IN THE INTERNATIONAL BUREAU OF WIPO

International Application of: PARAGON THERAPEUTICS, INC.

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For: TL1A BINDING PROTEINS AND METHODS OF USE

Submitted via ePCT

International Bureau of WIPO
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AMENDMENT AND STATEMENT UNDER PCT ARTICLE 19

Dear Sir:

Pursuant to PCT Article 19, Applicant respectfully requests that pages 233-268 be deleted, and that replacement sheets 233-268, submitted herewith, be substituted therefor. In the replacement sheets, claims 1, 2, 4-10, and 20 have been amended. Amended Claims 1, 2, and 4-10 and 20 are presented below.

AMENDMENTS TO THE CLAIMS

Pursuant to PCT Rule 46.5 and as set forth in the Administrative Instructions Under the PCT Section 205, Applicant respectfully requests that the claims be amended by substituting originally-submitted claim pages 233-268 with the enclosed substitute claim pages 233-268. The replacement sheets of pages 233-268 contain the following:

Claims 3, 11-19 and 21-44 remain unchanged; and

Claims 1, 2, 4-10 and 20 have been amended.

Applicant provides the following basis for the amendments.

(i) Basis for the amendment: Claims 1, 2 and 20 have been amended to correct a clerical error in the numbering of the sequence identifiers of CDR1 of VL of Antibody 70. In particular, Sequence identifier of CDR1 of VL of Antibody 70 has been renumbered SEQ ID NO: 699 as initially intended. The basis for these amendments can be found

at least at Table 1.1.C at page 83 which lists the correct SEQ ID NOs of CDR1 of VL of Antibody 70.

(ii) Basis for the amendment: Claims 1, 2, 4, 7, and 8 have been amended to correct a clerical error in the numbering of the sequence identifiers of CDR1, CDR2, CDR3 of heavy chain variable region (VH) and sequence identifiers of CDR1, CDR2, CDR3 of light chain variable region (VL) of Antibody 5, Antibody 6, Antibody, Antibody 8, Antibody 9 and Antibody 10. The basis for these amendments can be found at least at Table 1.1B at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs of the CDR1, CDR2 and CDR3 of the VH and VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. In particular:

- With regard to Antibody 5: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 5, SEQ ID NO: 15, and SEQ ID NO: 25; and sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 35, SEQ ID NO: 45, and SEQ ID NO: 55, respectively as initially intended;
- With regard to Antibody 6: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 6, SEQ ID NO: 16, and SEQ ID NO: 26; and sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 36, SEQ ID NO: 46, and SEQ ID NO: 56, respectively as initially intended;
- With regard to Antibody 7: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 7, SEQ ID NO: 17, and SEQ ID NO: 27; and sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 37, SEQ ID NO: 47, and SEQ ID NO: 57, respectively as initially intended;
- With regard to Antibody 8: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 8, SEQ ID NO: 18, and SEQ ID NO: 28; and sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 38, SEQ ID NO: 48, and SEQ ID NO: 58, respectively as initially intended;
- With regard to Antibody 9: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 9, SEQ ID NO: 19, and SEQ ID NO: 29; and sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 39, SEQ ID NO: 49, and SEQ ID NO: 59, respectively as initially intended;
- With regard to Antibody 10: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 10, SEQ ID NO: 20, and SEQ ID NO: 30; and sequence

identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 40, SEQ ID NO: 50, and SEQ ID NO: 60, respectively as initially intended.

(iii) Basis for the amendment: Claims 5-6 have been amended to correct numbering a clerical error in the numbering of the sequence identifiers of heavy chain variable region (VH) and light chain variable region (VL) of Antibody 5, Antibody 6, Antibody, Antibody 8, Antibody 9 and Antibody 10. The basis for this amendment can be found throughout the specification and original claims, in particular at Table 2.1 at pages 106-017 of the application as originally filed. In particular:

- With regard to Antibody 5: Sequence identifiers of VH has been renumbered SEQ ID NO: 185, and sequence identifiers of VL have been renumbered SEQ ID NO: 195, as initially intended;
- With regard to Antibody 6: Sequence identifiers of VH has been renumbered SEQ ID NO: 186, and sequence identifiers of VL have been renumbered SEQ ID NO: 196, as initially intended;
- With regard to Antibody 7: Sequence identifiers of VH has been renumbered SEQ ID NO: 187, and sequence identifiers of VL have been renumbered SEQ ID NO: 197, as initially intended;
- With regard to Antibody 8: Sequence identifiers of VH has been renumbered SEQ ID NO: 188, and sequence identifiers of VL have been renumbered SEQ ID NO: 198, as initially intended;
- With regard to Antibody 9: Sequence identifiers of VH has been renumbered SEQ ID NO: 189, and sequence identifiers of VL have been renumbered SEQ ID NO: 199, as initially intended;
- With regard to Antibody 10: Sequence identifiers of VH has been renumbered SEQ ID NO: 190, and sequence identifiers of VL have been renumbered SEQ ID NO: 200, as initially intended.

(iv) Basis for the amendment: Claim 9 has been amended to correct a clerical error in the numbering of the sequence identifiers of CDR1, CDR2, CDR3 of heavy chain variable region (VH) of Antibody 5, Antibody 6, Antibody, Antibody 8, Antibody 9 and Antibody 10. The basis for these amendments can be found at least at Table 1.1B at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs

of the CDR1, CDR2 and CDR3 of the VH and VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. In particular:

- With regard to Antibody 5: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 5, SEQ ID NO: 15, and SEQ ID NO: 25, respectively as initially intended;
- With regard to Antibody 6: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 6, SEQ ID NO: 16, and SEQ ID NO: 26, respectively as initially intended;
- With regard to Antibody 7: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 7, SEQ ID NO: 17, and SEQ ID NO: 27, respectively as initially intended;
- With regard to Antibody 8: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 8, SEQ ID NO: 18, and SEQ ID NO: 28, respectively as initially intended;
- With regard to Antibody 9: CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 9, SEQ ID NO: 19, and SEQ ID NO: 29, respectively as initially intended;
- With regard to Antibody 10: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 10, SEQ ID NO: 20, and SEQ ID NO: 30, respectively as initially intended.

(v) Basis for the amendment: Claim 10 has been amended to correct a clerical error in the numbering of the sequence identifiers of CDR1, CDR2, CDR3 of light chain variable region (VL) of Antibody 5, Antibody 6, Antibody, Antibody 8, Antibody 9 and Antibody 10. The basis for these amendments can be found at least at Table 1.1B at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs of the CDR1, CDR2 and CDR3 of the VH and VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. In particular:

- With regard to Antibody 5: Sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 35, SEQ ID NO: 45, and SEQ ID NO: 55, respectively as initially intended;
- With regard to Antibody 6: Sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 36, SEQ ID NO: 46, and SEQ ID NO: 56, respectively as initially intended;

- With regard to Antibody 7: Sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 37, SEQ ID NO: 47, and SEQ ID NO: 57, respectively as initially intended;
- With regard to Antibody 8: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 38, SEQ ID NO: 48, and SEQ ID NO: 58, respectively as initially intended;
- With regard to Antibody 9: Sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 39, SEQ ID NO: 49, and SEQ ID NO: 59, respectively as initially intended;
- With regard to Antibody 10: Sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 40, SEQ ID NO: 50, and SEQ ID NO: 60, respectively as initially intended.

The amendments to claims 1, 2, 4-10 and 20 are indicated below, wherein the added claim language is indicated by underlining and deletions are indicated by strikethrough:

1. A TL1A binding protein, wherein the TL1A binding protein comprises:

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~3~~ 5, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~3~~ 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~9~~ 15, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~9~~ 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~15~~ 25, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~15~~ 25; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~21~~ 35, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~21~~ 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~27~~ 45, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~27~~ 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~33~~ 55, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~33~~ 55; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~4~~ 6, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~4~~ 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~10~~ 16, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~10~~ 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~16~~ 26, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~16~~ 26; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~22~~ 36, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~22~~ 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~28~~ 46, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~28~~ 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~34~~ 56, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~34~~ 56; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~5~~ 7, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~5~~ 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~11~~ 17, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~11~~ 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~17~~ 27, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~17~~ 27; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~23~~ 37, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~23~~ 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~29~~ 47, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~29~~ 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~35~~ 57, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~35~~ 57; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~6~~ 8, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~6~~ 8, (ii) a CDR2 having an amino

acid sequence according to SEQ ID NO: ~~12~~ 18, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~12~~ 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~18~~ 28, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~18~~ 28; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~24~~ 38, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~24~~ 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~30~~ 48, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~30~~ 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~36~~ 58, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~36~~ 58; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~7~~ 9, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~7~~ 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~13~~ 19, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~13~~ 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~19~~ 29, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~19~~ 29; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~25~~ 39, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~25~~ 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~31~~ 49, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~31~~ 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~37~~ 59, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~37~~ 59; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~8~~ 10, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~8~~ 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~14~~ 20, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~14~~ 20, and (iii) a CDR3

having an amino acid sequence according to SEQ ID NO: ~~20~~ 30, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~20~~ 30; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~26~~ 40, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~26~~ 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~32~~ 50, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~32~~ 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~38~~ 60, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~38~~ 60; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 21; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 51; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 22; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 52; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO:23; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 53; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 24; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 34, (ii) a CDR2 having an amino

acid sequence according to SEQ ID NO: 44, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 54; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 539; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 866; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 559; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 777, and (iii) a CDR3

having an amino acid sequence according to SEQ ID NO: 886, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 886; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 563; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 890; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 567, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 567; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 894; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 460; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 569; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 787; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 896; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 572; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 899; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 365, (ii) a CDR2 having an

amino acid sequence according to SEQ ID NO: 474, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 583; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 910; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 589; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 916; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 481, and (iii) a CDR3

having an amino acid sequence according to SEQ ID NO: 590, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 590; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~691~~ 699, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~691~~ 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 917; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 591; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 918; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 606; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 933; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 612; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 939; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 618; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 727, (ii) a CDR2 having an

amino acid sequence according to SEQ ID NO: 836, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 945.

2. The TL1A binding protein of claim 1, comprising:

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~3~~ 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~9~~ 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~15~~ 25; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~21~~ 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~27~~ 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~33~~ 55; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~4~~ 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~10~~ 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~16~~ 26; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~22~~ 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~28~~ 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~34~~ 56; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~5~~ 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~11~~ 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~17~~ 27; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~23~~ 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~29~~ 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~35~~ 57; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~6~~ 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~12~~ 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~18~~ 28; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~24~~ 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~30~~ 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~36~~ 58; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~7~~ 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~13~~ 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~19~~ 29; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~25~~ 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~31~~ 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~37~~ 59; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~8~~ 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~14~~ 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~20~~ 30; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~26~~ 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~32~~ 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~38~~ 60; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence

according to SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence

according to SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 567; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~691~~ 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945.

4. A TL1A binding protein comprising:

(a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: ~~3-8~~ 5-10, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: ~~3-8~~ 5-10, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: ~~9-14~~ 15-20, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: ~~9-14~~ 15-20, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: ~~15-20~~ 25-30, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: ~~15-20~~ 25-30; and

(b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: ~~21-26~~ 35-40, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: ~~21-26~~ 35-40, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: ~~27-32~~ 45-50, or having an amino acid

sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: ~~27-32~~ 45-50, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: ~~33-38~~ 55-60, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: ~~33-38~~ 55-60.

5. The TL1A binding protein of claim 4, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: ~~111~~185-~~116~~190 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: ~~117~~195-~~122~~200.

6. The TL1A binding protein of claim 4 or claim 5, wherein

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: ~~111~~-185 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: ~~117~~-195,

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: ~~112~~-186 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: ~~118~~-196,

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: ~~113~~-187 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: ~~119~~-197,

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: ~~114~~-188 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: ~~120~~-198,

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: ~~115~~-189 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: ~~121~~-199, or

wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: ~~116~~-190 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: ~~122~~-200.

7. A TL1A binding protein, wherein the TL1A binding protein comprises:

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~3~~ 5, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~3~~ 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~9~~ 15, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~9~~ 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~15~~ 25, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~15~~ 25; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~21~~ 35, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~21~~ 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~27~~ 45, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~27~~ 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~33~~ 55, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~33~~ 55; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~4~~ 6, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~4~~ 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~10~~ 16, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~10~~ 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~16~~ 26, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~16~~ 26; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~22~~ 36, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~22~~ 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~28~~ 46, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~28~~ 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~34~~ 56, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~34~~ 56; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~5~~ 7, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~5~~ 7, (ii) a CDR2 having an amino

acid sequence according to SEQ ID NO: ~~11~~ 17, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~11~~ 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~17~~ 27, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~17~~ 27; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~23~~ 37, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~23~~ 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~29~~ 47, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~29~~ 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~35~~ 57, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~35~~ 57; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~6~~ 8, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~6~~ 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~12~~ 18, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~12~~ 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~18~~ 28, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~18~~ 28; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~24~~ 38, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~24~~ 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~30~~ 48, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~30~~ 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~36~~ 58, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~36~~ 58; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~7~~ 9, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~7~~ 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~13~~ 19, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~13~~ 19, and (iii) a CDR3 having

an amino acid sequence according to SEQ ID NO: ~~19~~ 29, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~19~~ 29; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~25~~ 39, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~25~~ 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~31~~ 49, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~31~~ 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~37~~ 59, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~37~~ 59; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~8~~ 10, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~8~~ 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~14~~ 20, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~14~~ 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~20~~ 30, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~20~~ 30; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~26~~ 40, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~26~~ 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~32~~ 50, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~32~~ 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~38~~ 60, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~38~~ 60.

8. The TL1A binding protein of claim 7, comprising:

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~3~~ 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~9~~ 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~15~~ 25; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~21~~ 35, (ii) a CDR2 having an amino acid sequence

according to SEQ ID NO: ~~27~~ 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~33~~ 55; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~4~~ 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~10~~ 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~16~~ 26; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~22~~ 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~28~~ 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~34~~ 56; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~5~~ 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~11~~ 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~17~~ 27; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~23~~ 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~29~~ 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~35~~ 57; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~6~~ 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~12~~ 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~18~~ 28; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~24~~ 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~30~~ 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~36~~ 58; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~7~~ 9, (ii) a CDR2 having an amino acid sequence

according to SEQ ID NO: ~~13~~ 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~19~~ 29; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~25~~ 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~31~~ 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~37~~ 59; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~8~~ 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~14~~ 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~20~~ 30; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~26~~ 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: ~~32~~ 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: ~~38~~ 60.

9. A TL1A binding protein comprising a heavy chain variable region (VH) comprising:

(i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: ~~3 8~~ 5-10, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: ~~3 8~~ 5-10;

(ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: ~~9 14~~ 15-20, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: ~~9 14~~ 15-20; and

(iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: ~~15 20~~ 25-30, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: ~~15 20~~ 25-30.

10. A TL1A binding protein comprising a light chain variable region (VL) comprising:

(i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: ~~21 26~~ 35-40, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: ~~21 26~~ 35-40;

(ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: ~~27-32~~ 45-50, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: ~~27-32~~ 45-50; and

(iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: ~~33-38~~ 55-60, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: ~~33-38~~ 55-60.

20. A TL1A binding protein comprising:

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 21; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 51; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 22; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, or a CDR2 having one to two amino acid

substitutions as compared to the sequence of SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 52; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO:23; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 53; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 24; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 34, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 44, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 54; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 539; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 866; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 559; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 886; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, or a CDR1 having one to two amino acid

substitutions as compared to the sequence of SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 563; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 890; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 567, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 567; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 894; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 460; and (iii) a CDR3

having an amino acid sequence according to SEQ ID NO: 569, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 569; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 787; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 896; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 572; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 899; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 583; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 910; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 589; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 916; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 590; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: ~~691~~ 699, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: ~~691~~ 699, (ii) a CDR2 having an

amino acid sequence according to SEQ ID NO: 808, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 917; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 591; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 918; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 606; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 824, and (iii) a CDR3

having an amino acid sequence according to SEQ ID NO: 933, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 933; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 612; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 939; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 618; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 945.

AMENDED CLAIMS
received by the International Bureau on
31 December 2024 (31.12.2024)

CLAIMS

1. A TL1A binding protein, wherein the TL1A binding protein comprises:

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 5, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 15, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 25, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 25; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 35, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 45, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 55, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 55; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 6, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 16, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 26, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 26; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 36, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 46, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 56, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 56; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 7, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 17, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 27, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 27; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 37, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 47, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 57, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 57; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 8, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 18, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 28, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 28; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 38, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 48, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 58, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 58; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 9, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 9, (ii) a CDR2 having an amino acid sequence

according to SEQ ID NO: 19, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 29, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 29; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 39, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 49, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 59, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 59; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 10, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 20, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 30, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 30; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 40, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 50, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 60, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 60; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence

according to SEQ ID NO: 21, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 21; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 51; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 22; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 52; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO:23; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 53; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 24; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 34, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 44, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 54; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 539; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence

according to SEQ ID NO: 757, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 866; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 559; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 886; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 563; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence

according to SEQ ID NO: 890, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 890; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 567, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 567; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 894; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 460; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 569; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 787; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 896; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 572; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 899; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 583; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 910; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence

according to SEQ ID NO: 480, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 589; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 916; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 590; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 699, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 917; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence

according to SEQ ID NO: 591, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 591; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 918; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 606; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 933; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 612; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 939; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 618; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 945.

2. The TL1A binding protein of claim 1, comprising:

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 25; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 55; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 26; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 56; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 27; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 57; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 28; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 58; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 29; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 59; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 30; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 60; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 567; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945.

3. The TL1A binding protein of claim 1 or claim 2 comprising an immunoglobin Fc domain.

4. A TL1A binding protein comprising:

(a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 5-10, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 5-10, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 15-20, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 15-20, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 25-30, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 25-30; and

(b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 35-40, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 35-40, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 45-50, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 45-50, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 55-60, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 55-60.

5. The TL1A binding protein of claim 4, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 185-190 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 195-200.

6. The TL1A binding protein of claim 4 or claim 5, wherein

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 185 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 195,

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 186 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 196,

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 187 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 197,

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 188 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 198,

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 189 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 199, or

wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 190 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 200.

7. A TL1A binding protein, wherein the TL1A binding protein comprises:

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 5, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 15, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 25, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 25; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 35, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 45, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 55, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 55; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 6, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 16, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 26, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 26; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 36, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 46, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 56, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 56; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 7, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 17, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 27, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 27; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 37, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 37, (ii) a CDR2 having an amino acid sequence

according to SEQ ID NO: 47, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 57, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 57; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 8, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 18, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 28, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 28; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 38, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 48, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 58, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 58; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 9, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 19, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 29, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 29; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 39, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 49, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 49, and (iii) a CDR3 having an amino acid sequence

according to SEQ ID NO: 59, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 59; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 10, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 20, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 30, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 30; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 40, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 50, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 60, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 60.

8. The TL1A binding protein of claim 7, comprising:

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 25; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 55; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 26; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 56; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 27; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 57; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 28; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 58; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 29; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 59; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 30; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 60.

9. A TL1A binding protein comprising a heavy chain variable region (VH) comprising:

(i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 5-10, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 5-10;

(ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 15-20, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 15-20; and

(iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 25-30, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 25-30.

10. A TL1A binding protein comprising a light chain variable region (VL) comprising:

(i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 35-40, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 35-40;

(ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 45-50, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 45-50; and

(iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 55-60, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 55-60.

11. The TL1A binding protein of any one of claims 1-8, wherein the TL1A binding protein is an antibody having IgG1, IgG2 or IgG4 immunoglobulin Fc domain.

12. The TL1A binding protein of claim 11, wherein the Fc domain is a modified Fc that extends half-life of the TL1A binding protein as compared to a TL1A binding protein that does not comprise the modified Fc domain.

13. The TL1A binding protein of claim 11 or claim 12, wherein the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

14. A TL1A binding antibody, wherein the TL1A binding antibody specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156.

15. The TL1A binding antibody of claim 14, wherein the TL1A binding antibody specifically binds to the TL1A sequences at amino acid residues Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156.

16. The TL1A binding protein or the TL1A binding antibody of any one of claims 1-15, wherein the TL1A binding protein binds TL1A with a K_D less than about 0.5 nanomolar (nM).

17. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 1-4 and 313-421, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 1-4 and 313-421, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 11-14 and 422-530, or having an amino acid sequence with one or two amino acid substitution as compared to any one of to any one of SEQ ID NOs: 11-14 and 422-530, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 21-24 and 531-639, or having an amino acid sequence with one or two amino acid substitution as compared to any one of to any one of SEQ ID NOs: 21-24 and 531-639; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 31-34 and 640-748, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 1-4 and 313-421, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 41-44 and 749-857, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 41-44 and 749-857, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 51-54 and 858-966, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 51-54 and 858-966.

18. The TL1A binding protein of claim 17, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 181-184 and 2275-2383 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 191-194 and 2384-2492.

19. The TL1A binding protein of claim 17 or claim 18, wherein

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 181 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 191;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 182 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 192;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 183 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 193;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 184 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 194;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2283 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2392;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2303 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2412;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2307 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2416;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2311 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2420;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2313 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2422;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2316 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2425;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2327 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2436;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2333 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2442;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2334 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2443;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2335 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2444;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2350 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2459;

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2356 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2465; or

the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2362 and the VL comprises a sequence having at least 80% sequence to SEQ ID NO: 2471.

20. A TL1A binding protein comprising:

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 21; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence

according to SEQ ID NO: 51, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 51; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 22; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 52; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO:23; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 53; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 24; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 34, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 44, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 54; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 539; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 866; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence

according to SEQ ID NO: 450, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 559; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 886; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 563; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 890; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence

according to SEQ ID NO: 567, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 567; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 894; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 460; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 569; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 787; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 896; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 572; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 899; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 583; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 910; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 589; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence

according to SEQ ID NO: 807, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 916; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 590; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 699, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 917; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 591; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence

according to SEQ ID NO: 918, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 918; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 606; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 933; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 612; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 939; or

a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 618; and

a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 945.

21. A TL1A binding protein comprising a heavy chain variable region (VH) comprising:

(i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 1-4 and 313-421, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 1-4 and 313-421;

(ii)a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 11-14 and 422-530, or having an amino acid sequence with one or two amino acid substitution as compared to any one of to any one of SEQ ID NOs: 11-14 and 422-530; and

(iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 21-24 and 531-639, or having an amino acid sequence with one or two amino acid substitution as compared to any one of to any one of SEQ ID NOs: 21-24 and 531-639.

22. A TL1A binding protein comprising a light chain variable region (VL) comprising:

(i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 31-34 and 640-748, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 31-34 and 640-748;

(ii)a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 41-44 and 749-857, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 41-44 and 749-857; and

(iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 51-54 and 858-966, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 51-54 and 858-966.

23. The TL1A binding protein of any one of claims 17-20, wherein the TL1A binding protein is an antibody comprising an IgG1, IgG2 or IgG4 immunoglobulin Fc domain.

24. The TL1A binding protein of claim 23, wherein the Fc domain is a modified Fc that extends half-life of the TL1A binding protein as compared to a TL1A binding protein that does not comprise the modified Fc domain.

25. The TL1A binding protein of claim 24, wherein the modified Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

26. A TL1A binding antibody, wherein the TL1A binding antibody specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Lys243, Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Ile233, Asp232, Met158, Arg156, Trp119, His118, Lys111, Phe110, His109, Gln108, Thr107, Pro106, Thr105, Gln104, Arg103, Val102, and Val101.

27. A TL1A binding antibody, wherein the TL1A binding antibody specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Gln104, and Arg103.

28. The TL1A binding protein of any one of claims 17-27, wherein the TL1A binding protein binds TL1A with a K_D less than about 0.5 nanomolar (nM).

29. A method of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A binding protein of any one of claims 1-28, or

a TL1A binding antibody that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Gln104, and Arg103, or

a TL1A binding antibody that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156.

30. The method of claim 29, wherein the inflammatory disease is a gastrointestinal inflammatory disease or an inflammatory bowel disease.

31. The method of claim 30, wherein the inflammatory bowel disease is Crohn's disease.

32. The method of claim 31, wherein the inflammatory bowel disease is ulcerative colitis.

33. The method of claim 32, wherein the inflammatory disease is psoriasis, psoriatic arthritis, or hidradenitis suppurativa.

34. The method of any one of claims 29-33, wherein administration of the TL1A binding protein is subcutaneous.

35. The method of any one of claims 29-33, wherein administration of the TL1A binding protein is intravenous.

36. The method of any one of claims 29-33, comprising administering the TL1A binding protein to the patient 2 or more times at an interval of from about 2 weeks to about 12 weeks or more.

37. A composition comprising the TL1A binding protein of any one of claims 1-28 and a pharmaceutically acceptable carrier.

38. An injectable liquid composition comprising the TL1A binding protein of any one of claims 1-28 and a pharmaceutically acceptable carrier.

39. An isolated nucleic acid encoding the TL1A binding protein of any one of claims 1-28.

40. A recombinant host cell comprising the isolated nucleic acid of claim 39.

41. A method for producing a TL1A binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Table 12, 13, or 14, wherein the TL1A antigen binding protein is an antibody.

42. The method of claim 41, wherein the TL1A binding antibody specifically binds to the TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Gln104, and Arg103.

43. The method of claim 41, wherein the TL1A binding antibody specifically binds to the TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156.

44. A method to obtain an antibody that specifically binds to a certain epitope portion of a TL1A sequence comprising SEQ ID NO: 2493 or SEQ ID NO: 2494, wherein the method comprises:

a) assessing whether an antibody binds specifically to the certain epitope portion, wherein the certain epitope portion

i) is recognized by an antibody of any of claims 1-28; or

ii) has amino acid residues Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156 of SEQ ID NO: 2493, or

iii) has amino acid residues Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Gln104, and Arg103 of SEQ ID NO: 2493, and

b) isolating or selecting the antibody that binds to the certain epitope portion.

IN THE EUROPEAN PATENT OFFICE

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For: TL1A BINDING PROTEINS AND METHODS OF USE

Via ePCT
International Preliminary Examining Authority
European Patent Office
Munich
Germany

LETTER ACCOMPANYING AMENDMENTS UNDER PCT ARTICLE 34

Pursuant to PCT Article 34(2)(b), Applicant hereby requests entry of the following amendments and remarks in the above-identified international application. A Demand for International Preliminary Examination using Form PCT/IPEA/401 and the requisite fees are filed concurrently herewith, within twenty-two (22) months from the date of priority (11 June 2025). Accordingly, the instant Amendment and Demand are timely filed.

This amendment is to amend the specification to correct inadvertent clerical errors in the numbering of the sequence identifiers of the complementarity-determining regions CDR1, CDR2 and CDR3 of the heavy chain variable region (VH), CDR1, CDR2 and CDR3 of the light chain variable region (VL), VH and VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10, consistent with and as supported by the SEQ ID NOS of CDR1, CDR2 and CDR3 of the VH, CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10 listed at **Table 1.1B**, and with the SEQ ID NOS of the VH and the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10 listed **Table 2.1** of the application as originally filed, and to correct the SEQ ID NO of the CDR1 of the VL of Antibody 70 to be consistent with the SEQ ID NO of the CDR1 of the VL of Antibody 70 listed at **Table 1.1B**.

This amendment also amends paragraph [0002] of the specification to correct an inadvertent clerical error and reference the size of the sequence listing xml file in bytes and not in kilobytes

consistent with and as supported by the Sequence Listing which has been submitted electronically on August 8, 2024.

No new matter has been added by these amendments to the specification.

Basis for the amendments to the Specification

The basis for the amendments to the numbering of the sequence identifiers of the complementarity-determining regions CDR1, CDR2 and CDR3 of the heavy chain variable region (VH), CDR1, CDR2 and CDR3 of the light chain variable region (VL), VH and VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10 can be found at least at Table 1.1B at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs of the CDR1, CDR2 and CDR3 of the VH and VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. In particular:

- With regard to Antibody 5: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 5, SEQ ID NO: 15, and SEQ ID NO: 25; and sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 35, SEQ ID NO: 45, and SEQ ID NO: 55, respectively, as disclosed in Table 1.1B;
- With regard to Antibody 6: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 6, SEQ ID NO: 16, and SEQ ID NO: 26; and sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 36, SEQ ID NO: 46, and SEQ ID NO: 56, respectively, as disclosed in Table 1.1B;
- With regard to Antibody 7: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 7, SEQ ID NO: 17, and SEQ ID NO: 27; and sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 37, SEQ ID NO: 47, and SEQ ID NO: 57, respectively, as disclosed in Table 1.1B;
- With regard to Antibody 8: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 8, SEQ ID NO: 18, and SEQ ID NO: 28; and sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 38, SEQ ID NO: 48, and SEQ ID NO: 58, respectively, as disclosed in Table 1.1B;
- With regard to Antibody 9: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 9, SEQ ID NO: 19, and SEQ ID NO: 29; and sequence identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 39, SEQ ID NO: 49, and SEQ ID NO: 59, respectively, as disclosed in Table 1.1B;
- With regard to Antibody 10: Sequence identifiers of CDR1, CDR2, CDR3 of VH have been renumbered SEQ ID NO: 10, SEQ ID NO: 20, and SEQ ID NO: 30; and sequence

identifiers of CDR1, CDR2, CDR3 of VL have been renumbered SEQ ID NO: 40, SEQ ID NO: 50, and SEQ ID NO: 60, respectively, as disclosed in Table 1.1B.

The basis for the amendments to the numbering of the sequence identifiers of the heavy chain variable region (VH) and light chain variable region (VL) of Antibody 5, Antibody 6, Antibody, Antibody 8, Antibody 9 and Antibody 10 can be found at least at Table 2.1 at pages 106-107 of the application as originally filed which lists the correct SEQ ID NOs of the VH and the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. In particular:

- With regard to Antibody 5: Sequence identifiers of VH has been renumbered SEQ ID NO: 185, and sequence identifiers of VL have been renumbered SEQ ID NO: 195, as disclosed in Table 2.1;
- With regard to Antibody 6: Sequence identifiers of VH has been renumbered SEQ ID NO: 186, and sequence identifiers of VL have been renumbered SEQ ID NO: 196, as disclosed in Table 2.1;
- With regard to Antibody 7: Sequence identifiers of VH has been renumbered SEQ ID NO: 187, and sequence identifiers of VL have been renumbered SEQ ID NO: 197, as disclosed in Table 2.1;
- With regard to Antibody 8: Sequence identifiers of VH has been renumbered SEQ ID NO: 188, and sequence identifiers of VL have been renumbered SEQ ID NO: 198, as disclosed in Table 2.1;
- With regard to Antibody 9: Sequence identifiers of VH has been renumbered SEQ ID NO: 189, and sequence identifiers of VL have been renumbered SEQ ID NO: 199, as disclosed in Table 2.1;
- With regard to Antibody 10: Sequence identifiers of VH has been renumbered SEQ ID NO: 190, and sequence identifiers of VL have been renumbered SEQ ID NO: 200, as disclosed in Table 2.1.

The basis for the amendments to the numbering of the sequence identifier of the CDR1 of the light chain variable region (VL) of Antibody 70 can be found at least at Table 1.1C at page 83 of the application as originally filed which lists the correct SEQ ID NO of the CDR1 of the VL of Antibody 70. In particular, the sequence identifier of VL has been renumbered SEQ ID NO: 699, as disclosed in Table 1.1C.

Amendment to the Specification

Paragraph [0002] at page 1 of the specification as originally filed has been amended to correct an inadvertent clerical error and reference the size of the sequence listing xml file in bytes and not in kilobytes consistent with and as supported by the Sequence Listing which has been submitted electronically on August 8, 2024.

Paragraphs [0004]-[0009] at pages 1-5 of the specification as originally filed have been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VH, and the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL, of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH, and of the CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10.

Paragraph [0022] at page 14 of the specification as originally filed has been amended to correct inadvertent clerical errors the sequence identifier numbering of the CDR1 of the VL of Antibody 70 to SEQ ID NO: 699. Support for the amendments can be found at least at **Table 1.1C** at page 83 of the application as originally filed which lists the correct SEQ ID NO. 699 of the CDR1 of the VL of Antibody 70.

Paragraph [0030] at page 18 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VH, the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH, and of the CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10.

Paragraphs [0031]-[0037] at pages 18-19 of the specification as originally filed have been amended to inadvertent correct clerical errors in: the sequence identifier numbering of the VH and the sequence identifier numbering of VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. Support for the amendments can be found at least at **Table 2.1** at pages 106-107 of the application as originally filed which lists the correct SEQ ID NOs. of the VH and VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10.

Paragraph [0038]-[0043] at pages 19-23 of the specification as originally filed have been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the CDR1,

CDR2 and CDR3 of the VH, and the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH, and of the CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10.

Paragraph [0044] at page 23 of the specification as originally filed has been amended to correct inadvertent clerical errors in the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VH. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10.

Paragraph [0045] at page 23 of the specification as originally filed has been amended to correct inadvertent clerical errors in the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10.

Paragraph [0079] at pages 34-35 of the specification as originally filed has been amended to correct inadvertent clerical errors the sequence identifier numbering of the CDR1 of the VL of Antibody 70 to SEQ ID NO: 699. Support for the amendments can be found at least at **Table 1.1C** at page 83 of the application as originally filed which lists the correct SEQ ID NO. 699 of the CDR1 of the VL of Antibody 70.

Paragraphs [0126]-[0131] at pages 45-49 of the specification as originally filed have been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VH, and the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH, and of the CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10.

Paragraph [0161] at pages 60-61 of the specification as originally filed has been amended to correct inadvertent clerical errors the sequence identifier numbering of the CDR1 of the VL of Antibody 70 to SEQ ID NO: 699. Support for the amendments can be found at least at **Table 1.1C**

at page 83 of the application as originally filed which lists the correct SEQ ID NO. 699 of the CDR1 of the VL of Antibody 70.

Paragraph [0222] at page 105 of the specification as originally filed has been amended to correct inadvertent clerical errors the sequence identifier numbering of the CDR1 of the VL of Antibody 70 to SEQ ID NO: 699. Support for the amendments can be found at least at **Table 1.1C** at page 83 of the application as originally filed which lists the correct SEQ ID NO. 699 of the CDR1 of the VL of Antibody 70.

Paragraph [0364] at page 200 of the specification as originally filed has been amended to correct inadvertent clerical errors the sequence identifier numbering of the CDR1 of the VL of Antibody 70 to SEQ ID NO: 699. Support for the amendments can be found at least at **Table 1.1C** at page 83 of the application as originally filed which lists the correct SEQ ID NO. 699 of the CDR1 of the VL of Antibody 70.

Paragraph [0413] at page 206 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VH, and the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH, and of the CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10.

Paragraph [0414] at page 206 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the VH and the sequence identifier numbering of VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. Support for the amendments can be found at least at **Table 2.1** at pages 106-107 of the application as originally filed which lists the correct SEQ ID NOs. of the VH and VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10.

Paragraph [0421] at page 207 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VH, and the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL of Antibody 5. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH, and of the CDR1, CDR2 and CDR3 of the VL of Antibody 5.

Paragraph [0422] at page 207 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the VH, and the sequence identifier numbering of the VL of Antibody 5. Support for the amendments can be found at least at **Table 2.1** at pages 106-107 of the application as originally filed which lists the correct SEQ ID NOs. of the VH and VL of Antibody 5.

Paragraph [0424] at page 207 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VH, and the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL of Antibody 6. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH, and of the CDR1, CDR2 and CDR3 of the VL of Antibody 6.

Paragraph [0425] at page 207 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the VH, and the sequence identifier numbering of the the VL of Antibody 6. Support for the amendments can be found at least at **Table 2.1** at pages 106-107 of the application as originally filed which lists the correct SEQ ID NOs. of the VH and VL of Antibody 6.

Paragraph [0427] at page 208 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VH, and the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL of Antibody 7. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH, and of the CDR1, CDR2 and CDR3 of the VL of Antibody 7.

Paragraph [0428] at page 208 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the VH, and the sequence identifier numbering of the the VL of Antibody 7. Support for the amendments can be found at least at **Table 2.1** at pages 106-107 of the application as originally filed which lists the correct SEQ ID NOs. of the VH and VL of Antibody 7.

Paragraph [0430] at page 208 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VH, and the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL of Antibody 8. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH, and of the CDR1, CDR2 and CDR3 of the VL of Antibody 8.

Paragraph [0431] at page 208 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the VH, and the sequence identifier numbering of the VL of Antibody 8. Support for the amendments can be found at least at **Table 2.1** at pages 106-107 of the application as originally filed which lists the correct SEQ ID NOs. of the VH and VL of Antibody 8.

Paragraph [0433] at page 209 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VH, and the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL of Antibody 9. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH, and of the CDR1, CDR2 and CDR3 of the VL of Antibody 9.

Paragraph [0434] at page 209 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the VH, and the sequence identifier numbering of the VL of Antibody 9. Support for the amendments can be found at least at **Table 2.1** at pages 106-107 of the application as originally filed which lists the correct SEQ ID NOs. of the VH and VL of Antibody 9.

Paragraph [0436] at page 209 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VH, and the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL of Antibody 10. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH, and of the CDR1, CDR2 and CDR3 of the VL of Antibody 10.

Paragraph [0437] at page 209 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the VH, and the sequence identifier numbering of the the VL of Antibody 10. Support for the amendments can be found at least at **Table 2.1** at pages 106-107 of the application as originally filed which lists the correct SEQ ID NOs. of the VH and VL of Antibody 10.

Paragraph [0439] at page 210 of the specification as originally filed has been amended to correct inadvertent clerical errors in: the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VH, and the sequence identifier numbering of the CDR1, CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10. Support for the amendments can be found at least at **Table 1.1B** at pages 76-77 of the application as originally filed which lists the correct SEQ ID NOs. of the CDR1, CDR2 and CDR3 of the VH, and of the CDR1,

CDR2 and CDR3 of the VL of Antibody 5, Antibody 6, Antibody 7, Antibody 8, Antibody 9 and Antibody 10.

No new matter has been added by these amendments to the specification.

Attached hereto are clean and marked-up replacement sheets of the specification and the claims of the present application.

Applicant requests entry of the replacement sheets 1-236 be accepted. The marked up version of the portions that were changed in the replacement sheets are shown at paragraphs [0002], [0004]-[0009], [0022], [0030]-[0045], [0079], [0126]-[0131], [0161], [0222], [0364], [0413]-[0414], [0421]-[0422], [0424]-[0425], [0427]-[0428], [0430]-[0431], [0433]-[0434], [0436]-[0437] and [0439] wherein the strikethrough text indicates the text to be removed while the underlined text indicates the text to be added.

Applicant confirms that the amendments requested herein do not go beyond the disclosure of the international application as originally filed.

If there are any questions concerning this amendment or any irregularities or errors in the enclosed submission, it is respectfully requested that the Authorized Officer kindly notify the undersigned.

Respectfully submitted,

GREENBERG TRAURIG LLP

Dated: 11 June 2025

By: /Natalie Salem, Reg. No. 58731/

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TL1A BINDING PROTEINS AND METHODS OF USE

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of and priority to U.S. Provisional Application No. 63/519,056, filed on August 11, 2023; U.S. Provisional Application No. 63/592,535, filed on October 23, 2023; U.S. Provisional Application No. 63/599,923, filed on November 16, 2023; U.S. Provisional Application No. 63/604,104, filed on November 29, 2023; U.S. Provisional Application No. 63/554,897, filed on February 16, 2024; U.S. Provisional Application No. 63/554,916, filed on February 16, 2024; U.S. Provisional Application No. 63/559,060, filed on February 28, 2024; and U.S. Provisional Application No. 63/559,071, filed on February 28, 2024, the entire contents of each of which are incorporated herein by reference.

SEQUENCE LISTING

[0002] This application contains a Sequence Listing which has been submitted electronically in XML format and is hereby incorporated by reference in its entirety. The XML copy, created on August 8, 2024, is titled 220703-010508_PCT_SL.xml and is 2,191,113 bytes in size.

BACKGROUND

[0003] Tumor necrosis factor (TNF)-like cytokine 1A (TL1A) is part of the TNF superfamily and is a transmembrane protein expressed by myeloid mononuclear cells and endothelial cells. TL1A interacts with its receptors, death receptor 3 (DR3) and decoy receptor 3 (DcR3) to trigger signaling. TL1A is elevated in individuals with inflammatory diseases including Crohn's disease and ulcerative colitis, and DR3 expression is upregulated in inflamed tissue. As such, TL1A along with other members of the TNF superfamily have been investigated as therapeutic targets to treat inflammatory diseases including inflammatory bowel diseases. Current biologics targeting TNF are associated with serious side effects highlighting the need for improved therapies targeting TL1A.

SUMMARY OF THE DISCLOSURE

[0004] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 5, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 15, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 15, and (iii) a CDR3 having an amino acid sequence

according to SEQ ID NO: 25, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 25; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 35, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 45, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 55, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 55. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 25; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 55. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0005] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 6, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 16, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 26, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 26; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 36, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 46, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 56, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 56. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 16, and (iii) a CDR3 having an amino

acid sequence according to SEQ ID NO: 26; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 56. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0006] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 7, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 17, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 27, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 27; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 37, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 47, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 57, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 57. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 27; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 57. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0007] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 8, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 8, (ii) a CDR2 having an amino acid sequence

according to SEQ ID NO: 18, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 28, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 28; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 38, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 48, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 58, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 58. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 28; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 58. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0008] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 9, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 19, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 29, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 29; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 39, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 49, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 59, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 59. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH)

comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 29; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 59. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0009] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 10, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 20, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 30, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 30; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 40, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 50, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 60, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 60. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 30; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 60. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0010] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid

sequence according to SEQ ID NO: 1, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 21; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 51. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0011] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 22; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52, or a CDR3 having one to two

amino acid substitutions as compared to the sequence of SEQ ID NO: 52. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0012] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 23; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 53. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0013] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 24; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 34, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 44, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 54. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0014] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 539; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, or a CDR2

having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 866. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0015] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 559; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 886. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886. In some embodiments, the TL1A

binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0016] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 563; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 890. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0017] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence

according to SEQ ID NO: 567, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 567; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 894. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 567; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0018] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 460; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 569; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 787; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 896. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, (ii) a

CDR2 having an amino acid sequence according to SEQ ID NO: 460; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0019] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 572; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 899. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0020] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 583; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 910. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0021] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 589; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO:

698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 916. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0022] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 590; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 699, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 917. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, and (iii) a CDR3 having

an amino acid sequence according to SEQ ID NO: 917. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0023] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 591; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 918. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918 . In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0024] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, or a CDR2 having one to two amino acid substitutions as

compared to the sequence of SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 606; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 933. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0025] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 612; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 939. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH)

comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0026] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 618; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 945. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0027] Aspects of the disclosure relate to TL1A binding antibody that specifically binds to an epitope on a TL1A polypeptide recognized by an antibody disclosed herein. Aspects of the disclosure relate to TL1A binding antibody that specifically binds to an epitope on a TL1A polypeptide recognized by antibody 1, 2, 3, 4, 6, 8, 10, 47, 49, 63, or 69 disclosed herein.

[0028] Aspects of the disclosure relate to TL1A binding antibody that binds specifically to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Thr 107, Gln 108, His 109, Phe 110, Lys 111, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 231, Asp 232, Ile 233, Ser 234, Tyr 238, Thr 239, Lys 240, and Lys 243. In some embodiments, the TL1A binding antibody specifically binds to the TL1A sequences at ten or more amino acid residues selected from Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 231, Asp 232, Ile 233, Ser 234, Leu 235, Val 236, Asp 237, Tyr 238, Thr 239, Lys 240, and Lys 243.

[0029] Aspects of the disclosure relate to TL1A binding antibody that binds specifically to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, and Thr 239. In some embodiments, the TL1A binding antibody specifically binds to the TL1A sequences at amino acid residues Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, and Thr 239.

[0030] Aspects of the disclosure relate to a TL1A binding protein comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 5-10, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 5-10, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 15-20, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 15-20, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 25-30, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 25-30; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 35-40, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 35-40, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 45-50, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 45-50, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID

NOs: 55-60, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 55-60.

[0031] In some embodiments, the TL1A binding protein comprises a VH comprising a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 185-190 and a VL comprising a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 195-200.

[0032] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 185 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 195.

[0033] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 186 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 196.

[0034] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 187 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 197.

[0035] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 188 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 198.

[0036] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 189 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 199.

[0037] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 190 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 200.

[0038] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 5, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 15, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 25, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 25; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 35, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 35, (ii)

a CDR2 having an amino acid sequence according to SEQ ID NO: 45, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 55, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 55. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 25; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 55. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0039] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 6, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 16, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 26, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 26; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 36, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 46, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 56, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 56. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 26; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 56. In some embodiments, the TL1A binding

protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0040] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 7, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 17, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 27, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 27; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 37, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 47, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 57, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 57. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 27; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 57. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0041] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 8, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 18, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 28, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 28; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 38, or a CDR1

having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 48, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 58, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 58. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 28; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 58. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0042] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 9, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 19, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 29, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 29; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 39, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 49, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 59, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 59. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 29; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 49, and (iii) a CDR3 having an amino acid

sequence according to SEQ ID NO: 59. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0043] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 10, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 20, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 30, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 30; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 40, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 50, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 60, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 60. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 30; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 60. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE). In some embodiments, the TL1A binding protein or the TL1A binding antibody, wherein the TL1A binding protein binds TL1A with a K_D less than about 0.5 nanomolar (nM).

[0044] Described herein is a TL1A binding protein comprising a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 5-10, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 5-10; (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 15-20, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 15-20; and (ii) a CDR3 having

an amino acid sequence according to any one of SEQ ID NOs: 25-30, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 25-30.

[0045] Described herein is a TL1A binding protein TL1A binding protein comprising a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 35-40, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 35-40; (i) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 45-50, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 45-50; and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 55-60, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 55-60.

[0046] Described herein is a method to obtain an antibody that specifically binds to a certain epitope portion of a TL1A sequence comprising SEQ ID NO: 2493, wherein the method comprises assessing whether an antibody binds specifically to the certain epitope portion, wherein the certain epitope portion has amino acid residues Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 227, Tyr 231, and Thr 232 of SEQ ID NO: 2493, and isolating or selecting the an antibody that binds to the certain epitope portion.

[0047] Also, described herein are TL1A binding proteins that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 or 2494, wherein the TL1A binding protein is an antibody.

[0048] Described herein are TL1A binding proteins comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 1-4 and 313-421, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 1-4 and 313-421, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 11-14 and 422-530, or having an amino acid sequence with one or two amino acid substitution as compared to any one of to any one of SEQ ID NOs: 11-14 and 422-530, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 21-24 and 531-639, or having an amino acid sequence with one or two amino acid substitution as compared to any one of to any one of SEQ ID NOs: 21-24 and 531-639; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 31-34 and 640-748, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID

NOs: 1-4 and 313-421, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 41-44 and 749-857, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 41-44 and 749-857, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 51-54 and 858-966, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 51-54 and 858-966.

[0049] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 181-184 and 2275-2383 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 191-194 and 2384-2492.

[0050] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 181 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 191.

[0051] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 182 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 192.

[0052] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 183 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 193.

[0053] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 184 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 194.

[0054] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2283 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2392.

[0055] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2303 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2412.

[0056] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2307 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2416.

[0057] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2311 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2420.

[0058] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2313 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2422.

[0059] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2316 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2425.

[0060] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2327 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2436.

[0061] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2333 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2442.

[0062] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2334 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2443.

[0063] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2335 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2444.

[0064] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2350 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2459.

[0065] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2356 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2465.

[0066] In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2362 and the VL comprises a sequence having at least 80% sequence to SEQ ID NO: 2471.

[0067] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21, or a CDR3 having one to two amino acid substitutions as

compared to the sequence of SEQ ID NO: 21; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 51. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0068] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 22; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 52. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22; and b) a light chain variable region (VL)

comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0069] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 23; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 53. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0070] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence

according to SEQ ID NO: 24, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 24; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 34, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 44, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 54. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0071] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 539; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 866. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, and (iii) a CDR3 having

an amino acid sequence according to SEQ ID NO: 539; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0072] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 559; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 886. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0073] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, or a CDR1 having one to two amino acid substitutions

as compared to the sequence of SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 563; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 890. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0074] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 567, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 567; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894, or a CDR3

having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 894. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 567; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0075] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 460; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 569; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 787; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 896. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain

comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0076] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 572; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 899. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0077] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 583; and a light chain variable region (VL)

comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 910. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0078] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 589; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 916. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589; and b) a light chain variable region (VL)

comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0079] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 590; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 699, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 917. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0080] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence

according to SEQ ID NO: 482, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 591; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 918. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918 . In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0081] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 606; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 933. In

some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0082] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 612; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 939. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0083] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 618; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 945. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0084] Described herein is a TL1A binding protein comprising a heavy chain variable region (VH) comprising: (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 1-4 and 313-421, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 1-4 and 313-421; (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 11-14 and 422-530, or having an amino acid sequence with one or two amino acid substitution as compared to any one of to any one of SEQ ID NOs: 11-14 and 422-530; and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 21-24 and 531-639, or having an amino acid sequence with one or two amino acid substitution as compared to any one of to any one of SEQ ID NOs: 21-24 and 531-639.

[0085] Described herein is a TL1A binding protein comprising a light chain variable region (VL) comprising: (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 31-34 and 640-748, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 1-4 and 313-421; (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 41-44 and 749-857, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 41-44 and 749-857; and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 51-54 and 858-966, or having an amino acid sequence with one or two amino acid substitution as compared to any one of SEQ ID NOs: 51-54 and 858-966.

[0086] Aspects of the disclosure relate to a composition comprising the TL1A binding protein described herein and a pharmaceutically acceptable carrier. Aspects of the disclosure relate to an injectable liquid composition comprising the TL1A binding protein described herein and a pharmaceutically acceptable carrier.

[0087] Aspects of the disclosure relate to an isolated nucleic acid encoding the TL1A binding protein described herein.

[0088] Aspects of the disclosure relate to a recombinant host cell comprising the isolated nucleic acid.

[0089] Described herein is a method for producing a TL1A binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 or 2494, wherein the TL1A antigen binding protein is an antibody.

[0090] Aspects of the disclosure relate to a method to obtain an antibody that specifically binds to a certain epitope portion of a TL1A sequence comprising SEQ ID NO: 2493, wherein the method comprises assessing whether an antibody binds specifically to the certain epitope portion, wherein the certain epitope portion has ten or more amino acid residues selected from Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Thr 107, Gln 108, His 109, Phe 110, Lys 111, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, and Thr 239 of SEQ ID NO: 2493, and isolating or selecting the an antibody that binds to the certain epitope portion.

[0091] Aspects of the disclosure relate to a method to obtain an antibody that specifically binds to a certain epitope portion of a TL1A sequence comprising SEQ ID NO: 2493, wherein the method comprises assessing whether an antibody binds specifically to the certain epitope portion, wherein the certain epitope portion has amino acid residues Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg

156, Gly 157, Met 158, Ser 234, Tyr 238, and Thr 239 of SEQ ID NO: 2493, and isolating or selecting the an antibody that binds to the certain epitope portion.

[0092] Aspects of the disclosure relate to a method for producing a TL1A binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Table 12, 13, or 14, wherein the TL1A antigen binding protein is an antibody. In some embodiments, the TL1A binding antibody specifically binds to the TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Gln104, and Arg103. In some embodiments, the TL1A binding antibody specifically binds to the TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156.

[0093] Aspects of the disclosure relate to method to obtain an antibody that specifically binds to a certain epitope portion of a TL1A sequence comprising SEQ ID NO: 2493 or SEQ ID NO: 2494, wherein the method comprises: assessing whether an antibody binds specifically to the certain epitope portion, and isolating or selecting the antibody that binds to the certain epitope portion wherein the certain epitope portion is recognized by an antibody described herein; or has amino acid residues Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156 of SEQ ID NO: 2493, or has amino acid residues Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Gln104, and Arg103 of SEQ ID NO: 2493.

[0094] Aspects of the disclosure relate to a method to obtain an antibody that specifically binds to a certain epitope portion of a TL1A by competitively inhibiting binding of an antibody disclosed herein, such as antibody 1, 2, 3, 4, 6, 8, 10, 47, 49, 63, or 69 disclosed herein.

[0095] Aspects of the disclosure relate to a method of treating a gastrointestinal inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A binding protein described herein. In some embodiments, administration of the TL1A binding protein is subcutaneous. In some embodiments, administration of the TL1A binding protein is intravenous. In some embodiments, the method comprises administering the TL1A binding protein to the patient 2 or more times at an interval of from about 2 weeks to about 12 weeks or more.

[0096] Aspects of the disclosure relate to a method of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A binding protein described herein. In some embodiments, the inflammatory bowel disease is Crohn's disease or ulcerative colitis. In some embodiments, administration of the TL1A binding protein is subcutaneous. In some

embodiments, administration of the TL1A binding protein is intravenous. In some embodiments, the method comprises administering the TL1A binding protein to the patient 2 or more times at an interval of from about 2 weeks to about 12 weeks or more.

[0097] Aspects of the disclosure relate to a method of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A binding protein described herein. In some embodiments, the inflammatory disease is psoriasis, psoriatic arthritis, or hidradenitis suppurativa.

[0098] In some embodiments, administration of the TL1A binding protein is subcutaneous. In some embodiments, administration of the TL1A binding protein is intravenous. In some embodiments, the method comprises administering the TL1A binding protein to the patient 2 or more times at an interval of from about 2 weeks to about 12 weeks or more.

BRIEF DESCRIPTION OF THE DRAWINGS

[0099] **FIG. 1** is a graph depicting TL1A binding antibody described herein (Antibody 10) and various comparator antibodies binding membrane TL1A. Comparator antibody 1 has an amino acid sequence substantially identical to RVT-3101 and is referred herein as RVT-3101; Comparator antibody 2 has an amino acid sequence substantially identical to MK-7240 and is referred herein as MK-7240; Comparator antibody 3 has an amino acid sequence substantially identical to TEV-48574 and is referred herein as TEV-48574.

[0100] **FIGs. 2A-2B** depict TL1A monomer and TL1A trimer binding of various comparator antibodies compared to TL1A binding antibodies disclosed herein.

[0101] **FIGs. 3A-3D** depict apoptosis inhibition of various comparator antibodies compared to TL1A binding antibodies disclosed herein.

[0102] **FIGs. 4A-4E** depict half-life of TL1A binding antibodies disclosed herein in non-human primates. **FIG. 4F** depicts half-life of TL1A binding antibodies disclosed herein in Tg276 mice expressing human FcRn.

[0103] **FIGs. 5A and 5B** depict inhibition of TL1A-induced apoptosis in response to various comparator antibodies and TL1A binding antibodies described herein.

[0104] **FIGs. 6A-6C** depict formulation data of TL1A binding antibodies described herein compared to various comparator antibodies.

[0105] **FIGs. 7A-7F** depict chemical and pharmacokinetic data of TL1A binding antibodies described herein compared to various comparator antibodies.

[0106] **FIG. 8A** depicts a CryoEM image of epitope for comparator TL1A binding antibodies. **FIG. 8B** depicts a CryoEM image of epitope for TL1A binding antibody 10.

DETAILED DESCRIPTION

[0107] It is to be understood that both the foregoing general description and the following detailed description are exemplary, and explanatory only, and are not restrictive of the disclosure.

[0108] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[0109] All documents, or portions of documents, cited in this application, including, but not limited to, patents, patent applications, articles, books, and treatises, are hereby expressly incorporated by reference in their entirety for any purpose.

Definitions

[0110] Unless otherwise indicated, all technical terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Unless otherwise indicated or obvious from context, the following terms have the following meanings:

[0111] As used herein, unless otherwise indicated, the term "antibody" is understood to mean an intact antibody (*e.g.*, an intact monoclonal antibody), or a fragment thereof, such as a Fc fragment of an antibody (*e.g.*, an Fc fragment of a monoclonal antibody), or an antigen-binding fragment of an antibody (*e.g.*, an antigen-binding fragment of a monoclonal antibody), including an intact antibody, antigen-binding fragment, or Fc fragment that has been modified, engineered, or chemically conjugated. In general, antibodies are multimeric proteins that contain four polypeptide chains. Two of the polypeptide chains are called immunoglobulin heavy chains (H chains), and two of the polypeptide chains are called immunoglobulin light chains (L chains). The immunoglobulin heavy and light chains are connected by an interchain disulfide bond. The immunoglobulin heavy chains are connected by interchain disulfide bonds. A light chain consists of one variable region (VL) and one constant region (CL). The heavy chain consists of one variable region (VH) and at least three constant regions (CH1, CH2 and CH3). The variable regions determine the binding specificity of the antibody. Each variable region contains three hypervariable regions known as complementarity determining regions (CDRs) flanked by four relatively conserved regions known as framework regions (FRs). The extent of the FRs and CDRs has been defined (Kabat et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242;

and Chothia, C. et al. (1987) J. Mol. Biol. 196:901-917). The three CDRs, referred to as CDR1, CDR2, and CDR3, contribute to the antibody binding specificity. Naturally occurring antibodies have been used as starting material for engineered antibodies, such as chimeric antibodies and humanized antibodies. Examples of antibody-based antigen-binding fragments include Fab, Fab', (Fab')2, Fv, single chain antibodies (*e.g.*, scFv), minibodies, and diabodies. Examples of antibodies that have been modified or engineered include chimeric antibodies, humanized antibodies, and multispecific antibodies (*e.g.*, bispecific antibodies). An example of a chemically conjugated antibody is an antibody conjugated to a toxin moiety.

[0112] The terms "variable domain" and "variable region" are used interchangeably and refer to the portions of the antibody or immunoglobulin domains that exhibit variability in their sequence and that are involved in determining the specificity and binding affinity of a particular antibody. Variability is not evenly distributed throughout the variable domains of antibodies; it is concentrated in sub-domains of each of the heavy and light chain variable regions. These sub-domains are called "hypervariable regions" or "complementarity determining regions" (CDRs). The more conserved (*i.e.,* non-hypervariable) portions of the variable domains are called the "framework" regions (FRM or FR) and provide a scaffold for the six CDRs in three-dimensional space to form an antigen-binding surface.

[0113] An "Fc polypeptide" of a dimeric Fc as used herein refers to one of the two polypeptides forming the dimeric Fc domain, *i.e.* a polypeptide comprising C-terminal constant regions of an immunoglobulin heavy chain, capable of stable self-association. For example, an Fc polypeptide of a dimeric IgG Fc comprises an IgG CH2 and an IgG CH3 constant domain sequence. An Fc can be of the class IgA, IgD, IgE, IgG, and IgM. These classes are also designated α, δ, ε, γ, and μ, respectively. Several of these may be further divided into subclasses (isotypes), *e.g.*, IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

[0114] The terms "Fc receptor" and "FcR" are used to describe a receptor that binds to the Fc region of an antibody. For example, an FcR can be a native sequence human FcR. Generally, an FcR is one which binds an IgG antibody (a gamma receptor) and includes receptors of the FcγRI, FcγRII, and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors. FcγRII receptors include FcγRIIA (an "activating receptor") and FcγRIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Immunoglobulins of other isotypes can also be bound by certain FcRs (see, *e.g.*, Janeway *et al.*, *Immuno Biology*: the immune system in health and disease, (Elsevier Science Ltd., NY) (4th ed., 1999)). Activating receptor FcγRIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting

receptor FcγRIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain (reviewed in Daëron, *Annu. Rev. Immunol*. 15:203-234 (1997)). FcRs are reviewed in Ravetch and Kinet, *Annu. Rev*. Immunol 9:457-92 (1991); Capel *et al.*, *Immunomethods* 4:25-34 (1994); and de Haas *et al.*, J. Lab. Clin. Med. 126:330-41 (1995). Other FcRs, including those to be identified in the future, are encompassed by the term "FcR" herein. The term also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus (Guyer *et al.*, *J. Immunol*. 117:587 (1976); and Kim *et al.*, *J. Immunol.* 24:249 (1994)).

[0115] The terms "recipient", "individual", "subject", "host", and "patient", are used interchangeably herein and in some embodiments, refer to any mammalian subject for whom diagnosis, treatment, or therapy is desired, particularly humans. "Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and laboratory, zoo, sports, or pet animals, such as dogs, horses, cats, cows, sheep, goats, pigs, mice, rats, rabbits, guinea pigs, monkeys etc. In some embodiments, the mammal is human. None of these terms require the supervision of medical personnel.

[0116] As used herein, the term "effective amount" refers to the amount of a compound (*e.g.*, a compound of the present disclosure) sufficient to effect beneficial or desired results. An effective amount can be administered in one or more administrations, applications or dosages and is not intended to be limited to a particular formulation or administration route. As used herein, the term "treating" includes any effect, *e.g.*, lessening, reducing, modulating, ameliorating or eliminating, that results in the improvement of the condition, disease, disorder, and the like, or ameliorating a symptom thereof.

[0117] As used herein, the term "pharmaceutical composition" refers to the combination of an active agent with a carrier, inert or active, making the composition especially suitable for diagnostic or therapeutic use *in vivo* or *ex vivo*.

[0118] As used herein, the term "pharmaceutically acceptable carrier" refers to any of the standard pharmaceutical carriers, such as a phosphate buffered saline solution, water, emulsions (*e.g.*, such as an oil/water or water/oil emulsions), and various types of wetting agents. The compositions also can include stabilizers and preservatives. For examples of carriers, stabilizers and adjuvants, *see e.g.*, Martin, Remington's Pharmaceutical Sciences, 15th Ed., Mack Publ. Co., Easton, PA (1975).

[0119] The terms "a" and "an" as used herein mean "one or more" and include the plural unless the context is inappropriate.

[0120] As used herein, all numerical values or numerical ranges include whole integers within or encompassing such ranges and fractions of the values or the integers within or encompassing ranges unless the context clearly indicates otherwise. Thus, for example, reference to a range of 90-100%, includes 91%, 92%, 93%, 94%, 95%, 95%, 96%, 97%, etc., as well as 91.1%, 91.2%, 91.3%, 91.4%, 91.5%, etc., 92.1%, 92.2%, 92.3%, 92.4%, 92.5%, etc., and so forth. In another example, reference to a range of 1-5,000-fold includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, fold, etc., as well as 1.1, 1.2, 1.3, 1.4, 1.5, fold, etc., 2.1, 2.2, 2.3, 2.4, 2.5, fold, etc., and so forth.

[0121] "About" a number, as used herein, refers to range including the number and ranging from 10% below that number to 10% above that number. "About" a range refers to 10% below the lower limit of the range, spanning to 10% above the upper limit of the range.

[0122] "Percent (%) identity" refers to the extent to which two sequences (nucleotide or amino acid) have the same residue at the same positions in an alignment. For example, "an amino acid sequence is X% identical to SEQ ID NO: Y" refers to % identity of the amino acid sequence to SEQ ID NO: Y and is elaborated as X% of residues in the amino acid sequence are identical to the residues of sequence disclosed in SEQ ID NO: Y. Generally, computer programs are employed for such calculations. Exemplary programs that compare and align pairs of sequences include ALIGN (Myers and Miller, 1988), FASTA (Pearson and Lipman, 1988; Pearson, 1990) and gapped BLAST (Altschul et al., 1997), BLASTP, BLASTN, or GCG (Devereux et al., 1984).

[0123] Throughout the description, where compositions are described as having, including, or comprising specific components, or where processes and methods are described as having, including, or comprising specific steps, it is contemplated that, additionally, there are compositions of the present disclosure that consist essentially of, or consist of, the recited components, and that there are processes and methods according to the present disclosure that consist essentially of, or consist of, the recited processing steps.

[0124] As a general matter, compositions specifying a percentage are by weight unless otherwise specified. Further, if a variable is not accompanied by a definition, then the previous definition of the variable controls.

TL1A Binding Proteins

[0125] Provided herein are compositions, systems, and methods comprising a TL1A binding protein. The TL1A binding proteins described herein can bind to TL1A monomers, TL1A trimers, or both, may have picomolar potency against TL1A monomers, TL1A trimers, or both, and may have extended half-life (*e.g.,* as compared to known TL1A directed antibodies), or

combinations thereof. In some embodiments, the TL1A binding proteins described herein allow for subcutaneous administration. In some embodiments, the TL1A binding proteins described herein allow for dosing *e.g.*, every 8 weeks or every 12 weeks, or more. TL1A binding proteins binding proteins described herein may also have improved specificity. TL1A binding proteins binding proteins described herein may have specificity for monomeric and trimeric TL1A and not to related TNF super family proteins TNF, FasL, TRAIL, or LIGHT.

[0126] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 5, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 15, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 25, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 25; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 35, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 45, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 55, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 55. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 25; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 55. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0127] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 6, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 16, or a CDR2 having one to two amino acid substitutions as

compared to the sequence of SEQ ID NO: 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 26, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 26; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 36, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 46, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 56, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 56. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 26; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 56. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0128] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 7, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 17, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 27, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 27; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 37, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 47, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 57, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 57. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 7, (ii) a CDR2

having an amino acid sequence according to SEQ ID NO: 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 27; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 57. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0129] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 8, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 18, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 28, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 28; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 38, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 48, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 58, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 58. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 28; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 58. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0130] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 9, or a CDR1 having one to two amino acid substitutions as

compared to the sequence of SEQ ID NO: 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 19, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 29, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 29; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 39, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 49, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 59, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 59. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 29; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 59. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0131] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 10, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 20, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 30, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 30; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 40, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 50, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 60, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 60. In some

embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 30; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 60. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0132] In some embodiments the TL1A binding antibody specifically binds to an epitope on a TL1A polypeptide recognized by an antibody disclosed herein. In some embodiments the TL1A binding antibody specifically binds to an epitope on a TL1A polypeptide recognized by antibody 1, 2, 3, 4, 6, 8, 10, 47, 49, 63, or 69 disclosed herein.

[0133] In some embodiments the TL1A binding antibody binds specifically to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Thr 107, Gln 108, His 109, Phe 110, Lys 111, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 231, Asp 232, Ile 233, Ser 234, Tyr 238, Thr 239, Lys 240, and Lys 243. In some embodiments, the TL1A binding antibody specifically binds to the TL1A sequences at ten or more amino acid residues selected from Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 231, Asp 232, Ile 233, Ser 234, Leu 235, Val 236, Asp 237, Tyr 238, Thr 239, Lys 240, and Lys 243 of SEQ ID NO: 2493. In some embodiments, the TL1A binding antibody specifically binds to the TL1A sequences at ten or more amino acid residues selected from Arg103, Gln104, Ser234, Leu235, Val236, Asp237, Tyr238, Thr239, and Lys240 of SEQ ID NO: 2493. In some embodiments, the TL1A antigen binding protein is an antibody.

[0134] In some embodiments the TL1A binding protein specifically binds to an epitope of TL1A. In some embodiments, the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, and Thr 239. In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at amino acid residues Arg103, Gln104, Ser234, Leu235, Val236, Asp237, Tyr238, Thr239, and Lys240.

[0135] Described herein, in some embodiments, are TL1A binding proteins, wherein the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 15 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tye 238, and Trh 239, wherein the TL1A binding protein is an antibody. In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at amino acid residues Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tye 238, and Thr 239.

[0136] In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at least at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or all 19 of amino acid residues Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tye 238, and Thr 239 of SEQ ID NO: 2493.

[0137] In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at least at 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or all of amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Thr 107, His 118, Trp 119, Glu 120, His 121, Glu 122, Leu 123, Gly 124, Tyr 134, Asn 136, Arg 156, Gly 157, Met 158, Thr 159, Ser 206, Asn 207, Ser 234, Leu 235, Val 236, Asp 237, Tyr 238, Thr 239, and Lys 240 of SEQ ID NO: 2493.

[0138] In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at least at 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or all of amino acid residues Arg 103, Gln 104, Thr 105, Pro 106, Thr 107, Gln 108, His 109, Phe 110, Lys 111, Pro 115, Arg 156, Met 158, Thr 159, Ser 160, Glu 161, Ala 168, Gly 169, Arg 170, Pro 171, Lys 173, Asp 175, Gln 193, Ser 206, Asn 207, Ser 231, Asp 232, Ile 233, Ser 234, Leu 235, Val 236, Asp 237, Tyr 238, Thr 239, Lys 240, and Lys 243 of SEQ ID NO: 2493.

[0139] In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at least at 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 21, 22, or all of amino acid residues Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Thr 107, Gln 108, His 109, Asn 112, Pro 115, Leu 117, Arg 156, Gly 157, Met 158, Thr 159, Ser 160, Glu 161, Arg 170, Lys 173, Asp 175, Ser 176, Val 201, Ser 206, Asn 207, Trp 208, Phe 209, Asp 232, Ile 233, Ser 234, Leu 235, Val 236, Asp 237, Tyr 238, Thr 239, Lys 240, and Lys 243 of SEQ ID NO: 2493.

[0140] In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at least at 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, or all of amino acid residues Val 101, Val 102, Arg 103, Gln 104, His 118, Trp 119, Glu 120, His 121, Glu 122, Leu 123, Gly 124, Tyr 134, Thr 135, Lys 137, Tyr 188, Glu 190, Pro 191, Thr 192, Gln 193, Thr 239, Lys 240, Glu 241, and Asp 272 of SEQ ID NO: 2493.

[0141] In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at least at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or all of amino acid residues Val 102, Arg 103, Gln 104, Pro 106, His 118, Glu 120, Glu 122, Leu 123, Gly 124, Asn 136, Arg 156, Gly 157, Ser 234, Tyr 238, and Thr 239 of SEQ ID NO: 2493.

[0142] In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at least at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or all of amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Gln 108, Glu 120, Glu 122, Leu 123, Arg 156, Gly 157, Met 158, and Tyr 238 of SEQ ID NO: 2493.

[0143] In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at least at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or all of amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, His 118, Glu 120, Glu 122, Leu 123, Gly 124, Arg 156, Ser 234, Tyr 238, and Thr 239 of SEQ ID NO: 2493.

[0144] In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at least at 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or all of amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Thr 107, Gln 108, His 109, Phe 110, Lys 111, Leu 117, His 118, Trp 119, Arg 156, Gly 157, Lys 173, Met 196, Ser 206, Ser 231, Asp 232, Ile 233, Ser 234, Leu 235, Val 236, Asp 237, Tyr 238, Thr 239, Lys 240, and Lys 243 of SEQ ID NO: 2493.

[0145] In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at least at 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or all of amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Thr 107, Gln 108, His 109, Phe 110, Lys 111, Gln 113, Pro 115, Leu 117, His 118, Trp 119, Arg 156, Lys 173, Ser 206, Asn 207, Ser 231, Asp 232, Ile 233, Ser 234, Leu 235, Val 236, Asp 237, Tyr 238, Thr 239, Lys 240, and Lys 243 of SEQ ID NO: 2493.

[0146] In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at least at 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or all of amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Thr 107, Gln 108,

His 109, Phe 110, Lys 111, Leu 117, His 118, Trp 119, Arg 156, Lys 173, Ser 231, Asp 232, Ile 233, Ser 234, Leu 235, Val 236, Asp 237, Tyr 238, Thr 239, Lys 240, and Lys 243 of SEQ ID NO: 2493.

[0147] In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at least at 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or all of amino acid residues Thr 100, Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Thr 107, Gln 108, His 109, Phe 110, Lys 111, Gln 113, Pro 115, His 118, Trp 119, Glu 120, Arg 156, Asp 232, Ile 233, Ser 234, Leu 235, Val 236, Asp 237, Tyr 238, Thr 239, Lys 240, and Lys 243 of SEQ ID NO: 2493.

[0148] In some embodiments the amino acid residue of the TL1A epitope bind the paratope of the antibody with a distance of 6 Angstroms or less, 5 Angstroms or less, 4 Angstroms or less, 3 Angstroms or less, or 2 Angstroms or less.

[0149] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 21; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 51. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51. In some embodiments, the TL1A binding

protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0150] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 22; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 52. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0151] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 23; and b) a light chain variable region (VL)

comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 53. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0152] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 24; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 34, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 44, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 54. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, (ii) a

CDR2 having an amino acid sequence according to SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0153] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 539; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 866. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0154] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, or a CDR2 having one to two amino acid substitutions as

compared to the sequence of SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 559; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 886. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0155] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 563; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 890. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH)

comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0156] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 567, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 567; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 894. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 567; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0157] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 460; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 569; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 787; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 896. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787; and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0158] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 572; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO:

681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 899. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0159] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 583; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 910. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, and (iii) a CDR3 having

an amino acid sequence according to SEQ ID NO: 910. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0160] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 589; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 916. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0161] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, or a CDR2 having one to two amino acid substitutions as

compared to the sequence of SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 590; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 699, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 917. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0162] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 591; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 918. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH)

comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918 . In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0163] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 606; and a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 933. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0164] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 612; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 939. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0165] Described herein is a TL1A binding protein, wherein the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 618; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, or a CDR1 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO:

727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, or a CDR2 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945, or a CDR3 having one to two amino acid substitutions as compared to the sequence of SEQ ID NO: 945. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945. In some embodiments, the TL1A binding protein comprises an immunoglobin Fc domain. In some embodiments, the Fc domain comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0166] Described herein, in some embodiments, are TL1A binding proteins comprising a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 1-10 and 313-421, or having one to two amino acid substitutions as compared to any one of SEQ ID NOs: 1-10 and 313-421, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 11-20 and 422-530, or having one to two amino acid substitutions as compared to any one of SEQ ID NOs: 11-20 and 422-530, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 21-30 and 531-639, or having one to two amino acid substitutions as compared to any one of SEQ ID NOs: 21-30 and 531-639; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 31-40 and 640-748, or having one to two amino acid substitutions as compared to any one of SEQ ID NOs: 31-40 and 640-748, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 41-50 and 749-857, or having one to two amino acid substitutions as compared to any one of SEQ ID NOs: 41-50 and 749-857, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 51-60 and 858-966 or having one to two amino acid substitutions as compared to any one of SEQ ID NOs: 51-60 and 858-966.

[0167] Described herein, in some embodiments, are TL1A binding proteins comprising a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 1-10 and 313-421, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 11-20 and 422-530, and (iii) a CDR3 having an

amino acid sequence according to any one of SEQ ID NOs: 21-30 and 531-639; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 31-40 and 640-748, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 41-50 and 749-857, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 51-60 and 858-966.

[0168] Described herein, in some embodiments, are TL1A binding proteins comprising a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C.

[0169] Further described herein, in some embodiments, are TL1A binding proteins comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 1-10 and 313-421, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 11-20 and 422-530, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 21-30 and 531-639; b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 31-40 and 640-748, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 41-50 and 749-857, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 51-60 and 858-966; and c) a modified Fc that extends half-life of the TL1A binding protein as compared to a TL1A binding protein that does not comprise the modified Fc.

[0170] In some embodiments, provided are TL1A binding antibodies, wherein the TL1A binding proteins specifically bind to a TL1A polypeptide comprising SEQ ID NO: 2493 or 2494. In some embodiments, provided are antibodies that bind to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 13 or Table 14. In some embodiments, provided are antibodies that bind to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Lys243, Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234,

Ile233, Asp232, Met158, Arg156, Trp119, His118, Lys111, Phe110, His109, Gln108, Thr107, Pro106, Thr105, Gln104, Arg103, Val102, and Val101. In some embodiments, provided are antibodies that bind to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Gln104, and Arg103, Val102, and Val101

[0171] In some embodiments, the TL1A binding proteins comprises: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; and c) a modified Fc that extends half-life of the TL1A binding protein as compared to a TL1A binding protein that does not comprise the modified Fc.

[0172] Described herein, in some embodiments, are TL1A binding proteins comprising a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C.

[0173] Further described herein, in some embodiments, are TL1A binding proteins comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2

sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C; b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C; and c) a modified Fc that extends half-life of the TL1A binding protein as compared to a TL1A binding protein that does not comprise the modified Fc.

[0174] Described herein, in some embodiments, are TL1A binding proteins comprising a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C.

[0175] Further described herein, in some embodiments, are TL1A binding proteins comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C; b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C; and c) a modified Fc that extends half-life of

the TL1A binding protein as compared to a TL1A binding protein that does not comprise the modified Fc.

[0176] Described herein, in some embodiments, are TL1A binding proteins comprising a VH comprising a sequence having at least 80% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.1 and TABLE 2.2, and a VL comprising a sequence having at least 80% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a VH comprising a sequence having at least 85% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.1 and TABLE 2.2, and a VL comprising a sequence having at least 85% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a VH comprising a sequence having at least 90% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.1 and TABLE 2.2, and a VL comprising a sequence having at least 90% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a VH comprising a sequence having at least 95% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.1 and TABLE 2.2, and a VL comprising a sequence having at least 95% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a VH comprising a sequence having at least 96% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.1 and TABLE 2.2, and a VL comprising a sequence having at least 96% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a VH comprising a sequence having at least 97% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.1 and TABLE 2.2, and a VL comprising a sequence having at least 97% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a VH comprising a sequence having at least 98% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.1 and TABLE 2.2, and a VL comprising a sequence having at least 98% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a VH comprising a sequence having at least 99% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.1 and TABLE 2.2, and a VL comprising a sequence

having at least 99% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.1 and TABLE 2.2.

[0177] In some embodiments, the TL1A binding protein comprises a Fc domain. In some embodiments, the Fc domain is an IgG1, IgG2 or IgG4 immunoglobulin Fc domain. In some embodiments, the Fc domain is an IgG1 immunoglobulin domain. In some embodiments, the Fc domain is an IgG2 immunoglobulin domain. In some embodiments, the Fc domain is an IgG4 immunoglobulin domain. In some embodiments, the Fc domain amino acid comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE). In some embodiments, the TL1A binding protein is a TL1A binding antibody.

[0178] Further described herein, in, are TL1A binding antibodies, wherein the TL1A binding antibodies specifically bind to an epitope of TL1A and comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0179] Described herein, in some embodiments, are TL1A binding proteins, comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to CDRH1 sequences listed in TABLE 1.1 A, (ii) a CDR2 having an amino acid sequence according to CDRH2 sequences listed in TABLE 1.1 A, and (iii) a CDR3 having an amino acid sequence according to CDRH3 sequences listed in TABLE 1.1 A; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to CDRL1 sequences listed in TABLE 1.1 A, (ii) a CDR2 having an amino acid sequence according to CDRL2 sequences listed in TABLE 1.1 A, and (iii) a CDR3 having an amino acid sequence according to CDRL3 sequences listed in TABLE 1.1 A. In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.2 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0180] Described herein, in some embodiments, are TL1A binding proteins, comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to CDRH1 sequences listed in TABLE 1.2 A, (ii) a CDR2 having an amino acid sequence according to CDRH2 sequences listed in TABLE 1.2 A, and (iii) a CDR3 having an amino acid sequence according to CDRH3 sequences listed in TABLE 1.2 A; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to CDRL1 sequences listed in TABLE 1.2 A, (ii) a CDR2 having an amino acid sequence

according to CDRL2 sequences listed in TABLE 1.2 A, and (iii) a CDR3 having an amino acid sequence according to CDRL3 sequences listed in TABLE 1.2 A. In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.2 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0181] Described herein, in some embodiments, are TL1A binding proteins, comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to CDRH1 sequences listed in TABLE 1.3 A, (ii) a CDR2 having an amino acid sequence according to CDRH2 sequences listed in TABLE 1.3 A, and (iii) a CDR3 having an amino acid sequence according to CDRH3 sequences listed in TABLE 1.3 A; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to CDRL1 sequences listed in TABLE 1.3 A, (ii) a CDR2 having an amino acid sequence according to CDRL2 sequences listed in TABLE 1.3 A, and (iii) a CDR3 having an amino acid sequence according to CDRL3 sequences listed in TABLE 1.3 A. In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.2 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0182] Described herein, in some embodiments, are TL1A binding proteins, comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to CDRH1 sequences listed in TABLE 1.1 B, (ii) a CDR2 having an amino acid sequence according to CDRH2 sequences listed in TABLE 1.1 B, and (iii) a CDR3 having an amino acid sequence according to CDRH3 sequences listed in TABLE 1.1 B; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to CDRL1 sequences listed in TABLE 1.1 B, (ii) a CDR2 having an amino acid sequence according to CDRL2 sequences listed in TABLE 1.1 B, and (iii) a CDR3 having an amino acid sequence according to CDRL3 sequences listed in TABLE 1.1 B. In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.2 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.1.

In some embodiments, the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0183] Described herein, in some embodiments, are TL1A binding proteins, comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to CDRH1 sequences listed in TABLE 1.2 B, (ii) a CDR2 having an amino acid sequence according to CDRH2 sequences listed in TABLE 1.2 B, and (iii) a CDR3 having an amino acid sequence according to CDRH3 sequences listed in TABLE 1.2 B; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to CDRL1 sequences listed in TABLE 1.2 B, (ii) a CDR2 having an amino acid sequence according to CDRL2 sequences listed in TABLE 1.2 B, and (iii) a CDR3 having an amino acid sequence according to CDRL3 sequences listed in TABLE 1.2 B. In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.2 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.1. In some embodiments, the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0184] Described herein, in some embodiments, are TL1A binding proteins, comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to CDRH1 sequences listed in TABLE 1.3 B, (ii) a CDR2 having an amino acid sequence according to CDRH2 sequences listed in TABLE 1.3 B, and (iii) a CDR3 having an amino acid sequence according to CDRH3 sequences listed in TABLE 1.3 B; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to CDRL1 sequences listed in TABLE 1.3 B, (ii) a CDR2 having an amino acid sequence according to CDRL2 sequences listed in TABLE 1.3 B, and (iii) a CDR3 having an amino acid sequence according to CDRL3 sequences listed in TABLE 1.3 B. In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.2 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.1. In some embodiments, the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0185] Described herein, in some embodiments, are TL1A binding proteins, comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to CDRH1 sequences listed in TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to CDRH2 sequences listed in TABLE 1.1 C, and (iii) a CDR3 having an

amino acid sequence according to CDRH3 sequences listed in TABLE 1.1 C; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to CDRL1 sequences listed in TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to CDRL2 sequences listed in TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to CDRL3 sequences listed in TABLE 1.1 C. In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.2 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0186] Described herein, in some embodiments, are TL1A binding proteins, comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to CDRH1 sequences listed in TABLE 1.2 C, (ii) a CDR2 having an amino acid sequence according to CDRH2 sequences listed in TABLE 1.2 C, and (iii) a CDR3 having an amino acid sequence according to CDRH3 sequences listed in TABLE 1.2 C; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to CDRL1 sequences listed in TABLE 1.2 C, (ii) a CDR2 having an amino acid sequence according to CDRL2 sequences listed in TABLE 1.2 C, and (iii) a CDR3 having an amino acid sequence according to CDRL3 sequences listed in TABLE 1.2 C. In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VH sequences listed in TABLE 2.2 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0187] Described herein, in some embodiments, are TL1A binding proteins, comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to CDRH1 sequences listed in TABLE 1.3 C, (ii) a CDR2 having an amino acid sequence according to CDRH2 sequences listed in TABLE 1.3 C, and (iii) a CDR3 having an amino acid sequence according to CDRH3 sequences listed in TABLE 1.3 C; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to CDRL1 sequences listed in TABLE 1.3 C, (ii) a CDR2 having an amino acid sequence according to CDRL2 sequences listed in TABLE 1.3 C, and (iii) a CDR3 having an amino acid sequence according to CDRL3 sequences listed in TABLE 1.3 C. In some embodiments, the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any

one of VH sequences listed in TABLE 2.2 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0188] Described herein, in some embodiments, are TL1A binding proteins comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; and c) a modified Fc that extends half-life of the TL1A binding protein as compared to a TL1A binding protein that does not comprise the modified Fc.

[0189] Described herein, in some embodiments, are TL1A binding proteins, wherein the TL1A binding protein specifically binds to an epitope of TL1A and comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE). In some embodiments, the TL1A binding protein binds TL1A with a K_D less than about 0.5 nanomolar (nM). In some embodiments, the TL1A binding protein binds TL1A with a K_D less than about 0.4 nanomolar (nM). In some embodiments, the TL1A binding protein comprises a binding affinity to TL1A at least 2-fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein is a TL1A binding antibody. In some embodiments, the TL1A binding protein reduces TL1A-induced apoptosis by at least 2-fold more than a comparator antibody.

[0190] In some embodiments, are TL1A binding antibodies, wherein the TL1A binding proteins specifically bind to a TL1A polypeptide comprising SEQ ID NO: 2493 or 2494.

[0191] In some the TL1A binding protein specifically binds to an epitope of TL1A. In some embodiments, the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 12. In some embodiments, the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 13. In some embodiments, the TL1A binding protein

specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 14. In some embodiments, the TL1A antigen binding protein is an antibody.

[0192] In some embodiments, the TL1A binding protein specifically to the TL1A polypeptide at least at 2 or more amino acid residues of Table 12. In some embodiments, the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at least at 2 or more amino acid residues of Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Gln 108, His 118, Glu 120, Glu 122, Leu 123, Gly 124, Asn 136, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, Thr 239. In some embodiments, the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at least at 2 or more amino acid residues of Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156. In some embodiments, the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at least at 2 or more amino acid residues of Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, Arg 156 and Tyr 238.

[0193] In some embodiments, the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at least at 2 or more amino acid residues of Table 13. In some embodiments, the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at least at 2 or more amino acid residues of Table 14. In some embodiments, the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at least at 2 or more amino acid residues of Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Thr 107, Gln 108, His 109, Phe 110, Lys 111, Leu 117, His 118, Trp 119, Arg 156, Asp 232, Ile 233, Ser 234, Leu 235, Val 236, Asp 237, Tyr 238, Thr 239, Lys 240. In some embodiments, the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at least at 2 or more amino acid residues of Table 14. In some embodiments, the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at least at 2 or more amino acid residues of Arg103, Gln104, Arg 156, Ser234, Leu235, Val236, Asp237, Tyr238, Thr239, and Lys240.

[0194] In some embodiments the amino acid residue of the TL1A epitope bind the paratope of the antibody with a distance of 6 Angstroms or less, 5 Angstroms or less, 4 Angstroms or less, 3 Angstroms or less, or 2 Angstroms or less.

`TABLE 1. TL1A SEQUENCES

Name	SEQ ID NO.	Sequence
Human TL1A (TNF15)-1	2493	MAEDLGLSFGETASVEMLPEHGSCRPKARSSSARWALTCCLVLLPFLAGLTTYLLVSQLRAQGEACVQF QALKGQEFAPSHQQVYAPLRADGDKPRAHLTVVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNYTN KFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTKSVCEVGSN WFQPIYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL
Human TL1A (TNF15)-2	2494	MQLTKGRLHFSHPLSHTKHISPFVTDAPLRADGDKPRAHLTVVRQTPTQHFKNQFPALHWEHELGLAFT KNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTK SVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL

TABLE 1.1 A. AMINO ACID SEQUENCES OF EXEMPLARY CDRS OF ANTIBODY 1-4

Kabat Numbering (EU index)											
Antibody	**CDR H1 SEQ ID NO**	**CDRH1**	**CDRH 2 SEQ ID NO**	**CDRH2**	**CDRH 3 SEQ ID NO**	**CDRH3**	**CDRL 1 SEQ ID NO**	**CDRL1**	**CDR L2 SEQ ID NO**	**CDRL2**	**CDR L3 SEQ ID NO**	**CDRL3**
Antibody 1	1	SYAMH	11	VVSYEGSQNY YADSVKG	21	LESAYYFDY	31	RSSQSLLYS NGYNSLD	41	LGSNRAS	51	MQALQ TPYT
Antibody 2	2	SYYWS	12	LIYYSGSTNYN PSLKS	22	ADVVTIDY	32	RASQTISSYF N	42	AASSLQS	52	QQSYST PIT
Antibody 3	3	TYNMN	13	SIHSSSNYLYY ADSVKG	23	DRAMVDFDY	33	RASQSISTYL N	43	AASSLQS	53	QQSYST PLT
Antibody 4	4	SNSATWN	14	RTYYRSKWY NDYAVSVKS	24	EAVGPTKDFDY	34	RASQSFSSY LN	44	AASSLQS	54	QQSYFT PRT

TABLE 1.2 A. AMINO ACID SEQUENCES OF EXEMPLARY CDRS OF ANTIBODY 1-4

Chothia Numbering											
Antibody	**CDR H1 SEQ ID NO**	**CDRH1**	**CDRH 2 SEQ ID NO**	**CDRH2**	**CDRH 3 SEQ ID NO**	**CDRH3**	**CDRL 1 SEQ ID NO**	**CDRL1**	**CDR L2 SEQ ID NO**	**CDRL2**	**CDR L3 SEQ ID NO**	**CDRL3**

Antibody 1	61	GFTFSSY	71	SYEGSQ	81	ESAYYFD	91	SQSLLYSNGYNS		LGS	111	ALQTPY
Antibody 2	62	GGSISSY	72	YYSGS	82	DVVTID	92	SQTISSY		AAS	112	SYSTPI
Antibody 3	63	GFTFSTY	73	HSSSNY	83	RAMVDFD	93	SQSISTY		AAS	113	SYSTPL
Antibody 4	64	GDSVSSNSA	74	YYRSKWY	84	AVGPTKDFD	94	SQSFSSY		AAS	114	SYFTPR

TABLE 1.3 A. AMINO ACID SEQUENCES OF EXEMPLARY CDRS OF ANTIBODY 1-4

IMGT Numbering												
Antibody	**CDRH1 SEQ ID NO**	**CDRH1**	**CDRH2 SEQ ID NO**	**CDRH2**	**CDRH3 SEQ ID NO**	**CDRH3**	**CDRL1 SEQ ID NO**	**CDRL1**	**CDRL2 SEQ ID NO**	**CDRL2**	**CDRL3 SEQ ID NO**	**CDRL3**
Antibody 1	121	GFTFSSYA	131	VSYEGSQN	141	ANLESAYYFDY	151	QSLLYSNGYNS		LGS	171	MQALQTPYT
Antibody 2	122	GGSISSYY	132	IYYSGST	142	ARADVVTIDY	152	QTISSY		AAS	172	QQSYSTPIT
Antibody 3	123	GFTFSTYN	133	IHSSSNYL	143	ATDRAMVDFDY	153	QSISTY		AAS	173	QQSYSTPLT
Antibody 4	124	GDSVSSNSAT	134	TYYRSKWYN	144	AREAVGPTKDFDY	154	QSFSSY		AAS	174	QQSYFTPRT

TABLE 1.1 B. AMINO ACID SEQUENCES OF EXEMPLARY CDRS OF ANTIBODY 5-10

Kabat Numbering (EU index)												
Antibody	**CDRH1 SEQ ID NO**	**CDRH1**	**CDRH2 SEQ ID NO**	**CDRH2**	**CDRH3 SEQ ID NO**	**CDRH3**	**CDRL1 SEQ ID NO**	**CDRL1**	**CDRL2 SEQ ID NO**	**CDRL2**	**CDRL3 SEQ ID NO**	**CDRL3**
Antibody 5	5	NVWMN	15	LIKSKTDAGTTDYAAPVKG	25	DRGWGENY	35	RASQIFSSSYLV	45	GASSRAT	55	QQYGNSPYT

Antibody 6	6	NVWMN	16	RIKSKIDAGTT DYVAPVKG	26	DRGWGENY	36	RASQSVSSS YLV	46	GASSRAT	56	QQYGG SPYT
Antibody 7	7	NAWMS	17	RIKSKIDAGTT DYAAPVKG	27	DLGWGENY	37	RASQSISRSY LV	47	GASSRAT	57	HQYGS SPYT
Antibody 8	8	NAWMS	18	RIKSKIDAGTT DYAAPVKG	28	DLGWGENY	38	RASQRVSSS YLV	48	GASSRAT	58	QQYGS SPYT
Antibody 9	9	NAWMT	19	RIKSKIDAGTT DYAAPVKG	29	DLGWGENY	39	RASQRVSSS YLV	49	GASSRAT	59	QQYGS SPYT
Antibody 10	10	NAWMT	20	RIKSKIDAGTT DYAAPVKG	30	DLGWGENY	40	RASQRVSSS YLV	50	GASSRAT	60	QQYGS SPYT

TABLE 1.2 B. AMINO ACID SEQUENCES OF EXEMPLARY CDRS OF ANTIBODY 5-10

Chothia Numbering												
Antibody	**CDR H1 SEQ ID NO**	**CDRH1**	**CDRH 2 SEQ ID NO**	**CDRH2**	**CDRH 3 SEQ ID NO**	**CDRH3**	**CDRL 1 SEQ ID NO**	**CDRL1**	**CDR L2 SEQ ID NO**	**CDRL2**	**CDR L3 SEQ ID NO**	**CDRL3**
Antibody 5	65	GFTFSNV	75	KSKTDAGT	85	RGWGEN	95	SQIFSSSY		GAS	115	YGNSP Y
Antibody 6	66	GFIFSNV	76	KSKIDAGT	86	RGWGEN	96	SQSVSSSY		GAS	116	YGGSP Y
Antibody 7	67	GFTFSNA	77	KSKIDAGT	87	LGWGEN	97	SQSISRSY		GAS	117	YGSSPY
Antibody 8	68	GFTFSNA	78	KSKIDAGT	88	LGWGEN	98	SQRVSSSY		GAS	118	YGSSPY
Antibody 9	69	GFTFSNA	79	KSKIDAGT	89	LGWGEN	99	SQRVSSSY		GAS	119	YGSSPY
Antibody 10	70	GFTFSNA	80	KSKIDAGT	90	LGWGEN	100	SQRVSSSY		GAS	120	YGSSPY

TABLE 1.3 B. AMINO ACID SEQUENCES OF EXEMPLARY CDRS OF ANTIBODY 5-10

IMGT Numbering												
Antibody	**CDR H1 SEQ**	**CDRH1**	**CDRH 2 SEQ ID NO**	**CDRH2**	**CDRH 3 SEQ ID NO**	**CDRH3**	**CDRL 1 SEQ ID NO**	**CDRL1**	**CDR L2 SEQ**	**CDRL2**	**CDR L3 SEQ**	**CDRL3**

AMENDED SHEET

PCT/US 2024/041 774 - 11.06.2025
Attorney Docket No. 220703-010508/PCT
Replacement Sheets

	ID NO								ID NO		ID NO	
Antibody 5	125	GFTFSNVW	135	IKSKTDAGTT	145	TTDRGWGENY	155	QIFSSSY		GAS	175	QQYGN SPYT
Antibody 6	126	GFIFSNVW	136	IKSKIDAGTT	146	ITDRGWGENY	156	QSVSSSY		GAS	176	QQYGG SPYT
Antibody 7	127	GFTFSNAW	137	IKSKIDAGTT	147	TTDLGWGENY	157	QSISRSY		GAS	177	HQYGS SPYT
Antibody 8	128	GFTFSNAW	138	IKSKIDAGTT	148	TTDLGWGENY	158	QRVSSSY		GAS	178	QQYGS SPYT
Antibody 9	129	GFTFSNAW	139	IKSKIDAGTT	149	TTDLGWGENY	159	QRVSSSY		GAS	179	QQYGS SPYT
Antibody 10	130	GFTFSNAW	140	IKSKIDAGTT	150	TTDLGWGENY	160	QRVSSSY		GAS	180	QQYGS SPYT

TABLE 1.1 C. AMINO ACID SEQUENCES OF EXEMPLARY CDRS OF ANTIBODY 11-119

Kabat Numbering (EU index)												
Name	**CDRH1 SEQ ID NO**	**CDRH1**	**CDRH2 SEQ ID NO**	**CDRH2**	**CDRH3 SEQ ID NO**	**CDRH3**	**CDRL1 SEQ ID NO**	**CDRL1**	**CDRL2 SEQ ID NO**	**CDRL2**	**CDRL3 SEQ ID NO**	**CDRL3**
Antibody 11	313	GYYMH	422	WINPKSG GTIYAQK FQG	531	GGSFDAF DI	640	RASQSIS RYLY	749	GASSLQS	858	QQGFSAP LT
Antibody 12	314	GYYWS	423	EITHSGIT NYNPSLE S	532	GQVGTT DYYYFY MDV	641	RASQSIR RYLN	750	AASSLQS	859	QQSYRTI T
Antibody 13	315	GYYMH	424	WINPNSG GTNYAQ NFQG	533	GGSFDAF DI	642	RASQSIS RYLN	751	GASSVQS	860	QQGDSSP FT
Antibody 14	316	GYYMH	425	WINPKSG GTNYAQ NFQG	534	GGSFDAF DI	643	RASQSIS RYLN	752	GASSVQS	861	QQGDSSP FT
Antibody 15	317	GYYMH	426	WINPNSG GTNYAQ KFQG	535	GGSFDAF DI	644	RASQSISS YLN	753	GASSLQS	862	QQGHSTP FT

Antibody 16	318	AYYMH	427	WINPNSG GTNYAQ SFQG	536	GGSFDAF D1	645	RASQSIS RYLN	754	GASSVQS	863	QQGDSSP FT
Antibody 17	319	AYYMH	428	WINPKSG GTNYAQ SFQG	537	GGSFDAF D1	646	RASQSIS RYLN	755	GASSVQS	864	QQGDSSP FT
Antibody 18	320	AYYMH	429	WINPNSG GTNYAQ QFQG	538	GGSYDA FD1	647	RASQSISS YLN	756	GASRLQS	865	QQGHSTP FT
Antibody 19	321	AYYMH	430	WINPKSG GTNYAQ QFQG	539	GGSYDA FD1	648	RASQSISS YLN	757	GASRLQS	866	QQGHSTP FT
Antibody 20	322	AYYIH	431	WINPNSG GTNYAQ KFQG	540	GGSFDAF D1	649	RASQSISS YLN	758	GASSLQS	867	QQGDSTP FT
Antibody 21	323	AYYIH	432	WINPKSG GTNYAQ KFQG	541	GGSFDAF D1	650	RASQSISS YLN	759	GASSLQS	868	QQGDSTP FT
Antibody 22	324	GYYLH	433	WINPNSG GTNFAQ KFQG	542	GGSYDA FD1	651	RASQSISS YLN	760	GASRLQS	869	QQGDSTP FT
Antibody 23	325	GYYLH	434	WINPKSG GTNFAQ KFQG	543	GGSYDA FD1	652	RASQSISS YLN	761	GASRLQS	870	QQGDSTP FT
Antibody 24	326	GYYMH	435	WINPNSG GTNYAQ KFQG	544	GGSYDA FD1	653	RASQSISS YLN	762	GASRLQS	871	QQGDSTP FT
Antibody 25	327	GYYMH	436	WINPKSG GTNYAQ KFQG	545	GGSYDA FD1	654	RASQSISS YLN	763	GASRLQS	872	QQGDSTP FT
Antibody 26	328	GYYLH	437	WINPNSG GTNYAQ RFQG	546	GGSFDAF D1	655	RASQSISS YLN	764	GASRLQS	873	QQGDSSP FT
Antibody 27	329	GYYLH	438	WINPKSG GTNYAQ RFQG	547	GGSFDAF D1	656	RASQSISS YLN	765	GASRLQS	874	QQGDSSP FT
Antibody 28	330	GYYMH	439	WINPKSG GTIYAQK FQG	548	GGSFDAF D1	657	RASQSISS YLN	766	GASSLQS	875	QQGHSTP FT

Antibody 29	331	GYYMH	440	WINPKSG GTNYAQ KFQG	549	GGSFDAF D1	658	RASQSISS YLN	767	GASSLQS	876	QQGDSTP FT
Antibody 30	332	GYYMH	441	WINPKSG GTSYAQ KFQG	550	GGSYDA FD1	659	RASQSISS YLN	768	GASSLQS	877	QQGHSTP FT
Antibody 31	333	GYYMH	442	WINPKSG GTNYAQ KFQG	551	GGSYDA FD1	660	RASQSISS YLN	769	GASRLQS	878	QQGYSSP FT
Antibody 32	334	AYYIH	443	WINPNSG GTNYAQ NFQG	552	GGSFDAF D1	661	QASQDIS NYLN	770	GASSLQS	879	QQGDSTP FT
Antibody 33	335	AYYIH	444	WINPKSG GTNYAQ NFQG	553	GGSFDAF D1	662	QASQDIS NYLN	771	GASSLQS	880	QQGDSTP FT
Antibody 34	336	GYYMH	445	WINPKSG GTNYAQ NFQG	554	GGSFDAF D1	663	RASQGIS RYLH	772	GASSLQS	881	QQGFSTP FT
Antibody 35	337	GYYMH	446	WINPNSG GTNYAQ KFQG	555	GGSYDA FD1	664	RASQSISS YLN	773	GASRLQS	882	QQGSSPP FT
Antibody 36	338	GYYMH	447	WINPKSG GTNYAQ KFQG	556	GGSYDA FD1	665	RASQSISS YLN	774	GASRLQS	883	QQGSSPP FT
Antibody 37	339	AYYMH	448	WINPNSG GTKYAQ KFQG	557	GGSYDA FD1	666	RASQSISS YLN	775	GASRLQS	884	QQGYSSP FT
Antibody 38	340	AYYMH	449	WINPKSG GTKYAQ KFQG	558	GGSYDA FD1	667	RASQSISS YLN	776	GASRLQS	885	QQGYSSP FT
Antibody 39	341	AYYLH	450	WINPNSG GTNYAQ KFQG	559	GGSFDAF D1	668	RASQSIS RYLN	777	GASSVQS	886	QQGDSSP FT
Antibody 40	342	AYYLH	451	WINPKSG GTNYAQ KFQG	560	GGSFDAF D1	669	RASQSIS RYLN	778	GASSVQS	887	QQGDSSP FT
Antibody 41	343	GYFIH	452	WINPKSG GTNYAQ KFQD	561	GGSYDA FD1	670	RASQSISS YLN	779	GASRLQS	888	QQGHSTP FT

Antibody 42	344	AYYMH	453	WINPNSG GTKYAQ KFQG	562	GGSYDA FDI	671	RASQSISS YLN	780	GASRLQS	889	QQGDSTP FT
Antibody 43	345	AYYMH	454	WINPKSG GTKYAQ KFQG	563	GGSYDA FDI	672	RASQSISS YLN	781	GASRLQS	890	QQGDSTP FT
Antibody 44	346	AYYIH	455	WINPNSG GTSSAQK FQG	564	GGSFDAF DI	673	RASQSISS YLN	782	GASRLQS	891	QQGYSSP FT
Antibody 45	347	AYYIH	456	WINPKSG GTSSAQK FQG	565	GGSFDAF DI	674	RASQSISS YLN	783	GASRLQS	892	QQGYSSP FT
Antibody 46	348	AYYIH	457	WVNPNS GGTNYA QSFQG	566	GGSFDAF DI	675	RASQSISS YLN	784	GASSLQS	893	QQGHSTP FT
Antibody 47	349	AYYIH	458	WVNPKS GGTNYA QSFQG	567	GGSFDAF DI	676	RASQSISS YLN	785	GASSLQS	894	QQGHSTP FT
Antibody 48	350	AYYMH	459	WINPNSG GTKYAQ KFQG	568	GGSFDAF DI	677	RASQSISS YLN	786	GASSLQS	895	QQGDSTP FT
Antibody 49	351	AYYMH	460	WINPKSG GTKYAQ KFQG	569	GGSFDAF DI	678	RASQSISS YLN	787	GASSLQS	896	QQGDSTP FT
Antibody 50	352	GYYIH	461	WINPKSG GTNYAQ KFQG	570	GGSYDA FDI	679	RASQSISS YLN	788	GASSLQS	897	QQGDSTP FT
Antibody 51	353	GYYMH	462	WINPNSG GTNYAQ KFQG	571	GGSYDA FDI	680	RASQSISS YLN	789	GASSLQS	898	QQGDSTP FT
Antibody 52	354	GYYMH	463	WINPKSG GTNYAQ KFQG	572	GGSYDA FDI	681	RASQSISS YLN	790	GASSLQS	899	QQGDSTP FT
Antibody 53	355	GYYMH	464	WIHPNSG GTNSAQ KFQG	573	GGSYDA FDI	682	RASQSISS YLN	791	GASRLQS	900	QQGYSSP FT
Antibody 54	356	GYYMH	465	WIHPKSG GTNTAQ KFQG	574	GGSYDA FDI	683	RASQSISS YLN	792	GASRLQS	901	QQGYSSP FT

Antibody 55	357	GYFIH	466	WINPKSG GTNYAQ KFQG	575	GGSFDAF D1	684	RASQSIS RYLN	793	GASSVQS	902	QQGDSSP FT
Antibody 56	358	GYYMH	467	WINPNSG GTNYAQ KFQG	576	GGSFDAF D1	685	RASQSISS YLN	794	GASRLQS	903	QQGYSSP FT
Antibody 57	359	GYYMH	468	WINPKSG GTNYAQ KFQG	577	GGSFDAF D1	686	RASQSISS YLN	795	GASRLQS	904	QQGYSSP FT
Antibody 58	360	GYYMH	469	WINPNSG GPNYAQ KFQD	578	GGSFDAF D1	687	RASQSIS NYLN	796	GTSRLQS	905	QQGYSSP FT
Antibody 59	361	GYYMH	470	WINPKSG GPNYAQ KFQD	579	GGSFDAF D1	688	RASQSIS NYLN	797	GTSRLQS	906	QQGYSSP FT
Antibody 60	362	GYFMH	471	WINPNSG GTNYAQ RFQG	580	GGSFDAF D1	689	RASQSISS YLN	798	GASRLQS	907	QQGYSSP FT
Antibody 61	363	GYFMH	472	WINPKSG GTNYAQ RFQG	581	GGSFDAF D1	690	RASQSISS YLN	799	GASRLQS	908	QQGYSSP FT
Antibody 62	364	GYYMH	473	WINPNSG GTNYAQ KFQG	582	GGSFDAF DV	691	RASQSISS YLN	800	GASRLQS	909	QQGDNT PFT
Antibody 63	365	GYYMH	474	WINPKSG GTNYAQ KFQG	583	GGSFDAF DV	692	RASQSISS YLN	801	GASRLQS	910	QQGDNT PFT
Antibody 64	366	GYYMQ	475	WINPNSG GTIYAQK FQG	584	GGSFDAF D1	693	RASQSISS YLN	802	GASRLQS	911	QQGHSTP FT
Antibody 65	367	GYYMQ	476	WINPKSG GTIYAQK FQG	585	GGSFDAF D1	694	RASQSISS YLN	803	GASRLQS	912	QQGHSTP FT
Antibody 66	368	GYYLH	477	WIKPNSG GTNYAQ KFQG	586	GGSYDA FD1	695	RASQSISS YLN	804	GASRLQS	913	QQGYSSP FT
Antibody 67	369	GYYLH	478	WIKPKSG GTNYAQ KFQG	587	GGSYDA FD1	696	RASQSISS YLN	805	GASRLQS	914	QQGYSSP FT

Antibody 68	370	AYYMH	479	WVNPNS GGTNYA QNFQG	588	GGSFDAF D1	697	RASQSISS YLN	806	GASSLQS	915	QQGHSTP FT
Antibody 69	371	AYYMH	480	WVNPKS GGTNYA QNFQG	589	GGSFDAF D1	698	RASQSISS YLN	807	GASSLQS	916	QQGHSTP FT
Antibody 70	372	GYYMH	481	WINPNSG GTNYAQ KFQG	590	GGSFDAF D1	699	RASQTIS SYLN	808	GASSLQS	917	QQGDSTP FT
Antibody 71	373	GYYMH	482	WINPKSG GTNYAQ KFQG	591	GGSFDAF D1	700	RASQTIS SYLN	809	GASSLQS	918	QQGDSTP FT
Antibody 72	374	GYYMH	483	WINPNSG GTNYAQ RFQG	592	GGSFDAF D1	701	RASQSIS KYLI	810	GASSLQS	919	QQGHSTP FT
Antibody 73	375	GYYMH	484	WINPKSG GTNYAQ RFQG	593	GGSFDAF D1	702	RASQSIS KYLI	811	GASSLQS	920	QQGHSTP FT
Antibody 74	376	GYYMH	485	WIKPNSG GTNYAQ KFQG	594	GGSYDA FD1	703	RASQSISS YLN	812	GASRLQS	921	QQGDSTP FT
Antibody 75	377	GYYMH	486	WIKPKSG GTNYAQ KFQG	595	GGSYDA FD1	704	RASQSISS YLN	813	GASRLQS	922	QQGDSTP FT
Antibody 76	378	GYYIH	487	WINPNSG GTNYAQ KFQG	596	GGSFDAF D1	705	RASQSISS YLN	814	GASRLQS	923	QQGYSSP FT
Antibody 77	379	GYYIH	488	WINPKSG GTNYAQ KFQG	597	GGSFDAF D1	706	RASQSISS YLN	815	GASRLQS	924	QQGYSSP FT
Antibody 78	380	AYYMH	489	WINPNSG GTKYAQ KFQG	598	GGSYDA FD1	707	RASLSISS YLN	816	GASSLQS	925	QQGHSTP FT
Antibody 79	381	AYYMH	490	WINPKSG GTKYAQ KFQG	599	GGSYDA FD1	708	RASLSISS YLN	817	GASSLQS	926	QQGHSTP FT
Antibody 80	382	GYYMH	491	WINPNSG GTNYAQ KFQG	600	GGSFDAF D1	709	RASQSISS YLN	818	GASSLQS	927	QQGDSTP FT

Antibody 81	383	GYYMH	492	WINPNSG GTNYAQ KFQG	601	GGSYDA FDI	710	RSSQSISS YLN	819	GASSLQS	928	QQGDSTP FT
Antibody 82	384	GYYMH	493	WINPKSG GTNYAQ KFQG	602	GGSYDA FDI	711	RSSQSISS YLN	820	GASSLQS	929	QQGDSTP FT
Antibody 83	385	GYYMH	494	WINPNSG ATNFAQ KFQG	603	GGSFDAF DI	712	RASRSISS YLN	821	GASRLQT	930	QQGYSSP FT
Antibody 84	386	GYYMH	495	WINPKSG ATNFAQ KFQG	604	GGSFDAF DI	713	RASRSISS YLN	822	GASRLQT	931	QQGYSSP FT
Antibody 85	387	AYYLH	496	WINPNSG GTNYAQ KFQD	605	GGSYDA FDI	714	RASQSIN SYLN	823	GASSLQS	932	QQGYSTP FT
Antibody 86	388	AYYLH	497	WINPKSG GTNYAQ KFQD	606	GGSYDA FDI	715	RASQSIQ SYLN	824	GASSLQS	933	QQGYSTP FT
Antibody 87	389	AYYMH	498	WINPNSG GTKYAQ KFQG	607	GGSYDA FDI	716	RASQSISS YLN	825	GASRLQS	934	QQGDNT PFT
Antibody 88	390	AYYMH	499	WINPKSG GTKYAQ KFQG	608	GGSYDA FDI	717	RASQSISS YLN	826	GASRLQS	935	QQGDNT PFT
Antibody 89	391	GYYMH	500	WINPKSG GTNYAQ KFQG	609	GGSYDA FDI	718	RASQSIN SYLY	827	GASSLQS	936	QQGYSTP FT
Antibody 90	392	GYYMH	501	WINPKSG GTNYAQ KFQG	610	GGSYDA FDI	719	RASQSIQ SYLY	828	GASSLQS	937	QQGYSTP FT
Antibody 91	393	AYYLH	502	WINPNSG GTSSAQK FQG	611	GGSFDAF DI	720	RASQSISS YLN	829	GASSLQS	938	QQGDSTP FT
Antibody 92	394	AYYLH	503	WINPKSG GTSSAQK FQG	612	GGSFDAF DI	721	RASQSISS YLN	830	GASSLQS	939	QQGDSTP FT
Antibody 93	395	GYYMH	504	WINPNSG GTHYAQ KFQG	613	GGSFDAF DI	722	RASLSISS YLN	831	GASSLQS	940	QQGHSTP FT

Antibody 94	396	GYYMH	505	WINPKSG GTHYAQ KFQG	614	GGSFDAF DI	723	RASLSISS YLN	832	GASSLQS	941	QQGHSTP FT
Antibody 95	397	GYYIH	506	WINPNSG GTNYAQ RFQG	615	GGSFDAF DI	724	RASQSISS YLN	833	GASRLQS	942	QQGYSSP FT
Antibody 96	398	GYYMH	507	WINPKSG GTIYAQK FQG	616	GGSFDAF DI	725	RASQTIS RYLN	834	GASSLQS	943	QQSYSTP FT
Antibody 97	399	AYYIH	508	WINPNSG GTNYAQ KFQG	617	GGSYDA FDI	726	RASQTIS RYLN	835	GASSLQS	944	QQGYSTP FT
Antibody 98	400	GYFMH	509	WINPKSG GTNYAQ KFQG	618	GGSFDAF DI	727	RASQSISS YLN	836	GASRLQS	945	QQGDSTP FT
Antibody 99	401	GYYMH	510	WINPNSG GTKYAQ KFQG	619	GGSFDAF DI	728	RASQSISS YLN	837	GASRLQS	946	QQGYSSP FT
Antibody 100	402	GYYMH	511	WINPNSG GTNYAQ KFQG	620	GGSFDAF DI	729	RASQSIS RYLN	838	GASSVQS	947	QQGDSSP FT
Antibody 101	403	GYYMH	512	WINPNSG GTNYAQ KFQG	621	GGSYDA FDI	730	RASQSIS RYLN	839	GASSLQS	948	QQGYSTL FT
Antibody 102	404	GYYMH	513	WINPNSG GTKYSQ KFQG	622	GGSFDAF DI	731	RASQSISS YLN	840	GASRLQS	949	QQGYSSP FT
Antibody 103	405	GYYMH	514	WINPNSG GTNYAQ KFQG	623	GGSYDA FDI	732	RASQSISS YLN	841	GASRLQS	950	QQGYSN PFT
Antibody 104	406	AYYMH	515	WINPNSG GTNYAQ KFQG	624	GGSIDAF DI	733	RASQSISS YLN	842	GASRLQS	951	QQGFSTP FT
Antibody 105	407	AYYIH	516	WINPNSG GTNYAQ KFQD	625	GGSYDA FDI	734	RASQSISS YLN	843	GASRLQS	952	QQGYSSP FT
Antibody 106	408	GYYIH	517	WINPNSG GTKYAQ KFHG	626	GGSFDAF DI	735	RASQSIS RYLN	844	GASRLQS	953	QQGYSSP FT

Antibody 107	409	GYYMH	518	WINPNSG GTNYAQ KFQG	627	GGSFDAF DV	736	RASQSISS YLN	845	GASSLQS	954	QQGDSTP FT
Antibody 108	410	GYYMH	519	WINPNSG GTNYAQ KFQG	628	GGSFDAF DI	737	RASQSISS FLN	846	GASRLQS	955	QQGDSTP FT
Antibody 109	411	AYYIH	520	WINPNSG GTNYAQ RFQG	629	GGSFDAF DI	738	RASQSISS YLN	847	GASSLQS	956	QQGHSTP FT
Antibody 110	412	GYYMH	521	WINPKSG GTNYAQ KFQG	630	GGSFDAF DI	739	RASQSISS YLN	848	GASSLQS	957	QQGHSTP FT
Antibody 111	413	AYYIH	522	WINPNSG GTSSAQK FQG	631	GGSFDAF DI	740	RASQSISS YLN	849	GASRLQS	958	QQGHSTP IT
Antibody 112	414	GYYMH	523	WINPNSG GTNYAQ KFQG	632	GGSYDA FDI	741	RASQSISS YLN	850	GASRLQS	959	QQGYSSP FT
Antibody 113	415	GYYMH	524	WINPNSG GTKYAQ KFQG	633	GGSYDA FDI	742	RASQSIS RYLY	851	AASSLQS	960	QQGYDT PFT
Antibody 114	416	GYYMH	525	WINPKSG GTNYAQ KFQG	634	GGSFDAF DI	743	QASQDIS NYLN	852	AASSLQT	961	QQGDSTP FT
Antibody 115	417	RYGMN	526	WINTNTG NPTYAQ DFTG	635	DNWNYV SDY	744	RASQSVS DSYLA	853	GASSRAT	962	QQYGTSP IT
Antibody 116	418	GYYMH	527	WINPKSG GTIYAQK FQG	636	GGSFDAF DI	745	RASQSISS YLN	854	GASSLQS	963	QQAKSFP LT
Antibody 117	419	VYYMH	528	WINPNSG GTNYAQ KFQG	637	GGSFDAF DI	746	RASQSISS YLN	855	GASRLQS	964	QQGYSSP FT
Antibody 118	420	RYGMN	529	WINTNTG NPTYAQ GFTG	638	DNWNYD FDY	747	KSSQSLV HSDGNT YLS	856	KISNRFS	965	MQVTQF PIT
Antibody 119	421	TYGMN	530	WINTNTG NPTYAQ GFTG	639	DNWNYD LDY	748	RSSQSLV HSDGNT YLS	857	KISNRFS	966	MQATQF PIT

TABLE 1.2 C. AMINO ACID SEQUENCES OF EXEMPLARY CDRS OF ANTIBODY 11-119

Chothia Numbering												
Name	**CDRH1 SEQ ID NO**	**CDRH1**	**CDRH2 SEQ ID NO**	**CDRH2**	**CDRH3 SEQ ID NO**	**CDRH3**	**CDRL1 SEQ ID NO**	**CDRL1**	CDRL2 SEQ ID NO	**CDRL2**	**CDRL3 SEQ ID NO**	**CDRL3**
Antibody 11	967	GYTFTGY	1076	NPKSGG	1185	GSFDAFD	1294	SQSISRY		GAS	1512	GFSAPL
Antibody 12	968	GGSFSGY	1077	THSGI	1186	QVGTTD YYYFYM D	1295	SQSIRRY		AAS	1513	SYRTI
Antibody 13	969	GYTFTGY	1078	NPNSGG	1187	GSFDAFD	1296	SQSISRY		GAS	1514	GDSSPF
Antibody 14	970	GYTFTGY	1079	NPKSGG	1188	GSFDAFD	1297	SQSISRY		GAS	1515	GDSSPF
Antibody 15	971	GYTFTGY	1080	NPNSGG	1189	GSFDAFD	1298	SQSISSY		GAS	1516	GHSTPF
Antibody 16	972	GYTFTAY	1081	NPNSGG	1190	GSFDAFD	1299	SQSISRY		GAS	1517	GDSSPF
Antibody 17	973	GYTFTAY	1082	NPKSGG	1191	GSFDAFD	1300	SQSISRY		GAS	1518	GDSSPF
Antibody 18	974	GYTFTAY	1083	NPNSGG	1192	GSYDAF D	1301	SQSISSY		GAS	1519	GHSTPF
Antibody 19	975	GYTFTAY	1084	NPKSGG	1193	GSYDAF D	1302	SQSISSY		GAS	1520	GHSTPF
Antibody 20	976	GYTFTAY	1085	NPNSGG	1194	GSFDAFD	1303	SQSISSY		GAS	1521	GDSTPF
Antibody 21	977	GYTFTAY	1086	NPKSGG	1195	GSFDAFD	1304	SQSISSY		GAS	1522	GDSTPF
Antibody 22	978	GYTFTGY	1087	NPNSGG	1196	GSYDAF D	1305	SQSISSY		GAS	1523	GDSTPF
Antibody 23	979	GYTFTGY	1088	NPKSGG	1197	GSYDAF D	1306	SQSISSY		GAS	1524	GDSTPF
Antibody 24	980	GYTFTGY	1089	NPNSGG	1198	GSYDAF D	1307	SQSISSY		GAS	1525	GDSTPF
Antibody 25	981	GYTFTGY	1090	NPKSGG	1199	GSYDAF D	1308	SQSISSY		GAS	1526	GDSTPF

Antibody 26	982	GYTFTGY	1091	NPNSGG	1200	GSFDAFD	1309	SQSISSY		GAS	1527	GDSSPF
Antibody 27	983	GYTFTGY	1092	NPKSGG	1201	GSFDAFD	1310	SQSISSY		GAS	1528	GDSSPF
Antibody 28	984	GYTFTGY	1093	NPKSGG	1202	GSFDAFD	1311	SQSISSY		GAS	1529	GHSTPF
Antibody 29	985	GYTFTGY	1094	NPKSGG	1203	GSFDAFD	1312	SQSISSY		GAS	1530	GDSTPF
Antibody 30	986	GYTFTGY	1095	NPKSGG	1204	GSYDAFD	1313	SQSISSY		GAS	1531	GHSTPF
Antibody 31	987	GYTFTGY	1096	NPKSGG	1205	GSYDAFD	1314	SQSISSY		GAS	1532	GYSSPF
Antibody 32	988	GYTFTAY	1097	NPNSGG	1206	GSFDAFD	1315	SQDISNY		GAS	1533	GDSTPF
Antibody 33	989	GYTFTAY	1098	NPKSGG	1207	GSFDAFD	1316	SQDISNY		GAS	1534	GDSTPF
Antibody 34	990	GYTFTGY	1099	NPKSGG	1208	GSFDAFD	1317	SQGISRY		GAS	1535	GFSTPF
Antibody 35	991	GYTFTGY	1100	NPNSGG	1209	GSYDAFD	1318	SQSISSY		GAS	1536	GSSPPF
Antibody 36	992	GYTFTGY	1101	NPKSGG	1210	GSYDAFD	1319	SQSISSY		GAS	1537	GSSPPF
Antibody 37	993	GYTFTAY	1102	NPNSGG	1211	GSYDAFD	1320	SQSISSY		GAS	1538	GYSSPF
Antibody 38	994	GYTFTAY	1103	NPKSGG	1212	GSYDAFD	1321	SQSISSY		GAS	1539	GYSSPF
Antibody 39	995	GYTFTAY	1104	NPNSGG	1213	GSFDAFD	1322	SQSISRY		GAS	1540	GDSSPF
Antibody 40	996	GYTFTAY	1105	NPKSGG	1214	GSFDAFD	1323	SQSISRY		GAS	1541	GDSSPF
Antibody 41	997	GYTFTGY	1106	NPKSGG	1215	GSYDAFD	1324	SQSISSY		GAS	1542	GHSTPF
Antibody 42	998	GYTFTAY	1107	NPNSGG	1216	GSYDAFD	1325	SQSISSY		GAS	1543	GDSTPF
Antibody 43	999	GYTFTAY	1108	NPKSGG	1217	GSYDAFD	1326	SQSISSY		GAS	1544	GDSTPF
Antibody 44	1000	GYTFTAY	1109	NPNSGG	1218	GSFDAFD	1327	SQSISSY		GAS	1545	GYSSPF

Antibody 45	1001	GYTFTAY	1110	NPKSGG	1219	GSFDAFD	1328	SQSISSY		GAS	1546	GYSSPF
Antibody 46	1002	GYTFTAY	1111	NPNSGG	1220	GSFDAFD	1329	SQSISSY		GAS	1547	GHSTPF
Antibody 47	1003	GYTFTAY	1112	NPKSGG	1221	GSFDAFD	1330	SQSISSY		GAS	1548	GHSTPF
Antibody 48	1004	GYTFTAY	1113	NPNSGG	1222	GSFDAFD	1331	SQSISSY		GAS	1549	GDSTPF
Antibody 49	1005	GYTFTAY	1114	NPKSGG	1223	GSFDAFD	1332	SQSISSY		GAS	1550	GDSTPF
Antibody 50	1006	GYTFTGY	1115	NPKSGG	1224	GSYDAF D	1333	SQSISSY		GAS	1551	GDSTPF
Antibody 51	1007	GYTFTGY	1116	NPNSGG	1225	GSYDAF D	1334	SQSISSY		GAS	1552	GDSTPF
Antibody 52	1008	GYTFTGY	1117	NPKSGG	1226	GSYDAF D	1335	SQSISSY		GAS	1553	GDSTPF
Antibody 53	1009	GYTFTGY	1118	HPNSGG	1227	GSYDAF D	1336	SQSISSY		GAS	1554	GYSSPF
Antibody 54	1010	GYTFTGY	1119	HPKSGG	1228	GSYDAF D	1337	SQSISSY		GAS	1555	GYSSPF
Antibody 55	1011	GYTFTGY	1120	NPKSGG	1229	GSFDAFD	1338	SQSISRY		GAS	1556	GDSSPF
Antibody 56	1012	GYTFTGY	1121	NPNSGG	1230	GSFDAFD	1339	SQSISSY		GAS	1557	GYSSPF
Antibody 57	1013	GYTFTGY	1122	NPKSGG	1231	GSFDAFD	1340	SQSISSY		GAS	1558	GYSSPF
Antibody 58	1014	GYTFTGY	1123	NPNSGG	1232	GSFDAFD	1341	SQSISNY		GTS	1559	GYSSPF
Antibody 59	1015	GYTFTGY	1124	NPKSGG	1233	GSFDAFD	1342	SQSISNY		GTS	1560	GYSSPF
Antibody 60	1016	GYTFTGY	1125	NPNSGG	1234	GSFDAFD	1343	SQSISSY		GAS	1561	GYSSPF
Antibody 61	1017	GYTFTGY	1126	NPKSGG	1235	GSFDAFD	1344	SQSISSY		GAS	1562	GYSSPF
Antibody 62	1018	GYTFTGY	1127	NPNSGG	1236	GSFDAFD	1345	SQSISSY		GAS	1563	GDNTPF
Antibody 63	1019	GYTFTGY	1128	NPKSGG	1237	GSFDAFD	1346	SQSISSY		GAS	1564	GDNTPF

Antibody 64	1020	GYTFTGY	1129	NPNSGG	1238	GSFDAFD	1347	SQSISSY		GAS	1565	GHSTPF
Antibody 65	1021	GYTFTGY	1130	NPKSGG	1239	GSFDAFD	1348	SQSISSY		GAS	1566	GHSTPF
Antibody 66	1022	GYTFTGY	1131	KPNSGG	1240	GSYDAF D	1349	SQSISSY		GAS	1567	GYSSPF
Antibody 67	1023	GYTFTGY	1132	KPKSGG	1241	GSYDAF D	1350	SQSISSY		GAS	1568	GYSSPF
Antibody 68	1024	GYTFTAY	1133	NPNSGG	1242	GSFDAFD	1351	SQSISSY		GAS	1569	GHSTPF
Antibody 69	1025	GYTFTAY	1134	NPKSGG	1243	GSFDAFD	1352	SQSISSY		GAS	1570	GHSTPF
Antibody 70	1026	GYTFTGY	1135	NPNSGG	1244	GSFDAFD	1353	SQTISSY		GAS	1571	GDSTPF
Antibody 71	1027	GYTFTGY	1136	NPKSGG	1245	GSFDAFD	1354	SQTISSY		GAS	1572	GDSTPF
Antibody 72	1028	GYTFTGY	1137	NPNSGG	1246	GSFDAFD	1355	SQSISKY		GAS	1573	GHSTPF
Antibody 73	1029	GYTFTGY	1138	NPKSGG	1247	GSFDAFD	1356	SQSISKY		GAS	1574	GHSTPF
Antibody 74	1030	GYTFTGY	1139	KPNSGG	1248	GSYDAF D	1357	SQSISSY		GAS	1575	GDSTPF
Antibody 75	1031	GYTFTGY	1140	KPKSGG	1249	GSYDAF D	1358	SQSISSY		GAS	1576	GDSTPF
Antibody 76	1032	GYTFTGY	1141	NPNSGG	1250	GSFDAFD	1359	SQSISSY		GAS	1577	GYSSPF
Antibody 77	1033	GYTFTGY	1142	NPKSGG	1251	GSFDAFD	1360	SQSISSY		GAS	1578	GYSSPF
Antibody 78	1034	GYTFTAY	1143	NPNSGG	1252	GSYDAF D	1361	SLSISSY		GAS	1579	GHSTPF
Antibody 79	1035	GYTFTAY	1144	NPKSGG	1253	GSYDAF D	1362	SLSISSY		GAS	1580	GHSTPF
Antibody 80	1036	GYTFTGY	1145	NPNSGG	1254	GSFDAFD	1363	SQSISSY		GAS	1581	GDSTPF
Antibody 81	1037	GYTFTGY	1146	NPNSGG	1255	GSYDAF D	1364	SQSISSY		GAS	1582	GDSTPF
Antibody 82	1038	GYTFTGY	1147	NPKSGG	1256	GSYDAF D	1365	SQSISSY		GAS	1583	GDSTPF

Antibody 83	1039	GYTFTGY	1148	NPNSGA	1257	GSFDAFD	1366	SRSISSY		GAS	1584	GYSSPF
Antibody 84	1040	GYTFTGY	1149	NPKSGA	1258	GSFDAFD	1367	SRSISSY		GAS	1585	GYSSPF
Antibody 85	1041	GYTFTAY	1150	NPNSGG	1259	GSYDAFD	1368	SQSINSY		GAS	1586	GYSTPF
Antibody 86	1042	GYTFTAY	1151	NPKSGG	1260	GSYDAFD	1369	SQSIQSY		GAS	1587	GYSTPF
Antibody 87	1043	GYTFTAY	1152	NPNSGG	1261	GSYDAFD	1370	SQSISSY		GAS	1588	GDNTPF
Antibody 88	1044	GYTFTAY	1153	NPKSGG	1262	GSYDAFD	1371	SQSISSY		GAS	1589	GDNTPF
Antibody 89	1045	GYTFTGY	1154	NPKSGG	1263	GSYDAFD	1372	SQSINSY		GAS	1590	GYSTPF
Antibody 90	1046	GYTFTGY	1155	NPKSGG	1264	GSYDAFD	1373	SQSIQSY		GAS	1591	GYSTPF
Antibody 91	1047	GYTFTAY	1156	NPNSGG	1265	GSFDAFD	1374	SQSISSY		GAS	1592	GDSTPF
Antibody 92	1048	GYTFTAY	1157	NPKSGG	1266	GSFDAFD	1375	SQSISSY		GAS	1593	GDSTPF
Antibody 93	1049	GYTFTGY	1158	NPNSGG	1267	GSFDAFD	1376	SLSISSY		GAS	1594	GHSTPF
Antibody 94	1050	GYTFTGY	1159	NPKSGG	1268	GSFDAFD	1377	SLSISSY		GAS	1595	GHSTPF
Antibody 95	1051	GYTFTGY	1160	NPNSGG	1269	GSFDAFD	1378	SQSISSY		GAS	1596	GYSSPF
Antibody 96	1052	GYTFTGY	1161	NPKSGG	1270	GSFDAFD	1379	SQTISRY		GAS	1597	SYSTPF
Antibody 97	1053	GYTFTAY	1162	NPNSGG	1271	GSYDAFD	1380	SQTISRY		GAS	1598	GYSTPF
Antibody 98	1054	GYTFTGY	1163	NPKSGG	1272	GSFDAFD	1381	SQSISSY		GAS	1599	GDSTPF
Antibody 99	1055	GYTFTGY	1164	NPNSGG	1273	GSFDAFD	1382	SQSISSY		GAS	1600	GYSSPF
Antibody 100	1056	GYTFTGY	1165	NPNSGG	1274	GSFDAFD	1383	SQSISRY		GAS	1601	GDSSPF
Antibody 101	1057	GYTFTGY	1166	NPNSGG	1275	GSYDAFD	1384	SQSISRY		GAS	1602	GYSTLF

Antibody 102	1058	GYTFNG Y	1167	NPNSGG	1276	GSFDAFD	1385	SQSISSY		GAS	1603	GYSSPF
Antibody 103	1059	GYTFTGY	1168	NPNSGG	1277	GSYDAF D	1386	SQSISSY		GAS	1604	GYSNPF
Antibody 104	1060	GYTFTAY	1169	NPNSGG	1278	GSIDAFD	1387	SQSISSY		GAS	1605	GFSTPF
Antibody 105	1061	GYTFTAY	1170	NPNSGG	1279	GSYDAF D	1388	SQSISSY		GAS	1606	GYSSPF
Antibody 106	1062	GYTFTGY	1171	NPNSGG	1280	GSFDAFD	1389	SQSISRY		GAS	1607	GYSSPF
Antibody 107	1063	GYTFTGY	1172	NPNSGG	1281	GSFDAFD	1390	SQSISSY		GAS	1608	GDSTPF
Antibody 108	1064	GYTFTGY	1173	NPNSGG	1282	GSFDAFD	1391	SQSISSF		GAS	1609	GDSTPF
Antibody 109	1065	GYTFTAY	1174	NPNSGG	1283	GSFDAFD	1392	SQSISSY		GAS	1610	GHSTPF
Antibody 110	1066	GYTFTGY	1175	NPKSGG	1284	GSFDAFD	1393	SQSISSY		GAS	1611	GHSTPF
Antibody 111	1067	GYTFTAY	1176	NPNSGG	1285	GSFDAFD	1394	SQSISSY		GAS	1612	GHSTPI
Antibody 112	1068	GYTFTGY	1177	NPNSGG	1286	GSYDAF D	1395	SQSISSY		GAS	1613	GYSSPF
Antibody 113	1069	GYTFTGY	1178	NPNSGG	1287	GSYDAF D	1396	SQSISRY		AAS	1614	GYDTPF
Antibody 114	1070	GYTFTGY	1179	NPKSGG	1288	GSFDAFD	1397	SQDISNY		AAS	1615	GDSTPF
Antibody 115	1071	GYTFTRY	1180	NTNTGN	1289	NWNYVS D	1398	SQSVSDS Y		GAS	1616	YGTSPI
Antibody 116	1072	GYTFTGY	1181	NPKSGG	1290	GSFDAFD	1399	SQSISSY		GAS	1617	AKSFPL
Antibody 117	1073	GYTFTVY	1182	NPNSGG	1291	GSFDAFD	1400	SQSISSY		GAS	1618	GYSSPF
Antibody 118	1074	GYTFTRY	1183	NTNTGN	1292	NWNYDF D	1401	SQSLVHS DGNTY		KIS	1619	VTQFPI
Antibody 119	1075	GYTFTTY	1184	NTNTGN	1293	NWNYDL D	1402	SQSLVHS DGNTY		KIS	1620	ATQFPI

TABLE 1.3 C. AMINO ACID SEQUENCES OF EXEMPLARY CDRS OF ANTIBODY 11-119

IMGT Numbering												
Name	**CDRH1 SEQ ID NO**	**CDRH1**	**CDRH2 SEQ ID NO**	**CDRH2**	**CDRH3 SEQ ID NO**	**CDRH3**	**CDRL1 SEQ ID NO**	**CDRL1**	**CDRL2 SEQ ID NO**	**CDRL2**	**CDRL3 SEQ ID NO**	**CDRL3**
Antibody 11	1621	GYTFTGYY	1730	INPKSGGT	1839	ATGGSFDAFDI	1948	QSISRY		GAS	2166	QQGFSAPLT
Antibody 12	1622	GGSFSGYY	1731	ITHSGIT	1840	ARGQVGTTDYYYFYMDV	1949	QSIRRY		AAS	2167	QQSYRTIT
Antibody 13	1623	GYTFTGYY	1732	INPNSGGT	1841	AVGGSFDAFDI	1950	QSISRY		GAS	2168	QQGDSSPFT
Antibody 14	1624	GYTFTGYY	1733	INPKSGGT	1842	AVGGSFDAFDI	1951	QSISRY		GAS	2169	QQGDSSPFT
Antibody 15	1625	GYTFTGYY	1734	INPNSGGT	1843	AVGGSFDAFDI	1952	QSISSY		GAS	2170	QQGHSTPFT
Antibody 16	1626	GYTFTAYY	1735	INPNSGGT	1844	ATGGSFDAFDI	1953	QSISRY		GAS	2171	QQGDSSPFT
Antibody 17	1627	GYTFTAYY	1736	INPKSGGT	1845	ATGGSFDAFDI	1954	QSISRY		GAS	2172	QQGDSSPFT
Antibody 18	1628	GYTFTAYY	1737	INPNSGGT	1846	AVGGSYDAFDI	1955	QSISSY		GAS	2173	QQGHSTPFT
Antibody 19	1629	GYTFTAYY	1738	INPKSGGT	1847	AVGGSYDAFDI	1956	QSISSY		GAS	2174	QQGHSTPFT
Antibody 20	1630	GYTFTAYY	1739	INPNSGGT	1848	AVGGSFDAFDI	1957	QSISSY		GAS	2175	QQGDSTPFT
Antibody 21	1631	GYTFTAYY	1740	INPKSGGT	1849	AVGGSFDAFDI	1958	QSISSY		GAS	2176	QQGDSTPFT
Antibody 22	1632	GYTFTGYY	1741	INPNSGGT	1850	AVGGSYDAFDI	1959	QSISSY		GAS	2177	QQGDSTPFT
Antibody 23	1633	GYTFTGYY	1742	INPKSGGT	1851	AVGGSYDAFDI	1960	QSISSY		GAS	2178	QQGDSTPFT
Antibody 24	1634	GYTFTGYY	1743	INPNSGGT	1852	AVGGSYDAFDI	1961	QSISSY		GAS	2179	QQGDSTPFT
Antibody 25	1635	GYTFTGYY	1744	INPKSGGT	1853	AVGGSYDAFDI	1962	QSISSY		GAS	2180	QQGDSTPFT
Antibody 26	1636	GYTFTGYY	1745	INPNSGGT	1854	ATGGSFDAFDI	1963	QSISSY		GAS	2181	QQGDSSPFT

Antibody 27	1637	GYTFTGY Y	1746	INPKSGG T	1855	ATGGSFD AFD1	1964	QSISSY		GAS	2182	QQGDSSP FT
Antibody 28	1638	GYTFTGY Y	1747	INPKSGG T	1856	ATGGSFD AFD1	1965	QSISSY		GAS	2183	QQGHSTP FT
Antibody 29	1639	GYTFTGY Y	1748	INPKSGG T	1857	ATGGSFD AFD1	1966	QSISSY		GAS	2184	QQGDSTP FT
Antibody 30	1640	GYTFTGY Y	1749	INPKSGG T	1858	AVGGSY DAFD1	1967	QSISSY		GAS	2185	QQGHSTP FT
Antibody 31	1641	GYTFTGY Y	1750	INPKSGG T	1859	AVGGSY DAFD1	1968	QSISSY		GAS	2186	QQGYSSP FT
Antibody 32	1642	GYTFTAY Y	1751	INPNSGG T	1860	AVGGSF DAFD1	1969	QDISNY		GAS	2187	QQGDSTP FT
Antibody 33	1643	GYTFTAY Y	1752	INPKSGG T	1861	AVGGSF DAFD1	1970	QDISNY		GAS	2188	QQGDSTP FT
Antibody 34	1644	GYTFTGY Y	1753	INPKSGG T	1862	ATGGSFD AFD1	1971	QGISRY		GAS	2189	QQGFSTP FT
Antibody 35	1645	GYTFTGY Y	1754	INPNSGG T	1863	AVGGSY DAFD1	1972	QSISSY		GAS	2190	QQGSSPP FT
Antibody 36	1646	GYTFTGY Y	1755	INPKSGG T	1864	AVGGSY DAFD1	1973	QSISSY		GAS	2191	QQGSSPP FT
Antibody 37	1647	GYTFTAY Y	1756	INPNSGG T	1865	AVGGSY DAFD1	1974	QSISSY		GAS	2192	QQGYSSP FT
Antibody 38	1648	GYTFTAY Y	1757	INPKSGG T	1866	AVGGSY DAFD1	1975	QSISSY		GAS	2193	QQGYSSP FT
Antibody 39	1649	GYTFTAY Y	1758	INPNSGG T	1867	ASGGSFD AFD1	1976	QSISRY		GAS	2194	QQGDSSP FT
Antibody 40	1650	GYTFTAY Y	1759	INPKSGG T	1868	ASGGSFD AFD1	1977	QSISRY		GAS	2195	QQGDSSP FT
Antibody 41	1651	GYTFTGY F	1760	INPKSGG T	1869	AVGGSY DAFD1	1978	QSISSY		GAS	2196	QQGHSTP FT
Antibody 42	1652	GYTFTAY Y	1761	INPNSGG T	1870	AVGGSY DAFD1	1979	QSISSY		GAS	2197	QQGDSTP FT
Antibody 43	1653	GYTFTAY Y	1762	INPKSGG T	1871	AVGGSY DAFD1	1980	QSISSY		GAS	2198	QQGDSTP FT
Antibody 44	1654	GYTFTAY Y	1763	INPNSGG T	1872	AVGGSF DAFD1	1981	QSISSY		GAS	2199	QQGYSSP FT
Antibody 45	1655	GYTFTAY Y	1764	INPKSGG T	1873	AVGGSF DAFD1	1982	QSISSY		GAS	2200	QQGYSSP FT

Antibody 46	1656	GYTFTAY Y	1765	VNPNSG GT	1874	AVGGSF DAFDI	1983	QSISSY		GAS	2201	QQGHSTP FT
Antibody 47	1657	GYTFTAY Y	1766	VNPKSG GT	1875	AVGGSF DAFDI	1984	QSISSY		GAS	2202	QQGHSTP FT
Antibody 48	1658	GYTFTAY Y	1767	INPNSGG T	1876	ATGGSFD AFDI	1985	QSISSY		GAS	2203	QQGDSTP FT
Antibody 49	1659	GYTFTAY Y	1768	INPKSGG T	1877	ATGGSFD AFDI	1986	QSISSY		GAS	2204	QQGDSTP FT
Antibody 50	1660	GYTFTGY Y	1769	INPKSGG T	1878	AVGGSY DAFDI	1987	QSISSY		GAS	2205	QQGDSTP FT
Antibody 51	1661	GYTFTGY Y	1770	INPNSGG T	1879	AVGGSY DAFDI	1988	QSISSY		GAS	2206	QQGDSTP FT
Antibody 52	1662	GYTFTGY Y	1771	INPKSGG T	1880	AVGGSY DAFDI	1989	QSISSY		GAS	2207	QQGDSTP FT
Antibody 53	1663	GYTFTGY Y	1772	IHPNSGG T	1881	AVGGSY DAFDI	1990	QSISSY		GAS	2208	QQGYSSP FT
Antibody 54	1664	GYTFTGY Y	1773	IHPKSGG T	1882	AVGGSY DAFDI	1991	QSISSY		GAS	2209	QQGYSSP FT
Antibody 55	1665	GYTFTGY F	1774	INPKSGG T	1883	ASGGSFD AFDI	1992	QSISRY		GAS	2210	QQGDSSP FT
Antibody 56	1666	GYTFTGY Y	1775	INPNSGG T	1884	ATGGSFD AFDI	1993	QSISSY		GAS	2211	QQGYSSP FT
Antibody 57	1667	GYTFTGY Y	1776	INPKSGG T	1885	ATGGSFD AFDI	1994	QSISSY		GAS	2212	QQGYSSP FT
Antibody 58	1668	GYTFTGY Y	1777	INPNSGG P	1886	ATGGSFD AFDI	1995	QSISNY		GTS	2213	QQGYSSP FT
Antibody 59	1669	GYTFTGY Y	1778	INPKSGG P	1887	ATGGSFD AFDI	1996	QSISNY		GTS	2214	QQGYSSP FT
Antibody 60	1670	GYTFTGY F	1779	INPNSGG T	1888	ATGGSFD AFDI	1997	QSISSY		GAS	2215	QQGYSSP FT
Antibody 61	1671	GYTFTGY F	1780	INPKSGG T	1889	ATGGSFD AFDI	1998	QSISSY		GAS	2216	QQGYSSP FT
Antibody 62	1672	GYTFTGY Y	1781	INPNSGG T	1890	ATGGSFD AFDV	1999	QSISSY		GAS	2217	QQGDNT PFT
Antibody 63	1673	GYTFTGY Y	1782	INPKSGG T	1891	ATGGSFD AFDV	2000	QSISSY		GAS	2218	QQGDNT PFT
Antibody 64	1674	GYTFTGY Y	1783	INPNSGG T	1892	ATGGSFD AFDI	2001	QSISSY		GAS	2219	QQGHSTP FT

Antibody 65	1675	GYTFTGY Y	1784	INPKSGG T	1893	ATGGSFD AFDI	2002	QSISSY		GAS	2220	QQGHSTP FT
Antibody 66	1676	GYTFTGY Y	1785	IKPNSGG T	1894	AVGGSY DAFDI	2003	QSISSY		GAS	2221	QQGYSSP FT
Antibody 67	1677	GYTFTGY Y	1786	IKPKSGG T	1895	AVGGSY DAFDI	2004	QSISSY		GAS	2222	QQGYSSP FT
Antibody 68	1678	GYTFTAY Y	1787	VNPNSG GT	1896	AVGGSF DAFDI	2005	QSISSY		GAS	2223	QQGHSTP FT
Antibody 69	1679	GYTFTAY Y	1788	VNPKSG GT	1897	AVGGSF DAFDI	2006	QSISSY		GAS	2224	QQGHSTP FT
Antibody 70	1680	GYTFTGY Y	1789	INPNSGG T	1898	ATGGSFD AFDI	2007	QTISSY		GAS	2225	QQGDSTP FT
Antibody 71	1681	GYTFTGY Y	1790	INPKSGG T	1899	ATGGSFD AFDI	2008	QTISSY		GAS	2226	QQGDSTP FT
Antibody 72	1682	GYTFTGY Y	1791	INPNSGG T	1900	ATGGSFD AFDI	2009	QSISKY		GAS	2227	QQGHSTP FT
Antibody 73	1683	GYTFTGY Y	1792	INPKSGG T	1901	ATGGSFD AFDI	2010	QSISKY		GAS	2228	QQGHSTP FT
Antibody 74	1684	GYTFTGY Y	1793	IKPNSGG T	1902	AVGGSY DAFDI	2011	QSISSY		GAS	2229	QQGDSTP FT
Antibody 75	1685	GYTFTGY Y	1794	IKPKSGG T	1903	AVGGSY DAFDI	2012	QSISSY		GAS	2230	QQGDSTP FT
Antibody 76	1686	GYTFTGY Y	1795	INPNSGG T	1904	ATGGSFD AFDI	2013	QSISSY		GAS	2231	QQGYSSP FT
Antibody 77	1687	GYTFTGY Y	1796	INPKSGG T	1905	ATGGSFD AFDI	2014	QSISSY		GAS	2232	QQGYSSP FT
Antibody 78	1688	GYTFTAY Y	1797	INPNSGG T	1906	AVGGSY DAFDI	2015	LSISSY		GAS	2233	QQGHSTP FT
Antibody 79	1689	GYTFTAY Y	1798	INPKSGG T	1907	AVGGSY DAFDI	2016	LSISSY		GAS	2234	QQGHSTP FT
Antibody 80	1690	GYTFTGY Y	1799	INPNSGG T	1908	ATGGSFD AFDI	2017	QSISSY		GAS	2235	QQGDSTP FT
Antibody 81	1691	GYTFTGY Y	1800	INPNSGG T	1909	AVGGSY DAFDI	2018	QSISSY		GAS	2236	QQGDSTP FT
Antibody 82	1692	GYTFTGY Y	1801	INPKSGG T	1910	AVGGSY DAFDI	2019	QSISSY		GAS	2237	QQGDSTP FT
Antibody 83	1693	GYTFTGY Y	1802	INPNSGA T	1911	ATGGSFD AFDI	2020	RSISSY		GAS	2238	QQGYSSP FT

Antibody 84	1694	GYTFTGY Y	1803	INPKSGA T	1912	ATGGSFD AFDI	2021	RSISSY		GAS	2239	QQGYSSP FT
Antibody 85	1695	GYTFTAY Y	1804	INPNSGG T	1913	AVGGSY DAFDI	2022	QSINSY		GAS	2240	QQGYSTP FT
Antibody 86	1696	GYTFTAY Y	1805	INPKSGG T	1914	AVGGSY DAFDI	2023	QSIQSY		GAS	2241	QQGYSTP FT
Antibody 87	1697	GYTFTAY Y	1806	INPNSGG T	1915	AVGGSY DAFDI	2024	QSISSY		GAS	2242	QQGDNT PFT
Antibody 88	1698	GYTFTAY Y	1807	INPKSGG T	1916	AVGGSY DAFDI	2025	QSISSY		GAS	2243	QQGDNT PFT
Antibody 89	1699	GYTFTGY Y	1808	INPKSGG T	1917	ATGGSY DAFDI	2026	QSINSY		GAS	2244	QQGYSTP FT
Antibody 90	1700	GYTFTGY Y	1809	INPKSGG T	1918	ATGGSY DAFDI	2027	QSIQSY		GAS	2245	QQGYSTP FT
Antibody 91	1701	GYTFTAY Y	1810	INPNSGG T	1919	AVGGSF DAFDI	2028	QSISSY		GAS	2246	QQGDSTP FT
Antibody 92	1702	GYTFTAY Y	1811	INPKSGG T	1920	AVGGSF DAFDI	2029	QSISSY		GAS	2247	QQGDSTP FT
Antibody 93	1703	GYTFTGY Y	1812	INPNSGG T	1921	AVGGSF DAFDI	2030	LSISSY		GAS	2248	QQGHSTP FT
Antibody 94	1704	GYTFTGY Y	1813	INPKSGG T	1922	AVGGSF DAFDI	2031	LSISSY		GAS	2249	QQGHSTP FT
Antibody 95	1705	GYTFTGY Y	1814	INPNSGG T	1923	ATGGSFD AFDI	2032	QSISSY		GAS	2250	QQGYSSP FT
Antibody 96	1706	GYTFTGY Y	1815	INPKSGG T	1924	ATGGSFD AFDI	2033	QTISRY		GAS	2251	QQSYSTP FT
Antibody 97	1707	GYTFTAY Y	1816	INPNSGG T	1925	AVGGSY DAFDI	2034	QTISRY		GAS	2252	QQGYSTP FT
Antibody 98	1708	GYTFTGY F	1817	INPKSGG T	1926	ASGGSFD AFDI	2035	QSISSY		GAS	2253	QQGDSTP FT
Antibody 99	1709	GYTFTGY Y	1818	INPNSGG T	1927	ATGGSFD AFDI	2036	QSISSY		GAS	2254	QQGYSSP FT
Antibody 100	1710	GYTFTGY Y	1819	INPNSGG T	1928	ASGGSFD AFDI	2037	QSISRY		GAS	2255	QQGDSSP FT
Antibody 101	1711	GYTFTGY Y	1820	INPNSGG T	1929	AVGGSY DAFDI	2038	QSISRY		GAS	2256	QQGYSTL FT
Antibody 102	1712	GYTFNG YY	1821	INPNSGG T	1930	ATGGSFD AFDI	2039	QSISSY		GAS	2257	QQGYSSP FT

Antibody 103	1713	GYTFTGY Y	1822	INPNSGG T	1931	AVGGSY DAFDI	2040	QSISSY		GAS	2258	QQGYSN PFT
Antibody 104	1714	GYTFTAY Y	1823	INPNSGG T	1932	ASGGSID AFDI	2041	QSISSY		GAS	2259	QQGFSTP FT
Antibody 105	1715	GYTFTAY Y	1824	INPNSGG T	1933	AVGGSY DAFDI	2042	QSISSY		GAS	2260	QQGYSSP FT
Antibody 106	1716	GYTFTGY Y	1825	INPNSGG T	1934	AVGGSF DAFDI	2043	QSISRY		GAS	2261	QQGYSSP FT
Antibody 107	1717	GYTFTGY Y	1826	INPNSGG T	1935	VTGGSFD AFDV	2044	QSISSY		GAS	2262	QQGDSTP FT
Antibody 108	1718	GYTFTGY Y	1827	INPNSGG T	1936	TSGGSFD AFDI	2045	QSISSF		GAS	2263	QQGDSTP FT
Antibody 109	1719	GYTFTAY Y	1828	INPNSGG T	1937	ATGGSFD AFDI	2046	QSISSY		GAS	2264	QQGHSTP FT
Antibody 110	1720	GYTFTGY Y	1829	INPKSGG T	1938	ASGGSFD AFDI	2047	QSISSY		GAS	2265	QQGHSTP FT
Antibody 111	1721	GYTFTAY Y	1830	INPNSGG T	1939	AVGGSF DAFDI	2048	QSISSY		GAS	2266	QQGHSTP IT
Antibody 112	1722	GYTFTGY Y	1831	INPNSGG T	1940	ATGGSY DAFDI	2049	QSISSY		GAS	2267	QQGYSSP FT
Antibody 113	1723	GYTFTGY Y	1832	INPNSGG T	1941	ATGGSY DAFDI	2050	QSISRY		AAS	2268	QQGYDT PFT
Antibody 114	1724	GYTFTGY Y	1833	INPKSGG T	1942	ATGGSFD AFDI	2051	QDISNY		AAS	2269	QQGDSTP FT
Antibody 115	1725	GYTFTRY G	1834	INTNTGN P	1943	ARDNWN YVSDY	2052	QSVSDSY		GAS	2270	QQYGTSP IT
Antibody 116	1726	GYTFTGY Y	1835	INPKSGG T	1944	ATGGSFD AFDI	2053	QSISSY		GAS	2271	QQAKSFP LT
Antibody 117	1727	GYTFTVY Y	1836	INPNSGG T	1945	ASGGSFD AFDI	2054	QSISSY		GAS	2272	QQGYSSP FT
Antibody 118	1728	GYTFTRY G	1837	INTNTGN P	1946	ARDNWN YDFDY	2055	QSLVHSD GNTY		KIS	2273	MQVTQF PIT
Antibody 119	1729	GYTFTTY G	1838	INTNTGN P	1947	ARDNWN YDLDY	2056	QSLVHSD GNTY		KIS	2274	MQATQF PIT

[0195] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising a CDR1, CDR2, and CDR3 as listed in TABLE 1.1 A, TABLE 1.1 B, TABLE 1.1 C, TABLE 1.2 A, TABLE 1.2 B, TABLE 1.2 C, TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 1-10 and 313-421, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 11-20 and 422-530, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 21-30 and 531-639.

[0196] In some embodiments, the TL1A binding protein comprises a light chain variable region comprising a CDR1, CDR2, and CDR3 as listed in TABLE 1.1 A, TABLE 1.1 B, TABLE 1.1 C, TABLE 1.2 A, TABLE 1.2 B, TABLE 1.2 C, TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C. In some embodiments, the TL1A binding protein comprises a light chain variable region comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C. In some embodiments, the TL1A binding protein comprises a light chain variable region comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 31-40 and 640-748, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 41-50 and 749-857, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 51-60 and 858-966.

[0197] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 1-10 and 313-421, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 11-20 and 422-530, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 21-30 and 531-639; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID

NOs: 31-40 and 640-748, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 41-50 and 749-857, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 51-60 and 858-966. In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C. In some embodiments, the TL1A binding protein described herein, wherein the VH comprises a sequence having at least 80% sequence identity to any one of the amino acid sequences listed in TABLE 2.1 and TABLE 2.2, and the VL comprises a sequence having at least 80% sequence identity to any one of the amino acid sequences listed in TABLE 2.1 and TABLE 2.2.

[0198] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 61-70 and 967-1075, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 71-80 and 1076-1184, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 81-90 and 1185-1293.

[0199] In some embodiments, the TL1A binding protein comprises a light chain variable region comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 91-100 and 1294-1402, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 111-120 and 1512-1620.

[0200] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region comprising i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 61-70 and 967-1075, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 71-80 and 1076-1184, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 81-90 and 1185-1293; and b) a light chain variable region

comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 91-100 and 1294-1402, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.2 A, TABLE 1.2 B, and TABLE 1.2 C, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 111-120 and 1512-1620.

[0201] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 121-130 and 1621-1729, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 131-140 and 1730-1838, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 141-150 and 1839-1947.

[0202] In some embodiments, the TL1A binding protein comprises a light chain variable region comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 151-160 and 1948-2056, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 171-180 and 2166-2274.

[0203] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 121-130 and 1621-1729, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 131-140 and 1730-1838, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 141-150 and 1839-1947; and b) a light chain variable region comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 151-160 and 1948-2056, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.3 A, TABLE 1.3 B, and TABLE 1.3 C, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 171-180 and 2166-2274.

[0204] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51.

[0205] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2,

(ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52.

[0206] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53.

[0207] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54.

[0208] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 25; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 55.

[0209] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 26; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 56.

[0210] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 27; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 57.

[0211] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 28; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 58.

[0212] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 29; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 59.

[0213] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 30; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 60.

[0214] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ

ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866.

[0215] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886.

[0216] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890.

[0217] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 567; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894.

[0218] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896.

[0219] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572; and b) a light chain

variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899.

[0220] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910.

[0221] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916.

[0222] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917.

[0223] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918.

[0224] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, and (iii) a

CDR3 having an amino acid sequence according to SEQ ID NO: 606; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933.

[0225] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939.

[0226] In some embodiments, the TL1A binding protein comprises a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945.

[0227] Amino acid sequences of exemplary heavy chain variable regions (VH) and light chain variable regions (VL) of TL1A binding proteins are provided in TABLE 2.1 and TABLE 2.2.

TABLE 2.1. SEQUENCES OF HEAVY CHAIN VARIABLE REGIONS (VH) AND LIGHT CHAIN VARIABLE REGIONS (VL) OF TL1A BINDING PROTEINS (ANTIBODY 5-10)

Antibody	SEQ ID NO	VH	SEQ ID NO	VL
Antibody 5	185	EVQLVESGGGLVKPGGSLRLSCAAFGFTFSNVWMNWVRQAPGKGLEWVGLIKSKTDAGTTDYAAPVKGRFTISRDDSKNMLYLQMNSLKTEDTAVYYCTTDRGWGENYWGQGTLVTVSS	195	ENVLTQSPGTLSLSPGERATLSCRASQIFSSSYLVWYQKKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSPYTFGQGTKLEIK
Antibody 6	186	EVQLVESGGGLVKPGGSLRLSCAASGFIFSNVWMNWVRQAPGKGLEWVGRIKSKIDAGTTDYVAPVKGRFTISRDDSKNTLSLQMNSLKTEDTAVYYCITDRGWGENYWGQGTLVTVSS	196	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLVWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTFTISRLEPEDFAVYYCQQYGGSPYTFGQGTKLEIK

Antibody 7	187	EVQLVESGGGLVKPGGS LRLSCAASGFTFSNAWM SWVRQAPGKGLEWVGRI KSKIDAGTTDYAAPVKG RFTISRDDSRNTLYLQMN SLRTEDTADYYCTTDLG WGENYWGQGTLVTVSS	197	EIVLTQSPGTLSLSPGERATLSCR ASQSISRSYLVWYEQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTD FTLTISRLEPEDFAVYYCHQYGSS PYTFGQGTKLEIK
Antibody 8	188	EVQLVESGGGLVKPGGS LRLSCAASGFTFSNAWM SWVRQAPGKGLEWVGRI KSKIDAGTTDYAAPVKG RFTISRDDSKNTLYLQM NSLKTEDTAVYYCTTDL GWGENYWGQGTLVTVS S	198	ENVLTQSPGTLSLSPGERATLSCR ASQRVSSSYLVWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGT DFTLTISRLEPEDFAVYYCQQYGS SPYTFGQGTKLESK
Antibody 9	189	EVQLVESGGGLVKPGGS LRLSCAASGFTFSNAWM TWVRQAPGKGLEWVGR IKSKIDAGTTDYAAPVKG RFTISRYDSKNTLYLQM NSLKTEDTAVYYCTTDL GWGENYWGQGTLVTVS S	199	ENVLTQSPGTLSLSPGERATLSCR ASQRVSSSYLVWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGT DFTLTISRLEPEDFAVYYCQQYGS SPYTFGQGTKLEIK
Antibody 10	190	EVQLVESGGGLVKPGGS LRLSCAASGFTFSNAWM TWVRQAPGKGLEWVGR IKSKIDAGTTDYAAPVKG RFTISRDDSKNTLYLQM NSLKTEDTAVYYCTTDL GWGENYWGQGTLVTVS S	200	ENVLTQSPGTLSLSPGERATLSCR ASQRVSSSYLVWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGT DFTLTISRLEPEDFAVYYCQQYGS SPYTFGQGTKLEIK

TABLE 2.2. SEQUENCES OF HEAVY CHAIN VARIABLE REGIONS (VH) AND LIGHT CHAIN VARIABLE REGIONS (VL) OF TL1A BINDING PROTEINS (ANTIBODY 1-4, 11-119)

Antibody	**SEQ ID NO**	**VH**	**SEQ ID NO**	**VL**
Antibody 1	181	QVKLVESGGGVVQPGRS LRLSCAASGFTFSSYAM HWVRQAPGKGLEWVAV VSYEGSQNYYADSVKGR FTISRDNSKNTLYLQMNS LRAEDTAVYYCANLESA YYFDYWGQGTLVTVSS	191	DIVMTQSPLSLPVTPGEPASISCRS SQSLLYSNGYNSLDWYLQKTGQ SPQLLIYLGSNRASGVPDRFSGSG SGTDFTLKISRVEAEDVGVYYCM QALQTPYTFGQGTKLEIK
Antibody 2	182	QVQLQESGPGLVKPSETL SLTCTVSGGSISSYYWSW IRQPPGKGLEWIGLIYYS GSTNYNPSLKSRVTISVD TSKNQFSLKLSSVTAADT AVYYCARADVVTIDYW GQGTLVTVSS	192	DIQMTQSPSSLSASVGDRVTITCR ASQTISSYFNWYQQKAGEAPKLL IYAASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQSYSTPI TFGQGTRLEIK

Antibody 3	183	EVQLVESGGGLVKPGGS LRLSCAASGFTFSTYNM NWVRQAPGKGLEWISSI HSSSNYLYYADSVKGRF TISRDNAKNSLYLQMNS LRAEDTAVYYCATDRA MVDFDYWGQGTLVTVS S	193	DIQMTQSPSSLSASVGDRVTITCR ASQSISTYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFAAYYCQQSYSTP LTFGGGTRVEIK
Antibody 4	184	QVQLQQSGPGLVKPSQT LSLTCAISGDSVSSNSAT WNWIRQSPSRGLEWLGR TYYRSKWYNDYAVSVK SRLTINPDTSKNQFSLQL NSVTPEDTAVYYCAREA VGPTKDFDYWGQGTLVP VSS	194	DIQMTQSPSSLSASVGDRVTITCR ASQSFSSYLNWYQQTPGKAPKLL IYAASSLQSGVPSRFSGSGSGTYF TLTISSLQPEDLATYYCQQSYFTP RTFGQGTKVEIK
Antibody 11	2275	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTIYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYSCATGGS FDAFDIWGQGTMVTVSS	2384	DIQMTQSPSSLSASVGDRVTITCR ASQSISRYLYWYQQKPGKAPKLL IYGASSLQSGVPSRFSGSGSGTDF TLTVSSMQPEDFATYYCQQGFSA PLTFGGGTKVDIK
Antibody 12	2276	QVQLQQWGAGLLKPSET LSLTCAVYGGSFSGYYW SWIRQPPGKGLEWIGEIT HSGITNYNPSLESRVTMS VDTSKNQFSLKLSSVTA ADTAVYYCARGQVGTT DYYYFYMDVWGKGTLV TVSS	2385	DIQMTQSPSSLSASVGDRVTITCR ASQSIRRYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFASYFCQQSYRTIT FGQGTKLEIK
Antibody 13	2277	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQNFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS FDAFDIWGQGTMVTVSS	2386	DIQLTQSPSSLSASVGDRVTITCR ASQSISRYLNWYQQKPGKAPKILI YGASSVQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSSP FTFGPGTKVDIK
Antibody 14	2278	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQNFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS FDAFDIWGQGTMVTVSS	2387	DIQLTQSPSSLSASVGDRVTITCR ASQSISRYLNWYQQKPGKAPKILI YGASSVQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSSP FTFGPGTKVDIK
Antibody 15	2279	QVQLVQSGPEVEKPGAS VKVSCKASGYTFTGYYM HWMRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMDL SGLRSDDTAVYYCAVGG SFDAFDIWGQGTMVTVS S	2388	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGHSTP FTFGPGTKVEIK

Antibody 16	2280	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWIGW INPNSGGTNYAQSFQGR VTMTRDTSITTAYMDLS RLRSDDTAIYYCATGGSF DAFDIWGQGTMVTVSS	2389	DIVMTQSPSSLSASVGDRVTITCR ASQSISRYLNWYQQKPGKAPKILI YGASSVQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSSP FTFGPGTKVEIK
Antibody 17	2281	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWIGW INPKSGGTNYAQSFQGR VTMTRDTSITTAYMDLS RLRSDDTAIYYCATGGSF DAFDIWGQGTMVTVSS	2390	DIVMTQSPSSLSASVGDRVTITCR ASQSISRYLNWYQQKPGKAPKILI YGASSVQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSSP FTFGPGTKVEIK
Antibody 18	2282	QVQLVQSGAEVKEPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQQFQG RVTMTRDTSISTAYMELS RLTSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2391	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLSISSLQPEDFATYYCQQGHSTP FTFGPGTKLEIK
Antibody 19	2283	QVQLVQSGAEVKEPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQQFQG RVTMTRDTSISTAYMELS RLTSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2392	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLSISSLQPEDFATYYCQQGHSTP FTFGPGTKLEIK
Antibody 20	2284	EVQLVQSGVEVKKPGAS VKVSCQASGYTFTAYYI HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDSSISTAYMELS RLRSDDTAVYYCAVGGS FDAFDIWGQGTMVTVSS	2393	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVDIK
Antibody 21	2285	EVQLVQSGVEVKKPGAS VKVSCQASGYTFTAYYI HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDSSISTAYMELS RLRSDDTAVYYCAVGGS FDAFDIWGQGTMVTVSS	2394	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVDIK
Antibody 22	2286	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYL HWVRQAPGQGLEWMG WINPNSGGTNFAQKFQG RVTMTRDTSINTAYMEL SRLRSDDTAVYYCAVGG SYDAFDIWGQGTMVTVS S	2395	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKVPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSTP FTFGPGTKVDIK
Antibody 23	2287	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYL HWVRQAPGQGLEWMG WINPKSGGTNFAQKFQG RVTMTRDTSINTAYMEL	2396	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKVPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSTP FTFGPGTKVDIK

		SRLRSDDTAVYYCAVGG SYDAFDIWGQGTMVTVS S		
Antibody 24	2288	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS GLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2397	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQEKPGKAPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSTP FTFGPGTKVEIK
Antibody 25	2289	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS GLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2398	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQEKPGKAPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSTP FTFGPGTKVEIK
Antibody 26	2290	QVQLVQSGAEVKKPGAS VKFSCKASGYTFTGYYL HWVRQAPGQGLEWMG WINPNSGGTNYAQRFQG RVTMTRDTSINTAYMEL SRLRSDDTAVYYCATGG SFDAFDIWGQGTMVTVS S	2399	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQSPGKAPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSSP FTFGPGTKVEIK
Antibody 27	2291	QVQLVQSGAEVKKPGAS VKFSCKASGYTFTGYYL HWVRQAPGQGLEWMG WINPKSGGTNYAQRFQG RVTMTRDTSINTAYMEL SRLRSDDTAVYYCATGG SFDAFDIWGQGTMVTVS S	2400	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQSPGKAPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSSP FTFGPGTKVEIK
Antibody 28	2292	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTIYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYSCATGGS FDAFDIWGQGTMVTVSS	2401	DIVLTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGHSTP FTFGPGTKVDIK
Antibody 29	2293	EVQLVESGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCATGGS FDAFDIWGQGTMVTVSS	2402	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKLEIK
Antibody 30	2294	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTSYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2403	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGHSTP FTFGPGTKLEIK

Antibody 31	2295	EVQLVESGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2404	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVEIK
Antibody 32	2296	EVQLVQSGAEVRKPGAS VKVSCKASGYTFTAYYI HWVRQAPGQGLEWMG WINPNSGGTNYAQNFQG RVTMTRDTSISTAYMELS RLRPDDTAVYFCAVGGS FDAFDIWGQGTMVTVSS	2405	DIQLTQSPSSLSASVGDRVTITCQ ASQDISNYLNWYQQKPGKAPKIL IYGASSLQSGVPSRFSGSGSGTDF TLAISSLQPEDYATYYCQQGDST PFTFGPGTKVEIK
Antibody 33	2297	EVQLVQSGAEVRKPGAS VKVSCKASGYTFTAYYI HWVRQAPGQGLEWMG WINPKSGGTNYAQNFQG RVTMTRDTSISTAYMELS RLRPDDTAVYFCAVGGS FDAFDIWGQGTMVTVSS	2406	DIQLTQSPSSLSASVGDRVTITCQ ASQDISNYLNWYQQKPGKAPKIL IYGASSLQSGVPSRFSGSGSGTDF TLAISSLQPEDYATYYCQQGDST PFTFGPGTKVEIK
Antibody 34	2298	QVQLVQSGAEVKRPGAA VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQNFQG RVTMTRDTSISTAYMELS RLTSDDTAMYYCATGGS FDAFDIWGQGTMVTVSS	2407	DIQMTQSPSSVSASVGDRVTITCR ASQGISRYLHWYQQKPGKAPNFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGFSTP FTFGPGTKLEIK
Antibody 35	2299	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2408	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYHCQQGSSPP FTFGPGTKLEIK
Antibody 36	2300	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2409	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYHCQQGSSPP FTFGPGTKLEIK
Antibody 37	2301	EVQLVQSGAEVKSPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPNSGGTKYAQKFQG RVTVTRDTSISTAYMELN RLTSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2410	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPNFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVDIK
Antibody 38	2302	EVQLVQSGAEVKSPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPKSGGTKYAQKFQG RVTVTRDTSISTAYMELN	2411	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPNFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVDIK

		RLTSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS		
Antibody 39	2303	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTAYYL HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCASGGS FDAFDIWGQGTMVTVSS	2412	DIQMTQSPSSLSASVGDRVTITCR ASQSISRYLNWYQQKPGKAPKILI YGASSVQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSSP FTFGPGTKLEIK
Antibody 40	2304	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTAYYL HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCASGGS FDAFDIWGQGTMVTVSS	2413	DIQMTQSPSSLSASVGDRVTITCR ASQSISRYLNWYQQKPGKAPKILI YGASSVQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSSP FTFGPGTKLEIK
Antibody 41	2305	QVQLVESGAEVKKPGAS VKVSCKASGYTFTGYFIH WVRQAPGQGLEWMGWI NPKSGGTNYAQKFQDRV TMTRDTSISTAYMELSRL RSDDTAVYYCAVGGSY DAFDIWGQGTMVTVSS	2414	DIVLTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFVTYYCQQGHSTP FTFGPGTKVDIK
Antibody 42	2306	QVQLVQSGAEVKSPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPNSGGTKYAQKFQG RVTVTRDTSISTAYMELN RLTSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2415	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQSPGKAPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSTP FTFGPGTKVEIK
Antibody 43	2307	QVQLVQSGAEVKSPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPKSGGTKYAQKFQG RVTVTRDTSISTAYMELN RLTSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2416	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQSPGKAPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSTP FTFGPGTKVEIK
Antibody 44	2308	QVQLVQSGAEVKKPGAS VRVSCKASGYTFTAYYI HWVRQAPGQGLEWMG WINPNSGGTSSAQKFQG RVTMTRDTSISTAYMDL SRLRSDDTAVYYCAVGG SFDAFDIWGQGTMVTVS S	2417	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYSCQQGYSSP FTFGPGTKVDIK
Antibody 45	2309	QVQLVQSGAEVKKPGAS VRVSCKASGYTFTAYYI HWVRQAPGQGLEWMG WINPKSGGTSSAQKFQG RVTMTRDTSISTAYMDL SRLRSDDTAVYYCAVGG SFDAFDIWGQGTMVTVS S	2418	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYSCQQGYSSP FTFGPGTKVDIK

Antibody 46	2310	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTAYYI HWVRQAPGQGLEWMG WVNPNSGGTNYAQSFQ GRVTMTGDTSITTAYMD LSELRSDDTAVYYCAVG GSFDAFDIWGQGTMVTV SS	2419	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGHSTP FTFGPGTKVDIK
Antibody 47	2311	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTAYYI HWVRQAPGQGLEWMG WVNPKSGGTNYAQSFQ GRVTMTGDTSITTAYMD LSELRSDDTAVYYCAVG GSFDAFDIWGQGTMVTV SS	2420	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGHSTP FTFGPGTKVDIK
Antibody 48	2312	QVQLVQSGAEVKSPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPNSGGTKYAQKFQG RVTVTRDTSISTAYMELN RLTSDDTAVYYCATGGS FDAFDIWGQGTMVTVSS	2421	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVDIK
Antibody 49	2313	QVQLVQSGAEVKSPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPKSGGTKYAQKFQG RVTVTRDTSISTAYMELN RLTSDDTAVYYCATGGS FDAFDIWGQGTMVTVSS	2422	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVDIK
Antibody 50	2314	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYI HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2423	DIVLTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVDIK
Antibody 51	2315	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2424	DIVLTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVDIK
Antibody 52	2316	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2425	DIVLTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVDIK
Antibody 53	2317	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WIHPNSGGTNSAQKFQG	2426	DIVMTQSPSSLSASEGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF

		RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS		TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVEIK
Antibody 54	2318	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WIHPKSGGTNTAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2427	DIVMTQSPSSLSASEGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVEIK
Antibody 55	2319	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYFIH WVRQAPGQGLEWMGWI NPKSGGTNYAQKFQGRV TMTRDTSISTAYMELSRL SSDDTAVYYCASGGSFD AFDIWGQGTMVTVSS	2428	DIQMTQSPSSLSASVGDRVTITCR ASQSISRYLNWYQQKPGKAPKILI YGASSVQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSSP FTFGPGTKVEIK
Antibody 56	2320	QVQLVQAGAEVKKPGA SVKVSCKASGYTFTGYY MHWVRQAPGQGLEWM GWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYME LSRLRSDDTAVYYCATG GSFDAFDIWGQGTMVTV SS	2429	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVEIK
Antibody 57	2321	QVQLVQAGAEVKKPGA SVKVSCKASGYTFTGYY MHWVRQAPGQGLEWM GWINPKSGGTNYAQKFQ GRVTMTRDTSISTAYME LSRLRSDDTAVYYCATG GSFDAFDIWGQGTMVTV SS	2430	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVEIK
Antibody 58	2322	EVQLVQSGAEVKNPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGPNYAQKFQD RVTMTRDTSISTAYMELS RLRSDDTAVYYCATGGS FDAFDIWGQGTMVTVSS	2431	DIVMTQSPSSLSASVGDRVTITCR ASQSISNYLNWYQQKPGKAPKFL IYGTSRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVDIK
Antibody 59	2323	EVQLVQSGAEVKNPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGPNYAQKFQD RVTMTRDTSISTAYMELS RLRSDDTAVYYCATGGS FDAFDIWGQGTMVTVSS	2432	DIVMTQSPSSLSASVGDRVTITCR ASQSISNYLNWYQQKPGKAPKFL IYGTSRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVDIK
Antibody 60	2324	EVQLVESGAEVKKPGAS VKVSCKASGYTFTGYFM HWVRQAPGQGLEWMG WINPNSGGTNYAQRFQG RVTMTRDTSINTAYMEL SRLRSDDTAVYYCATGG	2433	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVDIK

		SFDAFDIWGQGTMVTVSS		
Antibody 61	2325	EVQLVESGAEVKKPGASVKVSCKASGYTFTGYFMHWVRQAPGQGLEWMGWINPKSGGTNYAQRFQGRVTMTRDTSINTAYMELSRLRSDDTAVYYCATGGSFDAFDIWGQGTMVTVSS	2434	DIVMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKFLIYGASRLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSSPFTFGPGTKVDIK
Antibody 62	2326	EVQLVQSGAEVKKPGASVNVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLISDDTAVYYCATGGSFDAFDVWGQGTMVTVSS	2435	DIVMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQSPGKAPKILIYGASRLQSGVPSRFSGSGSGTDFTLAISSLQPEDFATYYCQQGDNTPFTFGPGTKLEIK
Antibody 63	2327	EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPKSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLISDDTAVYYCATGGSFDAFDVWGQGTMVTVSS	2436	DIVMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQSPGKAPKILIYGASRLQSGVPSRFSGSGSGTDFTLAISSLQPEDFATYYCQQGDNTPFTFGPGTKLEIK
Antibody 64	2328	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMQWVRQAPGQGLEWMGWINPNSGGTIYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYSCATGGSFDAFDIWGQGTMVTVSS	2437	DIVLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKFLIYGASRLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGHSTPFTFGPGTKVDIK
Antibody 65	2329	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMQWVRQAPGQGLEWMGWINPKSGGTIYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYSCATGGSFDAFDIWGQGTMVTVSS	2438	DIVLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKFLIYGASRLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGHSTPFTFGPGTKVDIK
Antibody 66	2330	EVQLVESGAEVKNPGASVKVSCKASGYTFTGYYLHWVRQAPGQGLEWMGWIKPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAVGGSYDAFDIWGQGTMVTVSS	2439	DIVMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQQPGKAPKFLIYGASRLQSGVPSRFSGSGSGTDFTLTINSLQPEDFATYFCQQGYSSPFTFGPGTKVEIK
Antibody 67	2331	EVQLVESGAEVKNPGASVKVSCKASGYTFTGYYLHWVRQAPGQGLEWMGWIKPKSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAVGGSYDAFDIWGQGTMVTVSS	2440	DIVMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQQPGKAPKFLIYGASRLQSGVPSRFSGSGSGTDFTLTINSLQPEDFATYFCQQGYSSPFTFGPGTKVEIK

Antibody 68	2332	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WVNPNSGGTNYAQNFQ GRVTMTGDTSITTAYMD LSGLRSDDTAVYYCAVG GSFDAFDIWGQGTMVTV SS	2441	DIVLTQSPASLSASVGDRVAITCR ASQSISSYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGHSTP FTFGPGTKLEIK
Antibody 69	2333	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WVNPKSGGTNYAQNFQ GRVTMTGDTSITTAYMD LSGLRSDDTAVYYCAVG GSFDAFDIWGQGTMVTV SS	2442	DIVLTQSPASLSASVGDRVAITCR ASQSISSYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGHSTP FTFGPGTKLEIK
Antibody 70	2334	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLISDDTAVYYCATGGSF DAFDIWGQGTMVTVSS	2443	DIVMTQSPSSLSASVGDRVTITCR ASQTISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVDIK
Antibody 71	2335	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLISDDTAVYYCATGGSF DAFDIWGQGTMVTVSS	2444	DIVMTQSPSSLSASVGDRVTITCR ASQTISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVDIK
Antibody 72	2336	QVQLVQSGAEVKKPGAS MKVSCKASGYTFTGYY MHWVRQAPGQGLEWM GWINPNSGGTNYAQRFQ GRVTMTRDTSVSTAYM DLSRLRSDDTAVYYCAT GGSFDAFDIWGQGTMVT VSS	2445	DIVLTQSPSSLSASVGDRVTITCR ASQSISKYLIWYQQKPGKAPNLLI YGASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQGHSTPF TFGPGTKVDIK
Antibody 73	2337	QVQLVQSGAEVKKPGAS MKVSCKASGYTFTGYY MHWVRQAPGQGLEWM GWINPKSGGTNYAQRFQ GRVTMTRDTSVSTAYM DLSRLRSDDTAVYYCAT GGSFDAFDIWGQGTMVT VSS	2446	DIVLTQSPSSLSASVGDRVTITCR ASQSISKYLIWYQQKPGKAPNLLI YGASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQGHSTPF TFGPGTKVDIK
Antibody 74	2338	EVQLVESGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WIKPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2447	DIQLTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQSPGKAPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSTP FTFGPGTKVDIK

Antibody 75	2339	EVQLVESGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WIKPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2448	DIQLTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQSPGKAPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSTP FTFGPGTKVDIK
Antibody 76	2340	EVQLVESGAEVKKPGAS VKVSCKASGYTFTGYYI HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMDL SRLRSDDTAVYYCATGG SFDAFDIWGQGTMVTVS S	2449	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVDIK
Antibody 77	2341	EVQLVESGAEVKKPGAS VKVSCKASGYTFTGYYI HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMDL SRLRSDDTAVYYCATGG SFDAFDIWGQGTMVTVS S	2450	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVDIK
Antibody 78	2342	EVQLVQSGAEVKSPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPNSGGTKYAQKFQG RVTVTRDTSISTAYMELN RLTSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2451	DIVLTQSPSSLSASVGDRVTITCR ASLSISSYLNWYQQKPGKAPKLLI YGASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQGHSTPF TFGPGTKLEIK
Antibody 79	2343	EVQLVQSGAEVKSPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPKSGGTKYAQKFQG RVTVTRDTSISTAYMELN RLTSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2452	DIVLTQSPSSLSASVGDRVTITCR ASLSISSYLNWYQQKPGKAPKLLI YGASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQGHSTPF TFGPGTKLEIK
Antibody 80	2344	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCATGGS FDAFDIWGQGTMVTVSS	2453	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVEIK
Antibody 81	2345	EVQLVQSGAEVKKPGAP VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2454	DIQMTQSPSSLSASVGDRVTITCR SSQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVEIK
Antibody 82	2346	EVQLVQSGAEVKKPGAP VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG	2455	DIQMTQSPSSLSASVGDRVTITCR SSQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT

		RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS		LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVEIK
Antibody 83	2347	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGATNFAQKFQG RVTMTRDTSITTAYMEL SRLRSDDTAVYYCATGG SFDAFDIWGQGTMVTVS S	2456	DIQMTQSPSSLSASVGDRVTITCR ASRSISSYLNWYQQRPGKAPKFLI YGASRLQTGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVDIK
Antibody 84	2348	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGATNFAQKFQG RVTMTRDTSITTAYMEL SRLRSDDTAVYYCATGG SFDAFDIWGQGTMVTVS S	2457	DIQMTQSPSSLSASVGDRVTITCR ASRSISSYLNWYQQRPGKAPKFLI YGASRLQTGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVDIK
Antibody 85	2349	QVQLVQSGAEVKRPGAS VKVSCKASGYTFTAYYL HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQD RVTMTGDTSISTAYMEL SRLRSDDTAVYYCAVGG SYDAFDIWGQGTMVTVS S	2458	DIQMTQSPSSLSASVGDRVTITCR ASQSINSYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSTP FTFGPGTKVEIK
Antibody 86	2350	QVQLVQSGAEVKRPGAS VKVSCKASGYTFTAYYL HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQD RVTMTGDTSISTAYMEL SRLRSDDTAVYYCAVGG SYDAFDIWGQGTMVTVS S	2459	DIQMTQSPSSLSASVGDRVTITCR ASQSIQSYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSTP FTFGPGTKVEIK
Antibody 87	2351	QVQLVQSGAEVKSPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPNSGGTKYAQKFQG RVTVTRDTSISTAYMELN RLTSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2460	DIQMTQSPSTLSASVGDRVTITCR ASQSISSYLNWYQQSPGKAPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDNT PFTFGPGTKVDIK
Antibody 88	2352	QVQLVQSGAEVKSPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPKSGGTKYAQKFQG RVTVTRDTSISTAYMELN RLTSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2461	DIQMTQSPSTLSASVGDRVTITCR ASQSISSYLNWYQQSPGKAPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDNT PFTFGPGTKVDIK
Antibody 89	2353	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS	2462	DIQMTQSPSSLSASVGDRVTITCR ASQSINSYLYWYQQKPGKAPKLL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDSATYYCQQGYSTP FTFGPGTKVEIK

		RLRSDDTAVYYCATGGS YDAFDIWGQGTMVTVSS		
Antibody 90	2354	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCATGGS YDAFDIWGQGTMVTVSS	2463	DIQMTQSPSSLSASVGDRVTITCR ASQSIQSYLYWYQQKPGKAPKLL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDSATYYCQQGYSTP FTFGPGTKVEIK
Antibody 91	2355	EVQLVQSGAEVKKPGAS VKVSCKTSGYTFTAYYL HWVRQAPGQGLEWMG WINPNSGGTSSAQKFQG RVTMTRDTSISTAYMDL TRLRSDDTAVYYCAVGG SFDAFDIWGQGTMVTVS S	2464	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVDIK
Antibody 92	2356	EVQLVQSGAEVKKPGAS VKVSCKTSGYTFTAYYL HWVRQAPGQGLEWMG WINPKSGGTSSAQKFQG RVTMTRDTSISTAYMDL TRLRSDDTAVYYCAVGG SFDAFDIWGQGTMVTVS S	2465	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVDIK
Antibody 93	2357	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTHYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYFCAVGGS FDAFDIWGQGTMVTVSS	2466	DIVMTQSPSSLSASVGDRVTITCR ASLSISSYLNWYQQKPGKAPKLLI YGASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQGHSTPF TFGPGTKLEIK
Antibody 94	2358	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTHYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYFCAVGGS FDAFDIWGQGTMVTVSS	2467	DIVMTQSPSSLSASVGDRVTITCR ASLSISSYLNWYQQKPGKAPKLLI YGASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQGHSTPF TFGPGTKLEIK
Antibody 95	2359	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYI HWVRQAPGQGLEWMG WINPNSGGTNYAQRFQG RVTMTRDTSISTAYMDL SRLRSDDTAVYYCATGG SFDAFDIWGQGTMVTVS S	2468	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYFCQQGYSSP FTFGPGTKLEIK
Antibody 96	2360	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTIYAQKFQG RVTMTRDTSISTAYMELS	2469	EIVMTQSPASLSASVGDRVTITCR ASQTISRYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQSYSTP FTFGPGTKVDIK

		RLRSDDTAVYSCATGGS FDAFDIWGQGTMVTVSS		
Antibody 97	2361	QVQLVQSGAEVKRPGAS LTVSCKSSGYTFTAYYIH WVRQAPGQGLEWMGWI NPNSGGTNYAQKFQGRV TMTRDTSITTAYMELSRL RSDDTAVYYCAVGGSY DAFDIWGQGTMVTVSS	2470	EIVMTQSPASLSASVGDRVTITCR ASQTISRYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSTP FTFGPGTKVDIK
Antibody 98	2362	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYFM HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRFDDTAVYYCASGGS FDAFDIWGQGTMVTVSS	2471	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQSPGKAPKILI YGASRLQSGVPSRFRGSGSGTDF TLAISSLQPEDFATYYCQQGDSTP FTFGPGTKVDIK
Antibody 99	2363	EVQLVESGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGRGLEWMG WINPNSGGTKYAQKFQG RVTMTRDTSINTAYMEL SRLRPDDTAVYYCATGG SFDAFDIWGQGTMVTVS S	2472	DIVLTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYFCQQGYSSP FTFGPGTKLEIK
Antibody 100	2364	EVQLVESGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCASGGS FDAFDIWGQGTMVTVSS	2473	DIQMTQSPSSLSASVGDRVTITCR ASQSISRYLNWYQQKPGKAPKILI YGASSVQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSSP FTFGPGTKVDIK
Antibody 101	2365	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2474	DIQMTQSPSSLSASVGDRVTITCR ASQSISRYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQGYSTLF TFGPGTKLEIK
Antibody 102	2366	EVQLVQSGAEVKKPGAS VKVSCKASGYTFNGYY MHWIRQAPGQGLEWMG WINPNSGGTKYSQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCATGGS FDAFDIWGQGTMVTVSS	2475	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVDIK
Antibody 103	2367	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCAVGGS YDAFDIWGQGTMVTVSS	2476	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSNP FTFGPGTKVDIK

Antibody 104	2368	EVQLVESGAEVKKPGAS VKVSCKASGYTFTAYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSINTAYMEL SRLRSDDTAVYYCASGG SIDAFDIWGQGTMVTVS S	2477	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKLL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGFSTP FTFGPGTKLEIK
Antibody 105	2369	QVQLVQSEAEVKKPGAS VKVSCKASGYTFTAYYI HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQD RVTMTGDTSISTAYMEL RRLRSDDTAVYYCAVGG SYDAFDIWGQGTMVTVS S	2478	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVDIK
Antibody 106	2370	EVQLVQSGAEVKKPGAS MKVSCKASGYTFTGYYI HWVRQAPGQGLEWMG WINPNSGGTKYAQKFHG RVTLTRDTSVNTAYMDL SGLRSDDTAVYYCAVGG SFDAFDIWGQGTMVTVS S	2479	DIVMTQSPSSLSASVGDRVTITCR ASQSISRYLNWYQQKPGKAPNFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGPGTKVDIK
Antibody 107	2371	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLISDDTAVYYCVTGGSF DAFDVWGQGTMVTVSS	2480	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKILI YGASSLQSGVPSRFSGSGSGTDFT LAISSLQPEDFATYYCQQGDSTPF TFGPGTKVDIK
Antibody 108	2372	QVQLVQSGAEVKKPGAS VRVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTVTRDTSISTAYMELS RLRSDDTAVYYCTSGGS FDAFDIWGQGTMVTVSS	2481	DIVMTQSPSSLSASVGDRVTITCR ASQSISSFLNWYQQSPGKAPKILI YGASRLQSGVPSRFSGSGSGTDF TLAISSLQPEDFATYYCQQGDSTP FTFGPGTKVDIK
Antibody 109	2373	EVQLVQSGAEVKRPGAS LTVSCKSSGYTFTAYYIH WVRQAPGQGLEWMGWI NPNSGGTNYAQRFQGRV TMTRDTSISTAYMELSRL RSDDTAVYYCATGGSFD AFDIWGQGTMVTVSS	2482	DIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGHSTP FTFGPGTKVDIK
Antibody 110	2374	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCASGGS FDAFDIWGQGTMVTVSS	2483	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFAAYYCQQGHSTP FTFGPGTKVDIK

Antibody 111	2375	EVQLVESGAEVKKPGAS VRVSCKASGYTFTAYYI HWVRQAPGQGLEWMG WINPNSGGTSSAQKFQG RVTMTRDTSISTAYMDL NRLRSDDTAMYYCAVG GSFDAFDIWGQGTMVTV SS	2484	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKLL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFASYFCQQGHSTPI TFGQGTKLEIK
Antibody 112	2376	EVQLVQSGAEVKRPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYLELS RLRSDDTAVYYCATGGS YDAFDIWGQGTMVTVSS	2485	DIQLTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYFCQQGYSSP FTFGPGTKVDIK
Antibody 113	2377	QVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPNSGGTKYAQKFQG RVTMTRDTSISTAYMELS SLRSDDTAVYYCATGGS YDAFDIWGQGTMVTVSS	2486	DIVLTQSPSSLSASVGDRVTITCR ASQSISRYLYWYQQNPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYDTP FTFGPGTKVDIK
Antibody 114	2378	EVQLVESGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCATGGS FDAFDIWGQGTMVTVSS	2487	DIQLTQSPSSLSASVGDRVTITCQ ASQDISNYLNWYQQKPGKAPKL LIYAASSLQTGVPSRFSGSGSGTD FTLAISSLQPEDFATYYCQQGDST PFTFGPGTKLEIK
Antibody 115	2379	QVQLVQSGSDLKKPGAS VKVSCKASGYTFTRYGM NWVRQAPGQGLEWMG WINTNTGNPTYAQDFTG RFVFSLDTSVSTAYLQISS LKAEDTAVYYCARDNW NYVSDYWGQGTLVTVSS	2488	EIVLTQSPGTLSLSPGERATLSCR ASQSVSDSYLAWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGT DFTLTISRLEPEDFAVYYCQQYG TSPITFGQGTKLEIK
Antibody 116	2380	EVQLVQSGAEVKKPGAS VKVSCKASGYTFTGYYM HWVRQAPGQGLEWMG WINPKSGGTIYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYSCATGGS FDAFDIWGQGTMVTVSS	2489	DIQMTQSPSSLSASVGDRVIITCR ASQSISSYLNWYQQKPGKAPKLL IYGASSLQSGVPSRFSGSGAGTEF TLTISSLQPEDFATYYCQQAKSFP LTFGGGTKVEIK
Antibody 117	2381	EVQLVESGAEVKKPGAS VKVSCKASGYTFTVYYM HWVRQAPGQGLEWMG WINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELS RLRSDDTAVYYCASGGS FDAFDIWGQGTMVTVSS	2490	DIVMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKFL IYGASRLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGYSSP FTFGGGTKVDIK
Antibody 118	2382	QVQLVQSGSELQKPGAS VKVSCKTSGYTFTRYGM NWVRQAPGQGLEWMG WINTNTGNPTYAQGFTG RFVFSLDTSVSTAYLQISS	2491	DIVMTQTPLSSPVPLGQPASISCK SSQSLVHSDGNTYLSWLQQRPGQ PPRLLIYKISNRFSGVPDRFSGSG AGTDFTLKISRVEAEDVGVYYC MQVTQFPITLGQGTKLEIK

		LKAEDTAVYYCARDNW NYDFDYWGQGTTVTVSS		
Antibody 119	2383	QVQLVQSGSELKRPGAS VKVSCKASGYTFTTYGM NWVRQAPGQGLEWMG WINTNTGNPTYAQGFTG RFVFSLDTSVSTAYLQISS LKAEDTAVYYCARDNW NYDLDYWGQGTLVTVS S	2492	DIVMTQTPLSSPVTLGQPASISCR SSQSLVHSDGNTYLSWLQQRPGQ PPRLLIYKISNRFSGVPDRFSGSG AGTDFTLKISRVEAEDVGVYYC MQATQFPITLGQGTKLEIK

[0228] In some embodiments, the TL1A binding protein comprises a heavy chain variable region (VH) comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region (VH) comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 181-190 and 2275-2383). In some embodiments, the TL1A binding protein comprises a heavy chain variable region (VH) comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region (VH) comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region (VH) comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region (VH) comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region (VH) comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region (VH) comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a

heavy chain variable region (VH) comprising an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2.

[0229] In some embodiments, the TL1A binding protein comprises a light chain variable region (VL) comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 191-200 and 2384-2492). In some embodiments, the TL1A binding protein comprises a light chain variable region (VL) comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein antibody comprises a light chain variable region (VL) comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a light chain variable region (VL) comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a light chain variable region (VL) comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a light chain variable region (VL) comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a light chain variable region (VL) comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a light chain variable region (VL) comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2. In some embodiments, the TL1A binding protein comprises a light chain variable region (VL) comprising an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2.

[0230] In some embodiments, the TL1A binding protein comprises a heavy chain variable region (VH) that comprises an amino acid sequence at least 60% (*e.g.*, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%) identical to the heavy chain variable region (VH) of an TL1A binding protein disclosed in TABLE 2.1 and TABLE 2.2, and

a light chain variable region (VL) that comprises an amino acid sequence at least 60% (*e.g.*, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%) identical to the light chain variable region (VL) of the same TL1A binding protein disclosed in TABLE 2.1 and TABLE 2.2.

[0231] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 181-190 and 2275-2383); and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 191-200 and 2384-2492). In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 181-190 and 2275-2383); and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 191-200 and 2384-2492). In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 181-190 and 2275-2383); and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 191-200 and 2384-2492). In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 181-190 and 2275-2383); and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 191-200 and 2384-2492). In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 181-190 and 2275-2383); and a light chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to any

one of VL sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 191-200 and 2384-2492). In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 181-190 and 2275-2383); and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 191-200 and 2384-2492). In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 181-190 and 2275-2383); and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 191-200 and 2384-2492). In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 181-190 and 2275-2383); and a light chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according any one of VL sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 191-200 and 2384-2492). In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence according to any one of VH sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 181-190 and 2275-2383); and a light chain variable region comprising an amino acid sequence according to any one of VL sequences listed in TABLE 2.1 and TABLE 2.2 (SEQ ID NOs: 191-200 and 2384-2492).

[0232] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence listed in TABLE 2.1; and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence listed in TABLE 2.1. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence listed in TABLE 2.1; and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence listed in TABLE 2.1. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid

sequence listed in TABLE 2.1; and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence listed in TABLE 2.1. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence listed in TABLE 2.1; and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence listed in TABLE 2.1. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence listed in TABLE 2.1; and a light chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence listed in TABLE 2.1. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence listed in TABLE 2.1; and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence listed in TABLE 2.1. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence listed in TABLE 2.1; and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence listed in TABLE 2.1. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence listed in TABLE 2.1; and a light chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence listed in TABLE 2.1. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence listed in TABLE 2.1; and a light chain variable region comprising an amino acid sequence listed in TABLE 2.1.

[0233] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence listed in TABLE 2.2; and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence listed in TABLE 2.2; and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region

comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence listed in TABLE 2.2; and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence listed in TABLE 2.2; and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence listed in TABLE 2.2; and a light chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence listed in TABLE 2.2; and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence listed in TABLE 2.2; and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence listed in TABLE 2.2; and a light chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence listed in TABLE 2.2. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence listed in TABLE 2.2; and a light chain variable region comprising an amino acid sequence listed in TABLE 2.2.

[0234] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 181; and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 191. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 181; and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino

acid sequence according to SEQ ID NO: 191. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 181; and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 191. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 181; and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 191. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 181; and a light chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 191. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 181; and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 191. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 181; and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 191. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to SEQ ID NO: 181; and a light chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according SEQ ID NO: 191. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence according to SEQ ID NO: 181; and a light chain variable region comprising an amino acid sequence according to SEQ ID NO: 191.

[0235] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 182; and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 192. In some embodiments, the TL1A binding protein comprises a

heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 182; and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 192. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 182; and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 192. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 182; and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 192. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 182; and a light chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 192. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 182; and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 192. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 182; and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 192. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to SEQ ID NO: 182; and a light chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according SEQ ID NO: 192. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence according to SEQ ID NO: 182; and a light chain variable region comprising an amino acid sequence according to SEQ ID NO: 192.

[0236] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino

acid sequence according to SEQ ID NO: 183; and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 193. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 183; and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 193. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 183; and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 193. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 183; and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 193. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 183; and a light chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 193. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 183; and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 193. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 183; and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 193. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to SEQ ID NO: 183; and a light chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according SEQ ID NO: 193. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence according to

SEQ ID NO: 183; and a light chain variable region comprising an amino acid sequence according to SEQ ID NO: 193.

[0237] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 184; and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 194. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 184; and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 194. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 184; and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 194. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 184; and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 194. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 184; and a light chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 194. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 184; and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 194. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 184; and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 194. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to SEQ ID NO: 184; and a light chain

variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according SEQ ID NO: 194. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence according to SEQ ID NO: 184; and a light chain variable region comprising an amino acid sequence according to SEQ ID NO: 194.

[0238] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 185; and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 195. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 185; and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 195. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 185; and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 195. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 185; and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 195. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 185; and a light chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 195. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 185; and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 195. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 185; and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino

acid sequence according to SEQ ID NO: 195. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to SEQ ID NO: 185; and a light chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according SEQ ID NO: 195. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence according to SEQ ID NO: 185; and a light chain variable region comprising an amino acid sequence according to SEQ ID NO: 195.

[0239] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 186; and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 196. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 186; and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 196. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 186; and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 196. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 186; and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 196. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 186; and a light chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 196. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 186; and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 196. In some embodiments, the TL1A binding protein comprises a

heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 186; and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 196. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to SEQ ID NO: 186; and a light chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according SEQ ID NO: 196. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence according to SEQ ID NO: 186; and a light chain variable region comprising an amino acid sequence according to SEQ ID NO: 196.

[0240] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 187; and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 197. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 187; and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 197. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 187; and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 197. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 187; and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 197. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 187; and a light chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 197. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino

acid sequence according to SEQ ID NO: 187; and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 197. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 187; and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 197. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to SEQ ID NO: 187; and a light chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according SEQ ID NO: 197. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence according to SEQ ID NO: 187; and a light chain variable region comprising an amino acid sequence according to SEQ ID NO: 197.

[0241] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 188; and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 198. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 188; and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 198. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 188; and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 198. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 188; and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 198. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 188; and a light chain variable region comprising an amino acid

sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 198. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 188; and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 198. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 188; and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 198. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to SEQ ID NO: 188; and a light chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according SEQ ID NO: 198. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence according to SEQ ID NO: 188; and a light chain variable region comprising an amino acid sequence according to SEQ ID NO: 198.

[0242] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 189; and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 199. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 189; and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 199. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 189; and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 199. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 189; and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 199. In some

embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 189; and a light chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 199. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 189; and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 199. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 189; and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 199. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to SEQ ID NO: 189; and a light chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according SEQ ID NO: 199. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence according to SEQ ID NO: 189; and a light chain variable region comprising an amino acid sequence according to SEQ ID NO: 199.

[0243] In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 190; and a light chain variable region comprising an amino acid sequence having at least 80% sequence identity with an amino acid sequence according to SEQ ID NO: 200. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 190; and a light chain variable region comprising an amino acid sequence having at least 85% sequence identity with an amino acid sequence according to SEQ ID NO: 200. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 190; and a light chain variable region comprising an amino acid sequence having at least 90% sequence identity with an amino acid sequence according to SEQ ID NO: 200. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence

having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 190; and a light chain variable region comprising an amino acid sequence having at least 95% sequence identity with an amino acid sequence according to SEQ ID NO: 200. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 190; and a light chain variable region comprising an amino acid sequence having at least 96% sequence identity with an amino acid sequence according to SEQ ID NO: 200. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 190; and a light chain variable region comprising an amino acid sequence having at least 97% sequence identity with an amino acid sequence according to SEQ ID NO: 200. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 190; and a light chain variable region comprising an amino acid sequence having at least 98% sequence identity with an amino acid sequence according to SEQ ID NO: 200. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according to SEQ ID NO: 190; and a light chain variable region comprising an amino acid sequence having at least 99% sequence identity with an amino acid sequence according SEQ ID NO: 200. In some embodiments, the TL1A binding protein comprises a heavy chain variable region comprising an amino acid sequence according to SEQ ID NO: 190; and a light chain variable region comprising an amino acid sequence according to SEQ ID NO: 200.

[0244] In some embodiments, the TL1A binding protein binds TL1A with a K_D lower than or equal to 10 nanomolar (nM), 9 nM, 8 nM, 7 nM, 6 nM, 5 nM, 4 nM, 3 nM, 2 nM, 1 nM, 0.9 nM, 0.8 nM, 0.7 nM, 0.6 nM, 0.5 nM, 0.4 nM, 0.3 nM, 0.2 nM, 0.1 nM, 90 pM, 80 pM, 70 pM, 60 pM, 50 pM, 40 pM, 30 pM, 20 pM, or 10 pM. In some embodiments, the TL1A binding protein binds TL1A with a K_D within the range of about 10 pM – about 1 nM, about 10 pM – about 0.9 nM, about 10 pM – about 0.8 nM, about 10 pM – about 0.7 nM, about 10 pM – about 0.6 nM, about 10 pM – about 0.5 nM, about 10 pM – about 0.4 nM, about 10 pM – about 0.3 nM, about 10 pM – about 0.2 nM, about 10 pM – about 0.1 nM, about 10 pM – about 50 pM, 0.1 nM – about 10 nM, about 0.1 nM – about 9 nM, about 0.1 nM – about 8 nM, about 0.1 nM – about 7 nM, about 0.1 nM – about 6 nM, about 0.1 nM – about 5 nM, about 0.1 nM – about 4 nM, about 0.1 nM – about 3 nM, about 0.1 nM – about 2 nM, about 0.1 nM – about 1 nM, or about 0.1 nM

– about 0.5 nM. In some embodiments, the TL1A binding protein binds TL1A with a K_D less than about 1 nanomolar (nM). In some embodiments, the TL1A binding protein binds TL1A with a K_D less than about 0.9 nanomolar (nM). In some embodiments, the TL1A binding protein binds TL1A with a K_D less than about 0.8 nanomolar (nM). In some embodiments, the TL1A binding protein binds TL1A with a K_D less than about 0.7 nanomolar (nM). In some embodiments, the TL1A binding protein binds TL1A with a K_D less than about 0.6 nanomolar (nM). In some embodiments, the TL1A binding protein binds TL1A with a K_D less than about 0.5 nanomolar (nM). In some embodiments, the TL1A binding protein binds TL1A with a K_D less than about 0.4 nanomolar (nM). In some embodiments, the TL1A binding protein binds TL1A with a K_D less than about 0.3 nanomolar (nM). In some embodiments, the TL1A binding protein binds TL1A with a K_D less than about 0.2 nanomolar (nM). In some embodiments, the TL1A binding protein binds TL1A with a K_D less than about 0.1 nanomolar (nM). In some embodiments, the K_D is measured by surface plasmon resonance (SPR). In some embodiments, the K_D is measured by Biolayer Interferometry (BLI).

[0245] In some embodiments, the TL1A binding protein comprises a binding affinity to TL1A at least 1.5 fold, 2 fold, 3 fold, 4 fold, 5 fold, 6 fold, 7 fold, 8 fold, 9 fold, 10 fold, 15 fold, or 20 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein comprises a binding affinity to TL1A at least 1.5 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein comprises a binding affinity to TL1A at least 2 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein comprises a binding affinity to TL1A at least 3 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein comprises a binding affinity to TL1A at least 4 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein comprises a binding affinity to TL1A at least 5 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein comprises a binding affinity to TL1A at least 6 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein comprises a binding affinity to TL1A at least 7 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein comprises a binding affinity to TL1A at least 8 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein comprises a binding affinity to TL1A at least 9 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the

TL1A binding protein comprises a binding affinity to TL1A at least 10 fold more than a binding affinity of a comparator antibody to TL1A.

[0246] In some embodiments, the TL1A binding protein inhibits receptor (e.g., death receptor 3 (DR3) and decoy receptor 3 (DcR3)) binding to TL1A by at least 1.5 fold, 2 fold, 3 fold, 4 fold, 5 fold, 6 fold, 7 fold, 8 fold, 9 fold, 10 fold, 15 fold, or 20 fold more than a comparator antibody to TL1A. In some embodiments, the TL1A binding protein inhibits receptor binding to TL1A by at least 1.5 fold more than a comparator antibody to TL1A. In some embodiments, the TL1A binding protein inhibits receptor binding to TL1A by at least 2 fold more than a comparator antibody to TL1A. In some embodiments, the TL1A binding protein inhibits receptor binding to TL1A by at least 3 fold more than a comparator antibody to TL1A. In some embodiments, the TL1A binding protein inhibits receptor binding to TL1A by at least 4 fold more than a comparator antibody to TL1A. In some embodiments, the TL1A binding protein inhibits receptor binding to TL1A by at least 5 fold more than a comparator antibody to TL1A. In some embodiments, the TL1A binding protein inhibits receptor binding to TL1A by at least 6 fold more than a comparator antibody to TL1A. In some embodiments, the TL1A binding protein inhibits receptor binding to TL1A by at least 7 fold more than a comparator antibody to TL1A. In some embodiments, the TL1A binding protein inhibits receptor binding to TL1A by at least 8 fold more than a comparator antibody to TL1A. In some embodiments, the TL1A binding protein inhibits receptor binding to TL1A by at least 9 fold more than a comparator antibody to TL1A. In some embodiments, the TL1A binding protein inhibits receptor binding to TL1A by at least 10 fold more than a comparator antibody to TL1A.

[0247] In some embodiments, the TL1A binding protein reduces TL1A-induced apoptosis by at least 1.5 fold, 2 fold, 3 fold, 4 fold, 5 fold, 6 fold, 7 fold, 8 fold, 9 fold, 10 fold, 15 fold, or 20 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein reduces TL1A-induced apoptosis by at least 1.5 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein reduces TL1A-induced apoptosis by at least 2 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein reduces TL1A-induced apoptosis by at least 3 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein reduces TL1A-induced apoptosis by at least 4 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein reduces TL1A-induced apoptosis by at least 5 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein reduces TL1A-induced apoptosis by at least 6 fold more than a binding affinity of a comparator

antibody to TL1A. In some embodiments, the TL1A binding protein reduces TL1A-induced apoptosis by at least 7 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein reduces TL1A-induced apoptosis by at least 8 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein reduces TL1A-induced apoptosis by at least 9 fold more than a binding affinity of a comparator antibody to TL1A. In some embodiments, the TL1A binding protein reduces TL1A-induced apoptosis by at least 10 fold more than a binding affinity of a comparator antibody to TL1A.

[0248] In some embodiments, the TL1A binding protein exhibits improved solubility and/or developability. In some embodiments, the TL1A binding protein is formulated at high concentrations. In some embodiments, the TL1A binding protein is formulated at high concentrations for subcutaneous administration (*e.g.,* by an autoinjector). In some embodiments, the TL1A binding protein is formulated at a concentration of at least about 75, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, or more than 300 milligrams per milliliter (mg/mL). In some embodiments, the TL1A binding protein is formulated at a concentration in a range of about 50 to about 300, about 50 to about 200, about 50 to about 150, about 50 to about 100, about 75 to about 300, about 75 to about 200, about 75 to about 150, about 75 to about 100, about 100 to about 200, about 100 to about 150, or about 150 to about 200 mg/mL.

[0249] In some embodiments, the TL1A binding protein is formulated a pH range from about 5 to about 7. In some embodiments, the TL1A binding protein is formulated a pH range from about 5.5 to about 6.5. In some embodiments, the TL1A binding protein is formulated a pH range of about 4, 4.5, 5, 5.5, 6, 6.5, 7, or 7.5. In some embodiments, the TL1A binding protein is formulated a pH range ranging from about 4-4.5, 4.5-5, 5-5.5, 5.5-6, 6-6.5, 6.5-7, or 7-7.5.

Fc Modifications

[0250] Provided herein are compositions, systems, and methods comprising a TL1A binding protein comprising a modified Fc region. Unless otherwise specified herein, numbering of amino acid residues in the Fc region or constant region is according to the EU numbering system, also called the EU index, as described in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD, 1991.

[0251] In some embodiments, the TL1A binding proteins comprise a modified Fc comprising one or more modifications. In some embodiments, the one or more modifications are located in a Fc from IgG1 (*e.g.,* human IgG1 (hIgG1). In some embodiments, the one or more modifications are located in a Fc from IgG4 (*e.g.,* human IgG4 (hIgG4). In some embodiments,

the one or more modifications are located in a Fc from IgG2. In some embodiments, the one or more modifications promote selective binding of Fc-gamma receptors.

[0252] Amino acid sequences of exemplary Fc sequences are provided in Table 3.

TABLE 3. EXEMPLARY FC AMINO ACID SEQUENCES

Name	SEQ ID NO	Fc Sequence
hIgG1	201	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG4	202	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK
IgG2	203	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVD HKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSP
IgG4-SP	204	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK
IgG4-SPLE	205	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK

hIgG1-N297A	206	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-D265A	207	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALA	208	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LAGA	209	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALAGA	210	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALAPG	211	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-YTE	212	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH

		KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-N297A/YTE	213	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-D265A/YTE	214	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYITREPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALA/YTE	215	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LAGA/YTE	216	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALAGA/YTE	217	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALAPG/YTE	218	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK

		TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LS	219	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHSHYTQKSLSLSPG
hIgG1-N297A/LS	220	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHSHYTQKSLSLSPG
hIgG1-D265A/LS	221	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHSHYTQKSLSLSPG
hIgG1-LALA/LS	222	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHSHYTQKSLSLSPG
hIgG1-LAGA/LS	223	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHSHYTQKSLSLSPG
hIgG1-LALAGA/LS	224	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY

		PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHSHYTQKSLSLSPG
hIgG1- LALAPG/LS	225	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHSHYTQKSLSLSPG
hIgG1-DHS	226	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHSHYTQKSLSLSPG
hIgG1- N297A/DHS	227	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVDHHDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHSHYTQKSLSLSPG
hIgG1- D265A/DHS	228	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHSHYTQKSLSLSPG
hIgG1- LALA/DHS	229	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHSHYTQKSLSLSPG
hIgG1- LAGA/DHS	230	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHSHYTQKSLSLSPG

hIgG1-LALAGA/DHS	231	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHSHYTQKSLSLSPG
hIgG1-LALAPG/DHS	232	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHSHYTQKSLSLSPG
hIgG4-YTE	233	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDT LYITREPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPR EEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK TISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK
hIgG4-SP/YTE	234	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDT LYITREPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPR EEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK TISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK
hIgG4-SPLE/YTE	235	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFLFPPKPKDT LYITREPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPR EEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK TISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK
hIgG4-LS	236	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVLHEALHSYTQKSLSLSLGK
hIgG4-SP/LS	237	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD

		HKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVLHEALHSHYTQKSLSLSLGK
hIgG4- SPLE/LS	238	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVLHEALHSHYTQKSLSLSLGK
hIgG4-DHS	239	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHSHYTQKSLSLSLGK
hIgG4- SP/DHS	240	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHSHYTQKSLSLSLGK
hIgG4- SPLE/DHS	241	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHSHYTQKSLSLSLGK
hIgG2-YTE	242	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVD HKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT LYITREPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSP
hIgG2-LS	243	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVD HKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP

		REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSP
hIgG2-DHS	244	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVD HKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTFRVVSVLTVDHHDWLNGKEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHSHYTQKSLSLSP
IgG4-SP	245	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK
hIgG1-LA	246	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHAHYTQKSLSLSPG
hIgG1- N297A/LA	247	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHAHYTQKSLSLSPG
hIgG1- D265A/LA	248	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHAHYTQKSLSLSPG
hIgG1- LALA/LA	249	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY

		PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHAHYTQKSLSLSPG
hIgG1-LAGA/LA	250	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHAHYTQKSLSLSPG
hIgG1-LALAGA/LA	251	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHAHYTQKSLSLSPG
hIgG1-LALAPG/LA	252	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHAHYTQKSLSLSPG
hIgG1-N434A	253	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHAHYTQKSLSLSPG
hIgG1-N297A/N434A	254	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHAHYTQKSLSLSPG
hIgG1-D265A/N434A	255	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHAHYTQKSLSLSPG

hIgG1-LALA/N434A	256	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHAHYTQKSLSLSPG
hIgG1-LAGA/N434A	257	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHAHYTQKSLSLSPG
hIgG1-LALAGA/N434A	258	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHAHYTQKSLSLSPG
hIgG1-LALAPG/N434A	259	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHAHYTQKSLSLSPG
hIgG1-N434W	260	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHWHYTQKSLSLSPG
hIgG1-N297A/N434W	261	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHWHYTQKSLSLSPG

hIgG1-D265A/N434W	262	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHWHYTQKSLSLSPG
hIgG1-LALA/N434W	263	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHWHYTQKSLSLSPG
hIgG1-LAGA/N434W	264	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHWHYTQKSLSLSPG
hIgG1-LALAGA/N434W	265	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHWHYTQKSLSLSPG
hIgG1-LALAPG/N434W	266	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHWHYTQKSLSLSPG
hIgG1/DQ	267	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLQVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG

hIgG1-N297A/DQ	268	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLQVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-D265A/DQ	269	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLQVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALA/DQ	270	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LAGA/DQ	271	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALAGA/DQ	272	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALAPG/DQ	273	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1/DW	274	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH

		KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLWVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-N297A/DW	275	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLWVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-D265A/DW	276	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLWVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALA/DW	277	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLWVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LAGA/DW	278	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLWVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALAGA/DW	279	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLWVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG

hIgG1-LALAPG/DW	280	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLWVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1/YD	281	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-N297A/YD	282	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-D265A/YD	283	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYISRDPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALA/YD	284	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLYISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LAGA/YD	285	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLYISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG

hIgG1-LALAGA/YD	286	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLYISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALAPG/YD	287	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLYISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1/QVV	288	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLQVLHVDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-N297A/QVV	289	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLQVLHVDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-D265A/QVV	290	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLQVLHVDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALA/QVV	291	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHVDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG

hIgG1-LAGA/QVV	292	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHVDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALAGA/QVV	293	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHVDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALAPG/QVV	294	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHVDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1/DDRVV	295	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVDNAKT KPREEQYNSTYRVVSVLRVLHVDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-N297A/DDRVV	296	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVDNAKT KPREEQYASTYRVVSVLRVLHVDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-D265A/DDRVV	297	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVAVSHEDPEVKFNWYVDGVEVDNAKT KPREEQYNSTYRVVSVLRVLHVDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG

hIgG1-LALA/DDRVV	298	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVDNAK TKPREEQYNSTYRVVSVLRVLHVDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LAGA/DDRVV	299	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVDNAK TKPREEQYNSTYRVVSVLRVLHVDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALAGA/DDRVV	300	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVDNAK TKPREEQYNSTYRVVSVLRVLHVDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-LALAPG/DDRVV	301	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVDNAK TKPREEQYNSTYRVVSVLRVLHVDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
hIgG1-Q311R/M428L	302	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHNHYTQKSLSLSPG
hIgG4-Q311R/M428L	303	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVLHEALHNHYTQKSLSLSLGK

IgG4-SP/Q311R/M428L	304	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVLHEALHNHYTQKSLSLSLGK
IgG4-SPLE/Q311R/M428L	305	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVLHEALHNHYTQKSLSLSLGK
IgG2-Q311R/M428L	306	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVD HKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTFRVVSVLTVVHRDWLNGKEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHNHYTQKSLSLSP
hIgG1-N297A/Q311R/M428L	307	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHRDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHNHYTQKSLSLSPG
hIgG1-D265A/Q311R/M428L	308	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHNHYTQKSLSLSPG
hIgG1-LALA/Q311R/M428L	309	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHNHYTQKSLSLSPG

hIgG1-LAGA/Q311R/M428L	310	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHNHYTQKSLSLSPG
hIgG1-LALAGA/Q311R/M428L	311	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHNHYTQKSLSLSPG
hIgG1-LALAPG/Q311R/M428L	312	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHNHYTQKSLSLSPG
hIgG1 (with C-terminal lysine)	2495	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-N297A	2496	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-D265A	2497	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal	2498	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH

lysine)-LALA		KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LAGA	2499	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAGA	2500	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAPG	2501	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-YTE	2502	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-N297A/YTE	2503	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal	2504	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYITREPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT

lysine)-D265A/YTE		KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALA/YTE	2505	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LAGA/YTE	2506	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAGA/YTE	2507	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAPG/YTE	2508	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LS	2509	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHSHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-N297A/LS	2510	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP

		SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHSHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-D265A/LS	2511	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHSHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALA/LS	2512	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHSHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LAGA/LS	2513	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHSHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAGA/LS	2514	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHSHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAPG/LS	2515	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHSHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-DHS	2516	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHSHYTQKSLSLSPGK

hIgG1 (with C-terminal lysine)-N297A/DHS	2517	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVDHHDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHSHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-D265A/DHS	2518	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHSHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALA/DHS	2519	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHSHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LAGA/DHS	2520	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHSHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAGA/DHS	2521	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHSHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAPG/DHS	2522	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHSHYTQKSLSLSPGK

hIgG1 (with C-terminal lysine)-LA	2523	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-N297A/LA	2524	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-D265A/LA	2525	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALA/LA	2526	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LAGA/LA	2527	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAGA/LA	2528	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal	2529	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH

lysine)-LALAPG/LA		KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-N434A	2530	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-N297A/N434A	2531	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-D265A/N434A	2532	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALA/N434A	2533	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LAGA/N434A	2534	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-	2535	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK

LALAGA/ N434A		TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)- LALAPG/ N434A	2536	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHAHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)- N434W	2537	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHWHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)- N297A/ N434W	2538	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHWHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)- D265A/ N434W	2539	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHWHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)- LALA/ N434W	2540	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHWHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)- LAGA/ N434W	2541	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY

		PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHWHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAGA/N434W	2542	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHWHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAPG/N434W	2543	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHWHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)/DQ	2544	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLQVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-N297A/DQ	2545	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLQVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-D265A/DQ	2546	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLQVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALA/DQ	2547	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY

		PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LAGA/DQ	2548	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAGA/DQ	2549	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAPG/DQ	2550	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)/DW	2551	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLWVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-N297A/DW	2552	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLWVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-D265A/DW	2553	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLWVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

hIgG1 (with C-terminal lysine)-LALA/DW	2554	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLWVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LAGA/DW	2555	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLWVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAGA/DW	2556	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLWVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAPG/DW	2557	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLWVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)/YD	2558	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-N297A/YD	2559	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal	2560	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH

lysine)-D265A/YD		KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYISRDPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALA/YD	2561	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLYISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LAGA/YD	2562	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLYISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAGA/YD	2563	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLYISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAPG/YD	2564	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLYISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)/QVV	2565	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLQVLHVDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal	2566	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT

lysine)-N297A/QVV		KPREEQYASTYRVVSVLQVLHVDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-D265A/QVV	2567	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLQVLHVDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALA/QVV	2568	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHVDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LAGA/QVV	2569	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHVDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAGA/QVV	2570	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHVDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAPG/QVV	2571	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLQVLHVDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)/DDRVV	2572	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVDNAKT KPREEQYNSTYRVVSVLRVLHVDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP

		SDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-N297A/DDRVV	2573	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVDNAKT KPREEQYASTYRVVSVLRVLHVDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-D265A/DDRVV	2574	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRDPEVTCVVVAVSHEDPEVKFNWYVDGVEVDNAKT KPREEQYNSTYRVVSVLRVLHVDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALA/DDRVV	2575	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVDNAK TKPREEQYNSTYRVVSVLRVLHVDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LAGA/DDRVV	2576	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVDNAK TKPREEQYNSTYRVVSVLRVLHVDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAGA/DDRVV	2577	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVDNAK TKPREEQYNSTYRVVSVLRVLHVDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAPG/DDRVV	2578	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRDPEVTCVVVDVSHEDPEVKFNWYVDGVEVDNAK TKPREEQYNSTYRVVSVLRVLHVDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIVVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

hIgG1 (with C-terminal lysine)-Q311R/M428L	2579	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-N297A/Q311R/M428L	2580	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHRDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-D265A/Q311R/M428L	2581	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALA/Q311R/M428L	2582	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LAGA/Q311R/M428L	2583	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal lysine)-LALAGA/Q311R/M428L	2584	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVLHEALHNHYTQKSLSLSPGK
hIgG1 (with C-terminal	2585	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH

lysine)-LALAPG/Q311R/M428L		KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHRDWLNGKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHNHYTQKSLSLSPGK

[0253] In some embodiments, the Fc comprises an amino acid sequence having at least 80% sequence identity with any one of the amino acid sequences listed in TABLE 3. In some embodiments, the Fc comprises an amino acid sequence having at least 85% sequence identity with any one of the amino acid sequences listed in TABLE 3. In some embodiments, the Fc comprises an amino acid sequence having at least 90% sequence identity with any one of the amino acid sequences listed in TABLE 3. In some embodiments, the Fc comprises an amino acid sequence having at least 95% sequence identity with any one of the amino acid sequences listed in TABLE 3. In some embodiments, the Fc comprises an amino acid sequence having at least 96% sequence identity with any one of the amino acid sequences listed in TABLE 3. In some embodiments, the Fc comprises an amino acid sequence having at least 97% sequence identity with any one of the amino acid sequences listed in TABLE 3. In some embodiments, the Fc comprises an amino acid sequence having at least 98% sequence identity with any one of the amino acid sequences listed in TABLE 3. In some embodiments, the Fc comprises an amino acid sequence having at least 99% sequence identity with any one of the amino acid sequences listed in TABLE 3. In some embodiments, the Fc comprises the amino acid sequence according to any one of the amino acid sequences listed in TABLE 3.

[0254] In some embodiments, the TL1A binding protein comprises a Fc comprising one or more modifications in SEQ ID NO: 201. In some embodiments, the TL1A binding protein comprises a Fc comprising one or more modifications in SEQ ID NO: 202. In some embodiments, the TL1A binding protein comprises a Fc comprising one or more modifications in SEQ ID NO: 203. In some embodiments, the Fc comprises an amino acid sequence having at least 80% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 201-203. In some embodiments, the Fc comprises an amino acid sequence having at least 85% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 201-203. In some embodiments, the Fc comprises an amino acid sequence having at least 90% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 201-203. In some embodiments, the Fc comprises an amino acid sequence having at least 95% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 201-203. In some embodiments, the Fc comprises an amino acid sequence having at least 96% sequence identity

with the amino acid sequence according to any one of SEQ ID NOs: 201-203. In some embodiments, the Fc comprises an amino acid sequence having at least 97% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 201-203. In some embodiments, the Fc comprises an amino acid sequence having at least 98% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 201-203. In some embodiments, the Fc comprises an amino acid sequence having at least 99% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 201-203. In some embodiments, the Fc comprises the amino acid sequence according to any one of SEQ ID NOs: 201-203.

[0255] In some embodiments, one or more modifications in the modified Fc is selected from the group consisting of: S298A, E333A, K334A, K326A, F243L, R292P, Y300L, V305I, P396L, F243L, R292P, Y300L, L235V, P396L, F243L, S239D, I332E, A330L, S267E, L328F, D265S, S239E, K326A, A327H, G237F, K326E, G236A, D270L, H268D, S324T, L234F, N325L, V266L, and S267D. In some embodiments, one or more modifications in the modified Fc is selected from the group consisting of S228P, M252Y, S254T, T256E, T256D, T250Q, H285D, T307A, T307Q, T307R, T307W, L309D, Q411H, Q311V, A378V, E380A, M428L, N434A, N434S, N297A, D265A, L234A, L235A, and N434W.

[0256] In some embodiments, the modified Fc comprises a specific combination of amino acid substitutions selected from the group consisting of: L234A/L235A; V234A/G237A; L235A/G237A/E318A; S228P/L236E; H268Q/V309L/A330S/A331S; C220S/C226S/C229S/P238S; C226S/C229S/E3233P/L235V/L235A; L234F/L235E/P331S; C226S/P230S; L234A/G237A; L234A/L235A/G237A; Q311R/M428L; and L234A/L235A/P329G.

[0257] In some embodiments, the modified Fc comprises a specific combination of amino acid substitutions selected from the group consisting of M428L/N434S (LS); M252Y/S254T/T256E (YTE); T250Q/M428L; T307A/E380A/N434A; T256D/T307Q (DQ); T256D/T307W (DW); M252Y/T256D (YD); T307Q/Q311V/A378V (QVV); T256D/H285D/T307R/Q311V/A378V (DDRVV); L309D/Q311H/N434S (DHS); S228P/L235E (SPLE); L234A/L235A (LALA); M428L/N434A (LA); L234A/G237A (LAGA); L234A/L235A/G237A (LALAGA); L234A/L235A/P329G (LALAPG); N297A/YTE; D265A/YTE; LALA/YTE; LAGA/YTE; LALAGA/YTE; LALAPG/YTE; N297A/LS; D265A/LS; LALA/LS; LAGA/LS; LALAGA/LS; LALAPG/LS; N297A/DHS; D265A/DHS; LALA/DHS; LAGA/DHS; LALAGA/DHS; LALAPG/DHS; SP/YTE; SPLE/YTE; SP/LS; SPLE/LS; SP/DHS; SPLE/DHS; N297A/LA; D265A/LA; LALA/LA; LAGA/LA;

LALAGA/LA; LALAPG/LA; N297A/N434A; D265A/N434A; LALA/N434A; LAGA/N434A; LALAGA/N434A; LALAPG/N434A; N297A/N434W; D265A/N434W; LALA/N434W; LAGA/N434W; LALAGA/N434W; LALAPG/N434W; N297A/DQ; D265A/DQ; LALA/DQ; LAGA/DQ; LALAGA/DQ; LALAPG/DQ; N297A/DW; D265A/DW; LALA/DW; LAGA/DW; LALAGA/DW; LALAPG/DW; N297A/YD; D265A/YD; LALA/YD; LAGA/YD; LALAGA/YD; LALAPG/YD; N297A/QVV; D265A/QVV; LALA/QVV; LAGA/QVV, LALAGA/QVV; LALAPG/QVV; N297A/DDRVV; D265A/DDRVV; LALA/DDRVV; LAGA/DDRVV; LALAGA/DDRVV; LALAPG/DDRVV; SP/Q311R/M428L; SPLE/Q311R/M428L; N297A/Q311R/M428L; D265A/Q311R/M428L; LALA/Q311R/M428L; LAGA/Q311R/M428L; LALAGA/Q311R/M428L; and LALAPG/Q311R/M428L. In some embodiments, the modified Fc comprises a specific combination of amino acid substitutions selected from the group consisting of M428L/N434S (LS) and M252Y/S254T/T256E (YTE). In some embodiments, the modified Fc comprises M428L/N434S (LS) (e.g., SEQ ID NO: 219, SEQ ID NO: 236, SEQ ID NO: 243) modifications. In some embodiments, the modified Fc comprises M252Y/S254T/T256E (YTE) (e.g., SEQ ID NO: 212, SEQ ID NO: 233, SEQ ID NO: 242) modifications.

[0258] In some embodiments, the TL1A binding proteins described herein include modifications to improve its ability to mediate effector function. Such modifications are known in the art and include afucosylation, or engineering of the affinity of the Fc towards an activating receptor, mainly FCGR3a for antibody-dependent cellular cytotoxicity (ADCC), and towards C1q for complement-dependent cytotoxicity (CDC).

[0259] In some aspects, an antibody provided herein comprises a Fc domain (e.g., IgG1) with reduced fucose content at position Asn 297 (EU numbering) compared to a naturally occurring Fc domain. Such Fc domains are known to have improved ADCC. In some aspects, such antibodies do not comprise any fucose at position Asn 297.

[0260] In some embodiments, the TL1A binding proteins described herein comprise an Fc region with one or more amino acid substitutions which improve ADCC, such as a substitution at one or more of positions 298, 333, and 334 of the Fc region. In some embodiments, an antibody provided herein comprises an Fc region with one or more amino acid substitutions at positions 239, 332, and 330.

[0261] In some embodiments, the Fc comprises an amino acid sequence having at least 80% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 204-312. In some embodiments, the Fc comprises an amino acid sequence having at least 85% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 204-312. In some

embodiments, the Fc comprises an amino acid sequence having at least 90% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 204-312. In some embodiments, the Fc comprises an amino acid sequence having at least 95% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 204-312. In some embodiments, the Fc comprises an amino acid sequence having at least 96% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 204-312. In some embodiments, the Fc comprises an amino acid sequence having at least 97% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 204-312. In some embodiments, the Fc comprises an amino acid sequence having at least 98% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 204-312. In some embodiments, the Fc comprises an amino acid sequence having at least 99% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 204-312. In some embodiments, the Fc comprises the amino acid sequence according to any one of SEQ ID NOs: 204-312.

[0262] In some embodiments, the Fc comprises a C-terminal lysine (e.g., SEQ ID NOs: 2495-2585) for use as disclosed herein. In some embodiments, the Fc comprises an amino acid sequence having at least 80% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 2495-2585. In some embodiments, the Fc comprises an amino acid sequence having at least 85% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 2495-2585. In some embodiments, the Fc comprises an amino acid sequence having at least 90% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 2495-2585. In some embodiments, the Fc comprises an amino acid sequence having at least 95% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 2495-2585. In some embodiments, the Fc comprises an amino acid sequence having at least 96% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 2495-2585. In some embodiments, the Fc comprises an amino acid sequence having at least 97% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 2495-2585. In some embodiments, the Fc comprises an amino acid sequence having at least 98% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 2495-2585. In some embodiments, the Fc comprises an amino acid sequence having at least 99% sequence identity with the amino acid sequence according to any one of SEQ ID NOs: 2495-2585. In some embodiments, the Fc comprises the amino acid sequence according to any one of SEQ ID NOs: 2495-2585.

[0263] In some embodiments, the TL1A binding proteins described herein comprise an Fc region with at least one galactose residue in the oligosaccharide attached to the Fc region. Such antibody variants may have improved CDC function.

[0264] In some embodiments, the TL1A binding proteins described herein comprise one or more alterations that improve or diminish C1q binding and/or CDC.

[0265] In some embodiments, the Fc region comprises one or more amino acid substitutions, wherein the one or more substitutions result in an increase in one or more of antibody half-life, ADCC activity, ADCP activity, or CDC activity compared with the Fc without the one or more substitutions. In some embodiments, the one or more amino acid substitutions results in increased antibody half-life at pH 6.0 compared to an antibody comprising a wild-type Fc region. In some embodiments, the antibody has an increased half-life that is about 10,000-fold, 1,000-fold, 500-fold, 100-fold, 50-fold, 20-fold, 10-fold, 9-fold, 8-fold, 7-fold, 6-fold, 5-fold, 4.5-fold, 4-fold, 3.5-fold, 3-fold, 2.5-fold, 2-fold, 1.95-fold, 1.9-fold, 1.85-fold, 1.8-fold, 1.75-fold, 1.7-fold, 1.65-fold, 1.6-fold, 1.55-fold, 1.50-fold, 1.45-fold, 1.4-fold, 1.35-fold, 1.3-fold, 1.25-fold, 1.2-fold, 1.15-fold, 1.1-fold, or 1.05-fold longer compared to an antibody comprising a wild-type Fc region.

[0266] In some embodiments, the Fc region comprises one or more amino acid substitutions, wherein the one or more substitutions result in a decrease in one or more of ADCC activity, ADCP activity, or CDC activity compared with the Fc without the one or more substitutions.

[0267] In some embodiments, the Fc region binds an Fcγ Receptor selected from the group consisting of: FcγRI, FcγRIIa, FcγRIIb, FcγRIIc, FcγRIIIa, and FcγRIIIb. In some embodiments, the Fc region binds an Fcγ Receptor with higher affinity at pH 6.0 compared to an antibody comprising a wild-type Fc region.

[0268] In some embodiments, the TL1A binding proteins described herein comprise an extended half-life (i.e., serum half-life). In some embodiments, the TL1A binding proteins described herein comprise a half-life of at least about 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 42, 56, 70, 84, 96, or more than 96 days. In some embodiments, the TL1A binding proteins described herein comprise a half-life in a range of about 10 to about 20 days, about 10 to about 30 days, about 18 days to about 30 days, about 14 days to about 96 days, about 14 days to about 84 days, about 14 days to about 70 days, about 14 days to about 56 days, about 14 days to about 42 days, about 14 days to about 28 days, of about 28 days to about 96 days, about 28 days to about 84 days, about 28 days to about 70 days, about 28 days to about 56 days, about 28 days to about 42 days, of about 42 days to about 96 days, about 42 days to about 84 days, about 42 days to about 70 days, or about 42 days to about 56 days. In some embodiments, the TL1A binding

proteins described herein comprise a half-life in a range of about 42 days to about 56 days. In some embodiments, the TL1A binding proteins described herein comprise a half-life of at least about 18 days. In some embodiments, the TL1A binding proteins described herein comprise a half-life of about 18 days. In some embodiments, the TL1A binding proteins described herein comprise a half-life of at least about 50 days. In some embodiments, the TL1A binding proteins described herein comprise a half-life of about 50 days. Methods of measuring half-life are known in the art. In some embodiments, the half-life is measured in a rodent model, such as Tg276 mice. In some embodiments, the half-life is measured in a non-human primate. In some embodiments, the half-life is measured in a human. In some embodiments, the half-life is measured following intravenous administration. In some embodiments, the half-life is measured following subcutaneous administration.

[0269] In some embodiments, the TL1A binding proteins described herein have a half-life that is at least 20% longer than a comparator antibody. In some embodiments, the comparator antibody comprises the same complementarity determining regions and variable regions but different Fc regions. In some embodiments, the half-life of the TL1A binding proteins described herein is at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% longer than the half-life of the comparator antibody. In some embodiments, the half-life of the TL1A binding proteins described herein is longer than the half-life of the comparator antibody by at least 2 fold, at least 3 fold, at least 4 fold, at least 5 fold, at least 6 fold, at least 7 fold, at least 8 fold, at least 9 fold, or at least 10 fold.

METHODS OF TREATMENT

[0270] Provided herein are methods of treatment comprising administering a TL1A binding protein. Described herein, in some embodiments, are methods of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of an TL1A binding protein comprising a modified Fc region. Described herein, in some embodiments, are methods of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of an TL1A binding protein comprising a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.1 A,

TABLE 1.1 B, and TABLE 1.1 C; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C.

[0271] In some embodiments, are methods of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of an TL1A binding protein comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; and c) a modified Fc that extends half-life of the TL1A binding protein as compared to a TL1A binding protein that does not comprise the modified Fc.

[0272] In some embodiments, are methods of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of an TL1A binding protein, wherein the TL1A binding protein specifically binds to an epitope of TL1A and comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0273] In some embodiments, the inflammatory bowel disease is Crohn's disease or ulcerative colitis. In some embodiments, the inflammatory bowel disease is ulcerative colitis. In some embodiments, the inflammatory bowel disease is Crohn's disease.

[0274] Described herein, iIn some embodiments, are methods of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of an TL1A binding protein comprising a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE

1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C.

[0275] In some embodiments, are methods of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of an TL1A binding protein comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; and c) a modified Fc that extends half-life of the TL1A binding protein as compared to a TL1A binding protein that does not comprise the modified Fc.

[0276] In some embodiments, are methods of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of an TL1A binding protein, wherein the TL1A binding protein specifically binds to an epitope of TL1A and comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0277] In some embodiments, are methods of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A binding protein described herein. In some embodiments, the inflammatory disease is psoriasis. In some embodiments, the inflammatory disease is psoriatic arthritis. In some embodiments, the inflammatory disease is hidradenitis suppurativa. In

some embodiments, administration of the TL1A binding protein is subcutaneous. In some embodiments, administration of the TL1A binding protein is intravenous.

[0278] Described herein, in certain embodiments, are methods of treating a gastrointestinal inflammatory disease in a patient in need thereof. As used herein, the term "gastrointestinal inflammatory disease" refers to a disease of the gastrointestinal tract that involves inflammatory pathways. For example, the gastrointestinal inflammatory disease includes, but is not limited to, inflammatory bowel disease, ulcerative colitis (with or without exposure to anti-tumor necrosis factor (anti-TNF), Crohn's disease (including fistulizing Crohn's Disease), chronic pouchitis, collagenous gastritis, microscopic or collagenous colitis, colitis (including immune mediated colitis), sclerosing cholangitis (including in subjects with underlying inflammatory bowel disease, celiac enteritis, ileitis. In other aspects of the disclosure, provided herein are methods of treating Intestinal Acute Graft Versus Host Disease (aGVHD) (e.g. in subjects undergoing allogeneic hematopoietic stem cell transplantation (Allo-HSCT)), steroid-refractory acute intestinal graft-versus-host disease (GvHD) (e.g. in subjects who have undergone Allo-HSCT), Type 1 diabetes (T1D) (e.g. with or without anti-TNF pre-treatment), immune checkpoint inhibitor-related colitis in subjects with genitourinary cancer or melanoma.

[0279] In some embodiments, the disease is a gastrointestinal inflammatory disease. In some embodiments, the disease is an inflammatory bowel disease. In some embodiments, the inflammatory bowel disease is Crohn's disease. In some embodiments, the inflammatory bowel disease is ulcerative colitis.

[0280] In some embodiments, are methods of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A binding protein described herein. In some embodiments, the inflammatory bowel disease is Crohn's disease or ulcerative colitis. In some embodiments, the inflammatory bowel disease is ulcerative colitis. In some embodiments, the inflammatory bowel disease is Crohn's disease. In some embodiments, administration of the TL1A binding protein is subcutaneous. In some embodiments, administration of the TL1A binding protein is intravenous.

[0281] In some embodiments, are methods of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 or 2494, wherein the TL1A antigen binding protein is an antibody.

[0282] In some embodiments, are methods of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 or 2494, wherein the TL1A antigen binding protein is an antibody.

[0283] In some embodiments, are methods of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein described herein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 12. In some embodiments, are methods of treating an inflammatory disease in an patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein described herein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156, and Tyr 238, wherein the TL1A antigen binding protein is an antibody. In some embodiments, the TL1A antigen binding protein specifically binds to the TL1A sequences at amino acid residues Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156, and Tyr 238. In some embodiments, are methods of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein described herein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 13. In some embodiments, are methods of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein described herein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 14. In some embodiments, are methods of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein described herein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Lys243, Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Ile233, Asp232, Met158, Arg156, Trp119, His118, Lys111, Phe110, His109, Gln108, Thr107, Pro106, Thr105, Gln104, Arg103, Val102, and Val101. . In some embodiments, are methods of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein described herein that

specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Gln104, and Arg103, Val102, and Val101. In some embodiments, the inflammatory disease is psoriasis. In some embodiments, the inflammatory disease is psoriatic arthritis. In some embodiments, the inflammatory disease is hidradenitis suppurativa. In some embodiments, administration of the TL1A binding protein is subcutaneous. In some embodiments, administration of the TL1A binding protein is intravenous.

[0284] In some embodiments, are methods of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein described herein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 12. In some embodiments, are methods of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein described herein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156, and Tyr 238, wherein the TL1A antigen binding protein is an antibody. In some embodiments, the TL1A antigen binding protein specifically binds to the TL1A sequences at amino acid residues Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156, and Tyr 238. In some embodiments, are methods of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein described herein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 13. In some embodiments, are methods of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein described herein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 14. In some embodiments, are methods of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein described herein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Lys243, Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Ile233, Asp232, Met158, Arg156, Trp119, His118, Lys111, Phe110, His109, Gln108, Thr107, Pro106, Thr105, Gln104, Arg103, Val102, and Val101. . In some embodiments, are methods of treating

an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein described herein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Gln104, and Arg103, Val102, and Val101. In some embodiments, the inflammatory bowel disease is Crohn's disease or ulcerative colitis. In some embodiments, the inflammatory bowel disease is ulcerative colitis. In some embodiments, the inflammatory bowel disease is Crohn's disease. In some embodiments, administration of the TL1A binding protein is subcutaneous. In some embodiments, administration of the TL1A binding protein is intravenous.

[0285] In some embodiments, the inflammatory disease is psoriasis. In some embodiments, the inflammatory disease is psoriatic arthritis. In some embodiments, the inflammatory disease is hidradenitis suppurativa.

[0286] In some embodiments, administration of the TL1A binding protein is intravenous, intratumoral, intramuscular, subcutaneous, intralesional, intraintestinal, intracolonic, intrarectal, intrapouch, or intraperitoneal. In some embodiments, administration of the TL1A binding protein is through a parenteral route such as intravenous, intramuscular, subcutaneous, intraarterial, or intraperitoneal administration. In some embodiments, administration of the TL1A binding protein is intravenous or subcutaneous. In some embodiments, administration of the TL1A binding protein is intravenous. In some embodiments, administration of the TL1A binding protein is subcutaneous.

Administration of the TL1A binding protein can occur at various intervals. In some embodiments, the TL1A binding protein is administered to the patient at least once at an interval more than 8 weeks. In some embodiments, the interval is about 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 7 weeks, 8 weeks, 9 weeks, 10 weeks, 11 weeks, 12 weeks, 13 weeks, 14 weeks, 15 weeks, 16 weeks, 17 weeks, 18 weeks, 19 weeks, 20 weeks, 21 weeks, 22 weeks, 23, weeks, 24, weeks, 25 weeks, 26 weeks or more than 26 weeks. In some embodiments, the interval is about 12 to about 22 weeks. In some embodiments, the interval is about 12 to about 20 weeks. In some embodiments, the interval is about 12 to about 18 weeks. In some embodiments, the interval is about 12 to about 16 weeks. In some embodiments, the interval is about 12 to about 14 weeks. In some embodiments, the interval is about 16 to about 26 weeks. In some embodiments, the interval is about 16 to about 24 weeks. In some embodiments, the interval is about 16 to about 22 weeks. In some embodiments, the interval is about 16 to about 20 weeks. In some embodiments, the interval is about 16 to about 18 weeks. In some

embodiments, the interval is about 20 to about 26 weeks. In some embodiments, the interval is about 20 to about 24 weeks. In some embodiments, the interval is about 20 to about 22 weeks. In some embodiments, the interval is 8 about 12 weeks. In some embodiments, the interval is 8 about 10 weeks. In some embodiments, the interval is about 12 weeks. In some embodiments, the interval is about 8 weeks.

PHARMACEUTICAL COMPOSITIONS

[0287] Provided herein are compositions, and systems, comprising a TL1A binding protein. The present disclosure also features pharmaceutical compositions that contain a therapeutically effective amount of the TL1A binding proteins described herein. The composition can be formulated for use in a variety of drug delivery systems. One or more physiologically acceptable excipients or carriers can also be included in the composition for proper formulation. Suitable formulations for use in the present disclosure are found in Remington's Pharmaceutical Sciences, Mack Publishing Company, Philadelphia, Pa., 17th ed., 1985. For a brief review of methods for drug delivery, *see, e.g.*, Langer (Science 249:1527-1533, 1990).

[0288] In some embodiments, a pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. In such embodiments, suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine (*e.g.*, arginine-HCl), histidine, or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin); fillers; monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrins); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate 80, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity

enhancing agents (such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants (see, *Remington's Pharmaceutical Sciences*, 18th ed. (Mack Publishing Company, 1990)).

[0289] In some embodiments, a pharmaceutical composition comprises one or more of: histidine; arginine or a salt thereof; ethylenediaminetetraacetic acid (EDTA); and polysorbate 80. In some embodiments, a pharmaceutical composition comprises one or more of: histidine; arginine or a salt thereof; ethylenediaminetetraacetic acid (EDTA); and poloxamer 188. In some embodiments, a pharmaceutical composition comprises one or more of: histidine; sucrose; and polysorbate 80.

[0290] In some embodiments, a pharmaceutical composition is citrate-free.

[0291] In some embodiments, a pharmaceutical composition may contain nanoparticles, *e.g.*, polymeric nanoparticles, liposomes, or micelles.

[0292] In some embodiments, a pharmaceutical composition may contain a sustained- or controlled-delivery formulation. Techniques for formulating sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. Sustained-release preparations may include, *e.g.*, porous polymeric microparticles or semipermeable polymer matrices in the form of shaped articles, *e.g.*, films, or microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides, copolymers of L-glutamic acid and gamma ethyl-L-glutamate, poly (2-hydroxyethyl-inethacrylate), ethylene vinyl acetate, or poly-D(−)-3-hydroxybutyric acid. Sustained release compositions may also include liposomes that can be prepared by any of several methods known in the art.

[0293] Pharmaceutical compositions containing an TL1A binding protein disclosed herein can be presented in a dosage unit form and can be prepared by any suitable method. A pharmaceutical composition should be formulated to be compatible with its intended route of administration. Examples of routes of administration are intravenous (IV), intradermal, inhalation, transdermal, topical, transmucosal, intrathecal and rectal administration. In some embodiments, the TL1A binding protein disclosed herein is administered intravenously or subcutaneously. In some embodiments, the TL1A binding protein disclosed herein is administered intravenously. In some embodiments, the TL1A binding protein disclosed herein is administered subcutaneously.

[0294] Useful formulations can be prepared by methods known in the pharmaceutical art. For example, see *Remington's Pharmaceutical Sciences*, 18th ed. (Mack Publishing Company, 1990). Formulation components suitable for parenteral administration include a sterile diluent

such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerin, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as EDTA; buffers such as acetates, citrates or phosphates; and agents for the adjustment of tonicity such as sodium chloride or dextrose. In some embodiments, a pharmaceutical composition is an injectable liquid formulation. In some embodiments, the formulation for parenteral administration is citrate-free. In some embodiments, the injectable liquid formulation comprises one or more of: histidine; arginine or a salt thereof; EDTA; and polysorbate 80. In some embodiments, the injectable liquid formulation comprises one or more of: histidine; arginine or a salt thereof; EDTA; and poloxamer 188.

[0295] In some embodiments, the injectable dosage form comprises at least about 100 mg/ml, at least about 150 mg/ml, at least about 180 mg/ml, or at least about 200 mg/ml of the α4β7 binding antibody. For example, the injectable dosage form comprises from at least about 100 mg/ml to at least 110 mg/ml, from at least about 110 mg/ml to at least 120 mg/ml, from at least about 120 mg/ml to at least 130 mg/ml, from at least about 130 mg/ml to at least 140 mg/ml, from at least about 140 mg/ml to at least 150 mg/ml, from at least about 150 mg/ml to at least 160 mg/ml, from at least about 160 mg/ml to at least 170 mg/ml, from at least about 170 mg/ml to at least 180 mg/ml, from at least about 180 mg/ml to at least 190 mg/ml, from at least about 190 mg/ml to at least 200 mg/ml, from at least about 200 mg/ml to at least 210 mg/ml or more of the TL1A binding protein described herein.

[0296] For intravenous or subcutaneous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor ELTM (BASF, Parsippany, NJ) or phosphate buffered saline (PBS). The carrier should be stable under the conditions of manufacture and storage, and should be preserved against microorganisms. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyetheylene glycol), and suitable mixtures thereof.

[0297] An intravenous or subcutaneous drug delivery formulation may be contained in a syringe, pen, or bag. In some embodiments, the bag is connected to a channel comprising a tube and/or a needle. In some embodiments, the formulation is a lyophilized formulation or a liquid formulation. Various devices can be used to deliver liquid formulations by subcutaneous route of administration, including on-body infusion devices, autoinjector devices, prefilled syringes, and syringes. Generally, administration time depends on volume and device, and can range from seconds to minutes.

[0298] These compositions may be sterilized by conventional sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as-is, or lyophilized, the lyophilized preparation being combined with a sterile aqueous carrier prior to administration.

[0299] A polyol, which acts as a tonicifier and may stabilize the TL1A binding protein, may also be included in the formulation. The polyol is added to the formulation in an amount which may vary with respect to the desired isotonicity of the formulation. In some embodiments, the aqueous formulation is isotonic. The amount of polyol added may also be altered with respect to the molecular weight of the polyol. For example, a lower amount of a monosaccharide (*e.g.*, mannitol) is added, compared to a disaccharide (such as trehalose). In some embodiments, the polyol which is used in the formulation as a tonicity agent is mannitol.

[0300] A detergent or surfactant may also be added to the formulation. Exemplary detergents include nonionic detergents such as polysorbates (*e.g.*, polysorbates 20, 80 etc.) or poloxamers (*e.g.*, poloxamer 188). The amount of detergent added is such that it reduces aggregation of the formulated antibody and/or minimizes the formation of particulates in the formulation and/or reduces adsorption. In some embodiments, the formulation may include a surfactant which is a polysorbate. In some embodiments, the formulation may contain the detergent polysorbate 80 or Tween 80. Tween 80 is a term used to describe polyoxyethylene (20) sorbitanmonooleate (see Fiedler, Lexikon der Hifsstoffe, Editio Cantor Verlag Aulendorf, 4th edi., 1996).

[0301] In embodiments, the protein product of the present disclosure is formulated as a liquid formulation. In some embodiments, the liquid formulation is prepared in combination with a sugar at stabilizing levels. In some embodiments, the liquid formulation is prepared in an aqueous carrier. In some embodiments, a stabilizer is added in an amount no greater than that which may result in a viscosity undesirable or unsuitable for intravenous administration. In some embodiments, the sugar is disaccharides, *e.g.*, sucrose. In some embodiments, the liquid formulation may also include one or more of a buffering agent, a surfactant, and a preservative.

[0302] In some embodiments, the pH of the liquid formulation is set by addition of a pharmaceutically acceptable acid and/or base. In some embodiments, the pharmaceutically acceptable acid is hydrochloric acid. In some embodiments, the base is sodium hydroxide.

[0303] The aqueous carrier of interest herein is one which is pharmaceutically acceptable (safe and non-toxic for administration to a human) and is useful for the preparation of a liquid formulation. Illustrative carriers include sterile water for injection (SWFI), bacteriostatic water for injection (BWFI), a pH buffered solution (*e.g.*, phosphate-buffered saline), sterile saline solution, Ringer's solution or dextrose solution.

[0304] A preservative may be optionally added to the formulations herein to reduce bacterial action. The addition of a preservative may, for example, facilitate the production of a multi-use (multiple-dose) formulation.

[0305] The TL1A binding protein may be lyophilized to produce a lyophilized formulation including the proteins and a lyoprotectant. The lyoprotectant may be sugar, *e.g.*, disaccharides. In some embodiments, the lyoprotectant is sucrose or maltose. The lyophilized formulation may also include one or more of a buffering agent, a surfactant, a bulking agent, and/or a preservative.

[0306] The amount of sucrose or maltose useful for stabilization of the lyophilized drug product may be in a weight ratio of at least 1:2 protein to sucrose or maltose. In some embodiments, the protein to sucrose or maltose weight ratio is of from 1:2 to 1:5. In some embodiments, the pH of the formulation, prior to lyophilization, is set by addition of a pharmaceutically acceptable acid and/or base. In some embodiments, the pharmaceutically acceptable acid is hydrochloric acid. In some embodiments, the pharmaceutically acceptable base is sodium hydroxide.

[0307] A patient's dose can be tailored to the approximate body weight or surface area of the patient. Other factors in determining the appropriate dosage can include the disease or condition to be treated or prevented, the severity of the disease, the route of administration, and the age, sex, and medical condition of the patient. Further refinement of the calculations necessary to determine the appropriate dosage for treatment is routinely made by those skilled in the art, especially in light of the dosage information and assays disclosed herein. The dosage can also be determined through the use of known assays for determining dosages used in conjunction with appropriate dose-response data. An individual patient's dosage can be adjusted as the progress of the disease is monitored. Blood levels of the targetable construct or complex in a patient can be measured to see if the dosage needs to be adjusted to reach or maintain an effective concentration. Pharmacogenomics may be used to determine which targetable constructs and/or complexes, and dosages thereof, are most likely to be effective for a given individual (Schmitz *et al.*, *Clinica Chimica Acta* 308: 43-53, 2001; Steimer *et al.*, *Clinica Chimica Acta* 308: 33-41, 2001).

METHODS OF PREPARATION

[0308] The TL1A binding proteins described above can be made using recombinant DNA technology well known to a skilled person in the art. For example, one or more isolated polynucleotides encoding the TL1A binding protein can be ligated to other appropriate nucleotide sequences, including, for example, constant region coding sequences, and expression

control sequences, to produce conventional gene expression constructs (*i.e.*, expression vectors) encoding the desired TL1A binding proteins. Production of defined gene constructs is within routine skill in the art.

[0309] Nucleic acids encoding desired TL1A binding proteins are provided herein. Nucleic acids encoding desired TL1A binding proteins can be incorporated (ligated) into expression vectors, which can be introduced into host cells through conventional transfection or transformation techniques. Exemplary host cells are *E. coli* cells, Chinese hamster ovary (CHO) cells, human embryonic kidney 293 (HEK 293) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (*e.g.*, Hep G2), and myeloma cells that do not otherwise produce IgG protein. Transformed host cells can be grown under conditions that permit the host cells to express the genes that encode TL1A binding proteins. In some embodiments, the nucleic acid comprises a sequence as set forth in SEQ ID NOs: 2586-2595.

SEQ ID NO	**Antibody**
2586	Antibody 10 Heavy Chain (HC)
2587	Antibody 10 Light Chain (LC)
2588	Antibody 19 Heavy Chain (HC)
2589	Antibody 19 Light Chain (LC)
2590	Antibody 47 Heavy Chain (HC)
2591	Antibody 47 Light Chain (LC)
2592	Antibody 63 Heavy Chain (HC)
2593	Antibody 63 Light Chain (LC)
2594	Antibody 86 Heavy Chain (HC)
2595	Antibody 86 Light Chain (LC)

[0310] Specific expression and purification conditions will vary depending upon the expression system employed. For example, if a gene is to be expressed in *E. coli*, it is first cloned into an expression vector by positioning the engineered gene downstream from a suitable bacterial promoter, *e.g.*, Trp or Tac, and a prokaryotic signal sequence. The expressed protein may be secreted. The expressed protein may accumulate in refractile or inclusion bodies, which can be harvested after disruption of the cells by French press or sonication. The refractile bodies then are solubilized, and the protein may be refolded and/or cleaved by methods known in the art.

[0311] If the engineered gene is to be expressed in eukaryotic host cells, *e.g.*, CHO cells, it is first inserted into an expression vector containing a suitable eukaryotic promoter, a secretion signal, a poly A sequence, and a stop codon. Optionally, the vector or gene construct may contain enhancers and introns. In embodiments involving fusion proteins comprising an TL1A

binding protein or portion thereof, the expression vector optionally contains sequences encoding all or part of a constant region, enabling an entire, or a part of, a heavy or light chain to be expressed. The gene construct can be introduced into eukaryotic host cells using conventional techniques.

[0312] In some embodiments, in order to express an TL1A binding protein, an N-terminal signal sequence is included in the protein construct. Exemplary N-terminal signal sequences include signal sequences from interleukin-2, CD-5, IgG kappa light chain, trypsinogen, serum albumin, and prolactin.

[0313] After transfection, single clones can be isolated for cell bank generation using methods known in the art, such as limited dilution, ELISA, FACS, microscopy, or Clonepix. Clones can be cultured under conditions suitable for bio-reactor scale-up and maintained expression of the TL1A binding proteins.

[0314] The TL1A binding proteins can be isolated and purified using methods known in the art including centrifugation, depth filtration, cell lysis, homogenization, freeze-thawing, affinity purification, gel filtration, ion exchange chromatography, hydrophobic interaction exchange chromatography, and mixed-mode chromatography.

[0315] In some embodiments, the titer for the TL1A antibodies ranges from about 7 g/L about 8 g/L, about 9 g/L, about 10 g/L or more. In some embodiments, the yield ranges from about 70%, about 80%, about 90% or more.

[0316] In some embodiments, are methods for producing the TL1A binding protein described herein, the method comprising expressing the TL1A binding protein in a host cell and isolating the expressed TL1A binding protein.

[0317] In some embodiments, are methods for producing a TL1A binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 or 2494. In some embodiments, are methods for producing a TL1A binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 12. In some embodiments, are methods for producing a TL1A binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 13. In some embodiments, are methods for producing a TL1A binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Table 14. In some embodiments, are methods for producing a TL1A binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues of Val 102, Arg 103, Gln 104, Glu 120, Glu 122, Leu 123, and Arg 156, and Tyr 238, wherein the TL1A antigen binding protein is an antibody. In some embodiments, the TL1A

binding protein specifically binds to the TL1A sequences at amino acid residues Lys243, Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Ile233, Asp232, Met158, Arg156, Trp119, His118, Lys111, Phe110, His109, Gln108, Thr107, Pro106, Thr105, Gln104, Arg103, Val102, and Val101. In some embodiments, the TL1A binding protein specifically binds to the TL1A sequences at amino acid residues Lys240, Thr239, Tyr238, Asp237, Val236, Leu235, Ser234, Gln104, and Arg103, Val102, and Val101.

[0318] In some embodiments, are methods to obtain an antibody that specifically binds to a certain epitope portion of a TL1A sequence comprising SEQ ID NO: 2493 or 2494. In some embodiments, the method comprises assessing whether an antibody binds specifically to the certain epitope portion, wherein the certain epitope portion has amino acid residues Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 25 227, Tyr 231, and Thr 232 of SEQ ID NO: 2493, and isolating or selecting the an antibody that binds to the certain epitope portion.

SPECIFIC EMBODIMENTS

[0319] Non-limiting specific embodiments are described below, each of which is considered to be within the present disclosure.

[0320] Embodiment 1. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 1-4 and 313-421, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 11-14 and 422-530, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 21-24 and 531-639; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 31-34 and 640-748, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 41-44 and 749-857, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 51-54 and 858-966.

[0321] Embodiment 2. The TL1A binding protein of embodiment 1, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 181-184 and 2275-2383 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 191-194 and 2384-2492.

[0322] Embodiment 3. The TL1A binding protein of any one of embodiments 1-2, wherein the TL1A binding protein comprises a Fc domain.

[0323] Embodiment 4. The TL1A binding protein of embodiment 3, wherein the Fc domain is an IgG1, IgG2 or IgG4 immunoglobulin Fc domain.

[0324] Embodiment 5. The TL1A binding protein of embodiment 3, wherein the Fc domain is an IgG1 immunoglobulin domain.

[0325] Embodiment 6. The TL1A binding protein of embodiment 3, wherein the Fc domain is an IgG2 immunoglobulin domain.

[0326] Embodiment 7. The TL1A binding protein of embodiment 3, wherein the Fc domain is an IgG4 immunoglobulin domain.

[0327] Embodiment 8. The TL1A binding protein of any one of embodiments 3-7, wherein the Fc domain amino acid comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0328] Embodiment 9. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 1, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 11, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 21; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 31, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 41, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 51.

[0329] Embodiment 10. The TL1A binding protein of embodiment 9, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 181 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 191.

[0330] Embodiment 11. The TL1A binding protein of any one of embodiments 9-10, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0331] Embodiment 12. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 2, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 12, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 22; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 32, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 42, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 52.

[0332] Embodiment 13. The TL1A binding protein of embodiment 12, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 182 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 192.

[0333] Embodiment 14. The TL1A binding protein of any one of embodiments 12-13, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0334] Embodiment 15. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 3, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 13, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 23; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 33, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 43, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 53.

[0335] Embodiment 16. The TL1A binding protein of embodiment 15, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 183 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 193.

[0336] Embodiment 17. The TL1A binding protein of any one of embodiments 15-16, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0337] Embodiment 18. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 4, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 14, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 24; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 34, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 44, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 54.

[0338] Embodiment 19. The TL1A binding protein of embodiment 18, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 184 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 194.

[0339] Embodiment 20. The TL1A binding protein of any one of embodiments 18-19, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0340] Embodiment 21. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 321, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 430, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 539; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 648, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 757, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 866.

[0341] Embodiment 22. The TL1A binding protein of embodiment 21, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2283 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2392.

[0342] Embodiment 23. The TL1A binding protein of any one of embodiments 21-22, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0343] Embodiment 24. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 341, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 450, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 559; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 668, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 777, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 886.

[0344] Embodiment 25. The TL1A binding protein of embodiment 24, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2303 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2412.

[0345] Embodiment 26. The TL1A binding protein of any one of embodiments 24-25, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0346] Embodiment 27. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 345, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 454, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 563; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 672, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 781, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 890.

[0347] Embodiment 28. The TL1A binding protein of embodiment 27, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2307 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2416.

[0348] Embodiment 29. The TL1A binding protein of any one of embodiments 27-28, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0349] Embodiment 30. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 349, (ii) a CDR2 having an amino acid sequence according

to SEQ ID NO: 458, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 567; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 676, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 785, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 894.

[0350] Embodiment 31. The TL1A binding protein of embodiment 30, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2311 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2420.

[0351] Embodiment 32. The TL1A binding protein of any one of embodiments 30-31, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0352] Embodiment 33. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 351, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 460, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 569; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 678, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 787, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 896.

[0353] Embodiment 34. The TL1A binding protein of embodiment 33, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2313 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2422.

[0354] Embodiment 35. The TL1A binding protein of any one of embodiments 33-34, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0355] Embodiment 36. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 354, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 463, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 572; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 681, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 790, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 899.

[0356] Embodiment 37. The TL1A binding protein of embodiment 36, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2316 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2425.

[0357] Embodiment 38. The TL1A binding protein of any one of embodiments 36-37, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0358] Embodiment 39. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 365, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 474, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 583; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 692, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 801, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 910.

[0359] Embodiment 40. The TL1A binding protein of embodiment 39, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2327 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2436.

[0360] Embodiment 41. The TL1A binding protein of any one of embodiments 39-40, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0361] Embodiment 42. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 371, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 480, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 589; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 698, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 807, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 916.

[0362] Embodiment 43. The TL1A binding protein of embodiment 42, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2333 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2442.

[0363] Embodiment 44. The TL1A binding protein of any one of embodiments 42-43, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0364] Embodiment 45. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 372, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 481, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 590; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 699, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 808, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 917.

[0365] Embodiment 46. The TL1A binding protein of embodiment 45, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2334 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2443.

[0366] Embodiment 47. The TL1A binding protein of any one of embodiments 45-46, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0367] Embodiment 48. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 373, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 482, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 591; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 700, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 809, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 918.

[0368] Embodiment 49. The TL1A binding protein of embodiment 48, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2335 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2444.

[0369] Embodiment 50. The TL1A binding protein of any one of embodiments 48-49, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0370] Embodiment 51. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 388, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 497, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 606; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 715, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 824, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 933.

[0371] Embodiment 52. The TL1A binding protein of embodiment 51, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ

ID NO: 2350 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2459.

[0372] Embodiment 53. The TL1A binding protein of any one of embodiments 51-52, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0373] Embodiment 54. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 394, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 503, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 612; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 721, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 830, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 939.

[0374] Embodiment 55. The TL1A binding protein of embodiment 54, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2356 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2465.

[0375] Embodiment 56. The TL1A binding protein of any one of embodiments 54-55, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0376] Embodiment 57. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 400, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 509, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 618; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 727, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 836, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 945.

[0377] Embodiment 58. The TL1A binding protein of embodiment 57, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 2362 and the VL comprises a sequence having at least 80% sequence to SEQ ID NO: 2471.

[0378] Embodiment 59. The TL1A binding protein of any one of embodiments 57-58, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0379] Embodiment 60. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 1-4 and 313-421, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 11-14 and 422-530, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 21-24 and 531-639;

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 31-34 and 640-748, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 41-44 and 749-857, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 51-54 and 858-966; and

c) a modified Fc that extends half-life of the TL1A binding protein as compared to a TL1A binding protein that does not comprise the modified Fc.

[0380] Embodiment 61. A TL1A binding protein, wherein the TL1A binding protein specifically binds to an epitope of TL1A and comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0381] Embodiment 62. A TL1A binding protein, wherein the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 or 2494, wherein the TL1A antigen binding protein is an antibody.

[0382] Embodiment 63. The TL1A binding protein of any one of embodiments 1-62, wherein the TL1A binding protein binds TL1A with a KD less than about 0.5 nanomolar (nM).

[0383] Embodiment 64. The TL1A binding protein of any one of embodiments 1-62, wherein the TL1A binding protein binds TL1A with a KD less than about 0.4 nanomolar (nM).

[0384] Embodiment 65. The TL1A binding protein of any one of embodiments 1-62, wherein the TL1A binding protein comprises a binding affinity to TL1A at least 2 fold more than a binding affinity of a comparator antibody to TL1A.

[0385] Embodiment 66. The TL1A binding protein of any one of embodiments 1-62, wherein the TL1A binding protein reduces TL1A-induced apoptosis by at least 2 fold more than a comparator antibody.

[0386] Embodiment 67. A method of treating an inflammatory bowel disease in an patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A binding protein of any one of embodiments 1-66.

[0387] Embodiment 68. The method of embodiment 67, wherein the inflammatory bowel disease is Crohn's disease or ulcerative colitis.

[0388] Embodiment 69. The method of embodiment 68, wherein the inflammatory bowel disease is ulcerative colitis.

[0389] Embodiment 70. The method of embodiment 68, wherein the inflammatory bowel disease is Crohn's disease.

[0390] Embodiment 71. The method of any one of embodiments 67-70, wherein administration of the TL1A binding protein is subcutaneous.

[0391] Embodiment 72. The method of any one of embodiments 67-70, wherein administration of the TL1A binding protein is intravenous.

[0392] Embodiment 73. A method of treating an inflammatory disease in an patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A binding protein of any one of embodiments 1-66.

[0393] Embodiment 74. The method of embodiment 73, wherein the inflammatory disease is psoriasis.

[0394] Embodiment 75. The method of embodiment 73, wherein the inflammatory disease is psoriatic arthritis.

[0395] Embodiment 76. The method of embodiment 73, wherein the inflammatory disease is hidradenitis suppurativa.

[0396] Embodiment 77. The method of any one of embodiments 73-76, wherein administration of the TL1A binding protein is subcutaneous.

[0397] Embodiment 78. The method of any one of embodiments 73-76, wherein administration of the TL1A binding protein is intravenous.

[0398] Embodiment 79. A method of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 or 2494, wherein the TL1A antigen binding protein is an antibody.

[0399] Embodiment 80. The method of embodiment 79, wherein the inflammatory bowel disease is Crohn's disease or ulcerative colitis.

[0400] Embodiment 81. The method of embodiment 80, wherein the inflammatory bowel disease is ulcerative colitis.

[0401] Embodiment 82. The method of embodiment 80, wherein the inflammatory bowel disease is Crohn's disease.

[0402] Embodiment 83. The method of any one of embodiments 79-82, wherein administration of the TL1A binding protein is subcutaneous.

[0403] Embodiment 84. The method of any one of embodiments 79-82, wherein administration of the TL1A binding protein is intravenous.

[0404] Embodiment 85. A method of treating an inflammatory disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 or 2494, wherein the TL1A antigen binding protein is an antibody characterized by:

binding to an epitope on TL1A recognized by an antibody disclosed herein, such as antibody 1, 2, 3, 4, 6, 8, 10, 47, 49, 63, or 69; or

bidning specifically to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Thr 107, Gln 108, His 109, Phe 110, Lys 111, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 231, Asp 232, Ile 233, Ser 234, Tyr 238, Thr 239, Lys 240, and Lys 243; or

bidning to the TL1A sequences at ten or more amino acid residues Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 231, Asp 232, Ile 233, Ser 234, Leu 235, Val 236, Asp 237, Tyr 238, Thr 239, Lys 240, and Lys 243; or

having a CDR sequence of an antibody of Table 1.1B; or

having a having a heavy chain-light chain of an antibody of Table 2.1.

[0405] Embodiment 86. The method of embodiment 85, wherein the inflammatory disease is psoriasis.

[0406] Embodiment 87. The method of embodiment 85, wherein the inflammatory disease is psoriatic arthritis.

[0407] Embodiment 88. The method of embodiment 85, wherein the inflammatory disease is hidradenitis suppurativa.

[0408] Embodiment 89. The method of any one of embodiments 85-88, wherein administration of the TL1A binding protein is subcutaneous.

[0409] Embodiment 90. The method of any one of embodiments 85-88, wherein administration of the TL1A binding protein is intravenous.

[0410] Embodiment 91. A method for producing the TL1A binding protein of any one of embodiments 1-66, the method comprising expressing the TL1A binding protein in a host cell and isolating the expressed TL1A binding protein.

[0411] Embodiment 92. A method for producing a TL1A binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 or 2494, wherein the TL1A antigen binding protein is an antibody.

[0412] Embodiment 93. A method to obtain an antibody that specifically binds to a certain epitope portion of a TL1A sequence comprising SEQ ID NO: 2493 or 2494, wherein the method comprises assessing whether an antibody binds specifically to the certain epitope portion, and isolating or selecting the antibody that binds to the certain epitope portion.

[0413] Embodiment 94. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 5-10, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 15-20, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 25-30; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 35-40, (ii) a CDR2 having an amino acid

sequence according to any one of SEQ ID NOs: 45-50, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 55-60.

[0414] Embodiment 95. The TL1A binding protein of embodiment 94, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 185-190 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 195-200.

[0415] Embodiment 96. The TL1A binding protein of any one of embodiments 94-95, wherein the TL1A binding protein comprises a Fc domain.

[0416] Embodiment 97. The TL1A binding protein of embodiment 96, wherein the Fc domain is an IgG1, IgG2 or IgG4 immunoglobulin Fc domain.

[0417] Embodiment 98. The TL1A binding protein of embodiment 96, wherein the Fc domain is an IgG1 immunoglobulin domain.

[0418] Embodiment 99. The TL1A binding protein of embodiment 96, wherein the Fc domain is an IgG2 immunoglobulin domain.

[0419] Embodiment 100. The TL1A binding protein of embodiment 96, wherein the Fc domain is an IgG4 immunoglobulin domain.

[0420] Embodiment 101. The TL1A binding protein of any one of embodiments 96-100, wherein the Fc domain amino acid comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0421] Embodiment 102. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 5, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 15, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 25; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 35, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 45, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 50.

[0422] Embodiment 103. The TL1A binding protein of embodiment 102, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 185 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 195.

[0423] Embodiment 104. The TL1A binding protein of any one of embodiments 102-103, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0424] Embodiment 105. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 6, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 16, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 26; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 36, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 46, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 56.

[0425] Embodiment 106. The TL1A binding protein of embodiment 105, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 186 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 196.

[0426] Embodiment 107. The TL1A binding protein of any one of embodiments 105-106, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0427] Embodiment 108. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 7, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 17, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 27; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 37, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 47, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 57.

[0428] Embodiment 109. The TL1A binding protein of embodiment 108, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 187 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 197.

[0429] Embodiment 110. The TL1A binding protein of any one of embodiments 108-109, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0430] Embodiment 111. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 8, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 18, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 28; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 38, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 48, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 58.

[0431] Embodiment 112. The TL1A binding protein of embodiment 111, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 188 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 198.

[0432] Embodiment 113. The TL1A binding protein of any one of embodiments 111-112, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0433] Embodiment 114. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 9, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 19, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 29; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 39, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 49, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 59.

[0434] Embodiment 115. The TL1A binding protein of embodiment 114, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 189 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 199.

[0435] Embodiment 116. The TL1A binding protein of any one of embodiments 114-115, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0436] Embodiment 117. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 10, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 20, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 30; and

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to SEQ ID NO: 40, (ii) a CDR2 having an amino acid sequence according to SEQ ID NO: 50, and (iii) a CDR3 having an amino acid sequence according to SEQ ID NO: 60.

[0437] Embodiment 118. The TL1A binding protein of embodiment 117, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 190 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 200.

[0438] Embodiment 119. The TL1A binding protein of any one of embodiments 117-118, wherein the TL1A binding protein comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0439] Embodiment 120. A TL1A binding protein comprising:

a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 5-10, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 15-20, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 25-30;

b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of SEQ ID NOs: 35-40, (ii) a CDR2 having an amino acid sequence according to any one of SEQ ID NOs: 45-50, and (iii) a CDR3 having an amino acid sequence according to any one of SEQ ID NOs: 55-60; and

c) a modified Fc that extends half-life of the TL1A binding protein as compared to a TL1A binding protein that does not comprise the modified Fc.

[0440] Embodiment 121. A TL1A binding protein, wherein the TL1A binding protein specifically binds to an epitope of TL1A and comprises a Fc domain comprising amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0441] Embodiment 122. A TL1A binding protein, wherein the TL1A binding protein specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 102, Arg 103, Gln 104, Thr 105, Thr 107, Gln 108, His 118, Trp 119, Glu 120, Glu 122, Leu 123, Gly 124, Lys 137, Arg 156, Gly 157, Met 158, Ser 227, Tyr 231, and Thr 232, wherein the TL1A antigen binding protein is an antibody.

[0442] Embodiment 123. The TL1A binding protein of embodiment 122, wherein the TL1A binding protein specifically binds to the TL1A sequences at amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Gln 108, His 118, Glu 120, Glu 122, Leu 123, Gly 124, Asn 136, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, Thr 239.

[0443] Embodiment 124. The TL1A binding protein of any one of embodiments 94-123, wherein the TL1A binding protein binds TL1A with a KD less than about 0.5 nanomolar (nM).

[0444] Embodiment 125. The TL1A binding protein of any one of embodiments 94-123, wherein the TL1A binding protein binds TL1A with a KD less than about 0.4 nanomolar (nM).

[0445] Embodiment 126. The TL1A binding protein of any one of embodiments 94-123, wherein the TL1A binding protein comprises a binding affinity to TL1A at least 2 fold more than a binding affinity of a comparator antibody to TL1A.

[0446] Embodiment 127. The TL1A binding protein of any one of embodiments 94-123, wherein the TL1A binding protein reduces TL1A-induced apoptosis by at least 2 fold more than a comparator antibody.

[0447] Embodiment 128. A method of treating an inflammatory bowel disease in a patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A binding protein of any one of embodiments 94-127.

[0448] Embodiment 129. The method of embodiment 128, wherein the inflammatory bowel disease is Crohn's disease or ulcerative colitis.

[0449] Embodiment 130. The method of embodiment 129, wherein the inflammatory bowel disease is ulcerative colitis.

[0450] Embodiment 131. The method of embodiment 129, wherein the inflammatory bowel disease is Crohn's disease.

[0451] Embodiment 132. The method of any one of embodiments 128-131, wherein administration of the TL1A binding protein is subcutaneous.

[0452] Embodiment 133. The method of any one of embodiments 128-131, wherein administration of the TL1A binding protein is intravenous.

[0453] Embodiment 134. A method of treating an inflammatory disease in an patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A binding protein of any one of embodiments 94-127.

[0454] Embodiment 135. The method of embodiment 134, wherein the inflammatory disease is psoriasis.

[0455] Embodiment 136. The method of embodiment 134, wherein the inflammatory disease is psoriatic arthritis.

[0456] Embodiment 137. The method of embodiment 134, wherein the inflammatory disease is hidradenitis suppurativa.

[0457] Embodiment 138. The method of any one of embodiments 134-137, wherein administration of the TL1A binding protein is subcutaneous.

[0458] Embodiment 139. The method of any one of embodiments 134-137, wherein administration of the TL1A binding protein is intravenous.

[0459] Embodiment 140. A method of treating an inflammatory bowel disease in an patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Gln 108, His 118, Glu 120, Glu 122, Leu 123, Gly 124, Asn 136, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, Thr 239, wherein the TL1A antigen binding protein is an antibody.

[0460] Embodiment 141. The method of embodiment 140, wherein the TL1A antigen binding protein specifically binds to the TL1A sequences at amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Gln 108, His 118, Glu 120, Glu 122, Leu 123, Gly 124, Asn 136, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, Thr 239.

[0461] Embodiment 142. The method of any one of embodiments 140-141, wherein the inflammatory bowel disease is Crohn's disease or ulcerative colitis.

[0462] Embodiment 143. The method of embodiment 142, wherein the inflammatory bowel disease is ulcerative colitis.

[0463] Embodiment 144. The method of embodiment 142, wherein the inflammatory bowel disease is Crohn's disease.

[0464] Embodiment 145. The method of any one of embodiments 140-144, wherein administration of the TL1A binding protein is subcutaneous.

[0465] Embodiment 146. The method of any one of embodiments 140-144, wherein administration of the TL1A binding protein is intravenous.

[0466] Embodiment 147. A method of treating an inflammatory disease in an patient in need thereof, the method comprising subcutaneously or intravenously administering to the patient an effective amount of a TL1A antigen binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Gln 108, His 118, Glu 120, Glu 122, Leu 123, Gly 124, Asn 136, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, Thr 239, wherein the TL1A antigen binding protein is an antibody.

[0467] Embodiment 148. The method of embodiment 147, wherein the TL1A antigen binding protein specifically binds to the TL1A sequences at amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Gln 108, His 118, Glu 120, Glu 122, Leu 123, Gly 124, Asn 136, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, Thr 239.

[0468] Embodiment 149. The method of any one of embodiments 147-148, wherein the inflammatory disease is psoriasis.

[0469] Embodiment 150. The method of any one of embodiments 147-148, wherein the inflammatory disease is psoriatic arthritis.

[0470] Embodiment 151. The method of any one of embodiments 147-148, wherein the inflammatory disease is hidradenitis suppurativa.

[0471] Embodiment 152. The method of any one of embodiments 147-151, wherein administration of the TL1A binding protein is subcutaneous.

[0472] Embodiment 153. The method of any one of embodiments 147-151, wherein administration of the TL1A binding protein is intravenous.

[0473] Embodiment 154. A method for producing the TL1A binding protein of any one of embodiments 94-127, the method comprising expressing the TL1A binding protein in a host cell and isolating the expressed TL1A binding protein.

[0474] Embodiment 155. A method for producing a TL1A binding protein that specifically binds to a TL1A polypeptide comprising SEQ ID NO: 2493 at any one of amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Gln 108, His 118, Glu 120, Glu 122, Leu 123, Gly 124, Asn 136, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, Thr 239, wherein the TL1A antigen binding protein is an antibody.

[0475] Embodiment 156. The method of embodiment 155, wherein the TL1A binding protein specifically binds to the TL1A sequences at amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Gln 108, His 118, Glu 120, Glu 122, Leu 123, Gly 124, Asn 136, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, Thr 239.

[0476] Embodiment 157. A method to obtain an antibody that specifically binds to a certain epitope portion of a TL1A sequence comprising SEQ ID NO: 2493, wherein the method comprises assessing whether an antibody binds specifically to the certain epitope portion, wherein the certain epitope portion has amino acid residues Val 101, Val 102, Arg 103, Gln 104, Thr 105, Pro 106, Gln 108, His 118, Glu 120, Glu 122, Leu 123, Gly 124, Asn 136, Lys 137, Arg 156, Gly 157, Met 158, Ser 234, Tyr 238, Thr 239 of SEQ ID NO: 2493, and isolating or selecting the an antibody that binds to the certain epitope portion.

[0477] Embodiment 158. A TL1A binding protein comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C , (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; and b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C.

[0478] Embodiment 159. The TL1A binding protein of embodiment 159, wherein the VH comprises a sequence having at least 80% sequence identity to the amino acid sequence of any

one of VH sequences listed in TABLE 2.1 and TABLE 2.2 and the VL comprises a sequence having at least 80% sequence identity to the amino acid sequence of any one of VL sequences listed in TABLE 2.1 and TABLE 2.2.

[0479] Embodiment 160. The TL1A binding protein of embodiment 159 or embodiment 160 comprising a Fc domain, optionally wherein the Fc domain comprises any one of the amino acid sequences listed in TABLE 3.

[0480] Embodiment 161. The TL1A binding protein of embodiment 159 or embodiment 160 comprising a Fc domain, wherein the Fc domain is an IgG1, IgG2 or IgG4 immunoglobulin Fc domain.

[0481] Embodiment 162. The TL1A binding protein of embodiment 159, wherein the Fc domain amino acid comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

[0482] Embodiment 163. A TL1A binding protein comprising: a) a heavy chain variable region (VH) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRH1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRH2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRH3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; b) a light chain variable region (VL) comprising (i) a CDR1 having an amino acid sequence according to any one of CDRL1 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, (ii) a CDR2 having an amino acid sequence according to any one of CDRL2 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C, and (iii) a CDR3 having an amino acid sequence according to any one of CDRL3 sequences listed in TABLE 1.1 A, TABLE 1.1 B, and TABLE 1.1 C; and c) a modified Fc that extends half-life of the TL1A binding protein as compared to a TL1A binding protein that does not comprise the modified Fc.

[0483] Embodiment 164. The TL1A binding protein of embodiment 163, wherein the modified Fc domain amino acid comprises amino acid modifications L234A/L235A (LALA) and/or M252Y, S254T, and T256E (YTE).

EXAMPLES

[0484] The disclosure now being generally described, will be more readily understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present disclosure, and is not intended to limit the disclosure.

Example 1. Determination of Antibody Affinity to TL1A

[0485] This Example describes the binding affinity of TL1A binding proteins described herein.

[0486] Binding affinity (K_D) of antibodies to human TL1A was determined through surface plasmon resonance (SPR) using a Biacore 8K. Briefly, a SPR chip functionalized with Protein G was used to capture purified antibodies at a flow rate of 10 μL/min for 60 seconds. A paired channel with only buffer was used as reference. Subsequently, concentrations of TL1A ranging from 100 nM to 1.23 nM were injected over the surface with captured purified antibody as well as the reference channel. Regeneration of the chip between different concentrations of TL1A was performed with 10 mM Glycine HCl, pH 1.5 and antibody was again captured as previously described. Association and dissociation rate constants were subsequently determined through fitting to a 1:1 Langmuir binding model using the Biacore Insight Evaluation Software from which a K_D value was derived. Results are summarized in **Table 4A and Table 4B**. Comparator antibody 1 has an amino acid sequence substantially identical to RVT-3101 and is referred herein as RVT-3101; Comparator antibody 2 has an amino acid sequence substantially identical to MK-7240 and is referred herein as MK-7240; Comparator antibody 3 has an amino acid sequence substantially identical to TEV-48574 and is referred herein as TEV-48574. *See also* **FIGs. 2A–2B**.

Table 4A.

Antibody	Human TL1A K_D (nM)
Comparator Antibody 1 (RVT-3101)	0.60
Comparator Antibody 2 (MK-7240)	0.64
Comparator Antibody 3 (TEV-48574)	0.43
Antibody 1	0.50
Antibody 2	0.43
Antibody 3	0.01
Antibody 4	0.47
Antibody 5	0.46
Antibody 6	0.24
Antibody 7	0.33
Antibody 8	0.32
Antibody 9	0.38
Antibody 10	0.28
Antibody 11	0.770
Antibody 12	0.255
Antibody 13	0.596
Antibody 14	0.582

Antibody 15	0.408
Antibody 16	0.464
Antibody 17	0.573
Antibody 18	0.709
Antibody 19	0.451
Antibody 20	0.398
Antibody 21	0.545
Antibody 22	0.349
Antibody 23	0.575
Antibody 24	0.562
Antibody 25	0.373
Antibody 26	0.351
Antibody 27	0.522
Antibody 28	0.527
Antibody 29	0.397
Antibody 30	0.473
Antibody 31	0.694
Antibody 32	0.582
Antibody 33	0.655
Antibody 34	0.540
Antibody 35	0.171
Antibody 36	0.382
Antibody 37	0.475
Antibody 38	0.656
Antibody 39	0.279
Antibody 40	0.543
Antibody 41	0.782
Antibody 42	0.397
Antibody 43	0.365
Antibody 44	0.640
Antibody 45	0.707
Antibody 46	0.591
Antibody 47	0.451
Antibody 48	0.329
Antibody 49	0.247
Antibody 50	0.437
Antibody 51	0.646
Antibody 52	0.347
Antibody 53	0.542
Antibody 54	0.686
Antibody 55	0.588
Antibody 56	0.518
Antibody 57	0.564
Antibody 58	0.713
Antibody 59	0.755
Antibody 60	0.971
Antibody 61	0.664
Antibody 62	0.510
Antibody 63	0.249

Antibody 64	0.449
Antibody 65	0.505
Antibody 66	0.597
Antibody 67	0.648
Antibody 68	0.374
Antibody 69	0.247
Antibody 70	0.286
Antibody 71	0.312
Antibody 72	0.691
Antibody 73	0.750
Antibody 74	0.868
Antibody 75	0.611
Antibody 76	0.871
Antibody 77	0.883
Antibody 78	0.712
Antibody 79	0.929
Antibody 80	0.267
Antibody 81	0.332
Antibody 82	0.631
Antibody 83	0.859
Antibody 84	0.701
Antibody 85	0.275
Antibody 86	0.221
Antibody 87	1.07
Antibody 88	1.08
Antibody 89	0.628
Antibody 90	0.609
Antibody 91	0.525
Antibody 92	0.428
Antibody 93	0.685
Antibody 94	0.823
Antibody 95	0.607
Antibody 96	0.858
Antibody 97	0.784
Antibody 98	0.431
Antibody 99	0.614
Antibody 100	0.455
Antibody 101	0.872
Antibody 102	0.835
Antibody 103	0.760
Antibody 104	0.724
Antibody 105	0.579
Antibody 106	0.983
Antibody 107	0.527
Antibody 108	0.724
Antibody 109	0.493
Antibody 110	0.741
Antibody 111	2.36
Antibody 112	0.531

Antibody 113	0.983
Antibody 114	0.758
Antibody 115	0.294
Antibody 116	1.16
Antibody 117	1.00
Antibody 118	0.345
Antibody 119	0.450

Table 4B.

Antibody	TL1A	FasL	TRAIL	LIGHT
Antibody 10	0.15 nM	NB	NB	NB
MK-7240	0.71 nM	NB	NB	NB
RVT-3101	0.57 nM	NB	NB	NB
TEV-48574	0.44 nM	NB	NB	NB

NB = no binding

Example 2. Antibody Binding to Membrane TL1A

[0487] This Example describes antibody binding of TL1A binding proteins described herein.

[0488] Antibody binding to membrane TL1A was determined using FACS and a TL1A overexpression cell line. Briefly, HEK293 previously transduced to stably express human TL1A were cultured and harvested. The cells were stained with either 100 nM or 10 nM of purified antibody at 4 °C for 1 hour. Cells were subsequently stained with a FITC-conjugated goat anti-human IgG secondary antibody at a 1:500 dilution. Cells were incubated 4 °C for 30 minutes, protected from light. Cells were then washed and the MFI of cells in each well was recorded by FACS. The data is seen in **FIG. 1** (MFI, mean fluorescence intensity).

Example 3. Inhibition of TL1A Binding to DR3 and DcR3

[0489] This Example describes the functional blockade of TL1A binding proteins described herein.

[0490] Recombinant TL1A binding to either recombinant DR3 or DcR3 by ELISA was used to evaluate the functional blockade of antibodies against these two binding interactions. Briefly, an ELISA plate was coated with either 4 μg/mL recombinant hDR3 or 1 μg/mL recombinant hDcR3 at 4 °C overnight. This was followed by incubation with 1% BSA to block nonspecific binding, at room temperature for 2 hours. Recombinant hTL1A biotinylated at an N-terminal AviTag™ was premixed with purified antibody, with the final concentration of TL1A being 1 μg/mL in the DR3 assay or 3 ng/mL in the DcR3 assay and antibody ranging from 200 nM to

0.006 nM. This was then incubated on the plate at room temperature for 1 hour. TL1A was detected using a streptavidin-peroxidase polymer and the plate developed using TMB substrate. Between all steps, ELISA plates were thoroughly washed with washing buffer. The TMB reaction was stopped with HCl and absorbances at 450 nm were read on a microplate reader. IC_{50} values were determined as the concentration of antibody required to inhibit 50% of the maximum absorbance of TL1A detected with no antibody.

Example 4. Inhibition of TL1A-Induced Apoptosis in TF-1 Cells

[0491] This Example describes the inhibition of TL1A-induced apoptosis by TL1A binding proteins described herein.

[0492] Inhibition of apoptosis in TF-1 cells was used to evaluate the functional activity of antibodies to block TL1A-induced biological activity. Briefly, TF-1 cells were collected and seeded at 20,000 cells per well. Concurrently, human TL1A, purified antibody, and cycloheximide were premixed before adding to the wells. The final concentration of human TL1A was 25 ng/mL; the final concentration of purified antibody ranged from 50 nM to 0.023 nM, and the final concentration of cycloheximide was 1 µg/mL. Cells were incubated at 37 °C for 6 hours before using Caspase-Glo 3/7 reagent to determine degree of apoptosis. Luminescence was read on a microplate reader. IC_{50} values were determined as the concentrations of antibody required to inhibit 50% of the maximum apoptosis detected with incubation of 25 ng/mL of TL1A alone. Results are summarized in **Table 5** and **Table 6.** *See also* **FIGs. 3A–3D**.

Table 5.

Antibody	TF-1 Apoptosis Inhibition IC_{50} (nM)
Comparator Antibody 1 (RVT-3101)	0.29
Comparator Antibody 2 (MK-7240)	1.23
Comparator Antibody 3 (TEV-48574)	0.28
Antibody 1	0.36
Antibody 2	0.26
Antibody 3	0.31
Antibody 4	0.37
Antibody 5	0.32
Antibody 6	0.16
Antibody 7	0.22
Antibody 8	0.21
Antibody 9	0.21
Antibody 10	0.22

Table 6.

Antibody	TF-1 Apoptosis Inhibition IC_{50} (nM)
Comparator Antibody 1 (RVT-3101)	0.188
Comparator Antibody 2 (MK-7240)	0.857
Comparator Antibody 3 (TEV-48574)	0.204
Antibody 11	0.151
Antibody 12	0.153
Antibody 13	0.142
Antibody 14	0.125
Antibody 15	0.176
Antibody 16	0.122
Antibody 17	0.114
Antibody 18	0.175
Antibody 19	0.140
Antibody 20	0.098
Antibody 21	0.112
Antibody 22	0.128
Antibody 23	0.110
Antibody 24	0.152
Antibody 25	0.105
Antibody 26	0.167
Antibody 27	0.150
Antibody 28	0.203
Antibody 29	0.107
Antibody 30	0.193
Antibody 31	0.253
Antibody 32	0.106
Antibody 33	0.111
Antibody 34	0.137
Antibody 35	0.207
Antibody 36	0.123
Antibody 37	0.178
Antibody 38	0.159
Antibody 39	0.103
Antibody 40	0.105
Antibody 41	0.201
Antibody 42	0.127
Antibody 43	0.084
Antibody 44	0.217
Antibody 45	0.199
Antibody 46	0.121
Antibody 47	0.099
Antibody 48	0.083
Antibody 49	0.076
Antibody 50	0.090

Antibody 51	0.079
Antibody 52	0.078
Antibody 53	0.172
Antibody 54	0.175
Antibody 55	0.109
Antibody 56	0.137
Antibody 57	0.138
Antibody 58	0.205
Antibody 59	0.145
Antibody 60	0.183
Antibody 61	0.162
Antibody 62	0.131
Antibody 63	0.100
Antibody 64	0.137
Antibody 65	0.133
Antibody 66	0.293
Antibody 67	0.234
Antibody 68	0.113
Antibody 69	0.111
Antibody 70	0.097
Antibody 71	0.091
Antibody 72	0.168
Antibody 73	0.147
Antibody 74	0.183
Antibody 75	0.143
Antibody 76	0.221
Antibody 77	0.224
Antibody 78	0.230
Antibody 79	0.193
Antibody 80	0.107
Antibody 81	0.107
Antibody 82	0.098
Antibody 83	0.268
Antibody 84	0.210
Antibody 85	0.143
Antibody 86	0.120
Antibody 87	0.136
Antibody 88	0.115
Antibody 89	0.134
Antibody 90	0.189
Antibody 91	0.093
Antibody 92	0.092
Antibody 93	0.126
Antibody 94	0.147
Antibody 95	0.190
Antibody 96	0.175
Antibody 97	0.226
Antibody 98	0.105
Antibody 99	0.141

Antibody 100	0.151
Antibody 101	0.266
Antibody 102	0.194
Antibody 103	0.189
Antibody 104	0.411
Antibody 105	0.225
Antibody 106	0.219
Antibody 107	0.107
Antibody 108	0.170
Antibody 109	0.130
Antibody 110	0.183
Antibody 111	1.610
Antibody 112	0.501
Antibody 113	0.276
Antibody 114	0.133
Antibody 115	0.522
Antibody 116	0.376
Antibody 117	0.385
Antibody 118	0.608
Antibody 119	0.604

Example 5. Inhibition of IFNγ secretion

[0493] A primary human whole blood-based assay measuring IFNγ secretion was used to assess functional blockade of exogenously added TL1A. For measuring IFNγ, whole blood was added to plates precoated with Human IgG at 1 mg/mL followed by 0.04 mg/mL mouse anti-human IgG in the presence of 2.5 ng/mL IL-12 and 0.25 ng/mL IL-18. Antibodies were added directly to the wells containing whole blood and cytokines at the indicated concentrations and incubated for 24 hr at 37 °C. After 24 hr IFNγ levels are determined by ELISA.

[0494] **FIGs. 5A and 5B** show that the TL1A antibodies described herein inhibit TL1A-induced apoptosis and IFNγ secretion with comparable or lower IC50 values vs. comparator antibodies.

Example 6. Inhibition of Human IL-23 and TL1A-induced IL-17 Response in Human PBMCs

[0495] Inhibition of IL-17 response induced by human IL-23 and TL1A was used to evaluate activity of anti-TL1A antibodies in human peripheral blood mononuclear cells (PBMCs). Briefly, frozen human PBMCs from healthy donors (N=6) were seeded into 96-well plate at 5 x 10^5 cells/well. Cells were then treated with 0–500 nM of antibody, 300 ng/ml of human IL-23 and 300 ng/ml of human TL1A for 72 hours at 37°C in a 5% CO_2 incubator. After 72 hours,

supernatants were harvested, and IL-17 measured by ELISA. Anti-TL1A antibody showed a dose-dependent inhibition of IL-17 production.

Example 7. Activity and Half-life of TL1A Antibodies

[0496] This Example describes determination of half-life of TL1A antibodies *in vitro* and *in vivo* (i.e., in non-human primates (NHP)).

[0497] Half-life extension was measured via pharmacokinetic analysis in both Tg276 transgenic mice (hemizygous for human FcRn) and non-human primates given a single bolus of the TL1A antibody by intravenous and/or subcutaneous administration.

[0498] The data is seen in **FIGs. 4A-4B**. The half-life of an anti-TL1A antibody disclosed herein was determined compared to Comparator Antibody (Ab) 1 (RVT-3101) and Comparator Antibody 2 (MK-7240). The TL1A antibody disclosed herein exhibited a half-life of ~25 days versus 10–13 days for competing TL1A antibodies. Comparator Antibody 1 and Comparator Antibody 2 exhibited half-lives in humans of 20 and 19 days, respectively.

[0499] The half-life of Antibody 63 described herein is significantly extended in Tg276 mice (13–17 days) compared to RVT-3101 (~3 days) and MK-7240 (~10 days). In cynomolgus monkeys, the half-life of the TL1A antibodies described herein is at least 18 days (~19–28 days, *See* **FIG. 4D)** including about 26–28 days for Antibody 63 (*See* **FIG. 4C**), compared to an observed half-life of about 7–12 days for RVT-3101 and MK-7240. *See* **FIGs. 4C-4D** and **Table 7**.

Table 7. Half-Life

	$t_{1/2}$ (days)
Antibody 19	25.2
Antibody 47	19.0
Antibody 63	27.9
MK-7240	12.2
RVT-3101	8.5

[0500] The half-life of Antibody 10 (~13 days) is significantly extended in Tg276 mice compared to RVT-3101 (~3 days) and MK-7240 (~10 days) (*See* **FIG. 4F**). In cynomolgus monkeys, the half-life of the TL1A antibodies described herein is at least 18 days, including ~24 days for Antibody 10, compared to an observed half-life of 7–12 days for RVT-3101 and MK-7240. *See* ***FIG.* 4E**.

Example 8. TL1A Antibody Formulations

[0501] This Example describes formulations of TL1A antibodies disclosed herein.

[0502] Briefly, TL1A antibodies disclosed herein were formulated as high concentration formulations. Subcutaneous (SC) formulation concentrations in mg/mL of disclosed TL1A antibodies were measured against Comparator Antibody 1 (RVT-3101) and Comparator Antibody 2 (MK-7240). As seen in **FIGs. 6A–6C and Table 8**, TL1A antibodies disclosed herein can be formulated to high concentrations (≥200 mg/mL). In addition, the viscosity of the TL1A antibodies disclosed herein is comparable or lower than the viscosity of the comparator antibodies (*See* **FIGs. 6B-6C and Table 8**)

Table 8.

Parameter	Antibody 10	Antibody 63	RVT-3101	MK-7240	TEV-48574
Route of Admin	SC autoinjector	SC autoinjector	SC autoinjector	IV load / SC autoinjector	SC infusion (high volume)
Dose Frequency	Q12W+	Q12W+	Q4W	Q4W	Q2-4W
Concentration	≥200 mg/mL	≥200 mg/mL	100 mg/mL	60–200 mg/mL	100 mg/mL
Bioavailability	TBD	TBD	45%	>80%	ND
pH range	5.5–6.5	5.5–6.5	ND	ND	ND
Viscosity (150 g/L)	7.1 cP	10.5 cP	8.3 cP	7.3 cP	10.4 cP

Example 9. TL1A Antibody Properties

[0503] This Example describes properties of TL1A antibodies described herein.

[0504] TL1A antibodies described herein were evaluated in multiple *in vitro* and *ex vivo* assays compared to other anti-TL1A mAbs (MK-7240, RVT-3101, and TEV-48574). Binding affinity to soluble TL1A was determined by surface plasmon resonance (SPR) and binding to membrane-bound TL1A was confirmed by flow cytometry. Competitive blockade of TL1A binding to cell-surface DR3 was determined by flow cytometry, and competition against the decoy receptor, DcR3, was evaluated by ELISA.

[0505] Various parameters including half-life, viscosity, solubility, and IFNγ release in whole blood were measured of TL1A antibodies including Antibody 10 and Antibody 63 as compared to RVT-3101, MK-7240, and TEV-48574.

[0506] The data is summarized in **Table 9** and **FIGs. 7A–7F**. The data shows that the TL1A antibodies are highly stable following accelerated stress testing and have cleaner profiles compared to MK-7240 that exhibited fragmentation and RVT-3101 that exhibited chemical stability issues. Antibody 63 exhibited a 2–3X increased half-life in non-human primates (NHPs). Antibody 10 exhibited a 2–3X increased half-life in non-human primates (NHPs).

Table 9.

Parameter	**Antibody 10**	**Antibody 63**	**RVT-3101**	**MK-7240**	**TEV-48574**
NHP PK $t_{1/2}$	~24–27 days	~24–28 days	~7–13 days	~10-12 days-	~6 days
Human TL1A K_D	280 pM	250 pM	600 pM	640 pM	430 pM
Viscosity (150 g/L)	7.1 cP	10.5 cP	8.3 cP	7.3 cP	10.4 cP
Solubility	>200 mg/mL	>200 mg/mL	>200 mg/mL	>200 mg/mL	~155 mg/mL
pI	8.8	8.7	9.0	8.7	7.0
T_{onset}	59 °C	59 °C	66 °C	60 °C	59 °C
Thermal Stability (D% / week)	SEC: -0.7 ICIEF: -6.3 CE-SDS: -0.7 PTM, CDR: N/A	SEC: -0.5 ICIEF: -6.6 CE-SDS: -1.3 PTM, CDR: N/A	SEC: -0.4 ICIEF: -9.4 CE-SDS: -0.6 N55: +0.6 M63: +0.9 N100: +4.7	SEC: -0.7 ICIEF: -8.2 CE-SDS: -4.5 PTM, CDR: N/A	SEC: NT ICIEF: NT CE-SDS: NT PTM (CDR): NT
pH Stability, Acidic (D% / day)	SEC: -3.2 ICIEF: 0.5	SEC: -4.5 ICIEF: -0.7	SEC: -2.4 ICIEF: -5.0	SEC: -7.2 ICIEF: -2.0	SEC: NT ICIEF: NT
pH Stability, Basic (D% / day)	SEC: -1.5 ICIEF: -3.1	SEC: -2.6 ICIEF: -4.5	SEC: -2.8 ICIEF: -14.3	SEC: -2.9 ICIEF: -4.3	SEC: NT ICIEF: NT

Binds monomer mutant	No	Yes (K_D 170 pM)	No	Yes (K_D 130 pM)	
Relative DR3 IC_{50}	0.98	1.2	1	33	
Relative DcR3 IC_{50}	2.8	7.2	1	51	
Relative TF-1 IC_{50}	0.86	0.53	1	4.9	
Relative IFNγ IC_{50}	0.39	0.21	1	6.85	
Species cross-reactivity	Hu, Cy, Pig, Dog	Hu, Cy, Rt, Pig, Dog	Hu, Cy, Rt, Rb, Pig, Dog	Hu, Cy, Rb, Pig, Dog	

Example 9. Epitope Mapping of TL1A Antibodies

[0507] This Example describes the epitope mapping of TL1A antibodies described herein.

[0508] The epitope binding of Antibody 10 to TL1A was determined using cryogenic electron microscopy. The data is seen in **Table 10**. Antibody 5, Antibody 6, Antibody 7, Antibody 8, and Antibody 9 were also found to bind to an epitope on a single TL1A subunit distinct from RVT-3101 and TEV-48574. *See also* **FIGs. 8A–8B**.

Table 10.

Type	**Antibody 10**	**TL1A amino acid residue of SEQ ID NO: 2493**	**Energy**	**Distance (Angstrom)**
D	LC Ser32	Val102	-0.38	3.86
D	LC Tyr33	Val102	-0.76	3.89
D	HC Trp104	Val102	-0.05	3.71
D	HC Trp33	Arg103	-2.59	3.93
D	LC Tyr33	Arg103	0.16	3.94
DH	HC Asp101	Arg103	-0.09	4.1
DH	HC Leu102	Arg103	-0.69	3.95
D	HC Gly103	Arg103	0.84	3.78
DH	HC Trp104	Arg103	-2.88	3.78
DH	HC Trp104	Gln104	-0.67	4.15
D	HC Asn31	Thr105	0.39	3.79

D	HC Ala32	Thr105	-0.27	4.37
DH	HC Glu1	Thr107	-2.58	3.76
D	HC Val2	Thr107	-0.15	4.42
D	HC Gly26	Thr107	-0.02	4.27
D	HC Phe27	Thr107	-0.11	3.96
DH	HC Thr28	Thr107	0.22	3.48
D	HC Tyr108	Thr107	-0.24	4.19
D	HC Gly26	Gln108	0.03	3.88
D	HC Phe27	Gln108	-0.09	3.86
D	HC Thr28	Gln108	-0.06	4.04
DH	LC Ser32	His118	-1.96	3.72
DA	HC Trp104	His118	-1.9	3.9
D	LC Ser32	Trp119	0	4.48
DH	LC Ser30	Glu120	-4.02	3.79
D	LC Ser32	Glu120	0	4.23
DH	LC Arg28	Glu122	-2.82	3.87
DH	LC Ser31	Glu122	-3.17	3.94
H	LC Ser68	Glu122	-0.7	3.8
D	LC Arg28	Leu123	-0.42	4.09
D	LC Val29	Leu123	-0.25	4.21
D	LC Ser30	Leu123	-0.79	4.14
D	LC Arg28	Gly124	0.12	4.19
D	HC Trp104	Lys137	-0.55	4
DH	HC Ile55	Arg156	-2.62	3.9
DIH	HC Asp56	Arg156	-16.13	3.78
D	HC Ile55	Gly157	-0.55	4.14
D	HC Lys54	Met158	-0.43	3.92
D	HC Ile55	Met158	-0.8	4.01
D	HC Asn31	Ser234	0.21	4.04
D	HC Trp33	Tyr238	-0.52	4.1
D	HC Ser53	Tyr238	-0.02	3.72
D	HC Ile55	Tyr238	-0.15	3.96
D	HC Asp56	Tyr238	3.49	3.66
D	HC Asp56	Thr239	0.16	3.89

D = distance; H = hydrogen bond; I = ionic / salt bridge; A = aromatic / stacking

[0509] Open-source Software PyMol was used to identify and output a list of the epitope residues in soluble TL1A polypeptide for binding for TL1A binding antibodies described herein. Soluble TL1A polypeptide amino acid sequence is underlined in Table 11 below and corresponds to Leu72-Leu251 of SEQ ID NO: 2393.

Table 11

Name	SEQ ID NO.	Sequence
Human TL1A (TNF15)-1	2493	MAEDLGLSFGETASVEMLPEHGSCRPKARSSSARWALTCCL VLLPFLAGLTTYLLVSQLRAQGEACVQFQALKGQEFAPSHQ QVYAPLRADGDKPRAHLTVVRQTPTQHFKNQFPALHWEHE LGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSE IRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTKSVCEVGS NWFQPIYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFF GAFLL

[0510] Open-source Software PyMol was used to identify and output a list of epitope residues of the soluble TL1A polypeptide that bind Antibodies 6, 8 and 10 (Table 12), Antibodies 1-4 (Table 13) and Antibodies 47, 49, 63 and 69 (Table 14) based on the cryoEM structures. Table 12 shows TL1A epitopes for Antibodies 6, 8 and 10.

Table 12.

ANTIBODY No.	6	8	10
TL1A EPITOPE RESIDUES**	SER163 (SER234)	TYR167 (TYR238)	SER163 (SER234)
	TYR167 (TYR238)	VAL30 (VAL101)	TYR167 (TYR238)
	THR168 (THR239)	VAL31 (VAL102)	THR168 (THR239)
	VAL31 (VAL102)	ARG32 (ARG103)	VAL30 (VAL101)
	ARG32 (ARG103)	GLN33 (GLN104)	VAL31 (VAL102)
	GLN33 (GLN104)	THR34 (THR105)	ARG32 (ARG103)
	PRO35 (PRO106)	GLN37 (GLN108)	GLN33 (GLN104)
	HIS47 (HIS118)	GLU49 (GLU120)	THR34 (THR105)
	GLU49 (GLU120)	GLU51 (GLU122)	PRO35 (PRO106)
	GLU51 (GLU122)	LEU52 (LEU123)	HIS47 (HIS118)
	LEU52 (LEU123)	LYS66 (LYS137)	GLU49 (GLU120)
	GLY53 (GLY124)	ARG85 (ARG156)	GLU51 (GLU122)
	ASN65 (ASN136)	GLY86 (GLY157)	LEU52 (LEU123)
	ARG85 (ARG156)	MET87 (MET158)	GLY53 (GLY124)
	GLY86 (GLY157)		ARG85 (ARG156)

	MET87 (MET158)		

**corresponding amino acid residues of SEQ ID No.: 2493 noted in parenthesis

[0511] Table 13 shows TL1A epitopes for Antibodies 1-4.

Table 13

ANTIBODY No.	1	2	3	4
TL1A EPITOPE RESIDUES**	SER135 (SER206)	PRO100 (PRO171)	LYS102 (LYS173)	TYR117
	ASN136 (ASN207)	LYS102 (LYS173)	ASP104 (ASP175)	GLU119
	SER163 (SER234)	ASP104 (ASP175)	SER105 (SER176)	PRO120
	LEU164 (LEU235)	GLN122 (GLN193)	VAL130 (VAL201)	THR121
	VAL165 (VAL236)	SER135 (SER206)	SER135 (SER206)	GLN122 (GLN193)
	ASP166 (ASP237)	ASN136 (ASN207)	ASN136 (ASN207)	THR168 (THR239)
	TYR167 (TYR238)	SER160 (SER231)	TRP137 (TRP208)	LYS169 (LYS240)
	THR168 (THR239)	ASP161 (ASP232)	PHE138 (PHE209)	GLU170 (GLU241)
	LYS169 (LYS240)	ILE162 (ILE233)	ASP161 (ILE233)	ASP171 (ASP242)
	VAL30 (VAL101)	SER163 (SER234)	ILE162 (ILE233)	VAL30 (VAL101)
	VAL31 (VAL102)	LEU164 (LEU235)	SER163 (SER234)	VAL31 (VAL102)
	ARG32 (ARG103)	VAL165 (VAL236)	LEU164 (LEU235)	ARG32 (ARG103)
	GLN33 (GLN104)	ASP166 (ASP237)	VAL165 (VAL236)	GLN33 (GLN104)
	THR34 (THR105)	TYR167 (TYR238)	ASP166 (ASP237)	HIS47 (HIS118)
	PRO35 (PRO106)	THR168 (THR239)	TYR167 (TYR238)	TRP48 (TRP119)
	THR36 (THR107)	LYS169 (LYS240)	THR168 (THR239)	GLU49 (GLU120)
	HIS47 (HIS118)	LYS172 (LYS243)	LYS169 (LYS240)	HIS50 (HIS121)
	TRP48 (TRP119)	ARG32 (ARG103)	LYS172 (LYS243)	GLU51 (GLU122)
	GLU49 (GLU120)	GLN33 (GLN104)	VAL31 (VAL102)	LEU52 (LEU123)
	HIS50 (HIS121)	THR34 (THR105)	ARG32 (ARG103)	GLY53 (GLY124)
	GLU51	PRO35	GLN33	TYR63

	(HIS122)	(PRO106)	(GLN104)	(TYR134)
	LEU52 (LEU123)	THR36 (THR107)	THR34 (THR105)	THR64 (THR135)
	GLY53 (GLY124)	GLN37 (GLN108)	PRO35 (PRO106)	
	TYR63 (TYR134)	HIS38 (HIS109)	THR36 (THR107)	
	ASN65 (ASN136)	PHE39 (PHE110)	GLN37 (GLN108)	
	ARG85 (ARG156)	LYS40 (LYS111)	HIS38 (HIS109)	
	GLY86 (GLY157)	PRO44 (PRO115)	ASN41 (ASN112)	
	MET87 (MET158)	ARG85 (ARG156)	PRO44 (PRO115)	
	THR88 (THR159)	MET87 (MET158)	LEU46 (LEU117)	
		THR88 (THR159)	ARG85 (ARG156)	
		SER89 (SER160)	GLY86 (GLY157)	
		GLU90 (GLU161)	MET87 (MET158)	
		ALA97 (ALA168)	THR88 (THR159)	
		GLY98 (GLY169)	SER89 (SER160)	
		ARG99 (ARG170)	GLU90 (GLU161)	
			ARG99 (ARG170)	

**corresponding amino acid residues of SEQ ID No.: 2493 noted in parenthesis

[0512] Table 14 shows TL1A epitopes for Antibodies 47, 49, 63 and 69.

Table 14

ANTIBODY No.	47	49	63	69
TL1A EPITOPE RESIDUES**	LYS102 (LYS173)	LYS102 (LYS173)	LYS102 (LYS173)	ASP161 (ASP232)
	MET125 (MET196)	SER135 (SER206)	SER160 (SER231)	ILE162 (ILE233)
	SER135 (SER206)	ASN136 (ASN207)	ASP161 (ASP232)	SER163 (SER234)
	SER160 (SER231)	SER160 (SER231)	ILE162 (ILE233)	LEU164 (LEU235)
	ASP161 (ASP232)	ASP161 (ASP232)	SER163 (SER234)	VAL165 (VAL236)
	ILE162 (ILE233)	ILE162 (ILE233)	LEU164 (LEU235)	ASP166 (ASP237)

	SER163 (SER234)	SER163 (SER234)	VAL165 (VAL236)	TYR167 (TYR238)
	LEU164 (LEU235)	LEU164 (LEU235)	ASP166 (ASP237)	THR168 (THR239)
	VAL165 (VAL236)	VAL165 (VAL236)	TYR167 (TYR238)	LYS169 (LYS240)
	ASP166 (ASP237)	ASP166 (ASP237)	THR168 (THR239)	LYS172 (LYS243)
	TYR167 (TYR238)	TYR167 (TYR238)	LYS169 (LYS240)	THR29 (THR100)
	THR168 (THR239)	THR168 (THR239)	LYS172 (LYS243)	VAL30 (VAL101)
	LYS169 (LYS240)	LYS169 (LYS240)	VAL30 (VAL101)	VAL31 (VAL102)
	LYS172 (LYS243)	LYS172 (LYS243)	VAL31 (VAL102)	ARG32 (ARG103)
	VAL30 (VAL101)	VAL30 (VAL101)	ARG32 (ARG103)	GLN33 (GLN104)
	VAL31 (VAL102)	VAL31 (VAL102)	GLN33 (GLN104)	THR34 (THR105)
	ARG32 (ARG103)	ARG32 (ARG103)	THR34 (THR105)	PRO35 (PRO106)
	GLN33 (GLN104)	GLN33 (GLN104)	PRO35 (PRO106)	THR36 (THR107)
	THR34 (THR105)	THR34 (THR105)	THR36 (THR107)	GLN37 (GLN108)
	PRO35 (PRO106)	PRO35 (PRO106)	GLN37 (GLN108)	HIS38 (HIS109)
	THR36 (THR107)	THR36 (THR107)	HIS38 (HIS109)	PHE39 (PHE110)
	GLN37 (GLN108)	GLN37 (GLN108)	PHE39 (PHE110)	LYS40 (LYS111)
	HIS38 (HIS109)	HIS38 (HIS109)	LYS40 (LYS111)	GLN42 (GLN113)
	PHE39 (PHE110)	PHE39 (PHE110)	LEU46 (LEU117)	PRO44 (PRO115)
	LYS40 (LYS111)	LYS40 (LYS111)	HIS47 (HIS118)	HIS47 (HIS118)
	LEU46 (LEU117)	GLN42 (GLN113)	TRP48 (TRP119)	TRP48 (TRP119)
	HIS47 (HIS118)	PRO44 (PRO115)	ARG85 (ARG156)	GLU49 (GLU120)
	TRP48 (TRP119)	LEU46 (LEU117)	MET87 (MET158)	ARG85 (ARG156)
	ARG85 (ARG156)	HIS47 (HIS118)	ARG99 (ARG170)	MET87 (MET158)
	GLY86 (GLY157)	TRP48 (TRP119)		
	MET87 (MET158)	ARG85 (ARG156)		

	ARG99 (ARG170)	MET87 (MET158)		

**corresponding amino acid residues of SEQ ID No.: 2493 noted in parenthesis

INCORPORATION BY REFERENCE

[0513] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

EQUIVALENTS

[0514] The disclosure may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The foregoing embodiments are therefore to be considered in all respects illustrative rather than limiting the disclosure described herein. Scope of the disclosure is thus indicated by the appended claims rather than by the foregoing description, and all changes that come within the meaning and range of equivalency of the claims are intended to be embraced therein.