

Señor Director

NUEVAS CREACIONES

Superintendencia de Industria y Comercio

E. S. D.

Referencia: Expediente No. **14191567**

Asunto: Solicitud de patente para: **“Moléculas de ácido nucléico que codifican enzimas EPSPS que confieren resistencia a glifosato.”**

Solicitante: DOW AGROSCIENCES LLC

Fecha de solicitud: 01 de septiembre de 2014

RESPUESTA A SEGUNDO EXÁMEN DE PATENTABILIDAD

ANDRÉS RINCÓN USCÁTEGUI, identificado como aparece al pie de mi firma, en mi condición de apoderado de la sociedad solicitante de la patente de la referencia, doy respuesta al Oficio 16212, notificado por su despacho el 30 de diciembre de 2016, para lo cual pedí plazo adicional el 24 de marzo de 2017.

I. MODIFICACIONES AL CAPÍTULO REIVINDICATORIO

En respuesta al examen de patentabilidad el solicitante decide aportar un nuevo capítulo reivindicatorio conformado por 6 reivindicaciones en las que se han incluido las siguientes modificaciones:

1. Las antiguas Reivindicaciones 5 y 7 a 10 han sido eliminadas.
2. La nueva Reivindicación 1 incluye las SEC ID NO: 185-193, las cuales tienen sustento en el listado de secuencias anexo al presente documento. Cabe aclarar que dicho listado no introduce materia nueva a la previamente divulgada en la Descripción. (ver Anexos).
3. La nueva Reivindicación 2 tiene sustento en la nueva Reivindicación 1 y en el párrafo 00241, de la página 91 de la Descripción.
4. Las nuevas Reivindicaciones 3, 4 y 5 tienen sustento en las antiguas Reivindicaciones 2, 3 y 4, respectivamente.

“EXCELENCIA LEGAL EN UN MUNDO SIN FRONTERAS”

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5. La nueva Reivindicación 6 tiene sustento en la antigua Reivindicación 6 y en el párrafo 0013 de la Descripción.

Estas modificaciones se ajustan al Artículo 34 de la Decisión 486 de 2000, ya que no constituyen una ampliación de la protección que correspondería a la divulgación contenida en la solicitud inicial.

A pesar de eliminar materia del pliego reivindicatorio originalmente presentado, mi representada no renuncia a la protección que pueda obtener sobre dicha materia y se reserva el derecho de presentar una solicitud divisional que la contenga durante el trámite de la presente solicitud.

II. EN CUANTO A LA SUPUESTA FALTA DE CLARIDAD

1. El Examinador señala que la Reivindicación 1 no es clara, puesto que no define una enzima 5-enolpiruvilshikimato-3-fosfato sintasa (EPSPS), en términos de sus características técnicas esenciales. Como resultado, la solicitante ha modificado la Reivindicación 1, la cual lista en adelante la secuencia de aminoácidos codificada por los polinucleótidos de la Reivindicación 2. Acorde a lo anterior, la objeción a este respecto se toma por superada.

2. El Examinador señala que las Reivindicaciones 2 y 3 no son claras porque no definen el vector plasmídico, especificando la secuencia recombinante que contiene. Por tanto, las Reivindicaciones 2 y 3 incluyen ahora la secuencia de nucleótidos que codifican los polipéptidos de la Reivindicación 1. Acorde a lo anterior, la objeción a este respecto se toma por superada.

3. El Examinador señala que las Reivindicaciones 4, 5 y 10 no se encuentran soportadas en la descripción, ya que no se menciona ni identifica el proceso para producir células como una línea celular. Como resultado, la solicitante desea aclarar que las Reivindicaciones han sido modificadas para mencionar que las líneas celulares comprenden polinucleótidos heterólogos, desde los cuales los polipéptidos son expresados. Acorde a lo anterior, la objeción a este respecto se toma por superada.

4. El Examinador señala que las Reivindicaciones 5 y 7 no son claras porque definen una línea celular vegetal y un método para generar una planta transgénica en términos de su resultado a alcanzar, lo cual llevaría a abarcar todas las alternativas presentes o futuras que lleguen a ese resultado. Por tanto, la solicitante desea aclarar que las antiguas Reivindicaciones 5 y 7 han sido canceladas.

También desea aclarar que, no debería ser necesario listar líneas celulares particulares, debido a que la persona versada en la materia entendería que, acorde a las divulgaciones de la Descripción y a las metodologías de rutina convencionales en el estado de la técnica, cualquier célula vegetal puede ser transformada con el fin de producir las células reclamadas en la presente invención. Acorde a lo anterior, la objeción a este respecto se toma por superada.

5. El Examinador señala que las Reivindicaciones 6 y 7 no son claras ya que no definen un método para generar una planta transgénica, a partir de sus características técnicas esenciales, es decir indicado una secuencia lógica de etapas y condiciones específicas. Como resultado, la solicitante desea aclarar que dichas reivindicaciones muestran la secuencia de codificación y el paso de transformación: no hay otras etapas o características técnicas esenciales.

El paso de Transformación es definido en el párrafo 00108 de la página 36 de la Descripción: *“tal como se usa en la presente, el término “transformación” se refiere a la transferencia e integración de un ácido nucleico o fragmento derivado dentro de un organismo huésped, lo cual resulta en la herencia genética estable. Los organismos huésped que contienen un ácido nucleico transformante se llaman organismos “transgénicos”, “recombinantes” o transformados”. Los métodos conocidos de transformación incluyen, por ejemplo la Agrobacterium tumefaciens- o transformación mediada por A. rhizogenes; transformación de fosfato de calcio; transformación de polibreno; fusión de protoplasto; electroporación; métodos ultrasónicos (por ejemplo, sonoporación); transformación de liposoma; microinyección; transformación con ADN desnudo; transformación con vectores plásmidos; transformación con vectores virales; transformación biolística (bombardeo de micropartículas); transformación mediada con WHISKERS de carburo de silicio; emisión de aerosol; y transformación mediada por PEG.”*

Acorde a lo anterior, la objeción a este respecto se toma por superada.

6. El Examinador señala que las Reivindicaciones 8 y 9 no son claras, ya que no definen un método para controlar semillas en un área bajo cultivo que contiene plantas resistentes a herbicida. A este respecto, la solicitante desea aclarar que dichas reivindicaciones han sido canceladas y por tanto la objeción a este respecto se toma por superada.

V. ESTADO DE LA TÉCNICA

Su Despacho determinó el siguiente documento como relevante para realizar el análisis de patentabilidad de la presente patente de invención:

D1, referido al documento CO2014/189988 titulado *“Péptidos sintéticos de tránsito al cloroplasto”* que se relaciona con la presentación internacional WO2013116764.

VI. EN CUANTO A LA SUPUESTA FALTA DE NOVEDAD

Con relación a las objeciones de Novedad, la solicitante desea resaltar que la presente solicitud reivindica prioridad sobre las Patentes No. 61/593,555 (1 de febrero de 2012), y 61/625,222 (17 de abril de 2012). El documento señalado como D4 fue publicado el 8 de agosto de 2013, más de un año después de las fechas de reivindicación de prioridad la presente solicitud.

Por tanto, el documento D4 no es considerado como arte previo válido para objetar la novedad de la presente solicitud, y se considera superada la objeción a este respecto.

VII. PETICIÓN

1. Puesto que se ha dado respuesta a todas las objeciones formuladas por la Dirección de Nuevas Creaciones, se solicita proceder al otorgamiento de la solicitud de patente.

VIII. ANEXOS

1. Nuevo capítulo reivindicatorio conformado por 6 reivindicaciones;
2. Listado de Secuencias.

Señor Director,

ANDRÉS RINCÓN USCÁTEGUI

C.C. 79.780.910 de Bogotá

T.P. 114.908

COLO-10975-0841-0236-4

SGC\SGC\ID-295586\WPC10975

No. M-2017-295586\SGC

CAPÍTULO REIVINDICATORIO

1. Un polímero quimérico que consiste de una 5-enolpiruvilshikimato-3-fosfato sintasa (EPSPS) y un péptido de tránsito de cloroplasto (CTP), en donde el polímero quimérico se selecciona del grupo que consiste de SEQ ID NOs: 185-193.
2. Una molécula aislada de ácido nucleico que codifica un polímero quimérico que consiste de una 5-enolpiruvilshikimato-3-fosfato sintasa (EPSPS) y un péptido de tránsito de cloroplasto (CTP), en donde la secuencia de codificación se selecciona del grupo que consiste de SEQ ID NOs: SEQ ID NO:42, SEQ ID NO:43, SEQ ID NOs:79-84, y SEQ ID NO:143.
3. La molécula de ácido nucleico de acuerdo con la Reivindicación 2, en donde la molécula es un vector plásmido.
4. El vector de acuerdo con la Reivindicación 3, en donde la secuencia nucleotídica está operativamente unida a un promotor *Arabidopsis thaliana* Ubiquitina-10 (AtUbi10).
5. Una línea celular vegetal resistente al glifosato que comprende un polinucleótido heterólogo del grupo que consiste de SEQ ID NOs: SEQ ID NO:42, SEQ ID NO:43, SEQ ID NOs:79-84, y SEQ ID NO:143, en donde la línea celular vegetal comprende además un polímero quimérico que consiste de una 5-enolpiruvilshikimato-3-fosfato sintasa (EPSPS) y un péptido de tránsito de cloroplasto (CTP), en donde el polímero quimérico se selecciona del grupo que consiste de SEQ ID NOs: 185-193.
6. Un método para generar un material de planta transgénica resistente al glifosato, que comprende:
transformar el material de planta con la molécula de ácido nucleico de acuerdo con la Reivindicación 2; de este modo produciendo un material de planta transgénica que es resistente al glifosato,
en donde el material de planta es una planta, parte de planta, órgano de planta, semilla de planta o célula de planta.

SEQUENCE LISTING

<110> Dow AgroSciences, LLC

Lira, Justin M

Cicchillo, Rob

Nair, Satish

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<151> 2012-02-01

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<151> 2012-04-17

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65 70 75 80

Arg Asp Gly Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Ala Ala Ala

85 90 95

Gly His Gly Thr Tyr Arg Phe Asp Ala Ser Pro Gln Met Arg Arg Arg

100 105 110

Pro Leu Leu Pro Leu Ser Arg Ala Leu Arg Asp Leu Gly Val Asp Leu

115 120 125

Arg His Glu Glu Ala Glu Gly His His Pro Leu Thr Val Arg Ala Ala

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260 265 270

Val Ser Val Gly Ala Asp Ala Thr Thr Val Arg Gly Thr Gly Glu Leu

275 280 285

Arg Gly Leu Thr Ala Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr

290 295 300

Leu Ala Ala Ile Ala Pro Phe Ala Ser Ala Pro Val Arg Ile Glu Asp

305 310 315 320

Val Ala Asn Thr Arg Val Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala

325 330 335

Glu Asn Leu Arg Arg Leu Gly Val Arg Val Ala Thr Gly Pro Asp Trp

340 345 350

Ile Glu Ile His Pro Gly Pro Ala Thr Gly Ala Gln Val Thr Ser Tyr

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agctgggatc gtttcttgt aaagggtggg cagaagtaca agtctcctgg caatgcttat 960

gtggaagggt acgcttcttc agctagttac ttcttggtg gtgcagccat aactggcgag 1020

acagttaccg tggaaggatg cggaactacc agcctccaag gtgatgtcaa gttcgagag 1080

gtgttgaaa agatggggtg caaagtttcc tggacagaga actcagttac tgtaacggga 1140

cctagtaggg atgcttttgg gatgcgtcac ctagggcag ttgacgtgaa catgaacaag 1200

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gagcttcgta agttgggtgc cacagttgaa gaaggggtccg attactgcgt gattactcct 1380

ccagctaaag ttaagcctgc tgagattgat acctatgatg accacagaat ggctatggcc 1440

tttagcctcg ctgcatgtgc cgatgttcca gtcacgatca aggaccctgg ctgtactaga 1500

aagacatttc ccgactactt tcaagtgctt gagtcaatca cgaaacactg a 1551

<210> 7

<211> 1551

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-3 v3 (G173A; P178S) (codon optimized)

<400> 7

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ctcagtaaga gcaatcagaa caaatcaccc ttctctgtct ccctcaaaac tcatcaacca 120

cgatcatcta gttggggatt gaagaaaagc ggaacaatgc tgaacggatc agtcattagg 180

cctgtaaagg ttactgcacg tgtgtccacg agtgaaaagg caagcgagat cgtcttacia 240

ccgattagag aaatctctgg gcttatcaag ttgcctggct ccaaactact ctccaatagg 300

atacttcttt tggctgcact gagtgaaggc acaactgttg tggacaactt gctcaactcc 360

gatgatatca actacatgct tgacgccttg aagaagttag gactcaatgt ggagagagat 420

agcgtaaca atcgtgctgt cgtagaagga tgtggtggaa tcttcctgc atctctggat 480

tctaagagcg acatcgagct ttactgggc aatgctgcaa cagccatgag atccttaact 540

gctgctgta ccgagctgg tggaaatgct agttatgtgc ttgatggtgt tccaagaatg 600

agggaaagcg caatagggga ttggtcgtc ggactcaaac agtcggtgc tgacgttgaa 660

tgtactttag gcacaaactg tcctcccgctc cgtgttaacg caaatggtgg actgcctggt 720

ggaaaagtca agtgtctgg ctccatttcc agtcaatacc ttacggcttt gctcatggct 780

gcaccacttg ccttaggtga tgtggagatt gagatcattg acaagctcat atctgttccg 840

tacgtggaaa tgacactta gctgatggaa agattcggag ttccagccga acattccgat 900

agctgggatc gtttcttgt aaaggaggcg cagaagtaca agtctcctgg aaacgcatac 960

gtggaagggt acgcttcttc agctagttac ttctggctg gtgcagccat aactggcgag 1020

acagttaccg tggaaggatg cggaactacc agcctccaag gtgatgtcaa gttcgagag 1080

gtgttgaaa agatggggtg caaagtttcc tggacagaga actcagttac tgtaacggga 1140

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gagcttcgta agttgggtgc cacagttgaa gaagggtccg attactgcgt gattactcct 1380

ccagctaaag ttaagccagc agagattgat acctatgatg accacagaat ggctatggct 1440

ttcagcctcg ctgcatgtgc cgatgttcca gtcacgatca aggacctgg ctgtactaga 1500

aagacatttc ccgactactt tcaagtgctt gagtcaatca cgaaacactg a 1551

<210> 8

<211> 1551

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-3 v4 (T174I; P178S) (codon optimized)

<400> 8

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ctcagtaaga gcaatcagaa caaatcaccc ttctctgtct ccctgaaaac tcatcaacca 120

cgatcatcta gttggggatt gaagaaaagt ggcacaatgc tgaacggatc agtcattagg 180

cctgtaaagg ttacagcctc tgtgtccacg agtgaaaagg caagcgagat cgtcttacia 240

ccgattagag aaatctctgg gcttatcaag ttgcctggct ccaaatact ctccaatagg 300

atattctttt tggctgcact gagtgaaggg acaactgttg tggacaactt gctcaactcc 360

gatgatatca actacatgct tgacgccttg aagaagttag gactcaatgt ggagagagat 420

agcgtaaca atcgtgctgt cgtagaagga tgtggtggaa tcttcctgc atctctggat 480

tctaagagcg acatcgagct ttactgggc aatgctggca tcgcatgag atccttaact 540

gctgctgta ccgagctgg tggaaatgct agttatgtgc ttgatggtgt tccaagaatg 600

agggaaagcg caatagggga ttggtgtc ggactcaaac agctcgtgc tgacgttgaa 660

tgtactttag gcacaaactg tcctcccggtg cgtgttaacg caaatggtgg actgcctggt 720

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gcaccactg ccttaggtga tgtggagatt gagatcattg acaagctcat atctgttccg 840

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agctgggatc gtttcttctg aaaggaggcg cagaagtaca agtctcctgg gaacgcatac 960

gtggaaggta acgcttctc agctagttac ttctggctg gtgcagccat aactggcgag 1020

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gtgttgaaa agatggggtg caaagtttc tggacagaga actcagttac tgtaacggga 1140

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atgccagatg tcgctatgac tttagctgta gtggcactgt tcgcagatgg tcctacaacg 1260

ataagggacg tagcctcttg gagagtcaaa gaaaccgaga ggatgatcgc catttgact 1320

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ccagctaaag ttaagccagc agagattgat acctatgatg accacagaat ggctatggcc 1440

tttagcctcg ctgcatgtgc cgatgttcca gtcacgatca aggaccctgg ctgtactaga 1500

aagacatttc ccgactactt tcaagtgctt gagtcaatca cgaaacactg a 1551

<210> 9

<211> 1533

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-7 v4 (T168I; P172S) (codon optimized)

<400> 9

atggcaatgg ctgctgtgc tactatggct gcaagcgctt cctcttccgc tgtgagctta 60

gacagagcag ctccagcacc atctaggcgt ctgccaatgc cagcagctag accagctagg 120

agaggtgcag tccgttttg gggaccaagg ggagcagctg cacgtgctac aagtgtcgca 180

gcaccagcag caccgagtgg agctgaggaa gtcgtgcttc aacctatcag agagatcagc 240

ggtgccgtcc agtccctgg gtcaaagtca ctagcaaca gaatacttct ttgagcgca 300

ttgtcagagg gcacgacagt ggtggataac cttctgaact ctgaagatgt tcactacatg 360

cttgaggctt tggaggcatt aggtctttct gttgaagccg ataaggttgc taagcgtgct 420

gtggtggttg gttgcggagg gagattccca gttgagaaag atgctcaaga ggaagttaag 480

ctgtttctgg gaaatgctgg gattgcaatg aggagcttga ctgctgctgt ggttgctgct 540

ggtggaaatg ccacatacgt cttgatgga gtcctagaa tgagagagag accgattggg 600

gatctggtgg ttggccttca gcaacttga gcagacgctg actgctttct tggaacaaac 660

tgtccacccg ttaggatcaa cgggaaagga ggtctccctg gtgggaaggt taagttgtct 720

ggatcaatct ctatgcagta tctgtcatca cttctcatgg ctgcacctct tgcacttgaa 780

gatgttgaga ttgaaatcat agacaaactc atatcagttc catacgtgga aatgacgctg 840

aagctgatgg agaggttcgg agtgacagca gagcactcag attcttggga taggttctac 900

atcaagggag gtcagaagta caaatcacct gggaacgctt acgtggaagg tgatgcctct 960

tctgcttcct acttctctgc tggagcagca atcaccggag gaactgttac tgtcgaaggt 1020

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gctaaagtta cttggaccga tacaagtgtt acagtgactg gtcctccag tcaacccttt 1140

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acgcttgccg ttgtggctct gttcgcatg ggtcccacag ccattagaga cgtggccagc 1260

tggaggggtga aagaaactga aaggatgggc gccattagaa cagagttaac caaacttgga 1320

gctactgtgg aagagggacc cgactattgc atcattacac ctcccagaa gctgaacata 1380

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gctgaggtgc cagtaacct tagagatcct ggggtgtacta ggaaaacttt ccctaactac 1500

ttcgatgtcc tttcaacatt cgtgaagaat tga 1533

<210> 10

<211> 1281

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-32 v3 (codon optimized)

<400> 10

atgacggtga tagagatacc tgggtctaag tctgttacag ccagagcact gttcttggca 60

gctgctgccg atgggacgac tactcttctt agaccattgc gtagcgatga cactgagggc 120

ttcgcagaag gactgaggaa tctgggctat gctgtggaac aagaggctga taggtggcgt 180

gtccaaggca gaccagctgg accagcagcc acggaagcag atgtctattg cagagatggt 240

gccaccaccg ctaggttcct tccgacactg gcagcagcag ctgcttccgg aacctacaga 300

ttcgacgctt cagcacagat gcgtcgtcgt ccccttgctc cattgacaag ggcaactaca 360

gccttgggtg tggatcttag acacgaagga gcagacggac atcatccgct caccgttcgt 420

gcagctggca tcgaaggagg agaattgacg ctcgacgctg gcgagtcag ccaatacttg 480

acagcactgc tcatgctcgg acctcttaca acaaagggaac ttcgcatcga agttacagaa 540

ctcgtctctg caccctacgt ggaaatcacc ctcgctatga tgagagactt tgggtggag 600

gttgagaggg aggggaatac cttcaccgtt ccaagcccat cttcaagact taggtccaat 660

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caccgcatag tcatgtcatt tgccgtcgtt ggcttcgca ctctggcct cacttacgac 1200

gaccctggct gcgtgcgtaa gaccttcctt agatttcacg aggtgtttgc cgacttcgct 1260

<210> 11

<211> 1248

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-33 v3 (codon optimized)

<400> 11

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ttcttggcag cagcagccga tggaacgaca acactgcttc gtcctctgag gtcagacgac120

acggaggggt ttgccgaggg tcttaagaat ctcggttatg ccgttgagca agaggctgac180

cgttggaggg tcgaaggcag accggatggt ccagctgctc cggatgcaga tgtctactgc240

cgtgatggtg caacgactgc acgctttctt ccaaccctcg tcgcagcagc agcttctgga300

acgtatcggt tcgacgcctc agcacagatg aggagacgtc ctttggtccc actcactagg360

gcactgacag ctcttggcgt ggatttgaga catggtggag aggaggggtca tcatccactg420

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ggagttgatg ttagcagaga aggaaacact ttcaccgtgc cgtccggagg ctatagagct 660

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gctatgggaa tcacggtgca tactgggcac gattggattg agattctccc tgggactcca 1080

aagccaacgg gaatagctac gcacggagat cacagaatcg ttatgtcctt cgcagtggt 1140

ggtttgtga cccctgggct gacatacgat gatcctggct gcgtccgcaa gactttcca 1200

aggttccacg aagttttcgc tgactttgct gcatcacccc aagcctga 1248

- <210> 12
- <211> 1368
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> DGT-1 v5 (E.coli optimized)

<400> 12

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attaaagatt ttagcggcac cattaccctg cctggtagca aaagcctgag caatcgtatt 120

ctgctgctgg cagcactgag cgaaggcacc accgttgtg ataactgct gtatagcgaa 180

gatattcatt atatgctggg tgactgcgt accctgggtc tgcgtgttga agatgataaa 240

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gcagtgttg cagccggtgg taatgcaagc tatgttctgg atggtgttc gcgtatgcgt 420

gaacgtccga ttggtgatct ggttgccggt ctgaaacagc tgggtgcaga tgttgattgt 480

tttctgggca ccaattgtcc tccggttcgt gttaatggta aaggtggtct gccgggtggt 540

aaagttaaac tgagcggtag cgtagcagc cagtatctga ccgcactgct gatggcagct 600

ccgctggcac tgggtgatgt tgaaattgaa attgtggata aactgatttc tgtgccgtat 660

gttgaaatga ccctgaaact gatggaacgt ttggtgtta gcgttgaaca tagcggtaat 720

tgggatcgtt ttctggttca tggtgccag aaatataaat ctccgggtaa tgcctttgtt 780

gaagtgatg caagcagcgc aagctatctg ctggcaggcg cagcaattac cgggtgtaca 840

attaccgtta atggttgtgg caccagcagc ctgcaggcg atgttaaatt tgccgaagtg 900

ctggaaaaaa tgggtgcaaa agtgacctgg tctgaaaata gcgttaccgt tagcgggtccg 960

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ctgcgtaaac tgggtgcaac cgttgaagaa ggtccggatt attgcgttat tacaccgccg 1200

gaaaaactga atgttaccgc cattgatacc tatgatgatc atcgtatggc aatggcattt 1260

agcctggcag catgtggtga tgttccggtg accattaaag atccgggttg tacacgtaaa 1320

acctttccag attattttga agttctggaa cgcctgacca aacattaa 1368

<210> 13

<211> 1368

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-1 v6 (G112A) (E. coli optimized)

<400> 13

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attaaagatt ttagcggcac cattaccctg cctggtagca aaagcctgag caatcgtatt 120

ctgctgctgg cagcactgag cgaaggcacc accgttgttg ataatctgct gtatagcgaa 180

gatattcatt atatgctggg tgactgcgt accctgggtc tgcgtgttga agatgataaa 240

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gaacgtccga ttggtgatct ggttgccggt ctgaaacagc tgggtgcaga tgttgattgt 480

tttctgggca ccaattgtcc tccggttcgt gttaatggta aaggtggtct gccgggtggt 540

aaagttaaac tgagcggtag cgtagcagc cagtatctga ccgactgct gatggcagct 600

ccgctggcac tgggtgatgt tgaaattgaa attgtggata aactgatttc tgtgccgtat 660

gttgaaatga ccctgaaact gatggaacgt tttggtgtta gcgttgaaca tagcggtaat 720

tgggatcggt ttctggttca tgggtgccag aaatataaat ctccgggtaa tgcctttgtt 780

gaagtgatg caagcagcgc aagctatctg ctggcaggcg cagcaattac cggtggtaca 840

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ctggaaaaaa tgggtgcaaa agtgacctgg tctgaaaata gcgttaccgt tagcgggtccg 960

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ctgcgtaaac tgggtgcaac cgttgaagaa ggtccggatt attgcgttat tacaccgccg 1200

gaaaaactga atgttaccgc cattgatacc tatgatgatc atcgatggc aatggcattt 1260

agcctggcag catgtgggta tgttccggg accattaaag atccgggttg tacacgtaaa 1320

acctttccag attattttga agttctggaa cgcctgacca aacattaa 1368

<210> 14

<211> 1368

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-1 v7 (G112A; P117S) (E. coli optimized)

<400> 14

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attaaagatt ttagcggcac cattaccctg cctggtagca aaagcctgag caatcgtatt 120

ctgctgctgg cagcactgag cgaaggcacc accgttgttg ataatctgct gtagcgaa 180

gatattcatt atatgctggg tgactgcgt accctgggtc tgcgtgttga agatgataaa 240

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gcagttgttg cagccggtgg taatgcaagc tatgttctgg atggtgttcc gcgtatgcgt 420

gaacgtccga ttggtgatct ggttgccggt ctgaaacagc tgggtgcaga tgttgattgt 480

tttctgggca ccaattgtcc tccggttcgt gttaatggta aaggtggtct gccgggtggt 540

aaagttaaac tgagcggtag cgtagcagc cagtatctga ccgcactgct gatggcagct 600

ccgctggcac tgggtgatgt tgaaattgaa attgtggata aactgatttc tgtgccgtat 660

gttgaaatga ccctgaaact gatggaacgt ttggtgtta gcgttgaaca tagcggtaat 720

tgggatcggt ttctggttca tgggtggccag aaatataaat ctccgggtaa tgcctttgtt 780

gaaggtgatg caagcagcgc aagctatctg ctggcaggcg cagcaattac cgggtgtaca 840

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ctggaaaaaa tgggtgcaaa agtgacctgg tctgaaaata gcgttaccgt tagcgggtccg 960

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ctgcgtaaac tgggtgcaac cgttgaagaa ggtccggatt attgcgttat tacaccgccg 1200

gaaaaactga atgttaccgc cattgatacc tatgatgatc atcgtatggc aatggcattt 1260

agcctggcag catgtggtga tgttccggtg accattaaag atccgggttg tacacgtaa 1320

acctttccag attattttga agttctggaa cgctgacca aacattaa 1368

<210> 15

<211> 1368

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-1 v8 (T113I; P117S) (E. coli optimized)

<400> 15

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attaaagatt ttagcggcac cattaccctg cctggtagca aaagcctgag caatcgatt 120

ctgctgctgg cagcactgag cgaaggcacc accgttgttg ataatctgct gtatagcgaa 180

gatattcatt atatgctggg tgactgcgt accctgggtc tgcgtgttga agatgataaa 240

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gcagttgttg cagccggtgg taatgcaagc tatgttctgg atggtgttcc gcgtatgcgt 420

gaacgtccga ttggtgatct ggttgccggt ctgaaacagc tgggtgcaga tgttgattgt 480

tttctgggca ccaattgtcc tccggttcgt gttaatggta aagtggtct gccgggtggt 540

aaagttaaac tgagcggtag cgtagcagc cagtatctga ccgcactgct gatggcagct 600

ccgctggcac tgggtgatgt tgaaattgaa attgtggata aactgatttc tgtccgtat 660

gttgaaatga ccctgaaact gatggaacgt tttggtgta gcgttgaaca tagcggtaat 720

tgggatcggt tctgtgtca tggtgccag aaatataaat ctccgggtaa tgcctttgtt 780

gaagtgatg caagcagcgc aagctatctg ctggcaggcg cagcaattac cggtggtaca 840

attaccgtta atggttggtg caccagcagc ctgcaggcg atgttaaatt tgccgaagt 900

ctggaaaaaa tgggtgcaaa agtgacctgg tctgaaaata gcgttaccgt tagcggtcg 960

ccgcgtgatt ttagcgtcg taaagtctg cgtggcattg atgtgaatat gaacaaaatg 1020

ccggatgttg ccatgacctt ggagttgtt gccctgttg caaatggtcc gaccgcaatt 1080

cgtgatgttg caagctggcg tgttaaagaa accgaacgca tgattgcaat ttgtaccgaa 1140

ctgcgtaaac tgggtgcaac cgttgaagaa ggtccggatt attgcgttat tacaccgccg 1200

gaaaaactga atgttaccgc cattgatacc tatgatgatc atcgatggc aatggcattt 1260

agcctggcag catgtggtga tgtccggtg accattaaag atccgggttg tacacgtaaa 1320

acctttccag attattttga agttctggaa cgctgacca aacattaa 1368

<210> 16

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-3 v6 (G105A) (E. coli optimized)

<400> 16

atgaccagcg aaaaagccag cgaaattggt ctgcagccga ttcgtgaaat tagcgggtctg 60

attaaactgc ctggtagcaa aagcctgagc aatcgtattc tgctgctggc agcactgagc 120

gaaggcacca ccgttggtga taatctgctg aacagcgacg atattaacta tatgctggat 180

gccctgaaaa aactgggtct gaatgttgaa cgtgatagcg ttaataatcg tgccgttggt 240

gaaggttggt gtggcatttt tccggcaagc ctggatagca aatccgatat cgaactgtat 300

ctgggtaatg cagccaccgc aatgcgtccg ctgaccgcag cagttaccgc agccgggtggt 360

aatgcaagct atgttctgga tgggtgtccg cgtatgcgtg aacgtccgat tggatgatctg 420

gttggtggtc tgaaacagct ggggtgcagat gttgaatgta ccctgggcac caattgtccg 480

cctgttcgtg ttaatgcaaa tgggtggtctg cctgggtgta aagttaaact gagcggtagc 540

attagcagcc agtatctgac cgactgctg atggcagctc cgctggcact gggatgatgtt 600

gaaatcgaga ttattgataa actgatcagc gttccgtatg ttgaaatgac cctgaaactg 660

atggaacgtt ttggtgttag cgagaacat agcgatagct gggatcgctt tttgttaaa 720

ggtggccaga aatataaatc tccgggtaac gcctatgttg aaggatgatgc aagcagcgca 780

tcttattttc tggcaggcgc agcaattacc ggtgaaaccg ttaccgttga aggttgcggt 840

acaaccagcc tgcagggtga tgttaaattt gccgaagtgc tggaaaaaat gggttgtaaa 900

gtgagctgga ccgaaaatag cgttaccgtt accgggccga gccgtgatgc atttggtatg 960

cgatcatctgc gtgcagttga tgtgaacatg aacaaaatgc cggatgttgc catgaccctg 1020

gcagttgttg cactgtttgc agatgggccg accaccattc gtgatgttgc aagctggcgt 1080

gttaaagaaa ccgaacgcat gattgcaatt tgtaccgaac tgcgtaaact ggtgcaacc 1140

gttgaagaag gtagcgatta ttgcgttatt acccctccgg caaaagttaa accggcagaa 1200

atcgatacct atgatgatca tcgtatggca atggcattta gcctggcagc atgtgcagat 1260

gttccggtga ccattaaaga tccgggttgt acacgtaaaa ctttccgga ttattttcag 1320

gtgctggaaa gcatcaccaa acactaataa 1350

<210> 17

<211> 1347

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-3 v7 (G105A; P112S) (codon optimized)

<400> 17

atgaccagcg aaaaagccag cgaaattgtt ctgcagccga ttcgtgaaat tagcggctctg 60

attaaactgc ctggtagcaa aagcctgagc aatcgattc tgctgctggc agcactgagc 120

gaaggcacca ccgttggtga taatctgctg aacagcgacg atattaacta tatgctggat 180

gccctgaaaa aactgggtct gaatgttgaa cgtgatagcg ttaataatcg tgccgttggt 240

gaaggttgtg gtggcathtt tccggcaagc ctggatagca aatccgatat cgaactgtat 300

ctgggtaatg cagccaccgc aatgcgtagc ctgaccgcag cagttaccgc agccgggtggt 360

aatgcaagct atgttctgga tgggtttccg cgtatgcgtg aacgtccgat tggatgatctg 420

gttggtggtc tgaaacagct ggggtgcagat gttgaatgta ccctgggcac caattgtccg 480

cctgttcgtg ttaatgcaaa tgggtggtctg cctggtggta aagttaaact gagcggtagc 540

attagcagcc agtatctgac cgactgctg atggcagctc cgctggcact gggatgatgtt 600

gaaatcgaga ttattgataa actgatcagc gttccgtatg ttgaaatgac cctgaaactg 660

atggaacgtt ttggtgttag cgagaacat agcgatagct gggatcgctt tttgttaaa 720

ggtaggccaga aatataaatc tccgggtaac gcctatgttg aaggatgatgc aagcagcgca 780

tcttattttc tggcaggcgc agcaattacc ggtgaaaccg ttaccgttga aggttgcggt 840

acaaccagcc tgcagggtga tgttaaattt gccgaagtgc tggaaaaaat gggttgtaaa 900

gtgagctgga ccgaaaatag cgttaccgtt accgggtccga gccgtgatgc atttggtatg 960

cgtcactctgc gtgcagttga tgtgaacatg aacaaaatgc cggatgttgc catgaccctg 1020

gcagttgttg cactgtttgc agatgggtccg accaccattc gtgatgttgc aagctggcgt 1080

gttaaagaaa ccgaacgcat gattgcaatt tgtaccgaac tgcgtaaact gggtgcaacc 1140

gttgaagaag gtagcgatta ttgcgttatt acccctccgg caaaagttaa accggcagaa 1200

atcgatacct atgatgatca tcgtatggca atggcattta gcctggcagc atgtgcagat 1260

gttccggtga ccattaaaga tccgggttgt acacgtaaaa cttttccgga ttattttcag 1320

gtgctggaaa gcatcaccaa acactaa 1347

<210> 18

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-3 v8 (T106I; P112S) (codon optimized)

<400> 18

atgaccagcg aaaaagccag cgaaattgtt ctgcagccga ttcgtgaaat tagcggctctg 60

attaaactgc ctggtagcaa aagcctgagc aatcgtattc tgctgctggc agcactgagc 120

gaaggcacca ccgttggtga taatctgctg aacagcgacg atattaacta tatgctggat 180

gccctgaaaa aactgggtct gaatgttgaa cgtgatagcg ttaataatcg tgccgttggt 240

gaaggttggtg gtggcatttt tccggcaagc ctggatagca aatccgatat cgaactgtat 300

ctgggtaatg caggtattgc aatgcgtagc ctgaccgag cagttaccgc agccggtggt 360

aatgcaagct atgttctgga tgggttccg cgtatgctg aacgtccgat tggatgctg 420

gtgttggtc tgaacagct gggtcagat gttgaatga ccctgggcac caattgtccg 480

cctgttcgtg ttaatgcaaa tgggtgctg cctggtgta aagttaaact gagcggtagc 540

attagcagcc agtatctgac cgactgctg atggcagctc cgctggcact gggatgatt 600

gaaatcgaga ttattgataa actgatcagc gttccgatg ttgaaatgac cctgaaactg 660

atggaacgtt ttggtgttag cgagaacat agcgatagct gggatcgctt tttgttaa 720

ggtggccaga aatataaatc tccgggtaac gcctatgtg aaggtgatgc aagcagcgca 780

tcttatttc tggcaggcgc agcaattacc ggtgaaaccg ttaccgttga aggttgcggt 840

acaaccagcc tgcagggtga tgttaaattt gccgaagtgc tggaaaaaat ggggtgtaa 900

gtgagctgga ccgaaaatag cgttaccgtt accggtccga gccgtgatgc atttggtatg 960

cgatcatctg gtgcagttga tgtgaacatg aacaaaatgc cggatgttgc catgaccctg 1020

gcagttgtg cactgtttgc agatgggccg accaccattc gtgatgttg aagctggcgt 1080

gttaaagaaa ccgaacgcat gattgcaatt tgtaccgaac tgcgtaaact gggcgcaacc 1140

gttgaagaag gtagcgatta ttgcgttatt acccctccgg caaaagttaa accggcagaa 1200

atcgatacct atgatgatca tcgtatggca atggcattta gcctggcagc atgtgcagat 1260

gttccggtga ccattaaaga tccgggttgt acacgtaaaa ctttccgga ttattttcag 1320

gtgctggaaa gcatcaccaa acactaataa 1350

<210> 19

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-7 v5 (E. coli optimized)

<400> 19

atggcaacca gcgttcagc accggcagct ccgtctggtg ccgaagaagt tgttctgcag 60

ccgattctg aaattagcgg tgcagttcag ctgcctggta gaaaagcct gagcaatcgt 120

attctgctgc tgtctgcact gagcgaaggc accaccgttg tgataatct gctgaatagc 180

gaagatgtgc attatatgct ggaagcactg gaagccctgg gtctgagcgt tgaagcagat 240

aaagtgcaa aacgtgccgt tgttgttgtg tgggtggtc gttttccggt tgaaaaagat 300

gcacaggaag aagttaaact gtttctgggt aatgccggta ccgcaatgcg tccgctgacc 360

gcagcagttg ttgcagccgg tggtaatgca acctatgttc tggatgggtg tccgcgtatg 420

cgtaacgtc cgattggtga tctggtgtt ggtctgcagc agctgggtgc agatgcagat 480

tgttttctgg gcaccaattg tcctccggtt cgtattaatg gtaaagggtg tctgccgggt 540

ggtaaagtta aactgagcgg tagcattagc agccagtatc tgagcagcct gctgatggca 600

gcaccgctgg cactggaaga tgtggaaatt gaaattattg ataaactgat tagcgtgccg 660

tatgttgaaa tgaccctgaa actgatggaa cgttttgggt ttaccgcaga acatagcgat 720

agctgggatc gcttttatat taaagggtgc cagaaatata aatctccggg taatgcctat 780

gttgaagggt atgcaagcag cgcaagctat tttctggcag gcgcagcaat taccggtggc 840

accgttaccg ttgaagggtg tggtaacaac agcctgcagg gtgatgttaa attgccgaa 900

gtgctggaaa tgatgggtgc aaaagttacc tggaccgata ccagcggtac cgttaccggt 960

ccgccgcgtc agccgtttgg tcgtaaacad ctgaaagccg tggatgtgaa tatgaataaa 1020

atgccggatg ttgcatgac cctggcagtt gttgccctgt ttgcagatgg tccgaccgca 1080

attcgtgatg ttgcaagctg gcgtgttaaa gaaaccgaac gtatgggtgc aattcgtacc 1140

gaactgacca aactgggtgc aaccgttgaa gaaggtccgg attattgcat tattacaccg 1200

ccgaaaaaac tgaatattac cgccattgat acctatgatg atcatcgtat ggcaatggca 1260

tttagcctgg cagcatgtgc agaagttccg gttaccattc gtgatccggg ttgtacacgt 1320

aaaacctttc cgaattattt tgatgttctg agcacctttg tgaaaaatta a 1371

<210> 20

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-7 v6 (G113A) (E. coli optimized)

<400> 20

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ccgattcgtg aaattagcgg tgcagttcag ctgcctggta gcaaaagcct gagcaatcgt 120

attctgctgc tgtctgcact gagcgaaggc accaccgttg ttgataatct gctgaatagc 180

gaagatgtgc attatatgct ggaagcactg gaagccctgg gtctgagcgt tgaagcagat 240

aaagttgcaa aacgtgccgt tgttggtggt tgtggtggtc gttttccggt tgaaaaagat 300

gcacaggaag aagttaaact gtttctgggt aatgccgcaa ccgcaatgcg tccgctgacc 360

gcagcagttg ttgcagccgg tggtaatgca acctatgttc tggatggtgt tccgcgtatg 420

cgtaacgtc cgattggtga tctggtgtt ggtctgcagc agctgggtgc agatgcagat 480

tgttttctgg gcaccaattg tcctccggtt cgtattaatg gtaaaggtgg tctgccgggt 540

ggtaaagtta aactgagcgg tagcattagc agccagtatc tgagcagcct gctgatggca 600

gcaccgctgg cactggaaga tgtggaaatt gaaattattg ataaactgat tagcgtgccg 660

tatgttgaaa tgaccctgaa actgatggaa cgttttggtg ttaccgcaga acatagcgat 720

agctgggatc gcttttatat taaaggtggc cagaaatata aatctccggg taatgcctat 780

gttgaagtg atgcaagcag cgcaagctat tttctggcag gcgcagcaat taccggtggc 840

accgttaccg ttgaaggttg tggtaacaac agcctgcagg gtgatgttaa atttgccgaa 900

gtgctggaaa tgatgggtgc aaaagttacc tggaccgata ccagcggtac cgttaccggt 960

ccgccgcgtc agccgtttgg tcgtaaacad ctgaaagccg tggatgtgaa tatgaataaa 1020

atgccgatg ttgcatgac cctggcagtt gttgccctgt ttgcagatgg tccgaccgca 1080

attcgtgatg ttgaagctg gcgtgttaaa gaaaccgaac gtatggttgc aattcgtacc 1140

gaactgacca aactgggtgc aaccgttgaa gaaggtccgg attattgcat tattacaccg 1200

ccggaaaaac tgaatattac cgccattgat acctatgatg atcatcgtat ggcaatggca 1260

tttagcctgg cagcatgtgc agaagttccg gttaccattc gtgatccggg ttgtacacgt 1320

aaaacctttc cgaattattt tgatgttctg agcacctttg tgaaaaatta a 1371

<210> 21

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-7 v7 (G113A; P117S) (codon optimized)

<400> 21

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ccgattcgtg aaattagcgg tgcagttcag ctgcctggta gcaaaagcct gagcaatcgt 120

attctgctgc tgtctgcact gagcgaaggc accaccgttg ttgataatct gctgaatagc 180

gaagatgtgc attatatgct ggaagcactg gaagccctgg gtctgagcgt tgaagcagat 240

aaagtgcaa aacgtgccgt tgttgttggg tgtggtgggc gttttccggt tgaaaaagat 300

gcacaggaag aagttaaact gtttctgggt aatgccgcaa ccgcaatgcg tagcctgacc 360

gcagcagttg ttgcagccgg tggtaatgca acctatgttc tggatggtgt tccgcgtatg 420

cgtgaacgtc cgattggtga tctggttgtt ggtctgcagc agctgggtgc agatgcagat 480

tgttttctgg gcaccaattg tcctccggtt cgtattaatg gtaaaggtgg tctgccgggt 540

ggtaaagtta aactgagcgg tagcattagc agccagtatc tgagcagcct gctgatggca 600

gcaccgctgg cactggaaga tgtggaaatt gaaattattg ataaactgat tagcgtgccg 660

tatgttgaaa tgaccctgaa actgatggaa cgttttggtg ttaccgcaga acatagcga 720

agctgggatc gcttttatat taaaggtggc cagaaatata aatctccggg taatgcctat 780

gttgaagggtg atgcaagcag cgcaagctat tttctggcag gcgcagcaat taccggtggc 840

accgttaccg ttgaaggttg tggtaacaacc agcctgcagg gtgatgttaa attgccgaa 900

gtgctggaaa tgatgggtgc aaaagttacc tggaccgata ccagcggtac cgttaccggt 960

ccgccgcgtc agccgtttgg tcgtaaacad ctgaaagccg tggatgtgaa tatgaataaa 1020

atgccggatg ttgcatgac cctggcagtt gttgccctgt ttgcagatgg tccgaccgca 1080

attcgtgatg ttgcaagctg gcgtgttaaa gaaaccgaac gtatggttgc aattcgtacc 1140

gaactgacca aactgggtgc aaccgttgaa gaaggtccgg attattgcat tattacaccg 1200

ccggaaaaac tgaatattac cgccattgat acctatgatg atcatcgtat ggcaatggca 1260

tttagcctgg cagcatgtgc agaagttccg gttaccattc gtgatccggg ttgtacacgt 1320

aaaacctttc cgaattattt tgatgttctg agcaccttgc tgaaaaatta a 1371

<210> 22

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-7 v8 (T114I; P117S) (E. coli optimized)

<400> 22

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ccgattcgtg aaattagcgg tgcagttcag ctgcctggta gcaaaagcct gagcaatcgt 120

attctgctgc tgtctgcact gagcgaaggc accaccgttg ttgataatct gctgaatagc 180

gaagatgtgc attatatgct ggaagcactg gaagccctgg gtctgagcgt tgaagcagat 240

aaagttgcaa aacgtgccgt tgttggtggt tgtgggtggtc gttttccggt tgaaaaagat 300

gcacaggaag aagttaaact gtttctgggt aatgccggtg ttgcaatgcg tagcctgacc 360

gcagcagttg ttgcagccgg tggtaatgca acctatgttc tggatggtgt tccgcgtatg 420

cgtgaacgtc cgattggtga tctggttgtt ggtctgcagc agctgggtgc agatgcagat 480

tgttttctgg gcaccaattg tcctccggtt cgtattaatg gtaaagggtg tctgccgggt 540

ggtaaagtta aactgagcgg tagcattagc agccagtatc tgagcagcct gctgatggca 600

gcaccgctgg cactggaaga tgtggaaatt gaaattattg ataaactgat tagcgtgccg 660

tatgttgaaa tgaccctgaa actgatggaa cgttttggtg ttaccgcaga acatagcgat 720

agctgggatc gcttttatat taaagggtggc cagaaatata aatctccggg taatgcctat 780

gttgaagggtg atgcaagcag cgcaagctat tttctggcag gcgcagcaat taccggtggc 840

accgttaccg ttgaaggttg tggtaacaacc agcctgcagg gtgatgttaa atttgccgaa 900

gtgctggaaa tgatgggtgc aaaagttacc tggaccgata ccagcgttac cgttaccggt 960

ccgccgcgtc agccgttttg tcgtaaacad ctgaaagccg tggatgtgaa tatgaataaa 1020

atgccggatg ttgcatgac cctggcagtt gttgccctgt ttgcagatgg tccgaccgca 1080

attcgtgatg ttgaagctg gcgtgttaaa gaaaccgaac gtatggttgc aattcgtacc 1140

gaactgacca aactgggtgc aaccgttgaa gaaggtccgg attattgcat tattacaccg 1200

ccggaaaaac tgaatattac cgccattgat acctatgatg atcatcgtat ggcaatggca 1260

tttagcctgg cagcatgtgc agaagttccg gttaccattc gtgatccggg ttgtacacgt 1320

aaaacctttc cgaattattt tgatgttctg agcacctttg tgaaaaatta a 1371

<210> 23

<211> 1281

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-32 v5 (E. coli optimized)

<400> 23

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gcagcagcag atggcaccac caccctgctg cgtccgctgc gtagtgatga taccgaaggt 120

tttcagaag gtctgcgtaa tctgggttat gcagttgaac aggaagcaga tcgttggcgc 180

gttcagggtc gtccggcagg tccggctgca accgaagcag atgtttattg tcgtgatggt 240

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gcactgggtg ttgatctgcg tcatgaaggt gcagatggtc atcatccgct gaccgttcgt 420

gcagcaggta ttgaaggtagg tgaactgacc ctggatgccg gtgaaagcag ccagtatctg 480

accgctctgc tgatgctggg tcctctgacc accaaaggct tgcgcattga agttaccgaa 540

ctggtagcgc caccgtatgt ggaaattacc ctggcaatga tgcgcgattt tgggtttgaa 600

gttgaacgtg aaggcaatac ctttaccgtt ccgagcccga gcagccgtct gcgtagcaat 660

ctgggtggtc cgattggtgg ttatcgtgca accacctatg ccgttgaacc ggatgcaagc 720

accgaagct attttttgc agcagcagcc ctgaccggtc gtgaagttac cgttccgggt 780

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gcagaagtta gcgttgggtc ggatgccacc accgttcgta gcaccggtcg tctgcgtggt 900

attaccgtta atatgcgtga tattagcgt accatgccga cactggctgc aattgcaccg 960

tatgcagatg gtccggttgt tattgaagat gttgcaaata cccgtgtgaa agaattgat 1020

cgctcggaag catgtgcaga aaatctgcgt gccatgggta ttaccgtgca taccgggtccg 1080

gatcgtattg aaattcatcc gggtacaccg aaaccgaccg gtattgcaac ccatgggtgat 1140

catcgtattg ttatgagctt tgcagttgca ggtctgcgta caccgggtct gacctatgat 1200

gatccgggtt gtgttcgtaa aacctttccg cgttttcatg aagtgtttgc agattttgcc 1260

catgatctgg aaggtcgta a 1281

<210> 24

<211> 1248

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-33 v5 (E. coli optimized)

<400> 24

atgggtgcag ttaccgttat tgatattccg ggtagcaaaa gcgttaccgc acgtgcactg 60

tttctggcag cagcagcaga tggcaccacc accctgctgc gtccgctgcg tagtgatgat 120

accgaaggtt ttgcagaagg tctgaaaaat ctgggttatg cagttgaaca ggaagcagat 180

cgttggcgcg ttgaaggctg tccggatggt ccggcagcac cggatgcaga tgtttattgt 240

cgtgatggtg caaccaccgc acgttttctg ccgaccctgg ttgcagcagc agccagcggc 300

acctatcggtt ttgatgcaag cgcacagatg cgtcgtcgtc cgctggcacc gctgaccgt 360

gcactgaccg cactgggtgt tgatctcgt catggtggtg aagaaggtca tcatccgctg 420

accgttcgtg cagcaggtat tgaagtggt gatgtgttc tggatgccg tgaaagcagc 480

cagtatctga ccgctctgt gatgctgggt cctctgaccg caaaaggctt gcgtattgaa 540

gttaccgatc tggtagcgc accgtatgt gaaattacc tggcaatgat gcgcgatttt 600

ggtgttgatg ttagccgtga aggtaatacc ttaccgttc cgagcgggtg ttatcgtgca 660

accgcctatg ccgtgaacc ggatgcaagc accgcaagct attttttgc agcagccgca 720

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accgttcgta gcaccggtc tctgcgtggt attaccgtta ccatcgtga tattagtgat 900

accatgccga cactggcagc aattgcaccg catgccgatg gtccggttcg tattgaagat 960

gttgcaaata cccgtgtgaa agaattgat cgtctggaag catgtgcaca gaatctcgt 1020

gcaatgggta ttaccgtga taccggtcat gattgattg aaattctgcc tggtaaccg 1080

aaaccgaccg gtattgcaac ccatggtgat catcgtattg ttatgagctt tcagttgca 1140

ggtctgctga caccgggtct gacctatgat gatccgggtt gtgttcgtaa aacctttccg 1200

cgttttcatg aagtgttgc agattttgca gcaagtccgc aggcataa 1248

<210> 25

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide DGT28 MutF

<400> 25

gatgtttatt gccgtgatgg tggaaccacc gcacgttttc 40

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<223> Primer oligonucleotide DGT28 MutR

<400> 26

gaaaacgtgc ggtggttcca ccatcacggc aataaacatc 40

<210> 27

<211> 33

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<223> Primer oligonucleotide DGT28 Mut2F

<400> 27

gggtccgctg gcacgtcagg gtctgcgtat tcg 33

<210> 28

<211> 39

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<213> Artificial Sequence

<220>

<223> Primer oligonucleotide DGT28 Mut2R

<400> 28

cgaatacgca gaccctgacg tgccagcgga cccagcagc 39

<210> 29

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<223> Primer oligonucleotide pMALDGT32F

<400> 29

catatgaccg ttattgaaat tccggg 26

<210> 30

<211> 27

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<213> Artificial Sequence

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<223> Primer oligonucleotide pMALDGT32R

<400> 30

gatatcctat tattaacgac cttccag 27

<210> 31

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Primer oligonucleotide pMALDGT33F

<400> 31

catatgggtg cagttaccgt tattga 26

<210> 32

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide pMALDGT33R

<400> 32

gatatcctat tattatgcct gcggac 26

<210> 33

<211> 213

<212> DNA

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP4 v2

<400> 33

atgcttgcta gacaaggtgg aagtctgaga gcttctcaat gcaacgctgg acttgctaga 60

agagttgaag ttggtgctct tgtgttcct agacctatct ctgttaacga cgttgttcct 120

cacgtttact ctgctccact ttctgttgct agaaggtctt gctctaagtc ctccattagg 180

tccactagaa ggcttcaaac tactgtgtgc tct 213

<210> 34

<211> 186

<212> DNA

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP5 v2

<400> 34
atgcaactcc tgaatcagag gcaagccctg cgtcttggtc gttcatctgc ttcaaagaac 60

cagcaagttg ctccactggc ctctaggcct gcttcttcct tgagcgtcag cgcatccagc 120

gtcgcacctg cacctgcttg ctcagctcct gctggagctg gaaggcgtgc tgtgtcgtg 180

agagca 186

<210> 35
<211> 198
<212> DNA
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<223> Chloroplast transit peptide TraP8 v2

<400> 35
atgggtcaat ctagcagaat ctgccacggt gtgcagaacc catgtgtgat cattccaat 60

ctctccaaat ccaaccagaa caaatctcct ttctcagtca gcctcaagac tcaccagcag 120

cagcgtcgtg cttaccagat atctagctgg ggattgaaga agtcaaacia cgggtccgtg 180

attcgtccgg ttaaggca 198

<210> 36
<211> 198
<212> DNA

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP9 v2

<400> 36

atggcacaag ccagccgtat ctgccagaat ccatgtgtga tatccaatct ccccaaaagc 60

aaccaccgta agtccccctt ctctgtctca ctcaagacgc atcagcctag agcctcttca 120

tggggactta agaagtctgg caccatgctg aacggttcag tgattagacc cgtcaaggtg 180

acagcttctg tttccgca 198

<210> 37

<211> 225

<212> DNA

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP12 v2

<400> 37

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ctctcaaagt ccaatcagaa caaatcacct ttctccgtct ccctcaagac acaccagcat 120

ccaagggcat acccgataag cagctcatgg ggactcaaga agagcggaat gactctgatt 180

ggctctgagc ttcgtctct taaggttatg tcctctgttt ccgca 225

<210> 38
<211> 207
<212> DNA
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<220>
<223> Chloroplast transit peptide TraP13 v2

<400> 38
atggcacaag ttagcagaat ctgtaatggg gtcgagaacc catctcttat ctccaatctc 60

tcaaagtcca gccaacgtaa gtctcccctc agcgtgtctc tgaaaactca gcagcccaga 120

gcttcttcat ggggtttgaa gaaatctgga acgatgctta acggctcagt cattcgtccg 180

gttaaggtga cagcctccgt ctccgct 207

<210> 39
<211> 186
<212> DNA
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<220>
<223> Chloroplast transit peptide TraP14 v2

<400> 39
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gccagaccga tttcagtga cgcgctcggt ccccatgtct actccgctcc tctctccgtg 120

gctaggcggt cttgtagcaa gtccagcatt aggtctacgc gtagattgca gaccacagtc 180

tgctca 186

<210> 40

<211> 186

<212> DNA

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP23 v2

<400> 40

atggcacaga tcaacaagtc tgctaatggg gttaggaacg cttcactgat aagcaacttc 60

tccaataccc gtcaagccaa atcccccttc tccctctcat gcggaacaag actgaagaac 120

agcagcagag gtttgaagaa ggtggcagtt aggtctattg gctcccgtgt caaagtgtct 180

gcctca 186

<210> 41

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP24 v2

<400> 41

atgcaactgc tcaaccagag acaagccttg aggctcggga ggtcctctgc ctctaagaat 60

cagcaagtgg caccgcttgc cagccgtccc atttctgtga acgacgtcgt gccacacgtc 120

tacagcgcac ctctgtccgt tgctagacgc tcctgctcta agtcatcaat ccgcagcact 180

agaaggcttc agacgaccgt ttgttca 207

<210> 42

<211> 1467

<212> DNA

<213> Artificial Sequence

<220>

<223> In-frame fusion of dgt-32 v3 and TraP14 v2

<400> 42

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gccagaccga tttcagtga cgacgtcgtt ccccatgtct actccgctcc tctctccgtg 120

gctaggcggtt cttgtagcaa gtccagcatt aggtctacgc gtagattgca gaccacagtc 180

tgctcaatga cggatgata gatactggg tctaagtctg ttacagccag agcactgttc 240

ttggcagctg ctgccgatgg gacgactact cttcttagac cattgcgtag cgatgacact 300

gagggttcg cagaaggact gaggaatctg ggctatgctg tggaacaaga ggctgatagg 360

tggcgtgtcc aaggcagacc agctggacca gcagccacgg aagcagatgt ctattgcaga 420

gatggtgcc aaccgctag gttccttcg aactggcag cagcagctgc ttcggaacc 480

tacagattcg acgcttcagc acagatgcgt cgtcgtccc ttgtccatt gacaaggga 540

cttacagcct tgggtgtgga tcttagacac gaaggagcag acggacatca tccgtcacc 600

gttcgtgcag ctggcatcga aggaggagaa ttgacgctcg acgtggcga gtccagcaa 660

tacttgacag cactgctcat gctcgacat cttacaaca agggacttcg catcgaagt 720

acagaactcg tctctgcacc ctactggaa atcacctcg ctatgatgag agactttgt 780

gtggaggttg agaggaggga gaatacttc accgttcaa gccatcttc aagacttagg 840

tccaatagag gtggacccat aggaggctat agagctacta cgtatgctgt cgagccagat 900

gcctcaactg cctcttactt ctttcagct gctgccctca ctggtcgcga ggtcacagt 960

cctggattgg ggactggagc ttgcaaggt gatttcggt tcgtggatgt gctgagagaa 1020

atgggtgcc aggtgtctgt tggccggac gccacaactg tgcgtcaac tggcagattg 1080

aggggaatca ctgtgaacat gagagatatc tcagacacga tgcctacact cgagctatt 1140

gcaccttatg ccgatgttc agtggtgatt gaagatgtt ccaacaccg tgtgaaggag 1200

tgtgaccgtc tggaggcttg tgctgagaat ctgagggcaa tgggaatcac cgtccatag 1260

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ggagatcacc gcatagtcac gtcatttggc gtcgctggcc ttcgactcc tggcctcact 1380

tacgacgacc ctggctgcgt gcgtaagacc ttcctagat ttcacgaggt gtttccgac 1440

ttcgtcacg accttgaggg aaggatga 1467

<210> 43

<211> 1455

<212> DNA

<213> Artificial Sequence

<220>

<223> In-frame fusion of dgt-33 v3 and TraP24 v2

<400> 43

atgcaactgc tcaaccagag acaagccttg aggctcggga ggtcctctgc ctctaagaat 60

cagcaagtgg caccgcttg cagccgtccc atttctgtga acgacgtcgt gccacacgtc 120

tacagcgac ctctgtccgt tgctagacgc tctgtctta agtcatcaat ccgacgact 180

agaaggcttc agacgaccgt ttgttcaatg ggtgcagtga cagtcacga cattcctgga 240

agcaagagcg tgacagcaag ggcaactctt ttggcagcag cagccgatgg aacgacaaca 300

ctgcttcgtc ctctgaggtc agacgacacg gaggggtttg ccgaggtct taagaatctc 360

ggttatccg ttgagcaaga ggctgaccgt tggagggtcg aaggcagacc ggatgggtcca 420

gctgctccgg atgcagatgt ctactgccgt gatggtgcaa cgactgcacg ctttcttcca 480

accctcgtcg cagcagcagc ttctggaacg tatcgtttcg acgcctcagc acagatgagg 540

agacgtccct tggctccact cactagggca ctgacagctc ttggcgtgga tttgagacat 600

ggtggagagg agggtcacg tccactgact gtcagagctg ctggcataga aggtggcgat 660

gttgctcttg acgctggtga atcttctcag tatctcacag cccttcttat gttgggtccg 720

ttgactgcca aaggtcttag aatcgaagtc actgatctcg tgagcgctcc ttacgttgaa 780

atcactctgg ccatgatgag agatttcgga gttgatgtta gcagagaagg aaacactttc 840

accgtgccgt ccggaggcta tagagctaca gcctacgctg tggagccaga cgcaagcacg 900

gcttcttact tctttgcagc agctgccctc actggacgcg aggtgacggt ccctgggctg 960

ggaattggtg ctcttcaagg agaccttcgt tttgtggacg tgctgcgtga tatgggagca 1020

gaggtgtctg ttggaccaga tgccacgaca gtgcgctcaa ctggcagact ccgtggcatt 1080

acagttacta tgagagacat ttcagacacg atgccaacac tcgctgctat tgcacctcac 1140

gctgatggac ccgtccgtat tgaggacgtg gcaaacactc gtgtcaagga atgtgatagg 1200

cttgaggcat gtgctcaaaa ccttagagct atgggaatca cggtgcatac tgggcacgat 1260

tggattgaga ttctccctgg gactccaaag ccaacgggaa tagctacgca cggagatcac 1320

agaatcgta tgccttcgc agtggctggt ttgttgaccc ctgggctgac atacgatgat 1380

cctggctgcg tccgaagac tttccaagg ttccacgaag ttttcgctga ctttgctgca 1440

tcacccaag cctga 1455

<210> 44

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide DSM2A

<400> 44

agccacatcc cagtaacga 19

<210> 45

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer DSM2S

<400> 45

cctccctctt tgacgcc 17

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe oligonucleotide DSM2

<400> 46
cagcccaatg aggcatcagc 20

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer oligonucleotide DGT28F

<400> 47
cttcaaggag atttgggatt tgt 23

<210> 48
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer oligonucleotide DGT28R

<400> 48

gagggtcggc atcgatat 17

<210> 49

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe oligonucleotide TAFFY

<400> 49

agagaagttt cgacggattt cgggc 25

<210> 50

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide TAFII15-F

<400> 50

gaggattagg gtttcaacgg ag 22

<210> 51

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide TAFII15-R

<400> 51

gagaattgag ctgagacgag g 21

<210> 52

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide Dgt-28 Cassette Forward

<400> 52

ctgcaggtca acggatcagg atat 24

<210> 53

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide Dgt-28 Cassette Reverse

<400> 53

tgggctgaat tgaagacatg ctcc24

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide AT26410LP

<400> 54

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<210> 55

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide AT26410RP

<400> 55

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<210> 56

<211> 23

<212> DNA

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<220>

<223> Primer oligonucleotide DGT28F

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<210> 57

<211> 17

<212> DNA

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<220>

<223> Primer oligonucleotide DGT28R

<400> 57

gagggtcggc atcgtat 17

<210> 58

<211> 20

<212> DNA

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<223> Primer oligonucleotide GAAD1F

<400> 58

tggtcgggtc cctctaccaa 20

<210> 59

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe oligonucleotide GAAD1P

<400> 59

cacagaaccg tcgcttcagc aaca 24

<210> 60

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide GAAD1R

<400> 60

caacatccat caccttgact ga 22

<210> 61

<211> 26

<212> DNA

<213> Artificial Sequence

<220>
<223> Probe oligonucleotide IV-Probe

<400> 61
cgagcagacc gccgtgtact tctacc 26

<210> 62
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer oligonucleotide IVF-Taq

<400> 62
tggcggacga cgacttgt 18

<210> 63
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer oligonucleotide IVR-Taq

<400> 63
aaagtttgga ggctgccgt 19

<210> 64
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer oligonucleotide zmDGT28 F

<400> 64
ttcagcaccc gtcagaat 18

<210> 65
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe oligonucleotide zmDGT28

<400> 65
tgccgagaac ttgaggaggt 20

<210> 66
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer oligonucleotide zmDGT28 R

<400> 66

tggtcgccat agcttgt 17

<210> 67

<211> 415

<212> PRT

<213> Streptomyces griseus subsp. griseus NBRC 13350

<400> 67

Met Gly Ala Val Thr Val Ile Asp Ile Pro Gly Ser Lys Ser Val Thr

1 5 10 15

Ala Arg Ala Leu Phe Leu Ala Ala Ala Asp Gly Thr Thr Thr Leu

20 25 30

Leu Arg Pro Leu Arg Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu

35 40 45

Lys Asn Leu Gly Tyr Ala Val Glu Gln Glu Ala Asp Arg Trp Arg Val

50 55 60

Glu Gly Arg Pro Asp Gly Pro Ala Ala Pro Asp Ala Asp Val Tyr Cys

65 70 75 80

Arg Asp Gly Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Val Ala Ala

85 90 95

Ala Ala Ser Gly Thr Tyr Arg Phe Asp Ala Ser Ala Gln Met Arg Arg

100 105 110

Arg Pro Leu Ala Pro Leu Thr Arg Ala Leu Thr Ala Leu Gly Val Asp

115 120 125

Leu Arg His Gly Gly Glu Glu Gly His His Pro Leu Thr Val Arg Ala

130 135 140

Ala Gly Ile Glu Gly Gly Asp Val Val Leu Asp Ala Gly Glu Ser Ser

145 150 155 160

Gln Tyr Leu Thr Ala Leu Leu Met Leu Gly Pro Leu Thr Ala Lys Gly

165 170 175

Leu Arg Ile Glu Val Thr Asp Leu Val Ser Ala Pro Tyr Val Glu Ile

180 185 190

Thr Leu Ala Met Met Arg Asp Phe Gly Val Asp Val Ser Arg Glu Gly

195 200 205

Asn Thr Phe Thr Val Pro Ser Gly Gly Tyr Arg Ala Thr Ala Tyr Ala
210 215 220

Val Glu Pro Asp Ala Ser Thr Ala Ser Tyr Phe Phe Ala Ala Ala Ala
225 230 235 240

Leu Thr Gly Arg Glu Val Thr Val Pro Gly Leu Gly Ile Gly Ala Leu
 245 250 255

Gln Gly Asp Leu Arg Phe Val Asp Val Leu Arg Asp Met Gly Ala Glu
 260 265 270

Val Ser Val Gly Pro Asp Ala Thr Thr Val Arg Ser Thr Gly Arg Leu
 275 280 285

Arg Gly Ile Thr Val Thr Met Arg Asp Ile Ser Asp Thr Met Pro Thr
 290 295 300

Leu Ala Ala Ile Ala Pro His Ala Asp Gly Pro Val Arg Ile Glu Asp
305 310 315 320

Val Ala Asn Thr Arg Val Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala

325 330 335

Gln Asn Leu Arg Ala Met Gly Ile Thr Val His Thr Gly His Asp Trp

340 345 350

Ile Glu Ile Leu Pro Gly Thr Pro Lys Pro Thr Gly Ile Ala Thr His

355 360 365

Gly Asp His Arg Ile Val Met Ser Phe Ala Val Ala Gly Leu Leu Thr

370 375 380

Pro Gly Leu Thr Tyr Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro

385 390 395 400

Arg Phe His Glu Val Phe Ala Asp Phe Ala Ala Ser Pro Gln Ala

405 410 415

<210> 68

<211> 426

<212> PRT

<213> Streptomyces roseosporus NRRL 15998

<400> 68

Met Thr Val Ile Glu Ile Pro Gly Ser Lys Ser Val Thr Ala Arg Ala

1 5 10 15

Leu Phe Leu Ala Ala Ala Ala Asp Gly Thr Thr Thr Leu Leu Arg Pro

20 25 30

Leu Arg Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu Arg Asn Leu

35 40 45

Gly Tyr Ala Val Glu Gln Glu Ala Asp Arg Trp Arg Val Gln Gly Arg

50 55 60

Pro Ala Gly Pro Ala Ala Thr Glu Ala Asp Val Tyr Cys Arg Asp Gly

65 70 75 80

Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Ala Ala Ala Ala Ala Ser

85 90 95

Gly Thr Tyr Arg Phe Asp Ala Ser Ala Gln Met Arg Arg Arg Pro Leu

100 105 110

Ala Pro Leu Thr Arg Ala Leu Thr Ala Leu Gly Val Asp Leu Arg His

115 120 125

Glu Gly Ala Asp Gly His His Pro Leu Thr Val Arg Ala Ala Gly Ile
130 135 140

Glu Gly Gly Glu Leu Thr Leu Asp Ala Gly Glu Ser Ser Gln Tyr Leu
145 150 155 160

Thr Ala Leu Leu Met Leu Gly Pro Leu Thr Thr Lys Gly Leu Arg Ile
165 170 175

Glu Val Thr Glu Leu Val Ser Ala Pro Tyr Val Glu Ile Thr Leu Ala
180 185 190

Met Met Arg Asp Phe Gly Val Glu Val Glu Arg Glu Gly Asn Thr Phe
195 200 205

Thr Val Pro Ser Pro Ser Ser Arg Leu Arg Ser Asn Arg Gly Gly Pro
210 215 220

Ile Gly Gly Tyr Arg Ala Thr Thr Tyr Ala Val Glu Pro Asp Ala Ser
225 230 235 240

Thr Ala Ser Tyr Phe Phe Ala Ala Ala Ala Leu Thr Gly Arg Glu Val
245 250 255

Thr Val Pro Gly Leu Gly Thr Gly Ala Leu Gln Gly Asp Leu Arg Phe
260 265 270

Val Asp Val Leu Arg Glu Met Gly Ala Glu Val Ser Val Gly Pro Asp
275 280 285

Ala Thr Thr Val Arg Ser Thr Gly Arg Leu Arg Gly Ile Thr Val Asn
290 295 300

Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala Ile Ala Pro
305 310 315 320

Tyr Ala Asp Gly Pro Val Val Ile Glu Asp Val Ala Asn Thr Arg Val
325 330 335

Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala Glu Asn Leu Arg Ala Met
340 345 350

Gly Ile Thr Val His Thr Gly Pro Asp Arg Ile Glu Ile His Pro Gly
355 360 365

Thr Pro Lys Pro Thr Gly Ile Ala Thr His Gly Asp His Arg Ile Val
370 375 380

Met Ser Phe Ala Val Ala Gly Leu Arg Thr Pro Gly Leu Thr Tyr Asp

385 390 395 400

Asp Pro Gly Cys Val Arg Lys Thr Phe Pro Arg Phe His Glu Val Phe

405 410 415

Ala Asp Phe Ala His Asp Leu Glu Gly Arg

420 425

<210> 69

<211> 71

<212> PRT

<213> Streptomyces svaceus

<400> 69

Asp Thr Trp Gln Val Asp Gly Arg Pro Gln Gly Pro Ala Val Ala Glu

1 5 10 15

Ala Asp Val Tyr Cys Arg Asp Gly Ala Thr Thr Ala Arg Phe Leu Pro

20 25 30

Thr Leu Ala Ala Ala Gly His Gly Thr Tyr Arg Phe Asp Ala Ser Pro

35 40 45

Gln Met Arg Arg Arg Pro Leu Leu Pro Leu Ser Arg Ala Leu Arg Asp

50 55 60

Leu Gly Val Asp Leu Arg His

65 70

<210> 70

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Core EPSPS domain from GRG-23 variant sequence (ace3) (R173K)

<400> 70

Asp Asp Trp Val Val Glu Gly Leu Gly Gln Ala Pro Asn Leu Asp Ala

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Asp Ile Trp Cys Glu Asp Ala Gly Thr Val Ala Arg Phe Leu Pro Pro

20 25 30

Phe Val Ala Ala Gly Gln Gly Lys Phe Thr Phe Asp Gly Ser Glu Gln

35 40 45

Leu Arg Arg Arg Pro Leu Arg Pro Val Val Asp Gly Ile Arg His Leu

50 55 60

Gly Ala Arg Val Ser Ser

65 70

<210> 71

<211> 72

<212> PRT

<213> Agrobacterium tumefaciens

<400> 71

Asp Thr Trp Ile Ile Asp Gly Val Gly Asn Gly Gly Leu Leu Ala Pro

1 5 10 15

Glu Ala Pro Leu Asp Phe Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr

20 25 30

Met Gly Leu Val Gly Val Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp

35 40 45

Ala Ser Leu Thr Lys Arg Pro Met Gly Arg Val Leu Asn Pro Leu Arg

50 55 60

Glu Met Gly Val Gln Val Lys Ser

65 70

<210> 72

<211> 80

<212> PRT

<213> Brassica napus

<400> 72

Val Asn Asn Arg Ala Val Val Glu Gly Cys Gly Gly Ile Phe Pro Ala

1 5 10 15

Ser Leu Asp Ser Lys Ser Asp Ile Glu Leu Tyr Leu Gly Asn Ala Gly

20 25 30

Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr Ala Ala Gly Gly Asn

35 40 45

Ala Ser Tyr Val Leu Asp Gly Val Pro Arg Met Arg Glu Arg Pro Ile

50 55 60

Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly Ala Asp Val Glu Cys

65 70 75 80

<210> 73

<211> 80

<212> PRT

<213> Glycine max

<400> 73

Thr Thr Lys Gln Ala Ile Val Glu Gly Cys Gly Gly Leu Phe Pro Thr

1 5 10 15

Ser Lys Glu Ser Lys Asp Glu Ile Asn Leu Phe Leu Gly Asn Ala Gly

20 25 30

Thr Ala Met Arg Pro Leu Thr Ala Ala Val Val Ala Ala Gly Gly Asn

35 40 45

Ala Ser Tyr Val Leu Asp Gly Val Pro Arg Met Arg Glu Arg Pro Ile

50 55 60

Gly Asp Leu Val Ala Gly Leu Lys Gln Leu Gly Ala Asp Val Asp Cys

65 70 75 80

<210> 74

<211> 80

<212> PRT

<213> Triticum aestivum

<400> 74

Val Ala Lys Arg Ala Val Val Val Gly Cys Gly Gly Arg Phe Pro Val
1 5 10 15

Glu Lys Asp Ala Gln Glu Glu Val Lys Leu Phe Leu Gly Asn Ala Gly
 20 25 30

Thr Ala Met Arg Pro Leu Thr Ala Ala Val Val Ala Ala Gly Gly Asn
 35 40 45

Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met Arg Glu Arg Pro Ile
 50 55 60

Gly Asp Leu Val Val Gly Leu Gln Gln Leu Gly Ala Asp Ala Asp Cys
65 70 75 80

<210> 75

<211> 74

<212> PRT

<213> Escherichia coli

<400> 75

Asp Arg Thr Arg Cys Glu Ile Ile Gly Asn Gly Gly Pro Leu His Ala

1 5 10 15

Asp Gly Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly Thr Ala Met Arg

20 25 30

Pro Leu Ala Ala Ala Leu Cys Leu Gly Ser Asn Asp Ile Val Leu Thr

35 40 45

Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His Leu Val Asp Ala

50 55 60

Leu Arg Leu Gly Gly Ala Lys Ile Thr Tyr

65 70

<210> 76

<211> 516

<212> PRT

<213> Brassica napus

<400> 76

Met Ala Gln Ser Ser Arg Ile Cys His Gly Val Gln Asn Pro Cys Val

1 5 10 15

Ile Ile Ser Asn Leu Ser Lys Ser Asn Gln Asn Lys Ser Pro Phe Ser
20 25 30

Val Ser Leu Lys Thr His Gln Pro Arg Ala Ser Ser Trp Gly Leu Lys
35 40 45

Lys Ser Gly Thr Met Leu Asn Gly Ser Val Ile Arg Pro Val Lys Val
50 55 60

Thr Ala Ser Val Ser Thr Ser Glu Lys Ala Ser Glu Ile Val Leu Gln
65 70 75 80

Pro Ile Arg Glu Ile Ser Gly Leu Ile Lys Leu Pro Gly Ser Lys Ser
85 90 95

Leu Ser Asn Arg Ile Leu Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr
100 105 110

Val Val Asp Asn Leu Leu Asn Ser Asp Asp Ile Asn Tyr Met Leu Asp
115 120 125

Ala Leu Lys Lys Leu Gly Leu Asn Val Glu Arg Asp Ser Val Asn Asn
130 135 140

Arg Ala Val Val Glu Gly Cys Gly Gly Ile Phe Pro Ala Ser Leu Asp
145 150 155 160

Ser Lys Ser Asp Ile Glu Leu Tyr Leu Gly Asn Ala Gly Thr Ala Met
 165 170 175

Arg Pro Leu Thr Ala Ala Val Thr Ala Ala Gly Gly Asn Ala Ser Tyr
 180 185 190

Val Leu Asp Gly Val Pro Arg Met Arg Glu Arg Pro Ile Gly Asp Leu
 195 200 205

Val Val Gly Leu Lys Gln Leu Gly Ala Asp Val Glu Cys Thr Leu Gly
 210 215 220

Thr Asn Cys Pro Pro Val Arg Val Asn Ala Asn Gly Gly Leu Pro Gly
225 230 235 240

Gly Lys Val Lys Leu Ser Gly Ser Ile Ser Ser Gln Tyr Leu Thr Ala
 245 250 255

Leu Leu Met Ala Ala Pro Leu Ala Leu Gly Asp Val Glu Ile Glu Ile
 260 265 270

Ile Asp Lys Leu Ile Ser Val Pro Tyr Val Glu Met Thr Leu Lys Leu

275 280 285

Met Glu Arg Phe Gly Val Ser Ala Glu His Ser Asp Ser Trp Asp Arg

290 295 300

Phe Phe Val Lys Gly Gly Gln Lys Tyr Lys Ser Pro Gly Asn Ala Tyr

305 310 315 320

Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Gly Ala Ala

325 330 335

Ile Thr Gly Glu Thr Val Thr Val Glu Gly Cys Gly Thr Thr Ser Leu

340 345 350

Gln Gly Asp Val Lys Phe Ala Glu Val Leu Glu Lys Met Gly Cys Lys

355 360 365

Val Ser Trp Thr Glu Asn Ser Val Thr Val Thr Gly Pro Ser Arg Asp

370 375 380

Ala Phe Gly Met Arg His Leu Arg Ala Val Asp Val Asn Met Asn Lys

385 390 395 400

Met Pro Asp Val Ala Met Thr Leu Ala Val Val Ala Leu Phe Ala Asp

405 410 415

Gly Pro Thr Thr Ile Arg Asp Val Ala Ser Trp Arg Val Lys Glu Thr

420 425 430

Glu Arg Met Ile Ala Ile Cys Thr Glu Leu Arg Lys Leu Gly Ala Thr

435 440 445

Val Glu Glu Gly Ser Asp Tyr Cys Val Ile Thr Pro Pro Ala Lys Val

450 455 460

Lys Pro Ala Glu Ile Asp Thr Tyr Asp Asp His Arg Met Ala Met Ala

465 470 475 480

Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Val Thr Ile Lys Asp Pro

485 490 495

Gly Cys Thr Arg Lys Thr Phe Pro Asp Tyr Phe Gln Val Leu Glu Ser

500 505 510

Ile Thr Lys His

515

<210> 77

<211> 455

<212> PRT

<213> Glycine max

<400> 77

Met Ala Ser Val Ala Ala Ala Glu Lys Pro Ser Thr Ser Pro Glu Ile

1 5 10 15

Val Leu Glu Pro Ile Lys Asp Phe Ser Gly Thr Ile Thr Leu Pro Gly

20 25 30

Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu Ala Ala Leu Ser Glu

35 40 45

Gly Thr Thr Val Val Asp Asn Leu Leu Tyr Ser Glu Asp Ile His Tyr

50 55 60

Met Leu Gly Ala Leu Arg Thr Leu Gly Leu Arg Val Glu Asp Asp Lys

65 70 75 80

Thr Thr Lys Gln Ala Ile Val Glu Gly Cys Gly Gly Leu Phe Pro Thr
85 90 95

Ser Lys Glu Ser Lys Asp Glu Ile Asn Leu Phe Leu Gly Asn Ala Gly
100 105 110

Thr Ala Met Arg Pro Leu Thr Ala Ala Val Val Ala Ala Gly Gly Asn
115 120 125

Ala Ser Tyr Val Leu Asp Gly Val Pro Arg Met Arg Glu Arg Pro Ile
130 135 140

Gly Asp Leu Val Ala Gly Leu Lys Gln Leu Gly Ala Asp Val Asp Cys
145 150 155 160

Phe Leu Gly Thr Asn Cys Pro Pro Val Arg Val Asn Gly Lys Gly Gly
165 170 175

Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser Val Ser Ser Gln Tyr
180 185 190

Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala Leu Gly Asp Val Glu
195 200 205

Ile Glu Ile Val Asp Lys Leu Ile Ser Val Pro Tyr Val Glu Met Thr

210 215 220

Leu Lys Leu Met Glu Arg Phe Gly Val Ser Val Glu His Ser Gly Asn

225 230 235 240

Trp Asp Arg Phe Leu Val His Gly Gly Gln Lys Tyr Lys Ser Pro Gly

245 250 255

Asn Ala Phe Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Leu Leu Ala

260 265 270

Gly Ala Ala Ile Thr Gly Gly Thr Ile Thr Val Asn Gly Cys Gly Thr

275 280 285

Ser Ser Leu Gln Gly Asp Val Lys Phe Ala Glu Val Leu Glu Lys Met

290 295 300

Gly Ala Lys Val Thr Trp Ser Glu Asn Ser Val Thr Val Ser Gly Pro

305 310 315 320

Pro Arg Asp Phe Ser Gly Arg Lys Val Leu Arg Gly Ile Asp Val Asn

325 330 335

Met Asn Lys Met Pro Asp Val Ala Met Thr Leu Ala Val Val Ala Leu

340 345 350

Phe Ala Asn Gly Pro Thr Ala Ile Arg Asp Val Ala Ser Trp Arg Val

355 360 365

Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr Glu Leu Arg Lys Leu

370 375 380

Gly Ala Thr Val Glu Glu Gly Pro Asp Tyr Cys Val Ile Thr Pro Pro

385 390 395 400

Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr Asp Asp His Arg Met

405 410 415

Ala Met Ala Phe Ser Leu Ala Ala Cys Gly Asp Val Pro Val Thr Ile

420 425 430

Lys Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro Asp Tyr Phe Glu Val

435 440 445

Leu Glu Arg Leu Thr Lys His

450 455

<210> 78

<211> 456

<212> PRT

<213> Triticum aestivum

<400> 78

Met Ala Thr Ser Val Ala Ala Pro Ala Ala Pro Ser Gly Ala Glu Glu

1 5 10 15

Val Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Ala Val Gln Leu Pro

20 25 30

Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu Ser Ala Leu Ser

35 40 45

Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn Ser Glu Asp Val His

50 55 60

Tyr Met Leu Glu Ala Leu Glu Ala Leu Gly Leu Ser Val Glu Ala Asp

65 70 75 80

Lys Val Ala Lys Arg Ala Val Val Val Gly Cys Gly Gly Arg Phe Pro

85 90 95

Val Glu Lys Asp Ala Gln Glu Glu Val Lys Leu Phe Leu Gly Asn Ala

100 105 110

Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Val Ala Ala Gly Gly

115 120 125

Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met Arg Glu Arg Pro

130 135 140

Ile Gly Asp Leu Val Val Gly Leu Gln Gln Leu Gly Ala Asp Ala Asp

145 150 155 160

Cys Phe Leu Gly Thr Asn Cys Pro Pro Val Arg Ile Asn Gly Lys Gly

165 170 175

Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser Ile Ser Ser Gln

180 185 190

Tyr Leu Ser Ser Leu Leu Met Ala Ala Pro Leu Ala Leu Glu Asp Val

195 200 205

Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Val Pro Tyr Val Glu Met

210 215 220

Thr Leu Lys Leu Met Glu Arg Phe Gly Val Thr Ala Glu His Ser Asp

225 230 235 240

Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys Tyr Lys Ser Pro

245 250 255

Gly Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu

260 265 270

Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val Glu Gly Cys Gly

275 280 285

Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu Val Leu Glu Met

290 295 300

Met Gly Ala Lys Val Thr Trp Thr Asp Thr Ser Val Thr Val Thr Gly

305 310 315 320

Pro Pro Arg Gln Pro Phe Gly Arg Lys His Leu Lys Ala Val Asp Val

325 330 335

Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu Ala Val Val Ala

340 345 350

Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val Ala Ser Trp Arg

355 360 365

Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr Glu Leu Thr Lys

370 375 380

Leu Gly Ala Thr Val Glu Glu Gly Pro Asp Tyr Cys Ile Ile Thr Pro

385 390 395 400

Pro Glu Lys Leu Asn Ile Thr Ala Ile Asp Thr Tyr Asp Asp His Arg

405 410 415

Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu Val Pro Val Thr

420 425 430

Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro Asn Tyr Phe Asp

435 440 445

Val Leu Ser Thr Phe Val Lys Asn

450 455

<210> 79

<211> 1464

<212> DNA

<213> Artificial Sequence

<220>

<223> In-frame fusion of dgt-28 v5 and TraP4 v2

<400> 79

atgcttgcta gacaaggtgg aagtctgaga gcttctcaat gcaacgctgg acttgctaga 60

agagttgaag ttggtgctct tgtgttcct agacctatct ctgttaacga cgttgttcct 120

cacgtttact ctgctccact ttctgttgct agaaggtctt gctctaagtc ctccattagg 180

tccactagaa ggcttcaaac tactgtgtgc tctgtgcaa gagggatgcc agccttgtct 240

ttacctggat caaagagtat cacagctagg gcactctttc ttgctgctgc tgctgatggg 300

gttactactt tggtagggcc attgagaagt gacgacacag aaggattcgc tgaggggtta 360

gttcgttttag gctatcgtgt agggaggaca cccgatactt ggcaagtcga tggcagacca 420

caaggaccag cagtggtgta ggctgacgtc tactgtagag acggagcaac caccgctaga 480

ttcttgccaa ccttagcagc tgctggtcac ggaacataca gatttgatgc ttcaccacag 540

atgaggagac gtctctttt gcccttaagc agagccttga gggatttggg tgcgatctt 600

agacacgaag aagctgaagg tcatcacct ctgactgtcc gtgctgctgg ggtgaagga 660

ggagaggta ctttgatgc tggcagtca agtcagtatc tactgcctt gttgctcctt 720

ggcccccta caagacaagg actgaggata agggttactg atttggtgc agcaccatac 780

gtggagatta cgcttgaat gatgagggt ttcggagttg aagtggaag ggaggagat 840

gtgttcgtt ttccacctg tggatcgt gcaactacgt atgctataga accgacgca 900

agtactgctt ctacttctt cgagctgct gcttgactc ctggagctga agtgactga 960

cctgggtag gcacgggagc actcaagga gattgggat tttagatgt ctaaggaga 1020

atgggagccg aggtgtccgt aggagctgat gcaaccactg ttagaggaa tggtgaattg 1080

cgtagccta cagcaacat gagagacata agtgatacga tgccgaccct cgctgcaata 1140

gcacccttg ctagtgtcc agttagaatc gaggatgtt ccaacactcg tgtcaaagaa 1200

tgtgacagac ttgaggctt tgagagaac ctaggaggt tggagtaag gttgcaacg 1260

ggtccggact ggattgagat acaccctgt ccagctactg gtgctcaagt cacaagctat 1320

ggtgatcaca gaattgtgat gtcatttga gtgactggac ttcgtgtcc tgggatcagc 1380

ttcagcacc ctggctgtg tcgaagact ttcctgggt ttcagaggc ttcgcagaa 1440

ttgaggcgtg gcattgggag ctga 1464

<210> 80

<211> 1434

<212> DNA

<213> Artificial Sequence

<220>

<223> In-frame fusion of dgt-28 v5 and TraP5 v2

<400> 80

atgcaactcc tgaatcagag gcaagccctg cgtcttggtc gttcatctgc ttcaaagaac 60

cagcaagttg ctccactggc ctctaggcct gttcttcct tgagcgtcag cgcatccagc 120

gtcgcacctg cacctgcttg ctcagctcct gctggagctg gaaggcgtgc tgttgtcgtg 180

agagcagcaa gagggatgcc agccttgtct ttacctggat caaagagtat cacagctagg 240

gcactctttc ttgctgctgc tgctgatggg gttactactt tggtagggcc attgagaagt 300

gacgacacag aaggattcgc tgaggggtta gttcgtttag gctatcgtgt agggaggaca 360

cccatactt ggcaagtcga tggcagacca caaggaccag cagtggctga ggctgacgtc 420

tactgtagag acggagcaac caccgctaga ttcttgccaa ccttagcagc tgctggtcac 480

ggaacataca gatttgatgc ttcaccacag atgaggagac gtcctctttt gcccttaagc 540

agagccttga gggatttggg tgtcgatctt agacacgaag aagctgaagg tcatcacctt 600

ctgactgtcc gtgctgctgg ggttgaagga ggagaggtta ctttgatgc tggtcagtca 660

agtcagtatc tcactgcctt gttgctcctt ggtcccctta caagacaagg actgaggata 720

agggttactg atttggtgtc agcaccatac gtggagatta cgcttgcaat gatgagggct 780

ttcggagttg aagtggcaag ggagggagat gtgttcgttg ttccacctgg tggatatcgt 840

gcaactacgt atgctataga acccgacgca agtactgctt cttacttctt cgcagctgct 900

gctttgactc ctggagctga agtgactgta cctgggtag gcacgggagc acttcaagga 960

gatttgggat tttagatgt cctaaggaga atgggagccg aggtgtccgt aggagctgat 1020

gcaaccactg ttagaggaac tggatgaattg cgtggcctta cagccaacat gagagacata 1080

agtgatacga tgccgaccct cgctgcaata gcacccttg ctagtgctcc agttagaatc 1140

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cttaggaggt tgggagtaag ggttgcaacg ggtccggact ggattgagat acaccctggt 1260

ccagctactg gtgctcaagt cacaagctat ggtgatcaca gaattgtgat gtcatttgca 1320

gtgactggac ttcgtgtgcc tgggatcagc ttcgacgacc ctggctgtgt tcgtaagact 1380

tttctgggt ttcacgaggc ttgcgagaa ttgaggcgtg gcattgggag ctga 1434

<210> 81

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> In-frame fusion of dgt-28 v5 and TraP8 v2

<400> 81

atggctcaat ctagcagaat ctgccacggt gtgcagaacc catgtgtgat catttccaat 60

ctctccaaat ccaaccagaa caaatctcct ttctcagtca gcctcaagac tcaccagcag 120

cagcgtcgtg cttaccagat atctagctgg ggattgaaga agtcaaacia cgggtccgtg 180

attcgtccgg ttaaggcagc aagagggatg ccagccttgt cttacctgg atcaaagagt 240

atcacagcta gggcactctt tcttgctgct gctgctgatg gggttactac ttggtgagg 300

ccattgagaa gtgacgacac agaaggattc gctgaggggt tagttcgttt aggctatcgt 360

gtagggagga caccgatac ttggcaagtc gatggcagac cacaaggacc agcagtggct 420

gaggctgacg tctactgtag agacggagca accaccgta gattcttgcc aaccttagca 480

gctgctggtc acggaacata cagatttgat gcttcaccac agatgaggag acgtcctctt 540

ttgcccttaa gcagagcctt gagggatttg ggtgtcgatc ttagacacga agaagctgaa 600

ggcatcacc ctctgactgt ccgtgctgct ggggttgaag gaggagaggt tactttggat 660

gctggtcagt caagtcagta tctcactgcc ttgttgctcc ttggtcccct tacaagacia 720

ggactgagga taagggttac tgatttggtg tcagcaccat acgtggagat tacgcttgca 780

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ttcgagctg ctgcttgac tcctggagct gaagtgactg tacctgggtt aggcacggga 960

gcacttcaag gagatttggg attttagat gtcttaagga gaatgggagc cgaggtgtcc 1020

gtaggagctg atgcaaccac tgtagagga actggtgaat tgcgtgcct tacagccaac 1080

atgagagaca taagtatac gatccgacc ctcgtgcaa tagcaccctt tgctagtgt 1140

ccagtagaa tcgaggatgt tgccaacact cgtgtcaaag aatgtgacag acttgaggct 1200

tgtgcagaga accttaggag gttgggagta aggggtgcaa cgggtccgga ctggattgag 1260

atacacctg gtccagctac tgggtctcaa gtcacaagct atggtgatca cagaatttg 1320

atgtcatttg cagtactgg acttcgtgtg cctgggatca gcttcgacga ccctggctgt 1380

gttcgtaaga ctttcttg gtttcacgag gctttcgag aattgaggcg tggcattggg 1440

agctga 1446

<210> 82

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> In-frame fusion of dgt-28 v5 and TraP9 v2

<400> 82

atggcacaag ccagccgtat ctgccagaat ccatgtgtga tatccaatct ccccaaaagc 60

aaccaccgta agtccccctt ctctgtctca ctcaagacgc atcagcctag agcctcttca 120

tggggactta agaagtctgg caccatgctg aacggttcag tgattagacc cgtaagggtg 180

acagcttctg ttccgcgacg aagagggatg ccagccttgt ctttacctgg atcaaagagt 240

atcacagcta gggcactctt tcttgctgct gctgctgatg gggttactac ttggtgagg 300

ccattgagaa gtgacgacac agaaggattc gctgaggggt tagttcggtt aggctatcgt 360

gtagggagga caccgatac ttggcaagtc gatggcagac cacaaggacc agcagtggct 420

gaggctgacg tctactgtag agacggagca accaccgcta gattcttgcc aaccttagca 480

gctgctggtc acggaacata cagatttgat gcttcaccac agatgaggag acgtcctctt 540

ttgcccttaa gcagagcctt gagggatttg ggtgtcgatc ttagacacga agaagctgaa 600

ggtcacaccc ctctgactgt ccgtgctgct ggggttgaag gaggagaggt tactttggat 660

gctggtcagt caagtcagta tctcactgcc ttgttgctcc ttggtcccct tacaagacaa 720

ggactgagga taagggttac tgatttggtg tcagcaccat acgtggagat tacgcttgca 780

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gtaggagctg atgcaaccac tgtagagga actggtgaat tgcgtggcct tacagccaac 1080

atgagagaca taagtatac gatgccgacc ctcgtgcaa tagcaccctt tgctagtgt 1140

ccagttgaa tcgaggatgt tgccaacact cgtgtcaaag aatgtgacag acttgaggct 1200

tgtgcagaga accttaggag gttgggagta agggttgcaa cgggtccgga ctggattgag 1260

atacaccctg gtccagctac tgggtctcaa gtcacaagct atggtgatca cagaattgtg 1320

atgtcatttg cagtactgg acttcgttg cctgggatca gcttcgacga ccctggctgt 1380

gttcgtaaga ctttcctgg gtttcacgag gctttcgag aattgaggcg tggcattggg 1440

agctga 1446

- <210> 83
- <211> 1473
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> In-frame fusion of dgt-28 v5 and TraP12 v2

<400> 83

atggcacaat ctagcagaat ctgccacggt gtgcagaacc catgtgtgat catttcaaat 60

ctctcaaagt ccaatcagaa caaatcacct ttctccgtct ccctcaagac acaccagcat 120

ccaagggcat acccgataag cagctcatgg ggactcaaga agagcggaat gactctgatt 180

ggctctgagc ttctctctct taaggttatg tcctctgttt ccgcagcaag agggatgcca 240

gccttgtctt tacctggatc aaagagtatc acagctaggg cactctttct tgctgctgct 300

gctgatgggg ttactacttt ggtgaggcca ttgagaagtg acgacacaga aggattcgct 360

gaggggtagg ttcgtttagg ctatcgtgta gggaggacac ccgatacttg gcaagtcgat 420

ggcagaccac aaggaccagc agtggctgag gctgacgtct actgtagaga cggagcaacc 480

accgctagat tcttgccaac ctagcagct gctggtcacg gaacatacag atttgatgct 540

tcaccacaga tgaggagacg tcctcttttg cccttaagca gagccttgag ggatttgggt 600

gtcgatctta gacacgaaga agctgaaggt catcacctc tgactgtccg tgctgctggg 660

gttgaaggag gagaggttac ttggatgct ggtcagtcaa gtcagtatct cactgccttg 720

ttgtccttg gtccccttac aagacaagga ctgaggataa gggttactga tttggtgtca 780

gcaccatacg tggagattac gcttgcaatg atgagggctt tcggagtga agtggcaagg 840

gagggagatg tgttcgttgt tccacctggt ggatatcgtg caactacgta tgctatagaa 900

cccgcgcaa gtactgcttc ttacttcttc gcagctgctg ctttgactcc tggagctgaa 960

gtgactgtac ctgggttagg cacgggagca cttcaaggag atttgggatt tgtagatgtc 1020

ttaaggagaa tgggagccga ggtgtccgta ggagctgatg caaccactgt tagaggaact 1080

ggtgaattgc gtggccttac agccaacatg agagacataa gtgatacgat gccgaccctc 1140

gtgcaatag caccctttgc tagtgctcca gttagaatcg aggatgttgc caacactcgt 1200

gtcaaagaat gtgacagact tgaggcttgt gcagagaacc ttaggaggtt gggagtaagg 1260

gttgcaacgg gtccggactg gattgagata caccctggtc cagctactgg tgctcaagtc 1320

acaagctatg gtgatcacag aattgtgatg tcatttgag tgactggact tcgtgtgcct 1380

gggatcagct tcgacgaccc tggctgtgtt cgtaagactt ttcctgggtt tcacgaggct 1440

ttcgcagaat tgaggcgtgg cattgggagc tga 1473

<210> 84

<211> 1455

<212> DNA

<213> Artificial Sequence

<220>

<223> In-frame fusion of dgt-28 v5 and TraP13 v2

<400> 84

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tcaaagtcca gccaacgtaa gtctcccctc agcgtgtctc tgaaaactca gcagcccaga 120

gcttcttcat ggggtttgaa gaaatctgga acgatgctta acggctcagt cattcgtccg 180

gttaaggtga cagcctccgt ctccgctgct agagggatgc cagccttgtc ttacctgga 240

tcaaagagta tcacagctag ggcactcttt cttgctgctg ctgctgatgg ggttactact 300

ttggtgaggc cattgagaag tgacgacaca gaaggattcg ctgaggggtt agttcgttta 360

ggctatcgtg tagggaggac acccgatact tggcaagtcg atggcagacc acaaggacca 420

gcagtggctg aggctgacgt ctactgtaga gacggagcaa ccaccgctag attcttgcca 480

accttagcag ctgctggta cggaacatac agatttgatg cttcaccaca gatgaggaga 540

cgctctcttt tgcccttaag cagagccttg agggatttgg gtgtgatct tagacacgaa 600

gaagtgaag gtcatcacc tctgactgtc cgtgctgctg gggttgaagg aggagaggtt 660

actttggatg ctggtcagtc aagtcagtat ctactgcct tgttgctcct tggccccctt 720

acaagacaag gactgaggat aagggttact gatttgggtg cagcaccata cgtggagatt 780

acgcttgcaa tgatgagggc ttctggagtt gaagtggcaa gggagggaga tgtgttcgtt 840

gttcacctg gtggatatcg tgcaactacg tatgctatag aaccgacgc aagtactgct 900

tcttacttct tcgcagctgc tgctttgact cctggagctg aagtgactgt acctgggtta 960

ggcacgggag cacttcaagg agatttgga ttgtagatg tcttaaggag aatgggagcc 1020

gaggtgtccg taggagctga tgcaaccact gtagaggaa ctggtgaatt gcgtggcctt 1080

acagccaaca tgagagacat aagtatacg atgccgaccc tcgtgcaat agcacccttt 1140

gctagtgtc cagttagaat cgaggatgtt gccaacactc gtgtcaaaga atgtgacaga 1200

cttgaggctt gtgcagagaa ccttaggagg ttgggagtaa gggttgcaac ggggccggac 1260

tggattgaga tacaccctgg tccagctact ggtgtcaag tcacaagcta tggatcac 1320

agaatttga tgcatttgc agtgactgga cttcgtgtc ctgggatcag cttcgacgac 1380

cctggctgtg ttcgtaagac ttttctggg tttcacgagg ctttcgaga attgaggcgt 1440

ggcattggga gctga 1455

- <210> 85
- <211> 20
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Primer oligonucleotide Ubiquitin Forward

<400> 85

gcgaagatcc aggacaagga 20

<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer oligonucleotide Ubiquitin Reverse

<400> 86
ctgcttaccg gcaaagatga g 21

<210> 87
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe oligonucleotide Ubiquitin Probe

<400> 87
ttcccccgga ccagcagcgt 20

<210> 88
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer oligonucleotide VirC Forward

<400> 88

ccgacgagaa agaccagcaa20

<210> 89

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide VirC reverse

<400> 89

cttaagttgt cgatcgggac tgt23

<210> 90

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Probe oligonucleotide VirC Probe

<400> 90

tgagcctctc gtcgccgatc acat24

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide Pinb Forward

<400> 91

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<210> 92

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide Pinb Reverse

<400> 92

tgctatctgg ctcagctgc 19

<210> 93

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe oligonucleotide Pinb Probe

<400> 93

atggtggaag ggcggttg a

21

<210> 94

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide Act1 Promoter Forward

<400> 94

ctcccgcga ccgatctg

18

<210> 95

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide Act1 Promoter Reverse

<400> 95

ccgcccctc tcctcttc

19

<210> 96

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe oligonucleotide Act1 Promoter Probe

<400> 96

aagccgcctc tcgccaccc a 21

<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6678-2-1 Primer 1

<400> 97

ggtttgtga atccctctgt tgg 24

<210> 98

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6678-2-1 Primer 2

<400> 98

gtggatcatga cagtatgata acagg 25

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer oligonucleotide hh08-6678-8-1 Primer 1

<400> 99
gggtctgccc aatgaagcga 20

<210> 100
<211> 26
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<220>
<223> Primer oligonucleotide hh08-6678-8-1 Primer 2

<400> 100
tctcgcttct ctcataacac atcgtg 26

<210> 101
<211> 22
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<220>

<223> Primer oligonucleotide hh08-6729-5-1 Primer 1

<400> 101

gacctctctc accctcctcc tc 22

<210> 102

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Primer oligonucleotide hh08-6729-5-1 Primer 2

<400> 102

ccaaataata agtgagagag gggcat 26

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide mp45-6739-14-1 Primer 1

<400> 103

tagttcccct gtcgtgtgca aa 22

<210> 104

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide mp45-6739-14-1 Primer 2

<400> 104

caacagcagc ctcaccaatc ac 22

<210> 105

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide mp45-6739-5-1 Primer 1

<400> 105

caagaacggt gctcctttt taag 24

<210> 106

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide mp45-6739-5-1 Primer 2

<400> 106
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<210> 107
<211> 24
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<220>
<223> Primer oligonucleotide yl02-6762-8-1 Primer 1

<400> 107
ggctgtgttg cacacaaata gaga 24

<210> 108
<211> 23
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<220>
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<400> 108
cagcagcacg gtaggtagat tgt 23

<210> 109
<211> 24
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<213> Artificial Sequence

<220>

<223> Primer oligonucleotide gt19-6752-4-1 Primer 1

<400> 109

ccgataagac ggcaactgat taaa 24

<210> 110

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide gt19-6752-4-1 Primer 2

<400> 110

aggctggctt ctagtgaag gag 23

<210> 111

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6761-1-1 Primer 1

<400> 111

gggtttccgg ctggagacg 19

<210> 112

<211> 28

<212> DNA

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<220>

<223> Primer oligonucleotide hh08-6761-1-1 Primer 2

<400> 112

ccaaaagcaa ttttcgttat aagatgcc 28

<210> 113

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide yl02-6762-6-1 Primer 1

<400> 113

ccagataatc tgtgggctcc tg 22

<210> 114

<211> 20

<212> DNA

<213> Artificial Sequence

<220>
<223> Primer oligonucleotide yl02-6762-6-1 Primer 2

<400> 114
gcagcagctt gccttaagca 20

<210> 115
<211> 27
<212> DNA
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<220>
<223> Primer oligonucleotide hh08-6780-10-1 Primer 1

<400> 115
tgcttgtttc tggtgtcatc ataggtt 27

<210> 116
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer oligonucleotide hh08-6780-10-1 Primer 2

<400> 116
catttgttgg gttccacgt acg 23

<210> 117

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6780-8-1 Primer 1

<400> 117

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<210> 118

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6780-8-1 Primer 2

<400> 118

ccgatttaca tggacttgat ggagt	25
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<210> 119

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6678-2-1 Primer 1

ggtttgttga atccctctgt tgggt 24

<213> Artificial Sequence

<223> Primer oligonucleotide hh08-6678-2-1 Primer 2

gccgcctcca gtgagtgtg ctgcttgtgt ag 32

<213> Artificial Sequence

<223> Primer oligonucleotide hh08-6678-8-1 Primer 1

gggtctgccc aatgaagcga 20

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6678-8-1 Primer 2

<400> 122

gccgcctcca taatgtgtga gtagttcca gataagg 37

<210> 123

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6729-5-1 Primer 1

<400> 123

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<210> 124

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6729-5-1 Primer 2

<400> 124

ccaaataata agtgagagag gggcat 26

<210> 125

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide mp45-6739-14-1 Primer 1

<400> 125

gccgcctcca taatgtgtga gtagttcca gataagg 37

<210> 126

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide mp45-6739-14-1 Primer 2

<400> 126

caacagcagc ctcaccaatc ac 22

<210> 127

<211> 37

<212> DNA

<213> Artificial Sequence

<220>
<223> Primer oligonucleotide mp45-6739-5-1 Primer 1

<400> 127
gccgcctcca taatgtgtga gtagttcca gataagg 37

<210> 128
<211> 21
<212> DNA
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<220>
<223> Primer oligonucleotide mp45-6739-5-1 Primer 2

<400> 128
agcccttcct ctgcatcctt a 21

<210> 129
<211> 37
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<220>
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<400> 129
gccgcctcca taatgtgtga gtagttcca gataagg 37

<210> 130

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide yl02-6762-8-1 Primer 2

<400> 130

cagcagcacg gtaggtagat tgt 23

<210> 131

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide gt19-6752-4-1 Primer 1

<400> 131

gccgcctcca gtgagtgttg ctgcttgtgt ag 32

<210> 132

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide gt19-6752-4-1 Primer 2

<400> 132

aggctggctt ctagtgaag gag 23

<210> 133

<211> 37

<212> DNA

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<220>

<223> Primer oligonucleotide hh08-6761-1-1 Primer 1

<400> 133

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<210> 134

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6761-1-1 Primer 2

<400> 134

ccaaaagcaa ttttcgttat aagatgcc 28

<210> 135

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide yl02-6762-6-1 Primer 1

<400> 135

gccgcctcca gtgagtgttg ctgcttgtgt ag 32

<210> 136

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Primer oligonucleotide yl02-6762-6-1 SEQ ID NO:2

<400> 136

gcagcagctt gccttaagca 20

<210> 137

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6780-10-1 Primer 1

<400> 137

gccgcctcca taatgtgtga gtagttcca gataagg 37

<210> 138

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6780-10-1 Primer 2

<400> 138

catttggtgg gtttcacgt acg 23

<210> 139

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6780-8-1 Primer 1

<400> 139

gccgcctcca gtgagtgttg ctgcttgtgt ag 32

<210> 140

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer oligonucleotide hh08-6780-8-1 Primer 2

<400> 140

ccgatttaca tggacttgat ggagt 25

<210> 141

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant Class I EPSPS motif

<400> 141

Leu Gly Asn Ala Ala Thr

1 5

<210> 142

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant Class I EPSPS motif

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa can be Ala, Ser, or Thr

<400> 142

Ala Leu Leu Met Xaa Ala Pro Leu Thr

1 5

<210> 143

<211> 1431

<212> DNA

<213> Artificial Sequence

<220>

<223> In-frame fusion of dgt-31 v3 and TraP23 v2

<400> 143

atggcacaga tcaacaagtc tgctaatggg gttaggaacg cttcactgat aagcaacttc 60

tccaataccc gtcaagccaa atcccctttc tccctctcat gcggaacaag actgaagaac 120

agcagcagag gtttgaagaa ggtggcagtt aggctcattg gctcccgtgt caaagtgtct 180

gcctcaatga ctgtgattga catccctggc tcaaagtcag ttactgccag agcattgttc 240

ctcgacgag ctgctgatgg cactacaact cttttgagac ctcttcacag cgatgacacg 300

gaaggcttca ctgagggctct cactcgtttg ggatacgagcag tggtagaga acccgatagg 360

tggcacatag aaggacgtcc ctccgtcca gcagcagcag atgcagaagt tcaactgtagg 420

gacggtgcta caactgctcg ctttctcca acccttgagcag ctgctgctgc ctccggaacg 480

tatcgtttcg acgcatcagc tcagatgagg cgtagacccc tcgtcccct cacggaagct 540

cttagaacac ttggagtga ccttaggcag gatggagctg aaggccacca ccccttgaca 600

attcaagcct ctggtgttaa gggtaggagga cttacgctcg acgctggtga gtcattcag 660

tacttgacag ctctgctcat gcttggtcct ctgaccgagcag agggactgag aatagaagtt 720

acggagcttg tctctgctcc ttatgtggag atcacccttg caatgatgag aggccttggt 780

gtggaggttg ttagggaggg gaatacttc actgtgcctc ctggaggta cagagctaca 840

acttatgcca tagaaccgga cgcaagcaca gcttcctact tctttgcagc agcagccctc 900

actgggaggg aagtgcggt gcctggcttg ggcactggag cacttcaagg tgatcttagg 960

ttcacggagg tcctcagaag gatggacgct gatgttcgca caacgtccga ctctacaaca 1020

gtgcgctcag atggtgcct tgctgggttg actgtcaaca tgaggacat aagcgacaca 1080

atgccaacac tggcagctat agtccgtac gcaagctcac cagtaggat cgaggatgtc 1140

gaaacaccc gtgtgaagga atgtgatagg ctggaggctt gcgctcagaa tctccgctca 1200

atgggcatca ccgttcgac tggaccagat tggattgaga tccatcctgg gactcctaga 1260

ccgaccgaga tagccacaca cggatgatcat agaatcgtca tgcattttgc cgtggctgga 1320

cttagaacc ctgggatgtc ttacgatgac cctggctgcg ttcgaagac tttcctcgt 1380

tttcatgaag agtttgacgc ctcgtggag cgctcatccg ctggagagtg a 1431

<210> 144

<211> 1245

<212> DNA

<213> Artificial Sequence

<220>

<223> DGT-31 v3 (codon optimized)

<400> 144

atgactgtga ttgacatccc tggctcaaag tcagttactg ccagagcatt gttcctcgca 60

gcagctgctg atggcactac aactcttttg agacctcttc acagcgatga cacggaaggc 120

ttcactgagg gtctcactcg ttgggatac gcagtgggta gagaaccga taggtggcac 180

atagaaggac gtccctccgg tccagcagca gcagatgcag aagttcactg tagggacggt 240

gctacaactg ctgcttttct tccaaccctt gcagctgctg ctgcctccgg aacgtatcgt 300

ttcgacgcat cagctcagat gaggcgtaga cccctcgctc ccctcacgga agctcttaga 360

acacttgagaggac tggaccttag gcatgatgga gctgaaggcc accaccctt gacaattcaa 420

gcctctggtg ttaagggtgg aggacttacg ctgcacgctg gtgagtcac tcagtacttg 480

acagctctgc tcatgcttgg tcctctgacc gcagagggac tgagaataga agttacggag 540

cttgtctctg ctccttatgt ggagatcacc cttgcaatga tgagaggctt tgggtgaggag 600

gttgtagggg aggggaatac ttctactgtg cctctggag gttacagagc tacaacttat 660

gccatagaac cggacgcaag cacagcttcc tacttctttg cagcagcagc cctcactggg 720

agggaagtga cggcgcctgg cttgggcact ggagcacttc aaggtgatct taggttcacg 780

gaggtcctca gaaggatgga cgctgatgtt cgcaaacgt ccgactctac aacagtgcgc 840

tcagatggtc gccttgctgg gttgactgtc aacatgaggg acataagcga cacaatgcca 900

acactggcag ctatagctcc gtacgcaagc tcaccagtta ggatcgagga tgcgcaaac 960

acccgtgtga aggaatgtga taggctggag gcttgcgctc agaatctccg ctcaatgggc 1020

atcaccgttc gactggacc agattggatt gagatccac tcgggactcc tagaccgacc 1080

gagatagcca cacacggtga tcatagaatc gtcatgtcat ttgccgtggc tggacttaga 1140

accctggga tgtcttacga tgaccctggc tgcgttcgca agacttttcc tcgttttcat 1200

gaagagtttg cagccttcgt ggagcgctca tccgctggag agtga 1245

<210> 145

<211> 414

<212> PRT

<213> Streptomyces pratensis ATCC 33331

<400> 145

Met Thr Val Ile Asp Ile Pro Gly Ser Lys Ser Val Thr Ala Arg Ala

1 5 10 15

Leu Phe Leu Ala Ala Ala Ala Asp Gly Thr Thr Thr Leu Leu Arg Pro

20 25 30

Leu His Ser Asp Asp Thr Glu Gly Phe Thr Glu Gly Leu Thr Arg Leu

35 40 45

Gly Tyr Ala Val Val Arg Glu Pro Asp Arg Trp His Ile Glu Gly Arg

50 55 60

Pro Ser Gly Pro Ala Ala Ala Asp Ala Glu Val His Cys Arg Asp Gly

65 70 75 80

Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Ala Ala Ala Ala Ser

85 90 95

Gly Thr Tyr Arg Phe Asp Ala Ser Ala Gln Met Arg Arg Arg Pro Leu

100 105 110

Ala Pro Leu Thr Glu Ala Leu Arg Thr Leu Gly Val Asp Leu Arg His

115 120 125

Asp Gly Ala Glu Gly His His Pro Leu Thr Ile Gln Ala Ser Gly Val

130 135 140

Lys Gly Gly Gly Leu Thr Leu Asp Ala Gly Glu Ser Ser Gln Tyr Leu

145 150 155 160

Thr Ala Leu Leu Met Leu Gly Pro Leu Thr Ala Glu Gly Leu Arg Ile

165 170 175

Glu Val Thr Glu Leu Val Ser Ala Pro Tyr Val Glu Ile Thr Leu Ala

180 185 190

Met Met Arg Gly Phe Gly Val Glu Val Val Arg Glu Gly Asn Thr Phe

195 200 205

Thr Val Pro Pro Gly Gly Tyr Arg Ala Thr Thr Tyr Ala Ile Glu Pro

210 215 220

Asp Ala Ser Thr Ala Ser Tyr Phe Phe Ala Ala Ala Ala Leu Thr Gly

225 230 235 240

Arg Glu Val Thr Val Pro Gly Leu Gly Thr Gly Ala Leu Gln Gly Asp

245 250 255

Leu Arg Phe Thr Glu Val Leu Arg Arg Met Asp Ala Asp Val Arg Thr

260 265 270

Thr Ser Asp Ser Thr Thr Val Arg Ser Asp Gly Arg Leu Ala Gly Leu

275 280 285

Thr Val Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala

290 295 300

Ile Ala Pro Tyr Ala Ser Ser Pro Val Arg Ile Glu Asp Val Ala Asn

305 310 315 320

Thr Arg Val Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala Gln Asn Leu

325 330 335

Arg Ser Met Gly Ile Thr Val Arg Thr Gly Pro Asp Trp Ile Glu Ile

340 345 350

His Pro Gly Thr Pro Arg Pro Thr Glu Ile Ala Thr His Gly Asp His
355 360 365

Arg Ile Val Met Ser Phe Ala Val Ala Gly Leu Arg Thr Pro Gly Met
370 375 380

Ser Tyr Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro Arg Phe His
385 390 395 400

Glu Glu Phe Ala Ala Phe Val Glu Arg Ser Ser Ala Gly Glu
405 410

<210> 146
<211> 410
<212> PRT
<213> Streptomyces davawensis

<400> 146

Met Pro Val Ala Asp Ile Pro Gly Ser Lys Ser Ile Thr Ala Arg Ala
1 5 10 15

Leu Phe Leu Ala Ala Ala Asp Gly Val Thr Thr Leu Val Arg Pro
20 25 30

Leu Arg Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu Ala Arg Leu

35 40 45

Gly Tyr Arg Val Gly Arg Thr Pro Asp Ser Trp Gln Val Asp Gly Arg

50 55 60

Pro Gln Gly Pro Ala Val Ala Glu Ala Asp Val Tyr Cys Arg Asp Gly

65 70 75 80

Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Ala Ala Ala Gly His Gly

85 90 95

Thr Tyr Arg Phe Asp Ala Ser Glu Gln Met Arg Arg Arg Pro Leu Leu

100 105 110

Pro Leu Thr Arg Ala Leu Arg Glu Leu Gly Val Asp Leu Arg His Glu

115 120 125

Glu Arg Asp Gly His His Pro Leu Thr Val Arg Ala Ala Gly Val Ala

130 135 140

Gly Gly Glu Val Thr Leu Asp Ala Gly Gln Ser Ser Gln Tyr Leu Thr

145 150 155 160

Ala Leu Leu Leu Leu Gly Pro Leu Thr Glu Lys Gly Leu Arg Ile His

165 170 175

Val Thr Asp Leu Val Ser Val Pro Tyr Ile Glu Ile Thr Leu Ala Met

180 185 190

Met Arg Ala Phe Gly Val Glu Val Thr Arg Glu Gly His Asp Phe Val

195 200 205

Val Pro Pro Gly Gly Tyr Arg Ala Thr Thr Tyr Ala Ile Glu Pro Asp

210 215 220

Ala Ser Thr Ser Ser Tyr Phe Phe Ala Ala Ala Ala Leu Ser Gly Gly

225 230 235 240

Glu Val Thr Val Pro Gly Leu Gly Glu Gly Ala Leu Gln Gly Asp Leu

245 250 255

Gly Phe Val Asp Val Leu Arg Arg Met Gly Ala Glu Val Glu Ile Gly

260 265 270

Ala Asp Arg Thr Thr Val Arg Gly Thr Gly Glu Leu Arg Gly Leu Thr

275 280 285

Val Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala Ile

290 295 300

Ala Pro Phe Ala Ser Gly Pro Val Arg Ile Glu Asp Val Ala Asn Thr

305 310 315 320

Arg Val Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala Glu Asn Leu Arg

325 330 335

Arg Leu Gly Val Arg Val Glu Thr Gly Pro Asp Trp Ile Glu Ile His

340 345 350

Pro Gly Ala Thr Pro Thr Gly Ala Glu Ile Lys Thr Tyr Gly Asp His

355 360 365

Arg Ile Val Met Ser Phe Ala Val Thr Gly Leu Arg Val Pro Gly Ile

370 375 380

Ser Phe Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro Gly Phe His

385 390 395 400

Glu Glu Phe Gly Ala Leu Arg Ala Arg Leu

<210> 147

<211> 1233

<212> DNA

<213> *Streptomyces davawensis*

<400> 147

atgccagttg ccgacatccc cggttccaag tccatcaccg cgcgcgccct cttcctggcg 60

gcggcggccg acggagtac caccctcgtt cggccgctgc ggtcggacga caccgagggc 120

ttgccgagg ggctggccc gctcgggtac cgcgtcggga ggaccccga cagctggcag 180

gtggacggcc gccgcaggg cccgcggtc gccgaggcgg acgtctactg ccgggacggc 240

gcgacgacc cccgcttct gccgacgtg gccgcccg gccacggcac ctaccgctt 300

gacgcctcg agcagatgc ccgcgccc ctgctgccgc tcaccgggc cctgcgcgag 360

ctgggcgtgg acctgcggca caggagcgg gacggccacc acccgctgac cgtgcgggcg 420

gccggggtcg cgggcggcga ggtgacgtg gacgccggac agtcctcgca gtacctgacc 480

gccctgtgc tgctggccc gtcaccgag aaggcctgc gcatcatgt caccgacctg 540

gtctcgtgc cgtacatga gatcaccctc gcgatgatgc gggcggttcgg ggtggaggtg 600

accaggaag gccatgactt cgtcgtccc cgggcggct accgcgccac cacctacgcc 660

atcgaaccg acgcctccac ctccagctac ttcttcgccg ccgcggccct ctccggtggc 720

gaggtgaccg tgccgggtct cggtgagggc gcgctccagg gcgacctggg cttcgtcgac 780

gtactgcgcc ggatgggctc cgaggtggag atcggcgagg accgcaccac ggtccgcggc 840

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ctcgcccca tcgcccctt cgctcgggg ccggtgcgca tcgaggacgt cgccaacacc 960

cgggtgaagg agtgcgaccg cctggaggcc tgcgcggaga acctgcggcg gctcggcgtg 1020

cgggtggaga cgggccccga ctggatcgag atccaccccg gcgccacccc cacaggcgcg 1080

gagatcaaga cctacggcga ccaccgcatc gtcatgtcct tcgccgtcac cggcctccgc 1140

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gaggagttcg gggcgctgcg cgcgcggttg tga 1233

<210> 148

<211> 412

<212> PRT

<213> Streptomyces turgidiscabies

<400> 148

Met Ala Val Val Glu Ile Pro Gly Ser Lys Ser Ile Thr Ala Arg Ala

1 5 10 15

Leu Phe Leu Ala Ala Ala Ala Asp Gly Val Thr Thr Leu Val Arg Pro
20 25 30

Leu Arg Ser Asp Asp Ser Glu Gly Phe Ala Glu Gly Leu Val Gly Leu
35 40 45

Gly Tyr Arg Val Gly Arg Thr Pro Gly Ala Trp Gln Ile Asp Gly Arg
50 55 60

Pro Gln Gly Pro Ala Ala Thr Glu Ala Asp Val His Cys Arg Asp Gly
65 70 75 80

Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Val Ala Ala Gly His Gly
85 90 95

Thr Tyr Arg Phe Asp Ala Ser Pro Gln Met Arg Arg Arg Pro Leu Ala
100 105 110

Pro Leu Thr Arg Ala Leu Arg Asp Leu Gly Val Asp Leu Arg His Glu
115 120 125

Glu Ala Glu Gly His His Pro Leu Thr Val Glu Ala Ala Gly Val Glu
130 135 140

Gly Gly Asn Val Thr Leu Asp Ala Gly Gln Ser Ser Gln Tyr Leu Thr
145 150 155 160

Ala Leu Leu Leu Leu Gly Pro Leu Thr Arg Lys Gly Leu Arg Ile His
 165 170 175

Val Thr Asp Leu Val Ser Ala Pro Tyr Val Asp Ile Thr Ile Ala Met
 180 185 190

Met Arg Glu Phe Gly Ala Glu Val Arg Gln Asp Gly Asp Val Phe Val
 195 200 205

Val Pro Pro Gly Gly Tyr Arg Ala Thr Thr Tyr Ala Val Glu Pro Asp
 210 215 220

Ala Ser Thr Ala Ser Tyr Phe Phe Ala Ala Ala Ala Leu Thr Gly Gly
225 230 235 240

Glu Val Thr Val Pro Gly Leu Gly Thr Gly Ala Leu Gln Gly Asp Leu
 245 250 255

Gly Phe Val Asp Val Leu Arg Arg Met Gly Ala Arg Val Glu Ile Ala

260	265	270	
Glu Asp Arg Thr Thr Val Thr Gly Thr Gly Glu Leu Arg Gly Leu Thr			
275	280	285	
Val Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala Leu			
290	295	300	
Ala Pro Phe Ala Ser Gly Pro Val Arg Ile Glu Asp Val Ala Asn Thr			
305	310	315	320
Arg Val Lys Glu Cys Asp Arg Leu Asp Ala Cys Ala Glu Asn Leu Arg			
325	330	335	
Arg Leu Gly Val Arg Val Glu Thr Gly Pro Asp Trp Ile Glu Ile His			
340	345	350	
Pro Gly Ala Val Pro Ala Pro Gly Thr Asp Ile Lys Ser Tyr Gly Asp			
355	360	365	
His Arg Ile Val Met Ser Phe Ala Val Thr Gly Leu Arg Thr Pro Gly			
370	375	380	

Ile Thr Phe Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro Gly Phe

385 390 395 400

His Glu Ala Phe Gly Glu Leu Arg Arg Val Leu Gly

405 410

<210> 149

<211> 1239

<212> DNA

<213> Streptomyces turgidiscabies

<400> 149

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gcggcagccg acgggggtcac caccctcgta cgccccctgc gctcggacga ctcggagggc 120

ttcgccgagg gcctggtcgg cctcggctac cgggtcgggc ggacccccgg cgcctggcag 180

atcgacggcc gcccgcaggg ccccgcgcc accgaggccg acgtccactg ccgcgacggc 240

gccacgaccg ccgcttcct cccaccctc gtcgccgccc gccacggcac ctaccgcttc 300

gacgcctccc ccagatgcg ccgccgccc ctcgcccc tcaccgcgc cctgcgcgac 360

ctgggcgtgg acctgcggca cgaggaggcg gaggggcacc acccgctgac cgtcgaggcg 420

gcgggcgtgg agggcggaac cgtcacctc gacgccgggc agtcctcca gtacctcacc 480

gcgctgctcc tcctgggccc cctgaccgc aagggcctgc gcatccacgt caccgacctc 540

gtctcggccc cctacgtgga catcaccatc gcgatgatgc gggagttcgg ggcggaggta 600

cgccaggacg gcgacgtctt cgtggtcccg cccggcggct accgggccac cacctacgcc 660

gtcgagcccg atgcctccac cgccagctac ttcttcgagg cggcggccct caccggcggc 720

gaggtgacgg tcccgggcct cggcacccgc gcgtccagg gcgacctggg cttcgtcgac 780

gtactgcgcc gcatgggcgc ccgggtggag atcgccgagg accgcacgac ggtcacggga 840

accggtgaac tccggggcct gacggtcaac atgcgggaca tctccgacac catgcccacc 900

ctggcggcgc tcgccccctt cgcgtccggc cccgtacgca tcgaggacgt ggccaacacg 960

cgcgtgaagg agtgcgaccg cctggacgcc tgcgcggaga acctccggcg gctgggggta 1020

cgggtggaga ccggaccgga ctggatcgag atccaccccg gcgcggtccc tgccccggc 1080

acggacatca agtcgtacgg cgaccaccgc atcgtcatgt ctttcgcggt gaccggcctg 1140

cgcacaccgg ggatcacctt cgacgaccgg gggcgcgtac gcaagacgtt ccccggttc 1200

cacgaggcgt tcggagagct gaggcgggta ctgggctag 1239

<210> 150

<211> 423

<212> PRT

<213> Streptomyces acidiscabies

<400> 150

Met Pro Leu Val Asp Ile Pro Gly Ser Lys Ser Leu Thr Ala Arg Ala

1 5 10 15

Leu Phe Leu Ala Ala Ala Ala Asp Gly Val Thr Thr Leu Val Arg Pro

20 25 30

Leu Arg Ser Asp Asp Ser Glu Gly Phe Ala Glu Gly Leu Ser Ser Leu

35 40 45

Gly Tyr Arg Val Gly Arg Ala Pro Asp Val Trp Gln Val Asp Gly Arg

50 55 60

Pro Gln Gly Pro Ala Val Thr Asp Val Asp Val Tyr Cys Arg Asp Gly

65 70 75 80

Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Ala Ala Ala Gly His Gly

85 90 95

Thr Phe Arg Phe Asp Ala Ser Pro Gln Met Arg Arg Arg Pro Leu Leu

100 105 110

Pro Leu Thr Arg Ala Leu Arg Asp Leu Gly Val Asp Leu Arg His Glu

115

120

125

Asp Ala Glu Gly His His Pro Leu Thr Val Asn Ala Ala Gly Val Glu

130

135

140

Gly Gly Glu Val Val Leu Asp Ala Gly Gln Ser Ser Gln Tyr Leu Thr

145

150

155

160

Ala Leu Leu Leu Leu Gly Pro Leu Thr Arg Thr Gly Leu Arg Ile Arg

165

170

175

Val Thr Asp Leu Val Ser Val Pro Tyr Val Glu Ile Thr Ile Ala Met

180

185

190

Met Arg Ala Phe Gly Val Glu Val Lys Gln Glu Ala Thr Val Ser Thr

195

200

205

Asn Glu Pro Gly Ala Ser Gly Glu Arg Val Tyr Thr Val Pro Pro Gly

210

215

220

Gly Tyr Arg Ala Thr Thr Tyr Pro Ile Glu Pro Asp Ala Ser Thr Ala

225

230

235

240

Ser Tyr Phe Phe Ala Ala Ala Ala Leu Thr Gly Gly Glu Val Thr Val

245 250 255

Pro Gly Leu Gly Gln Gly Ala Leu Gln Gly Asp Leu Gly Phe Val Glu

260 265 270

Val Leu Arg Lys Met Gly Ala Tyr Val Glu Ile Ala Ala Asp Arg Thr

275 280 285

Thr Val Arg Gly Thr Gly Thr Leu Asn Gly Val Thr Val Thr Met Arg

290 295 300

Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala Ile Ala Pro Phe Ala

305 310 315 320

Thr Gly Pro Val Arg Ile Glu Asp Val Ala Asn Thr Arg Val Lys Glu

325 330 335

Cys Asp Arg Leu Asp Val Cys Ala Glu Asn Leu Arg Arg Leu Gly Ile

340 345 350

Asp Val Ala Thr Gly Pro Asp Trp Ile Glu Ile His Pro Gly Thr Pro

355 360 365

Lys Pro Ala Glu Ile Thr Thr His Gly Asp His Arg Ile Val Met Ser

370 375 380

Phe Ala Val Thr Gly Leu Arg Thr Pro Gly Ile Ser Phe Asp Asp Pro

385 390 395 400

Gly Cys Val Arg Lys Thr Phe Pro Gly Phe His Glu Ala Phe Ala Gln

405 410 415

Leu Arg Lys Asp Ile Thr Gly

420

<210> 151

<211> 1272

<212> DNA

<213> Streptomyces acidiscabies

<400> 151

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ttcgccgagg ggctgagcag cctcggttat cgggtcgggc gggcgccgga cgtctggcag 180

gtggacggcc gccgcaggg cccggcggtc acggacgtgg acgtgtactg ccgggacggc 240

gcgacgaccg cccgtttcct gccgacgctc gccgccgccg gccacggcac gttccgcttc 300

gacgcctcgc cccagatgcg ccgccgcccc ctctccac tcacccgcgc cctgcgcgac 360

ctcggcgtgg acctgcgcca cgaggacgcg gagggccacc acccctgac ggtcaacgcg 420

gccggggtgg agggcggcga ggttgcctc gacgccggcc agtcctcca gtacctcacc 480

gcgctgctcc tccttggtcc cctacccgc acgggcctgc gcatccgct caccgatctg 540

gtctccgtgc cgtacgtgga gatcacgatc gcgatgatga gggcgttcgg ggtggaggtg 600

aaacaggaag caaccgttc cacaacgaa ccggcgccct cggcgagcg cgtctacacc 660

gtccccccg gcggctaccg gccaccacc tacccatcg aaccgacgc ctccaccgcg 720

agctacttct tcgccgagc ggccctcacc ggcgcgagg tcaccgtccc cggcctcgga 780

caggcgcac ttcaggcgca ctgggcttc gtggagtcc tgcgaagat gggcgctac 840

gtcgagatcg ccgccgaccg tacgacgtg cggggaaccg gcacgtgaa cggcgtgacg 900

gtcacatgc gcgacatctc cgacacgatg cccaccctcg ccgcatcgc ccccttcgcc 960

accggccccg tccgcatcga ggacgtgcc aacaccgcg tcaaggagtg cgaccgctc 1020

gacgtctcgc cggagaacct gcgccgctc ggcacgacg ttgcgacggg ccccgactgg 1080

atcgagatcc acccggcac ccgaagccc gccgagatca cgaccacgg cgaccaccgc 1140

atcgtcatgt ccttcggt caccggcctg cgcacgccg gtatttcgtt cgacgaccc 1200

ggttgctcc gcaagacttt ccccggttc cacgaagcgt tcgcgagtt gaggaaggac 1260

atcacgggt ga 1272

<210> 152

<211> 431

<212> PRT

<213> Streptomyces ipomoeae

<400> 152

Met Pro Asp Ala Pro Ala His Pro Arg Pro Ile Gly Gln His Val Gly

1 5 10 15

Met Pro Leu Val Asp Ile Pro Gly Ser Lys Ser Ile Thr Ala Arg Ala

20 25 30

Leu Phe Leu Ala Ala Ala Asp Gly Val Thr Thr Leu Leu Arg Pro

35 40 45

Leu Arg Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu Thr Arg Leu

50 55 60

Gly Tyr Arg Val Gly Arg Thr Pro Asp Ser Trp Gln Ile Asp Gly Arg

65 70 75 80

Pro Gln Gly Pro Ala Val Lys Glu Ala Asp Val Tyr Cys Arg Asp Gly

85 90 95

Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Ala Ala Ala Gly His Gly

100 105 110

Thr Tyr Arg Phe Asp Ala Ser Ala Gln Met Arg Arg Arg Pro Leu Ala

115 120 125

Pro Leu Thr Arg Ala Leu Arg Asp Leu Gly Val Asp Leu Val His Glu

130 135 140

Glu Ala Glu Gly His His Pro Leu Arg Ile Ala Ala Asn Gly Val Thr

145 150 155 160

Gly Gly Asp Val Thr Leu Asp Ala Gly Gln Ser Ser Gln Tyr Leu Thr

165 170 175

Ala Leu Leu Leu Leu Gly Pro Leu Thr Arg Glu Gly Leu Arg Ile Thr

180 185 190

Val Thr Asp Leu Val Ser Glu Pro Tyr Val Glu Ile Thr Thr Ala Met

195

200

205

Met Arg Ala Phe Gly Ala Asp Val Arg Arg Glu Gly Arg Thr Tyr Val

210

215

220

Val Glu Pro Gly Gly Tyr Arg Ala Thr Thr Tyr Ala Val Glu Pro Asp

225

230

235

240

Ala Ser Thr Ser Ser Tyr Phe Phe Ala Ala Ala Ala Leu Thr Gly Gly

245

250

255

Glu Val Thr Val Pro Gly Leu Gly Thr Gly Ala Leu Gln Gly Asp Leu

260

265

270

Arg Phe Val Asp Val Leu Arg Arg Met Gly Ala Arg Val Asp Val Arg

275

280

285

Glu Asp Gly Thr Thr Val Thr Gly Thr Gly Glu Leu Arg Gly Leu Thr

290

295

300

Val Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala Ile

305

310

315

320

Ala Pro Phe Ala Ser Gly Pro Val Arg Ile Glu Asp Val Ala Asn Thr

325 330 335

Arg Val Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala Glu Asn Leu Arg

340 345 350

Arg Leu Gly Ala Glu Val Ala Thr Gly Pro Asp Trp Ile Glu Ile Arg

355 360 365

Pro Gly Ala Pro Leu Thr Ser Thr Thr Asp Ile Lys Thr Tyr Gly Asp

370 375 380

His Arg Ile Val Met Ser Phe Ala Val Thr Gly Leu Arg Val Pro Gly

385 390 395 400

Ile Thr Phe Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro Asp Phe

405 410 415

His Glu Val Phe Ala Glu Phe Arg Arg Glu Leu Pro Gly Ala Glu

420 425 430

<210> 153

<211> 1296

<212> DNA

<213> Streptomyces ipomoeae

<400> 153

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ggagtcacca cgctgctacg acccctcaga tccgacgaca ccgagggctt cgccgagggc 180

ctgaccgggc tcggctaccg cgtcggccgt acccccgact cctggcagat cgacggccgt 240

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cgcttcctgc ccaccctggc cgccgccggc cacggcacct accgcttcga cgcctccgcc 360

cagatgcgcc gccgccccct ggccccgctc accggggccc tgcgcgacct cggcgtcgac 420

ctcgtacag aggaggccga gggccaccac ccgctgcgga tcgccgcaa cggcgtcacc 480

ggcggtgacg tcaccctga cgccggccag tcctcccagt acctcaccgc cctgctctc 540

ctcgccccc tcaccgcga gggcctgcgc atcacggtga cggacctggt ctcggagccg 600

tacgtggaga tcaccacggc gatgatgcgg gcgttcggcg ccgacgtccg ccgcgagggc 660

cgtacctag tcgtgaacc cggcggctac cgcgccacca cctacgccgt cgaaccgcac 720

gcctccacct ccagctactt ctcgccgcc gcggccctca ccggcggcga ggtcaccgtc 780

cccgccctcg gcaccggcgc cctccagggc gacctgcgt tcgtggacgt actgcggcgg 840

atgggcgccc gtgtggacgt acgcgaggac ggcacgaccg tgaccggcac cggcgaactg 900

cgcggcctca ccgtcaacat gcgtgacatc tccgacacca tgccgaccct tgcccgatc 960

gcccccttcg cctccggccc cgtccgcatc gaggacgtcg ccaacacccg ggtcaaggag 1020

tgcgaccgcc tggaggcctg cgcggagaac ctccggcggc tgggggcgga ggtcgccacg 1080

ggccccgact ggatcgagat ccgccccggc gcaccgctga cctccaccac ggacatcaag 1140

acgtacggcg accaccgat cgtgatgtcc ttcgccgtga cgggacttcg ggtgccgggc 1200

atcacgttcg acgaccccg ctgcgtacgg aagacgttcc cggacttcca cgaggtgttc 1260

gcggagttcc ggcgggagtt gccgggcgcc gagtga 1296

<210> 154

<211> 412

<212> PRT

<213> Streptomyces sp. W007

<400> 154

Met Thr Val Ile Asp Ile Pro Gly Ser Lys Ser Val Thr Ala Arg Ala

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Leu Phe Leu Ala Ala Ala Asp Gly Thr Ser Thr Leu Leu Arg Pro

20 25 30

Leu Arg Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu Glu Asn Leu

35 40 45

Gly Tyr Arg Val Asp Arg Glu Ala Asp Arg Trp His Ile Glu Gly Arg

50 55 60

Pro Ala Gly Pro Ala Ala Pro Asp Ala Asp Val Tyr Cys Arg Asp Gly

65 70 75 80

Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Val Ala Ala Ala Ala Ser

85 90 95

Gly Thr Tyr Arg Phe Asp Ala Ser Ala Gln Met Arg Arg Arg Pro Leu

100 105 110

Ala Pro Leu Thr Arg Ala Leu Thr Ala Leu Gly Val Asp Leu Arg His

115 120 125

Gly Gly Ala Glu Gly His His Pro Leu Thr Val Arg Ala Ala Gly Ile

130 135 140

Ala Gly Gly Glu Leu Thr Leu Asp Ala Gly Glu Ser Ser Gln Tyr Leu

145 150 155 160

Thr Ala Leu Leu Met Leu Gly Pro Leu Thr Ala Gln Gly Leu Arg Ile

165 170 175

Glu Val Thr Glu Leu Val Ser Ala Pro Tyr Val Glu Ile Thr Leu Ala

180 185 190

Met Met Arg Asp Phe Gly Val Glu Val Glu Arg Glu Gly Asn Thr Phe

195 200 205

Thr Val Pro Pro Gly Gly Tyr Arg Ala Thr Ala Tyr Ala Val Glu Pro

210 215 220

Asp Ala Ser Thr Ala Ser Tyr Phe Phe Ala Ala Gly Ala Leu Thr Gly

225 230 235 240

Arg Glu Val Thr Val Pro Gly Leu Gly Thr Gly Ala Leu Gln Gly Asp

245 250 255

Leu Arg Phe Val Asp Val Leu Arg Asp Met Gly Ala Glu Val Glu Val

260 265 270

Gly Ala Asp Ala Thr Thr Val Arg Ser Thr Gly Arg Leu Arg Gly Leu

275	280	285	
Thr Val Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala			
290	295	300	
Ile Ala Pro Tyr Ala Asp Gly Pro Val Arg Ile Glu Asp Val Ala Asn			
305	310	315	320
Thr Arg Val Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala Glu Asn Leu			
325	330	335	
Arg Ala Met Gly Ile Thr Val His Thr Gly Pro Asp Trp Ile Glu Ile			
340	345	350	
His Pro Gly Thr Pro Lys Pro Thr Glu Ile Ala Thr His Gly Asp His			
355	360	365	
Arg Ile Val Met Ser Phe Ala Val Ser Gly Leu Arg Thr Pro Gly Leu			
370	375	380	
Thr Tyr Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro Gly Phe His			
385	390	395	400

Glu Val Phe Gln Asp Phe Ala Gly Ala Gly Leu Pro

405 410

<210> 155

<211> 1239

<212> DNA

<213> Streptomyces sp. W007

<400> 155

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gccgccgccg acggcaccag caccctgctg aggccgctgc gctcggacga caccgagggc 120

ttcgccgaag gcctggagaa cctcggctac cgggtcgcacc gggaagccga ccgctggcac 180

atcgagggcc gccccgccgg gcccgccgcc cccgacgccg acgtctactg ccgcgacggc 240

gcgaccaccg cccgcttctt gccaccctc gtcgcggccg ccgcctccgg cacgtaccgc 300

ttcgacgcct ccgccagat gcgccgccg ccgctcgccc cgctcaccg cgccctcacc 360

gccctcggcg tcgacctgcg ccacggagga gcggaagggc accaccgct gaccgtccgg 420

gccgccggga tcgcgggcgg cgaactcacc ctggacgcgg gggagtcgtc ccagtacctc 480

accgcactgc tgatgctcgg gccgctcacc gcgcaggggc tgcggatcga ggtcaccgag 540

ctggtctccg cgccgtacgt cgagatcact ctcgcgatga tgcgcgactt cggcgtggag 600

gtggagcggg aggggaacac cttcacgctc cctccggcg gctaccgggc caccgcctac 660

gccgtcgagc ccgacgcctc caccgcgagc tacttcttcg ccgccggggc cctcaccggc 720

cgcgagggtca ccgtccccgg cctcggcacc ggggcgctcc agggcgatct gcgcttcgtc 780

gacgtgctgc gggacatggg cgccgaggtg gaggtgggag ccgacgccac caccgtccgc 840

tccaccggcc ggctgcgcgg cctcaccgtc aacatgcgcg acatctccga caccatgccg 900

accctcgccg ccacgcccc gtacgcggac ggaccgtgc ggatcgagga cgtcgccaac 960

acccgggtca aggaatgcga ccggctggag gcgtgcgccg agaacctgcg cgccatgggc 1020

atcaccgtcc acaccggccc cgactggatc gagatccacc ccggcacacc gaagcccacc 1080

gagatcgcca ccacggcgga ccaccggatc gtgatgtcgt tcgcggtctc cggactgcgc 1140

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gaggtgttcc aggacttcgc cggggccggg ctcccgtaa 1239

<210> 156

<211> 412

<212> PRT

<213> Streptomyces sp. SirexAA-E

<400> 156

Met Thr Val Ile His Ile Pro Gly Ser Lys Ser Val Thr Ala Arg Ala

1 5 10 15

Leu Phe Leu Ala Ala Ala Ala Asp Gly Thr Thr Thr Leu Leu Arg Pro
20 25 30

Leu Ser Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu Thr Arg Leu
35 40 45

Gly His Gly Val Thr Arg Glu Pro Asp Arg Trp His Ile Glu Gly Arg
50 55 60

Pro Asp Gly Pro Ala Val Thr Glu Ala Glu Val His Cys Arg Asp Gly
65 70 75 80

Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Ala Ala Ala Ala Pro Arg
85 90 95

Gly Thr Tyr Arg Phe Asp Ala Ser Ala Gln Met Arg Arg Arg Pro Leu
100 105 110

Gly Pro Leu Thr Glu Ala Leu Arg Ala Leu Gly Val Asp Leu Arg His
115 120 125

Glu Gly Ala Glu Gly His His Pro Leu Thr Val Arg Ala Ser Gly Val

130 135 140

Lys Gly Gly Glu Leu Thr Leu Asn Ala Gly Glu Ser Ser Gln Tyr Leu

145 150 155 160

Thr Ala Leu Leu Met Leu Gly Pro Leu Thr Ala Glu Gly Leu Arg Ile

165 170 175

His Val Thr Glu Leu Val Ser Ala Pro Tyr Val Glu Ile Thr Leu Ala

180 185 190

Met Met Arg Ser Phe Gly Val Asp Val Val Arg Glu Gly Asn Thr Phe

195 200 205

Thr Val Pro Pro Gly Gly Tyr Arg Ala Thr Thr Tyr Ala Val Glu Pro

210 215 220

Asp Ala Ser Thr Ala Ser Tyr Phe Phe Ala Ala Ala Ala Leu Thr Gly

225 230 235 240

Arg Glu Val Thr Val Pro Gly Leu Gly Thr Gly Ala Leu Gln Gly Asp

245 250 255

Leu Arg Phe Thr Asp Val Leu Arg Arg Met Gly Ala Glu Val Thr Thr
260 265 270

Thr Asp Thr Gly Thr Thr Val Arg Ser Thr Gly Ala Leu Ser Gly Leu
275 280 285

Thr Val Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala
290 295 300

Val Ala Pro Phe Ala Ser Ser Pro Val Arg Ile Glu Asp Val Ala Asn
305 310 315 320

Thr Arg Val Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala Arg Asn Leu
325 330 335

Arg Ala Met Gly Val Thr Val His Thr Gly Pro Asp Trp Thr Glu Ile
340 345 350

His Pro Gly Thr Pro Arg Pro Ala Glu Ile Thr Thr Phe Gly Asp His
355 360 365

Arg Ile Val Met Ser Phe Ala Val Ala Ala Leu Arg Val Pro Gly Val
370 375 380

Thr Tyr Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro Glu Phe His

385 390 395 400

Glu Val Phe Ala Arg Phe Ala Ala Glu Gly Ala Gly

405 410

<210> 157

<211> 1239

<212> DNA

<213> Streptomyces sp. SirexAA-E

<400> 157

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gccgcggcgg acggcacgac caccctcctg cggcccctga gctccgacga cacggagggg 120

ttcgccgagg ggctcaccg cctcggacac ggggtgacac gcgagccgga ccgctggcac 180

atcgagggac gccccgacgg ccccgccgtc accgaggccg aggtccactg ccgggacggg 240

gccaccaccg cccgcttctt gccacgctc gccgccgccg cgccccgcgg gacgtaccgc 300

ttcgacgcct cggcccagat gcgccgccgc ccgctcggcc cgctcaccga ggcgctgcgc 360

gccctcggtg tggacctgcg ccacgagggg gccgagggcc accaccgct caccgtacgg 420

gcgtcgggcg tcaagggcgg cgaactcacc ctgaacgcgg gggagtcgtc ccagtacctc 480

accgcactgc tcatgctcgg cccgctcacc gccgaagggc tgcggatcca cgtcacggaa 540

ctggtgtccg ccccttacgt cgagatcacc ctgcgatga tgcggagctt cggcgtcgac 600

gtcgtccgtg aggggaacac cttaccgctc cccccgggcg gctaccgcgc caccacctac 660

gccgtggagc ccgacgcgtc caccgcgagc tacttcttcg ccgccgcggc gtcaccggc 720

cgcgaggta ccgtcccgga gctgggcacc ggcgcgctcc agggcgacct gcgcttcacc 780

gagtcctgc gccgcatggg cgccgaggtg acgaccacgg acacgggcac gacggtccgc 840

tccaccgggg cgctctcggg cctcaccgtc aacatgcgcg acatctccga caccatgccg 900

accctggcgc ccgtcgcacc gttcgctcc tcgccgtac ggatcgagga cgtcgccaac 960

acccgggtca aggagtgcga ccggctggag gcctgcgcgc ggaacctgcg cgccatgggc 1020

gtcaccgtgc acaccggccc cgactggacc gagatccacc ccggcacccc ccggcccgcc 1080

gagatcacca cgttcggcga ccaccgcac gtgatgtcgt tcgcggtcgc ggcgctgcgc 1140

gtgcccggcg tcacctacga cgaccccggc tgcgtccgca agacgttccc cgagttccac 1200

gaggtcttcg cccggttcgc cgcggaaggc gccggctga 1239

<210> 158

<211> 413

<212> PRT

<213> Streptomyces globisporus C-1027

<400> 158

Met Ser Val Ile Asp Ile Pro Gly Ser Lys Ser Val Thr Ala Arg Ala

1 5 10 15

Leu Phe Leu Ala Ala Ala Ala Asp Gly Thr Thr Thr Leu Leu Arg Pro

20 25 30

Leu Arg Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu Lys Ser Leu

35 40 45

Gly Tyr Ala Val Glu Gln Glu Ala Asp Arg Trp Arg Val Gln Gly Arg

50 55 60

Pro Ala Gly Pro Ala Ala Asp Asp Ala Asp Val Tyr Cys Arg Asp Gly

65 70 75 80

Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Val Ala Ala Ala Ala Ser

85 90 95

Gly Thr Tyr Arg Phe Asp Ala Ser Ala Gln Met Arg Arg Arg Pro Leu

100 105 110

Ala Pro Leu Thr Arg Ala Leu Thr Ala Leu Gly Val Asp Leu Arg His

115 120 125

Gly Gly Ala Gln Gly His His Pro Leu Thr Val Arg Ala Ala Gly Ile

130 135 140

Glu Gly Gly Asp Leu Thr Leu Asp Ala Gly Glu Ser Ser Gln Tyr Leu

145 150 155 160

Thr Ala Leu Leu Met Leu Gly Pro Leu Thr Ala Lys Gly Leu Arg Ile

165 170 175

Glu Val Thr Glu Leu Val Ser Ala Pro Tyr Val Glu Ile Thr Leu Ala

180 185 190

Met Met Arg Asp Phe Gly Val Glu Val Leu Arg Glu Gly Asn Thr Phe

195 200 205

Thr Val Pro Pro Gly Gly Tyr Arg Ala Thr Ala Tyr Ala Val Glu Pro

210 215 220

Asp Ala Ser Thr Ala Ser Tyr Phe Phe Ala Ala Ala Ala Leu Thr Gly

225 230 235 240

Arg Glu Val Thr Val Pro Gly Leu Gly Ile Gly Ala Leu Gln Gly Asp

245 250 255

Leu Arg Phe Val Asp Val Leu Arg Asp Met Gly Ala Glu Val Ser Val

260 265 270

Gly Ala Asp Ala Thr Thr Val Arg Ser Thr Gly Arg Leu Arg Gly Thr

275 280 285

Thr Val Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala

290 295 300

Ile Ala Pro Tyr Ala Asp Gly Pro Val Ile Ile Glu Asp Val Ala Asn

305 310 315 320

Thr Arg Val Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala Glu Asn Leu

325 330 335

Arg Ala Met Gly Ile Thr Val His Thr Gly Pro Asp Arg Ile Glu Ile

340 345 350

His Pro Gly Thr Pro Lys Pro Thr Glu Ile Ala Thr Arg Gly Asp His

355 360 365

Arg Ile Val Met Ser Phe Ala Val Ala Gly Leu Arg Thr Pro Gly Leu

370 375 380

Thr Tyr Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro Arg Phe His

385 390 395 400

Glu Val Phe Ala Asp Phe Ala His Asp Leu Glu Gly Arg

405 410

<210> 159

<211> 1242

<212> DNA

<213> Streptomyces globisporus C-1027

<400> 159

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ttcgccgagg ggctgaagag ctcggttac gccgtcgagc aggaggccga ccgctggcgc 180

gtccaggggc gtccggccgg gcccgccgcc gacgacgccg acgtgtactg ccgcgacggc 240

gcgaccaccg cccgcttctt gccaccctc gtcgcggccg ccgcctccgg cacgtaccgc 300

ttcgagcctt ccgccagat gcgccgccgc ccgctcgccc cgctcaccgc ggccctcacc 360

gccctcggcg tcgacctcg ccacggggga gcgcaggggc accacccgct gaccgtgcgc 420

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accgcgtgc tgatgctcgg gccgtcacc gcgaaggggc tgcgcatga ggtcaccgag 540

ctggtctccg cgccgtacgt cgagatcacc ctgcgatga tgcgcatgtt cggcgtggag 600

gtactcggg aggggaacac cttaccgtc cctccggcg gctaccgggc caccgcctac 660

gccgtcgcg ctgacgctc caccgcgagc tacttcttcg ccgccgggc ctcaccggc 720

cgcgaggtca ccgtccccg cctcggcatc ggcgcctcc agggcgacct gcgcttcgtc 780

gagtcctgc gggacatggg cgccgaggtg agcgtcggcg ccgacgccac caccgtccgc 840

tccaccggcc ggctgcgcg caccaccgtc aacatgcgcg acatctccga caccatgccg 900

accctcgcg cgatcgcgc gtacgcggac gggcccgtca tcatcgagga cgtcgccaac 960

accgcgtca aggagtgcga ccggctggag gcgtgcgccc agaacctccg cgccatgggc 1020

atcaccgtcc acaccgtcc ggaccggatc gagatccacc ccggcacgcc gaagcccacc 1080

gagatgccca ccgcggcga ccaccgatc gtgatgtcct tcgccgtgc cggactgcgc 1140

acacccggcc tgacgtacga cgacccggc tgcgtacga agacgttccc gcgcttcac 1200

gaggtgttcg ccgacttcg gcacgacctc gaaggcgct ga 1242

<210> 160

<211> 411

<212> PRT

<213> Streptomyces venezuelae ATCC 10712

<400> 160

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Leu Phe Leu Ala Ala Ala Ala Gln Gly Thr Thr Thr Leu Leu Arg Pro

20 25 30

Leu Val Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu Gly Ser Leu

35 40 45

Gly Tyr Ala Val Arg Arg Glu Ser Asp Ala Trp His Ile Glu Gly Arg

50 55 60

Pro Ala Gly Pro Gly Ala Asp Thr Ala Asp Val Tyr Cys Arg Asp Gly

65 70 75 80

Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Val Ala Ala Gly His Gly

85 90 95

Thr Tyr Arg Phe Asp Ala Ser Pro Gln Met Arg Arg Arg Pro Leu Gly
100 105 110

Pro Leu Ser Thr Ala Leu Arg Thr Leu Gly Val Asp Leu Arg His Gly
115 120 125

Gly Lys Asp Gly His His Pro Leu Asp Val His Ala His Gly Val Lys
130 135 140

Gly Gly Ala Leu Thr Leu Asp Ala Gly Gln Ser Ser Gln Tyr Leu Thr
145 150 155 160

Ala Leu Leu Met Leu Gly Pro Leu Thr Ala Glu Gly Leu Asp Ile Thr
165 170 175

Val Thr Asp Leu Val Ser Glu Pro Tyr Val Glu Ile Thr Leu Ala Met
180 185 190

Met Arg Ser Phe Gly Ala Glu Val Thr Gln Glu Gly Arg Thr Tyr Arg
195 200 205

Val Ala Pro Thr Gly Tyr Arg Ala Arg Thr Tyr Gly Ile Glu Pro Asp
210 215 220

Ala Ser Thr Ala Ser Tyr Phe Phe Ala Ala Ala Ala Leu Glu Pro Gly

225 230 235 240

Arg Ser Val Thr Val Pro Gly Leu Gly Thr Gly Ala Leu Gln Gly Asp

245 250 255

Leu Gly Phe Val Asp Val Leu Arg Arg Met Gly Ala Asp Val Glu Ile

260 265 270

Thr Asp Ala Gly Thr Thr Val Arg Ser Thr Gly Thr Leu Arg Gly Leu

275 280 285

Thr Val Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala

290 295 300

Ile Ala Pro Phe Ala Asp Gly Pro Val Arg Ile Glu Asp Val Ala Asn

305 310 315 320

Thr Arg Val Lys Glu Cys Asp Arg Leu Asp Ala Cys Ala Glu Asn Leu

325 330 335

Arg Arg Leu Gly Ile Thr Val Glu Thr Gly Pro Asp Trp Ile Glu Ile

340

345

350

His Pro Gly Thr Pro Thr Gly Pro Ala Glu Ile Ala Thr His Gly Asp

355

360

365

His Arg Ile Val Met Ser Phe Ala Val Thr Ala Leu Arg Thr Pro Gly

370

375

380

Ile Thr Phe Asp Asp Pro Gly Cys Val Lys Lys Thr Phe Pro Asp Phe

385

390

395

400

His Arg Val Phe Asp Ala Phe Val His Thr Pro

405

410

<210> 161

<211> 1236

<212> DNA

<213> Streptomyces venezuelae ATCC 10712

<400> 161

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gccgcggccc agggcaccac caccctctg cggccgctcg tctccgacga caccgagggc

120

ttcgccgagg ggctcggttc gctcggctac gccgtccgcc gcgagagcga cgcttggcac

180

atcgagggcc gccccgcggg ccccggcgcg gacaccgccg acgtctactg ccgcgacggc 240

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gacgcctccc cccagatgag gcgcgcggc ctcggccgcg tcagcaccgc cctgcgcacc 360

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cacggcgtga agggcggcgc gctcacctc gacgccggc agtcctcca gtacctgacg 480

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gacgtgctgc gccgcatggg cgccgacgtc gagatcaccg acgccggcac caccgtccgc 840

tccaccggca ccctgcgcgg cctcacggtc aacatgcggg acatctcgga caccatgccg 900

accctgcgcg cgatcgcccc cttgccgac ggcccgttc gcacgagga cgtcgccaac 960

accgggtca aggagtgcga ccggctcgac gcctgcgcg agaacctgcg ccgcctgggc 1020

atcaccgtcg agaccggccc cgactggatc gagatccacc ccggcacccc caccggaccg 1080

gccgagatcg ccaccacgg cgaccacagg atcgtgatgt ccttcgcggt caccgcctg 1140

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caccgggtct tcgacgcgtt cgtccacacc ccgtga 1236

<210> 162

<211> 415

<212> PRT

<213> Streptomyces griseus XylebKG-1

<400> 162

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Ala Arg Ala Leu Phe Leu Ala Ala Ala Asp Gly Thr Thr Thr Leu

20 25 30

Leu Arg Pro Leu Arg Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu

35 40 45

Lys Asn Leu Gly Tyr Ala Val Glu Gln Glu Ala Asp Arg Trp Arg Val

50 55 60

Glu Gly Arg Pro Asp Gly Pro Ala Ala Pro Asp Ala Asp Val Tyr Cys

65 70 75 80

Arg Asp Gly Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Val Ala Ala

85 90 95

Ala Ala Ser Gly Thr Tyr Arg Phe Asp Ala Ser Val Gln Met Arg Arg

100 105 110

Arg Pro Leu Ala Pro Leu Thr Arg Ala Leu Thr Ala Leu Gly Val Asp

115 120 125

Leu Arg His Gly Gly Glu Glu Gly His His Pro Leu Thr Val Arg Ala

130 135 140

Ala Gly Ile Glu Gly Gly Asp Val Val Leu Asp Ala Gly Glu Ser Ser

145 150 155 160

Gln Tyr Leu Thr Ala Leu Leu Met Leu Gly Pro Leu Thr Ala Lys Gly

165 170 175

Leu Arg Ile Glu Val Thr Asp Leu Val Ser Ala Pro Tyr Val Glu Ile

180 185 190

Thr Leu Ala Met Met Arg Asp Phe Gly Val Asp Val Thr Arg Glu Gly

195 200 205

Asn Thr Phe Thr Val Pro Ser Gly Gly Tyr Arg Ala Thr Ala Tyr Ala

210 215 220

Val Glu Pro Asp Ala Ser Thr Ala Ser Tyr Phe Phe Ala Ala Ala Ala

225 230 235 240

Leu Thr Gly Arg Glu Val Thr Val Pro Gly Leu Gly Ile Gly Ala Leu

245 250 255

Gln Gly Asp Leu Arg Phe Val Asp Val Leu Arg Asp Met Gly Ala Glu

260 265 270

Val Ser Val Gly Pro Asp Ala Thr Thr Val Arg Ser Thr Gly Arg Leu

275 280 285

Arg Gly Ile Thr Val Thr Met Arg Asp Ile Ser Asp Thr Met Pro Thr

290 295 300

Leu Ala Ala Ile Ala Pro His Ala Asp Gly Pro Val Arg Ile Glu Asp

305 310 315 320

Val Ala Asn Thr Arg Val Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala
325 330 335

Gln Asn Leu Arg Ala Met Gly Ile Thr Val His Thr Gly His Asp Trp
340 345 350

Ile Glu Ile Leu Pro Gly Thr Pro Lys Pro Thr Gly Ile Ala Thr His
355 360 365

Gly Asp His Arg Ile Val Met Ser Phe Ala Val Ala Gly Leu Leu Thr
370 375 380

Pro Gly Leu Thr Tyr Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro
385 390 395 400

Arg Phe His Glu Val Phe Ala Asp Phe Ala Ala Ser Pro Gln Ala
405 410 415

<210> 163

<211> 1248

<212> DNA

<213> Streptomyces griseus XylebKG-1

<400> 163

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accgagggct tcgccgaagg gctgaagaac ctcggttacg cggtcgagca ggaggccgac 180

cgctggcgcg tcgaaggacg cccggacggg cccgccgccc ccgacgccga cgtctactgc 240

cgcgacggcg cgaccaccgc ccgcttcctg cccaccctcg tcgcggccgc cgcctccggc 300

acgtaccgct tcgacgctc cgtccagatg cgcgccgcc cgctcgcccc gtcacccgc 360

gccctcaccg ccctcggcgt cgatctgcgc cacgggggag aagaggggca ccaccgctg 420

accgtgcgcg ccgccgggat cgaggggtggc gacgtcgtcc tggacgcggg ggagtcgtcg 480

cagtacctca ccgccctgct gatgctcggg ccgctcaccg cgaaggggct gcggatcgag 540

gtcaccgacc tggctccgc cccgtacgtc gagatcacc tcgcatgat gcgcgacttc 600

ggcgtggacg tgacgcggga ggggaacacc ttaccgtcc cctccggcgg ctaccgggcc 660

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cgcttcgtcg acgtcctgcg ggacatgggc gccgaggtga gcgtcgcccc cgacgccacc 840

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accatgccga cgctcgccgc catcgcccc caccggacg gaccgtgcg catcgaggac 960

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aagccgacgg ggatgccac ccacggcgac caccggatcg tgatgcctt cgcggtcgcc 1140

ggactgtca cccccgtct gacgtacgac gacccggct gcgtacgaa gacgttcccg 1200

cgcttcacg aggtgttcgc ggacttcgcc gcgagccgc aggcctga 1248

<210> 164

<211> 412

<212> PRT

<213> Amycolatopsis mediterranei U32

<400> 164

Met Thr Leu Val Glu Ile Pro Gly Ser Lys Ser Val Thr Ala Arg Gly

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Leu Phe Leu Ala Ala Ala Ala His Gly Thr Thr Val Leu Gly Arg Pro

20 25 30

Leu His Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu Ala Glu Leu

35 40 45

Gly Tyr Arg Val Asp Arg Gln Pro Gly Glu Trp Thr Ile Glu Gly Arg

50 55 60

Pro Ser Gly Pro Gly Val Ala Glu Ala Asp Val Phe Cys Arg Asp Gly

65 70 75 80

Ala Thr Thr Ala Arg Phe Leu Pro Ala Leu Ala Ala Ala Gly Thr Gly

85 90 95

Thr Phe Arg Phe Asp Ala Ser Gly Gln Met Arg Arg Arg Pro Leu Gly

100 105 110

Pro Leu Thr Asp Ala Leu Gln Glu Leu Gly Val Glu Leu Glu Phe Arg

115 120 125

Gly Glu Pro Gly His His Pro Leu Thr Val Arg Ala Asn Gly Ile Lys

130 135 140

Gly Gly Glu Leu Thr Leu Asp Ala Gly Leu Ser Ser Gln Phe Leu Thr

145 150 155 160

Ala Leu Leu Leu Val Gly Pro Leu Thr Ala Glu Gly Leu Arg Ile Thr

165 170 175

Val Thr Asp Leu Val Ser Val Pro Tyr Val Glu Ile Thr Leu Glu Met

180 185 190

Met Arg Arg Phe Gly Val Asp Val Arg Arg Glu Gly Gln Thr Phe Val

195 200 205

Val Pro Ala Gln Pro Tyr Gln Ala Cys Glu Tyr Pro Val Glu Pro Asp

210 215 220

Ala Ser Thr Ala Ser Tyr Phe Leu Ala Ala Ala Ala Leu Thr Gly Arg

225 230 235 240

Thr Val Thr Ile Pro Gly Leu Gly Ser Glu Ala Leu Gln Gly Asp Val

245 250 255

Lys Phe Ala Asp Val Leu Arg Glu Met Gly Ala His Val Asp Leu Gly

260 265 270

Pro Asp Ser Val Thr Val Ala Gly Pro Ser Asp Gly Leu Arg Gly Ile

275 280 285

Thr Val Asn Met Arg Asp Ile Ser Asp Thr Val Pro Thr Leu Ala Ala

290 295 300

Ile Ala Pro Phe Ala Ser Gly Pro Val Arg Ile Glu Asp Val Tyr Asn

305 310 315 320

Thr Arg Ile Lys Glu Cys Asp Arg Leu Asp Ala Cys Glu Glu Asn Leu

325 330 335

Arg Ala Met Gly Ile Ala Val Glu Thr Gly Arg Asp Trp Ile Glu Ile

340 345 350

Gln Pro Gly Arg Pro Thr Gly Thr Leu Val Ser Cys Arg Arg Asp His

355 360 365

Arg Ile Ala Met Ala Phe Ser Ile Thr Gly Leu Leu Val Asp Gly Val

370 375 380

Thr Leu Asp Asp Pro Asp Cys Val Lys Lys Thr Phe Pro Gly Phe His

385 390 395 400

Gln Ala Leu Gly Thr Leu Arg Glu Gly Trp Gly Ile

405 410

<210> 165

<211> 1239

<212> DNA

<213> Amycolatopsis mediterranei U32

<400> 165

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atcaggggcc gtccgtcagg tccgggggtc gccgaagccg acgtcttctg ccgggacggc 240

gccacgacgg cccggttcct gcccgcctg gccgcggccg gcaccggcac gttccgcttc 300

gacgcctccg gccagatgcg ccgccgcccg ctggggccgc tgaccgacgc cctgcaggag 360

ctgggcgtcg aactcgagtt ccgcggcgag ccgggccacc acccgctgac ggtccgcgcg 420

aacggcatca agggcggcga gctgaccctc gacgcggggt tgtcttcgca gttcctgacg 480

gcgttgctgc tggtcgggcc gctgaccgcg gagggcctgc ggatcacggt gaccgacctc 540

gtgtcgggtc cgtacgtcga gatcacgtg gagatgatgc gccgcttcgg tgtcgacgtc 600

cgccgcgagg ggcagacgtt cgtgggtccc gcgcagccgt accaggcgtg cgagtacccg 660

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gtgctgcggg agatgggcgc gcacgtcgac ctggggccgg actcggtgac ggtcgcgggc 840

ccgtcggacg gcctgcgcgg gatcacggtg aacatgcggg acatctccga cacgtcccg 900

accctggccg cgategcccc gttcgcttcc ggcccgggtgc gcatcgagga cgtctacaac 960

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atgccgtcg agacgggccg cgactggatc gagatccagc cgggccggcc gacgggcacg 1080

ctggtgtcgt gccgccgca ccaccggatc gcgatggcgt tcagcatcac cggcctgctg 1140

gtcgacggcg tgacctgga tgatccggac tgtgtgaaga agacgttccc cggcttcac 1200

caggcgctgg ggacctgcg ggagggctgg gggatctag 1239

<210> 166

<211> 414

<212> PRT

<213> Streptomyces cattleya

<400> 166

Met Thr Val Val Glu Ile Pro Gly Ser Lys Ser Val Thr Ala Arg Ala

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Leu Phe Leu Ala Ala Ala Ala Arg Gly Thr Thr Val Leu Arg Gly Pro

20 25 30

Leu Val Ser Asp Asp Ser Glu Gly Phe Ala Glu Gly Leu Ile Thr Leu

35 40 45

Gly Tyr Gln Val Glu Arg Gly Pro Asp Ala Trp Thr Ile Thr Gly Arg

50 55 60

Pro Glu Gly Pro Ala Val Asn Glu Ala Asp Val Tyr Cys Arg Asp Gly

65 70 75 80

Ala Thr Thr Ala Arg Phe Leu Pro Ala Leu Ala Ala Ala Gly His Gly

85 90 95

Leu Phe Arg Phe Asp Ala Ser Ala Gln Met Arg Arg Arg Pro Leu Gly

100 105 110

Pro Leu Thr Arg Ala Leu Arg Asp Leu Gly Val Asp Leu Thr His Gln

115 120 125

Glu Glu Glu Gly His His Pro Leu Thr Val Arg Ala Ala Gly Ile Lys

130 135 140

Gly Gly Gln Val Thr Leu Asp Ala Gly Leu Ser Ser Gln Phe Leu Thr

145 150 155 160

Ala Leu Leu Leu Leu Ala Pro Leu Thr Glu Glu Gly Leu Arg Ile Thr
165 170 175

Val Thr Asp Leu Val Ser Val Pro Tyr Val Glu Ile Thr Leu Val Met
180 185 190

Met Arg Arg Phe Gly Val Glu Thr Val Arg Glu Gly Asp Thr Phe Val
195 200 205

Val Pro Pro Gly Gly Tyr Arg Ala Thr Asp Tyr Pro Val Glu Pro Asp
210 215 220

Ala Ser Thr Ala Ser Tyr Phe Leu Ala Ala Ala Ala Leu Thr Gly Arg
225 230 235 240

Arg Val Thr Val Pro Gly Leu Gly Ala Gly Ser Leu Gln Gly Asp Leu
245 250 255

Arg Phe Ala Glu Val Leu Arg Ser Met Gly Ala Glu Val Thr Leu Thr
260 265 270

Arg Asp Ser Val Thr Val Thr Gly Ala Asp Gly Gly Arg Leu Arg Gly
275 280 285

Leu Thr Val Asn Met Arg Asp Ile Ser Asp Thr Val Pro Thr Leu Ala

290 295 300

Ala Ile Ala Pro Phe Ala Asp Gly Pro Val Arg Ile Glu Asp Val Tyr

305 310 315 320

Asn Thr Arg Ile Lys Glu Cys Asp Arg Leu Asp Ala Cys Ala Glu Asn

325 330 335

Leu Arg Ala Leu Gly Val Pro Val Ala Thr Gly Arg Asp Trp Ile Glu

340 345 350

Ile Arg Pro Ala Arg Pro Ala Ala Ala Arg Ile Ala Cys Arg Gly Asp

355 360 365

His Arg Ile Ala Met Ser Phe Ser Val Thr Gly Leu Arg Thr Pro Gly

370 375 380

Ile Thr Leu Asp Asp Pro Gly Cys Val Lys Lys Thr Phe Pro Gly Phe

385 390 395 400

His Glu Ala Leu Ala Ala Leu Arg Thr Ala Trp Glu Thr Glu

<210> 167

<211> 1245

<212> DNA

<213> Streptomyces cattleya

<400> 167

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ttcgcggagg gcctgatcac cctcggctac caggtcgaac ggggcccgga cgcctggacg 180

atcaccggcc gccccgaggg cccggccgtc aacgaggcgg acgtctactg ccgggacggc 240

gcgacgaccg cgcgcttctt gcccgcgtc gccgccgccc gacacggcct gttccgcttc 300

gacgcctccg cgcagatgcg ccgccgcccg ctgggcccgc tcaccgcgc cctgcgcgac 360

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cgcgtcaccg tgcccgggct cggcgccggt tcgctccagg gcgatctgcg cttcgccgag 780

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cacgaggcgc tcgccgcgct gcggacagcc tgggaaacgg agtga 1245

<210> 168

<211> 410

<212> PRT

<213> Kitasatospora setae KM-6054

<400> 168

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Leu Phe Leu Ala Ala Ala Ala Asp Gly Val Thr Thr Leu Val Arg Pro
20 25 30

Leu Ala Ser Asp Asp Thr Glu Gly Phe Thr Glu Gly Leu Arg Ala Leu
35 40 45

Gly Tyr Gln Val Glu Arg Ala Glu Arg Glu Trp Arg Ile Thr Gly Arg
50 55 60

Pro Gln Gly Pro Gly Val Asp Gly Ala Ser Val Phe Cys Arg Asp Gly
65 70 75 80

Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Ala Ala Ala Gly His Gly
85 90 95

Thr Phe His Phe Asp Ala Ser Glu Gln Met Arg Arg Arg Pro Leu Gly
100 105 110

Pro Leu Thr Thr Ala Leu Arg Asp Leu Gly Val Arg Leu Glu His Arg
115 120 125

Gly Ala Glu Gly His His Pro Leu Ser Ile Glu Ala Ser Gly Val Glu
130 135 140

Gly Gly Glu Val Thr Leu Asp Ala Gly Leu Ser Ser Gln Tyr Leu Thr
145 150 155 160

Ala Leu Leu Leu Leu Gly Pro Leu Thr Arg Thr Gly Leu Arg Ile His
 165 170 175

Val Thr Asp Leu Val Ser Ala Pro Tyr Ile Glu Ile Thr Leu Ala Met
 180 185 190

Met Arg Ser Phe Gly Val Glu Val Ala Arg Glu Gly Asn Val Phe Asp
 195 200 205

Val Pro Ala Gly Gly Tyr Thr Ala Ala Arg Tyr Pro Val Glu Pro Asp
 210 215 220

Ala Ser Thr Ala Ser Tyr Phe Phe Ala Ala Ala Ala Leu Thr Gly Arg
225 230 235 240

Glu Val Thr Val Pro Gly Leu Gly Arg Gly Ala Leu Gln Gly Asp Leu
 245 250 255

Lys Phe Val Glu Val Leu Glu Arg Leu Gly Ala Lys Val Glu Ile Gly

260265270

Thr Asp Ala Thr Thr Val Thr Gly Gly Thr Leu Thr Gly Gly Thr Val

275280285

Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala Ile Ala

290295300

Pro Phe Ala Ser Gly Pro Ile Arg Ile Glu Asp Val Tyr Asn Thr Arg

305310315320

Val Lys Glu Cys Asp Arg Leu Asp Ala Cys Ala Asp Asn Leu Arg Arg

325330335

Gln Gly Ile Asp Val Ala Thr Gly Arg Asp Trp Ile Glu Ile Arg Pro

340345350

Gly Ser Pro Lys Pro Val Glu Ile Glu Thr His Gly Asp His Arg Ile

355360365

Val Met Ser Phe Ala Val Ala Gly Leu Arg Thr Pro Gly Thr Ser Tyr

370375380

Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro Gly Phe His Asp Ala

385 390 395 400

Phe Ala Ala Trp Ala Ala Gln Pro Glu Gly

405 410

<210> 169

<211> 1233

<212> DNA

<213> Kitasatospora setae KM-6054

<400> 169

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ttcgccgcct gggccgccca gcccgagggc tga 1233

<210> 170

<211> 6

<212> PRT

<213> Artificial Sequence

<220>
<223> Class IV EPSPS conserved amino acid sequence

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Ala or Gly

<400> 170

Thr Ala Arg Xaa Leu Phe
1 5

<210> 171
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Class IV EPSPS conserved amino acid sequence

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Thr or Ala

<400> 171

Glu Gly Phe Xaa Glu Gly

1 5

<210> 172

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Class IV EPSPS conserved amino acid sequence

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa is Thr or Ala

<220>

<221> MISC_FEATURE

<222> (12)..(12)

<223> Xaa is Ala or Val

<400> 172

Gly Ala Thr Thr Ala Arg Phe Leu Pro Xaa Leu Xaa Ala Ala

1 5 10

<210> 173

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Class IV EPSPS conserved amino acid sequence

<400> 173

Phe Asp Ala Ser

1

<210> 174

<211> 72

<212> PRT

<213> Streptomyces griseus subsp. griseus NBRC 13350

<400> 174

Asp Arg Trp Arg Val Glu Gly Arg Pro Asp Gly Pro Ala Ala Pro Asp

1 5 10 15

Ala Asp Val Tyr Cys Arg Asp Gly Ala Thr Thr Ala Arg Phe Leu Pro

20 25 30

Thr Leu Val Ala Ala Ala Ala Ser Gly Thr Tyr Arg Phe Asp Ala Ser

35 40 45

Ala Gln Met Arg Arg Arg Pro Leu Ala Pro Leu Thr Arg Ala Leu Thr
50 55 60

Ala Leu Gly Val Asp Leu Arg His
65 70

<210> 175
<211> 72
<212> PRT
<213> Streptomyces roseosporus NRRL 15998

<400> 175

Asp Arg Trp Arg Val Gln Gly Arg Pro Ala Gly Pro Ala Ala Thr Glu
1 5 10 15

Ala Asp Val Tyr Cys Arg Asp Gly Ala Thr Thr Ala Arg Phe Leu Pro
20 25 30

Thr Leu Ala Ala Ala Ala Ala Ser Gly Thr Tyr Arg Phe Asp Ala Ser
35 40 45

Ala Gln Met Arg Arg Arg Pro Leu Ala Pro Leu Thr Arg Ala Leu Thr
50 55 60

Ala Leu Gly Val Asp Leu Arg His

65 70

<210> 176

<211> 71

<212> PRT

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP4

<400> 176

Met Leu Ala Arg Gln Gly Gly Ser Leu Arg Ala Ser Gln Cys Asn Ala

1 5 10 15

Gly Leu Ala Arg Arg Val Glu Val Gly Ala Leu Val Val Pro Arg Pro

20 25 30

Ile Ser Val Asn Asp Val Val Pro His Val Tyr Ser Ala Pro Leu Ser

35 40 45

Val Ala Arg Arg Ser Cys Ser Lys Ser Ser Ile Arg Ser Thr Arg Arg

50 55 60

Leu Gln Thr Thr Val Cys Ser

65 70

<210> 177

<211> 62

<212> PRT

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP5

<400> 177

Met Gln Leu Leu Asn Gln Arg Gln Ala Leu Arg Leu Gly Arg Ser Ser

1 5 10 15

Ala Ser Lys Asn Gln Gln Val Ala Pro Leu Ala Ser Arg Pro Ala Ser

20 25 30

Ser Leu Ser Val Ser Ala Ser Ser Val Ala Pro Ala Pro Ala Cys Ser

35 40 45

Ala Pro Ala Gly Ala Gly Arg Arg Ala Val Val Val Arg Ala

50 55 60

<210> 178

<211> 66

<212> PRT

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP8

<400> 178

Met Ala Gln Ser Ser Arg Ile Cys His Gly Val Gln Asn Pro Cys Val

1 5 10 15

Ile Ile Ser Asn Leu Ser Lys Ser Asn Gln Asn Lys Ser Pro Phe Ser

20 25 30

Val Ser Leu Lys Thr His Gln Gln Gln Arg Arg Ala Tyr Gln Ile Ser

35 40 45

Ser Trp Gly Leu Lys Lys Ser Asn Asn Gly Ser Val Ile Arg Pro Val

50 55 60

Lys Ala

65

<210> 179

<211> 66

<212> PRT

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP9

<400> 179

Met Ala Gln Ala Ser Arg Ile Cys Gln Asn Pro Cys Val Ile Ser Asn

1 5 10 15

Leu Pro Lys Ser Asn His Arg Lys Ser Pro Phe Ser Val Ser Leu Lys

20 25 30

Thr His Gln Pro Arg Ala Ser Ser Trp Gly Leu Lys Lys Ser Gly Thr

35 40 45

Met Leu Asn Gly Ser Val Ile Arg Pro Val Lys Val Thr Ala Ser Val

50 55 60

Ser Ala

65

<210> 180

<211> 75

<212> PRT

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP12

<400> 180

Met Ala Gln Ser Ser Arg Ile Cys His Gly Val Gln Asn Pro Cys Val

1 5 10 15

Ile Ile Ser Asn Leu Ser Lys Ser Asn Gln Asn Lys Ser Pro Phe Ser

20 25 30

Val Ser Leu Lys Thr His Gln His Pro Arg Ala Tyr Pro Ile Ser Ser

35 40 45

Ser Trp Gly Leu Lys Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu

50 55 60

Arg Pro Leu Lys Val Met Ser Ser Val Ser Ala

65 70 75

<210> 181

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP13

<400> 181

Met Ala Gln Val Ser Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu

1 5 10 15

Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val

20 25 30

Ser Leu Lys Thr Gln Gln Pro Arg Ala Ser Ser Trp Gly Leu Lys Lys

35 40 45

Ser Gly Thr Met Leu Asn Gly Ser Val Ile Arg Pro Val Lys Val Thr

50 55 60

Ala Ser Val Ser Ala

65

<210> 182

<211> 62

<212> PRT

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP14

<400> 182

Met Ile Leu Gly Ser Ser Pro Thr Leu Pro His Ala Ser His Pro Ala

1 5 10 15

Arg Pro Gly Pro Ala Arg Pro Ile Ser Val Asn Asp Val Val Pro His

20 25 30

Val Tyr Ser Ala Pro Leu Ser Val Ala Arg Arg Ser Cys Ser Lys Ser

35 40 45

Ser Ile Arg Ser Thr Arg Arg Leu Gln Thr Thr Val Cys Ser

50 55 60

<210> 183

<211> 62

<212> PRT

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP23

<400> 183

Met Ala Gln Ile Asn Lys Ser Ala Asn Gly Val Arg Asn Ala Ser Leu

1 5 10 15

Ile Ser Asn Phe Ser Asn Thr Arg Gln Ala Lys Ser Pro Phe Ser Leu

20 25 30

Ser Cys Gly Thr Arg Leu Lys Asn Ser Ser Arg Gly Leu Lys Lys Val

35 40 45

Ala Val Arg Leu Ile Gly Ser Arg Val Lys Val Ser Ala Ser

50 55 60

<210> 184

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> Chloroplast transit peptide TraP24

<400> 184

Met Gln Leu Leu Asn Gln Arg Gln Ala Leu Arg Leu Gly Arg Ser Ser

1 5 10 15

Ala Ser Lys Asn Gln Gln Val Ala Pro Leu Ala Ser Arg Pro Ile Ser

20 25 30

Val Asn Asp Val Val Pro His Val Tyr Ser Ala Pro Leu Ser Val Ala

35 40 45

Arg Arg Ser Cys Ser Lys Ser Ser Ile Arg Ser Thr Arg Arg Leu Gln

50 55 60

Thr Thr Val Cys Ser

65

<210> 185

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> TraP14:DGT-32 fusion protein

<400> 185

Met Ile Leu Gly Ser Ser Pro Thr Leu Pro His Ala Ser His Pro Ala

1 5 10 15

Arg Pro Gly Pro Ala Arg Pro Ile Ser Val Asn Asp Val Val Pro His

20 25 30

Val Tyr Ser Ala Pro Leu Ser Val Ala Arg Arg Ser Cys Ser Lys Ser

35 40 45

Ser Ile Arg Ser Thr Arg Arg Leu Gln Thr Thr Val Cys Ser Met Thr

50 55 60

Val Ile Glu Ile Pro Gly Ser Lys Ser Val Thr Ala Arg Ala Leu Phe

65 70 75 80

Leu Ala Ala Ala Ala Asp Gly Thr Thr Thr Leu Leu Arg Pro Leu Arg

85 90 95

Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu Arg Asn Leu Gly Tyr

100 105 110

Ala Val Glu Gln Glu Ala Asp Arg Trp Arg Val Gln Gly Arg Pro Ala

115 120 125

Gly Pro Ala Ala Thr Glu Ala Asp Val Tyr Cys Arg Asp Gly Ala Thr

130 135 140

Thr Ala Arg Phe Leu Pro Thr Leu Ala Ala Ala Ala Ala Ser Gly Thr

145 150 155 160

Tyr Arg Phe Asp Ala Ser Ala Gln Met Arg Arg Arg Pro Leu Ala Pro

165 170 175

Leu Thr Arg Ala Leu Thr Ala Leu Gly Val Asp Leu Arg His Glu Gly

180 185 190

Ala Asp Gly His His Pro Leu Thr Val Arg Ala Ala Gly Ile Glu Gly

195 200 205

Gly Glu Leu Thr Leu Asp Ala Gly Glu Ser Ser Gln Tyr Leu Thr Ala

210 215 220

Leu Leu Met Leu Gly Pro Leu Thr Thr Lys Gly Leu Arg Ile Glu Val

225 230 235 240

Thr Glu Leu Val Ser Ala Pro Tyr Val Glu Ile Thr Leu Ala Met Met

245 250 255

Arg Asp Phe Gly Val Glu Val Glu Arg Glu Gly Asn Thr Phe Thr Val

260 265 270

Pro Ser Pro Ser Ser Arg Leu Arg Ser Asn Arg Gly Gly Pro Ile Gly

275

280

285

Gly Tyr Arg Ala Thr Thr Tyr Ala Val Glu Pro Asp Ala Ser Thr Ala

290

295

300

Ser Tyr Phe Phe Ala Ala Ala Ala Leu Thr Gly Arg Glu Val Thr Val

305

310

315

320

Pro Gly Leu Gly Thr Gly Ala Leu Gln Gly Asp Leu Arg Phe Val Asp

325

330

335

Val Leu Arg Glu Met Gly Ala Glu Val Ser Val Gly Pro Asp Ala Thr

340

345

350

Thr Val Arg Ser Thr Gly Arg Leu Arg Gly Ile Thr Val Asn Met Arg

355

360

365

Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala Ile Ala Pro Tyr Ala

370

375

380

Asp Gly Pro Val Val Ile Glu Asp Val Ala Asn Thr Arg Val Lys Glu

385

390

395

400

Cys Asp Arg Leu Glu Ala Cys Ala Glu Asn Leu Arg Ala Met Gly Ile
405 410 415

Thr Val His Thr Gly Pro Asp Arg Ile Glu Ile His Pro Gly Thr Pro
420 425 430

Lys Pro Thr Gly Ile Ala Thr His Gly Asp His Arg Ile Val Met Ser
435 440 445

Phe Ala Val Ala Gly Leu Arg Thr Pro Gly Leu Thr Tyr Asp Asp Pro
450 455 460

Gly Cys Val Arg Lys Thr Phe Pro Arg Phe His Glu Val Phe Ala Asp
465 470 475 480

Phe Ala His Asp Leu Glu Gly Arg
485

- <210> 186
- <211> 484
- <212> PRT
- <213> Artificial Sequence
- <220>
- <223> TraP24:DGT-33 fusion protein

<400> 186

Met Gln Leu Leu Asn Gln Arg Gln Ala Leu Arg Leu Gly Arg Ser Ser

1 5 10 15

Ala Ser Lys Asn Gln Gln Val Ala Pro Leu Ala Ser Arg Pro Ile Ser

20 25 30

Val Asn Asp Val Val Pro His Val Tyr Ser Ala Pro Leu Ser Val Ala

35 40 45

Arg Arg Ser Cys Ser Lys Ser Ser Ile Arg Ser Thr Arg Arg Leu Gln

50 55 60

Thr Thr Val Cys Ser Met Gly Ala Val Thr Val Ile Asp Ile Pro Gly

65 70 75 80

Ser Lys Ser Val Thr Ala Arg Ala Leu Phe Leu Ala Ala Ala Asp

85 90 95

Gly Thr Thr Thr Leu Leu Arg Pro Leu Arg Ser Asp Asp Thr Glu Gly

100 105 110

Phe Ala Glu Gly Leu Lys Asn Leu Gly Tyr Ala Val Glu Gln Glu Ala

115 120 125

Asp Arg Trp Arg Val Glu Gly Arg Pro Asp Gly Pro Ala Ala Pro Asp

130 135 140

Ala Asp Val Tyr Cys Arg Asp Gly Ala Thr Thr Ala Arg Phe Leu Pro

145 150 155 160

Thr Leu Val Ala Ala Ala Ala Ser Gly Thr Tyr Arg Phe Asp Ala Ser

165 170 175

Ala Gln Met Arg Arg Arg Pro Leu Ala Pro Leu Thr Arg Ala Leu Thr

180 185 190

Ala Leu Gly Val Asp Leu Arg His Gly Gly Glu Glu Gly His His Pro

195 200 205

Leu Thr Val Arg Ala Ala Gly Ile Glu Gly Gly Asp Val Val Leu Asp

210 215 220

Ala Gly Glu Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Leu Gly Pro

225 230 235 240

Leu Thr Ala Lys Gly Leu Arg Ile Glu Val Thr Asp Leu Val Ser Ala

245 250 255

Pro Tyr Val Glu Ile Thr Leu Ala Met Met Arg Asp Phe Gly Val Asp

260 265 270

Val Ser Arg Glu Gly Asn Thr Phe Thr Val Pro Ser Gly Gly Tyr Arg

275 280 285

Ala Thr Ala Tyr Ala Val Glu Pro Asp Ala Ser Thr Ala Ser Tyr Phe

290 295 300

Phe Ala Ala Ala Ala Leu Thr Gly Arg Glu Val Thr Val Pro Gly Leu

305 310 315 320

Gly Ile Gly Ala Leu Gln Gly Asp Leu Arg Phe Val Asp Val Leu Arg

325 330 335

Asp Met Gly Ala Glu Val Ser Val Gly Pro Asp Ala Thr Thr Val Arg

340 345 350

Ser Thr Gly Arg Leu Arg Gly Ile Thr Val Thr Met Arg Asp Ile Ser

355 360 365

Asp Thr Met Pro Thr Leu Ala Ala Ile Ala Pro His Ala Asp Gly Pro

370 375 380

Val Arg Ile Glu Asp Val Ala Asn Thr Arg Val Lys Glu Cys Asp Arg

385 390 395 400

Leu Glu Ala Cys Ala Gln Asn Leu Arg Ala Met Gly Ile Thr Val His

405 410 415

Thr Gly His Asp Trp Ile Glu Ile Leu Pro Gly Thr Pro Lys Pro Thr

420 425 430

Gly Ile Ala Thr His Gly Asp His Arg Ile Val Met Ser Phe Ala Val

435 440 445

Ala Gly Leu Leu Thr Pro Gly Leu Thr Tyr Asp Asp Pro Gly Cys Val

450 455 460

Arg Lys Thr Phe Pro Arg Phe His Glu Val Phe Ala Asp Phe Ala Ala

465 470 475 480

Ser Pro Gln Ala

<210> 187

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> TraP4:DGT-28 fusion protein

<400> 187

Met Leu Ala Arg Gln Gly Gly Ser Leu Arg Ala Ser Gln Cys Asn Ala

1 5 10 15

Gly Leu Ala Arg Arg Val Glu Val Gly Ala Leu Val Val Pro Arg Pro

20 25 30

Ile Ser Val Asn Asp Val Val Pro His Val Tyr Ser Ala Pro Leu Ser

35 40 45

Val Ala Arg Arg Ser Cys Ser Lys Ser Ser Ile Arg Ser Thr Arg Arg

50 55 60

Leu Gln Thr Thr Val Cys Ser Ala Ala Arg Gly Met Pro Ala Leu Ser

65 70 75 80

Leu Pro Gly Ser Lys Ser Ile Thr Ala Arg Ala Leu Phe Leu Ala Ala

85 90 95

Ala Ala Asp Gly Val Thr Thr Leu Val Arg Pro Leu Arg Ser Asp Asp

100 105 110

Thr Glu Gly Phe Ala Glu Gly Leu Val Arg Leu Gly Tyr Arg Val Gly

115 120 125

Arg Thr Pro Asp Thr Trp Gln Val Asp Gly Arg Pro Gln Gly Pro Ala

130 135 140

Val Ala Glu Ala Asp Val Tyr Cys Arg Asp Gly Ala Thr Thr Ala Arg

145 150 155 160

Phe Leu Pro Thr Leu Ala Ala Ala Gly His Gly Thr Tyr Arg Phe Asp

165 170 175

Ala Ser Pro Gln Met Arg Arg Arg Pro Leu Leu Pro Leu Ser Arg Ala

180 185 190

Leu Arg Asp Leu Gly Val Asp Leu Arg His Glu Glu Ala Glu Gly His

195 200 205

His Pro Leu Thr Val Arg Ala Ala Gly Val Glu Gly Gly Glu Val Thr

210 215 220

Leu Asp Ala Gly Gln Ser Ser Gln Tyr Leu Thr Ala Leu Leu Leu Leu

225 230 235 240

Gly Pro Leu Thr Arg Gln Gly Leu Arg Ile Arg Val Thr Asp Leu Val

245 250 255

Ser Ala Pro Tyr Val Glu Ile Thr Leu Ala Met Met Arg Ala Phe Gly

260 265 270

Val Glu Val Ala Arg Glu Gly Asp Val Phe Val Val Pro Pro Gly Gly

275 280 285

Tyr Arg Ala Thr Thr Tyr Ala Ile Glu Pro Asp Ala Ser Thr Ala Ser

290 295 300

Tyr Phe Phe Ala Ala Ala Ala Leu Thr Pro Gly Ala Glu Val Thr Val

305 310 315 320

Pro Gly Leu Gly Thr Gly Ala Leu Gln Gly Asp Leu Gly Phe Val Asp
325 330 335

Val Leu Arg Arg Met Gly Ala Glu Val Ser Val Gly Ala Asp Ala Thr
340 345 350

Thr Val Arg Gly Thr Gly Glu Leu Arg Gly Leu Thr Ala Asn Met Arg
355 360 365

Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala Ile Ala Pro Phe Ala
370 375 380

Ser Ala Pro Val Arg Ile Glu Asp Val Ala Asn Thr Arg Val Lys Glu
385 390 395 400

Cys Asp Arg Leu Glu Ala Cys Ala Glu Asn Leu Arg Arg Leu Gly Val
405 410 415

Arg Val Ala Thr Gly Pro Asp Trp Ile Glu Ile His Pro Gly Pro Ala
420 425 430

Thr Gly Ala Gln Val Thr Ser Tyr Gly Asp His Arg Ile Val Met Ser
435 440 445

Phe Ala Val Thr Gly Leu Arg Val Pro Gly Ile Ser Phe Asp Asp Pro

450 455 460

Gly Cys Val Arg Lys Thr Phe Pro Gly Phe His Glu Ala Phe Ala Glu

465 470 475 480

Leu Arg Arg Gly Ile Gly Ser

485

<210> 188

<211> 477

<212> PRT

<213> Artificial Sequence

<220>

<223> TraP5:DGT-28 fusion protein

<400> 188

Met Gln Leu Leu Asn Gln Arg Gln Ala Leu Arg Leu Gly Arg Ser Ser

1 5 10 15

Ala Ser Lys Asn Gln Gln Val Ala Pro Leu Ala Ser Arg Pro Ala Ser

20 25 30

Ser Leu Ser Val Ser Ala Ser Ser Val Ala Pro Ala Pro Ala Cys Ser

35 40 45

Ala Pro Ala Gly Ala Gly Arg Arg Ala Val Val Val Arg Ala Ala Arg

50 55 60

Gly Met Pro Ala Leu Ser Leu Pro Gly Ser Lys Ser Ile Thr Ala Arg

65 70 75 80

Ala Leu Phe Leu Ala Ala Ala Ala Asp Gly Val Thr Thr Leu Val Arg

85 90 95

Pro Leu Arg Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu Val Arg

100 105 110

Leu Gly Tyr Arg Val Gly Arg Thr Pro Asp Thr Trp Gln Val Asp Gly

115 120 125

Arg Pro Gln Gly Pro Ala Val Ala Glu Ala Asp Val Tyr Cys Arg Asp

130 135 140

Gly Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Ala Ala Ala Gly His

145 150 155 160

Gly Thr Tyr Arg Phe Asp Ala Ser Pro Gln Met Arg Arg Arg Pro Leu
165 170 175

Leu Pro Leu Ser Arg Ala Leu Arg Asp Leu Gly Val Asp Leu Arg His
180 185 190

Glu Glu Ala Glu Gly His His Pro Leu Thr Val Arg Ala Ala Gly Val
195 200 205

Glu Gly Gly Glu Val Thr Leu Asp Ala Gly Gln Ser Ser Gln Tyr Leu
210 215 220

Thr Ala Leu Leu Leu Leu Gly Pro Leu Thr Arg Gln Gly Leu Arg Ile
225 230 235 240

Arg Val Thr Asp Leu Val Ser Ala Pro Tyr Val Glu Ile Thr Leu Ala
245 250 255

Met Met Arg Ala Phe Gly Val Glu Val Ala Arg Glu Gly Asp Val Phe
260 265 270

Val Val Pro Pro Gly Gly Tyr Arg Ala Thr Thr Tyr Ala Ile Glu Pro
275 280 285

Asp Ala Ser Thr Ala Ser Tyr Phe Phe Ala Ala Ala Ala Leu Thr Pro

290 295 300

Gly Ala Glu Val Thr Val Pro Gly Leu Gly Thr Gly Ala Leu Gln Gly

305 310 315 320

Asp Leu Gly Phe Val Asp Val Leu Arg Arg Met Gly Ala Glu Val Ser

325 330 335

Val Gly Ala Asp Ala Thr Thr Val Arg Gly Thr Gly Glu Leu Arg Gly

340 345 350

Leu Thr Ala Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala

355 360 365

Ala Ile Ala Pro Phe Ala Ser Ala Pro Val Arg Ile Glu Asp Val Ala

370 375 380

Asn Thr Arg Val Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala Glu Asn

385 390 395 400

Leu Arg Arg Leu Gly Val Arg Val Ala Thr Gly Pro Asp Trp Ile Glu

405 410 415

Ile His Pro Gly Pro Ala Thr Gly Ala Gln Val Thr Ser Tyr Gly Asp

420 425 430

His Arg Ile Val Met Ser Phe Ala Val Thr Gly Leu Arg Val Pro Gly

435 440 445

Ile Ser Phe Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro Gly Phe

450 455 460

His Glu Ala Phe Ala Glu Leu Arg Arg Gly Ile Gly Ser

465 470 475

<210> 189

<211> 481

<212> PRT

<213> Artificial Sequence

<220>

<223> TraP8:DGT-28 fusion protein

<400> 189

Met Ala Gln Ser Ser Arg Ile Cys His Gly Val Gln Asn Pro Cys Val

1 5 10 15

Ile Ile Ser Asn Leu Ser Lys Ser Asn Gln Asn Lys Ser Pro Phe Ser

20 25 30

Val Ser Leu Lys Thr His Gln Gln Gln Arg Arg Ala Tyr Gln Ile Ser

35 40 45

Ser Trp Gly Leu Lys Lys Ser Asn Asn Gly Ser Val Ile Arg Pro Val

50 55 60

Lys Ala Ala Arg Gly Met Pro Ala Leu Ser Leu Pro Gly Ser Lys Ser

65 70 75 80

Ile Thr Ala Arg Ala Leu Phe Leu Ala Ala Ala Ala Asp Gly Val Thr

85 90 95

Thr Leu Val Arg Pro Leu Arg Ser Asp Asp Thr Glu Gly Phe Ala Glu

100 105 110

Gly Leu Val Arg Leu Gly Tyr Arg Val Gly Arg Thr Pro Asp Thr Trp

115 120 125

Gln Val Asp Gly Arg Pro Gln Gly Pro Ala Val Ala Glu Ala Asp Val

130 135 140

Tyr Cys Arg Asp Gly Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Ala

145 150 155 160

Ala Ala Gly His Gly Thr Tyr Arg Phe Asp Ala Ser Pro Gln Met Arg

165 170 175

Arg Arg Pro Leu Leu Pro Leu Ser Arg Ala Leu Arg Asp Leu Gly Val

180 185 190

Asp Leu Arg His Glu Glu Ala Glu Gly His His Pro Leu Thr Val Arg

195 200 205

Ala Ala Gly Val Glu Gly Gly Glu Val Thr Leu Asp Ala Gly Gln Ser

210 215 220

Ser Gln Tyr Leu Thr Ala Leu Leu Leu Leu Gly Pro Leu Thr Arg Gln

225 230 235 240

Gly Leu Arg Ile Arg Val Thr Asp Leu Val Ser Ala Pro Tyr Val Glu

245 250 255

Ile Thr Leu Ala Met Met Arg Ala Phe Gly Val Glu Val Ala Arg Glu
260 265 270

Gly Asp Val Phe Val Val Pro Pro Gly Gly Tyr Arg Ala Thr Thr Tyr
275 280 285

Ala Ile Glu Pro Asp Ala Ser Thr Ala Ser Tyr Phe Phe Ala Ala Ala
290 295 300

Ala Leu Thr Pro Gly Ala Glu Val Thr Val Pro Gly Leu Gly Thr Gly
305 310 315 320

Ala Leu Gln Gly Asp Leu Gly Phe Val Asp Val Leu Arg Arg Met Gly
325 330 335

Ala Glu Val Ser Val Gly Ala Asp Ala Thr Thr Val Arg Gly Thr Gly
340 345 350

Glu Leu Arg Gly Leu Thr Ala Asn Met Arg Asp Ile Ser Asp Thr Met
355 360 365

Pro Thr Leu Ala Ala Ile Ala Pro Phe Ala Ser Ala Pro Val Arg Ile
370 375 380

Glu Asp Val Ala Asn Thr Arg Val Lys Glu Cys Asp Arg Leu Glu Ala
385 390 395 400

Cys Ala Glu Asn Leu Arg Arg Leu Gly Val Arg Val Ala Thr Gly Pro
 405 410 415

Asp Trp Ile Glu Ile His Pro Gly Pro Ala Thr Gly Ala Gln Val Thr
 420 425 430

Ser Tyr Gly Asp His Arg Ile Val Met Ser Phe Ala Val Thr Gly Leu
 435 440 445

Arg Val Pro Gly Ile Ser Phe Asp Asp Pro Gly Cys Val Arg Lys Thr
 450 455 460

Phe Pro Gly Phe His Glu Ala Phe Ala Glu Leu Arg Arg Gly Ile Gly
465 470 475 480

Ser

<210> 190

<211> 481

<212> PRT

<213> Artificial Sequence

<220>

<223> TraP9:DGT-28 fusion protein

<400> 190

Met Ala Gln Ala Ser Arg Ile Cys Gln Asn Pro Cys Val Ile Ser Asn

1 5 10 15

Leu Pro Lys Ser Asn His Arg Lys Ser Pro Phe Ser Val Ser Leu Lys

20 25 30

Thr His Gln Pro Arg Ala Ser Ser Trp Gly Leu Lys Lys Ser Gly Thr

35 40 45

Met Leu Asn Gly Ser Val Ile Arg Pro Val Lys Val Thr Ala Ser Val

50 55 60

Ser Ala Ala Arg Gly Met Pro Ala Leu Ser Leu Pro Gly Ser Lys Ser

65 70 75 80

Ile Thr Ala Arg Ala Leu Phe Leu Ala Ala Ala Asp Gly Val Thr

85 90 95

Thr Leu Val Arg Pro Leu Arg Ser Asp Asp Thr Glu Gly Phe Ala Glu
100 105 110

Gly Leu Val Arg Leu Gly Tyr Arg Val Gly Arg Thr Pro Asp Thr Trp
115 120 125

Gln Val Asp Gly Arg Pro Gln Gly Pro Ala Val Ala Glu Ala Asp Val
130 135 140

Tyr Cys Arg Asp Gly Ala Thr Thr Ala Arg Phe Leu Pro Thr Leu Ala
145 150 155 160

Ala Ala Gly His Gly Thr Tyr Arg Phe Asp Ala Ser Pro Gln Met Arg
165 170 175

Arg Arg Pro Leu Leu Pro Leu Ser Arg Ala Leu Arg Asp Leu Gly Val
180 185 190

Asp Leu Arg His Glu Glu Ala Glu Gly His His Pro Leu Thr Val Arg
195 200 205

Ala Ala Gly Val Glu Gly Gly Glu Val Thr Leu Asp Ala Gly Gln Ser
210 215 220

Ser Gln Tyr Leu Thr Ala Leu Leu Leu Leu Gly Pro Leu Thr Arg Gln

225 230 235 240

Gly Leu Arg Ile Arg Val Thr Asp Leu Val Ser Ala Pro Tyr Val Glu

245 250 255

Ile Thr Leu Ala Met Met Arg Ala Phe Gly Val Glu Val Ala Arg Glu

260 265 270

Gly Asp Val Phe Val Val Pro Pro Gly Gly Tyr Arg Ala Thr Thr Tyr

275 280 285

Ala Ile Glu Pro Asp Ala Ser Thr Ala Ser Tyr Phe Phe Ala Ala Ala

290 295 300

Ala Leu Thr Pro Gly Ala Glu Val Thr Val Pro Gly Leu Gly Thr Gly

305 310 315 320

Ala Leu Gln Gly Asp Leu Gly Phe Val Asp Val Leu Arg Arg Met Gly

325 330 335

Ala Glu Val Ser Val Gly Ala Asp Ala Thr Thr Val Arg Gly Thr Gly

340	345	350	
Glu Leu Arg Gly Leu Thr Ala Asn Met Arg Asp Ile Ser Asp Thr Met			
355	360	365	
Pro Thr Leu Ala Ala Ile Ala Pro Phe Ala Ser Ala Pro Val Arg Ile			
370	375	380	
Glu Asp Val Ala Asn Thr Arg Val Lys Glu Cys Asp Arg Leu Glu Ala			
385	390	395	400
Cys Ala Glu Asn Leu Arg Arg Leu Gly Val Arg Val Ala Thr Gly Pro			
405	410	415	
Asp Trp Ile Glu Ile His Pro Gly Pro Ala Thr Gly Ala Gln Val Thr			
420	425	430	
Ser Tyr Gly Asp His Arg Ile Val Met Ser Phe Ala Val Thr Gly Leu			
435	440	445	
Arg Val Pro Gly Ile Ser Phe Asp Asp Pro Gly Cys Val Arg Lys Thr			
450	455	460	

Phe Pro Gly Phe His Glu Ala Phe Ala Glu Leu Arg Arg Gly Ile Gly
465 470 475 480

Ser

<210> 191

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<223> TraP12:DGT-28 fusion protein

<400> 191

Met Ala Gln Ser Ser Arg Ile Cys His Gly Val Gln Asn Pro Cys Val
1 5 10 15

Ile Ile Ser Asn Leu Ser Lys Ser Asn Gln Asn Lys Ser Pro Phe Ser
20 25 30

Val Ser Leu Lys Thr His Gln His Pro Arg Ala Tyr Pro Ile Ser Ser
35 40 45

Ser Trp Gly Leu Lys Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu

50 55 60

Arg Pro Leu Lys Val Met Ser Ser Val Ser Ala Ala Arg Gly Met Pro

65 70 75 80

Ala Leu Ser Leu Pro Gly Ser Lys Ser Ile Thr Ala Arg Ala Leu Phe

85 90 95

Leu Ala Ala Ala Ala Asp Gly Val Thr Thr Leu Val Arg Pro Leu Arg

100 105 110

Ser Asp Asp Thr Glu Gly Phe Ala Glu Gly Leu Val Arg Leu Gly Tyr

115 120 125

Arg Val Gly Arg Thr Pro Asp Thr Trp Gln Val Asp Gly Arg Pro Gln

130 135 140

Gly Pro Ala Val Ala Glu Ala Asp Val Tyr Cys Arg Asp Gly Ala Thr

145 150 155 160

Thr Ala Arg Phe Leu Pro Thr Leu Ala Ala Ala Gly His Gly Thr Tyr

165 170 175

Arg Phe Asp Ala Ser Pro Gln Met Arg Arg Arg Pro Leu Leu Pro Leu

180 185 190

Ser Arg Ala Leu Arg Asp Leu Gly Val Asp Leu Arg His Glu Glu Ala

195 200 205

Glu Gly His His Pro Leu Thr Val Arg Ala Ala Gly Val Glu Gly Gly

210 215 220

Glu Val Thr Leu Asp Ala Gly Gln Ser Ser Gln Tyr Leu Thr Ala Leu

225 230 235 240

Leu Leu Leu Gly Pro Leu Thr Arg Gln Gly Leu Arg Ile Arg Val Thr

245 250 255

Asp Leu Val Ser Ala Pro Tyr Val Glu Ile Thr Leu Ala Met Met Arg

260 265 270

Ala Phe Gly Val Glu Val Ala Arg Glu Gly Asp Val Phe Val Val Pro

275 280 285

Pro Gly Gly Tyr Arg Ala Thr Thr Tyr Ala Ile Glu Pro Asp Ala Ser

290 295 300

Thr Ala Ser Tyr Phe Phe Ala Ala Ala Ala Leu Thr Pro Gly Ala Glu
305 310 315 320

Val Thr Val Pro Gly Leu Gly Thr Gly Ala Leu Gln Gly Asp Leu Gly
 325 330 335

Phe Val Asp Val Leu Arg Arg Met Gly Ala Glu Val Ser Val Gly Ala
 340 345 350

Asp Ala Thr Thr Val Arg Gly Thr Gly Glu Leu Arg Gly Leu Thr Ala
 355 360 365

Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala Ile Ala
370 375 380

Pro Phe Ala Ser Ala Pro Val Arg Ile Glu Asp Val Ala Asn Thr Arg
385 390 395 400

Val Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala Glu Asn Leu Arg Arg
 405 410 415

Leu Gly Val Arg Val Ala Thr Gly Pro Asp Trp Ile Glu Ile His Pro
 420 425 430

Gly Pro Ala Thr Gly Ala Gln Val Thr Ser Tyr Gly Asp His Arg Ile

435 440 445

Val Met Ser Phe Ala Val Thr Gly Leu Arg Val Pro Gly Ile Ser Phe

450 455 460

Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro Gly Phe His Glu Ala

465 470 475 480

Phe Ala Glu Leu Arg Arg Gly Ile Gly Ser

485 490

<210> 192

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> TraP13:DGT-28 fusion protein

<400> 192

Met Ala Gln Val Ser Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu

1 5 10 15

Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val

20 25 30

Ser Leu Lys Thr Gln Gln Pro Arg Ala Ser Ser Trp Gly Leu Lys Lys

35 40 45

Ser Gly Thr Met Leu Asn Gly Ser Val Ile Arg Pro Val Lys Val Thr

50 55 60

Ala Ser Val Ser Ala Ala Arg Gly Met Pro Ala Leu Ser Leu Pro Gly

65 70 75 80

Ser Lys Ser Ile Thr Ala Arg Ala Leu Phe Leu Ala Ala Ala Ala Asp

85 90 95

Gly Val Thr Thr Leu Val Arg Pro Leu Arg Ser Asp Asp Thr Glu Gly

100 105 110

Phe Ala Glu Gly Leu Val Arg Leu Gly Tyr Arg Val Gly Arg Thr Pro

115 120 125

Asp Thr Trp Gln Val Asp Gly Arg Pro Gln Gly Pro Ala Val Ala Glu

130 135 140

Ala Asp Val Tyr Cys Arg Asp Gly Ala Thr Thr Ala Arg Phe Leu Pro

145 150 155 160

Thr Leu Ala Ala Ala Gly His Gly Thr Tyr Arg Phe Asp Ala Ser Pro

165 170 175

Gln Met Arg Arg Arg Pro Leu Leu Pro Leu Ser Arg Ala Leu Arg Asp

180 185 190

Leu Gly Val Asp Leu Arg His Glu Glu Ala Glu Gly His His Pro Leu

195 200 205

Thr Val Arg Ala Ala Gly Val Glu Gly Gly Glu Val Thr Leu Asp Ala

210 215 220

Gly Gln Ser Ser Gln Tyr Leu Thr Ala Leu Leu Leu Leu Gly Pro Leu

225 230 235 240

Thr Arg Gln Gly Leu Arg Ile Arg Val Thr Asp Leu Val Ser Ala Pro

245 250 255

Tyr Val Glu Ile Thr Leu Ala Met Met Arg Ala Phe Gly Val Glu Val

260265270

Ala Arg Glu Gly Asp Val Phe Val Val Pro Pro Gly Gly Tyr Arg Ala

275280285

Thr Thr Tyr Ala Ile Glu Pro Asp Ala Ser Thr Ala Ser Tyr Phe Phe

290295300

Ala Ala Ala Ala Leu Thr Pro Gly Ala Glu Val Thr Val Pro Gly Leu

305310315320

Gly Thr Gly Ala Leu Gln Gly Asp Leu Gly Phe Val Asp Val Leu Arg

325330335

Arg Met Gly Ala Glu Val Ser Val Gly Ala Asp Ala Thr Thr Val Arg

340345350

Gly Thr Gly Glu Leu Arg Gly Leu Thr Ala Asn Met Arg Asp Ile Ser

355360365

Asp Thr Met Pro Thr Leu Ala Ala Ile Ala Pro Phe Ala Ser Ala Pro

370375380

Val Arg Ile Glu Asp Val Ala Asn Thr Arg Val Lys Glu Cys Asp Arg
385 390 395 400

Leu Glu Ala Cys Ala Glu Asn Leu Arg Arg Leu Gly Val Arg Val Ala
 405 410 415

Thr Gly Pro Asp Trp Ile Glu Ile His Pro Gly Pro Ala Thr Gly Ala
 420 425 430

Gln Val Thr Ser Tyr Gly Asp His Arg Ile Val Met Ser Phe Ala Val
 435 440 445

Thr Gly Leu Arg Val Pro Gly Ile Ser Phe Asp Asp Pro Gly Cys Val
 450 455 460

Arg Lys Thr Phe Pro Gly Phe His Glu Ala Phe Ala Glu Leu Arg Arg
465 470 475 480

Gly Ile Gly Ser

<210> 193
<211> 476
<212> PRT

<213> Artificial Sequence

<220>

<223> TraP23:DGT-31 fusion protein

<400> 193

Met Ala Gln Ile Asn Lys Ser Ala Asn Gly Val Arg Asn Ala Ser Leu

1 5 10 15

Ile Ser Asn Phe Ser Asn Thr Arg Gln Ala Lys Ser Pro Phe Ser Leu

20 25 30

Ser Cys Gly Thr Arg Leu Lys Asn Ser Ser Arg Gly Leu Lys Lys Val

35 40 45

Ala Val Arg Leu Ile Gly Ser Arg Val Lys Val Ser Ala Ser Met Thr

50 55 60

Val Ile Asp Ile Pro Gly Ser Lys Ser Val Thr Ala Arg Ala Leu Phe

65 70 75 80

Leu Ala Ala Ala Ala Asp Gly Thr Thr Thr Leu Leu Arg Pro Leu His

85 90 95

Ser Asp Asp Thr Glu Gly Phe Thr Glu Gly Leu Thr Arg Leu Gly Tyr
100 105 110

Ala Val Val Arg Glu Pro Asp Arg Trp His Ile Glu Gly Arg Pro Ser
115 120 125

Gly Pro Ala Ala Ala Asp Ala Glu Val His Cys Arg Asp Gly Ala Thr
130 135 140

Thr Ala Arg Phe Leu Pro Thr Leu Ala Ala Ala Ala Ala Ser Gly Thr
145 150 155 160

Tyr Arg Phe Asp Ala Ser Ala Gln Met Arg Arg Arg Pro Leu Ala Pro
165 170 175

Leu Thr Glu Ala Leu Arg Thr Leu Gly Val Asp Leu Arg His Asp Gly
180 185 190

Ala Glu Gly His His Pro Leu Thr Ile Gln Ala Ser Gly Val Lys Gly
195 200 205

Gly Gly Leu Thr Leu Asp Ala Gly Glu Ser Ser Gln Tyr Leu Thr Ala
210 215 220

Leu Leu Met Leu Gly Pro Leu Thr Ala Glu Gly Leu Arg Ile Glu Val
225 230 235 240

Thr Glu Leu Val Ser Ala Pro Tyr Val Glu Ile Thr Leu Ala Met Met
 245 250 255

Arg Gly Phe Gly Val Glu Val Val Arg Glu Gly Asn Thr Phe Thr Val
 260 265 270

Pro Pro Gly Gly Tyr Arg Ala Thr Thr Tyr Ala Ile Glu Pro Asp Ala
 275 280 285

Ser Thr Ala Ser Tyr Phe Phe Ala Ala Ala Ala Leu Thr Gly Arg Glu
290 295 300

Val Thr Val Pro Gly Leu Gly Thr Gly Ala Leu Gln Gly Asp Leu Arg
305 310 315 320

Phe Thr Glu Val Leu Arg Arg Met Asp Ala Asp Val Arg Thr Thr Ser
 325 330 335

Asp Ser Thr Thr Val Arg Ser Asp Gly Arg Leu Ala Gly Leu Thr Val
 340 345 350

Asn Met Arg Asp Ile Ser Asp Thr Met Pro Thr Leu Ala Ala Ile Ala

355 360 365

Pro Tyr Ala Ser Ser Pro Val Arg Ile Glu Asp Val Ala Asn Thr Arg

370 375 380

Val Lys Glu Cys Asp Arg Leu Glu Ala Cys Ala Gln Asn Leu Arg Ser

385 390 395 400

Met Gly Ile Thr Val Arg Thr Gly Pro Asp Trp Ile Glu Ile His Pro

405 410 415

Gly Thr Pro Arg Pro Thr Glu Ile Ala Thr His Gly Asp His Arg Ile

420 425 430

Val Met Ser Phe Ala Val Ala Gly Leu Arg Thr Pro Gly Met Ser Tyr

435 440 445

Asp Asp Pro Gly Cys Val Arg Lys Thr Phe Pro Arg Phe His Glu Glu

450 455 460

Phe Ala Ala Phe Val Glu Arg Ser Ser Ala Gly Glu

465 470 475