

UniProtKB - P33681 (CD80_HUMAN)

Protein **T-lymphocyte activation antigen CD80**

Gene **CD80**

Organism *Homo sapiens (Human)*

Status  **Reviewed** - Annotation score:  - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> T-lymphocyte activation antigen CD80 <i>Alternative name(s):</i> - Activation B7-1 antigen - BB1 - CTLA-4 counter-receptor B7.1 ▪ <i>Short name:</i> B7 <i>CD_antigen:</i> CD80
Gene names	<i>Name:</i> <u>CD80</u> Synonyms: CD28LG, CD28LG1, LAB7
Organism	<u>Homo sapiens (Human)</u>
Taxonomic identifier	<u>9606</u> [NCBI]
Taxonomic lineage	<u>Eukaryota</u> > <u>Metazoa</u> > <u>Chordata</u> > <u>Craniata</u> > <u>Vertebrata</u> > <u>Euteleostomi</u> > <u>Mammalia</u> > <u>Eutheria</u> > <u>Euarchontoglires</u> > <u>Primates</u> > <u>Haplorrhini</u> > <u>Catarrhini</u> > <u>Hominidae</u> > <u>Homo</u>
Proteomes	<u>UP000005640</u> Component: Chromosome 3

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000121594.11.</u>
HGNC	<u>HGNC:1700.</u> CD80.

Sequences (3)

Sequence status: Complete.
Sequence processing: The displayed sequence is further processed into a mature form.
This entry describes **3** isoforms produced by **alternative splicing**.

Isoform 1 (identifier: **P33681-1**) [UniParc]
This isoform has been chosen as the 'canonical' sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.
[« Hide](#)

10	20	30	40	50
MGHTRRQGTS	PSKCPYLNFF	QLLVLAGLSH	FCSGVIHVTK	EVKEVATLSC
60	70	80	90	100
GHNVSVEELA	QTRIWQKEK	KMVLTMMSGD	MNIWPEYKNR	TIFDITNNLS
110	120	130	140	150
IVILALRPSD	EGTYECVVLK	YEKDAFKREH	LAEVTLSVKA	DFPTPSISDF
160	170	180	190	200
EIPTSNIIRRI	ICSTSGGFPE	PHLSWLENCE	ELNAINTTVS	QDPETELYAV
210	220	230	240	250
SSKLDFNMTT	NHSFMCLIKY	GHLRVNQTFN	WNTTKQEHFP	DNLLPSWAIT
260	270	280		
LISVNGIFVI	CCLTYCFAPR	CRERRRNERL	RRESVRPV	

Length: 288
Mass (Da): 33,048
Last modified: February 1, 1994 - v1
Checksum: BA453EE34528B1F4

Isoform 2 (identifier: **P33681-2**) [[UniParc](#)]
Also known as: s1CD80
The sequence of this isoform differs from the canonical sequence as follows:
234-266: TKQEHFPDNLLPSWAITLISVNGIFVICCLTYC → S

Note: Soluble isoform. Expressed in unstimulated B-cells and monocytes, but not T-cells.
[Show »](#)

Length: 256
Mass (Da): 29,413
Checksum: DEB0A9FBA7B7D9A4

Isoform 3 (identifier: **P33681-3**) [[UniParc](#)]
Also known as: s2CD80
The sequence of this isoform differs from the canonical sequence as follows:
140-140: A → G
141-266: Missing.

Note: Soluble isoform. Expressed in T-cells activated by ConA, non-activated monocytes and monocytes activated w IFN- γ .
[Show »](#)

Length: 162
Mass (Da): 18,761
Checksum: 24DBC2D5BD70C4FA

Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_047698)	<u>140</u>	A → G in isoform <u>3</u> . Evidence: 1 Publication	

Alternative sequence (VSP_047699)	<u>141 – 266</u>	Missing in isoform <u>3</u> . Evidence: 1 Publication	
Alternative sequence (VSP_047700)	<u>234 – 266</u>	TKQEH...CLTYC → S in isoform <u>2</u> . Evidence: 1 Publication	

Sequence databases

Select the link destinations:	M27533 mRNA. Translation: <u>AAA36045.1</u> . M83077 M83074 Genomic DNA. Translation: <u>AAA58390.1</u> .
☒ EMBL	AY197777 mRNA. Translation: <u>AAO39208.1</u> .
☐ GenBank	AY197778 mRNA. Translation: <u>AAO39209.1</u> .
☐ DDBJ	AC073352 Genomic DNA. No translation available. BC042665 mRNA. Translation: <u>AAH42665.1</u> .
CCDS	<u>CCDS2989.1</u> . [P33681-1]
PIR	<u>I54495</u> . A45803.
RefSeq	<u>NP_005182.1</u> . <u>NM_005191.3</u> . [P33681-1]
UniGene	<u>Hs.838</u> .

Genome annotation databases

Ensembl	<u>ENST00000264246</u> ; <u>ENSP00000264246</u> ; <u>ENSG00000121594</u> . [P33681-1] <u>ENST00000383669</u> ; <u>ENSP00000373165</u> ; <u>ENSG00000121594</u> . [P33681-2] <u>ENST00000478182</u> ; <u>ENSP00000418364</u> ; <u>ENSG00000121594</u> . [P33681-1]
GeneID	<u>941</u> .
KEGG	<u>hsa:941</u> .
UCSC	<u>uc003ecq.4</u> . human. [P33681-1]

Keywords - Coding sequence diversity

Alternative splicing

UniProtKB - P42081 (CD86_HUMAN)

Protein **T-lymphocyte activation antigen CD86**

Gene **CD86**

Organism *Homo sapiens (Human)*

Status  **Reviewed** - Annotation score:  - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> T-lymphocyte activation antigen CD86 <i>Alternative name(s):</i> • Activation B7-2 antigen • B70 • BU63 • CTLA-4 counter-receptor B7.2 • FUN-1 • <i>CD_antigen</i>: CD86
Gene names	<i>Name:</i> <u>CD86</u> <i>Synonyms:</i> CD28LG2
Organism	<u>Homo sapiens (Human)</u>
Taxonomic identifier	<u>9606</u> [<u>NCBI</u>]
Taxonomic lineage	<u>Eukaryota</u> > <u>Metazoa</u> > <u>Chordata</u> > <u>Craniata</u> > <u>Vertebrata</u> > <u>Euteleostomi</u> > <u>Mammalia</u> > <u>Eutheria</u> > <u>Euarchontoglires</u> > <u>Primates</u> > <u>Haplorrhini</u> > <u>Catarrhini</u> > <u>Hominidae</u> > <u>Homo</u>
Proteomes	<u>UP000005640</u> Component: Chromosome 3

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000114013.15.</u>
HGNC	<u>HGNC:1705.</u> CD86.

Sequences (6)

Sequence status: Complete.
Sequence processing: The displayed sequence is further processed into a mature form.
This entry describes **6** isoforms produced by **alternative splicing**.

Isoform 1 (identifier: **P42081-1**) [UniParc]
This isoform has been chosen as the 'canonical' sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.
[« Hide](#)

10	20	30	40	50
MDPQCTMGLS	NILFVMAFLL	SGAAPLKIQA	YFNETADLPC	QFANSQNQSL
60	70	80	90	100
SELVVFWDQD	ENLVLNEVYL	GKEKFDSVHS	KYMGRTSFDS	DSWTLRLHNL
110	120	130	140	150
QIKDKGLYQC	IIHHKKPTGM	IRIHQMNSL	SVLANFSQPE	IVPISNITEN
160	170	180	190	200
VYINLTCCSI	HGYPEPKKMS	VLLRTKNSTI	EYDGVMQKSQ	DNVTELYDVS
210	220	230	240	250
ISLSVSFPDV	TSNMTIFCIL	ETDKTRLLSS	PFSIELEDPO	PPPDHIPWIT
260	270	280	290	300
AVLPTVIICV	MVFCLILWKW	KKKKRPRNSY	KCGTNTMERE	ESEQTKKREK
310	320			
IHIPERSDEA	QRVFKSSKTS	SCDKSDTCF		

Length: 329**Mass (Da):** 37,682**Last modified:** January 11, 2011 - v2**Checksum:** C249DAEEB889D911**Isoform 2** (identifier: **P42081-3**) [[UniParc](#)]*The sequence of this isoform differs from the canonical sequence as follows:*1-6: Missing.[Show »](#)**Length:** 323**Mass (Da):** 37,007**Checksum:** A492C705D89B65B7**Isoform 3** (identifier: **P42081-2**) [[UniParc](#)]*Also known as:* CD86 deltaEC*The sequence of this isoform differs from the canonical sequence as follows:*1-6: Missing.22-234: Missing.[Show »](#)**Length:** 110**Mass (Da):** 12,818**Checksum:** 0AE70C853C85F666**Isoform 4** (identifier: **P42081-4**) [[UniParc](#)]*Also known as:* CD86 deltaTM*The sequence of this isoform differs from the canonical sequence as follows:*1-6: Missing.235-282: Missing.[Show »](#)**Length:** 275

Mass (Da): 31,293**Checksum:** 137A523F73708BD5**Isoform 5** (identifier: **P42081-5**) [UniParc]*The sequence of this isoform differs from the canonical sequence as follows:*22-133: Missing.Note: No experimental confirmation available.Show »**Length:** 217**Mass (Da):** 24,773**Checksum:** 7AF72282EEF8B7CE**Isoform 6** (identifier: **P42081-6**) [UniParc]*The sequence of this isoform differs from the canonical sequence as follows:*1-82: Missing.Note: No experimental confirmation available.Show »**Length:** 247**Mass (Da):** 28,420**Checksum:** 60CBC08652F42C26**Experimental Info**

Feature key	Position(s)	Description	Graphical view
Sequence conflict	<u>27</u>	K → E in AAA86473 (PubMed: 7541777). Evidence: Curated	

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_021916)	<u>170</u>	S → N. Corresponds to variant dbSNP:rs9282642	
Natural variant (VAR_055003)	<u>185</u>	V → I Evidence: 8 Publications Corresponds to variant dbSNP:rs2681417	
Natural variant (VAR_014650)	<u>310</u>	A → T Evidence: 2 Publications Corresponds to variant dbSNP:rs1129055	
Natural variant (VAR_021917)	<u>323</u>	D → N. Corresponds to variant dbSNP:rs9282648	

Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_047220)	<u>1 – 82</u>	Missing in isoform <u>6</u> . Evidence: Curated	
Alternative sequence (VSP_023124)	<u>1 – 6</u>	Missing in isoform <u>2</u> , isoform <u>3</u> and isoform <u>4</u> . Evidence: 3 Publications	
Alternative sequence (VSP_009125)	<u>22 – 234</u>	Missing in isoform <u>3</u> . Evidence: 1 Publication	

Alternative sequence (VSP_047221)	<u>22 – 133</u>	Missing in isoform <u>5</u> . Evidence: 1 Publication	
Alternative sequence (VSP_040324)	<u>235 – 282</u>	Missing in isoform <u>4</u> . Evidence: 1 Publication	

Sequence databases

Select the link destinations:	☒ EMBL	<u>U04343</u> mRNA. Translation: <u>AAB03814.1</u> . <u>L25259</u> mRNA. Translation: <u>AAA58389.1</u> . <u>CR541844</u> mRNA. Translation: <u>CAG46642.1</u> . <u>EF064748</u> Genomic DNA. Translation: <u>ABK41931.1</u> . ☐ GenBank ☐ DDBJ
		<u>AK294663</u> mRNA. Translation: <u>BAH11839.1</u> . <u>AK301237</u> mRNA. Translation: <u>BAH13438.1</u> . <u>AK316203</u> mRNA. Translation: <u>BAH14574.1</u> . <u>AC068630</u> Genomic DNA. No translation available. <u>BC040261</u> mRNA. Translation: <u>AAH40261.1</u> . <u>U17722</u> <u>U17721</u> Genomic DNA. Translation: <u>AAA86473.1</u> .
	CCDS	<u>CCDS3009.1</u> . [P42081-1] <u>CCDS43138.1</u> . [P42081-3] <u>CCDS56272.1</u> . [P42081-5] <u>CCDS56273.1</u> . [P42081-6] <u>CCDS74991.1</u> . [P42081-4]
	PIR	<u>A48754</u> . <u>JC7605</u> .
	RefSeq	<u>NP_001193853.1</u> . <u>NM_001206924.1</u> . <u>NP_001193854.1</u> . <u>NM_001206925.1</u> . <u>NP_008820.3</u> . <u>NM_006889.4</u> . <u>NP_787058.4</u> . <u>NM_175862.4</u> . <u>NP_795711.1</u> . <u>NM_176892.1</u> .
	UniGene	<u>Hs.171182</u> .

Genome annotation databases

Ensembl	<u>ENST00000264468</u> ; <u>ENSP00000264468</u> ; <u>ENSG00000114013</u> . [P42081-4] <u>ENST00000330540</u> ; <u>ENSP00000332049</u> ; <u>ENSG00000114013</u> . [P42081-1] <u>ENST00000393627</u> ; <u>ENSP00000377248</u> ; <u>ENSG00000114013</u> . [P42081-3] <u>ENST00000469710</u> ; <u>ENSP00000418988</u> ; <u>ENSG00000114013</u> . [P42081-6] <u>ENST00000493101</u> ; <u>ENSP00000420230</u> ; <u>ENSG00000114013</u> . [P42081-5]
GeneID	<u>942</u> .
KEGG	<u>hsa:942</u> .
UCSC	<u>uc003eet.4</u> . human. [P42081-1]

Keywords - Coding sequence diversity

Alternative splicing, Polymorphism

UniProtKB - Q9BQ51 (PD1L2_HUMAN)

Protein **Programmed cell death 1 ligand 2**

Gene **PDCD1LG2**

Organism *Homo sapiens (Human)*

Status  **Reviewed** - Annotation score:  - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> Programmed cell death 1 ligand 2 ▪ <i>Short name:</i>PD-1 ligand 2 ▪ <i>Short name:</i>PD-L2 ▪ <i>Short name:</i>PDCD1 ligand 2 ▪ <i>Short name:</i>Programmed death ligand 2 <i>Alternative name(s):</i> • Butyrophilin B7-DC ▪ <i>Short name:</i>B7-DC • <i>CD_antigen:</i> CD273
Gene names	<i>Name:</i> <u>PDCD1LG2</u> Synonyms:B7DC, CD273, PDCD1L2, PDL2
Organism	<u>Homo sapiens (Human)</u>
Taxonomic identifier	9606 [NCBI]
Taxonomic lineage	<u>Eukaryota</u> > <u>Metazoa</u> > <u>Chordata</u> > <u>Craniata</u> > <u>Vertebrata</u> > <u>Euteleostomi</u> > <u>Mammalia</u> > <u>Eutheria</u> > <u>Euarchontoglires</u> > <u>Primates</u> > <u>Haplorrhini</u> > <u>Catarrhini</u> > <u>Hominidae</u> > <u>Homo</u>
Proteomes	<u>UP000005640</u> Component: Chromosome 9

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000197646.7.</u>
HGNC	<u>HGNC:18731.</u> PDCD1LG2.

Sequences (3)

Sequence status: Complete.

Sequence processing: The displayed sequence is further processed into a mature form.

This entry describes **3** isoforms produced by **alternative splicing**.

Isoform 1 (identifier: **Q9BQ51-1**) [UniParc]

Also known as: PD-L2I, Type I

This isoform has been chosen as the 'canonical' sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.

« Hide

```

      10           20           30           40           50
MIFLLLMLSL ELQLHQIAAL FTVTVPKELY IIEHGSNVTL ECNFDTGSHV
      60           70           80           90          100
NLGAITASLQ KVENDTSPHR ERATLLEEQL PLGKASFHIP QVQVRDEGQY
     110          120          130          140          150
QCIIIIYGVAV DYKYLTLKVK ASYRKINTHI LKVPETDEVE LTCQATGYPL
     160          170          180          190          200
AEVSWPNVSV PANTSHSRTP EGLYQVTSVL RLKPPPGRNF SCVFWNTHVR
     210          220          230          240          250
ELTLASIDLQ SQMEPRTHPT WLLHIFIFPC IIAFIFIATV IALRKQLCQK
     260          270
LYSSKDTTKR PVTITKREVN SAI

```

Length: 273

Mass (Da): 30,957

Last modified: May 10, 2005 - v2

Checksum: 8B7E963C9BA26ED9

Isoform 2 (identifier: **Q9BQ51-2**) [UniParc]

Also known as: PD-L2II, Type II

The sequence of this isoform differs from the canonical sequence as follows:

121-211: ASYRKINTHI...LTLASIDLQS → G

[Show »](#)

Length: 183

Mass (Da): 20,867

Checksum: ADFCD2E70205B137

Isoform 3 (identifier: **Q9BQ51-3**) [UniParc]

Also known as: PD-L2III, Type III

The sequence of this isoform differs from the canonical sequence as follows:

121-182: ASYRKINTHI...LYQVTSVLRL → DGTQDPSNLA...NKEGSEQCYL

183-273: Missing.

[Show »](#)

Length: 182

Mass (Da): 20,745

Checksum: 357E9952F65BCADC

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_049842)	<u>58</u>	S → T. Corresponds to variant dbSNP:rs12339171	
Natural variant (VAR_022449)	<u>229</u>	F → S Evidence: 4 Publications Corresponds to variant dbSNP:rs7854303	
Natural variant (VAR_049843)	<u>241</u>	I → T. Corresponds to variant dbSNP:rs7854413	

Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_013740)	<u>121 – 211</u>	ASYRK...IDLQS → G in isoform <u>2</u> . Evidence: 1 Publication	
Alternative sequence (VSP_013738)	<u>121 – 182</u>	ASYRK...SVLRL → DGTQDPSNLAASHFHPLLHH CFHFHSHSDSPKKTTLSKAV FFKRHNKKTCHHNKEGSEQC YL in isoform <u>3</u> . Evidence: 1 Publication	
Alternative sequence (VSP_013739)	<u>183 – 273</u>	Missing in isoform <u>3</u> . Evidence: 1 Publication	

Sequence databases

Select the link destinations:	AF329193 mRNA. Translation: AAK31105.1 .
☒ EMBL	AF344424 mRNA. Translation: AAK15370.1 .
☐ GenBank	AY254343 mRNA. Translation: AAP13471.1 .
☐ DDBJ	AY271901 mRNA. Translation: AAP49000.1 .
	AY271902 mRNA. Translation: AAP49001.1 .
	AL162253 Genomic DNA. Translation: CAI15984.1 .
	BC074766 mRNA. Translation: AAH74766.1 .
	BC113678 mRNA. Translation: AAI13679.1 .
	BC113680 mRNA. Translation: AAI13681.1 .
CCDS	CCDS6465.1 . [Q9BQ51-1]
RefSeq	NP_079515.2 . NM_025239.3 . [Q9BQ51-1]
UniGene	Hs.532279 .
	Hs.617872 .

Genome annotation databases

Ensembl	ENST00000397747 ; ENSP00000380855 ; ENSG00000197646 . [Q9BQ51-1]
GeneID	80380 .
KEGG	hsa:80380 .
UCSC	uc003zjg.5 . human. [Q9BQ51-1]

Keywords - Coding sequence diversity[Alternative splicing](#), [Polymorphism](#)

UniProtKB - Q9NZQ7 (PD1L1_HUMAN)

Protein **Programmed cell death 1 ligand 1**

Gene **CD274**

Organism *Homo sapiens (Human)*

Status  **Reviewed** - Annotation score:  - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> Programmed cell death 1 ligand 1 ▪ <i>Short name:</i>PD-L1 ▪ <i>Short name:</i>PDCD1 ligand 1 ▪ <i>Short name:</i>Programmed death ligand 1 <i>Alternative name(s):</i> • B7 homolog 1 ▪ <i>Short name:</i>B7-H1 • <i>CD_antigen:</i> CD274
Gene names	<i>Name:</i> <u>CD274</u> Synonyms:B7H1, PDCD1L1, PDCD1LG1, PDL1
Organism	<u>Homo sapiens (Human)</u>
Taxonomic identifier	<u>9606</u> [<u>NCBI</u>]
Taxonomic lineage	<u>Eukaryota</u> > <u>Metazoa</u> > <u>Chordata</u> > <u>Craniata</u> > <u>Vertebrata</u> > <u>Euteleostomi</u> > <u>Mammalia</u> > <u>Eutheria</u> > <u>Euarchontoglires</u> > <u>Primates</u> > <u>Haplorrhini</u> > <u>Catarrhini</u> > <u>Hominidae</u> > <u>Homo</u>
Proteomes	<u>UP000005640</u> Component: Chromosome 9

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000120217.13.</u>
HGNC	<u>HGNC:17635.</u> CD274.

Sequences (3)

Sequence status: Complete.

Sequence processing: The displayed sequence is further processed into a mature form.

This entry describes **3** isoforms produced by **alternative splicing**.

Isoform 1 (identifier: **Q9NZQ7-1**) [UniParc]

Also known as: PD-L1I

This isoform has been chosen as the 'canonical' sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.

« Hide

```

      10           20           30           40           50
MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL
      60           70           80           90          100
AALIVYWEME DKNIIQFVHG EEDLKVQHSS YRQARLLKD QLSLGNAALQ
     110          120          130          140          150
ITDVKLQDAG VYRCMISYGG ADYKRITVKV NAPYNKINQR ILVVDPTSE
     160          170          180          190          200
HELTCQAEGY PKAEVIWTSS DHQVLGKTT TTNSKREEKL FNVSTLRIN
     210          220          230          240          250
TTTNEIFYCT FRRLDPEENH TAEVIPPELP LAHPPNERTH LVILGAILLC
     260          270          280          290
LGVALTFIFR LRKGRMMDVK KCGIQDTNSK KQSDTHLEET

```

Length: 290**Mass (Da):** 33,275**Last modified:** October 1, 2000 - v1**Checksum:** FE957086E62A31A8**Isoform 2** (identifier: **Q9NZQ7-2**) [[UniParc](#)]*Also known as:* PD-L1II*The sequence of this isoform differs from the canonical sequence as follows:*19-132: Missing.[Show »](#)**Length:** 176**Mass (Da):** 20,246**Checksum:** B8BD0CFF9DEA722F**Isoform 3** (identifier: **Q9NZQ7-3**) [[UniParc](#)]*The sequence of this isoform differs from the canonical sequence as follows:*178-178: K → D179-290: Missing.**Note:** No experimental confirmation available. May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay.[Show »](#)**Length:** 178**Mass (Da):** 20,454**Checksum:** A306BF2018885F0B**Sequence caution**The sequence [BAA91966](#) differs from that shown. Reason: Erroneous initiation. Translation N-terminally extended.

Evidence: Curated

Alternative sequence

Feature key	Position(s)	Description	Graphical view
-------------	-------------	-------------	----------------

Alternative sequence (VSP_013735)	<u>19 – 132</u>	Missing in isoform <u>2</u> . Evidence: 2 Publications	
Alternative sequence (VSP_013736)	<u>178</u>	K → D in isoform <u>3</u> . Evidence: 2 Publications	
Alternative sequence (VSP_013737)	<u>179 – 290</u>	Missing in isoform <u>3</u> . Evidence: 2 Publications	

Sequence databases

Select the link destinations:	AF177937 mRNA. Translation: AAF25807.1 .
☒ EMBL	AF233516 mRNA. Translation: AAG18508.1 .
☐ GenBank	AY254342 mRNA. Translation: AAP13470.1 .
☐ DDBJ	AY291313 mRNA. Translation: AAP42144.1 .
	AY714881 mRNA. Translation: AAU09634.1 .
	DQ286582 mRNA. Translation: ABB90152.1 .
	AK001894 mRNA. Translation: BAA91966.1 . Different initiation.
	AK300470 mRNA. Translation: BAG62189.1 .
	AK314567 mRNA. Translation: BAG37149.1 .
	AL162253 Genomic DNA. Translation: CAI15983.1 .
	CH471071 Genomic DNA. Translation: EAW58763.1 .
	BC069381 mRNA. Translation: AAH69381.1 .
	BC074984 mRNA. Translation: AAH74984.1 .
	BC113734 mRNA. Translation: AAI13735.1 .
	BC113736 mRNA. Translation: AAI13737.1 .
CCDS	CCDS59118.1 . [Q9NZQ7-2] CCDS6464.1 . [Q9NZQ7-1]
RefSeq	NP_001254635.1 . NM_001267706.1 . [Q9NZQ7-2] NP_054862.1 . NM_014143.3 . [Q9NZQ7-1]
UniGene	Hs.521989 .

Genome annotation databases

Ensembl	ENST00000381573 ; ENSP00000370985 ; ENSG00000120217 . [Q9NZQ7-2] ENST00000381577 ; ENSP00000370989 ; ENSG00000120217 . [Q9NZQ7-1]
GeneID	29126 .
KEGG	hsa:29126 .
UCSC	uc003zje.4 . human. [Q9NZQ7-1]

Keywords - Coding sequence diversity

[Alternative splicing](#)

UniProtKB - O75144 (ICOSL_HUMAN)

Protein

ICOS ligand

Gene

ICOSLG

Organism

Homo sapiens (Human)

Status

 Reviewed - Annotation score:  - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> ICOS ligand <i>Alternative name(s):</i> - B7 homolog 2 - Short name: B7-H2 - B7-like protein GI50 - B7-related protein 1 - Short name: B7RP-1 - CD_antigen: CD275
Gene names	<i>Name:</i> ICOSLG Synonyms: B7H2, B7RP1, ICOSL, KIAA0653
Organism	Homo sapiens (Human)
Taxonomic identifier	9606 [NCBI]
Taxonomic lineage	Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Mammalia > Eutheria > Euarchontoglires > Primates > Haplorrhini > Catarrhini > Hominidae > Homo
Proteomes	UP000005640 Component: Chromosome 21

Organism-specific databases

EuPathDB	HostDB:ENSG00000160223.16. HostDB:ENSG00000277117.4.
HGNC	HGNC:17087 , ICOSLG.

Sequences (3)

Sequence status: Complete.

Sequence processing: The displayed sequence is further processed into a mature form.

This entry describes **3** isoforms produced by **alternative splicing**.

Note: Additional isoforms seem to exist.

Isoform 1 (identifier: **O75144-1**) [UniParc]

This isoform has been chosen as the 'canonical' sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.

« Hide

10	20	30	40	50
MRLGSPGLLF	LLFSSLRADT	QEKEVRAMVG	SDVELSCACP	EGSRFDLNDV
60	70	80	90	100
YVYWQTSESK	TVVTYHIPQN	SSLENVDSRY	RNRALMSPAG	MLRGDFSLRL
110	120	130	140	150
FNVTPQDEQK	FHCLVLSQSL	GFQEVLSVEV	TLHVAANFSV	PVVSAPHSPS
160	170	180	190	200
QDELTFCTCT	INGYPRPNVY	WINKTDNSLL	DQALQNDTVF	LNMRGLYDVV
210	220	230	240	250
SVLRIARTPS	VNIGCCIEINV	LLQQNLTVGS	QTGNDIGERD	KITENPVSTG
260	270	280	290	300
EKNAATWSIL	AVLCLLVVVA	VAIGWVCRDR	CLQHSYAGAW	AVSPETELTG
HV				

Length: 302

Mass (Da): 33,349

Last modified: August 14, 2001 - v2

Checksum: 647934E21B55E34A

Isoform 2 (identifier: **O75144-2**) [UniParc]

The sequence of this isoform differs from the canonical sequence as follows:

300-302: GHV → ESWNLLLLLS

Show »

Length: 309

Mass (Da): 34,225

Checksum: D019EC5307D796A5

Isoform 3 (identifier: **O75144-3**) [UniParc]

The sequence of this isoform differs from the canonical sequence as follows:

18-134: Missing.

Show »

Length: 185

Mass (Da): 20,120

Checksum: 0DAD5D52E6DE5F5F

Sequence caution

The sequence [BAA31628](#) differs from that shown. The sequence differs from that shown in position 300 onward for unknown reason. Evidence: Curated

The sequence [BAA31628](#) differs from that shown. Reason: Erroneous initiation. Translation N-terminally shortened. Evidence: Curated

Natural variant

Feature key	Position(s)	Description	Graphical view
-------------	-------------	-------------	----------------

Natural variant (VAR_049880)	<u>128</u>	V → I. Corresponds to variant dbSNP:rs11558819	
------------------------------	------------	--	--

Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_054718)	<u>18 – 134</u>	Missing in isoform <u>3</u> . Evidence: 1 Publication	
Alternative sequence (VSP_002520)	<u>300 – 302</u>	GHV → ESWNLLLLLS in isoform <u>2</u> . Evidence: 2 Publications	

Sequence databases

Select the link destinations:	AF199028 mRNA. Translation: <u>AAF34739.1</u> .
☒ EMBL	AF289028 mRNA. Translation: <u>AAG01176.1</u> .
☐ GenBank	AF216749 mRNA. Translation: <u>AAK16241.1</u> .
☐ DDBJ	AX100595 mRNA. Translation: <u>CAC36465.1</u> .
	AB014553 mRNA. Translation: <u>BAA31628.1</u> . Sequence problems.
	AK090492 mRNA. Translation: <u>BAG52170.1</u> .
	AP001058 Genomic DNA. No translation available.
	AP001059 Genomic DNA. No translation available.
	CH471079 Genomic DNA. Translation: <u>EAX09446.1</u> .
	BC064637 mRNA. Translation: <u>AAH64637.1</u> .
CCDS	<u>CCDS42952.1</u> . [O75144-1] <u>CCDS63377.1</u> . [O75144-3] <u>CCDS63379.1</u> . [O75144-2]
RefSeq	NP_001269979.1. NM_001283050.1. [O75144-2] NP_001269980.1. NM_001283051.1. [O75144-3] NP_056074.1. NM_015259.5. [O75144-1] XP_006723963.1. XM_006723900.2. [O75144-1]
UniGene	<u>Hs.14155</u> .

Genome annotation databases

Ensembl	<u>ENST00000344330</u> ; <u>ENSP00000339477</u> ; <u>ENSG00000160223</u> . [O75144-2] <u>ENST00000400377</u> ; <u>ENSP00000383228</u> ; <u>ENSG00000160223</u> . [O75144-3] <u>ENST00000407780</u> ; <u>ENSP00000384432</u> ; <u>ENSG00000160223</u> . [O75144-1]
GeneID	<u>102723996</u> . <u>23308</u> .
KEGG	<u>hsa:102723996</u> . <u>hsa:23308</u> .
UCSC	<u>uc002zee.5</u> . human. [O75144-1]

Keywords - Coding sequence diversity

Alternative splicing, Polymorphism

UniProtKB - Q5ZPR3 (CD276_HUMAN)

Protein **CD276 antigen**

Gene **CD276**

Organism *Homo sapiens (Human)*

Status  **Reviewed** - Annotation score:  - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> CD276 antigen <i>Alternative name(s):</i> 4Ig-B7-H3 - B7 homolog 3 ▪ <i>Short name:</i> B7-H3 - Costimulatory molecule <i>CD_antigen:</i> CD276
Gene names	<i>Name:</i> <u>CD276</u> Synonyms: B7H3 ORF Names: PSEC0249, UNQ309/PRO352
Organism	<u>Homo sapiens (Human)</u>
Taxonomic identifier	<u>9606</u> [NCBI]
Taxonomic lineage	Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Mammalia > Eutheria > Euarchontoglires > Primates > Haplorrhini > Catarrhini > Hominidae > Homo
Proteomes	<u>UP000005640</u> Component: Chromosome 15

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000103855.17.</u>
HGNC	<u>HGNC:19137.</u> CD276.

Sequences (4)

Sequence status: Complete.

Sequence processing: The displayed sequence is further processed into a mature form.

This entry describes **4** isoforms produced by **alternative splicing**.

Isoform 1 (identifier: **Q5ZPR3-1**) [[UniParc](#)]

Also known as: 4Ig-B7-H3

This isoform has been chosen as the 'canonical' sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.

« [Hide](#)

10	20	30	40	50
MLRRRGSPGM	GVHVGAALGA	LWFCLTGALE	VQVPEDPVVA	LVGTDATLCC
60	70	80	90	100
SFSPEPGFSL	AQLNLIWQLT	DTKQLVHSFA	EGQDQGSAYA	NRTALFPDLL
110	120	130	140	150
AQGNASLRLQ	RVRVADEGSF	TCFVSIRDFG	SAAVSLQVAA	PYSKPSMTLE
160	170	180	190	200
PNKDLRPGDT	VTITCSSYQG	YPEAEVFWQD	GQGVPLTGNV	TTSQMANEQG
210	220	230	240	250
LFDVHSILRV	VLGANGTYSC	LVRNPVLQQD	AHSSVTITPQ	RSPTGAVEVQ
260	270	280	290	300
VPEDPVVALV	GTDATLRCSF	SPEPGFSLAQ	LNLIWQLTDT	KQLVHSFTEG
310	320	330	340	350
RDQGSAYANR	TALFPDLLAQ	GNASLRLQRV	RVADEGSFTC	FVSIRDFGSA
360	370	380	390	400
AVSLQVAAPY	SKPSMTLEPN	KDLRPGDTVT	ITCSSYRGYP	EAEVFWQDGQ
410	420	430	440	450
GVPLTGNVTT	SQMANEQGLF	DVHSVLRVVL	GANGTYSCLV	RNPVLQQDAH
460	470	480	490	500
GSVTITGQPM	TFPPEALWVT	VGLSVCLIAL	LVALAFVCWR	KIKQSCEEN
510	520	530		
AGAEDQDGEG	EGSKTALQPL	KHSDSKEDDG	QEIA	

Note: Contains tandemly repeated immunoglobulin-like V and C domains.

Length: 534

Mass (Da): 57,235

Last modified: November 23, 2004 - v1

Checksum: 2181A064404C7939

Isoform 2 (identifier: **Q5ZPR3-2**) [[UniParc](#)]

Also known as: B7-H3

The sequence of this isoform differs from the canonical sequence as follows:

159-376: Missing.

Note: Minor transcript. Contains one single set of immunoglobulin-like V and C domains.

[Show](#) »

Length: 316

Mass (Da): 33,791

Checksum: FF97007F191CCFA1

Isoform 3 (identifier: **Q5ZPR3-3**) [[UniParc](#)]

The sequence of this isoform differs from the canonical sequence as follows:

465-493: EALWVTVGLSVCLIALLVALAFVCWRKIK → GPASSAVPLSPAHPHGSMSHWFSGRL

494-534: Missing.

Note: Contains tandemly repeated immunoglobulin-like V and C domains.

[Show](#) »

Length: 493

Mass (Da): 52,761

Checksum: CD7C5591CC4822D2**Isoform 4** (identifier: **Q5ZPR3-4**) [UniParc]*The sequence of this isoform differs from the canonical sequence as follows:*528-534: DDGQEIA → GKDTWANote: Contains tandemly repeated immunoglobulin-like V and C domains.Show »**Length:** 533**Mass (Da):** 57,165**Checksum:** BC38033295EBE978**Sequence caution**The sequence BAC11344 differs from that shown. Reason: Erroneous initiation. Evidence: Curated**Experimental Info**

Feature key	Position(s)	Description	Graphical view
Sequence conflict	<u>387</u>	R → Q in <u>AAQ88709</u> (PubMed: <u>12975309</u>). Evidence: Curated	
Sequence conflict	<u>473</u>	L → P in <u>BAC11243</u> (PubMed: <u>14702039</u>). Evidence: Curated	

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_049857)	<u>97</u>	P → L. Corresponds to variant <u>dbSNP:rs7173448</u>	
Natural variant (VAR_049858)	<u>111</u>	R → S. Corresponds to variant <u>dbSNP:rs7173476</u>	
Natural variant (VAR_049859)	<u>137</u>	Q → L. Corresponds to variant <u>dbSNP:rs11574477</u>	
Natural variant (VAR_049860)	<u>160</u>	T → M Evidence: 2 Publications Corresponds to variant <u>dbSNP:rs11574479</u>	
Natural variant (VAR_049861)	<u>267</u>	R → H. Corresponds to variant <u>dbSNP:rs11574483</u>	
Natural variant (VAR_049862)	<u>279</u>	A → T. Corresponds to variant <u>dbSNP:rs10083681</u>	
Natural variant (VAR_049863)	<u>315</u>	P → L. Corresponds to variant <u>dbSNP:rs7173448</u>	
Natural variant (VAR_049864)	<u>329</u>	R → S. Corresponds to variant <u>dbSNP:rs7173476</u>	
Natural variant (VAR_049865)	<u>378</u>	T → M. Corresponds to variant <u>dbSNP:rs11574479</u>	

Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_017088)	<u>159 – 376</u>	Missing in isoform 2. Evidence: 2 Publications	
Alternative sequence (VSP_017089)	<u>465 – 493</u>	EALWV..WRKIK → GPASSAVPLSPAHPHGSMC WSHWFSRGL in isoform 3. Evidence: 1 Publication	
Alternative sequence (VSP_017090)	<u>494 – 534</u>	Missing in isoform 3. Evidence: 1 Publication	

Alternative sequence (VSP_017091)	<u>528 – 534</u>	DDGQEIA → GKDTWA in isoform <u>4</u> . Evidence: 1 Publication
--------------------------------------	------------------	---

Sequence databases

Select the link destinations: ☒ EMBL ☐ GenBank ☐ DDBJ	<u>AF302102</u> mRNA. Translation: <u>AAK15438.1</u> . <u>AJ583695</u> mRNA. Translation: <u>CAE47548.1</u> . <u>AY358343</u> mRNA. Translation: <u>AAQ88709.1</u> . <u>AK074849</u> mRNA. Translation: <u>BAC11243.1</u> . <u>AK074997</u> mRNA. Translation: <u>BAC11344.1</u> . Different initiation. <u>AK075549</u> mRNA. Translation: <u>BAC11692.1</u> . <u>BC062581</u> mRNA. Translation: <u>AAH62581.1</u> .
CCDS	<u>CCDS10251.1</u> . [<u>Q5ZPR3-2</u>] <u>CCDS32288.1</u> . [<u>Q5ZPR3-1</u>]
RefSeq	<u>NP_001019907.1</u> . <u>NM_001024736.1</u> . [<u>Q5ZPR3-1</u>] <u>NP_001316557.1</u> . <u>NM_001329628.1</u> . [<u>Q5ZPR3-2</u>] <u>NP_001316558.1</u> . <u>NM_001329629.1</u> . <u>NP_079516.1</u> . <u>NM_025240.2</u> . [<u>Q5ZPR3-2</u>] <u>XP_005254757.1</u> . <u>XM_005254700.4</u> . <u>XP_011520397.1</u> . <u>XM_011522095.2</u> . [<u>Q5ZPR3-1</u>] <u>XP_011520398.1</u> . <u>XM_011522096.2</u> . [<u>Q5ZPR3-1</u>] <u>XP_016878127.1</u> . <u>XM_017022638.1</u> . [<u>Q5ZPR3-1</u>]
UniGene	<u>Hs.744915</u> .

Genome annotation databases

Ensembl	<u>ENST00000318424</u> ; <u>ENSP00000320058</u> ; <u>ENSG00000103855</u> . [<u>Q5ZPR3-2</u>] <u>ENST00000318443</u> ; <u>ENSP00000320084</u> ; <u>ENSG00000103855</u> . [<u>Q5ZPR3-1</u>] <u>ENST00000561213</u> ; <u>ENSP00000452736</u> ; <u>ENSG00000103855</u> . [<u>Q5ZPR3-4</u>] <u>ENST00000564751</u> ; <u>ENSP00000454940</u> ; <u>ENSG00000103855</u> . [<u>Q5ZPR3-2</u>]
GeneID	<u>80381</u> .
KEGG	<u>hsa:80381</u> .
UCSC	<u>uc002avu.2</u> . human. [<u>Q5ZPR3-1</u>]

Keywords - Coding sequence diversity

Alternative splicing, Polymorphism

UniProtKB - Q7Z7D3 (VTCN1_HUMAN)

Protein **V-set domain-containing T-cell activation inhibitor 1**

Gene **VTCN1**

Organism *Homo sapiens (Human)*

Status  **Reviewed** - Annotation score:  - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> V-set domain-containing T-cell activation inhibitor 1 <i>Alternative name(s):</i> - B7 homolog 4 - Short name: B7-H4 - B7h.5 - Immune costimulatory protein B7-H4 - Protein B7S1 - T-cell costimulatory molecule B7x
Gene names	<i>Name:</i> VTCN1 Evidence: Imported <i>Synonyms:</i> B7H4 Evidence: Imported <i>ORF Names:</i> UNQ659/PRO1291
Organism	<i>Homo sapiens (Human)</i>
Taxonomic identifier	9606 [NCBI]
Taxonomic lineage	Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Mammalia > Eutheria > Euarchontoglires > Primates > Haplorrhini > Catarrhini > Hominidae > Homo
Proteomes	UP000005640 Component: Chromosome 1

Organism-specific databases

EuPathDB	HostDB:ENSG00000134258.16.
HGNC	HGNC:28873 . VTCN1.

Sequences (4)

Sequence status: Complete.

Sequence processing: The displayed sequence is further processed into a mature form.

This entry describes **4** isoforms produced by **alternative splicing**.

Isoform 1 Evidence: 7 Publications (identifier: **Q7Z7D3-1**) [[UniParc](#)]

This isoform has been chosen as the 'canonical' sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.

[« Hide](#)

10	20	30	40	50
MASLGQILFW	SIISIIIIILA	GAIALIIGFG	ISGRHSITVT	TVASAGNIGE
60	70	80	90	100
DGILSCTFEP	DIKLSDIVIQ	WLKEGVLGLV	HEFKEGKDEL	SEQDEMFRGR
110	120	130	140	150
TAVFADQVIV	GNASLRLKNV	QLTDAGTYKC	YIITSKGKGN	ANLEYKTGAF
160	170	180	190	200
SMPEVNVVDYN	ASSETLRCEA	PRWFPQPTVV	WASQVDQGAN	FSEVSNTSFE
210	220	230	240	250
LNSENVTMKV	VSVLYNVTIN	NTYSCMIEND	IAKATGDIKV	TESEIKRRSH
260	270	280		
LQLLNSKASL	CVSSFFAISW	ALLPLSPYLM	LK	

Length: 282**Mass (Da):** 30,878**Last modified:** October 1, 2003 - v1**Checksum:** 1C9C565A9242E78C**Isoform 2** Evidence: 1 Publication (identifier: **Q7Z7D3-2**) [UniParc]*The sequence of this isoform differs from the canonical sequence as follows:*33-148: Missing.[Show »](#)**Length:** 166**Mass (Da):** 18,275**Checksum:** 30FFF157B8C66DE2**Isoform 3** Evidence: 1 Publication (identifier: **Q7Z7D3-3**) [UniParc]*The sequence of this isoform differs from the canonical sequence as follows:*33-87: GRHSITVTTV...GLVHEFKEGK → EVSVWLSAMK...WGGWNPELHF88-282: Missing.[Show »](#)**Length:** 87**Mass (Da):** 9,875**Checksum:** 1006690A861AB006**Isoform 4** (identifier: **Q7Z7D3-4**) [UniParc]*The sequence of this isoform differs from the canonical sequence as follows:*1-95: Missing.[Show »](#)**Length:** 187**Mass (Da):** 20,743**Checksum:** 9AED6155AEED4E63

Experimental Info

Feature key	Position(s)	Description	Graphical view
Sequence conflict	<u>29</u>	F → L in ABI16083 (Ref. 10) Evidence: Curated	
Sequence conflict	<u>54</u>	L → Q in BAB15349 (PubMed:14702039). Evidence: Curated	

Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_045423)	<u>1 – 95</u>	Missing in isoform 4. Evidence: 2 Publications	
Alternative sequence (VSP_052841)	<u>33 – 148</u>	Missing in isoform 2. Evidence: 1 Publication	
Alternative sequence (VSP_052842)	<u>33 – 87</u>	GRHSI...FKEGK → EVS VWLSAMKGWCRSSKASL SIDLCFLNFRETLHHSHYCR LSWEHWGGWNPELHF in isoform 3. Evidence: 1 Publication	
Alternative sequence (VSP_052843)	<u>88 – 282</u>	Missing in isoform 3. Evidence: 1 Publication	

Sequence databases

Select the link destinations:	☒ EMBL ☐ GenBank ☐ DDBJ AY280972 mRNA. Translation: AAP37283.1. AY346100 mRNA. Translation: AAQ24206.1. DQ103757 mRNA. Translation: AAZ17406.1. AY442303 mRNA. Translation: AAS13400.1. AY358352 mRNA. Translation: AAQ88718.1. AK026071 mRNA. Translation: BAB15349.1. AK303466 mRNA. Translation: BAH13967.1. AL391476 Genomic DNA. Translation: CAI12739.1. CH471122 Genomic DNA. Translation: EAW56672.1. CH471122 Genomic DNA. Translation: EAW56673.1. BC065717 mRNA. Translation: AAH65717.1. BC074729 mRNA. Translation: AAH74729.1. DQ836392 mRNA. Translation: ABI16083.1.
CCDS	CCDS58019.1. [Q7Z7D3-4] CCDS58020.1. [Q7Z7D3-2] CCDS894.1. [Q7Z7D3-1]
RefSeq	NP_001240778.1. NM_001253849.1. [Q7Z7D3-4] NP_001240779.1. NM_001253850.1. [Q7Z7D3-2] NP_078902.2. NM_024626.3. [Q7Z7D3-1]
UniGene	Hs.546434 .

Genome annotation databases

Ensembl	ENST00000328189; ENSP00000328168; ENSG00000134258. [Q7Z7D3-2] ENST00000369458; ENSP00000358470; ENSG00000134258. [Q7Z7D3-1] ENST00000539893; ENSP00000444724; ENSG00000134258. [Q7Z7D3-4]
GeneID	79679 .
KEGG	hsa:79679 .
UCSC	uc001ehb.4 . human. [Q7Z7D3-1]

Keywords - Coding sequence diversity

Alternative splicing

UniProtKB - Q9H7M9 (VISTA_HUMAN)

Protein **V-type immunoglobulin domain-containing suppressor of T-cell activation**

Gene **VSIR**

Organism *Homo sapiens (Human)*

Status  **Reviewed** - Annotation score:  - Experimental evidence at protein level

Names & Taxonomy

Protein names	Recommended name: V-type immunoglobulin domain-containing suppressor of T-cell activation Evidence: 1 Publication Alternative name(s): - Platelet receptor Gi24 Evidence: 1 Publication - Stress-induced secreted protein-1 Evidence: 1 Publication - Short name:Sisp-1 Evidence: 1 Publication - V-set domain-containing immunoregulatory receptor Evidence: By similarity - V-set immunoregulatory receptor Evidence: Imported
Gene names	Name: VSIR Evidence: Imported Synonyms: C10orf54, SISP1 Evidence: 1 Publication, VISTA ORF Names: PP2135, UNQ730/PRO1412
Organism	<i>Homo sapiens (Human)</i>
Taxonomic identifier	9606 [NCBI]
Taxonomic lineage	Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Mammalia > Eutheria > Euarchontoglires > Primates > Haplorrhini > Catarrhini > Hominidae > Homo
Proteomes	UP000005640 Component: Chromosome 10

Organism-specific databases

EuPathDB	HostDB:ENSG00000107738.19.
HGNC	HGNC:30085. VSIR.

Sequence

Sequence status: Complete.

Sequence processing: The displayed sequence is further processed into a mature form.

Q9H7M9-1 [UniParc]

« Hide

```
      10           20           30           40           50
MGVPTALEAG SWRWGSLLEA LFLAASLG PV AAFKVATPYS LYVCPEGQNV
      60           70           80           90          100
TLTCRLLGPV DKGHDVTFYK TWYRSSRGEV QTCSERRPIR NLTFQDLHLH
     110          120          130          140          150
HGGHQAANTS HDLAQRHGLE SASDHHGNFS ITMRNLTLTD SGLYCCLVVE
     160          170          180          190          200
IRHHHSEHRV HGAMELQVQT GKDAPSNCVV YPSSSQDSEN ITAAALATGA
     210          220          230          240          250
CIVGILCLPL ILLLVYKQRQ AASNRRQAEL VRMDSNIQGI ENPGFEASPP
     260          270          280          290          300
AQGIPEAKVR HPLSYVAQRQ PSESGRHLLS EPSTPLSPPG PGDVFFPSLD
     310
PVPDSPNFEV I
```

Length: 311**Mass (Da):** 33,908**Last modified:** November 2, 2010 - v3**Checksum:** 321862EC650623CD

Sequence caution

The sequence [AAL55778](#) differs from that shown. Contaminating sequence. Sequence of unknown origin in the N-terminal part. [Evidence: Curated](#)

The sequence [AAL55778](#) differs from that shown. Reason: Erroneous termination at position [84](#). Translated as Ser. [Evidence: Curated](#)

The sequence [BAB15739](#) differs from that shown. Reason: Erroneous initiation. Translation N-terminally shortened. [Evidence: Curated](#)

Experimental Info

Feature key	Position(s)	Description	Graphical view
Sequence conflict	33	F → L in AAL55778 (PubMed: 15498874). Evidence: Curated	
Sequence conflict	85	E → K in AAL55778 (PubMed: 15498874). Evidence: Curated	

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_028036)	187	D → E Evidence: 5 Publications Corresponds to variant dbSNP:rs3747869	

Sequence databases

Select the link destinations:	AY265805 mRNA. Translation: AAP03084.1 .
☒ EMBL	EF506490 mRNA. Translation: ABP88253.1 .
☐ GenBank	AF289594 mRNA. Translation: AAL55778.1 . Sequence problems.
☐ DDBJ	AK024449 mRNA. Translation: BAB15739.1 . Different initiation.
	AY358379 mRNA. Translation: AAQ88745.1 .
	AL731541 Genomic DNA. No translation available.
	BC020568 mRNA. Translation: AAH20568.1 .
	BC127257 mRNA. Translation: AAI27258.1 .
CCDS	CCDS31218.1 .
RefSeq	NP_071436.1 . NM_022153.1 .
UniGene	Hs.47382 .

Genome annotation databases

Ensembl	ENST00000394957 ; ENSP00000378409 ; ENSG00000107738 .
GeneID	64115 .
KEGG	hsa:64115 .
UCSC	uc001jsd.5 . human.

Keywords - Coding sequence diversity

[Polymorphism](#)

UniProtKB - Q68D85 (NR3L1_HUMAN)

Protein **Natural cytotoxicity triggering receptor 3 ligand 1**

Gene **NCR3LG1**

Organism *Homo sapiens (Human)*

Status  **Reviewed** - Annotation score:  - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> Natural cytotoxicity triggering receptor 3 ligand 1 <i>Alternative name(s):</i> - B7 homolog 6 <i>Short name:</i> B7-H6
Gene names	<i>Name:</i> <u>NCR3LG1</u> <i>Synonyms:</i> B7H6
Organism	<u>Homo sapiens (Human)</u>
Taxonomic identifier	9606 [<u>NCBI</u>]
Taxonomic lineage	<u>Eukaryota</u> > <u>Metazoa</u> > <u>Chordata</u> > <u>Craniata</u> > <u>Vertebrata</u> > <u>Euteleostomi</u> > <u>Mammalia</u> > <u>Eutheria</u> > <u>Euarchontoglires</u> > <u>Primates</u> > <u>Haplorrhini</u> > <u>Catarrhini</u> > <u>Hominidae</u> > <u>Homo</u>
Proteomes	<u>UP000005640</u> Component: Chromosome 11

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000188211.8.</u>
HGNC	<u>HGNC:42400.</u> NCR3LG1.

Sequence

Sequence status: Complete.

Sequence processing: The displayed sequence is further processed into a mature form.

Q68D85-1 [UniParc]

[« Hide](#)

10	20	30	40	50
MTWRAAASTC	AALLILLWAL	TTEGDLKVEM	MAGGTQITPL	NDNVTIFCNI
60	70	80	90	100
FYSQPLNITS	MGITWFWKSL	TFDKEVKVFE	FFGDHQEAFR	PGAIVSPWRL
110	120	130	140	150
KSGDASLRLP	GIQLEEAGEY	RCEVVVTPLK	AQGTVQLEVV	ASPASRLLLD
160	170	180	190	200
QVGMKENEDK	YMCESSGFYP	EAINITWEKQ	TQKFPHPIEI	SEDVITGPTI
210	220	230	240	250
KNMDGTFNVT	SCLKLNSSQE	DPGTVYQCVV	RHASLHTPLR	SNFTLTAAARH
260	270	280	290	300
SLSETEKTDN	FSIHWWPISF	IGVGLVLLIV	LIPWKKICNK	SSSAYTPLKC
310	320	330	340	350
ILKHWNSFDT	QTLKKEHLIF	FCTRAWPSYQ	LQDGEAWPPE	GSVNINTIQQ
360	370	380	390	400
LDVFCRQEGK	WSEVPYVQAF	FALRDNPDLG	QCCRIDPALL	TVTSGKSIDD
410	420	430	440	450
NSTKSEKQTP	REHSDAVPDA	PILPVSPIWE	PPPATTSTTP	VLSSQPPTLL
LPLQ				

Length: 454

Mass (Da): 50,827

Last modified: October 11, 2004 - v1

Checksum: 433CE0B0EE0A4470

Sequence caution

The sequence [CAD97811](#) differs from that shown. Reason: Erroneous initiation. Translation N-terminally shortened.
Evidence: Curated

Experimental Info

Feature key	Position(s)	Description	Graphical view
Sequence conflict	37	I → V in CAD97811 (PubMed: 17974005). Evidence: Curated	
Sequence conflict	211	S → N in CAD97811 (PubMed: 17974005). Evidence: Curated	

Sequence databases

Select the link destinations: ●EMBL ○GenBank ○DDBJ	BX537685 mRNA. Translation: CAD97811.1 . Different initiation.
	CR749521 mRNA. Translation: CAH18335.1 .
	AC124798 Genomic DNA. No translation available.
	BC136800 mRNA. No translation available.
	BC136797 mRNA. No translation available.
CCDS	CCDS55748.1 .
RefSeq	NP_001189368.1 . NM_001202439.2 .
UniGene	Hs.146274 .

Genome annotation databases

Ensembl	ENST00000338965 ; ENSP00000341637 ; ENSG00000188211 . ENST00000530403 ; ENSP00000434394 ; ENSG00000188211 .
GeneID	374383 .
KEGG	hsa:374383 .
UCSC	uc001mmz.5 . human.