

UniProtKB - Q07011 (TNR9_HUMAN)

Protein | **Tumor necrosis factor receptor superfamily member 9**

Gene | **TNFRSF9**

Organism | *Homo sapiens* (Human)

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

Names & Taxonomy

Protein names	<i>Recommended name:</i> Tumor necrosis factor receptor superfamily member 9 <i>Alternative name(s):</i> • 4-1BB ligand receptor • CDw137 • T-cell antigen 4-1BB homolog • T-cell antigen ILA • <i>CD_antigen</i>: CD137
Gene names	<i>Name:</i> <u>TNFRSF9</u> <i>Synonyms:</i> CD137, ILA
Organism	<u>Homo sapiens</u> (Human)
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 1

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000049249.8.</u>
HGNC	<u>HGNC:11924.</u> TNFRSF9.

Sequence

Sequence status: Complete.

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

Q07011-1 [UniParc]

« Hide

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      10           20           30           40           50
MGNSCYNIVA TLLLVLNFER TRSLQDPCSN CPAGTFCDNN RNQICSPCPP
      60           70           80           90          100
NSFSAGGQR TCDICRQCKG VFRTRKECSS TSNAECDCTP GFHCLGAGCS
      110          120          130          140          150
MCEQDCKQGQ ELTKKGCKDC CFGTFNDQKR GICRPWTNCS LDGKSVLVNG
      160          170          180          190          200
TKERDVVCGP SPADLSPGAS SVTPPAPARE PGHSPQIISF FLALTSTALL
      210          220          230          240          250
FLLFFLTIRF SVVKRGRKKL LYIFKQPFMR PVQTTQEEDG CSCRFPEEEE

GGCEL
```

Length: 255**Mass (Da):** 27,899**Last modified:** February 1, 1995 - v1**Checksum:** F3A563FE5EF00460

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_018920)	56	A → T Evidence: 1 Publication Corresponds to variant dbSNP:rs9657963	
Natural variant (VAR_018921)	115	K → N Evidence: 1 Publication Corresponds to variant dbSNP:rs9657965	
Natural variant (VAR_018922)	176	A → D Evidence: 1 Publication Corresponds to variant dbSNP:rs9657979	
Natural variant (VAR_035478)	250	E → G in a colorectal cancer sample; somatic mutation. Evidence: 1 Publication Corresponds to variant dbSNP:rs776878260	

Sequence databases

Select the link destinations:	U03397 mRNA. Translation: AAA53133.1 .
	L12964 mRNA. Translation: AAA62478.2 .
☒ EMBL	AY438976 Genomic DNA. Translation: AAR05440.1 .
☐ GenBank	AL009183 Genomic DNA. No translation available.
☐ DDBJ	BC006196 mRNA. Translation: AAH06196.1 .
CCDS	CCDS92.1 .
PIR	I38426 .
RefSeq	NP_001552.2 . NM_001561.5 . XP_011539688.1 . XM_011541386.2 .
UniGene	Hs.738942 . Hs.86447 .

Genome annotation databases

Ensembl	ENST00000377507 ; ENSP00000366729 ; ENSG00000049249 . ENST00000615230 ; ENSP00000478699 ; ENSG00000049249 .
GeneID	3604 .
KEGG	hsa:3604 .
UCSC	uc001aot.4 . human.

Keywords - Coding sequence diversity

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	Recommended name: CD276 antigen Alternative name(s): 4Ig-B7-H3 - B7 homolog 3 - Short name: B7-H3 - Costimulatory molecule - CD_antigen: CD276
Gene names	Name: <u>CD276</u> Synonyms: B7H3 ORF Names: PSEC0249, UNQ309/PRO352
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 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.

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10	20	30	40	50
MLRRRGSPGM	GVHVGAAALGA	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
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Sequence databases

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

Genome annotation databases

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

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	Name: VTCN1 Evidence: Imported Synonyms: B7H4 Evidence: Imported ORF Names: UNQ659/PRO1291
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 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.

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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 SIDLCFLNFRET LHHSHYCR 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:	AY280972 mRNA. Translation: AAP37283.1 . AY346100 mRNA. Translation: AAQ24206.1 . ☒ EMBL DQ103757 mRNA. Translation: AAZ17406.1 . ☐ GenBank AY442303 mRNA. Translation: AAS13400.1 . ☐ DDBJ 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 - Q7Z6A9 (BTLA_HUMAN)

Protein

B- and T-lymphocyte attenuator

Gene

BTLA

Organism

Homo sapiens (Human)

Status



Reviewed - Annotation score:

- Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> B- and T-lymphocyte attenuator <i>Alternative name(s):</i> - B- and T-lymphocyte-associated protein <i>CD_antigen</i>: CD272
Gene names	<i>Name</i> : <u>BTLA</u>
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:ENSG00000186265.9.</u>
HGNC	<u>HGNC:21087.</u> BTLA.

Sequences (2)

Sequence status: Complete.

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

This entry describes **2** isoforms produced by **alternative splicing**.

Isoform 1 (identifier: **Q7Z6A9-1**) [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
MKTLPAMLGT	GKLFVWFFLI	PYLDIWNHIG	KESCDVQLYI	KRQSEHSILA
60	70	80	90	100
GDPFELECPV	KYCANRPHVT	WCKLNGTTTCV	KLEDRQTSWK	EEKNISFFIL
110	120	130	140	150
HFEPVLPNDN	GSYRCSANFQ	SNLIESHSTT	LYVTDVKSAS	ERPSKDEMAS
160	170	180	190	200
RPWLLYRLLP	LGGLPLLITT	CFCLFCCLRR	HQGKQNELSD	TAGREINLVD
210	220	230	240	250
AHLKSEQTEA	STRQNSQVLL	SETGIYDNDP	DLCFRMQEGS	EVYSNPCLEE
260	270	280		
NKPGIVYASL	NHSVIGPNSR	LARNVKEAPT	EYASICVRS	

Length: 289

Mass (Da): 32,834

Last modified: May 18, 2010 - v3

Checksum: F4D1FF775D7D33F3

Isoform 2 (identifier: **Q7Z6A9-2**) [UniParc]

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

135-182: Missing.

Show »

Length: 241

Mass (Da): 27,317

Checksum: 991AFF2495C3F612

Sequence caution

The sequence BAD18396 differs from that shown. Reason: Erroneous initiation. Translation N-terminally extended.

Evidence: Curated

Experimental Info

Feature key	Position(s)	Description	Graphical view
Sequence conflict	<u>105</u>	V → M in <u>AAP44003</u> (PubMed: <u>12796776</u>). Evidence: Curated	
Sequence conflict	<u>138</u>	S → G in <u>AAP44003</u> (PubMed: <u>12796776</u>). Evidence: Curated	
Sequence conflict	<u>148</u>	M → V in <u>AAP44003</u> (PubMed: <u>12796776</u>). Evidence: Curated	
Sequence conflict	<u>171</u>	C → W in <u>AAP44003</u> (PubMed: <u>12796776</u>). Evidence: Curated	
Sequence conflict	<u>219</u>	L → P in <u>BAD18396</u> (PubMed: <u>14702039</u>). Evidence: Curated	
Sequence conflict	<u>223</u>	T → A in <u>AAP44003</u> (PubMed: <u>12796776</u>). Evidence: Curated	
Sequence conflict	<u>243</u>	Y → C in <u>AAP44003</u> (PubMed: <u>12796776</u>). Evidence: Curated	

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_056027)	<u>124</u>	<u>I → V</u> . Corresponds to variant <u>dbSNP:rs16859633</u>	
Natural variant (VAR_027607)	<u>157</u>	<u>R → S</u> Evidence: 3 Publications Corresponds to variant <u>dbSNP:rs2931761</u>	
Natural variant (VAR_027608)	<u>267</u>	<u>P → L</u> Evidence: 5 Publications Corresponds to variant <u>dbSNP:rs9288952</u>	

Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_040305)	<u>135 – 182</u>	Missing in isoform <u>2</u> . Evidence: 3 Publications	

Sequence databases

Select the link destinations:	AY293286 mRNA. Translation: AAP44003.1 . AY599411 mRNA. Translation: AAT44901.1 . ☒ EMBL DQ198368 mRNA. Translation: ABA54407.1 . ☐ GenBank AC092894 Genomic DNA. No translation available. ☐ DDBJ BC107091 mRNA. Translation: AAI07092.1 . BC107092 mRNA. Translation: AAI07093.1 . AK131204 mRNA. Translation: BAD18396.1 . Different initiation.
CCDS	CCDS33819.1 . [Q7Z6A9-1] CCDS43130.1 . [Q7Z6A9-2]
RefSeq	NP_001078826.1 . NM_001085357.1 . [Q7Z6A9-2] NP_861445.3 . NM_181780.3 . XP_016861237.1 . XM_017005748.1 . [Q7Z6A9-1]
UniGene	Hs.445162 .

Genome annotation databases

Ensembl	ENST00000334529 ; ENSP00000333919 ; ENSG00000186265 . [Q7Z6A9-1] ENST00000383680 ; ENSP00000373178 ; ENSG00000186265 . [Q7Z6A9-2]
GeneID	151888 .
KEGG	hsa:151888 .
UCSC	uc003dza.5 . human. [Q7Z6A9-1]

Keywords - Coding sequence diversity

[Alternative splicing](#), [Polymorphism](#)

UniProtKB - P13500 (CCL2_HUMAN)

Protein

C-C motif chemokine 2

Gene

CCL2

Organism

Homo sapiens (Human)

Status

 Reviewed - Annotation score:  - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> C-C motif chemokine 2 <i>Alternative name(s):</i> - HC11 - Monocyte chemoattractant protein 1 - Monocyte chemotactic and activating factor <i>Short name:</i>MCAF - Monocyte chemotactic protein 1 <i>Short name:</i>MCP-1 - Monocyte secretory protein JE - Small-inducible cytokine A2
Gene names	<i>Name:</i> <u>CCL2</u> Synonyms:MCP1, SCYA2
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 17

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000108691.9.</u>
HGNC	<u>HGNC:10618.</u> CCL2.

Sequence

Sequence status: Complete.

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

P13500-1 [UniParc]

[« Hide](#)

10	20	30	40	50
MKVSAALLCL	LLIAATFIPQ	GLAQPDAINA	PVTCCYNFTN	RKISVQRLAS
60	70	80	90	
YRRITSSKCP	KEAVIFKTIV	AKEICADPKQ	KWVQDSMDHL	DKQTQTPKT

Length: 99

Mass (Da): 11,025

Last modified: January 1, 1990 - v1

Checksum: 45EC72361435302F

Polymorphism

Genetic variations in CCL2 determine Mycobacterium tuberculosis susceptibility [MIM:607948].

Evidence: 1 Publication

Sequence databases

Select the link destinations:	M24545 mRNA. Translation: AAA18164.1 .
☒ EMBL	M28225, M28223, M28224 Genomic DNA. Translation: AAA60308.1 . M28226 mRNA. Translation: AAA60309.1 .
☐ GenBank	M31626, M30816, M31625 Genomic DNA. Translation: AAA36330.1 .
☐ DDBJ	X14768 mRNA. Translation: CAA32876.1 . M37719 Genomic DNA. Translation: AAA18102.1 . S71513 mRNA. Translation: AAB20651.1 . S69738 mRNA. Translation: AAB29926.1 . Y18933 Genomic DNA. Translation: CAC14049.1 . A17786 mRNA. Translation: CAA01352.1 . BT007329 mRNA. Translation: AAP35993.1 . AF519531 Genomic DNA. Translation: AAM54046.1 . AK311960 mRNA. Translation: BAG34900.1 . CH471147 Genomic DNA. Translation: EAW80212.1 . BC009716 mRNA. Translation: AAH09716.1 .
CCDS	CCDS11277.1 .
PIR	A35474 . A60299 .
RefSeq	NP_002973.1 . NM_002982.3 .
UniGene	Hs.303649 .

Genome annotation databases

Ensembl	ENST00000225831 ; ENSP00000225831 ; ENSG00000108691 .
GeneID	6347 .
KEGG	hsa:6347 .
UCSC	uc002hhy.4 . human.

UniProtKB - P13501 (CCL5_HUMAN)

Protein

C-C motif chemokine 5

Gene

CCL5

Organism

Homo sapiens (Human)

Status

 Reviewed - Annotation score:  - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> C-C motif chemokine 5 <i>Alternative name(s):</i> - EoCP - Eosinophil chemotactic cytokine - SIS-delta - Small-inducible cytokine A5 - T cell-specific protein P228 <i>Short name:</i>TCP228 - T-cell-specific protein RANTES <i>Cleaved into the following 2 chains:</i> <u>RANTES(3-68)</u> <u>RANTES(4-68)</u>
Gene names	<i>Name:</i> <u>CCL5</u> Synonyms:D17S136E, SCYA5
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 17

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000271503.5</u> .
HGNC	<u>HGNC:10632</u> . CCL5.

Sequence

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

P13501-1 [[UniParc](#)]

« Hide

10	20	30	40	50
MKVSAAALAV	ILIATALCAP	ASASPYSSDT	TPCCFAYIAR	PLPRAHIKEY
60	70	80	90	
FYTSGKCSNP	AVVFVTRKNR	QVCANPEKKW	VREYINSLEM	S

Length: 91

Mass (Da): 9,990**Last modified:** July 15, 1999 - v3**Checksum:** FB0BFAF9A87C620F

Experimental Info

Feature key	Position(s)	Description	Graphical view
Sequence conflict	<u>7</u>	A → R in AAA36725 (PubMed: 2456327). Evidence: Curated	
Sequence conflict	<u>7</u>	A → R in AAF73070 (Ref. 5) Evidence: Curated	
Sequence conflict	<u>14</u>	A → V in AAF73070 (Ref. 5) Evidence: Curated	

Mass spectrometry

Molecular mass is 7515±1 Da from positions 27 - 91. Determined by SELDI. Evidence: 1 Publication

Molecular mass is 7862.8±1.1 Da from positions 24 - 91. Determined by ESI. Evidence: 1 Publication

Molecular mass is 8355±10 Da from positions 24 - 91. Determined by ESI. O-glycosylated. Evidence: 1 Publication

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_043043)	<u>24</u>	<u>S → F</u> Polymorphism; antagonist of the chemokine receptors CCR1 and CCR3. Evidence: 1 Publication Corresponds to variant dbSNP:rs377415776	

Sequence databases

Select the link destinations:	M21121 mRNA. Translation: AAA36725.1 .
☒ EMBL	AF088219 Genomic DNA. Translation: AAC63331.1 .
☐ GenBank	DQ230537 mRNA. Translation: ABB69929.1 .
☐ DDBJ	AF043341 mRNA. Translation: AAC03541.1 .
	AF266753 mRNA. Translation: AAF73070.1 .
	DQ017060 Genomic DNA. Translation: AAY22177.1 .
	BC008600 mRNA. Translation: AAH08600.1 .
CCDS	CCDS11300.1 .
PIR	A28815 .
RefSeq	NP_002976.2 . NM_002985.2 .
UniGene	Hs.514821 .

Genome annotation databases

Ensembl	ENST00000603197 ; ENSP00000474412 ; ENSG00000271503 . ENST00000605140 ; ENSP00000475057 ; ENSG00000271503 . ENST00000613606 ; ENSP00000479894 ; ENSG00000274233 . ENST00000618639 ; ENSP00000484921 ; ENSG00000274233 .
GeneID	6352 .
KEGG	hsa:6352 .
UCSC	uc002hkf.5 . human.

Keywords - Coding sequence diversity

Polymorphism

UniProtKB - Q92583 (CCL17_HUMAN)

Protein

C-C motif chemokine 17

Gene

CCL17

Organism

Homo sapiens (Human)

Status

 Reviewed

 - Annotation score: - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> C-C motif chemokine 17 <i>Alternative name(s):</i> - CC chemokine TARC - Small-inducible cytokine A17 - Thymus and activation-regulated chemokine
Gene names	<i>Name:</i>CCL17 Synonyms:SCYA17, TARC
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 16

Organism-specific databases

EuPathDB	HostDB:ENSG00000102970.10 .
HGNC	HGNC:10615 , CCL17.

Sequence

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

Q92583-1 [UniParc]

« Hide

1020304050

MAPLKMLALV TLLLGASLQH IHAARGTNVG RECCLEYFKG AIPLRKCLKTW

60708090

YQTSEDCSRDAIVFVTVQGR AICSDPNNKR VKNAVLYLQS LERS

Length:

94

Mass (Da):

10,507

Last modified:

February 1, 1997 - v1

Checksum:

7959C56BA8FDAF08

Natural variant			
Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_048708)	5	K → N . Corresponds to variant dbSNP:rs34693308	
Natural variant (VAR_048709)	67	V → M . Corresponds to variant dbSNP:rs34379253	

Sequence databases

Select the link destinations: EMBL GenBank ODDBJ	D43767 mRNA. Translation: BAA07824.1 .
	EF064767 Genomic DNA. Translation: ABK41950.1 .
	AC004382 Genomic DNA. Translation: AAC24308.1 .
	CH471092 Genomic DNA. Translation: EAW82921.1 .
	BC069107 mRNA. Translation: AAH69107.1 .
CCDS	BC112066 mRNA. Translation: AAI12067.1 .
	BC112068 mRNA. Translation: AAI12069.1 .
	CCDS10780.1 .
RefSeq	NP_002978.1 , NM_002987.2 .
UniGene	Hs.546294 .

Genome annotation databases

Ensembl	ENST00000219244 ; ENSP00000219244 ; ENSG00000102970 . ENST00000616880 ; ENSP00000480147 ; ENSG00000102970 .
GeneID	6361 .
KEGG	hsa:6361 .
UCSC	uc002elj.1 , human.

Keywords - Coding sequence diversity
[Polymorphism](#)

UniProtKB - Q99731 (CCL19_HUMAN)

Protein

C-C motif chemokine 19

Gene

CCL19

Organism

Homo sapiens (Human)

Status

 Reviewed

 - Annotation score: - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> C-C motif chemokine 19 <i>Alternative name(s):</i> - Beta-chemokine exodus-3 - CK beta-11 - Epstein-Barr virus-induced molecule 1 ligand chemokine <i>Short name:</i>EBI1 ligand chemokine <i>Short name:</i>ELC - Macrophage inflammatory protein 3 beta <i>Short name:</i>MIP-3-beta - Small-inducible cytokine A19
Gene names	<i>Name:</i> <u>CCL19</u> Synonyms:ELC, MIP3B, SCYA19
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:ENSG00000172724.11.</u>
HGNC	<u>HGNC:10617.</u> CCL19.

Sequence

Sequence status: Complete.

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

Q99731-1 [[UniParc](#)]

[« Hide](#)

10	20	30	40	50
MALLLLALSLL	VLWTSPAPTL	SGTND AEDCC	LSVTQKPIPG	YIVRNFHYLL
60	70	80	90	
IKDGC RVP AV	VFTTLRGRQL	CAPPDQ PWVE	RIIQRLQRTS	AKMKRRSS

Length: 98

Mass (Da): 10,993

Last modified: May 1, 1997 - v1

Checksum: 0D2516DB2EB1C81B

Sequence databases

Select the link destinations:	U77180 mRNA. Translation: AAC50944.1 .
☒ EMBL	AB000887 mRNA. Translation: BAA20383.1 .
☐ GenBank	U88321 mRNA. Translation: AAC23905.1 .
☐ DDBJ	AJ223410 Genomic DNA. Translation: CAA11307.1 .
	BC027968 mRNA. Translation: AAH27968.1 .
CCDS	CCDS6570.1 .
RefSeq	NP_006265.1 . NM_006274.2 .
UniGene	Hs.50002 .

Genome annotation databases

Ensembl	ENST00000311925 ; ENSP00000308815 ; ENSG00000172724 .
GeneID	6363 .
KEGG	hsa:6363 .
UCSC	uc003zvn.4 . human.

UniProtKB - P78556 (CCL20_HUMAN)

Protein

C-C motif chemokine 20

Gene

CCL20

Organism

Homo sapiens (Human)

Status

 Reviewed - Annotation score:  - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> C-C motif chemokine 20 <i>Alternative name(s):</i> - Beta-chemokine exodus-1 - CC chemokine LARC - Liver and activation-regulated chemokine - Macrophage inflammatory protein 3 alpha <i>Short name:</i> MIP-3-alpha - Small-inducible cytokine A20 <i>Cleaved into the following 3 chains:</i> CCL20(1-67) CCL20(1-64) CCL20(2-70)
Gene names	<i>Name:</i> CCL20 Synonyms: LARC, MIP3A, SCYA20
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 2

Organism-specific databases

EuPathDB	HostDB:ENSG00000115009.11.
HGNC	HGNC:10619 . CCL20.

Sequences (2)

Sequence status: Complete.

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

This entry describes **2** isoforms produced by **alternative splicing**.

Isoform 1 (identifier: **P78556-1**) [[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
MCCTKSLLLA	ALMSVLLLHL	CGESEASNF	DCCLGYTDRI	LHPKFIVGFT
60	70	80	90	
RQLANEGCDI	NAIIFHTKKK	LSVCANPKQT	WVKYIVRLLS	KKVKNM

Length: 96

Mass (Da): 10,762

Last modified: May 1, 1997 - v1

Checksum: 1ED19EC2E1AC70AD

Isoform 2 (identifier: **P78556-2**) [UniParc]

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

26-26: Missing.

Show »

Length: 95

Mass (Da): 10,691

Checksum: BFDB243C51B59960

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_011915)	<u>47</u>	V → M. Corresponds to variant dbSNP:rs1049617	

Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_001061)	<u>26</u>	Missing in isoform 2. Evidence: 3 Publications	

Sequence databases

Select the link destinations:	●EMBL	U77035 mRNA. Translation: AAC50943.1 .
	○GenBank	D86955 mRNA. Translation: BAA13191.1 .
	○ODDBJ	U64197 mRNA. Translation: AAB61534.1 .
		AC073065 Genomic DNA. Translation: AAX93214.1 .
CCDS		BC020698 mRNA. Translation: AAH20698.1 .
RefSeq		CCDS2469.1 . [P78556-1]
		CCDS46536.1 . [P78556-2]
UniGene		NP_001123518.1 . NM_001130046.1 . [P78556-2]
		NP_004582.1 . NM_004591.2 . [P78556-1]
UniGene		Hs.75498 .

Genome annotation databases

Ensembl	ENST00000358813 ; ENSP00000351671 ; ENSG00000115009 . [P78556-1] ENST00000409189 ; ENSP00000386273 ; ENSG00000115009 . [P78556-2]
GeneID	6364 .
KEGG	hsa:6364 .

UCSC	uc002vpl.3. human. [P78556-1]
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Keywords - Coding sequence diversity

[Alternative splicing](#), [Polymorphism](#)

UniProtKB - O00626 (CCL22_HUMAN)

Protein

C-C motif chemokine 22

Gene

CCL22

Organism

Homo sapiens (Human)

Status

 Reviewed

 - Annotation score: - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> C-C motif chemokine 22 <i>Alternative name(s):</i> - CC chemokine STCP-1 - MDC(1-69) - Macrophage-derived chemokine - Small-inducible cytokine A22 - Stimulated T-cell chemotactic protein 1 <u>Cleaved into the following 3 chains:</u> <u>MDC(3-69)</u> <u>MDC(5-69)</u> <u>MDC(7-69)</u>
Gene names	<i>Name:</i> <u>CCL22</u> Synonyms:MDC, SCYA22 ORF Names:A-152E5.1
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 16

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000102962.4.</u>
HGNC	<u>HGNC:10621.</u> CCL22.

Sequence

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

O00626-1 [UniParc]

« Hide

10	20	30	40	50
MDRLQTALLV	VLVLLAVALQ	ATEAGPYGAN	MEDSVCCRDY	VR YRLPLRVV
60	70	80	90	
KHFYWTSDSC	PRPGVLLTTF	RDKEICADPR	VPWVKMILNK	LSQ

Length: 93

Mass (Da): 10,625

Last modified: November 2, 2010 - v2

Checksum: 641FCE999586A7D2

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_055117)	<u>2</u>	<u>D → A</u> Evidence: 6 Publications Corresponds to variant <u>dbSNP:rs4359426</u>	

Sequence databases

Select the link destinations:	<u>U83239</u> mRNA. Translation: <u>AAB53372.1</u> . <u>U83171</u> mRNA. Translation: <u>AAB58360.1</u> . ☒ EMBL <u>EF064764</u> Genomic DNA. Translation: <u>ABK41947.1</u> . ☐ GenBank <u>AK311970</u> mRNA. Translation: <u>BAG34909.1</u> . ☐ DDBJ <u>AC004382</u> Genomic DNA. Translation: <u>AAC24306.1</u> . <u>AC009052</u> Genomic DNA. No translation available. <u>CH471092</u> Genomic DNA. Translation: <u>EAW82918.1</u> . <u>BC027952</u> mRNA. Translation: <u>AAH27952.1</u> .
CCDS	<u>CCDS10778.1</u> .
RefSeq	<u>NP_002981.2</u> . <u>NM_002990.4</u> . <u>XP_016879020.1</u> . <u>XM_017023531.1</u> .
UniGene	<u>Hs.534347</u> .

Genome annotation databases

Ensembl	<u>ENST00000219235</u> ; <u>ENSP00000219235</u> ; <u>ENSG00000102962</u> .
GeneID	<u>6367</u> .
KEGG	<u>hsa:6367</u> .
UCSC	<u>uc002elh.4</u> . human.

Keywords - Coding sequence diversity

Polymorphism

UniProtKB - P41597 (CCR2_HUMAN)

Protein

C-C chemokine receptor type 2

Gene

CCR2

Organism

Homo sapiens (Human)

Status

 Reviewed

 - Annotation score: - Experimental evidence at protein level

Names & Taxonomy

Protein names	Recommended name: C-C chemokine receptor type 2 ■ Short name:C-C CKR-2 ■ Short name:CC-CKR-2 ■ Short name:CCR-2 ■ Short name:CCR2 Alternative name(s): • Monocyte chemoattractant protein 1 receptor ■ Short name:MCP-1-R • CD_antigen: CD192
Gene names	Name:<u>CCR2</u> Synonyms:CMKBR2
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 3

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000121807.5</u> .
HGNC	<u>HGNC:1603</u> . CCR2.

Sequences (2)

Sequence status: Complete.
This entry describes **2** isoforms produced by **alternative splicing**.

Isoform A

Evidence: 1 Publication

(identifier: **P41597-1**) [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.

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      10           20           30           40           50
MLSTSRSRFI RNTNESGEEV TTFFDYDYGA PCHKFDVKQI GAQLLPPLYS
      60           70           80           90          100
LVFIFGFVGN MLVVLILINC KKLKCLTDIY LLNLAISDLL FLITLPLWAH
     110          120          130          140          150
SAANEWVFGN AMCKLFTGLY HIGYFGGIF F IILLTIDRYL AIVHAVFALK
     160          170          180          190          200
ARTVTFGVVT SVITWLVAVF ASVPGIIFTK CQKEDSVYVC GPYFPRGWNN
     210          220          230          240          250
FHTIMRNILG LVLPLLIMVI CYSGILKTLL RCRNEKKRHR AVRVIFTIMI
     260          270          280          290          300
VYFLFWTPYN IVILLNTFQE FFGLSNCEST SQLDQATQVT ETLGMTHCCI
     310          320          330          340          350
NPIIYAFVGE KFRSLFHIAL GCRIAPLQKP VCGGPGVRPG KNVKVTQGL
     360          370
LDGRGKGKSI GRAPEASLQD KEGA
```

Length: 374**Mass (Da):** 41,915**Last modified:** November 1, 1995 - v1**Checksum:** F865E0D39E74CF0F**Isoform B** Evidence: 1 Publication (identifier: **P41597-2**) [UniParc]*The sequence of this isoform differs from the canonical sequence as follows:*314-374: SLFHIALGCR...EASLQDKEGA → RYLSVFFRKH...TGEQEVSAGLNote: Mutagenesis of Leu-316 to Thr as well as Phe-320 to Asp decrease interaction with NUP85.

Evidence: 1 Publication

Show »**Length:** 360**Mass (Da):** 41,064**Checksum:** EA352636D724D470

Polymorphism

Variations in CCR2 are associated with relative resistance to immunodeficiency virus type 1 (resistance to HIV-1)

[MIM:609423]. Evidence: 1 Publication

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_020066)	<u>45</u>	<u>L → V</u> . Corresponds to variant dbSNP:rs4987052	
Natural variant (VAR_014339)	<u>64</u>	<u>V → I</u> Confers relative resistance to infection by HIV-1; delay in disease progression in African Americans but not in Caucasians. Evidence: 3 Publications Corresponds to variant dbSNP:rs1799864	
Natural variant (VAR_014340)	<u>355</u>	<u>G → E</u> Evidence: 1 Publication Corresponds to variant dbSNP:rs3918387	

Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_001893)	<u>314 – 374</u>	SLFHI...DKEGA → RYLSVFFRKHITKRFCKQCP VFYRETVDGVTSTNTPSTGE QEVSAGL in isoform <u>B</u> . Evidence: 2 Publications	

Sequence databases

Select the link destinations:	☒ EMBL	<u>U03882</u> mRNA. Translation: <u>AAA19119.1</u> .
	☐ GenBank	<u>U03905</u> mRNA. Translation: <u>AAA19120.1</u> .
	☐ DDBJ	<u>D29984</u> mRNA. Translation: <u>BAA06253.1</u> .
		<u>U80924</u> Genomic DNA. Translation: <u>AAC51637.1</u> .
		<u>U80924</u> Genomic DNA. Translation: <u>AAC51636.1</u> .
		<u>AF545480</u> Genomic DNA. Translation: <u>AAN16400.1</u> .
		<u>AK292685</u> mRNA. Translation: <u>BAF85374.1</u> .
		<u>AK292920</u> mRNA. Translation: <u>BAF85609.1</u> .
		<u>U95626</u> Genomic DNA. Translation: <u>AAB57791.1</u> .
		<u>U95626</u> Genomic DNA. Translation: <u>AAB57792.1</u> .
		<u>CH471055</u> Genomic DNA. Translation: <u>EAW64760.1</u> .
		<u>BC074751</u> mRNA. Translation: <u>AAH74751.1</u> .
		<u>BC095540</u> mRNA. Translation: <u>AAH95540.1</u> .
		<u>BC126452</u> mRNA. Translation: <u>AAI26453.1</u> .
		<u>BC136396</u> mRNA. Translation: <u>AAI36397.1</u> .
		<u>X95583</u> mRNA. Translation: <u>CAA64835.1</u> .
CCDS		<u>CCDS43078.1</u> . [<u>P41597-1</u>] <u>CCDS46813.1</u> . [<u>P41597-2</u>]
PIR		<u>I38450</u> . <u>JC2443</u> .
RefSeq		<u>NP_001116513.2</u> . <u>NM_001123041.2</u> . [<u>P41597-1</u>] <u>NP_001116868.1</u> . <u>NM_001123396.1</u> . [<u>P41597-2</u>] <u>XP_011532371.1</u> . <u>XM_011534069.1</u> . [<u>P41597-2</u>]
UniGene		<u>Hs.511794</u> . <u>Hs.705362</u> .

Genome annotation databases

Ensembl	<u>ENST00000292301</u> ; <u>ENSP00000292301</u> ; <u>ENSG00000121807</u> . [<u>P41597-1</u>] <u>ENST00000400888</u> ; <u>ENSP00000383681</u> ; <u>ENSG00000121807</u> . [<u>P41597-1</u>] <u>ENST00000445132</u> ; <u>ENSP00000399285</u> ; <u>ENSG00000121807</u> . [<u>P41597-2</u>]
GeneID	<u>729230</u> .
KEGG	<u>hsa:729230</u> .
UCSC	<u>uc003cpm.5</u> . human. [<u>P41597-1</u>]

Keywords - Coding sequence diversity

Alternative splicing, Polymorphism

UniProtKB - P51679 (CCR4_HUMAN)

Protein **C-C chemokine receptor type 4**

Gene **CCR4**

Organism *Homo sapiens (Human)*

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

Names & Taxonomy

Protein names	<i>Recommended name:</i> C-C chemokine receptor type 4 ▪ <i>Short name:</i>C-C CKR-4 ▪ <i>Short name:</i>CC-CKR-4 ▪ <i>Short name:</i>CCR-4 ▪ <i>Short name:</i>CCR4 <i>Alternative name(s):</i> • K5-5 • <i>CD_antigen:</i> CD194
Gene names	<i>Name:</i> <u>CCR4</u> <i>Synonyms:</i> CMKBR4
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:ENSG00000183813.6.</u>
HGNC	<u>HGNC:1605.</u> CCR4.

Sequence

Sequence status: Complete.

P51679-1 [UniParc]

[« Hide](#)

10	20	30	40	50
MNPTDIADTT	LDESIYSNYY	LYESIPKPCT	KEGIKAFGEL	FLPPLYSLVF
60	70	80	90	100
VFGLLGNSVV	VLVLFKYKRL	RSMTDVYLLN	LAISDLLFVF	SLPFWGYAA
110	120	130	140	150
DQWVFGGLGC	KMISWMYLVG	FYSGIFFVML	MSIDRYLAIV	HAVFSLRART
160	170	180	190	200
LTYGVITSLA	TWSVAVFASL	PGFLFSTCYT	ERNHTYCKTK	YSLNSTTWKV
210	220	230	240	250
LSSLEINILG	LVIPLGIMLF	CYSMIIRTLQ	HCKNEKKNKA	VKMIFAVVVL
260	270	280	290	300
FLGFWTPYNI	VLFLETLEVEL	EVLQDCTFER	YLDYAIQATE	TLAFVHCCLN
310	320	330	340	350
PIIYFFLGEK	FRKYILQLFK	TCRGLFVLCQ	YCGLLQIYSA	DTPSSSYTQS
360				
TMDHDLHDAL				

Length: 360

Mass (Da): 41,403

Last modified: October 1, 1996 - v1

Checksum: 51EBE12AD1FAFABF

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_010669)	<u>130</u>	<u>L → V</u> Evidence: 1 Publication	
Natural variant (VAR_010670)	<u>178</u>	<u>C → S</u> Evidence: 1 Publication Corresponds to variant <u>dbSNP:rs753825374</u>	

Sequence databases

Select the link destinations:	<u>X85740</u> mRNA. Translation: <u>CAA59743.1</u> .
☒ EMBL	<u>AB023888</u> Genomic DNA. Translation: <u>BAA86965.1</u> .
☐ GenBank	<u>AB023890</u> Genomic DNA. Translation: <u>BAA86967.1</u> .
☐ DDBJ	<u>AB023891</u> Genomic DNA. Translation: <u>BAA86968.1</u> .
	<u>AB023892</u> Genomic DNA. Translation: <u>BAA86969.1</u> .
	<u>AY322539</u> Genomic DNA. Translation: <u>AAP84352.1</u> .
	<u>BC069139</u> mRNA. Translation: <u>AAH69139.1</u> .
	<u>BC071751</u> mRNA. Translation: <u>AAH71751.1</u> .
	<u>BC074935</u> mRNA. Translation: <u>AAH74935.1</u> .
CCDS	<u>CCDS2656.1</u> .
PIR	<u>A57160</u> .
RefSeq	<u>NP_005499.1</u> . <u>NM_005508.4</u> . <u>XP_016861176.1</u> . <u>XM_017005687.1</u> .
UniGene	<u>Hs.184926</u> .

Genome annotation databases

Ensembl	<u>ENST00000330953</u> ; <u>ENSP00000332659</u> ; <u>ENSG00000183813</u> .
GeneID	<u>1233</u> .

KEGG	hsa:1233 .
UCSC	uc003cfg.2 . human.

Keywords - Coding sequence diversity

Polymorphism

UniProtKB - P51681 (CCR5_HUMAN)

Protein

C-C chemokine receptor type 5

Gene

CCR5

Organism

Homo sapiens (Human)

Status

 Reviewed

 - Annotation score: - Experimental evidence at protein level

Names & Taxonomy

Protein names	<i>Recommended name:</i> C-C chemokine receptor type 5 ▪ Short name: C-C CKR-5 ▪ Short name: CC-CKR-5 ▪ Short name: CCR-5 ▪ Short name: CCR5 <i>Alternative name(s):</i> • CHEMR13 • HIV-1 fusion coreceptor • <i>CD_antigen:</i> CD195
Gene names	<i>Name:</i><u>CCR5</u> Synonyms:CMKBR5
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 3

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000160791.13.</u>
HGNC	<u>HGNC:1606.</u> CCR5.

Sequence

Sequence status: Complete.

P51681-1 [UniParc]

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```
      10           20           30           40           50
MDYQVSSPIY DINYTSEPC QKINVKQIAA RLLPPLYSLV FIFGFVGNML
      60           70           80           90          100
VILILINCKR LKSMTDIYLL NLAISDLFFL LTVPFWAHYA AAQWDFGNTM
      110          120          130          140          150
CQLLTGLYFI GFFSGIFFII LLTIDRYLAV VHAVFALKAR TVTFGVVTSV
      160          170          180          190          200
ITWVVAVFAS LPGIIFTRSQ KEGLHYTCSS HFPYSQYQFW KNFQTLKIVI
      210          220          230          240          250
LGLVLPLLVM VICYSGILKT LLRCRNEKKR HRAVRLIFTI MIVYFLFWAP
      260          270          280          290          300
YNIVLLLNTF QEFFGLNNCS SSNRLDQAMQ VTETLGMTHC CINPIIYAFV
      310          320          330          340          350
GEKFRNYLLV FFQKHIAKRF CKCCSIFQQE APERASSVYT RSTGEQEISV
```

GL

Length: 352**Mass (Da):** 40,524**Last modified:** October 1, 1996 - v1**Checksum:** 88ECE1F38E6D45A7

Polymorphism

Variations in CCR5 are associated with resistance or susceptibility to immunodeficiency virus type 1 (resistance or susceptibility to HIV-1) [MIM:[609423](#)]. Variations in CCR5 gene also influence the rate of progression to AIDS after infection. [Evidence: 2 Publications](#)

Ser-60 variant, a naturally occurring mutation in a conserved residue in the first intracellular domain of CCR5, results in reduced amounts of the protein in the membrane and consequently may be associated with reduced susceptibility to infection by microbes that depend on these molecules as their receptors. [Evidence: 1 Publication](#)

Variations in CCR5 are associated with susceptibility to West Nile virus (WNV) infection [MIM:[610379](#)].

[Evidence: 1 Publication](#)

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_003481)	10	Y → D in INCCR5-71A; results in absent sulfation and greatly decreased binding CCL4 and CCL5 when associated with D-3, D-10 and D-15; restored most CCL4 binding when associated with D-3 and D-15. Evidence: 1 Publication	
Natural variant (VAR_024066)	12	I → L Evidence: 1 Publication	
Natural variant (VAR_024067)	20	C → S Evidence: 1 Publication Corresponds to variant dbSNP: rs145061115	
Natural variant (VAR_011839)	29	A → S Evidence: 1 Publication Corresponds to variant dbSNP: rs1800939	
Natural variant (VAR_003482)	31	R → H in INCCR5-72A. Corresponds to variant dbSNP: rs56340326	
Natural variant (VAR_003483)	34	P → L in TZCCR5-179.	
Natural variant (VAR_024068)	42	I → F Evidence: 1 Publication	

Natural variant (VAR_011840)	<u>55</u>	<u>L</u> → <u>Q</u> Evidence: 2 Publications Corresponds to variant dbSNP:rs1799863	
Natural variant (VAR_011841)	<u>60</u>	<u>R</u> → <u>S</u> Associated with susceptibility to HIV-1; reduced surface expression and function of CCR5 protein. Evidence: 2 Publications Corresponds to variant dbSNP:rs1800940	
Natural variant (VAR_003484)	<u>62</u>	<u>K</u> → <u>R</u> in UGCCR5-145B.	
Natural variant (VAR_003485)	<u>68</u>	<u>Y</u> → <u>H</u> in ZWCCR5-7. Corresponds to variant dbSNP:rs758090461	
Natural variant (VAR_024069)	<u>73</u>	<u>A</u> → <u>V</u> Evidence: 1 Publication Corresponds to variant dbSNP:rs56198941	
Natural variant (VAR_003486)	<u>95</u>	<u>D</u> → <u>N</u> in MWCCR5-107. Corresponds to variant dbSNP:rs149975182	
Natural variant (VAR_003487)	<u>97</u>	<u>G</u> → <u>E</u> in INCCR5-467.	
Natural variant (VAR_003488)	<u>122</u>	<u>L</u> → <u>P</u> in ZWCCR5-7.	
Natural variant (VAR_003489)	<u>158</u>	<u>F</u> → <u>S</u> in UGCCR5-145A.	
Natural variant (VAR_003490)	<u>176</u>	<u>Y</u> → <u>C</u> in KECCR5-116.	
Natural variant (VAR_003491)	<u>177</u>	<u>T</u> → <u>A</u> in INCCR5-45C.	
Natural variant (VAR_012481)	<u>178</u>	<u>C</u> → <u>R</u> Found in a HIV-resistant individual. Evidence: 1 Publication Corresponds to variant dbSNP:rs199824195	
Natural variant (VAR_003492)	<u>185</u>	<u>S</u> → <u>N</u> in UGCCR5-145A.	
Natural variant (VAR_003493)	<u>210</u>	<u>M</u> → <u>V</u> in ZWCCR5-7.	
Natural variant (VAR_003494)	<u>214</u>	<u>Y</u> → <u>C</u> in KECCR5-3B.	
Natural variant (VAR_024070)	<u>215</u>	<u>S</u> → <u>L</u> Evidence: 1 Publication	
Natural variant (VAR_011842)	<u>223</u>	<u>R</u> → <u>Q</u> Evidence: 2 Publications Corresponds to variant dbSNP:rs1800452	
Natural variant (VAR_024071)	<u>228</u>	Missing Evidence: 1 Publication	
Natural variant (VAR_003495)	<u>239</u>	<u>T</u> → <u>S</u> in INCCR5-71A.	
Natural variant (VAR_003496)	<u>246</u>	<u>L</u> → <u>P</u> in UGCCR5-145A. Corresponds to variant dbSNP:rs143181119	
Natural variant (VAR_003497)	<u>288</u>	<u>T</u> → <u>M</u> in INCCR5-72A. Corresponds to variant dbSNP:rs534088482	
Natural variant (VAR_011843)	<u>301</u>	<u>G</u> → <u>V</u> Evidence: 1 Publication Corresponds to variant dbSNP:rs1800943	
Natural variant (VAR_003498)	<u>302</u>	<u>E</u> → <u>G</u> in TZCCR5-179.	
Natural variant (VAR_003499)	<u>303</u>	<u>K</u> → <u>E</u> in THCCR5-5.	
Natural variant (VAR_003500)	<u>306</u>	<u>N</u> → <u>S</u> in MWCCR5-1567.	
Natural variant (VAR_003501)	<u>322</u>	<u>K</u> → <u>R</u> in THCCR5-5.	
Natural variant (VAR_003502)	<u>333</u>	<u>E</u> → <u>G</u> in THCCR5-2.	
Natural variant (VAR_003503)	<u>335</u>	<u>A</u> → <u>V</u> in MWCCR5-1567, MWCCR5-1568, ZWCCR5-14 and ZWCCR5-112. Evidence: 2 Publications Corresponds to variant dbSNP:rs1800944	
Natural variant (VAR_003504)	<u>339</u>	<u>Y</u> → <u>F</u> in TZCCR5-181A and MWCCR5-107. Evidence: 2 Publications Corresponds to variant dbSNP:rs1800945	
Natural variant (VAR_003505)	<u>345</u>	<u>E</u> → <u>G</u> in UGCCR5-145C.	

Sequence databases

Select the link destinations:	X91492 Genomic DNA. Translation: CAA62796.1 .
☒ EMBL	U54994 mRNA. Translation: AAC50598.1 .
☐ GenBank	U57840 mRNA. Translation: AAB17071.1 .
☐ DDBJ	U83326 Genomic DNA. Translation: AAC51797.1 .
	AF011500 mRNA. Translation: AAB65700.1 .
	AF011501 mRNA. Translation: AAB65701.1 .
	AF011502 mRNA. Translation: AAB65702.1 .
	AF011503 mRNA. Translation: AAB65703.1 .
	AF011505 mRNA. Translation: AAB65705.1 .
	AF011506 mRNA. Translation: AAB65706.1 .
	AF011507 mRNA. Translation: AAB65707.1 .
	AF011508 mRNA. Translation: AAB65708.1 .
	AF011509 mRNA. Translation: AAB65709.1 .
	AF011510 mRNA. Translation: AAB65710.1 .
	AF011511 mRNA. Translation: AAB65711.1 .
	AF011512 mRNA. Translation: AAB65712.1 .
	AF011513 mRNA. Translation: AAB65713.1 .
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	AF011517 mRNA. Translation: AAB65717.1 .
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	AF011523 mRNA. Translation: AAB65723.1 .
	AF011524 mRNA. Translation: AAB65724.1 .
	AF011525 mRNA. Translation: AAB65725.1 .
	AF011526 mRNA. Translation: AAB65726.1 .
	AF011527 mRNA. Translation: AAB65727.1 .
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	AF011535 mRNA. Translation: AAB65735.1 .
	AF011536 mRNA. Translation: AAB65736.1 .
	AF011537 mRNA. Translation: AAB65737.1 .
	AF031237 Genomic DNA. Translation: AAB94735.1 .
	AF052539 Genomic DNA. Translation: AAD18131.1 .
	AY221093 Genomic DNA. Translation: AAO65971.1 .
	U95626 Genomic DNA. Translation: AAB57793.1 .
	BC038398 mRNA. Translation: AAH38398.1 .
CCDS	CCDS2739.1 .
PIR	A43113 .
RefSeq	NP_000570.1 . NM_000579.3 . NP_001093638.1 . NM_001100168.1 .
UniGene	Hs.450802 .

Genome annotation databases

Ensembl	ENST00000292303 ; ENSP00000292303 ; ENSG00000160791 . ENST00000445772 ; ENSP00000404881 ; ENSG00000160791 .
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GeneID	1234.
KEGG	hsa:1234.

Keywords - Coding sequence diversity

Polymorphism

UniProtKB - P51684 (CCR6_HUMAN)

Protein  **C-C chemokine receptor type 6**

Gene  **CCR6**

Organism  *Homo sapiens (Human)*

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

Names & Taxonomy

Protein names	<i>Recommended name:</i> C-C chemokine receptor type 6 ▪ <i>Short name:</i>C-C CKR-6 ▪ <i>Short name:</i>CC-CKR-6 ▪ <i>Short name:</i>CCR-6 <i>Alternative name(s):</i> • Chemokine receptor-like 3 ▪ <i>Short name:</i>CKR-L3 • DRY6 • G-protein coupled receptor 29 • GPR-CY4 ▪ <i>Short name:</i>GPRCY4 • LARC receptor • <i>CD_antigen:</i> CD196
Gene names	<i>Name:</i> <u>CCR6</u> Synonyms:CKRL3, CMKBR6, GPR29, STRL22
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 6

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000112486.14.</u>
HGNC	<u>HGNC:1607.</u> CCR6.

Sequence

Sequence status: Complete.

P51684-1 [UniParc]
[« Hide](#)

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MSGESMNFSD	VFDSSSEDYFV	SVNTSYYSVD	SEMLLCSLQE	VRQFSRLFVP
60	70	80	90	100
IAYSLICVFG	LLGNILVVIT	FAFYKKARSM	TDVYLLNMAI	ADILFVLTLP
110	120	130	140	150
FWAVSHATGA	WVFSNATCKL	LKGIYAINFN	CGMLLLTCIS	MDRYIAIVQA
160	170	180	190	200
TKSFRLRSRT	LPRSKIICLV	VWGLSVIISS	STFVFNQKYN	TQGSDVCEPK
210	220	230	240	250
YQTVSEPIRW	KLLMLGLELL	FGFFIPLMFM	IFCYTFIVKT	LVQAQNSKRH
260	270	280	290	300
KAIRVIIAVV	LVFLACQIPH	NMVLLVTAAN	LGKMNRSQCS	EKLIGYTKTV
310	320	330	340	350
TEVLAFLHCC	LNPVLYAFIG	QKFRNYFLKI	LKDLWCVRRK	YKSSGFSCAG
360	370			
RYSENISRQT	SETADNDNAS	SFTM		

Length: 374

Mass (Da): 42,494

Last modified: July 15, 1998 - v2

Checksum: D7F963534E990BC4

Sequence caution

The sequence [CAB02144](#) differs from that shown. Reason: Erroneous initiation. Evidence: Curated

Experimental Info

Feature key	Position(s)	Description	Graphical view
Sequence conflict	60	G → A in AAB06949 (Ref. 4) Evidence: Curated	
Sequence conflict	74	Y → N in AAB06949 (Ref. 4) Evidence: Curated	
Sequence conflict	86	L → V in AAB06949 (Ref. 4) Evidence: Curated	
Sequence conflict	164	S → T in AAC51124 (PubMed: 9070937). Evidence: Curated	
Sequence conflict	164	S → T in AAC51125 (PubMed: 9070937). Evidence: Curated	
Sequence conflict	182	T → S in AAB06949 (Ref. 4) Evidence: Curated	
Sequence conflict	192	Q → L in AAB06949 (Ref. 4) Evidence: Curated	
Sequence conflict	206	E → V in AAB06949 (Ref. 4) Evidence: Curated	
Sequence conflict	225	I → F in AAB06949 (Ref. 4) Evidence: Curated	
Sequence conflict	370 – 374	SSFTM → VVLHYVIES in AAB06949 (Ref. 4) Evidence: Curated	

Sequence databases

Select the link destinations:	☒EMBL ☐GenBank ☐DDBJ U45984 Genomic DNA. Translation: AAB62714.1. Z79784 Genomic DNA. Translation: CAB02144.1. Different initiation. U60000 mRNA. Translation: AAB06949.1. U68030 mRNA. Translation: AAC51124.1. U68032 Genomic DNA. Translation: AAC51125.1. AY242126 mRNA. Translation: AAO92293.1. AL121935 Genomic DNA. No translation available. CH471051 Genomic DNA. Translation: EAW47506.1. CH471051 Genomic DNA. Translation: EAW47507.1. BC037960 mRNA. Translation: AAH37960.1.
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Genome annotation databases

Ensembl	ENST00000341935 ; ENSP00000343952 ; ENSG00000112486 . ENST00000349984 ; ENSP00000339393 ; ENSG00000112486 . ENST00000400926 ; ENSP00000383715 ; ENSG00000112486 .
GeneID	1235 .
KEGG	hsa:1235 .
UCSC	uc003qvm.5 . human.

UniProtKB - P32248 (CCR7_HUMAN)

Protein **C-C chemokine receptor type 7**

Gene **CCR7**

Organism *Homo sapiens (Human)*

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

Names & Taxonomy

Protein names	<i>Recommended name:</i> C-C chemokine receptor type 7 ▪ <i>Short name:</i>C-C CKR-7 ▪ <i>Short name:</i>CC-CKR-7 ▪ <i>Short name:</i>CCR-7 <i>Alternative name(s):</i> • BLR2 • CDw197 • Epstein-Barr virus-induced G-protein coupled receptor 1 ▪ <i>Short name:</i>EBI1 ▪ <i>Short name:</i>EBV-induced G-protein coupled receptor 1 • MIP-3 beta receptor • <i>CD_antigen:</i> CD197
Gene names	<i>Name:</i> <u>CCR7</u> Synonyms:CMKBR7, EBI1, EVI1
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 17

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000126353.3.</u>
HGNC	<u>HGNC:1608.</u> CCR7.

Sequence

Sequence status: Complete.

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

P32248-1 [UniParc]

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1020304050

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60708090100

KDVRNFKAWF LPIMYSIICF VGLLGNGLVV LTYIYFKRLK TMTDTYLLNL

110120130140150

AVADILFLLT LPFWAYSAAK SWVFGVHFCK LIFAIYKMSF FSGMLLLLCI

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SIDRYVAIVQ AVSAHRHRAR VLLISKLSKV GIWILATVLS IPELLYSDLQ

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260270280290300

LQARNFERNK AIKVIIAVVV VFIVFQLPYN GVVLAQTVAN FNITSSTCEL

310320330340350

SKQLNIAYDV TYSLACVRCC VNPFLYAFIG VKFRNDLFKL FKDLGCLSQE

360370

QLRQWSSCRH IRRSSMSVEA ETTTTFSP

Length: 378

Mass (Da): 42,874

Last modified: February 1, 1996 - v2

Checksum: D4CB4213841A1BD4

Experimental Info

Feature key	Position(s)	Description	Graphical view
Sequence conflict	<u>182 – 183</u>	IW → SA in AAA58615 (PubMed: 8383238). Evidence: Curated	
Sequence conflict	<u>337</u>	L → I in AAA58615 (PubMed: 8383238). Evidence: Curated	

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_049383)	<u>7</u>	M → V. Corresponds to variant dbSNP:rs45521932	

Sequence databases

Select the link destinations: ☒ EMBL ☐ GenBank ☐ DDBJ	L08176 mRNA. Translation: AAA58615.1 .
	L31584 , L31582 , L31583 Genomic DNA. Translation: AAA74230.1 .
	L31581 mRNA. Translation: AAA74231.1 .
	AY587876 mRNA. Translation: AAT52232.1 .
	BC035343 mRNA. Translation: AAH35343.1 .
CCDS	CCDS11369.1 .
PIR	A45680 . B55735 .
RefSeq	NP_001288643.1 . NM_001301714.1 . NP_001288645.1 . NM_001301716.1 . NP_001288646.1 . NM_001301717.1 . NP_001288647.1 . NM_001301718.1 . NP_001829.1 . NM_001838.3 .

UniGene	Hs.370036.
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Genome annotation databases

Ensembl	ENST00000246657 ; ENSP00000246657 ; ENSG00000126353 .
GeneID	1236.
KEGG	hsa:1236.
UCSC	uc002huw.4. human.

Keywords - Coding sequence diversity[Polymorphism](#)

UniProtKB - P51685 (CCR8_HUMAN)

Protein

C-C chemokine receptor type 8

Gene

CCR8

Organism

Homo sapiens (Human)

Status

 Reviewed

 - Annotation score: - Experimental evidence at protein level

Names & Taxonomy

Protein names	Recommended name: C-C chemokine receptor type 8 ▪ Short name:C-C CKR-8 ▪ Short name:CC-CKR-8 ▪ Short name:CCR-8 Alternative name(s): • CC chemokine receptor CHEMR1 • CMKBRL2 • Chemokine receptor-like 1 ▪ Short name:CKR-L1 • GPR-CY6 ▪ Short name:GPRCY6 • TER1 • CD_antigen: CDw198
Gene names	Name:<u>CCR8</u> Synonyms:CKRL1, CMKBR8, CMKBRL2
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:ENSG00000179934.6.</u>
HGNC	<u>HGNC:1609.</u> CCR8.

Sequences (2)

Sequence status: Complete.

This entry describes **2** isoforms produced by **alternative splicing**.

Isoform 1 (identifier: **P51685-1**) [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
MDYTLDL SVT	TVTDYYY PDI	FSSPCDA ELI	QTNGKLLL AV	FYCLLFV FSL
60	70	80	90	100
LGNSLVIL VL	VVCKKLRS IT	DVYLLNL ALS	DLLFVFS FPF	QTYYL LDQWV
110	120	130	140	150
FGTVMCKV VS	GFYYIGFY SS	MFFITLMS VD	RYLAVVHA VY	ALKVRTIR MG
160	170	180	190	200
TTLCLAVW LT	AIMATIPL LV	FYQVASED GV	LQCYSFY NQQ	TLKWKIFT NF
210	220	230	240	250
KMNILGLL IP	FTIFMFCY IK	ILHQLKRC QN	HNKTKAIR LV	LIVVIAS LLF
260	270	280	290	300
WVPFNVVL FL	TSLHSMHI LD	GCSISQQLT Y	ATHVTEI ISF	THCCVNP VIY
310	320	330	340	350
AFVGEKFKK H	LSEIFQKSC S	QIFNYLGR QM	PRESCEK SSS	CQQHSSR SSS
VDYIL				

Length: 355

Mass (Da): 40,844

Last modified: October 1, 1996 - v1

Checksum: BC14A153CF695361

Isoform 2 (identifier: **P51685-2**) [UniParc]

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

1-91: MDYTLDL SVT...LLFVFSFPFQ → MRNLFRQM

Note: No experimental confirmation available.

Show »

Length: 272

Mass (Da): 31,622

Checksum: 1A78F1429FE3A4A3

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_049384)	<u>27</u>	A → G Evidence: 1 Publication Corresponds to variant <u>dbSNP:rs2853699</u>	

Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_056340)	<u>1 – 91</u>	MDYTL...SF PFQ → MRNLFRQM in isoform <u>2</u> . Evidence: 1 Publication	

Sequence databases

Select the link destinations:	Z79782 Genomic DNA. Translation: CAB02142.1 . Y08456 Genomic DNA. Translation: CAA69712.1 . ☒ EMBL U45983 Genomic DNA. Translation: AAB61962.1 . ☐ GenBank AF005210 mRNA. Translation: AAB62547.1 . ☐ DDBJ U62556 Genomic DNA. Translation: AAB05542.1 . D49919 mRNA. Translation: BAA23387.1 . AY016370 Genomic DNA. Translation: AAK08628.1 . AK314957 mRNA. Translation: BAG37461.1 . AC104850 Genomic DNA. No translation available. CH471055 Genomic DNA. Translation: EAW64577.1 . BC069067 mRNA. Translation: AAH69067.1 . BC074743 mRNA. Translation: AAH74743.1 . BC107152 mRNA. Translation: AAI07153.1 . BC107159 mRNA. Translation: AAI07160.1 .
CCDS	CCDS2684.1 . [P51685-1]
PIR	JC5067 .
RefSeq	NP_005192.1 . NM_005201.3 . [P51685-1]
UniGene	Hs.113222 .

Genome annotation databases

Ensembl	ENST00000326306 ; ENSP00000326432 ; ENSG00000179934 . [P51685-1]
GeneID	1237 .
KEGG	hsa:1237 .
UCSC	uc010hhr.3 . human. [P51685-1]

Keywords - Coding sequence diversity

[Alternative splicing](#), [Polymorphism](#)

UniProtKB - P26842 (CD27_HUMAN)

Protein  **CD27 antigen**

Gene  **CD27**

Organism  *Homo sapiens (Human)*

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

Names & Taxonomy

Protein names	<i>Recommended name:</i> CD27 antigen <i>Alternative name(s):</i> - CD27L receptor - T-cell activation antigen CD27 - T14 - Tumor necrosis factor receptor superfamily member 7 <i>CD_antigen</i>: CD27
Gene names	<i>Name:</i> <u>CD27</u> Synonyms:TNFRSF7
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 12

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000139193.3.</u>
HGNC	<u>HGNC:11922.</u> CD27.

Sequence

Sequence status: Complete.

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

P26842-1 [[UniParc](#)]

[« Hide](#)

10	20	30	40	50
MARPHPWWLC	VLGTLVGLSA	TPAPKSCPER	HYWAQGKLCC	QMCEPGTFLV
60	70	80	90	100
KDCDQHRKAA	QCDPCIPGVS	FSPDHHTRPH	CESCRHCNSG	LLVRNCTITA
110	120	130	140	150
NAECACRNGW	QCRDKECTEC	DPLPNPSLTA	RSSQALSPHP	QPTHLPYVSE
160	170	180	190	200
MLEARTAGHM	QTLADFRQLP	ARTLSTHWPP	QRSLCSSDFI	RILVIFSGMF
210	220	230	240	250
LVFTLAGALF	LHQRKRYRSN	KGESPVEPAE	PCHYSCFREE	EGSTIPIQED
260				
YRKPEPACSP				

Length: 260

Mass (Da): 29,137

Last modified: November 24, 2009 - v2

Checksum: 43C38B895B2AD4E2

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_069793)	53	C → Y in LPFS2. Evidence: 1 Publication Corresponds to variant dbSNP:rs397514667	
Natural variant (VAR_016148)	59	A → T Evidence: 3 Publications Corresponds to variant dbSNP:rs25680	
Natural variant (VAR_052348)	233	H → R Evidence: 5 Publications Corresponds to variant dbSNP:rs2532502	

Sequence databases

Select the link destinations:	M63928 mRNA. Translation: AAA58411.1 .
☒ EMBL	AK315732 mRNA. Translation: BAG38087.1 .
☐ GenBank	AY504961 Genomic DNA. Translation: AAR84239.1 .
☐ DDBJ	AC005840 Genomic DNA. No translation available.
	BC012160 mRNA. Translation: AAH12160.1 .
CCDS	CCDS8545.1 .
PIR	A46517 .
RefSeq	NP_001233.1 . NM_001242.4 .
UniGene	Hs.355307 .

Genome annotation databases

Ensembl	ENST00000266557 ; ENSP00000266557 ; ENSG00000139193 .
GeneID	939 .
KEGG	hsa:939 .
UCSC	uc001qod.4 . human.

Keywords - Coding sequence diversity

Polymorphism

UniProtKB - P10747 (CD28_HUMAN)

Protein **T-cell-specific surface glycoprotein CD28**

Gene **CD28**

Organism *Homo sapiens (Human)*

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

Names & Taxonomy

Protein names	<i>Recommended name:</i> T-cell-specific surface glycoprotein CD28 <i>Alternative name(s):</i> - TP44 <i>CD_antigen</i>: CD28
Gene names	<i>Name</i> : <u>CD28</u>
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 2

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000178562.17.</u>
HGNC	<u>HGNC:1653.</u> CD28.

Sequences (7)

Sequence status: Complete.
Sequence processing: The displayed sequence is further processed into a mature form.
This entry describes **7** isoforms produced by **alternative splicing**.

Isoform 1 (identifier: **P10747-1**) [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
MLRLLLLALNL	FPSIQVTGNK	ILVKQSPMLV	AYDNAVNLSC	KYSYNLFSRE
60	70	80	90	100
FRASLHKGLD	SAVEVCVVYG	NYSQQLQVYS	KTGFNCDGKL	GNESVTFYQLQ
110	120	130	140	150
NLYVNQTDIY	FCKIEVMYPP	PYLDNEKSNG	TIIHVKGKHL	CPSPLFPGPS
160	170	180	190	200
KPFWVLVVVG	GVLACYSLLV	TVAFIIFWVR	SKRSRL LHSD	YMNMTPRRPG
210	220			
PTRKHYQPYA	PPRDFAAYRS			

Length: 220**Mass (Da):** 25,066**Last modified:** July 1, 1989 - v1**Checksum:** 1D9B6552A5878D0F

Isoform 2 (identifier: **P10747-2**) [[UniParc](#)]*Also known as:* CD28-S2*The sequence of this isoform differs from the canonical sequence as follows:*19-137: Missing.[Show »](#)**Length:** 101**Mass (Da):** 11,528**Checksum:** F9B205F1D1BBFDC9

Isoform 3 (identifier: **P10747-3**) [[UniParc](#)]*Also known as:* CD28i*The sequence of this isoform differs from the canonical sequence as follows:*40-124: CKYSYNLFSR...EVMYPPPYLD → Y[Show »](#)**Length:** 136**Mass (Da):** 15,369**Checksum:** C9AF33467706D2BE

Isoform 4 (identifier: **P10747-4**) [[UniParc](#)]*Also known as:* CD28-S1*The sequence of this isoform differs from the canonical sequence as follows:*40-137: CKYSYNLFSR...SNGTIIHVKG → W[Show »](#)**Length:** 123**Mass (Da):** 14,014**Checksum:** 3DE54211F2642520

Isoform 5 (identifier: **P10747-5**) [[UniParc](#)]*The sequence of this isoform differs from the canonical sequence as follows:*40-124: CKYSYNLFSR...EVMYPPPYLD → Y138-139: KH → EE140-220: Missing.[Show »](#)**Length:** 55**Mass (Da):** 6,099**Checksum:** A2F24E0CFBD16D90

Isoform 6 (identifier: **P10747-6**) [[UniParc](#)]*Also known as:* CD28-S3

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

40-124: CKYSYNLFSR...EVMYPPPYLD → Y

152-207: Missing.

[Show »](#)

Length: 80

Mass (Da): 8,823

Checksum: C09D0EC41F748AFC

Isoform 7 (identifier: **P10747-7**) [UniParc]

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

1-17: MLRLLLALNLFPSIQVT → MPCGLSALIMCPKGMVAVVVAVDDGDSQALA

[Show »](#)

Length: 234

Mass (Da): 26,186

Checksum: 02AD85397834E57E

Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_047701)	<u>1 – 17</u>	MLRLL...SIQVT → MPCGLSALIMCPKGMVAVVVAVDDGDSQALA in isoform <u>7</u> . Evidence: 1 Publication	
Alternative sequence (VSP_002494)	<u>19 – 137</u>	Missing in isoform <u>2</u> . Evidence: 1 Publication	
Alternative sequence (VSP_002496)	<u>40 – 137</u>	CKYSY...IHKVG → W in isoform <u>4</u> . Evidence: 1 Publication	
Alternative sequence (VSP_002495)	<u>40 – 124</u>	CKYSY...PPYLD → Y in isoform <u>3</u> , isoform <u>5</u> and isoform <u>6</u> . Evidence: 2 Publications	
Alternative sequence (VSP_002497)	<u>138 – 139</u>	KH → EE in isoform <u>5</u> . Evidence: 1 Publication	
Alternative sequence (VSP_002498)	<u>140 – 220</u>	Missing in isoform <u>5</u> . Evidence: 1 Publication	
Alternative sequence (VSP_002499)	<u>152 – 207</u>	Missing in isoform <u>6</u> . Evidence: 1 Publication	

Sequence databases

Select the link destinations:	J02988 mRNA. Translation: AAA60581.1 .
☒ EMBL	M37815 M37814 Genomic DNA. Translation: AAA51944.1 .
☐ GenBank	M37815 M37814 Genomic DNA. Translation: AAA51945.1 .
☐ DDBJ	AJ295273 mRNA. Translation: CAC29237.1 .
	AF222341 mRNA. Translation: AAF33792.1 .
	AF222342 mRNA. Translation: AAF33793.1 .
	AF222343 mRNA. Translation: AAF33794.1 .
	AJ517504 mRNA. Translation: CAD57003.1 .
	EF064755 Genomic DNA. Translation: ABK41938.1 .
	AK292986 mRNA. Translation: BAF85675.1 .
	AK313313 mRNA. Translation: BAG36118.1 .
	AC125238 Genomic DNA. Translation: AAY24123.1 .
	CH471063 Genomic DNA. Translation: EAW70348.1 .
	BC093698 mRNA. Translation: AAH93698.1 .
	BC112085 mRNA. Translation: AAI12086.1 .
	AF411057 Genomic DNA. Translation: AAL40931.1 .
CCDS	CCDS2361.1 . [P10747-1] CCDS58749.1 . [P10747-2]
PIR	A39983 . RWHU28 .
RefSeq	NP_001230006.1 . NM_001243077.1 . [P10747-4] NP_001230007.1 . NM_001243078.1 . [P10747-2] NP_006130.1 . NM_006139.3 . [P10747-1] XP_011510496.1 . XM_011512194.2 . [P10747-7] XP_011510499.1 . XM_011512197.2 . [P10747-3]
UniGene	Hs.443123 .

Genome annotation databases

Ensembl	ENST00000324106 ; ENSP00000324890 ; ENSG00000178562 . [P10747-1] ENST00000374481 ; ENSP00000363605 ; ENSG00000178562 . [P10747-2] ENST00000458610 ; ENSP00000393648 ; ENSG00000178562 . [P10747-7]
GeneID	940 .
KEGG	hsa:940 .
UCSC	uc002vah.6 . human. [P10747-1]

Keywords - Coding sequence diversity

[Alternative splicing](#)

UniProtKB - P28908 (TNR8_HUMAN)

Protein **Tumor necrosis factor receptor superfamily member 8**

Gene **TNFRSF8**

Organism *Homo sapiens (Human)*

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

Names & Taxonomy

Protein names	<i>Recommended name:</i> Tumor necrosis factor receptor superfamily member 8 Evidence: Imported <i>Alternative name(s):</i> - CD30L receptor - Ki-1 antigen - Lymphocyte activation antigen CD30 <i>CD_antigen</i>: CD30 Evidence: 1 Publication
Gene names	<i>Name</i> : TNFRSF8 Evidence: Imported <i>Synonyms</i> : CD30 Evidence: 1 Publication , D1S166E
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:ENSG00000120949.14.
HGNC	HGNC:11923 . TNFRSF8.

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** and **alternative initiation**.

Isoform 1 (identifier: **P28908-1**) [[UniParc](#)]

Also known as: Long

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
MRVLLAALGL	LFLGALRAFP	QDRPFEDTCH	GNPSHYDKA	VRRCCYRCPM
60	70	80	90	100
GLFPTQQCPQ	RPTDCRKQCE	PDYYLDEADR	CTACVTCSR	DLVEKTPCAW
110	120	130	140	150
NSSRVCECRP	GMFCSTSAVN	SCARCFHHSV	CPAGMIVKFP	GTAQKNTVCE
160	170	180	190	200
PASPGVSPAC	ASPENCKEPS	SGTIPQAKPT	PVSPATSSAS	TMPVRGGTRL
210	220	230	240	250
AQEAASKLTR	APDSPSSVGR	PSSDPGLSPT	QPCPEGSGDC	RKQCEPDYYL
260	270	280	290	300
DEAGRCTACV	SCSRDDLVEK	TPCAWNSSRT	CECRPGMICA	TSATNSCARC
310	320	330	340	350
VPYPICAAET	VTKPQDMAEK	DTTFEAPPLG	TQPD CNPTPE	NGEAPASTSP
360	370	380	390	400
TQSLLVDSQA	SKTLPIPTSA	PVALSSTGKP	VLDAGPVLFW	VILVLVVVVG
410	420	430	440	450
SSAFLLCRRR	ACRKRIKQKL	HLCYPVQTSQ	PKLELVDSRP	RRSSTQLRSG
460	470	480	490	500
ASVTEPVAAE	RGLMSQPLME	TCHSVGAAYL	ESLPLQDASP	AGGPSSPRDL
510	520	530	540	550
PEPRVSTEHT	NNKIEKIYIM	KADTVIVGTV	KAELPEGRGL	AGPAEPELEE
560	570	580	590	
ELEADHTPHY	PEQETEPPLG	SCSDVMLSVE	EEGKEDPLPT	AASGK

Length: 595**Mass (Da):** 63,747**Last modified:** December 1, 1992 - v1**Checksum:** 7A407CC78A6E0BC8**Isoform 2** (identifier: **P28908-2**) [[UniParc](#)]*Also known as:* Cytoplasmic, Short, C30V*The sequence of this isoform differs from the canonical sequence as follows:*1-463: Missing.[Show »](#)**Length:** 132**Mass (Da):** 14,088**Checksum:** 211648B504B6313F

Isoform 3 (identifier: **P28908-3**) [UniParc]

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

1-111: Missing.

446-446: Missing.

Show »

Length: 483

Mass (Da): 50,935

Checksum: 8EA95A0BEA6BD315

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_054213)	<u>273</u>	C → F. Corresponds to variant dbSNP:rs2230624	
Natural variant (VAR_018753)	<u>273</u>	C → Y Evidence: 1 Publication Corresponds to variant dbSNP:rs2230624	
Natural variant (VAR_055257)	<u>297</u>	C → R Evidence: 1 Publication Corresponds to variant dbSNP:rs1763642	
Natural variant (VAR_055258)	<u>314</u>	P → S. Corresponds to variant dbSNP:rs2275170	
Natural variant (VAR_018754)	<u>402</u>	S → G Evidence: 1 Publication Corresponds to variant dbSNP:rs2230625	
Natural variant (VAR_055259)	<u>466</u>	Q → R. Corresponds to variant dbSNP:rs35511003	

Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_018900)	<u>1 – 463</u>	Missing in isoform 2. Evidence: 2 Publications	
Alternative sequence (VSP_055032)	<u>1 – 111</u>	Missing in isoform 3. Evidence: 1 Publication	
Alternative sequence (VSP_055033)	<u>446</u>	Missing in isoform 3. Evidence: 1 Publication	

Sequence databases

Select the link destinations:	M83554 mRNA. Translation: AAA51947.1 . S75768 mRNA. Translation: AAD14188.1 . ☒ EMBL D86042 mRNA. Translation: BAA12973.1 . ☐ GenBank AJ289159 Genomic DNA. Translation: CAC16652.1 . ☐ DDBJ AY498860 Genomic DNA. Translation: AAR32099.1 . AL357835 Genomic DNA. No translation available. BC063482 mRNA. Translation: AAH63482.2 . BC136400 mRNA. Translation: AAI36401.1 .
CCDS	CCDS144.1 . [P28908-1] CCDS59989.1 . [P28908-3]
PIR	A42086 .
RefSeq	NP_001234.3 . NM_001243.4 . [P28908-1] NP_001268359.2 . NM_001281430.2 . [P28908-3]
UniGene	Hs.1314 .

Genome annotation databases

Ensembl	ENST00000263932 ; ENSP00000263932 ; ENSG00000120949 . [P28908-1] ENST00000413146 ; ENSP00000398337 ; ENSG00000120949 . [P28908-2] ENST00000417814 ; ENSP00000390650 ; ENSG00000120949 . [P28908-3]
GeneID	943 .
KEGG	hsa:943 .
UCSC	uc001atq.3 . human. [P28908-1]

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

UniProtKB - P29965 (CD40L_HUMAN)

Protein **CD40 ligand**

Gene **CD40LG**

Organism *Homo sapiens (Human)*

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

Names & Taxonomy

Protein names	<i>Recommended name:</i> CD40 ligand ▪ <i>Short name:</i>CD40-L <i>Alternative name(s):</i> • T-cell antigen Gp39 • TNF-related activation protein ▪ <i>Short name:</i>TRAP • Tumor necrosis factor ligand superfamily member 5 • <i>CD_antigen:</i> CD154 <i>Cleaved into the following 2 chains:</i> • <u>CD40 ligand, membrane form</u> • <u>CD40 ligand, soluble form</u>
Gene names	<i>Name:</i> <u>CD40LG</u> <i>Synonyms:</i> CD40L, TNFSF5, TRAP
Organism	<u>Homo sapiens (Human)</u>
Taxonomic identifier	<u>9606 [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 X

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000102245.7.</u>
HGNC	<u>HGNC:11935.</u> CD40LG.

Sequence

Sequence status: Complete.

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

P29965-1 [[UniParc](#)]

[« Hide](#)

10	20	30	40	50
MIETYNQTSP	RSAATGLPIS	MKIFMYLLTV	FLITQMIGSA	LFAVYLHRRL
60	70	80	90	100
DKIEDERNLH	EDFVFMKTIQ	RCNTGERSLS	LLNCEEIKSQ	FEGFVKDIML
110	120	130	140	150
NKEETKKENS	FEMQKGDQNP	QIAAHVISEA	SSKTTSVLQW	AEKGYTMSN
160	170	180	190	200
NLVTLENGKQ	LTVKRQGLYY	IYAQVTFCSN	REASSQAPFI	ASLCLKSPGR
210	220	230	240	250
FERILLRAAN	THSSAKPCGQ	QSIHLGGVFE	LQPGASVFN	VTDPSQVSHG
260				
TGFTSFGLLK	L			

Length: 261

Mass (Da): 29,274

Last modified: April 1, 1993 - v1

Checksum: 16F5CEB093BCC2BB

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_007513)	<u>36</u>	<u>M</u> → <u>R</u> in HIGM1. Evidence: 2 Publications Corresponds to variant <u>dbSNP:rs104894774</u>	
Natural variant (VAR_017925)	<u>38</u>	<u>G</u> → <u>R</u> in HIGM1. Evidence: 1 Publication	
Natural variant (VAR_017929)	<u>116</u>	<u>G</u> → <u>R</u> in HIGM1.	
Natural variant (VAR_017930)	<u>116</u>	<u>G</u> → <u>S</u> in HIGM1. Evidence: 2 Publications	
Natural variant (VAR_007514)	<u>123</u>	<u>A</u> → <u>E</u> in HIGM1. Evidence: 1 Publication Corresponds to variant <u>dbSNP:rs104894778</u>	
Natural variant (VAR_017926)	<u>125</u>	<u>H</u> → <u>R</u> in HIGM1. Evidence: 1 Publication	
Natural variant (VAR_007515)	<u>126</u>	<u>V</u> → <u>A</u> in HIGM1. Evidence: 1 Publication	
Natural variant (VAR_017931)	<u>126</u>	<u>V</u> → <u>D</u> in HIGM1.	
Natural variant (VAR_007516)	<u>128 – 129</u>	<u>SE</u> → <u>RG</u> in HIGM1.	
Natural variant (VAR_007517)	<u>140</u>	<u>W</u> → <u>C</u> in HIGM1. Evidence: 1 Publication	
Natural variant (VAR_007518)	<u>140</u>	<u>W</u> → <u>G</u> in HIGM1. Evidence: 1 Publication Corresponds to variant <u>dbSNP:rs104894777</u>	
Natural variant (VAR_007519)	<u>140</u>	<u>W</u> → <u>R</u> in HIGM1. Evidence: 1 Publication	
Natural variant (VAR_017932)	<u>143</u>	<u>K</u> → <u>T</u> in HIGM1.	
Natural variant (VAR_007520)	<u>144</u>	<u>G</u> → <u>E</u> in HIGM1. Evidence: 1 Publication	
Natural variant (VAR_017922)	<u>147</u>	<u>T</u> → <u>N</u> in HIGM1. Evidence: 1 Publication	
Natural variant (VAR_007521)	<u>155</u>	<u>L</u> → <u>P</u> in HIGM1. Evidence: 2 Publications Corresponds to variant <u>dbSNP:rs104894769</u>	
Natural variant (VAR_017923)	<u>170</u>	<u>Y</u> → <u>C</u> in HIGM1. Evidence: 1 Publication Corresponds to variant <u>dbSNP:rs756468554</u>	
Natural variant (VAR_017933)	<u>173</u>	<u>A</u> → <u>D</u> in HIGM1.	
Natural variant (VAR_017927)	<u>174</u>	<u>Q</u> → <u>R</u> in HIGM1. Evidence: 1 Publication	
Natural variant (VAR_017934)	<u>176</u>	<u>T</u> → <u>I</u> in HIGM1.	
Natural variant (VAR_017935)	<u>195</u>	<u>L</u> → <u>P</u> in HIGM1.	

Natural variant (VAR_017936)	208	A → D in HIGM1.		
Natural variant (VAR_007522)	211	T → N in HIGM1. Evidence: 1 Publication		
Natural variant (VAR_007523)	219	G → R Evidence: 1 Publication Corresponds to variant dbSNP:rs148594123		
Natural variant (VAR_017937)	224	H → Y in HIGM1.		
Natural variant (VAR_017938)	226	G → A in HIGM1.		
Natural variant (VAR_007524)	227	G → V in HIGM1. Evidence: 3 Publications Corresponds to variant dbSNP:rs104894768		
Natural variant (VAR_007525)	227	Missing in HIGM1. Evidence: 1 Publication		
Natural variant (VAR_007526)	231	L → S in HIGM1. Evidence: 2 Publications		
Natural variant (VAR_007527)	235	A → P in HIGM1. Evidence: 2 Publications Corresponds to variant dbSNP:rs104894771		
Natural variant (VAR_017939)	237	V → E in HIGM1. Evidence: 1 Publication		
Natural variant (VAR_007528)	254	T → M in HIGM1. Evidence: 2 Publications Corresponds to variant dbSNP:rs193922136		
Natural variant (VAR_017940)	257	G → D in HIGM1.		
Natural variant (VAR_017928)	257	G → S in HIGM1. Evidence: 1 Publication		
Natural variant (VAR_017924)	258	L → S in HIGM1. Evidence: 1 Publication		

Sequence databases

Select the link destinations:	X68550 mRNA. Translation: CAA48554.1 .
☒ EMBL	Z15017 mRNA. Translation: CAA78737.1 .
☐ GenBank	X67878 mRNA. Translation: CAA48077.1 .
☐ DDBJ	L07414 mRNA. Translation: AAA35662.1 .
	D31797 Genomic DNA. Translation: BAA06599.1 .
	BC071754 mRNA. Translation: AAH71754.1 .
	BC074950 mRNA. Translation: AAH74950.1 .
CCDS	CCDS14659.1 .
PIR	S28017 . I53476.
RefSeq	NP_000065.1 . NM_000074.2 .
UniGene	Hs.592244 .

Genome annotation databases

Ensembl	ENST00000370629 ; ENSP00000359663 ; ENSG00000102245 .
GeneID	959 .
KEGG	hsa:959 .
UCSC	uc004faa.4 . human.

Keywords - Coding sequence diversity

[Polymorphism](#)

UniProtKB - P25942 (TNR5_HUMAN)

Protein **Tumor necrosis factor receptor superfamily member 5**

Gene **CD40**

Organism *Homo sapiens (Human)*

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

Names & Taxonomy

Protein names	<i>Recommended name:</i> Tumor necrosis factor receptor superfamily member 5 <i>Alternative name(s):</i> - B-cell surface antigen CD40 - Bp50 - CD40L receptor - CDw40 <i>CD_antigen</i>: CD40
Gene names	<i>Name:</i> <u>CD40</u> <i>Synonyms:</i> TNFRSF5
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 20

Organism-specific databases

EuPathDB	<u>HostDB:ENSG00000101017.13.</u>
HGNC	<u>HGNC:11919.</u> CD40.

Sequences (2)

Sequence status: Complete.

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

This entry describes **2** isoforms produced by **alternative splicing**.

Note: Additional isoforms seem to exist.

Isoform I (identifier: **P25942-1**) [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
MVRLPLQCVL	WGCLLTAVHP	EPPTACREKQ	YLINSQCCSL	CQPGQKLVSD
60	70	80	90	100
CTEFTETECL	PCGESEFLDT	WNRETHCHQH	KYCDPNLGLR	VQQKGTSETD
110	120	130	140	150
TICTCEEGLWH	CTSEACESCV	LHRSCSPGFG	VKQIATGVSD	TICEPCPVGF
160	170	180	190	200
FSNVSSAFEK	CHPWTSCETK	DLVVQQAGTN	KTDVVCGPQD	RLRALVVIPI
210	220	230	240	250
IFGILFAILL	VLVFIKKVAK	KPTNKAPHPK	QEPQEINFPD	DLPGSNTAAP
260	270			
VQETLHGCQP	VTQEDGKESR	ISVQERQ		

Length: 277

Mass (Da): 30,619

Last modified: May 1, 1992 - v1

Checksum: BC8776EC2C4A5680

Isoform II (identifier: **P25942-2**) [UniParc]
The sequence of this isoform differs from the canonical sequence as follows:
166-203: SCETKDLVVQ...ALVVIPIIFG → RSPGSAESPG...YQKGGQEANQ
204-277: Missing.

Show »

Length: 203

Mass (Da): 22,259

Checksum: 07399D5F79D59A4F

Experimental Info

Feature key	Position(s)	Description	Graphical view
Sequence conflict	<u>112</u>	T → A in <u>BAD96616</u> (Ref. 4) Evidence: Curated	

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_039301)	<u>26</u>	C → Q in bladder carcinoma cell line Hu549; requires 2 nucleotide substitutions. Evidence: 1 Publication	
Natural variant (VAR_039302)	<u>35</u>	S → G in bladder carcinoma cell line Hu549. Evidence: 1 Publication Corresponds to variant <u>dbSNP:rs750234130</u>	
Natural variant (VAR_077569)	<u>37</u>	C → G in HIGM3. Evidence: 1 Publication	
Natural variant (VAR_039303)	<u>39</u>	S → T in bladder carcinoma cell line Hu549. Evidence: 1 Publication	
Natural variant (VAR_013628)	<u>83</u>	C → R in HIGM3. Evidence: 1 Publication Corresponds to variant <u>dbSNP:rs28931586</u>	
Natural variant (VAR_018751)	<u>124</u>	S → L Evidence: 1 Publication Corresponds to variant <u>dbSNP:rs11569321</u>	

Natural variant (VAR_018752)	227	P → A Evidence: 1 Publication Corresponds to variant dbSNP:rs11086998	
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Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_006472)	166 – 203	SCETK...PIIFG → RSPGSAESPGGDPHHLRDPV CHPLGAGLYQKGGQEANQ in isoform II . Evidence: 1 Publication	
Alternative sequence (VSP_006473)	204 – 277	Missing in isoform II . Evidence: 1 Publication	

Sequence databases

Select the link destinations:	X60592 mRNA. Translation: CAA43045.1 .
☒ EMBL	AJ300189 mRNA. Translation: CAC29424.1 .
☐ GenBank	BT019901 mRNA. Translation: AAV38704.1 .
☐ DDBJ	AK222896 mRNA. Translation: BAD96616.1 .
	AY504960 Genomic DNA. Translation: AAR84238.1 .
	EF064754 Genomic DNA. Translation: ABK41937.1 .
	AL035662 Genomic DNA. No translation available.
	CH471077 Genomic DNA. Translation: EAW75758.1 .
	CH471077 Genomic DNA. Translation: EAW75760.1 .
	CH471077 Genomic DNA. Translation: EAW75762.1 .
	BC012419 mRNA. Translation: AAH12419.1 .
	AY225405 mRNA. Translation: AAO43990.1 .
CCDS	CCDS13393.1 . [P25942-1] CCDS13394.1 . [P25942-2]
PIR	B60771 . S04460 . A60771.
RefSeq	NP_001241.1 . NM_001250.5 . [P25942-1] NP_001289682.1 . NM_001302753.1 . NP_001309351.1 . NM_001322422.1 . NP_690593.1 . NM_152854.3 . [P25942-2]
UniGene	Hs.472860 .

Genome annotation databases

Ensembl	ENST00000372276 ; ENSP00000361350 ; ENSG00000101017 . [P25942-2] ENST00000372285 ; ENSP00000361359 ; ENSG00000101017 . [P25942-1]
GeneID	958 .
KEGG	hsa:958 .
UCSC	uc002xrg.2 . human. [P25942-1]

Keywords - Coding sequence diversity

Alternative splicing, [Polymorphism](#)