

UniProtKB - P01834 (IGKC_HUMAN)

Protein	Immunoglobulin kappa constant
Gene	IGKC
Organism	<i>Homo sapiens (Human)</i>
Status	 <u>Reviewed</u> - Annotation score:  - Experimental evidence at protein level

Function

Constant region of immunoglobulin light chains. Immunoglobulins, also known as antibodies, are membrane-bound or secreted glycoproteins produced by B lymphocytes. In the recognition phase of humoral immunity, the membrane-bound immunoglobulins serve as receptors which, upon binding of a specific antigen, trigger the clonal expansion and differentiation of B lymphocytes into immunoglobulins-secreting plasma cells. Secreted immunoglobulins mediate the effector phase of humoral immunity, which results in the elimination of bound antigens (PubMed:[22158414](#), PubMed:[20176268](#)). The antigen binding site is formed by the variable domain of one heavy chain, together with that of its associated light chain. Thus, each immunoglobulin has two antigen binding sites with remarkable affinity for a particular antigen. The variable domains are assembled by a process called V-(D)-J rearrangement and can then be subjected to somatic hypermutations which, after exposure to antigen and selection, allow affinity maturation for a particular antigen (PubMed:[17576170](#), PubMed:[20176268](#)). Evidence: 3 Publications

Caution

For an example of a full-length immunoglobulin kappa light chain see AC [P0DOX7](#).

Evidence: Curated

GO - Molecular function

- [antigen binding](#) Evidence: Source: GO_Central
- [immunoglobulin receptor binding](#) Evidence: Source: GO_Central

GO - Biological process

- [B cell receptor signaling pathway](#) Evidence: Source: GO_Central
- [complement activation](#) Evidence: Source: Reactome
- [complement activation, classical pathway](#) Evidence: Source: GO_Central
- [defense response to bacterium](#) Evidence: Source: GO_Central
- [Fc-epsilon receptor signaling pathway](#) Evidence: Source: Reactome
- [Fc-gamma receptor signaling pathway involved in phagocytosis](#) Evidence: Source: Reactome
- [immune response](#) Evidence: Source: UniProtKB
- [innate immune response](#) Evidence: Source: GO_Central
- [leukocyte migration](#) Evidence: Source: Reactome
- [negative regulation of inflammatory response to antigenic stimulus](#) Evidence: Source: Reactome
- [opsonization](#) Evidence: Source: Reactome
- [peptide cross-linking](#) Evidence: Source: Reactome
- [phagocytosis, recognition](#) Evidence: Source: GO_Central
- [positive regulation of B cell activation](#) Evidence: Source: Reactome
- [receptor-mediated endocytosis](#) Evidence: Source: Reactome

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- [regulation of complement activation](#) Evidence: Source: Reactome
- [regulation of immune response](#) Evidence: Source: Reactome
- [retina homeostasis](#) Evidence: Source: UniProtKB

Keywords

Biological process	Adaptive immunity , Immunity
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Enzyme and pathway databases

PathwayCommons	P01834
Reactome	R-HSA-166663 , Initial triggering of complement R-HSA-173623 , Classical antibody-mediated complement activation R-HSA-198933 , Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell R-HSA-202733 , Cell surface interactions at the vascular wall R-HSA-2029481 , FCGR activation R-HSA-2029482 , Regulation of actin dynamics for phagocytic cup formation R-HSA-2029485 , Role of phospholipids in phagocytosis R-HSA-2168880 , Scavenging of heme from plasma R-HSA-2454202 , Fc epsilon receptor (FCERI) signaling R-HSA-2730905 , Role of LAT2/NTAL/LAB on calcium mobilization R-HSA-2871796 , FCERI mediated MAPK activation R-HSA-2871809 , FCERI mediated Ca+2 mobilization R-HSA-2871837 , FCERI mediated NF-kB activation R-HSA-5690714 , CD22 mediated BCR regulation R-HSA-9664323 , FCGR3A-mediated IL10 synthesis R-HSA-9664422 , FCGR3A-mediated phagocytosis R-HSA-977606 , Regulation of Complement cascade R-HSA-983695 , Antigen activates B Cell Receptor (BCR) leading to generation o second messengers

Protein family/group databases

IMGT/GENE-DB	IGKC
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Names & Taxonomy

Protein names	<i>Recommended name:</i> Immunoglobulin kappa constant Evidence: 2 Publications <i>Alternative name(s):</i> Ig kappa chain C region Evidence: Curated Ig kappa chain C region AG Evidence: 1 Publication Ig kappa chain C region CUM Evidence: 1 Publication Ig kappa chain C region EU Evidence: 1 Publication Ig kappa chain C region OU Evidence: 1 Publication Ig kappa chain C region ROY Evidence: 1 Publication Ig kappa chain C region TI Evidence: 1 Publication
Gene names	<i>Name:</i> IGKC Evidence: 2 Publications
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	UP0000005640 Component: Unplaced Do not show this banner again

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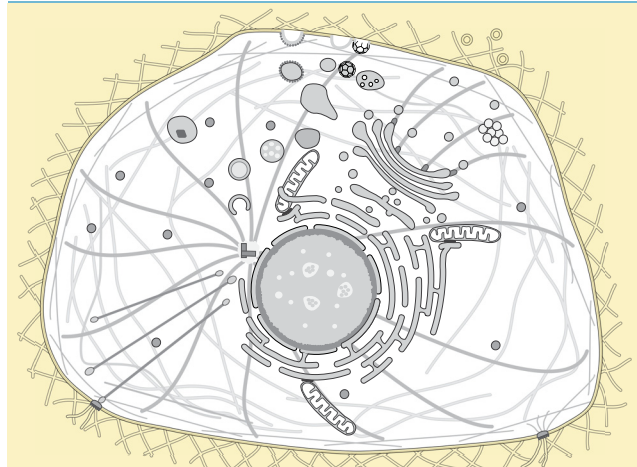
Organism-specific databases

HGNC	HGNC:5716 , IGKC
MIM	147200 , gene
neXtProt	NX_P01834
VEuPathDB	HostDB:ENSG00000211592.7

Subcellular location

[UniProt annotation](#)

[GO - Cellular component](#)



☐ Automatic annotation
☐ Manual annotation
Source: [SwissBioPics](#)

Plasma membrane

👁 [Cell membrane](#) [i](#)

Evidence: 2 Publications

Extracellular region or secreted

👁 [Secreted](#) [i](#)

Evidence: 2 Publications

Keywords - Cellular component

[Cell membrane](#), [Immunoglobulin](#), [Membrane](#), [Secreted](#)

Pathology & Biotech

Involvement in disease

[Immunoglobulin kappa light chain deficiency \(IGKCD\)](#) [Evidence: 1 Publication](#)

The disease is caused by variants affecting the gene represented in this entry.

Disease description: A disease characterized by the complete absence of immunoglobulin kappa chains.

Related information in OMIM

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_066403)	41	W → R in IGKCD. Evidence: 1 Publication	

Keywords - Disease

[Disease variant](#)

Organism-specific databases

MalaCards	IGKC
MIM	614102 , phenotype
Orphanet	183675 , Recurrent infections associated with rare immunoglobulin isotypes deficiency

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Miscellaneous databases

Pharos	P01834 , Tbio
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Chemistry databases

DrugBank	DB07909 , (1S,2S,5S)2-(4-GLUTARIDYLBENZYL)-5-PHENYL-1-CYCLOHEXANOL DB07416 , (2S)-2-(BUTYRYLOXY)-3-HYDROXYPROPYL NONANOATE DB07716 , (4Z)-2,8:7,12:11,15:14,18:17,22-PENTAANHYDRO-4,5,6,9,10,13,19,20,21-NONAEOXY-D-ARABINO-D-ALLO-D-ALLO-DOCOSA-4,9,20-TRIENITOL DB07441 , 3-{[(9-CYANO-9,10-DIHYDRO-10-METHYLACRIDIN-9-YL)CARBONYL]AMINO}PROPANOIC ACID DB08562 , 4-(4-STYRYL-PHENYLCARBAMOYL)-BUTYRIC ACID DB07882 , 4-{4-[2-(1A,7A-DIMETHYL-4-OXY-OCTAHYDRO-1-OXA-4-AZA-CYCLOPROPA[A]NAPHTHALEN-4-YL) -ACETYLAMINO]-PHENYLCARBAMOYL}-BUTYRIC ACID DB07784 , [4-(4-ACETYLAMINO-PHENYL)-3,5-DIOXO-4-AZA-TRICYCLO[5.2.2.0 ^{2,6}]UNDEC-1-YLCARBAMOYLOXY]-ACETIC ACID DB07375 , Etiocholanedione DB08413 , METHYL-PHOSPHONIC ACID MONO-(4-NITRO-PHENYL) ESTER DB04688 , Methylecgonine DB08289 , N-(PARA-GLUTARAMIDOPHENYL-ETHYL)-PIPERIDINIUM-N-OXIDE DB07893 , PHENYL[1-(N-SUCCINYLAMINO)PENTYL]PHOSPHONATE DB01851 , Tetrabutylammonium Ion DB08647 , TRAZEOLIDE
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Genetic variation databases

BioMuta	IGKC
DMDM	125145

PTM / Processing

Molecule processing

Feature key	Position(s)	Description	Graphical view
Chain (PRO_0000153596)	<1 – 107	Immunoglobulin kappa constant	

Amino acid modifications

Feature key	Position(s)	Description	Graphical view
Disulfide bond	27 ↔ 87	Evidence: PROSITE-ProRule annotation Evidence: 1 Publication	
Disulfide bond	107	Interchain (with a heavy chain) Evidence: 1 Publication	

Keywords - PTM

[Disulfide bond](#)

Proteomic databases

EPD	P01834
jPOST	P01834
MassIVE	P01834
PeptideAtlas	P01834
PRIDE	P01834
ProteomicsDB	51490

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2D gel databases

UCD-2DPAGE	P01834
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PTM databases

CarbonylDB	P01834
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iPTMnet	P01834
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PhosphoSitePlus	P01834
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SwissPalm	P01834
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Expression

Gene expression databases

Bgee	ENSG00000211592 , Expressed in lymph node and 114 other tissues
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Interaction

Subunit structure

Immunoglobulins are composed of two identical heavy chains and two identical light chains; disulfide-linked.

Evidence: 1 Publication

GO - Molecular function

- [immunoglobulin receptor binding](#) Evidence: Source: GO_Central

Protein-protein interaction databases

IntAct	P01834 , 67 interactors
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MINT	P01834
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Miscellaneous databases

RNAc	P01834 , protein
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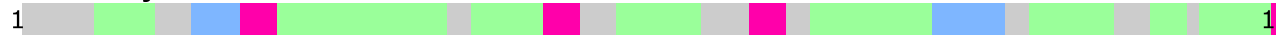
Structure

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PDB Entry	Method	Resolution	Chain	Position	Link
1A...	X-r...	2.1...	A/L	2-105	PD... RC... PDBj PD...
1A...	X-r...	2.4...	A/L	2-105	PD... RC... PDBj PD...
1C...	X-r...	2.5...	L	2-107	PD... RC... PDBj PD...
1D...	X-r...	2.8...	A/L	2-104	PD... RC... PDBj PD...
1D...	X-r...	2.0...	L	2-104	PD... RC... PDBj PD...
1D...	X-r...	2.0...	L	2-104	PD... RC... PDBj PD...

Secondary structure



Legend: ■ Helix ■ Turn ■ Beta strand ■ PDB Structure known for this area

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3D structure databases

SMR	P01834
ModBase	Search...
PDBe-KB	Search...

Miscellaneous databases

EvolutionaryTrace	P01834
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Family & Domains

Domains and Repeats

Feature key	Position(s)	Description	Graphical view
Domain	6 – 103	Ig-like Evidence: PROSITE-ProRule annotation	

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Keywords - Domain
Immunoglobulin domain

Phylogenomic databases

InParanoid	P01834
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Family and domain databases

Gene3D	2.60.40.10 , 1 hit
InterPro	View protein in InterPro IPR007110 , Ig-like_dom IPR036179 , Ig-like_dom_sf IPR013783 , Ig-like_fold IPR003006 , Ig/MHC_CS IPR003597 , Ig_C1-set
Pfam	View protein in Pfam PF07654 , C1-set, 1 hit
SMART	View protein in SMART SM00407 , IGc1, 1 hit
SUPFAM	SSF48726 , SSF48726, 1 hit
PROSITE	View protein in PROSITE PS50835 , IG_LIKE, 1 hit PS00290 , IG_MHC, 1 hit

Sequence (1+)

Sequence status: Complete.

This entry has 1 described isoform and 1 potential isoform that is computationally mapped.

P01834-1 [UniParc]

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```

          10           20           30           40           50
RTVAAPSVFI FPPSDEQLKS GTASVCLLN NFYPREAKVQ WKVDNALQSG
          60           70           80           90          100
NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK

SFNRGEC

```

Length: 107**Mass (Da):** 11,765**Last modified:** March 15, 2017 - v2**Checksum:** B97BEEBBA4D0B291

Computationally mapped potential isoform sequences

There is 1 potential isoform mapped to this entry.

☐	Entry	Entry name		Protein names	Gene names	Length	Annotation
☐	A0A5H1ZRQ3	A0A5H1ZRQ3_HUMAN		Immunoglobulin kappa constant	IGKC	107	Annotation score: 

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Sequence caution

The sequence [AAA58989](#) differs from that shown. Reason: Erroneous initiation. Truncated N-terminus. Evidence: Curated

Experimental Info

Feature key	Position(s)	Description	Graphical view
Non-terminal residue	1		
Sequence conflict	15	D → N AA sequence (PubMed: 4893682). Evidence: Curated	
Sequence conflict	15	D → N AA sequence (PubMed: 5447531). Evidence: Curated	
Sequence conflict	58	E → Q AA sequence (Ref. 3). Evidence: Curated	
Sequence conflict	58	E → Q AA sequence (PubMed: 5586923). Evidence: Curated	

Polymorphism

There are several alleles. The sequence shown is that of IMGT allele IGKC*01. Evidence: Curated

Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_066403)	41	W → R in IGKCD. Evidence: 1 Publication	
Natural variant (VAR_003897)	84	V → L Evidence: 1 Publication	

Sequence databases

Select the link destinations:	J00241 Genomic DNA Translation: AAA58989.1 Different initiation.
☒ EMBL	AC244205 Genomic DNA No translation available.
☐ GenBank	
☐ DDBJ	
PIR	B90562 , K3HU

Genome annotation databases

UCSC	uc061lpw.1 , human uc061lpy.1 , human
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Similar proteins

50% Identity

Protein	Similar proteins		Species	Score	Length	Source
P01834	Ig-like domain-containing protein		COLAP		151	UniRef50_P0183
	Ig-like domain-containing protein		PONAB		133	
	Burkitt's lymphoma translocation t(2;8) encoding kappa light chain, Chromosome 8q+ break point (Fragment)		HUMAN		13	

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Protein	Similar proteins		Species	Score	Length	Source
	Ig-like domain-containing protein		PONAB		120	
	IGKV1-5 isoform 1 (Fragment)		PONAB		117	
	+9					

Cross-references

Sequence databases

Select the link destinations:	J00241 Genomic DNA Translation: AAA58989.1 Different initiation.
☒ EMBL	AC244205 Genomic DNA No translation available.
☐ GenBank	
☐ DDBJ	
PIR	B90562 , K3HU

3D structure databases

Select the link destinations:	PDB entry	Method	Resolution (Å)	Chain	Positions	PDBsu
☒ PDBe	1A4J	X-ray	2.10	A/L	2-105	[>]
☐ RCSB PDB	1A4K	X-ray	2.40	A/L	2-105	[>]
☐ PDBj	1CLY	X-ray	2.50	L	2-107	[>]
	1D5B	X-ray	2.80	A/L	2-104	[>]
	1D5I	X-ray	2.00	L	2-104	[>]
	1D6V	X-ray	2.00	L	2-104	[>]
	1DFB	X-ray	2.70	L	2-107	[>]
	1GAF	X-ray	1.95	L	2-107	[>]
	1HEZ	X-ray	2.70	A/C	2-107	[>]
	1HKL	X-ray	2.68	L	2-107	[>]
	1HZH	X-ray	2.70	L/M	2-107	[>]
	1I7Z	X-ray	2.30	A/C	2-107	[>]
	1MIM	X-ray	2.60	L	2-106	[>]
	1N0X	X-ray	1.80	L/M	2-107	[>]
	1UCB	X-ray	2.50	L	2-107	[>]
	2NY7	X-ray	2.30	L	2-107	[>]
	2O5X	X-ray	2.05	L	2-107	[>]
	2O5Y	X-ray	2.85	L	2-107	[>]
	2O5Z	X-ray	2.40	L	2-107	[>]
	2QQK	X-ray	2.75	L	2-107	[>]
	2QQL	X-ray	3.10	L	2-107	[>]
	2QQN	X-ray	2.20	L	2-107	[>]
	2QSC	X-ray	2.80	L	2-107	[>]
	2R56	X-ray	2.80	L/M	2-104	[>]
	2RFX	X-ray	2.50	C	94-102	[>]
	2V6Q	X-ray	1.90	L	2-107	[>]
	3B2U	X-ray	2.58	D/G/K/L/O/R/U/X	2-105	[>]
	3B2V	X-ray	3.30	L	2-105	[>]
	3BDY	X-ray	2.60	L	2-107	[>]

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<u>3BE1</u>	X-ray	2.90	L	<u>2-107</u>	[»]
<u>3BKY</u>	X-ray	2.61	L	<u>2-107</u>	[»]
<u>3BN9</u>	X-ray	2.17	C/E	<u>2-107</u>	[»]
<u>3BQU</u>	X-ray	3.00	A	<u>2-107</u>	[»]
<u>3C08</u>	X-ray	2.15	L	<u>2-106</u>	[»]
<u>3C09</u>	X-ray	3.20	B/L	<u>2-106</u>	[»]
<u>3CFJ</u>	X-ray	2.60	A/C/E/L	<u>2-107</u>	[»]
<u>3CFK</u>	X-ray	2.60	A/C/E/G/J/L/M/O	<u>2-107</u>	[»]
<u>3CSY</u>	X-ray	3.40	B/D/F/H	<u>2-104</u>	[»]
<u>3D0L</u>	X-ray	2.35	A	<u>2-106</u>	[»]
<u>3D85</u>	X-ray	1.90	A	<u>2-107</u>	[»]
<u>3DVG</u>	X-ray	2.60	A	<u>2-107</u>	[»]
<u>3DVN</u>	X-ray	2.70	A/L	<u>2-107</u>	[»]
<u>3EYF</u>	X-ray	2.30	A/C	<u>2-107</u>	[»]
<u>3EYO</u>	X-ray	2.50	A/C	<u>2-107</u>	[»]
<u>3EYQ</u>	X-ray	2.40	C	<u>2-107</u>	[»]
<u>3IU3</u>	X-ray	2.90	B/D/L	<u>2-106</u>	[»]
<u>3O11</u>	X-ray	2.80	A/L	<u>2-107</u>	[»]
<u>3QCT</u>	X-ray	2.15	L	<u>3-106</u>	[»]
<u>3QCU</u>	X-ray	1.98	L/M	<u>3-106</u>	[»]
<u>3QCV</u>	X-ray	2.51	L/M	<u>3-106</u>	[»]
<u>3RU8</u>	X-ray	2.07	L	<u>2-107</u>	[»]
<u>3U0W</u>	X-ray	2.00	L	<u>2-107</u>	[»]
<u>3U7W</u>	X-ray	2.60	L	<u>2-107</u>	[»]
<u>3U7Y</u>	X-ray	2.45	L	<u>2-107</u>	[»]
<u>3VH8</u>	X-ray	1.80	C/F	<u>94-102</u>	[»]
<u>3WUW</u>	X-ray	2.00	C	<u>94-102</u>	[»]
<u>3X11</u>	X-ray	2.15	C	<u>94-102</u>	[»]
<u>3X12</u>	X-ray	1.80	C	<u>94-102</u>	[»]
<u>4D3C</u>	X-ray	2.62	L	<u>2-107</u>	[»]
<u>4D9R</u>	X-ray	2.42	D/L	<u>3-107</u>	[»]
<u>4HIX</u>	X-ray	2.20	L	<u>2-107</u>	[»]
<u>4NM4</u>	X-ray	2.65	L/M	<u>2-107</u>	[»]
<u>4NM8</u>	X-ray	4.00	L/M/N	<u>2-107</u>	[»]
<u>4XMP</u>	X-ray	1.78	L	<u>2-107</u>	[»]
<u>4XNY</u>	X-ray	2.30	L	<u>2-107</u>	[»]
<u>4XNZ</u>	X-ray	3.39	C/F/L	<u>2-107</u>	[»]
<u>4XXD</u>	X-ray	2.41	A/D	<u>2-107</u>	[»]
<u>4YDV</u>	X-ray	2.70	A/L	<u>2-107</u>	[»]
<u>5B38</u>	X-ray	2.30	C	<u>94-102</u>	[»]
<u>5B39</u>	X-ray	2.50	C	<u>94-102</u>	[»]
<u>5ESV</u>	X-ray	3.10	B/D/L	<u>2-107</u>	[»]
<u>5ESZ</u>	X-ray	4.19	B/L	<u>2-107</u>	[»]
<u>5VEB</u>	X-ray	2.34	B/L	<u>1-107</u>	[»]
<u>5V11</u>	electron microscopy	6.20	G/I	<u>1-107</u>	[»]
<u>6AU5</u>	X-ray	2.48	A/C	<u>1-106</u>	[»]
<u>6AXP</u>	X-ray	2.48	A/C	<u>1-106</u>	[»]

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	6AYN	X-ray	2.48	A/C	1-106	[»]
	6AZK	X-ray	2.48	A/C	1-106	[»]
	6AZL	X-ray	2.48	A/C	1-106	[»]
	6B9Y	X-ray	2.14	A	1-107	[»]
	6B9Z	X-ray	1.82	A	1-107	[»]
	6BAE	X-ray	2.14	A	1-107	[»]
	6BAH	X-ray	1.90	A	1-107	[»]
	6DCV	X-ray	1.90	A/L	1-107	[»]
	6DCW	X-ray	2.00	L	1-107	[»]
	6N2X	X-ray	3.00	K/L	2-106	[»]
	6N32	X-ray	2.20	L/M	2-106	[»]
	6N35	X-ray	1.75	K/L	2-106	[»]
	6OGE	electron microscopy	4.36	B/D	1-107	[»]
	6OKP	electron microscopy	3.28	N/P/R	1-107	[»]
SMR	P01834					
ModBase	Search...					
PDBe-KB	Search...					

Protein-protein interaction databases

IntAct	P01834 , 67 interactors
MINT	P01834

Chemistry databases

DrugBank	DB07909 , (1S,2S,5S)-2-(4-GLUTARIDYLBENZYL)-5-PHENYL-1-CYCLOHEXANOL DB07416 , (2S)-2-(BUTYRYLOXY)-3-HYDROXYPROPYL NONANOATE DB07716 , (4Z)-2,8:7,12:11,15:14,18:17,22-PENTAANHYDRO-4,5,6,9,10,13,19,20,21-NONADEXOXY-D-ARABINO-D-ALLO-D-ALLO-DOCOSA-4,9,20-TRIENITOL DB07441 , 3-{[(9-CYANO-9,10-DIHYDRO-10-METHYLACRIDIN-9-YL)CARBONYL]AMINO}PROPANOIC ACID DB08562 , 4-(4-STYRYL-PHENYLCARBAMOYL)-BUTYRIC ACID DB07882 , 4-{4-[2-(1A,7A-DIMETHYL-4-OXY-OCTAHYDRO-1-OXA-4-AZACYCLOPROPA[A]NAPHTHALEN-4-YL) -ACETYLAMINO]-PHENYLCARBAMOYL}-BUTYRIC ACID DB07784 , [4-(4-ACETYLAMINO-PHENYL)-3,5-DIOXO-4-AZA-TRICYCLO[5.2.2.0 ^{2,6}]UNDEC-1-YLCARBAMOYLOXY]-ACETIC ACID DB07375 , Etiocholanedione DB08413 , METHYL-PHOSPHONIC ACID MONO-(4-NITRO-PHENYL) ESTER DB04688 , Methylecgonine DB08289 , N-(PARA-GLUTARAMIDOPHENYL-ETHYL)-PIPERIDINIUM-N-OXIDE DB07893 , PHENYL[1-(N-SUCCINYLAMINO)PENTYL]PHOSPHONATE DB01851 , Tetrabutylammonium Ion DB08647 , TRAZEOLIDE
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Protein family/group databases

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PTM databases

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CarbonylDB	P01834
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iPTMnet	P01834
PhosphoSitePlus	P01834
SwissPalm	P01834

Genetic variation databases

BioMuta	IGKC
DMDM	125145

2D gel databases

UCD-2DPAGE	P01834
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Proteomic databases

EPD	P01834
jPOST	P01834
MassIVE	P01834
PeptideAtlas	P01834
PRIDE	P01834
ProteomicsDB	51490

Genome annotation databases

UCSC	uc061lpw.1 , human uc061lpy.1 , human
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Organism-specific databases

GeneCards	IGKC
HGNC	HGNC:5716 , IGKC
MalaCards	IGKC
MIM	147200 , gene 614102 , phenotype
neXtProt	NX_P01834
Orphanet	183675 , Recurrent infections associated with rare immunoglobulin isotypes deficiency
VEuPathDB	HostDB:ENSG00000211592.7
GenAtlas	Search...

Phylogenomic databases

InParanoid	P01834
PhylomeDB	P01834

Enzyme and pathway databases

PathwayCommons	P01834
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Reactome	R-HSA-166663 , Initial triggering of complement R-HSA-173623 , Classical antibody-mediated complement activation R-HSA-198933 , Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell R-HSA-202733 , Cell surface interactions at the vascular wall R-HSA-2029481 , FCGR activation R-HSA-2029482 , Regulation of actin dynamics for phagocytic cup formation R-HSA-2029485 , Role of phospholipids in phagocytosis R-HSA-2168880 , Scavenging of heme from plasma R-HSA-2454202 , Fc epsilon receptor (FCERI) signaling R-HSA-2730905 , Role of LAT2/NTAL/LAB on calcium mobilization R-HSA-2871796 , FCERI mediated MAPK activation R-HSA-2871809 , FCERI mediated Ca+2 mobilization R-HSA-2871837 , FCERI mediated NF-kB activation R-HSA-5690714 , CD22 mediated BCR regulation R-HSA-9664323 , FCGR3A-mediated IL10 synthesis R-HSA-9664422 , FCGR3A-mediated phagocytosis R-HSA-977606 , Regulation of Complement cascade R-HSA-983695 , Antigen activates B Cell Receptor (BCR) leading to generation o second messengers
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Miscellaneous databases

ChiTaRS	IGKC , human
EvolutionaryTrace	P01834
Pharos	P01834 , Tbio
PRO	PR:P01834
RNAct	P01834 , protein
SOURCE	Search...

Gene expression databases

Bgee	ENSG00000211592 , Expressed in lymph node and 114 other tissues
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Family and domain databases

Gene3D	2.60.40.10 , 1 hit
InterPro	View protein in InterPro IPR007110 , Ig-like_dom IPR036179 , Ig-like_dom_sf IPR013783 , Ig-like_fold IPR003006 , Ig/MHC_CS IPR003597 , Ig_C1-set
Pfam	View protein in Pfam PF07654 , C1-set, 1 hit
SMART	View protein in SMART SM00407 , IGc1, 1 hit
SUPFAM	SSF48726 , SSF48726, 1 hit
PROSITE	View protein in PROSITE PS50835 , IG_LIKE, 1 hit PS00290 , IG_MHC, 1 hit Search...
ProNet	Search...
MobiDB	Search...

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Entry information

Entry name	IGKC_HUMAN	
Accession	Primary (citable) accession number: P01834	
	Secondary accession number(s): A0A075B6H6, A0A087X130	
Entry history	Integrated into UniProtKB/Swiss-Prot:	July 21, 1986
	Last sequence update:	March 15, 2017
	Last modified:	April 7, 2021
	This is version 197 of the entry and version 2 of the sequence. See complete history.	
Entry status	Reviewed (UniProtKB/Swiss-Prot)	
Annotation program	Chordata Protein Annotation Program	
Disclaimer	Any medical or genetic information present in this entry is provided for research, educational and informational purposes only. It is not in any way intended to be used as a substitute for professional medical advice, diagnosis, treatment or care.	

Miscellaneous

Keywords - Technical term

[3D-structure](#), [Direct protein sequencing](#), [Reference proteome](#)

Documents

- [Human chromosome 2](#)
Human chromosome 2: entries, gene names and cross-references to MIM
- [Human entries with genetic variants](#)
List of human entries with genetic variants
- [Human variants curated from literature reports](#)
Index of human variants curated from literature reports
- [MIM cross-references](#)
Online Mendelian Inheritance in Man (MIM) cross-references in UniProtKB/Swiss-Prot
- [PDB cross-references](#)
Index of Protein Data Bank (PDB) cross-references



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