

# UniProtKB - Q70CQ3 (UBP30\_HUMAN)

12/7/2018

UBP30 - Ubiquitin carboxyl-terminal hydrolase 30 - Homo sapiens (Human) - USP30 gene & protein

Protein **Ubiquitin carboxyl-terminal hydrolase 30**

Gene **USP30**

Organism *Homo sapiens (Human)*

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

## Function

Deubiquitinating enzyme tethered to the mitochondrial outer membrane that acts as a key inhibitor of mitophagy by counteracting the action of parkin (PRKN): hydrolyzes ubiquitin attached by parkin on target proteins, such as RHOT1/MIRO1 and TOMM20, thereby blocking parkin's ability to drive mitophagy (PubMed:18287522, PubMed:24896179, PubMed:25527291, PubMed:25621951). Preferentially cleaves 'Lys-6'- and 'Lys-11'-linked polyubiquitin chains, 2 types of linkage that participate to mitophagic signaling (PubMed:25621951). Does not cleave efficiently polyubiquitin phosphorylated at 'Ser-65' (PubMed:25527291). Acts as negative regulator of mitochondrial fusion by mediating deubiquitination of MFN1 and MFN2 (By similarity). Evidence: By similarity

Evidence: 4 Publications



## Catalytic activity

- Thiol-dependent hydrolysis of ester, thioester, amide, peptide and isopeptide bonds formed by the C-terminal Gly of ubiquitin (a 76-residue protein attached to proteins as an intracellular targeting signal). Evidence: 1 Publication  
EC:3.4.19.12

## Activity regulation

Inhibited by the diterpenoid derivative 15-oxospiramilactone (S3). Evidence: By similarity

## Sites

Feature key	Position(s)	Description	Graphical view
Active site	<a href="#">77</a>	Nucleophile <span>Evidence: 3 Publications</span>	
Active site	<a href="#">452</a>	Proton acceptor <span>Evidence: PROSITE-ProRule annotation</span>	

## GO - Molecular function

- [cysteine-type endopeptidase activity](#) Evidence: Source: UniProtKB
- [thiol-dependent ubiquitin-specific protease activity](#) Evidence: Source: UniProtKB
- [thiol-dependent ubiquitinyl hydrolase activity](#) Evidence: Source: UniProtKB

## GO - Biological process

- [autophagy of mitochondrion](#) Evidence: Source: UniProtKB

- [mitochondrial fusion](#) Evidence: Source: UniProtKB

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- [negative regulation of mitophagy](#) Evidence: Source: Ensembl
- [protein deubiquitination](#) Evidence: Source: UniProtKB
- [protein K11-linked deubiquitination](#) Evidence: Source: UniProtKB
- [protein K6-linked deubiquitination](#) Evidence: Source: UniProtKB

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- [ubiquitin-dependent protein catabolic process](#) Evidence: Source: InterPro

## Keywords

Molecular function	<a href="#">Hydrolase</a> , <a href="#">Protease</a> , <a href="#">Thiol protease</a>
Biological process	<a href="#">Ubl conjugation pathway</a>

## Enzyme and pathway databases

Reactome	<a href="#">R-HSA-5689880</a> Ub-specific processing proteases
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## Protein family/group databases

MEROPS	<a href="#">C19.060</a>
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## Names & Taxonomy

Protein names	<p><i>Recommended name:</i>  <b>Ubiquitin carboxyl-terminal hydrolase 30</b> (EC:<a href="#">3.4.19.12</a> <span>Evidence: 1 Publication</span>)</p> <p><i>Alternative name(s):</i></p> <ul style="list-style-type: none"> <li>• Deubiquitinating enzyme 30</li> <li>• Ubiquitin thioesterase 30</li> <li>• Ubiquitin-specific-processing protease 30 <ul style="list-style-type: none"> <li>▪ <i>Short name:</i> Ub-specific protease 30</li> </ul> </li> </ul>
Gene names	<i>Name:</i> <a href="#">USP30</a> <span>Evidence: Imported</span>
Organism	<a href="#">Homo sapiens (Human)</a> .
Taxonomic identifier	<a href="#">9606</a> [NCBI]
Taxonomic lineage	<a href="#">Eukaryota</a> > <a href="#">Metazoa</a> > <a href="#">Chordata</a> > <a href="#">Craniata</a> > <a href="#">Vertebrata</a> > <a href="#">Euteleostomi</a> > <a href="#">Mammalia</a> > <a href="#">Eutheria</a> > <a href="#">Euarchontoglires</a> > <a href="#">Primates</a> > <a href="#">Haplorrhini</a> > <a href="#">Catarrhini</a> > <a href="#">Hominidae</a> > <a href="#">Homo</a>
Proteomes	<a href="#">UP000005640</a> Component: Chromosome 12

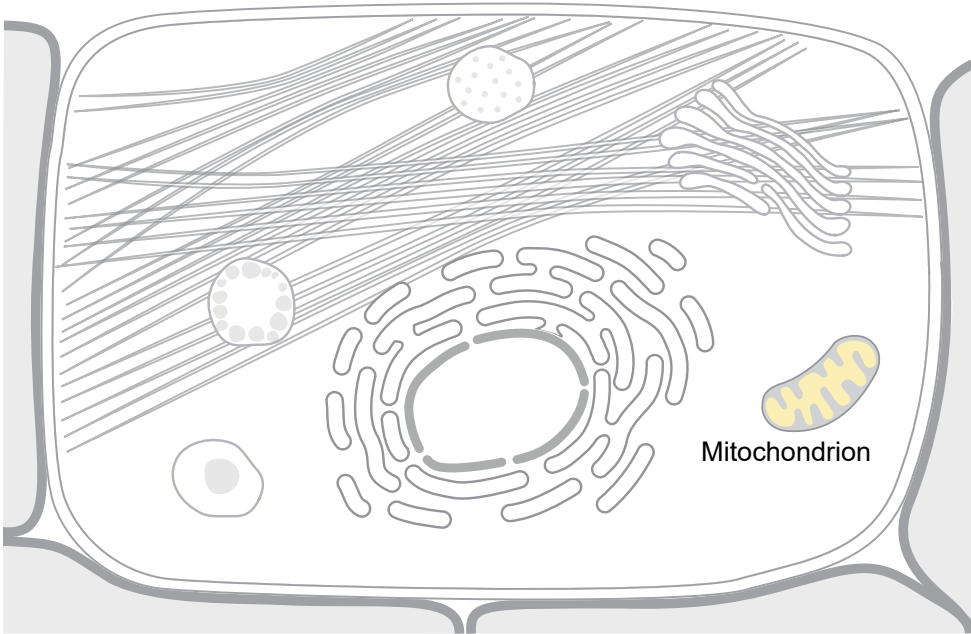
## Organism-specific databases

EuPathDB	<a href="#">HostDB:ENSG00000135093.12</a>
HGNC	<a href="#">HGNC:20065</a> USP30
MIM	<a href="#">612492</a> gene
neXtProt	<a href="#">NX_Q70CQ3</a>

## Subcellular location

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Graphics by Christian Stolte; Source: [COMPARTMENTS](#)

Manual annotation
  Automatic computational assertion

[UniProt annotation](#)

[GO - Cellular component](#)

## Mitochondrion

Mitochondrion outer membrane i

Evidence: 2 Publications

## Topology

Feature key	Position(s)	Description	Graphical view
Topological domain	<u>1 - 35</u>	Mitochondrial intermembrane Evidence: Sequence analysis	<span style="display: inline-block; width: 15px; height: 15px; background-color: orange;"></span>
Topological domain	<u>57 - 517</u>	Cytoplasmic Evidence: Sequence analysis	<span style="display: inline-block; width: 15px; height: 15px; background-color: orange;"></span>

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**Keywords - Cellular component**

## Pathology & Biotech

### Mutagenesis

Feature key	Position(s)	Description	Graphical view
Mutagenesis	<u>28</u>	R → T: No change in mitochondrial subcellular location; when associated with N-30 and N-33. <a href="#">Evidence: 1 Publication</a>	
Mutagenesis	<u>30</u>	K → N: No effect on subcellular location; when associated with N-28 and N-33. <a href="#">Evidence: 1 Publication</a>	
Mutagenesis	<u>33</u>	K → N: No effect on subcellular location; when associated with N-28 and N-30. <a href="#">Evidence: 1 Publication</a>	
Mutagenesis	<u>59 – 64</u>	RKKRRK → NNASNN: Loss of mitochondrial subcellular location. Located in the endoplasmic reticulum. <a href="#">Evidence: 1 Publication</a>	
Mutagenesis	<u>77</u>	C → S: Loss of deubiquitinase activity and impaired ability to inhibit mitophagy. Increased TOMM20 ubiquitination. <a href="#">Evidence: 3 Publications</a>	

### Organism-specific databases

DisGeNET	<a href="#">84749</a>
OpenTargets	<a href="#">ENSG00000135093</a>
PharmGKB	<a href="#">PA134971149</a>

### Polymorphism and mutation databases

BioMuta	<a href="#">USP30</a>
DMDM	<a href="#">52000872</a>

## PTM / Processing

### Molecule processing

Feature key	Position(s)	Description	Graphical view
Chain (PRO_0000080662)	<u>1 – 517</u>	Ubiquitin carboxyl-terminal hydrolase 30	

### Amino acid modifications

Feature key	Position(s)	Description	Graphical view
Cross-link	<u>235</u>	Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin) <a href="#">Evidence: 1 Publication</a>	
Cross-link	<u>289</u>	Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin) <a href="#">Evidence: 1 Publication</a>	

### Post-translational modification

Ubiquitin is hydrolyzed by parkin (PRKN) at lys-235 and lys-289, leading to its degradation. [Open Access Journal Article](#) European Central Data Protection Regulation (GDPR) that applies since 25 May 2018.

### Keywords - PTM

[Isopeptide bond](#), [Ubl conjugation](#)

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## Proteomic databases

EPD	<a href="#">Q70CQ3</a>
MaxQB	<a href="#">Q70CQ3</a>
PaxDb	<a href="#">Q70CQ3</a>
PeptideAtlas	<a href="#">Q70CQ3</a>
PRIDE	<a href="#">Q70CQ3</a>
ProteomicsDB	<a href="#">68524</a>

## PTM databases

iPTMnet	<a href="#">Q70CQ3</a>
PhosphoSitePlus	<a href="#">Q70CQ3</a>

## Expression

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### Tissue specificity

Expressed in skeletal muscle, pancreas, liver and kidney. Evidence: 1 Publication

### Gene expression databases

Bgee	<a href="#">ENSG00000135093</a> Expressed in 204 organ(s), highest expression level in cerebellar vermis
CleanEx	<a href="#">HS_USP30</a>
ExpressionAtlas	<a href="#">Q70CQ3</a> baseline and differential
Genevisible	<a href="#">Q70CQ3</a> HS

### Organism-specific databases

HPA	<a href="#">HPA016952</a>
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## Interaction

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### Protein-protein interaction databases

BioGrid	<a href="#">124238</a> , 39 interactors
DIP	<a href="#">DIP-53578N</a>
IntAct	<a href="#">Q70CQ3</a> , 14 interactors
STRING	<a href="#">9606.ENSP00000257548</a>

## Structure

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PDB Entry	Method	Resolution	Chain	Positions	Links
<b>5OHK</b>	X-ray	2.34 Å	A	64-178	<a href="#">PDBe</a>
			A	217-35	<a href="#">RCS...</a>
			A	432-50	<a href="#">PDBj</a> <a href="#">PDB...</a>
<b>5OHN</b>	X-ray	3.60 Å	A/C	64-357	<a href="#">PDBe</a>
			A/C	432-50	<a href="#">RCS...</a> <a href="#">PDBj</a> <a href="#">PDB...</a>
<b>5OHP</b>	X-ray	2.80 Å	A	64-178	<a href="#">PDBe</a>
			A	217-35	<a href="#">RCS...</a>
			A	432-50	<a href="#">PDBj</a> <a href="#">PDB...</a>

### Secondary structure



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

[Show more details](#)

### 3D structure databases

ProteinModelPortal	<a href="#">Q70CQ3</a>
SMR	<a href="#">Q70CQ3</a>
ModBase	<a href="#">Search...</a>
MobiDB	<a href="#">Search...</a>

## Family & Domains

### Domains and Repeats

Feature key	Position(s)	Description	Graphical view
Domain	<a href="#">68 – 502</a>	USP	

### Sequence similarities

Belongs to the [peptidase C19 family](#). Evidence: Curated

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[Keywords \(Domain\)](#)  
[Transmembrane](#), [Transmembrane helix](#)

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### Phylogenomic databases

eggNOG	<a href="#">KOG1867</a> Eukaryota <a href="#">ENOG410XQQ0</a> LUCA
GeneTree	<a href="#">ENSGT00550000075075</a>
HOGENOM	<a href="#">HOG000065744</a>
HOVERGEN	<a href="#">HBG079301</a>
InParanoid	<a href="#">Q70CQ3</a>
KO	<a href="#">K11851</a>
OMA	<a href="#">CNETTTH</a>
OrthoDB	<a href="#">EOG091G0D1P</a>
PhylomeDB	<a href="#">Q70CQ3</a>
TreeFam	<a href="#">TF105781</a>

## Family and domain databases

InterPro	<a href="#">View protein in InterPro</a> <a href="#">IPR038765</a> Papain_like_cys_pep_sf <a href="#">IPR001394</a> Peptidase_C19_UCH <a href="#">IPR018200</a> USP_CS <a href="#">IPR028889</a> USP_dom
Pfam	<a href="#">View protein in Pfam</a> <a href="#">PF00443</a> UCH, 1 hit
SUPFAM	<a href="#">SSF54001</a> SSF54001, 1 hit
PROSITE	<a href="#">View protein in PROSITE</a> <a href="#">PS00972</a> USP_1, 1 hit <a href="#">PS00973</a> USP_2, 1 hit <a href="#">PS50235</a> USP_3, 1 hit

## Sequence (1+)

Sequence status: Complete.

This entry has 1 described isoform and 6 potential isoforms that are computationally mapped.

Q70CQ3-1 [[UniParc](#)]

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```

      10      20      30      40      50
MLSSRAEAAM TAADRAIQRF LRTGAAVRYK VMKNWGVIGG IAAALAAGIY
      60      70      80      90     100
VIWGPITERK KRRKGLVPGL VNLGNTCFMN SLLQGLSACP AFIRWLEEFT
     110     120     130     140     150
SQYSRDQKEP PSHQYLSLTL LHLLKALSCQ EVTDDEVLDA SCLLDVLRMY
     160     170     180     190     200
RWQISSFEEQ DAHEL FHVIT SSLEDERDRQ PRVTHLFDVH SLEQQSEITP
     210     220     230     240     250
KQITCRTRGS PHPTSNHWKS QHPFHGRLTS NMVCKHCEHQ SPVRFDTFDS
     260     270     280     290     300
LSLSIPAATW GHPLTL DHCL HHFISSESVR DVVCDNCTKI EAKGTLNGEK
     310     320     330     340     350
VEHQRTTFVK QLKLGKLPQC LCIHLQRLSW SSHGTPLKRH EHVQFNEFLM
     360     370     380     390     400
MDIYKYHLLG HKPSQHNPKE NKNPGPTLEL QDGGAPTPV LNQPGAPKTQ
     410     420     430     440     450
IFMNGACSPS LLPTLSAPMP FPLPVVPDYS SSTYLFRLMA VVVHHGDMHS
     460     470     480     490     500
GHFVTYRRSP PSARNPLSTS NQWLWSDDT VRKASLQEV L SSSAYLLFYE
     510
RVLSRMQHQS QECKSEE

```

**Length:** 517

**Mass (Da):** 58,503

**Last modified:** July 5, 2004 - v1

**Checksum:** 68FA9B9BEB9CFF8DF

## Computationally mapped potential isoform sequences

There are 6 potential isoforms mapped to this entry.

<input type="checkbox"/>	Entry	Entry name		Protein names	Gene names	Length	Annotation
<input type="checkbox"/>	<a href="#">B3KUS5</a>	B3KUS5_HUMAN		Ubiquitin carboxyl-terminal hydrola...	<b>USP30</b>	486	Annotation score:
<input type="checkbox"/>	<a href="#">F5H8D3</a>	F5H8D3_HUMAN		Ubiquitin carboxyl-terminal hydrola...	<b>USP30</b>	177	Annotation score:
<input type="checkbox"/>	<a href="#">F5GXG2</a>	F5GXG2_HUMAN		Ubiquitin carboxyl-terminal hydrola...	<b>USP30</b>	95	Annotation score:
<input type="checkbox"/>	<a href="#">S4R3D1</a>	S4R3D1_HUMAN		Ubiquitin carboxyl-terminal hydrola...	<b>USP30</b>	91	Annotation score:
<input type="checkbox"/>	<a href="#">F5H3L3</a>	F5H3L3_HUMAN		Ubiquitin carboxyl-terminal hydrola...	<b>USP30</b>	146	Annotation score:
<input type="checkbox"/>	<a href="#">S4R354</a>	S4R354_HUMAN		Ubiquitin carboxyl-terminal hydrola...	<b>USP30</b>	35	Annotation score:


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The sequence [AAH04868](#) differs from that shown. Reason: Erroneous initiation. Evidence: Curated

The sequence [BAB55392](#) differs from that shown. Reason: Erroneous initiation. Evidence: Curated

## Natural variant

Feature key	Position(s)	Description	Graphical view
Natural variant (VAR_059751)	<a href="#">357</a>	<a href="#">H → R</a> . Corresponds to variant <a href="#">dbSNP:rs16939904</a>	

## Sequence databases

Select the link destinations:	<a href="#">AJ586136</a> mRNA Translation: <a href="#">CAE51936.1</a>
<input checked="" type="radio"/> EMBL	<a href="#">BC004868</a> mRNA Translation: <a href="#">AAH04868.1</a> Different initiation.
<input type="radio"/> GenBank	<a href="#">BC022094</a> mRNA Translation: <a href="#">AAH22094.2</a>
<input type="radio"/> DDBJ	<a href="#">AK027820</a> mRNA Translation: <a href="#">BAB55392.1</a> Different initiation.
CCDS	<a href="#">CCDS9123.2</a>
RefSeq	<a href="#">NP_001288104.1</a> , <a href="#">NM_001301175.1</a> <a href="#">NP_116052.2</a> , <a href="#">NM_032663.4</a> <a href="#">XP_006719716.1</a> , <a href="#">XM_006719653.3</a>
UniGene	<a href="#">Hs.486434</a> <a href="#">Hs.660996</a>

## Genome annotation databases











Ensembl	<a href="#">ENST00000257548</a> ; <a href="#">ENSP00000257548</a> ; <a href="#">ENSG00000135093</a>
GeneID	<a href="#">84749</a>
KEGG	<a href="#">hsa:84749</a>
UCSC	<a href="#">uc010sxi.3</a> human

## Keywords - Coding sequence diversity

[Polymorphism](#)

## Similar proteins

[100% Identity](#)   [90% Identity](#)   [50% Identity](#)

Protein	Similar proteins		Species	Score	Length	Source
Q70CQ3	<a href="#">Ubiquitin specific peptidase 30, isoform CRA_a</a>		<a href="#">HUMAN</a>		517	<a href="#">UniRef100_Q70CQ3</a>
	<a href="#">USP30 isoform 1</a>		<a href="#">PANTR</a>		517	
	<a href="#">Ubiquitin specific peptidase 30</a>		<a href="#">PANPA</a>		517	
	<a href="#">Ubiquitin specific peptidase 30</a>		<a href="#">GORGO</a>		517	
	<a href="#">Ubiquitin carboxyl-terminal hydrolase 30</a>		<a href="#">HUMAN</a>		486	
	<a href="#">+2</a>					

## Cross-references

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## Sequence databases

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Select the link destinations:	<a href="#">AJ586136</a> mRNA Translation: <a href="#">CAE51936.1</a>
<input checked="" type="radio"/> EMBL	<a href="#">BC004868</a> mRNA Translation: <a href="#">AAH04868.1</a> Different initiation.
<input type="radio"/> GenBank	<a href="#">BC022094</a> mRNA Translation: <a href="#">AAH22094.2</a>
<input type="radio"/> DDBJ	<a href="#">AK027820</a> mRNA Translation: <a href="#">BAB55392.1</a> Different initiation.
CCDS	<a href="#">CCDS9123.2</a>
RefSeq	<a href="#">NP_001288104.1</a> , <a href="#">NM_001301175.1</a> <a href="#">NP_116052.2</a> , <a href="#">NM_032663.4</a> <a href="#">XP_006719716.1</a> , <a href="#">XM_006719653.3</a>
UniGene	<a href="#">Hs.486434</a> <a href="#">Hs.660996</a>

### 3D structure databases

Select the link destinations:	PDB entry	Method	Resolution (Å)	Chain	Positions	PDBsum
	<a href="#">5OHK</a>	X-ray	2.34	A	<a href="#">64-178</a>	<a href="#">[&gt;&gt;]</a>
				A	<a href="#">217-357</a>	<a href="#">[&gt;&gt;]</a>
				A	<a href="#">432-502</a>	<a href="#">[&gt;&gt;]</a>
	<a href="#">5OHN</a>	X-ray	3.60	A/C	<a href="#">64-357</a>	<a href="#">[&gt;&gt;]</a>
				A/C	<a href="#">432-502</a>	<a href="#">[&gt;&gt;]</a>
	<a href="#">5OHP</a>	X-ray	2.80	A	<a href="#">64-178</a>	<a href="#">[&gt;&gt;]</a>
				A	<a href="#">217-357</a>	<a href="#">[&gt;&gt;]</a>
				A	<a href="#">432-502</a>	<a href="#">[&gt;&gt;]</a>
	ProteinModelPortal	<a href="#">Q70CQ3</a>				
SMR	<a href="#">Q70CQ3</a>					
ModBase	<a href="#">Search...</a>					
MobiDB	<a href="#">Search...</a>					

### Protein-protein interaction databases

BioGrid	<a href="#">124238</a> , 39 interactors
DIP	<a href="#">DIP-53578N</a>
IntAct	<a href="#">Q70CQ3</a> , 14 interactors
STRING	<a href="#">9606.ENSP00000257548</a>

### Protein family/group databases

MEROPS	<a href="#">C19.060</a>
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### PTM databases

iPTMnet	<a href="#">Q70CQ3</a>
PhosphoSitePlus	<a href="#">Q70CQ3</a>

### Polymorphism and mutation databases

BioMuta	<a href="#">USP30</a>
DMDM	<a href="#">52000872</a>

**Public databases** you that we have updated our [Privacy Notice](#) to comply with Europe's new General Data Protection Regulation (GDPR) that applies since 25 May 2018.

EPD	<a href="#">Q70CQ3</a>
MaxQB	<a href="#">Q70CQ3</a>
PaxDb	<a href="#">Q70CQ3</a>

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PeptideAtlas	<a href="#">Q70CQ3</a>
PRIDE	<a href="#">Q70CQ3</a>
ProteomicsDB	<a href="#">68524</a>

### Protocols and materials databases

DNASU	<a href="#">84749</a>
Structural Biology Knowledgebase	<a href="#">Search...</a>

### Genome annotation databases

Ensembl	<a href="#">ENST00000257548</a> ; <a href="#">ENSP00000257548</a> ; <a href="#">ENSG00000135093</a>
GeneID	<a href="#">84749</a>
KEGG	<a href="#">hsa:84749</a>
UCSC	<a href="#">uc010sxi.3</a> human

### Organism-specific databases

CTD	<a href="#">84749</a>
DisGeNET	<a href="#">84749</a>
EuPathDB	<a href="#">HostDB:ENSG00000135093.12</a>
GeneCards	<a href="#">USP30</a>
HGNC	<a href="#">HGNC:20065</a> USP30
HPA	<a href="#">HPA016952</a>
MIM	<a href="#">612492</a> gene
neXtProt	<a href="#">NX_Q70CQ3</a>
OpenTargets	<a href="#">ENSG00000135093</a>
PharmGKB	<a href="#">PA134971149</a>
GenAtlas	<a href="#">Search...</a>

### Phylogenomic databases

eggNOG	<a href="#">KOG1867</a> Eukaryota <a href="#">ENOG410XQQ0</a> LUCA
GeneTree	<a href="#">ENSGT00550000075075</a>
HOGENOM	<a href="#">HOG000065744</a>
HOVERGEN	<a href="#">HBG079301</a>
InParanoid	<a href="#">Q70CQ3</a>
KO	<a href="#">K11851</a>
OMA	<a href="#">CNETTTH</a>
OrthoDB	<a href="#">EOG091G0D1P</a>
PhylomeDB	<a href="#">Q70CQ3</a>
TreeFam	<a href="#">TF105781</a>

### Enzyme and pathway databases

Reactome	<a href="#">R-HSA-5689880</a> Ub-specific processing proteases
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### Miscellaneous databases

ChiTaRS	<a href="#">USP30</a> human	<a href="#">Do not show this banner again</a>
GenomeRNAi	<a href="#">84749</a>	
PRO	<a href="#">PR:Q70CQ3</a>	

SOURCE	<a href="#">Search...</a>
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## Gene expression databases

Bgee	<a href="#">ENSG00000135093</a> Expressed in 204 organ(s), highest expression level in cerebellar vermis
CleanEx	<a href="#">HS_USP30</a>
ExpressionAtlas	<a href="#">Q70CQ3</a> baseline and differential
Genevisible	<a href="#">Q70CQ3</a> HS

## Family and domain databases

InterPro	<a href="#">View protein in InterPro</a> <a href="#">IPR038765</a> Papain_like_cys_pep_sf <a href="#">IPR001394</a> Peptidase_C19_UCH <a href="#">IPR018200</a> USP_CS <a href="#">IPR028889</a> USP_dom
Pfam	<a href="#">View protein in Pfam</a> <a href="#">PF00443</a> UCH, 1 hit
SUPFAM	<a href="#">SSF54001</a> SSF54001, 1 hit
PROSITE	<a href="#">View protein in PROSITE</a> <a href="#">PS00972</a> USP_1, 1 hit <a href="#">PS00973</a> USP_2, 1 hit <a href="#">PS50235</a> USP_3, 1 hit
ProtoNet	<a href="#">Search...</a>

## Entry information

Entry name	UBP30_HUMAN	
Accession	Primary (citable) accession number: <b>Q70CQ3</b> Secondary accession number(s): Q8WTU7, Q96JX4, Q9BSS3	
Entry history	Integrated into UniProtKB/Swiss-Prot:	September 13, 2004
	Last sequence update:	July 5, 2004
	Last modified:	December 5, 2018
	This is version 138 of the entry and version 1 of the sequence. <a href="#">See complete history.</a>	
Entry status	Reviewed (UniProtKB/Swiss-Prot)	
Annotation program	<a href="#">Chordata Protein Annotation Program</a>	
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](#), [Complete proteome](#), [Reference proteome](#)

### Documents

• [WebDrops references](#)  
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- [SIMILARITY comments](#)

Index of protein domains and families

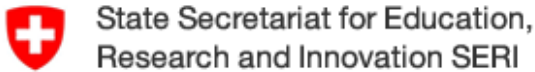
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- [Human chromosome 12](#)  
Human chromosome 12: entries, gene names and cross-references to MIM
- [Peptidase families](#)  
Classification of peptidase families and list of entries
- [Human polymorphisms and disease mutations](#)  
Index of human polymorphisms and disease mutations
- [Human entries with polymorphisms or disease mutations](#)  
List of human entries with polymorphisms or disease mutations
- [MIM cross-references](#)  
Online Mendelian Inheritance in Man (MIM) cross-references in UniProtKB/Swiss-Prot



UniProt is an ELIXIR core data resource

Main funding by: National Institutes of Health



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USP30

Contains
  Exact Match
  Begins With  
 Name
  Code
  Property
  Relationship

Source

NCIm Version: 201808 (Browser Version 2.9, using LexEVS 6.5.1)

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## Usp30 protein, human (CUI C2607345)

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### Terms & Properties

**Concept Unique Identifier (CUI):** C2607345

**Semantic Type:** Amino Acid, Peptide, or Protein

**Semantic Type:** Enzyme

**Synonyms & Abbreviations:** ([see Synonym Details](#))

ubiquitin-specific protease 30, human

Usp30 protein, human

**External Source Codes:** (none)

**Other Properties:** 

Name	Value	Source
FR	9	MSH
HM	D013869	MSH
HM	D024101	MSH
II	D010450	MSH
MDA	20081109	MSH
RN	EC 3.1.2.15	MSH
SC	1	MSH
SOS	a mitochondrial outer membrane protease	MSH
SRC	Mol Biol Cell 2008 May;19(5):1903-11	MSH
TERMUI	T729963	MSH
TERMUI	T729964	MSH
TH	NLM (2008)	MSH

**Additional Concept Data:** (none)

**URL to Bookmark:** [https://ncim.nci.nih.gov/ncimbrowser/ConceptReport.jsp?dictionary=NCI Metathesaurus&code=C2607345](https://ncim.nci.nih.gov/ncimbrowser/ConceptReport.jsp?dictionary=NCI%20Metathesaurus&code=C2607345)