

USP10

Contains
 Exact Match
 Begins With
 Name
 Code
 Property
 Relationship

Source: ALL

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

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USP10 protein, human (CUI C0967992)

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Terms & Properties

Concept Unique Identifier (CUI): C0967992

Semantic Type: Amino Acid, Peptide, or Protein

Semantic Type: Enzyme

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

ubiquitin specific protease 10, human

USP10 protein, human

USP32 protein, human

External Source Codes: (none)

Other Properties:

Name	Value	Source
FR	34	MSH
HM	D043222	MSH
II	D014452	MSH
MDA	20010725	MSH
MMR	20101215	MSH
PI	*ENDOPEPTIDASES (2001-2007)	MSH
RN	EC 3.1.2.15	MSH
SC	1	MSH
SOS	RefSeq NM_005153	MSH
SRC	Oncogene 2001 Jun 28;20(29):3869-79	MSH
TERMUI	T521043	MSH
TERMUI	T587279	MSH
TERMUI	T782269	MSH
TH	NLM (2002)	MSH
TH	NLM (2004)	MSH
TH	NLM (2011)	MSH

Additional Concept Data: (none)

URL to Bookmark: [https://ncim.nci.nih.gov/ncimbrowser/ConceptReport.jsp?dictionary=NCI Metathesaurus&code=C0967992](https://ncim.nci.nih.gov/ncimbrowser/ConceptReport.jsp?dictionary=NCI%20Metathesaurus&code=C0967992)

UniProtKB - Q14694 (UBP10_HUMAN)

Protein **Ubiquitin carboxyl-terminal hydrolase 10**

Gene **USP10**

Organism *Homo sapiens (Human)*

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

Function

Hydrolase that can remove conjugated ubiquitin from target proteins such as p53/TP53, BECN1, SNX3 and CFTR. Acts as an essential regulator of p53/TP53 stability: in unstressed cells, specifically deubiquitinates p53/TP53 in the cytoplasm, leading to counteract MDM2 action and stabilize p53/TP53. Following DNA damage, translocates to the nucleus and deubiquitinates p53/TP53, leading to regulate the p53/TP53-dependent DNA damage response. Component of a regulatory loop that controls autophagy and p53/TP53 levels: mediates deubiquitination of BECN1, a key regulator of autophagy, leading to stabilize the PIK3C3/VPS34-containing complexes. In turn, PIK3C3/VPS34-containing complexes regulate USP10 stability, suggesting the existence of a regulatory system by which PIK3C3/VPS34-containing complexes regulate p53/TP53 protein levels via USP10 and USP13. Does not deubiquitinate MDM2. Deubiquitinates CFTR in early endosomes, enhancing its endocytic recycling. Involved in a TANK-dependent negative feedback response to attenuate NF-kappaB activation via deubiquitinating IKBKG or TRAF6 in response to interleukin-1-beta (IL1B) stimulation or upon DNA damage (PubMed:25861989). Deubiquitinates TBX21 leading to its stabilization (PubMed:24845384). Evidence: 7 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

Specifically inhibited by spautin-1 (specific and potent autophagy inhibitor-1), a derivative of MBCQ that binds to USP10 and inhibits deubiquitinase activity. Regulated by PIK3C3/VPS34-containing complexes. Evidence: 1 Publication

Sites

Feature key	Position(s)	Description	Graphical view
Active site	424	Nucleophile	
Active site	749	Proton acceptor Evidence: PROSITE-ProRule annotation	

GO - Molecular function

- [cysteine-type endopeptidase activity](#) Evidence: Source: UniProtKB
- [ion channel binding](#) Evidence: Source: UniProtKB
- [p53 binding](#) Evidence: Source: UniProtKB

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

[Do not show this banner again](#)

GO - Biological process

- [autophagy](#) (Evidence: Source: UniProtKB-KW)
- [cellular response to DNA damage stimulus](#) (Evidence: Source: UniProtKB)
- [cellular response to interleukin-1](#) (Evidence: Source: UniProtKB)
- [DNA damage response, signal transduction by p53 class mediator](#) (Evidence: Source: UniProtKB)
- [negative regulation of I-kappaB kinase/NF-kappaB signaling](#) (Evidence: Source: UniProtKB)
- [protein deubiquitination](#) (Evidence: Source: UniProtKB)
- [regulation of autophagy](#) (Evidence: Source: UniProtKB)
- [translesion synthesis](#) (Evidence: Source: Reactome)
- [ubiquitin-dependent protein catabolic process](#) (Evidence: Source: InterPro)

Keywords

Molecular function	Hydrolase , Protease , Thiol protease
Biological process	Autophagy , DNA damage , DNA repair , Ubl conjugation pathway

Enzyme and pathway databases

Reactome	R-HSA-5656169 Termination of translesion DNA synthesis R-HSA-5689880 Ub-specific processing proteases
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Protein family/group databases

MEROPS	C19.018
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Names & Taxonomy

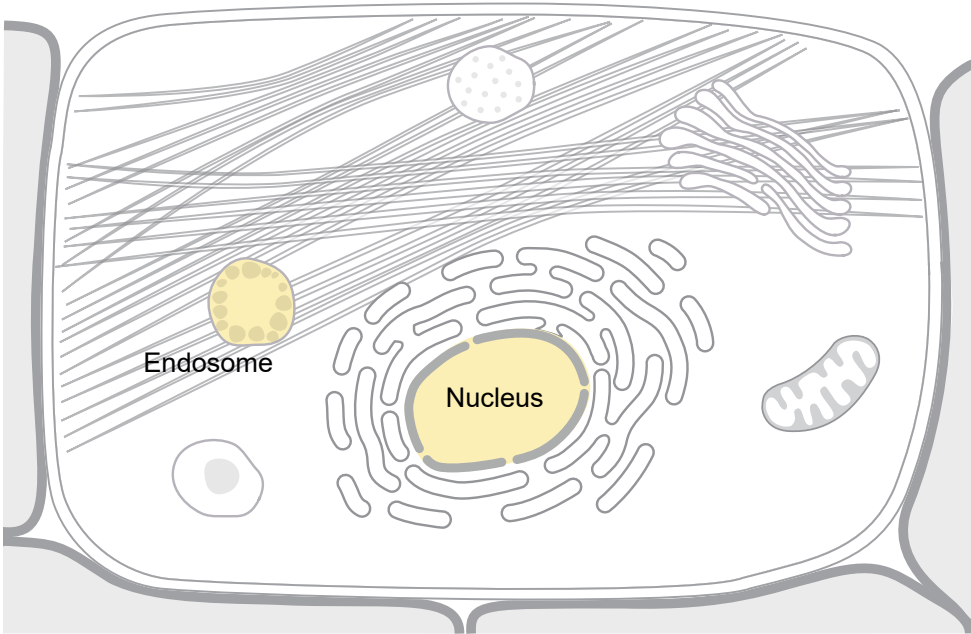
Protein names	<i>Recommended name:</i> Ubiquitin carboxyl-terminal hydrolase 10 (EC: 3.4.19.12 (Evidence: 1 Publication)) <i>Alternative name(s):</i> <ul style="list-style-type: none">• Deubiquitinating enzyme 10• Ubiquitin thioesterase 10• Ubiquitin-specific-processing protease 10
Gene names	<i>Name:</i> USP10 Synonyms: KIAA0190
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:ENSG00000103194.15
HGNC	HGNC:12608 USP10
MIM	609818 gene
neXtProt	NX_Q14694

Subcellular location

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

Manual annotation
 Automatic computational assertion

[UniProt annotation](#)

[GO - Cellular component](#)

Endosome

[Early endosome](#) i Evidence: 1 Publication

Nucleus

[Nucleus](#) i Evidence: 2 Publications

Other locations

[Cytoplasm](#) i Evidence: 1 Publication

Note: Cytoplasmic in normal conditions (PubMed:[20096447](#)). After DNA damage, translocates to the nucleus following phosphorylation by ATM (PubMed:[20096447](#)). Evidence: 1 Publication

Keywords - Cellular component

[Cytoplasm](#), [Endosome](#), [Nucleus](#)

Pathology & Biotech

Mutagenesis We'd like to inform 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.

Feature key	Position(s)	Description	Graphical view
Mutagenesis	42	T → A: Abolishes phosphorylation by ATM, when associated with A-337. Evidence: 1 Publication	do not show this banner again

Mutagenesis	42	T → E: Phospho-mimetic mutant that translocates to the nucleus in absence of genotoxic stress; when associated with D-337. (Evidence: 1 Publication)	
Mutagenesis	337	S → A: Abolishes phosphorylation by ATM; when associated with A-42. (Evidence: 1 Publication)	
Mutagenesis	337	S → D: Phospho-mimetic mutant that translocates to the nucleus in absence of genotoxic stress; when associated with E-42. (Evidence: 1 Publication)	
Mutagenesis	424	C → A: Abolishes de-ubiquitinating activity. (Evidence: 4 Publications)	

Organism-specific databases

DisGeNET	9100
OpenTargets	ENSG00000103194
PharmGKB	PA37234

Chemistry databases

ChEMBL	CHEMBL3407323
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Polymorphism and mutation databases

BioMuta	USP10
DMDM	2501458

PTM / Processing

Molecule processing

Feature key	Position(s)	Description	Graphical view
Initiator methionine		Removed (Evidence: Combined sources)	
Chain (PRO_0000080629)	2 – 798	Ubiquitin carboxyl-terminal hydrolase 10	

Amino acid modifications

Feature key	Position(s)	Description	Graphical view
Modified residue	2	N-acetylalanine (Evidence: Combined sources)	
Modified residue	24	Phosphothreonine (Evidence: Combined sources)	
Modified residue	42	Phosphothreonine; by ATM (Evidence: 1 Publication)	
Modified residue	100	Phosphothreonine (Evidence: Combined sources)	
Modified residue	211	Phosphoserine (Evidence: By similarity)	
Modified residue	226	Phosphoserine (Evidence: Combined sources)	
Modified residue	321	Phosphoserine (Evidence: Combined sources)	
Modified residue	337	Phosphoserine; by ATM (Evidence: 1 Publication)	
Modified residue	365	Phosphoserine (Evidence: Combined sources)	
Modified residue	370	Phosphoserine (Evidence: Combined sources)	
Modified residue	547	Phosphoserine (Evidence: Combined sources)	
Modified residue	563	Phosphoserine (Evidence: Combined sources)	
Modified residue	576	Phosphoserine (Evidence: Combined sources)	

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Post-translational modification

Phosphorylated by ATM following DNA damage, leading to stabilization and translocation it to the nucleus.

Evidence: 1 Publication

Ubiquitinated. Deubiquitinated by USP13. Evidence: 1 Publication

Keywords - PTM

Acetylation, Phosphoprotein, Ubl conjugation

Proteomic databases

EPD	Q14694
MaxQB	Q14694
PaxDb	Q14694
PeptideAtlas	Q14694
PRIDE	Q14694
ProteomicsDB	60132 60133 [Q14694-2] 60134 [Q14694-3]

PTM databases

iPTMnet	Q14694
PhosphoSitePlus	Q14694

Expression

Tissue specificity

Widely expressed. Evidence: 1 Publication

Induction

Following DNA damage. Down-regulated in renal cell carcinomas. Evidence: 1 Publication

Gene expression databases

Bgee	ENSG00000103194 Expressed in 219 organ(s), highest expression level in blood
CleanEx	HS_USP10
ExpressionAtlas	Q14694 baseline and differential
Genevisible	Q14694 HS

Organism-specific databases

HPA	HPA006731 HPA006749
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Interaction

Subunit structure

Found in a deubiquitination complex with TANK, USP10 and ZC3H12A; this complex inhibits genotoxic stress- or interleukin-1-beta (IL1B)-mediated NF-kappaB activation by promoting IKBKG or TRAF6 deubiquitination (PubMed:25861989). Interacts with IKBKG; this interaction increases in response to DNA damage (PubMed:25861989). Interacts with TANK; this interaction increases in response to DNA damage (PubMed:25861989). Interacts with TRAF6; this interaction increases in response to DNA damage (PubMed:25861989). Interacts with ZC3H12A; this interaction increases in response to DNA damage (PubMed:25861989). Interacts with G3BP, which may regulate its function

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(PubMed:[11439350](#)). Interacts with p53/TP53 (PubMed:[20096447](#)). Interacts with SNX3 (PubMed:[18632802](#)). Interacts with CFTR (PubMed:[19398555](#)). Interacts with TBX21 (PubMed:[24845384](#)). Evidence: 6 Publications

Binary interactions

Q14694 has binary interactions with 3 proteins

Subcellular location ▼

Reset filters

HUMAN
HUMAN
HUMAN
HUMAN

GO - Molecular function

- ion channel binding Evidence: Source: UniProtKB
- p53 binding Evidence: Source: UniProtKB

Protein-protein interaction databases

BioGrid	114554 , 69 interactors
ELM	Q14694
IntAct	Q14694 , 29 interactors
MINT	Q14694
STRING	9606.ENSP00000219473

Chemistry databases

BindingDB	Q14694
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Structure

3D structure databases

ProteinModelPortal	Q14694
ModBase	Search...
MobiDB	Search...

Family & Domains

Domains and Repeats

Feature key	Position(s)	Description	Graphical view
Domain	415 – 795	USP	

Region

Feature key	Position(s)	Description	Graphical view
Region	2 – 100	Interaction with p53/TP53 Evidence: 1 Publication	

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Belongs to the [peptidase C19 family](#). [USP10 subfamily](#). Evidence: Curated

Phylogenomic databases

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eggNOG	KOG1871 Eukaryota ENOG410XSIH LUCA
GeneTree	ENSGT00550000074994
HOGENOM	HOG000285959
HOVERGEN	HBG059823
InParanoid	Q14694
KO	K11841
OMA	ILSCTTS
OrthoDB	EOG091G023X
PhylomeDB	Q14694
TreeFam	TF323203

Family and domain databases

InterPro	View protein in InterPro IPR009818 Ataxin-2_C IPR038765 Papain_like_cys_pep_sf IPR001394 Peptidase_C19_UCH IPR018200 USP_CS IPR028889 USP_dom
Pfam	View protein in Pfam PF07145 PAM2, 1 hit PF00443 UCH, 1 hit
SUPFAM	SSF54001 SSF54001, 1 hit
PROSITE	View protein in PROSITE PS00972 USP_1, 1 hit PS00973 USP_2, 1 hit PS50235 USP_3, 1 hit

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**.

This entry has 3 described isoforms and 9 potential isoforms that are computationally mapped.

Isoform 1 (identifier: **Q14694-1**) [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
MALHSPQYIF	GDFSPDEFNQ	FFVTPRSSVE	LPPYSGTVLC	GTQAVDKLPD
60	70	80	90	100
GQEYQRIEFG	VDEVIEPSDT	LPRTPSYSIS	STLNPQAPEF	ILGCTASKIT
110	120	130	140	150
PDGITKEASY	GSIDCQYPGS	ALALDGSSNV	EAEVLENDGV	SGGLGQRERK
160	170	180	190	200
KKKKRPPGY	SYLKDGDDSD	ISTEALVNGH	ANSAVPNSVS	AEDAEFMGDM
210	220	230	240	250
PPSVTPRTC	SPQNSTDSVS	DIVPDSPPFG	ALGSDTRTAG	QPEGGPGADF
260	270	280	290	300
GQSCFPAEAG	RDTLSRTAGA	QPCVGTDTTE	NLGVANGQIL	ESSGEGTATN
310	320	330	340	350
GVELHTTESI	DLDPTKPESA	SPPADGTGSA	SGTLPVSQPK	SWASLFHDSK
360	370	380	390	400
PSSSSPVAYV	ETKYSPPAIS	PLVSEKQVEV	KEGLVPVSED	PVAIKIAELL
410	420	430	440	450
ENVTLIHKPV	SLQPRGLINK	GNWCYINATL	QALVACPPMY	HLMKFIPLYS
460	470	480	490	500
KVQRPCSTP	MIDSFVRLMN	EFTNMPVPPK	PRQALGDKIV	RDIRPGAAFE
510	520	530	540	550
PTYIYRLLTV	NKSSLSEKGR	QEDAEEYLG	ILNGLHEEML	NLKKLLSPSN
560	570	580	590	600
EKLTISNGPK	NHSVNEEEQE	EQGEGSEDEW	EQVGPRNKTS	VTRQADFVQT
610	620	630	640	650
PITGIFGGHI	RSVVYQSSK	ESATLQPFFT	LQLDIQSDKI	RTVQDALESL
660	670	680	690	700
VARESVQGYT	TKTKQEVEIS	RRVTLEKLPP	VLVLHLKRFV	YEKTGGCQKL
710	720	730	740	750
IKNIEYPVDL	EISKELLSPG	VKNKNFKCHR	TYRLFVVYH	HGNSATGGHY
760	770	780	790	
TTDVFQIGLN	GWLRIDDQTV	KVINQYQVVK	PTAERTAYLL	YYRRVDLL

Length: 798

Mass (Da): 87,134

Last modified: November 1, 1997 - v2

Checksum: E6BA77E2B5CE2B3F

Isoform 2 (identifier: **Q14694-2**) [[UniParc](#)]

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

1-1: M → MCKSKDTVLSVCALYWRKGIQSHTPLIGAWRRRGKQREQPEDRGVPMKRAA

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Length: 846

Mass (Da): 92,597

Checksum: 01C2CD6FC3709AE4

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Isoform 3 (identifier: **Q14694-3**) [[UniParc](#)]

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

1-6: MALHSP → MPWLSPGGIGNote: No experimental confirmation available.[Show »](#)**Length**: 802**Mass (Da)**: 87,533**Checksum**: CBA33D0F268AEF5A

Computationally mapped potential isoform sequences

There are 9 potential isoforms mapped to this entry.

<input type="checkbox"/>	Entry	Entry name		Protein names	Gene names	Length	Annotation
<input type="checkbox"/>	J3KT19	J3KT19_HUMAN		Ubiquitin carboxyl-terminal hydrola...	USP10	208	Annotation score:
<input type="checkbox"/>	H3BVF1	H3BVF1_HUMAN		Ubiquitin carboxyl-terminal hydrola...	USP10	158	Annotation score:
<input type="checkbox"/>	H3BNA1	H3BNA1_HUMAN		Ubiquitin carboxyl-terminal hydrola...	USP10	150	Annotation score:
<input type="checkbox"/>	H3BQP1	H3BQP1_HUMAN		Ubiquitin carboxyl-terminal hydrola...	USP10	110	Annotation score:
<input type="checkbox"/>	Q68D90	Q68D90_HUMAN		Ubiquitin carboxyl-terminal hydrola...	USP10 DKFZp686E14181	62	Annotation score:
<input type="checkbox"/>	H3BQC6	H3BQC6_HUMAN		Ubiquitin carboxyl-terminal hydrola...	USP10	141	Annotation score:
<input type="checkbox"/>	H3BNS8	H3BNS8_HUMAN		Ubiquitin carboxyl-terminal hydrola...	USP10	76	Annotation score:
<input type="checkbox"/>	H3BNL0	H3BNL0_HUMAN		Ubiquitin carboxyl-terminal hydrola...	USP10	35	Annotation score:
<input type="checkbox"/>	H3BNP1	H3BNP1_HUMAN		Ubiquitin carboxyl-terminal hydrola...	USP10	63	Annotation score:

Sequence caution

The sequence [CAD97644](#) differs from that shown. Reason: Erroneous initiation. Evidence: Curated

Experimental Info

Feature key	Position(s)	Description	Graphical view
Sequence conflict	<u>108</u>	A → V in BAG61546 (PubMed: 14702039). Evidence: Curated	
Sequence conflict	<u>263</u>	T → A in BAG61546 (PubMed: 14702039). Evidence: Curated	

Natural variant

Feature key	Position(s)	Description	Graphical view
Regulation (VAR_01589)	<u>200</u>	S → P Evidence: 1 Publication Corresponds to variant dbSNP:rs1862792	
Natural variant (VAR_015860)	<u>203</u>	S → P Evidence: 1 Publication Corresponds to variant dbSNP:rs2326391	

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Corresponds to [dbSNP:rs1862792](#) Do not show this banner again

Natural variant (VAR_015861)	204	V → L	Evidence: 1 Publication	Corresponds to variant dbSNP:rs1812061
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Alternative sequence

Feature key	Position(s)	Description	Graphical view
Alternative sequence (VSP_038868)	<u>1 – 6</u>	MALHSP → MPWLPSGIG in isoform <u>3</u> . Evidence: 1 Publication	
Alternative sequence (VSP_038869)	<u>1</u>	M → MCSKDTVLSVCALYWRKGIQ SHTPLIGAWRRGKQREQPED RGVPMKRAA in isoform <u>2</u> . Evidence: 1 Publication	

Sequence databases

Select the link destinations:	<input checked="" type="radio"/> EMBL D80012 mRNA Translation: BAA11507.1 <input type="radio"/> GenBank AK299618 mRNA Translation: BAG61546.1 <input type="radio"/> DDBJ AK315570 mRNA Translation: BAG37945.1 <input type="radio"/> GenBank AL162049 mRNA Translation: CAB82392.2 <input type="radio"/> DDBJ BX537402 mRNA Translation: CAD97644.1 Different initiation. AC009116 Genomic DNA No translation available. AC025280 Genomic DNA No translation available. BC000263 mRNA Translation: AAH00263.1
CCDS	CCDS45537.1 [Q14694-1] CCDS62004.1 [Q14694-3]
RefSeq	NP_001259004.1 , NM_001272075.1 [Q14694-3] NP_005144.2 , NM_005153.2 [Q14694-1]
UniGene	Hs.136778

Genome annotation databases

Ensembl	ENST00000219473 ; ENSP00000219473 ; ENSG00000103194 [Q14694-1] ENST00000570191 ; ENSP00000457411 ; ENSG00000103194 [Q14694-3]
GeneID	9100
KEGG	hsa:9100
UCSC	uc002fii.4 human [Q14694-1]

Keywords - Coding sequence diversity

Alternative splicing, Polymorphism











Similar proteins

90% Identity 50% Identity

Protein	Similar proteins	Species	Score	Length	Source
Q14694	Ubiquitin specific peptidase 10	MACFA	●○○○○	804	UniRef90_Q14694
	Ubiquitin specific peptidase 10	PANTR	●○○○○	803	
	Uncharacterized protein	MACMU	●●○○○	802	
	Uncharacterized protein	CERAT	●○○○○	802	
	Uncharacterized protein	MACNE	●○○○○	802	

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Protein	Similar proteins		Species	Score	Length	Source
Q14694-2	Ubiquitin specific peptidase 10		MACFA		810	UniRef90_Q14694-2
	Ubiquitin specific peptidase 10		SAIBB		803	
	Ubiquitin specific peptidase 10		CALJA		802	
	Ubiquitin specific peptidase 10		AOTNA		802	
	Ubiquitin specific peptidase 10		Cebus capucinus imitator		802	
	+39					

Cross-references

Sequence databases

Select the link destinations:	<input checked="" type="radio"/> EMBL <input type="radio"/> GenBank <input type="radio"/> DDBJ	D80012 mRNA Translation: BAA11507.1 AK299618 mRNA Translation: BAG61546.1 AK315570 mRNA Translation: BAG37945.1 AL162049 mRNA Translation: CAB82392.2 BX537402 mRNA Translation: CAD97644.1 Different initiation. AC009116 Genomic DNA No translation available. AC025280 Genomic DNA No translation available. BC000263 mRNA Translation: AAH00263.1
CCDS		CCDS45537.1 [Q14694-1] CCDS62004.1 [Q14694-3]
RefSeq		NP_001259004.1 , NM_001272075.1 [Q14694-3] NP_005144.2 , NM_005153.2 [Q14694-1]
UniGene		Hs.136778

3D structure databases

ProteinModelPortal	Q14694
ModBase	Search...
MobiDB	Search...

Protein-protein interaction databases

BioGrid	114554 , 69 interactors
ELM	Q14694
IntAct	Q14694 , 29 interactors
MINT	Q14694
STRING	9606.ENSP00000219473

Chemistry databases

BindingDB	Q14694
ChEMBL	CHEMBL3407323

Protein family/group databases

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PTM databases

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iPTMnet	Q14694
PhosphoSitePlus	Q14694

Polymorphism and mutation databases

BioMuta	USP10
DMDM	2501458

Proteomic databases

EPD	Q14694
MaxQB	Q14694
PaxDb	Q14694
PeptideAtlas	Q14694
PRIDE	Q14694
ProteomicsDB	60132 60133 [Q14694-2] 60134 [Q14694-3]

Protocols and materials databases

DNASU	9100
Structural Biology Knowledgebase	Search...

Genome annotation databases

Ensembl	ENST00000219473 ; ENSP00000219473 ; ENSG00000103194 [Q14694-1] ENST00000570191 ; ENSP00000457411 ; ENSG00000103194 [Q14694-3]
GeneID	9100
KEGG	hsa:9100
UCSC	uc002fii.4 human [Q14694-1]

Organism-specific databases

CTD	9100
DisGeNET	9100
EuPathDB	HostDB:ENSG00000103194.15
GeneCards	USP10
H-InvDB	HIX0173245
HGNC	HGNC:12608 USP10
HPA	HPA006731 HPA006749
MIM	609818 gene
neXtProt	NX_Q14694
OpenTargets	ENSG00000103194
PharmGKB	PA37234
HUGE	Search...
GenAtlas	Search...

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Phylogenomic databases

eggNOG	KOG1871 Eukaryota ENOG410XSIH LUCA	Do not show this banner again
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GeneTree	ENSGT00550000074994
HOGENOM	HOG000285959
HOVERGEN	HBG059823
InParanoid	Q14694
KO	K11841
OMA	ILSCTTS
OrthoDB	EOG091G023X
PhylomeDB	Q14694
TreeFam	TF323203

Enzyme and pathway databases

Reactome	R-HSA-5656169 Termination of translesion DNA synthesis R-HSA-5689880 Ub-specific processing proteases
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Miscellaneous databases

ChiTaRS	USP10 human
GeneWiki	USP10
GenomeRNAi	9100
PRO	PR:Q14694
SOURCE	Search...

Gene expression databases

Bgee	ENSG00000103194 Expressed in 219 organ(s), highest expression level in blood
CleanEx	HS_USP10
ExpressionAtlas	Q14694 baseline and differential
Genevisible	Q14694 HS

Family and domain databases

InterPro	View protein in InterPro IPR009818 Ataxin-2_C IPR038765 Papain_like_cys_pep_sf IPR001394 Peptidase_C19_UCH IPR018200 USP_CS IPR028889 USP_dom
Pfam	View protein in Pfam PF07145 PAM2, 1 hit PF00443 UCH, 1 hit
SUPFAM	SSF54001 SSF54001, 1 hit
PROSITE	View protein in PROSITE PS00972 USP_1, 1 hit PS00973 USP_2, 1 hit PS50235 USP_3, 1 hit
ProtoNet	Search...

Entry information

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Accession	Primary (citable) accession number: Q14694 Secondary accession number(s): B2RDJ8 Q9NSL7
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Entry history	Integrated into UniProtKB/Swiss-Prot:	November 1, 1997
	Last sequence update:	November 1, 1997
	Last modified:	December 5, 2018
	This is version 183 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

[Complete proteome](#), [Reference proteome](#)

Documents

- [SIMILARITY comments](#)
Index of protein domains and families
- [Human chromosome 16](#)
Human chromosome 16: 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



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