

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
P70398	USP9X_MOUSE	Mus musculus	Ubiquitin carboxyl-terminal hydrolase 9X	43.098091	NaN	S374;S375;S588;S1600;S2443;T2540;S2547;T2551	37507081;33300544;22645316;40885482	MTATTRGSPVGGNDNQQAPDQGS QPPLQONQTTSSPDSSNENSPATPPD EQGQGDAPPQIEDEEPAPFHTDLAK LDDMINRPRWVVPVLPKGELEVLLE AAIDLSKKGLDVKSEACQRFRRDGL TISFTKILTDEAVSGWKFEIHRCIINN THRLVELCVAKLAQDWFPLELLAM ALNPHCKFHINYNGTRPCESVSSVQ LPEDELFAFSPDPRSPKGWLVDLLN KFGTLNGFQILHDFINGSALNVQII AALIKPFGQCYEFLTLHTVKKYFLPII EMVPPQFLENLTDEELKKEAKNEAK NDALSMIIKSLKNLASRVPGQEETVK NLEIFRLKMLRLLQISSFNGKMNAL NEVNVKISSVSYTHRHGSEDEEW LTAERMAEWIQNNILSIVLRDSLH QPQYVEKLEKILRFVIKELTLQDL DNIWAAQAGKHEAIVKNVHDLAKL AWDFSPEQLDHLDFDCFKASWTNAS KKQREKLELIRLAEDDKDGVMAH KVLNLLWNLAHSDDVPDIMDLALS AHIKILDYSCSQRDRTQKIOWIDRFI EELRTNDKWVIPALKQIREICSLFGE APQNLQSQRSPHVFYRHDLINQLQ HNHALVTLVAENLATYMESMRMYG RDNEDYDPQTVRLGSRYSHVQEVQE RLNFLRFLLLKDGQLWLCAPQAKQIW KCLAENAVYLCDREACFKWYSKLM GDEPDLDPDINKDFFESNVQLDPS LLTENGMKCFERFFKAVNCREGKLV AKRRAYMDDLELIGLDYLWRVVIQ SNDDIACRAIDLLEKIYTNLGPRLQV NQVVIHEDFIQSCFDRLKASYDTLCV LDGDKDSINCARQEAVRMVRVLTVL REYINECSDSYHEERTILPMSRAFR GKHLSFIVRFPNQGRQVDDLEVWS HTNDTIGSVRRCILNRKANVAHTKI ELFVGGELIDPGDDRKLIGQLNLKDK SLITAKLTQISSNMPSSPDSSSDSST GSPGNHGNHYSDBGPNPEVESCLPG VIMSLHPRYISFLWQVADLGSSLNM PPLRDGARVLMKMLPDPSTTIEKLR AICLDHAKLGESSLSPSLDSLFFGPS ASQVLYLTVVYALLMPAGAPLTDDSD SDFQFHFLKSGGLPLVLSMLTRNNF LPNADMETRRGAYLNALKIAKLLLT AIGYGHVRAVAEACQPGVEGVNPM SVNQVTHDQAVVLSALQSI PNSSECM LRNVSVRLAQQISDEASRYMPD ICVIRAIQKIWTSGCGGLQVLFSPNE EVTKIYEKTNAGNEPDLLEDEQVCC E ALEVMTLCPALIPALDALSKEKAW QTFIIDLLLHCHSKTVRQVAQEQFFL MCTRCCMGHRPLFFITLLFTVLGS TARERAKHSGDYFTLLRHLNAYN SNINVPNAEVLNNEIDWLKRIRDD VKRTGETGVEETILEGHLGVTKELLA FQTPKPKFHIGCEKGGANLIKELIDD FIFPASNVYLYQYMRNGELPAEQAIPV CGSPATINAGFELLVALAVGCVRNK QIVDSLTEMYYIGTAITTCALTEWE YLPPVGRPPKGFVGLKNAGATCYM NSVIOQLYMIPSIIRNGILAIEGTGSDV DDDMSGDEKQDNESNVDPRDDVFG YPQQFEDKPPLSKTEDRKEYNIGVLR HLQVIFGHLAASRLQYVPRGFWKQ FRLWGPVNLREQHDALFFNSLV DSLDEALKALGHPAMLSKVLGGSFA DQKICQGCPHRYECEESFTTLNVDIR NHQNLLDSLEQYVKGDLLEGANAY HCEKCNKKVDTVKRLLIKKLPVLA QLKRFDYDWERECAIKFNDFEFPR ELDMPEYTVAGVAKLEGDNVNPES QLIQONEQSESEKAGSTKYRLVGVL VHSGQASGGHYYSIIQRNGDGEK NRWYKFDGDDVTECKMDDDEEMK NQCFGGEYMGVEFDHMMKRMSYR RQKRWWNAYILFYERMDTIGHDDE VIRYISEIAITTRPHQIVMPSAIERSVR KQNVQFMHNRMQYSLEYFQFMKK	True	False	4.53	2.249	1.959	1.687	1.246

