

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
Q93008	USP9X_HUMAN	Homo sapiens	Ubiquitin carboxyl-terminal hydrolase 9X	5.532164	NaN	S588;T590;S1600;S2443;T2540;S2547;T2551	37217939;30379171;38665916;34725712;40914422;34019948;35138101;28510447	MTATTRGSPVGGNDNQOAPDQGS QPPLQONQTSPPDSSNENSPPATPPD EQGGDAPPQLEDEEPAFPHDTLAK LDDMINRPRWVVPVLPKGELEVLLE AAIDLKSKGLDVKSEACQRFRRDGL TISFTKILTDEAVSGWKFEIHRCIINN THRLVELCVAKLSQDWFFLELLAM ALNPHCKFHINGRPCESVSSSVQ LPEDELFAFSPDRSPKGLVLDLLN KFGTLNGFQILHDFRINGSALNVQII AALIKPFGQCYEFLTLHTVKYFLPII EMVPPQFLENLTDEELKKEAKNEAK NDALSMIIKSLKNLASRVPGQEETVK NLEIFRLKMLRLLQISSFNGKMNAL NEVNKVISSVSYTHRHGNPEEEEW LTAERMAEWIQNNILSIVLRDSLH QPQYVEKLEKILRFVIKALTLQDL DNIWAAQAGKHEAIVKNVHDLAKL AWDFSPQLDHLDFCFKASWTNAS KKQREKLELIRRLAEDDKDGVMAH KVLNLLWNLAHSDDVPVIMDLALS AHIKILDYSCSQRDRDTQKIOWIDRFI EELRTNDKWVIPALKQIREICSLFGE APQNLSTQQRSPHFVYRHDLINQLQ HNHALVTLVAENLATYMESMRLYA RDHEDYDPQTVRLGSRYSHVQEVQE RLNFLRFLKDGQWLWCAPQAKQIW KCLAENAVYLCREACFKWYSKLM GDEPDLDPDINKDFFESNVLQLDPS LLENGMKCFERFFKAVNCREGKLV AKRRAYMDDLELIGLDYLWRVVIQ SNDDIASRAIDLKELYTNLGPRLQV NQVVIHEDFIQSCFDRLKASYDTLCV LDGDKDSVNCARQEAVRMVRVLT LREYINECSDYHEERTILPMSRAFR GKHLSEVVRFPNQGROVDDLEVWS HTNDTIGSVRRCILNRKANVAHTKI ELFVGGELIDPADDRKLIQNLKDKK SLITAKLTQISSNMSPDSSSDSST GSPGNHGNHYSDBGPNPEVESCLPG VIMSLHPRYISFLWQVADLGSLSNM PPLRDGARVLMKLMPPDSTTIEKLR AICLDHAKLGESSLSPSLDLSFFGPS ASQVLYLTVVYALLMPAGAPLADD SSDFQFHFLKSGGLPLVLSMLTRNN FLPNADMETRRGAYLNALKIALLLT AIGYGHVRAVAEACQPGVEGVNPMPT QINQVTHDQAVVLQSAEQSIPNPSE CMLRNVSVRLAQQISDEASRYMPDI CVIRAIQKIIWASGCGSLQLVFSPNE EITKIYEKTNAGNEPDLLEDEQVCEA LEVMTLFCFALIPTALDALSKEKAWQ TFIIDLLHCHSKTVRQVAQEQFFLM CTRCCMGHRPLLFFITLLFTVLGSTA RERAKHSGDYFTLLRHLLNYAYNSN INVPNAEVLNNEIDWLKRIRDDVK RTGETGIEETILEGHLGVTKELLAFO TSEKKFHIGCEKGGANLIKELIDDFIF PASNVYLQYMRNGELPAEQAIPVCG SPPTINAGFELLVALAVGCVRNLKQI VDSLTEMYIYGTAITTCEALTEWEYL PPVGPVPPKGFVGLKNAGATCYMNS VIQQLYMIPSIRNGILAIEGTGSDVDD DMSGDEKQDNESNVDPRDDVFGYP QQFEDKPALSKTEDRKEYNIGVLRH LQVIFGHLAASRLQYVPRGFWKQF RLWGEVNLREQHDALEFFNSLVD SLDEALKALGHPAMLKVLGGSFAD QKICQGCPHRYECEESFTLLNVDIR NHQNLDSLEQYVKGDLLEGANAY HCEKCNKKVDTVKRLLIKLPVLAI QLKRFYDWERECAIKFNDFEFPR ELDMEPYTVAGVAKLEGDNVNPES QLIQQSEQSESETAGSTKYRLVGLV HSGQASGGHYYSYIIRNNGDGGERN RWYKFDDGDVTECKMDDDEEMKN QCFGGEYMGEVFDHMMKRMSYRR QKRWWNAYILFYERMDTIDQDELI RYISELAITTRPHQIIMPASAIERSVRK QNVQFMHNRMQYSMEYFQFMKLL	True	False	5.0	3.929	2.016	1.764	1.364

