

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasm memt
A2AN08	UBR4_MOUSE	Mus musculus	E3 ubiquitin-protein ligase UBR4	33.214419	NaN	S178;S181;S212;T370;T905;S1401;S1646;S1651;S1746;S1753;S1876;S1902;T2712;S2716;S2719;T2721;T2941;S2949;S2603	33300544;37507081;22645316	MATSGGEEAAAAAPGAPATGQDT TPGWEVAVRPLLSASYSAFEMKELP QLVASVIESESEILHHEKQYEPFYSS FVALSTHYITTVCSLIPRNQLQSVA ACKVLIEFSLRLLENPDEACAVSQKH LILLIKGLCTGCSRLDRTEIITFTAMM KSAKLPQTVKTLSDVEDQKELASPV PELRQKEVQMNFLNQLTSVFNPRTV PSPPISPQALVEGENDEQSSPDQVSA AKTKSVFIAQNVASLQELGGSEKLLR VCLNLPYFLRYINRFQDAVVANSFFI MPATVADATAVRNGFHSLLVIDVTMA LDTLSLPVLEPLNPSRLQDVTVLSLS CLYAGVSVATCMAILHVGSAAQVVRT GSTSSKEDDYESDAATIVQKCLEIYD MIGQAISRRRAGGEHFQNFQLLGA WCLLNSLFLILNLSPTALADKGGKEK DPLAALRVRDILSRTEGEGVSPKLG GKGHGQFGVLSVILANHAIKLLASLF QDLQVEALHKGWETDGPVAVLSIMA QSTSTQRIQLRIDSVPLTNLLLTLLST SYRKACVLRQRKGSMSDASASTD SNTYYEDDFSSTEEDSSQDDSEPI GQWFEETISPSKEAAPPPIPPPPPL ESSPRVKSPNKQASGEKGNILASRK DPELFSGLASNILNFITSMNLSRNS FIRSYLSASLSEHHMATLASIIEVD KDGLKGSDEDAALYHFNHSLVT SDLQSPNLQNTLLQQLGVAPFSEGP WPLYIHPQGLSVLSRLLLIWQHKAG AQGDVPECLKVWDRFLTTMKQN ALQGVVPSSETEDLNVEHLQLLLI SFSEKGRRAILTMLVQSIQELSVNM EVQMRTAPLILARLLIFDYLLHOYS KAPVYLFEQVQHNLSPFGWASGS QDSSRRANTPLYHGFEVEENWS KHFSSDAAPQPRFYCVLSTEASEED LNRLDSEACEVLFSPVKYDELYSSL TTLAAGSQLDTRRKEKKNVTALE ACALQYYFLILWRILGILPPSKTYMN QLAMNSPEMSECDILHTRLRWSRL RISSYVSWIKDHILKQGMKPEHAGS LIELAASKCSSVKYDVEIVEYFARQI SSFCSIDCTAVLQLHEIPSLQSIYTL AAVSKVQVSLDEHFSKMAAETDPHK SSEITKNLLPATLQLIDTYASFTRAYL LQNLNEEGSTEKPSQEKLHGFAAVL AIGSSRCKANTLGPTLVQNLPSVQS VCESWNNINTNEFPNIGSWRNAFA NDTIPSESYISAVQAAHGLTLCGQSL PLAASLKHTLLSLVRLTGDIVWSDE MNPQAVIRTLPLLESSTESAAEIS SNSLERILGPAESDEFARVYEKLIT GCYNILANHADPNISGLDESILEECL QYLEKQLESSOARKAMEEFFSDGGE LVQIMMATANEDLSAKFCNRVLKFF TKLFQLTEKSPNPSLLHLCGSLAQLA CPEPVRQAOWLTRMTTSPPKDSDQL EVIQENRQLQLLTYIVRENSQVGE GVCVLLGTLTPMATDMLANGDGT GFPELMVVMATLASAGQAGHLQL HNAAVDWLGRCKKYLKQKNVVEKL NANVMHGKHMVLELECTCHIMSYLA DVTNALSQSNQGQPSHLSVDGGER AIEVDSWVEELAVEEEDSQAEDSD EDSLCNKCLTFTTITQKEFMNQHWY HCHTCKMVDGCVCTVCAKVCHKD HEISYAKYGSFFCDGAKEDGSCLA LVKRTPSGMSSTMKESAFQSEPRV SESLVRHASTSPADKAKVTISDGKVT DEEKPKKSSLCRTVEGCREELQNA NFSFAPLVLDMLSFLMDAIQTNFQQ ASAVGSSSRAQQALSELHTVDKQVE MTDQLMVPTLGSQEGAFENVRMNY SGDQGTIROLISAHVLRVAMCVL SSPHGRROHLAVSHEKGTIVLQLS ALLKQADSSKRKLTTRLASAPVFFT VLSLTGNPCKEYLAVCGLDKCHVL TFSSSGSVSDHLVHPQLATGNFIK AVWLPGSQTELAIVTADFVKIYDL	False	False	3.732	3.943	1.598	1.558	1.215	2.797

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