

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
B1AWL2	ZN462_MOUSE	Mus musculus	Zinc finger protein 462	25.875327	S694;S1762	S351;S355;S681;S1083;S1159;S2161;S2166	30059200	MEVLQCDGCDFRAPSYEDLKAHIQD VHTAFILQPTDVAEDNDDEPLSGSM NASNQTEVEFSSIKDEFVIAEDLPGQ SATALGSGGYGHSPGGYGHITPN PKPTNKFQCKFCVRYFRSKNLLIE HTRKVVHGAQAEESPTGPPVPGSLNY NIMMHEGFGKVFSCQFCTYKSPRR ARIKHQKMYHKNLSKESTAPPAPA PLPDPVLPVSLQDPCKELPAEVVER SILESMVKPLTKSRGNFCCEWCSYQ TPRRERWCDHMMKHKRSMVKILSS IROQEGPNVSEAQNDNEPSPSNTST YLSMNAASREMPNANVSNFRGSMG NSIMRPNSSSTSKFSSSSMYPQMKP KSPHNSGLVNLTERSRYGMSDMTN SSADLDTNSMLNDSSSEDLNEVD SENGLSVLDHQASGLSAEQLMGSD GNKLETKGIPFRFRFMNRFQCPFCP FLTMHRRSISRHIENIHLSGKTAVYK CDECPFTCKSSLKLGAKQCHTGTST DWDVTNSQSESLSSLNEMVMVSYE SSSINGRKSQVMLDPLQQQPPQPP PPLPPPPPPSQPLPQPPPPPLQSPH QVPPPTQQPPPTQAPPLHPYKCTM CSYSTMTLKGLRVHQHKSFCDN LPKFEGQPSLPLENETDSDHPSSSN TVKKSQTSILGLSSKNFVAKANRK LASDFPLDLSPVKKRTRIDEIASNLQ SKINQTKLQEDAIINVEDDEEEEDD NEVEIEVELDREEEATDPIMEVPTAF SAQQIWARDASEAQKEPNYSITHD YTATNGAEIELTLEDEEYDYGSSAS MKDQVSNAAALLNTQPAIYGTSPSNE NTDFGDSGRLYYCKHCFNNSAR SVSTHYQRMHPYIKFSFRYILDND HSAVYRCLECYIDYTNFEDLQQHYG EHHPEAMNVLNFDHSDLIYRCRFCS YTSPNVRSLMPHYQRMHPTVKINN AMIFSSYVVEQQEGLNAESQTLREIL NSAPKSMATSTPVARGGGLPATFNK NTPPKTFTPECESQKDPVNTVVVY DCDVCSFASPNMHVSVLVHYQKKHP EEKASYFRIQKTRMVMVSDRGSALS QLSFEVGA PMSPKMSNMGSPPPQ PPPPDLSEIYCKKCHS YSNR SVVGV LVHYQKRHPEIKVTAKYIRQAPPTAA MMRGAEGLQDSPRPPAPLQLNSSE RDCPPVETEMFFCQHC DYGNRTVK GVLIHYQKKHRDFKANADVIRQHTA TIRSLCDRNQK PASCVLLPASGMER DKTKLRALKCRQCSYSPYFYALRK HIKDDHPALKATVTSIMRWAFLDGLI EAGYHCEWCIYSHMEPSGLLLHYQR RHPEHYVDYTYMATKLWAGPDPSSP TLTMSAEAKTYRCRDCVFEAVSIWDI TNHYQAFHPWAMNGDES VLLDIIKE KDGVDKALLAPELIGPVN CENSIPN PLPEQEAEC PEDARLSPEKSIHLASA NPAISSTPYQCTVCQSEYNNLHGLLT HYGKHPGMKVKAA DFAQDIDINPG AVYKCRHCPYINTRIHGVLTHYQKR HPAIKVTAEDFVHDVEQSADISQND VEETSRIKQGYGAYRCKLCPYTHGT LELKIHYEKYHNQPEFDVFSPPPQ LPVLEPEITTEVSPSQVSVTEEEVG EDPMSTA HFSTSHLVSHTVFRCQLC KYFCSTRKGIARHYRIKHNNVRAQP EGKNLNFKALCAYTNPIRKGLAAH YQKRHDIDAYYTHCLAASRTISDKPN KVIIPSPKDDSPQLSEELRAVEKK KCSLCSFQSFSSKGVSHYMKRHPG VFPKQHASKLGGYFTAVYADEHEK PPLMEEERS SFERA VEVEGAQDIE WLPFRICIKCFKLSFSTAELLCMHYT DHHSRDLK RDFVILGSGPRFQNSTF QCKHCD SKLQSI AELTSHLNIHNEE FQKRAKRQERRKQLLSKQKYADGAF ADFKQERPFGLHEEVPIKIKERVVG YCKKFCVEVHPTLRAICNHLRKHVQ YGSVPAVSAVKGLRSHERSHLALA	None	None	None	None	None	None	None		

MFTREDKYSQYCSFVSAFRHNLDR
HMQTHHGHKPFRCCLCSFKSSYN
SRLKTHILKAHAGEHAYKCSWCSFS
TMTISOLKEHSLKVHGKALTLPRI
VSLSSHAPHSSQKATPAEEVEDSN
DSSYSEPPDVQQQLNHYQSAALARN
KSRVSPVPPSGTAAGTEQKAEAVLH
CEFCFSSGYIQSIRRHRYDKHGGK
KLFKCKDCSFYTGFKSAFTMHVEAG
HSAVPEEGPKDLRCPLCLYHTKYKR
NMIDHIVLHREERVVPIEVCRSKLSK
YLOGVVFRCDKCTFTCSSDESLOQH
IEKHNELKPYKCQLCYETKHTEEL
DTHLRDEHKVSRNFELVGRVNDQ
LEQMKIESSSSEDEDKDDMSSK
AEDRELMRFADRGPGVNTKRFPC
EFCGRAFSQGSEWERHVLRHGMSL
HDTNQVSRNEIHTKEMVEESMLP
SIEAKEDDEPIDFPLKSETVTICVV
AADKSLEDAEAKNE