

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
A0A1P8ARB7	A0A1P8ARB7_ARATH	Arabidopsis thaliana	NaN	27.144759	NaN	NaN	28154133	MTPSKVAGHTRFLLHSFHSDSDVDSI ALQLSQFVDFGVETSIPVLKTCLDCE TARRSHPNLQLEKVVSLFKHVLK LSNLATLLPHALNDFELTQESVDDL TTTLNFSISENIGFALALDFERLDA KTTGRNLLAQIEQLCANTGQILSSE LIHSVLSFLRKSEDLMSHLDSFLQFL SSAQPRDDFSFALTPMLAQQVHEAP VFRSMDFHDTSDADNDLDAILAEIDK EVSVDLMGELGCGFTADAQQCKEI LSSFAPLGEATISRVGNVSRTCADL EDNQTTFTFTVALGSCIPTELPTR SWNVLDLVDTIKQLAPGISWRKVIEN LDHDGFDIPNMEFSFFMRYKAAAC KEPFLDAVCGSVWKNMDGQLSFL KHAIAPPEVFTFMHSPRKLVIYDN MHSQEQQLGLSNHAWLSLDDLVDL CQLAERGHAVLVSSLLQYPLTQCPR TLLGMTHIKTAYNLIQREVVSAILPV IITSPQDSGFIHNLWHQNAELVLWGI IDAQHLKADSMRLRIEICHELKILSVV LESVPVSSIRLAVLASLRGLLDIEN WLPNCLYMYKDLFAEECLKFVKNV HFSESDDFRAKIFHPSDPLSDLHLE ATTSLLKVLKAHDNAITSSQLVEIE KVNAAILDCNPKLQNGEAKDSSAPN AYGDDVEAEANAYFHQMFSSHLSV DAMVQMLSRYSKESLVPREKLIFECM IANLFEYRFFPKYPERQLKIASILFG SVIKHQLISSLTGLMALRLVLDLRLK PADSKMFLFGSKALEQFVNRLVELP QYCNHILQISHLRSTHPELVTVIEQA LSRISSGNLESDASVSHPGPSQSFPG NGELSGSGIGQPALQLSSPLQLQOK NEVPSVPSNEAKPLPSTTSVDVS VNPKNPGIPTSSSTSTGFVRPARATT STRFGSALNIETLVAAAERRENAIEA PPSDVQDKVFSFIHNNISTTNIESKGGKE FAEILPQYYPWFAQYMMVKRASIE PNFHDLYLKFLDKVDSKLLFKEILO NTYENCKVLLGSELIKSSSEERSLLK NLGSWLGRLTIGRNYVLRAREIDPKS LIVEAYEKGLMAVIPFTSKVLEPCQ NSIAYQPPNPWTMAILGLLAEIYSMP NLKMNLFKFDIEVLFKNLGVEMKEV VPTSLDKDRKREIDGNPDFSNKDPG VTQISQPMIPEPKTISPLKQIDLPLD VANSPTDVPKLLSQYVAPQRVYT NTLMDEEKVATLGLPEQLPSPQGLF QSTPSPSISQQLSAAALPNIGNHVVI NQKLSAFGMHFPFQRVVPLAMDRAI KEIVSGIVQRSVCACQTTKELVLKDY ALEPDESRIYNAAHLMVASLAGSLA HVTCKEPLRTSISGHLRNSLQGLNIS NDALEQIVQLVTNDNLDLGCIAIEQ AATEKAIQTIDADIAQQLLRRKHRD GAGSSFFDPNLSQNSVSVFIPESLRP KPGHLSLSQQRVYEDFVQHPWQKQ STQTSGLSAASSSSGDVALGSGYG PVSGKVASEFLSNAGNARMDMVS PSDISVDGFESSPVLSLSSQVDPAGD SSSLQFTKSLPTSELNLAESSDAATK ETGTSLQTLTSAATMERLGASNITQP SLSTRDALDKCQIVTKMEELVANN AGDDEIQAVISEVPEIILRCISRDEAA FAVAQKAFKALYENASSNLHVSNANL AILVAIRDVCKRVVKELTSWVIYSEE DRKLNKIDITIGLIQRELLSLAEYNVH MAKHLDGRNKTATDFAILLQSLV TESSVISELHSLVDALAKLASKSGS SESLQQLIDHIRNPVTNTAGLSDSST GNDNNDROKDEKVACNTTNTTEEST SLDYVESDPAGFQNRVSTLTKFNWYQ ICELPGANETACSQYVHLHQTGLL KGDDTTESFFRILLELSVAHCISSEDI NSGAVQSPQPPSPFLIIDMYAKLV	None	None	None	None	None	None	None		

FSILKYFPEQESSRFLLEIMADTV
RFIQKDAEDKKTSLNSKPYFRLF
LLDLCSLDPGTDGANFQVLTAFANA
FHALQPLKIPAFSFAWLELVSHRSF
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SCIQMRNIISSFPNMRPDPSTPN
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GMQAIQQLQAGETQAQNVVALQMF
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PNNHTHYFSFIMLYLFFESDQEIIQE
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IKNPRYSFWKQAFIRCAPEIEKLFES
VARSCGGLKPVDEGMVSGGWVSDN
SH