

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
A0A178VTI3	A0A178VTI3_ARATH	Arabidopsis thaliana	NaN	27.144759	NaN	NaN	28154133	MTSSSHNIELEAAKFLHKLIQDSDK EPAKLATKLYVILQHMKTSKGENTM PYQVISRAMDTVVNQHGLDIEALKS SCLPHPGGTQTEDSGSAHLAGSSQA VGVSNEGKATLVENEMTKYDAFTSG RQLGGSNSASQTFYOGSGTQSNRSF DRESPNLDSTSGISQPHNRSETMN QRDVKSSGKRKRKGESSLWDQNM NSQIFDQSHKIDDQTGEVSKIEMPGN SGDIRNLHVGLSSDAFTTPOCGWQS SEATAIRPAIHKEPGNNVAGEGFLPS GSPFREQLKQLRAQCLVFLALRNG LVPKLLHVEIALRNTFREEDGFRGE LFDPKGRHTHTSSDLGGIPDVSALLSR TDNPTGRLEDEMDFSSKETERSRLGE KSFANTVFDGQKLLASRIPSSQAQT QVAVSHSQLTFSPGLTKNTPSEMVG WTGVKTNLDSLSAVQLDEFHSSAD EEEGNLQPSPKYTMQKWMGRQN KRLLVDRSWSLKQKADQAIGSRFN ELKESVSLDDISAKTKSVIELKKLQL LNLQRRLRSEFVYNFFKPIATDVEHL KSYKHKHGRRIKQLEKYEQKMKEE RQRRIRERQKEFFGGLVHKEKLED LFKVRRERLKGFNRYAKEFHKRKER LHREKIDKIQREKINLLKINDVEGYL RMVQDAKSDRVKQLLKEKTEKYLQKL GSKLKEAKLLTSRFENEADERTSN ATDDETLIENEDESQAKHYLESNE KYYLMAHSIKENINEQPSSLVGGKL REYQMNGLRWLVSLYNNHLNGILA DEMGLGKTQVISLICYLMETKNDR GPFLVVVPSVLPGWQSEINFWAPSI HKIVYCGTPDERRKLFKEQIVHQKF NVLLTTYEYLMNKHDRPKLSKIHHW YIIIDEGHRIKNASCKLNADLKHYVS SHRLLLTGTPLONNLEELWALLNFL LPNIFNSSEDFSQWFNPKPFQSNGES SAEEALLSEENLLIINRLHQVLRPF VLRRLKHKVENELPEKIERLIRCEAS AYQKLLMKRVEDNLGSGNAKSRV HNSVMELRNICNHPYLSQLHSEEV NNIIPKHFLLPPIVRLCGKLEMLDRML PKLKATDHRVLFSTMTRLLDVDMED YLTLLKGYKYLRLDGQTSGGDRGALID GFNKSGSPFFIFLLSIRAGGVGNLQ AADTVILFDTDWNQVDLQAQARAH RIGQKDVLLVRFETVNSVEEQVRA SAEHKLGVANQSITAGFFDNNTSAE DRKEYLESLLRESKKEEDAPVLDDD ALNDLIARRESEIDIFESIDKORKEN EMETWNTLVHGPGSDSFHIPSIPS RLVTEDDLKLLYETMKLNDVPMVAK ESTVGMKRKDGSMGGLDTHQYGRG KRAREVRSYEEKLTEEEFEKLCQTES PDSPOGKGESESLANDTNSNIPVE NSSDTLLPTSPTQAITVQPMEPVVRPQ SHTLKEETQPIKRGRGRPKRTDKALT PVLSAVSRTQATGNAISSAATGLDF VSSDKRLEAASHPTSSLALTSPLDLSG PPGFQSLPASPAPTPIRGRGRGRSRG RGAGRGRRVEGVLHGNSSSITORTE TATSLASDAEATKFAIPRSASEIVSR VPKANEGSTSNPDQVSPVHSATTAL RSDKAADKDLDAPPGFDSGSHVQTL NVLENSSERKAFVKKRPLIQGVSS QHPPGNKQPLDLPVSTSTLLGGGP VQNQNAVSSVCDGSKSPSEGRITYA LQGVTTAPSDATLPMSSQPSDATLP MSSQPVGSTVEAQEANVPSLPAALP AKRRVRNLP SRGETPKRQKRRGQP LPATDASSARSTGLTPQIEVKVGNLS GTKAKFDVAKEQPHFSQSVAPDIH SSGSLSQEIRRDTSGTGGARKQTA DVTDVARVMKEIFSETSLLKHVGE PSATTRTNVPAQSPGEMNLHTVET	None	None	None	None	None	None	None		

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SDRLDGESDGTIVATVEGTCVESNS
LVAEESNIEVPKDNEDV