	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	A0A1I9LPZ1	A0A1I9LPZ1_ARATH	Arabidopsis thaliana	NaN	27.144759	NaN	NaN	28154133	MVVLSRPRSSQNAGQKLSVPPPLNL PSLRKEHERVDSSGSSFHSGGGIAG SGTRPASSGIGWSKPAATATDGDIG NHTGEGVTRGSNGLNTSLASRVGAA EPMERAFHHVEKVATLRGEDFPSLK ASLPSASVSGQKQKEGLNQKQKQAA GEDFSKEPRGVSGMSSSLVDMRPQ NQSGRSRLGNELSESPSFSDGLHSS EHVRKKEYFAGPLPLVRLAPRSDWA DDERDTSHGLRDRDRDHGYSKNEP FWDRGFDLRPHVLPQKHAASNVFD KPGQRENEIAKSSLTQVRPVSGGGR EANAWRVSSPLQNEGANHNNYGAR PSSRGREAAKKSNYVLSSSRENVWN NSGAREAPYQHGGRQPWNNNMDS SSNRGTYNRDGYGIEHQNRDKRSFF KSDKPHVEDPFMKDFGDSGFDVHD PFPVLGVTKKKKEALKQTEFHDPVR ESFEAELERVQKMQEEERRRIIEEQ ERVIELARTEEEERLRLAREQDERQ RRLEEEAREAAFRNEQERLEATRRA EELRKSKEEEKHRLFMEEERRKQAA KQKLLELEEKISRRQAEAAKGCSSSS TISEDKFLDIVKEKDSADVVDWEDS ERMVDRITTSSTLDLSVPMRSFESN ATSQFSRDGSFGFPDRQKPTWRKED IESGSNSRFIPQNLENVPHSPQEEFF GTAGYLSAPSYFKPGFPEHSIDQSW RIPGDGRTHGRNYGMESESRENFG EQYGDPGWGQSQGRPRHGPYSPYP EKLYQNPEGDDYYPFGRPRYSVRQP RVLPPPQESRQKTSFRSEVEHPGPST SIGGINYSHKGRTNSTVLANYIEDHH VLPGSGIDEHRRFDTKLTGRCDSQS SLSVTSPPDSPVHLSHDDLDESADS TVLPTSRMGEDAGLLEKGGAPIISSD IGKDSLMMATGSVSCWDNEEWTLD SNERLQEQEEYDEDEDGYQEEDKIH GVDENIDLAQELEEMHLDDKDSNL VLGFNEGVEVEIPSDDFEKCQRNSE STFPLHQHTVDSLDDERPSIETSRGE QAAQPAVVSDPLGMHNASRTFQGA ETTMQNLTVHPNIGRQSFEVASKVD STSNSTVSTHPVIPLHSAALHPSSLQ TAIPPVSTTSAQMEEPVKFQFGLFSG PSLIPSPFPAIQIGSIQMPLPLHPQFG SSLTHMQQPQPPLIQFGQLPYTSPIS QGVLPPPHHSVVQANGLSTYALNQN PGSLVTVQLGQGNSANLLARNAATS VSHPQLSVLRRPTNVSDEGTLKNAN LPPARASIEAAVSPQKQPELSGNSQL PSRKMSHGKSNFAERQSGYQVQTD TSAVRNSGLRSSGTAEVSRVDSGGN RRYRRQRVEFRVRESNWPSSDENR NGNGRAQTSTKIGSRKYVVSNKSQK QALDSSASGLNAMQKTVSGGSFEN RLGKDAVVKNPLSPNSGQANLKRN MVSEKEIDAPLQIGIVRVFEQQGIEA PSDDDDFIEVRSKRQMLNDRREQR EKEIKEKSQAAKAFRKPRSTFQNNT TAARSNRSPPASRAANNKQFNPVSN RQTLAPIGTPSPKIDSHVDEKSGSNK STQESSALPVIPKNDQNPASGFVFS NKNKVLDNSHTPVGTWGNQLTYQP VMALTQSQLDEAMKPVSHLSCVSVE NGANRISESNSTSTSVVPKNNTFSS STSPINSLLAEGKIQFGAVTSSTVIPP CGGRTEKDSSLYFEKDNKHRNPSST GIEICEAEAEAAASAIAVAAITNDETS GNALSTGSVLPVETKIYGGTELDDGA ASGTVGGQTSRSKAEESLIVSLPADL SVDTPISLWPQLPSPHNSNQMITHF PPGPPHYPFYDVNPMLRGPIFAFGP HHDAGATQSQSQKGPVTVSGPPTT WQQQGHSGVDSFYAPPAGFTGPFLT PPGAIPGVQGPPHMFVYNHFAPVGQ	None	None	None	None	None	None	None	None	None

									FGGLSFMGTTYIPSGKQPDWKHNP NVSSSPVGGDGDVNNPNVASMQCN IVPASLQHLPMPMFDPSPFQSSSQE MPIRARWPYMPFSGPPTMQMQKQQ EGTDGSNLPSPQFNNNMLPPPPPN RYPNVQASTVVDAMVDSSNAYSSTT GAPPAKPTSTLSDPNSNNTQNPNGP GFKPPQQQQQQSSQEKNTQSQHVG GPSHHHQHQHHQNRRSGYHGRNQ PMARERGFPNNPKVKQIYVAKQTGN SCASASSTTTTTSPSI									