	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	extracellul region
0	Q2TAZ0	ATG2A_HUMAN	Homo sapiens	Autophagy-related protein 2 homolog A	18.379595	NaN	S765;S878;S892;S894;S1266;S1301;S1309;S1402	30379171	MSRWLWPWSNCVKERVCRYLLHH YLGHFFQEHLSLDQLSLDLYKGSVA LRDIHLEIWSVNEVLESMESPLELVE GFVGSIEVAVPWAALLTDHCTVRVS GLQLTLQPRRGPAPGAADSQSWASC MTTSLQLAQECLRDGLPEPSEPPQP LEGLEMFAQTIETVLRRIKVTFLDTV VRVEHSPGDGERGVAVEVRVQRLEY CDEAVRDPSQAPPVDVHQPPAFLHK LLQLAGVRLHYEELPAQEEPPEPPLQ IGSCSGYMELMVKLKQNEAFPGPKL EVAGQLGSLHLLLTPRQLQQLQELL SAVSLTDHEGLADKLNKSRPLGAED LWLIEQDLNQQLQAGAVAEPLSPDP LTNPLLNLDNTDLFFSMAGLTSSVA SALSELSLSDVDLASSVRSDMASRR LSAQAHPAGKMAPNPLLDTMRPDS LLKMTLGGVTLTLLQTSAPSSGPPDL ATHFFTEFDATKDGPFGSRDFHHLR PRFQRACPCSHVRLTGTAVQLSWEL RTGSRGRRTTSMEVHFGQLEVLECL WPRGTSEPEYTEILTFPGTLGSQASA RPCAHLRHTQILRRVPKSRPRRSVA CHCHSELALDLANFQADVELGALDR LAALLRLATVPAEPPAGLLTEPLPAM EQQTVFRLSAPRATLRLRFPIADLRP EPDPWAGQAVRAEQLRLELSEPQFR SELSSGPGPPVPTHLELTCSDLHGIY EDGGKPPVPCLRVSKALDPKSTGRK YFLPQVVVTVNPQSSSTQWEVAPEK GEELELSVESPCELREPEPSPFSSKR TMYETEEMVIPGDPEEMRTFQSRTL ALSRCSLEVILPSVHIFLPSKEVYESI YNRINNDLLMWEPADLLPTPDPAAQ PSGFPGPSGFWHDSFKMCKSAFKL ANCFDLTPDSDSDDEDAHFFSVGAS GGPQAAAPEAPSLHLQSTFSTLVTVL KGRITALCETKDEGGKRLEAVHGEL VLDMEHGTLFSVSQYCGQPGLGYFC LEAEKATLYHRAAVDDYPLPSHLDLP SFAPPAQLAPTIYPSEEGVTERGASG RKGQGRGPHMLSTAVRIHLDPHKN VKEFLVTLRLHKATLRHYMALPEQS WHSQLLEFLDVLDDPVLGYLPPTVIT ILHTHLFSCSVDYRPLYLPVRVLITAE TFTLSSNIIMDTSTFLLRFILDDSALY LSDKCEVETLDLRRDYVCVLDVDLL ELVIKTWKGSTEGKLSQPLFELRCS NNVVHVHSCADSCALLVNLLQYVM STGDLHPPPRPPSPTEIAGQKLSESP ASLPSCPPVETALINQRDLADALLDT ERSLRELAQPSGGHLPQASPISVYLF PGERSGAPPPSPPVGGPAGSLGSCSE EKEDEREEEGDGDTLDSDEFCILDA PGLGIPPRDGEPVVTQLHPGPIVVRD GYFSRPIGSTDLLRAPAHFPVPSTRV VLREVSLVWHLYGGRDFGPHPGHR ARTGLSGPRSSPSRCSGPNRPQNSW RTQGGSGRQHHVLMEIQLSKVSFQ HEVYPAEPATGPAAPSQELEERPLSR QVFIVQELEVRDRLASSQINKFLYLH TSERMPRRAHSNMLTIKALHVAPTT NLGGPECCLRVSLMPLRLNVDQDAL FFLKDFFTSLVAGINPVVPGETSAEA RPETRAQPSSPLEGQAEGVETTGSQ EAPGGGHSPSPPDQQPIYFREFRFTS EVPIWLDYHGKHVTMDQVGTFAGLL IGLAQLNCSELKLKRLCCRHGLLGV DKVLGYALNEWLQDIRKNQLPGLLG GVGPMHSVVQLFQGFRDLLWLPIEQ YRKDGRLMRGLQRGAASFGSSTASA ALELSNRLVQAIQATAETVYDILSPA APVSRSLQDKRSARRLRRGQQPADL REGVAKAYDTVREGILDTAQTICDVA SRGHEQKGLTGAVGGVIRQLPPTVV KPLILATEATSSLLGGMRNQIVPDAH KDHALKWRSDSAQD	False	False	3.733	2.936	1.869	3.787	1.705	1.529	1.289