

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum
E9QAT4	SC16A_MOUSE	Mus musculus	Protein transport protein Sec16A	46.058797	T60;S70;S121;S127;T2028;S2030;S2034	S311;S581;S591;S609;S611;S614;T615;S617;S1087;S1223;S1245;T1340;S1342;S1362;S1365;S1371;S1374;S1377;S1384;S1588;S1616;T1922;S1951;S2043;S2063;S2077;S2094;S2291	22645316;40885482	MOPPPQAVPSGVAGPPPAGNPRSM FWANSFYRKPANNAPVAPITRPLQ VTDPFANRQTLQNTPVGSSSSKSSL PNLPGPALSVSFQWPGPLVPTNAG DSSTGLHEPLSGTLSQPRADASFPP ASTPSSLPGLEVSRNAEADPSSGHE VQMLPHSAHYIPGVGPEQLGGQM NDSGSGPDQPMNRHAPHDGAVTHA ASPFLPQPMPGQWGAQGGPQPS YQHSPYLEGPVQNMGLQAASLPH FPPSSLHQGPGHESHAPQTFTPAS LASGEGNEIVHQSKNHPLSSFPFK HTFEQNSRIGNMWASPELKONPGV NKEHLLDPAHVNPFTQGNSPENQA HHPVAATNHALQEASGALSMFF QGEETENEENLSSEKAGLDKRLNLD SFSSTSRLGHPPPGASGVYQAFPRG PSSEAAQEGDAQPYFSQSVGVRLDK QSTVPPANDAWGDVPGTTRCASGP QCENVENLEFVONQEVLPRETLSDV PFPLSDQIRYGLPLGPAASRPATVGL TRGGGLNLEAPDTPLHPTRPDSVSS SYSSHSHRSPPGSARPQELVGTFIQQ EVGKLEDDTSGSFFKQIDSSPVGGET DEVTGSQNCSSLSQPSTPSPPKPT GVFQTSANSSFEVVKSHLVGVKPV ADRANMVVEVRGTQYCPKRRRAV APPDATSGNLEQPPDNMETPCAPQA CPLPLSTTGEAGQLVSNACTPLDVT RPVDPKRPSARAQGPVKCESPATT WAQNELPDPFGGNVLLAAPALYVP VKPKPSEVVHHEKGMGQKAWKQ GSVPPLQNDPPGASENLENPPKVG EEEALPVQASSGYASLLSPPTESLH NQPVLIAQPDQSYNLAQPINFSVLL NPNEKNQSWGDAVVGERSIVSNW ALGGDPEERAALSGVPASAVTGASLP SSIPQNCAPQGSSEMIASQSASW LVQQLSPOTPQSPHPNAEKGPSEFV SSPAGNTSVMLVPPASSTLVPSNKN AKHSSNQEEAVGALDFTLNRTLENP VRMYSPPSDGPASQQLPNNHPRQS GPLLHNQDHFYQQVTKDAQDQHRL ERAQPELVPPRQNSPQVPQASCPE PSNPESPTQGGQSESLAQPPASPASV NTGQLLPQPPQASSASVSTNSSQA AVRSEQLWLHPPPPNTFGPAPODLA SYYYRPLYDAYQSQYPSFYPSDPGT ASLYYQDMYGLYEPYRYPYDSSASAY AENHRYSEPERPSSRASHYSDQLAP RQGYPEGYYNSKSGWSSHSYDYANY YSGQYDYGDPNRWDYRYSRLRDP TWDRRYWDSEHDPYRKDHYAYS RPEKCDHWRYDPRFTGSFDDDAEI HRDPYGEADRRIHSEHSARSLRS THSLPSRRSSLSSHSHQSIYRSHH VTGGSFEAPHAGSFHGDYAYGTYA SNFSGAHGFPEYSYPADTSWPAVEQ VPSRPTSPEKFTVPHVCARFGPGGQ LLKVIPNLPSEGOPALVEIHSLETLL QHTPEQEMRSFPGPLGKDDTHKV DVINFAQNKATKCLQNESLIDKESAS LLWKFIILLCRQNGTVVGTDAIALL RDHRTVWLPKSPNEANLIDFTNEA VEQVEEESGEAQLSFLTDSQTVTTS VLEKETERFRELLLYGRKKDALESA MKNGLWGHALLLASKMDSRTHARV MTRFANSLPINDPLQTVYQLMSGR MPAASTCCGDEKWGDWRPHLAMV LSNLNNMDVESRTMATMGDTLAS KGLLDAAHFCYLMAQVGFVYTKKT TKLVLIGSNHSLPFLKFATNEAIQRT EAYEYAQSLGAHTCSLPNFQVFKFIY LCRLAEMGLATQAFHYCEVIKSVL TQPGAYSPVLISQLTOMASQLRFLDP QLKEKPEEESFVEPAWLVLQHQHVER QIQEGTVLWSQDGTPEQCRITSGS EVEQSDGPGLNQQAGPADNPLLM PSTEPLMHGVQLLPTAPQTLDPDQGP AHLSRVPMFVPMRSRPLELSPAYG	True	True	4.528	3.234	1.349	5.0

