

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
O15027	SC16A_HUMAN	Homo sapiens	Protein transport protein Sec16A	33.297277	S836;T1001;S1012;S1014;S1016;S1019;S1022;S1025;S1244;S2159	S296;S314;S331;S559;S569;S587;S589;S592;T593;S595;S1069;S1207;S1229;S1305;T1325;S1327;S1347;S1350;S1356;S1359;S1362;S1369;S1573;S1601;T1907;S1939;S1964;S2022;S2042;T2054;S2056;S2073;S2083;S2271;S2291	34229054;34019948;35254053;31373491;30397120;31637018;35138101;29237092;33214551;28314751;35289036;29351928;30620550;37340703;27655845;23301498;35132862;32574038	MQPPPTVPVPSGMAGPPPAGNPRSVF WASSPYRRRRANNAAVAPTTCPLOQP VTDPPAFSRQALQSTPLGSSSKSSPP VLQGPAPAGFSQHPGLLVPHTHARD SSQGPCPEPLPGPLTQPRAHASPFSG ALTSPAPPPEMNRSAEVEGSPSEPE VQTLPYLPHYIPGVDPETSHGGHPH GNMPGLDRPLSRQNPHDGVTTPAA SPSLPQPGLQMPGQWGPVQGGPQP SGQHRSPCPEGPVPSGVPCATSVPH FPTPSILHQPGGHEQHSPLVAPPAAL PSDGRDEVSHLQSGSHLANNSDPE STFRQNPRIVNHWASPELRQNPVK NEHRPASALVNPLARGDSPENRTH HPLGAGAGSGCAPLEADSGASGALA MFFQGGETENEENLSSEKAGLSGQ ADFDDFCSSPGLGRPPATHVVGAGS LCQALLPGPSNEAAGDVWGDASTG VPDASGSQYENVENLEFVQEQEVLP SEPLNLDPSSPSDQFRYGPLPGPAVP RHGAVCHTGPADATLHTVHPDSVSS SYSRSRSHGRLSGSARPQELVGTFIQQ EVGKPEDEASGSFFKQIDSSPVGGET DETTVSQNYRGSVSQPSTPSPKPTG IFQTSANSSFEVVKSHLVGVKPFVAD RANVVGVEVRETCVRQKQCRPAAALP DASPGNLEQPPDNMETLCAPQVCPL PLNSTTEAVHMLPHAGAPPLDTVYP APEKRPSARTQGPVKCESPATTLWA QSELPDFGGNVLLAPAAPALYVCAK PQPPVVQPPEEAMSGQQSRNPSSAA PVQSRGGIGASENLENPPKMGEEEA LQSQASSGYASLLSSPPTESLQNPV LIAQPDHSYNLAQPINFVSLNSHE KNQSWREALVGDRAVSSWALGGD SGENTSLSGIPTSSVLSLSPSSVAQ SNFPQGSASEMVSQNPANLLVQP PSQVPENLVPESQKDRKAGSALPG FANSPAGSTSVVLVPPAHGTLVDPG NKANHSSHQEDTYGALDFTLSRTLE NPVNVYNPSHSDSLASQQSVASHPR QSGPGAPNLDRFYQQVTKDAQGQP GLERAQQELVPPQQQASPPQLPKAM FSELSNPESLPAQQAQNSAQSPAS LVLVDAGQQLPPRPPQSSSVSLVSSG SGQAAVSEQPWPQPVPALAPGPPP QDLAAYYYRPLYDAYQPQYSLPYPP EPGAASLYYQDVVYSLYEPYRYPYDGA ASAYAQNYRYPEPERPSSRASHSSE RPPPRQGYPEGYYSSKSGWSSQSDY YASYSSQYDYGDPGHWDYRHYHYSAR VRDPRTYDRRYWCDAEYDAYRREHS AFGDRPEKRDNNWRYDPRFTGSFD DDPDPHRDPYGEEVDRRSVHSEHS ARSLHSAHSLARRSSLSHSHQSQ IYRSHNVAAGSYEAPLPPGSFHGDFA YGTYRSNFSSGPGFPEYGYPADTVW PAMEQVSSRPTSPEKFSVPHVCARF GPGGQLIKVIPNLPSEGQPALVEVHS MEALLQHTSEQEEMRAFPGLAKD DTHKVDVINFAQNKAMKCLQENLI DKESASLLWNFIVLLCRQNGTKVGT

DIAELLLRDHRTVWLP GKSPNEANLI
DFTNEAVEQVEEEESGEAQLSFLTG
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PGPGCVTPG PALGFLEPSGGLPPGV
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