

| UniprotKB ID | Entry name  | organism     | full name                        | oglcnacscore | oglcnac sites | phosphorylation sites      | PMIDS  | sequence  | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus | plasm memb |
|--------------|-------------|--------------|----------------------------------|--------------|---------------|----------------------------|--|---|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|------------|
| Q3UPL0       | SC31A_MOUSE | Mus musculus | Protein transport protein Sec31A | 31.506739    | S798          | S526;S531;S798;T1171;S1173 | 29187734;28528544;37453647;39627609;36064721;30059200;37507081 | MKLKEIDRTAMQAWSPAQNHPHYLA<br>TGTSAQQLDATFSTNASLEIFELDLS<br>DPSLDMKSCATFSSSHRYHKLWGP<br>HKMDSKGDVSGVLIAGGENGNILY<br>DPSKIIAGDKVEVIAQDKKHTGPVRA<br>LDVNIHQTNLIVASGANESIEIYIWDLN<br>NFATPMTPGAQTQPPEDISCIAWN<br>QVQHILASASPSGRATVWDLRKN<br>IHKVDHNSRMHCSGLAWHPDVAT<br>QMVLAIEDRLPVIQMWDLRFASSP<br>LRVLENHARGILAVAWSMADPELLL<br>SCGKDAKILCSNPNTGEVLYELPTNT<br>QWCFDIQWCPRNPVLSAASFDGRI<br>SVYSIMGGSIDGLRQKQVDKLSSSF<br>NLDPFGTGQPLPPLQIQQSAQHSIV<br>LPLKPPKWIRRPVGFASFSFGGKLV<br>FESVAVPLQQAEGQRRQPVFISQV<br>VTEKDFLNRSAQLQHAVQSQGFY<br>CQKKEASQTEFEKNVWVFLKVNFE<br>EDSRGKYLELLGYRKELDGQKIALAL<br>NKVDGPDVALKDSQVAQSDGEEESP<br>AAEFQLLGERIKEEKQECDFLPSAG<br>GTFNISVSGDIDGLITRALLTGNFES<br>AVDLCLHDNRMADAILAAGGQELL<br>AQTQKKYFAKSQSKITRLITAVVMKN<br>WREIVESCCLKNWRREALAALVYAK<br>PDEFSALCDLLGTRLEREGDSSLRT<br>QAACLCYICAGNVERLVACWTKAQDG<br>SSPLSLQDLIEKVILRKAVOLTAQAL<br>DTNTVGALLAEKMSQYASLLAAQGS<br>IAAALAFDPDNTNQPNIQLDRDLCK<br>AQQKPVSGQESSQSPYERQPLSKGR<br>PGPVAGHSQMPRVQTOQYYPHGEN<br>PPPPGFIMQGNVIPNPAAPLPTAPGH<br>MPSQLPPYQFPYQPAQYQYVSGTG<br>GAAAYRPOQPVAPPASNAYPNTPYIS<br>PVASYSGPQMYTAQQASSPTSSSA<br>ASFPPSSGASFOHGGPGAPSSSAY<br>ALPPGTTGTPPAASELPASQRTENQS<br>FODQASILEGPQNGWNPALNRP<br>PKKKMPENFMPVPTSPIMNPSG<br>DPQSQGLQQPSTPGPLSSHAFPPQ<br>QHLAGGQPFHGVQPLAQTMPPS<br>FSKPNTGAPGAPIGNTIQHVQALPT<br>EKITKPIPEHLIKTTFFEDLIQRCL<br>SSATDPQTKRKLDDASKRLEFLYDK<br>LREQTLSPHINGLHSIARSIEIRNYS<br>EGLSVHTHIVSTSNFSETSAFMPVLK<br>VVLSQASKLGV | False         | True          | 3.595   | 3.19    | 1.294         | 5.0                   | 2.214           | 1.492      |