

| UniprotKB ID | Entry name  | organism     | full name                              | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS  | sequence  | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus | plasma membrane | ext reg |
|--------------|-------------|--------------|--|--------------|---------------|-----------------------|--|---|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|-----------------|---------|
| Q7L576       | CYFP1_HUMAN | Homo sapiens | Cytoplasmic FMR1-interacting protein 1 | 23.663582    | S891          | S583;T1234            | 35138101;38665916;41350704;28510447;34725712;33214551;27655845;34019948;35008409 | MAAQVTLEDALSNDLLEELPLPDQ<br>QPCIEPPSSLLYQPNFNTNFEDRN<br>AFVVTGIARIYEQATVHSSMNEEMLEE<br>GQEYAVMLYTWRSRCSRAIPQVKCNE<br>QPNRVEIYEKTVLEPEVTKLMNF<br>MYFQRNAIERFCGEVRRRLCHAERRK<br>DFVSEAYLITLKGKFINMFAVLDELKN<br>MKCSVKNDHSAKRAAQFLRKMAD<br>PQSIQESQNLMSFLANHNKITQSLQ<br>QQLEVISGYEELLADIVNLCVDYYEN<br>RMYLTPSEKHMMLLKVMGFGLYLMD<br>GSVSNYKLDAKKRINLSKIDKYFKQ<br>LQVVPLFGDMQIELARYIKTSAHYEE<br>NKSRTWTCTSSGSSPOYNICEQMIQI<br>REDHMRFISELARYSNSEVVTGSGR<br>QEAQKTDAEYRKLFDLALQGLQLLS<br>QWSAHVMEVYSWKLVHPTDKYSNK<br>DCPDSAEYERATRYNYTSEEKFAV<br>EVIAMIKGLQVLMGRMESVFNHAIR<br>HTVYAALQDFSQVTLREPLRQAIAKKK<br>KNVIQSVLQAIRKTVCDWETGHEPF<br>NDPALRGEKDKPSGFDIKVPRRAVG<br>PSSTQLYMVRTMLES LIADKSGSKK<br>TLRSLEGPTILDIEKFHRESFFYTHL<br>INFSETLQCCDLSQLWFRFFLEL<br>TMGRRIQFPIEMSPWILTDHILETK<br>EASMMMEYVLYSLDLYNDSAHYALTR<br>FNKQFLYDEIEAEVNLCFDQFVYKL<br>ADQIFAYYKVMAGSLLLDKRLRSEC<br>KNQGATIHLPSPNRYETLLKQRHVQ<br>LLGRSIDLNRLITQRVSAAMYKSLEL<br>AIGRFESDLTSIVELDGLLEINRMT<br>HKLLSRYLTLDFDAMFREANHNV<br>SAPYGRITLHVFWELNYDFLPNYCY<br>NGSTNRFVRTVLPFSQEFQRDKQPN<br>AQPOYLHGSKALNLAYSIYGSYRNF<br>VGPPHFQVICRLLGYQGIAVVMEELL<br>KVVKSLQGTILQYVKTLMVEMPKIC<br>RLPRHEYGSPGILEFFHHQLKDIVEY<br>AELKTVCFONLREVGNAIFCLLIEQ<br>SLSLEEVCDLLHAAPFQNILPRVHVK<br>EGERLDAKMKRLESKYAPLHLVPLIE<br>RLGTPQQAIAAREGDLTKERLCCGL<br>SMFEVILTRIRFLDDPIWRGPLPSN<br>GVMHVDECEVFHRLWSAMQFVYCI<br>PVGTHEFTVEQCFGDGLHWAGCMII<br>VLLGQORRFVAVLDFCYHLLKVQKHD<br>GKDEIKNVPLKKMVERIRKQILND<br>EITILDKYLKSGDGEGTPVEHVRCF<br>QPIHQSLASS | True          | False         | 4.5     | 2.402   | 1.95          | 1.114                 | 0.893           | 1.814           | 4.2     |