| | UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochndrion | endoplasmic reticulum | golgi apparatus | plasm memb |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | Q3T8J9 | GON4L_HUMAN | Homo sapiens | GON-4-like protein | 21.108398 | S1197 | S206;S346;S775;S1268;S1426;S1896;S1902;S1977;S2107 | 28411811;30379171;29351928 | MLPCKKRRTTVTESLQHKGNQEEN<br>NVDLESAVKPESDQVKDLSSVSLSW<br>DPSHGRVAGFEVQSLQDAGNQLGM<br>EDTSLSSGMLTQNTNVPILEGVDVAI<br>SQGITLPSLESFHPLNIHIGKGKLHA<br>TGSKRGKKMTLRPGPVTQEDRCDH<br>LTLKEPFSGEPSEEVKEEGGKPQMN<br>SEGEIPSLPSGSQSAKPVSQPRKSTQ<br>PDVCASPQEKPLRTLFHQPEEEIEDG<br>GLFIPMEEQDNEESEKRRKKKKGTK<br>RKRDGRGQEGTLAYDLKLDDMLDR<br>TLEDGAKQHNLTAVNVRNILHEVIT<br>NEHVVAMMKAAISETEDMPMFEPK<br>MTRSKLKEVVEKGVVIPTWNISPIKK<br>ANEIKPPQFVDIHLEEDDSSDEEYQP<br>DDEEEDETAEESLLESDVESTASSPR<br>GAKKSRLRQSSEMTETDEESGILSE<br>AEKVTTPAIRHISAEVVPMGPPPPPK<br>PKQTRDSTFMEKLHAVDEELASSPV<br>CMDSFQPMDDSLIAFRTRSKMPLK<br>DVPLGQLEAELQAPDITPDMYDPNT<br>ADDEDWKMWLGGLMNDDVGNED<br>EADDDDDPEYNFLEDLDEPDTEDFR<br>TDRAVRITKKEVNELMEELFETFQD<br>EMGFSNMEDDGPEEEECVAEPRPN<br>FNTPQALRFEEPLANLLNEQHRTVK<br>ELFEQLKMKKSSAKQLQEVEKVKPQ<br>SEKVHQTLILDPAQRKRLQQQMQQ<br>HVQLLTQIHLLATCNPNLNPEATTT<br>RIFLKELGTFAQSSIALHHQYNPKFQ<br>TLFQPCNLMGAMQLIEDFSTHVSID<br>CSPHKTVKKTANEFPCLPKQVAWIL<br>ATSKVFMYPELLPVCSLKAKNPQDKI<br>VFTKAEDNLLALGLKHFEGTEFPNP<br>LISKYLLTCKTAHQLTVRIKNLNMNR<br>APDNIIKFYKKTKQLPVLGKCCEEIQ<br>PHQWKPPIEREEHRLPFWLKASLPSI<br>QEELRHMADGAREVGNMTGTTEIN<br>SDRSLEKDNLELGSESRYPLLLPKGV<br>VLKLKPVATRFPRKAWRQKRSSVLK<br>PLLIQPSPSLQPSFNPGKTPARSTHS<br>EAPPSKMVLRIPHPIQPATVLQTVPG<br>VPPLGVSGGESFESPAALPAVPPEAR<br>TSFPLSESQTLLSSAPVPKVMLPSLA<br>PSKFRKPYVRRRPSKRRGVKASPCM<br>KPAPVIHHPASVIFTVPATTVKIVSLG<br>GGCNMIQPVNAAVAQSPQTIPITTLL<br>VNPTSFPCPLNQSLVASSVSPLIVSG<br>NSVNLPIPSTPEDKAHVNVDIACAVA<br>DGENAFQGLEPKLEPQELSPLSATV<br>FPKVEHSPGPPLADAECQEGLSENS<br>ACRWTVVKTEEGRQALEPLPQGIQE<br>SLNNPTPGDLEEIVKMEPEEAREEIS<br>GSPERDICDDIKVEHAVELDTGAPSE<br>ELSSAGEVTKQTVLQKEEERSQPTK<br>TPSSSQEPPDEGTSGTDVNKGSSKN<br>ALSSMDPEVRLSSPPGKPEDSSSVD<br>GQSVGTPVGPETGGEKNGPEEEEEE<br>DFDDLTQDEEDEMSSASEESVLSVP<br>ELQETMEKLTWLASERRMSQEGES<br>EEENSQEENSEPEEEEEEEAEGME<br>SLQKEDEMTDEAVGDSAEKPPTFAS<br>PETAPEVETSRTPPGESIKAAGKGRN<br>NHRARNKRGSRARASKDTSKLLLLY<br>DEDILERDPLREQKDLAFAQAYLTRV<br>REALQHIPGKYEDFLQVIYEFESSTQ<br>RRTAVDLYKSLQILLQDWPQLLKDF<br>AAFLLPEQALACGLFEEQQAFEKSR<br>KFLRQLEICFAENPSHHQKIIKVLQG<br>CADCLPQEITELKTQMWQLLKGHD<br>HLQDEFSIFFDHLRPAASRMGDFEE<br>INWTEEKEYEFDGFEEVALPDVEEE<br>EEPPKIPTASKNKRKKEIGVQNHDK<br>ETEWPDGAKDCACSCHEGGPDSKL<br>KKSKRRSCSHCSSKVCDSKSYKSKE<br>PHELVGSSPHREASPMPGAKEAGQ<br>GKDMMEEEAPEERESTEATQSRTV<br>RTTRKGEMPVSAGLAVGSTLPSPRE<br>VTVTERLLLDGPPPHSPETPQFPPTT<br>GAVLYTVKRNQVGPEVRSCPKASPR | None | None | None | None | None | None | None | None |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | LQKEREGQKAVSESEALMLVWDAS<br>ETEKLPGTVEPPASFLSPVSSKTRDA<br>GRRHVSGKPDTQERWLPSSRARVKT<br>RDRTCPVHESPSGIDTSETSPKAPRG<br>GLAKDSGTQAKGPEGEQQPKAAEAT<br>VCANNSKVSSTGEKVVLWTREADRV<br>ILTMCQEQGAQPQTFNIISQQLGNK<br>TPAEVSHRFRELMQLFHTACEASSE<br>DEDDATSTSNADQLSDHGDLLSEEE<br>LDE | | | | | | | | |