

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|-------------|--------------|-------------------------------------|--------------|---|--|--|--|
| Q2KHR3 | QSER1_HUMAN | Homo sapiens | Glutamine and serine-rich protein 1 | 40.34384 | S5;T11;S17;T19;T20;T74;T104;S105;T108;T111;S131;T242;S245;S282;S299;T306;S308;T504;S521;S586;S595;T596;S600;S660;T959;T1270;T1271;S1272;T1274;T1277;T1278;T1283 | S586;S615;S886;T949;S987;S1211;S1230;S1231;S1239;T1341;S1348 | 29237092;21740066;34725712;34846842;28604694;38665916;37340703;30379171;34019948;30620550;28411811;22661428;32522876;35132862;35254053;20305658;31492838;35289036;32119511;33214551;20068230;21158410;30059200;28657654;23301498;32574038;35138101 | MNFLSTAESRTAQAAASGTTLLPQF RAPSWQTGMHSSAATELAFATGPLPS TGTLPPLSLAYQHPTTFNSRRNFATTS PLVLQDSTFNNTSNGILSHHDPLLQI KTSQGTVPALAFERLGSVLSNSIP PQSSTYRSAQESAPHLQPFQFLLPS ALGGSQQTTPQAYSSTLFTSSTASIER ALLRECSVIKHHQRPSGTQSIQAQLT GSQHSLHSHYLSNSSVVFQETTRQS SLSCSPIGDSTQVSNGLQKQTSQV SVELAQSYSSAIPSSGYPPSTTKIKSC STEQPLTSTKTPKQSIIPPVQTLSSY KPLHNQSSVISGQAQIYSTAQLPSLL SVSQSQNYGLVQPHNVPSIVHSQVY RSSKVEKLPPLYKTLTFSGSSQTVTP ENQTLNYSNQQEVLSSVTNENYPA QTRDLSSVSQSQSYSSGHSQGLSPV SQTQVSYSSQSQVLSVSVLSSESYASG ESLTLTAPSLSYSSASRAQNLPDSSP TQNYISMHSSQNVQTQESSSPQSQK FLPAVQSSSFASSTHCQTLQNNITSP DPKSYAERKLDSDVYPSSKQEDGFP MQELQVLQPQASLESSTQRLSDGEI NAQESTYKVKSKADDRYSQSVIRSN RLEDQVIGVALQASKKEESVVGSVT QLNQIQGVNNAATLDLKNSTNLIQ TPQIRLNTKDLKQQHPLILKVHESKV QEQHDQIINASSQIQIPNHALGHGH QASLPNTQVLLDSACDLQILQQSILQ AGLGQVKASLQAQRVQSPQQIVHPF LQMEGHVIQSNGDHSSQQQLHPQNS EVMKMDLSESSKPLQQLHTTKGHF SETNQHDSKNQFVSLGSMCFPEAV LLSDERNILSNVDDILAATAAACGVT PTDFSKSTSNETMQAVEDGDSKSHF QQSLDVRHVTSDFNSMTATVGKQP NINDTSLNGNQVTVNLSVPALQSK MTLDQQHIETPGQNIPTKVTSAVVG PSHEVQEQQSSGPFKKQSATNLESEE DSEAPVDSTLNNNRNQEYFVSSRSI SGENATSESEFTLGGDDSGVSMNPA RSALALLAMAQSGDAVSVKIEENQ DLMHFNLQKKRAKGGQVKEEDNS NOKQLKRP AQGKRONPRGTDIYLPY TPPSESCHDGYQHQEKMRQKIKEV EEKQPEVKTGFIAFLDFLKSQPKQQ FSTLAVRMPNRRRPGTQMVRTFCP PPLPKPSSTTPTPLVSETGGNSPSDK VDNELKNLEHLSSFSSDEDDPGYSQ DAYKSVSTPLTTLDATSDKTKKTEAL QVATTSPTANTTGTATTSTTVGAVK QEPLHSTSYAVNILENISSESSKPIE LDGLPSDQFAKGQDTVAIEGFTDEE DTESGGEGQYRERDEFVVKIEDIETF KEALKTGKEPPAIWKVQKALLQKQFV PEIRDGQREFAATNSYLGFGDAKS KYKRIYVKFIENANKKEYVRVCSKKP RNKPSQIRTIVQAKPSSSSKTS DPLA SKTTTTKAPSVKPKVKQPKVKAEP KKRKKWKEEFSSSQSDSSPEIHTSS SDDEEFEPAPFVTRFLNTRAMKET FKSYMELLVSIALDPDTMQALEKSN DELLPHMKKIDGMLNDNRKRLLL |

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| NLHLDQSFKNALESFPELTIITRDSK |
| AKSGGTAISKIKMNGKAYNKKTLRTS |
| KTTTKSAQEFVDPPEKIQLYSLYHSL |
| HHYKYHVYLICKDEISSVQKKNEDL |
| GQEEIVQLCMKNVWVEDLFEKFG |
| ELLNHVQQKCS |