

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	49.951009	S5;S17;T104;S105;S245;T306;T504;S600;T1270;T1271;S1272;T1274;T1277;T1278	S586;S615;S886;T949;S987;S1211;S1230;S1231;S1239;T1341;S1348	30379171;33214551;31492838;32119511;30620550;20068230;30059200;32522876;21740066;28657654;29237092;21158410;34019948;3626323;28411811;20305658;22661428;32574038;23301498;28604694	MNFLSTAESRTAQAAASGTTLLPQF RAPSWSQTMHSSAATELAFATGPLPS TGTLPPSLSAQYHPTTFNSNRNFATTS PLVLQDSTFNNTSNGILSHHDPLLQI KTSQGTVPALAFERLGSSVLSNSIP PQSSTYRSAQESAPHLLOPQFSLPS ALGGSQQTTPQAYSSTLFTSSTASIER ALLRECSVIKHHQRPSGTQSIQAQLT GSQHSLHSYLSNSSVVNFQETTRQS SLSCSPIGDSTQVSNNGGLQKTSQV SVELAQSYSSAIPSSGYPPSTTKIKSC STEQPLTSTKTPKQSIIPPVQTLSSY KPLHNQSSVISGQAQIYSTAQLPSLL SVSQSQNYGLVQPHNVPSIVHSQVY RSSKVEKLPPLYKTLTFSGSSQTVTP ENQTLNYSNQQEVLSSVTNENYPA QTRDLSSVSQSQSYSSGHSQGLSPV SQTQVSYSSQSQVLSVVSLSSESYASG ESLTLTAPSLSYSSASRAQNLDPDSSP TQNYISMHSSQNVQTQESSSPQSQK FLPAVQSSSFASSTHCQTLQNNITSP DPKSYAERKLDSDVYPSSKQEDGFP MQELQVLQPQASLESSTQRLSDGEI NAQESTYKVKADDRYSQSVIRSN RLEDQVIGVALQASKKEESVVGSVT QLNQIQGVNNAATLDLKNSTNLIQ TPQIRLNTKDLKQQHPLILKVHESKV QEQHDQIINASSQIQIPNHALGHGH QASLPNTQVLLDSACDLQILQQSILQ AGLGQVKASLQAQRVQSPQQIVHPF LQMEGHVIQSNGDHSQQQLHPQNS EVMKMDLSESSKPLQHLTTKGFH SETNQHDSKNQFVSLGSMCFPEAV LLSDERNILSNVDDILAATAAACGVT PTDFSKSTSNETMQAVEDGDSKSHF QQSLDVRHVTSDFNSMTATVGKQP NINDTSLNGNQVTVNLSVPALQSK MTLDQQHIETPGQNIPTKVTSAVVG PSHEVQEQSSGPFKKQSATNLESEE DSEAPVDSTLNNNRNQEFVSSRSI SGENATSESEFTLGGDDSGVSMNPA RSALALLAMAQSGDAVSVKIEENQ DLMHFNLQKKRAGKGVKQVEDNS NOKQLKRPQAGKRONPRGTDIYLPY TPPSSECHDGYQHQEKMRQKIKEV EEKQPEVKTGFIAFLDFLKSQPKQQ FSTLAVRMPNRRRPGTQMVRTFCP PPLPKPSSTTPTPLVSETGGNSPSDK VDNELKNLEHLSSFSSDEDDPGYSQ DAYKSVSTPLTLDATSDKTKKTEAL QVATTSPTANTTGTATTSTTVGAVK QEPLHSTSYAVNILENISSESSKPIE LDGLPSDQFAKGQDTVAIEGFTDEE DTESGGEGQYRERDEFVVKIEDIETF KEALKTGKEPPAIWKVQKALLQKQFV PEIRDGQREFAATNSYLGFGDAKS KYKRIYVKFIENANKKEYVRVCSKKP RNKPSQTIRTVOAKPSSSSKTS DPLA SKTTTTKAPSVKPKVKQPKVKAEP KKRKKWKEEFSSSQSDSSPEIHTSS SDDEEFEPAPFVTRFLNTRAMKET FKSYMELLVSIALDPDTMQALEKSN DELLPHMKKIDGMLNDNRKRLLL

