

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q86UR5	RIMS1_HUMAN	Homo sapiens	Regulating synaptic membrane exocytosis protein 1	11.700284	T398;T636;T1179;S1377	S500;S578;S728;S731;S881;S977;S1031;S1252;T1254;S1256;S1308;S1310;S1311;S1339;S1340;S1342;S1416;S1677;S1680;S1683;S1692	30379171;36240223;28657654	MSSAVGPRGPRPPTVPPPMQELPDL SHLTEEERNIIMAVMDRQKEEEEKE EAMLKCVVRDMAKPAACKTPRPAE NQPHQPSRRLHQQFESYKEQVRKIG EEARRYQGEHKDDAPTCGICHKTKF ADGCGHLCSYCRTKFCARCGRVSL RSNNEDKVMWVCNLCRKQQEILT KSGAWFFGSGPQOTSQDGTLSDTAT GAGSEVPREKKARLQERSRSQTPLS TAAASSQDAAPPSAPPDRSKGAEPS QQALGPEQKQASSRSRSEPPREKKA TPGLSEQNGKALKSERKRVKTS QPVEGAVEERERKERRESRRLEKGR SQDYPTPEKRDEGKADEEKQRKE EDYQTRYRSDPNLARYPVKPPPEEQ QMRMHARVSRARHERRHSDVALPR TEAGAALPEGKAGKRAPAAARASPP DSPRAYSAERTAETRAPGAKQLTNH SPPAPRHGPVPAEAPELKAQEPLRK QSRLDPSSAVLMRKAKREKVTMLR NDSLSSDQSESVRPSPPKPHRSKRG GKKRQMSVSSSEEEGVSTPEYTSCE DVELESESVSEKGDLDYYWLDPATW HSRETSPISHPVTWQPSKEGDRDIG RVILNKRTTMPKDSGALLGLKVGG KMTDLGRLGAFITKVKKGLADVVG HLRAGDEVLEWNGKPLPGATNEEV YNIILESKSEPQVEIIVSRPIGDIPRIPE SSHPPLESSSSSFESQKMERPSISVI SPTSPGALKDAPQVLPQQLSVKLWY DKVGHQLIVNVLQATDLPARVDGRP RNPYVKMYFLPDRSDKSKRRTKTVK KILEPKWNQTFVYSHVHRRDFRER MLEITVWDQPRVQEESEFLGEILIE LETALLDDEPHWYKLQTHDESSLPL PQPSPFMPRRHIHGESSKQLQRSQ RISDSDISDYEVDDGIGVPPVGYRS SARESKSTTLVPEQQRTHHRSRS VSPHRGNDQKPRSRLPNVPLQRS DEIHPTRRSRSPTRHHDASRSPVDH RTRDVDSQYLSEQDSELLMLPRAKR GRSAECLHTTRHLVRHYKTLPPKMP LLQSSSHWNIYSSILPAHTKTKSVTR QDISLHHECFNSTVLRFTDEILVSEL QPFLDRARSASTNCLRPDTSLHSPE RERGRWSPSLDRRRPPSPRIQIQHAS PENDRHSRKSERSSIQKQTRKGTAS DAERVLPTCLSRRGHAAPRATDQPI RGKHPARSRSSEHSSIRTLCSMHHL VPGGSAPPSLLTRMHRQRSPTQSP PADTSFSSRRGRQLQVPVRSQSIEQ ASLVVEERTRQMKMKVHRFKQTTG SGSSQELDREQYSKYNIHKDQYRSC DNVSAKSSSDSDVSAISRTSSASR LSSTSFMSEQSERPRGRISSTPKM QGRRMGTSGRSIMGKSTSVSGEMYTL EHNDGSQSDTAVGTVGAGGKKRRS

								SLSAKVVAIVSRRSRSTSQLSQTESG HKKLLKSTIQRSTETGMAAEMRKMV RQPSRESTDGSINSYSSEGNIIFPGV RLGADSQFSDFLDGLGPAQLVGRQT LATPAMGDIQIGMEDKKGQLEVEVI RARSLTQKPGSKSTPAPYVKVYLLEN GACIAKKKTRIARKTLDPLYQQSLVF DESPQGKVLQVIVWGDYGRMDHHC FMGVAQILLEELDLSMVGWYKLF PPSSLVDPTLTPLRRASQSSLESST GPPCIRS
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