	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	Q86VI3	IQGA3_HUMAN	Homo sapiens	Ras GTPase-activating-like protein IQGAP3	20.111456	S201;S944	T162;S539;S1424	30379171;29351928	MERRAAGPGWAAYERLTAEEMDEQ RRQNVAYQYLCRLEEAKRWMEACL KEELPSPVELEESLRNGVLLAKLGH CFAPSVVPLKKIYDVEQLRYQATGLH FRHTDNINFWLSAIAHIGLPSTFFPE TTDIYDKKNMPRVVYCIHALSLFLFR LGLAPQIHDLYGKVKFTAEELSNMA SELAKYGLQLPAFSKIGGILANELSV DEAAVHAAVLAINEAVERGVVEDTL AALQNPSALLENLREPLAAVYQEML AQAKMEKAANARNHDDRESQDIYD HYLTQAEIQGNINHVNVHGALEVVD DALERQSPEALLKALQDPALALRGV RRDFADWYLEQLNSDREQKAQELG LVELLEKEEVQAGVAAANTKGDQEQ AMLHAVQRINKAIRRRVAADTVKEL MCPEAQLPPVYPVASSMYQLELAVL QQQQGELGQEELFVAVEMLSAVVLI NRALEARDASGFWSSLVNPATGLAE VEGENAQRYFDALLKLRQERGMGE DFLSWNDLQATVSQVNAQTQEETD RVLAVSLINEALDKGSPEKTLSALLL PAAGLDDVSLPVAPRYHLLLVAAKR QKAQVTGDPGAVLWLEEIRQGVVRA NQDTNTAQRMALGVAAINQAIKEGK AAQTERVLRNPAVALRGVVPDCANG YQRALESAMAKKQRPADTAFWVQH DMKDGTAYYFHLQTFQGIWEQPPG CPLNTSHLTREEIQSAVTKVTAAYDR QQLWKANVGFVIQLQARLRGFLVRQ KFAEHSHFLRTWLPAVIKIQAHWRG YRQRKIYLEWLQYFKANLDAIIKIQA WARMWAARRQYLRRLHYFQKNVN SIVKIQAFFRARKAQDDYRILVHAPH PPLSVVRRFAHLLNQSQQDFLAEAE LLKLQEEVVRKIRSNQQLEQDLNIM DIKIGLLVKNRITLQEVVSHCKKLTK RNKEQLSDMMVLDKQKGLKSLSKE KRQKLEAYQHLFYLLQTQPIYLAKLI FQMPQNKTTKFMEAVIFSLYNYASS RREAYLLLQLFKTALQEEIKSKVEQP QDVVTGNPTVVRLVVRFYRNGRGQS ALQEILGKVIQDVLEDKVLSVHTDPV HLYKNWINQTEAQTGQRSHLPYDVT PEQALSHPEVQRRLDIALRNLLAMT DKFLLAITSSVDQIPYGMRYVAKVLK ATLAEKFPDATDSEVYKVVGNLLYYR FLNPAVVAPDAFDIVAMAAGGALAA PQRHALGAVAQLLQHAAAGKAFSGQ SQHLRVLNDYLEETHLKFRKFIHRA CQVPEPEERFAVDEYSDMVAVAKP MVYITVGELVNTHRLLLEHQDCIAP DHQDPLHELLEDLGELPTIPDLIGES IAADGHTDLSKLEVSLTLTNKFEGLE ADADDSNTRSLLLSTKQLLADIIQFH PGDTLKEILSLSASREQEAAHKQLM SRRQACTAQTPEPLRRHRSLTAHSL LPLAEKQRRVLRNLRRLEALGLVSA RNGYQGLVDELAKDIRNQHRHRHR RKAELVKLQATLQGLSTKTTFYEEQ GDYYSQYIRACLDHLAPDSKSSGKG KKQPSLHYTAAQLLEKGVLVEIEDLP ASHFRNVIFDITPGDEAGKFEVNAKF LGVDMERFQLHYQDLLQLQYEGVA VMKLFNKAKVNVNLLIFLLNKKFLR K	None	None	None	None	None	None	None	None	None