	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	ex re
0	Q99666	RGPD5_HUMAN	Homo sapiens	RANBP2-like and GRIP domain-containing protein 5/6	21.288829	S914;S918	T19;S21	36240223;31492838;35132862;34019948;30620550;38665916	MRRSKADVERYVASVLGLTPSPRQK SMKGFYFAKLYYEAKEYDLAKKYICT YINVQERDPKAHRFLGLLYELEENT EKAVECYRRSVELNPTQKDLVLKIAE LLCKNDVTDGRAKYWVERAAKLFPG SPAIYKLKEQLLDCEGEDGWNKLFD LIQSELYVRPDDVHVNIRLVELYRST KRLKDAVAHCHEAERNIALRSSLEW NSCVVQTLKEYLESLQCLESDKSDW QATNTDLLLAYANLMLLTLSTRDVQ ENRELLESFDSALQSAKSSLGGNDE LSATFLEMKGHFYMYAGSLLLKMG QHGNNVQWRALSELAALCYLIAFQV PRPKIKLREGKAGQNLLEMMACDRL SQSGHMLLSLSRGKQDFLKEVVETF ANKIGQSALYDALFSSQSPKDTSFLG SDDIGKIDVQEPELEDLARYDVGAIR AHNGSLQHLTWLGLQWNSLPALPG IRKWLKQLFHRLPHETSRLETNAPE SICILDLEVFLLGVVYTSHLQLKEKC NSHHSSYQPLCLPFPVCKQLCTERQ KSWWDAVCTLIHRKAVPGNLAKLRL LVQHEINTLRAQEKHGLQPALLVHW AKYLQKTGSGLNSFYGQLEYIGRSV HYWKKVLPLLKIIKKNSIPEPIDPLFK HFHSVDIQASEIVEYEEDAHITFAML DAVNGNIEDAVTAFESIKSVVSYWN LALIFHRKAEDIENDALSPEEQEECR NYLTKTRDYLIKIIDDGDSNLSVVKK LPVPLESVKQMLNSVMQELEDYSEG GPLYKNGSLRNADSEIKHSTPSPTKY SLSPSKSYKYSPETPPRWTEDRNSLL NMICQQVEAIKKEMQELKLNSSKSA SRHRWPTENYGPDSVPDGYQGSQT FHGAPLTVATTGPSVYYSQSPAYNSQ YLLRPAANVTPTKGSSNTEFKSTKEG FSIPVSADGFKFGISEPGNQEKKREK PLENDTGFQAQDISGRKKGRGVIFG QTSSTFTFADVAKSTSGEGFQFGKK DLNFKGFSGAGEKLFSSRYGKMAN KANTSGDFEKDDDAYKTEDSDDIHF EPVVQMPEKVELVTGEEGEKVLYSQ GVKLFRFDAEVRQWKERGLGNLKIL KNEVNGKLRMLMRREQVLKVCAN HWITTTMNLKPLSGSDRAWMWSAS DFSDGDAKLERLAAKFKTPELAEEF KQKFEECQRLLLDIPLQTPHKLVDT GRAAKLIQRAEEMKSGLKDFKTFLT NDQTKVTEEENKGSGTGAAGASDTT IKPNAENTGPTLEWDNYDLREDALD DSVSSSSVHASPLASSPVRKNLFRFD ESTTGSNFSFKSALSLSKSPAKLNQS GTSVGTDEESVVTQEEERDGQYFEP VVPLPDLVEVSSGEENEQVVFSHRA EIYRYDKDVGQWKERGIGDIKILQNY DNKQVRIVMRRDQVLKLCANHRITP DMSLQNMKGTERVWVWTACDFAD GERKVEHLAVRFKLQDVADSFKKIF DEAKTAQEKDSLITPHVSRSSTPRES PCGKIAVAILEETTRERTDVIQGDDV ADAASEVEVSSTSETTTKAVVSPPKF VFVSESVKRIFSSEKSKPFVFGNSSA TGSLFGFSFNAPLKSNNSETSSVAQ SGSESKVEPKKCELSKNSDIEQSSDS KVKNLSASFPTEESSINYTFKTPEKE PPLWHAEFTKEELVQKLRSTTKSAD HLNGLLREIEATNAVLMEQIKLLKSE IRRLERNQEREKSAANLEYLKNVLL QFIFLKPGSERERLLPVINTMLQLSP EEKGKLAAVAQDEEENASRSSG	None	None	None	None	None	None	None	None	N