

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	pl m
Q96PE2	ARHGH_HUMAN	Homo sapiens	Rho guanine nucleotide exchange factor 17	16.250926	S1961;T1963;T1970	S142;S152;S310;S326;S332;S383;S387;S395;S410;S420;S461;S546;S619;S696;T699;T702;S735;S914;S961;S1002;S1331	38253038;38665916	MADGAPRPQLYRSVSFKLLERWGGG PGLREEDTDTPLGLRRRASCRIPTAA RGQPSRRVSKLASGLAAPAQPRPL RSLSPSVRQLSRRFDAPRLDDGSAG TRDGGVLPAAAEAAEGPARGAWPS VTEMRKLFGGPGSRRPSADSESPGT PSPDGAAWEPPARESRQPTPPPPRT CFPLAGLRSARPLTGPETEGRLRRPQ QQQERAQRPADGLHSHWIFSQQA GARASCSSSIAASYPVRSRAASSS EEEEEGPPQLPGAQSPAYHGGHSSG SDDDDRDEGGHRWGGRPGLRPGSS LLDQDCRPDSGLNLSSMNSAGVS GSPEPTSPRAPREGLREWGGSGSP PCVPCPQEGLRPMSDSVGGAFRVAK VSFPYSYLASPAGSRGSSRYSTETLK DDDLWSSRGGGWVYRSPSFGAG EGLLRSQARTRAKGPGGTSRALRDG GFEPEKSRQRKSLSNPDIASETLTLL SFLRSDLSELVRKPGSSGDRGSN PLDGRDPSAGGPVQLEPIPIPAPA SPGTRPTLKDLTATLRRRAKSFTCSEK PMARRLPRTSALKSSSELLTGPGA EEDPLPLIVQDQYVQEARQVFEKIQR MGAQQDDGSDAPPGSPDWAGDVTR GQRSQEELSGPESLTDGEGIGADPEP PVA AFCGLGTTGMWRPLSSSSAQTN HHGPGTDSLGLGWALVSPETPPTPG ALRRRRKVPVPSGGSELSNGEAGE AYRSLSDPIPQRHRAATSEPTGFSV DSNLLGSLPKTGLPATSAMDEGLT SGHSDWSVGSEESKGYQEVISIVQ GPGLGRVDDRIAGKAPKKKSLSD PSRRGELAGPGFEGPGGPIREVEP MLPPSSSEPIVQRAEPEPEPGATRS RAQSERALPEALPPATAHRNFHLD PKLADILSPRLIRRGSKKRPARSSHQ ELRRDEGSDQDTGSLSRARPSRHV RHASVPATFMPVIVPEPPTSVGPPVA VPEPIGFPTRAHPTLQAPSLDVTQK YMLNLHSGEVPAPVPVDMPCPLPAA PPSAEAKPPEAARPADEPTPASKCCS KPQVDMRKHVAMTLLDTEQSYVES LRTLMOGYMQPLKQPENSVLCDPSL VDEIFDQIPELLEHHEQFLEQVRHC MQTWHAAQQKVGALLVQSFSDVLLV NIYSAYIDNFLNAKDAVRVAKEARPA FLKFLEQSMRENKEKQALSDLMIKP VQRIPRYELLVKDLLKHTPEDHPDH PLLEAQORNIQVAERINKGVRSAEE AERHARVLQEIIEAHIEGMEDLQAPL RRFLRQEMVIEVKAIGGKDRSLFLF TDLIVCTTLKRKSGSLRRSSMSLYTA ASVIDTASYKMLWKLPLEDADIKIG ASQATNRENIQKAISRLDEDLTLGQ MSKLSSELGFPHQSLDDALRDLAA MHRDLSEKQALCYALSFPTKLELC ATRPEGTDSYIFEFPHPDARLGFQA FDEAKRKLASSKSLDPEFLKAIPIM KTRSGMQFSCAAPTLNSCPEPSPEV WVCNSDGYVGVCLLSLRAEPDVEA CIAVCSARILCIGAVPGLQPRCHREP PPSLRSPPETAPEPAGPELDVEAAAD EEAATLAEPGPQCLHISAGSGLEM TPGLGEGDPRPELVFFDSDDESS PSPSGTLQSQASRSTISSFGNEETP SSKEATAETTSSEEEQEPFLPLSGS FGPGGPGTSPMDGRALRRSSHGSF TRGSLEDLLSVDPEAYQSSVWLGT DGCVHVYQSSDSIRDRRNSMKLQH AASVTCILYLNQVVFVSLANGELVY QREAGHFWDPNFKSVTLGTQGSPI TKMVSVGGRLWCGCQNRVVLSPD TLQLEHMFYVGQDSSRCVACMVDS SLGVVWTLKGSAAHVCLYHPDTFEQL AEVDVTPPVHRMLAGSDAIHQHKA ACLRLTALLVCELLWVGTSAAGVLT MPTSPGTVSCPRAPLSPGLGQGH GHVRFLLAAVQLPDGFNLLCPTPPPP PDTGPEKLPSEHRDSPWHRGPAPA	None	None	None	None	None	None	None	

