

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
A7KAX9	RHG32_HUMAN	Homo sapiens	Rho GTPase-activating protein 32	9.498347	NaN	S706;S709;S732;S738;S852;S856;S892;S952;S1203;S1585	35132862	METESESSTLGDDSVFWLESEVIIQV TDCEEEEREKFRMKSSVHSEED DFVPELHRNVHPRERPDWEETLSA MARGADVPEIPGDLTLKTCGSTASM KVKHVKKLPFTKGHFPKMAECAHF HYENVEFGSIQLSLSEEQNEVMKNG CESKELVYLVQIACQGKSWIVKRSYE DFRVLDKHLHLCIYDRRFSQLSELPR SDTLKDSPESVTQMLMAYLSRLSAIA GNKINCGPALTWMEIDNKGNHLLV HEESSINTPAVGAAHVIKRYTARAPD ELTLEVGDIVSVIDMPPKVLSTWWR GKHGFQVGLFPGHCVELINQKVPQS VTNSVPKPVSKKHGKLITFLRTFMKS RPTKQKLKQRGILKERVFGCDLGEH LLNSGFVQPVLQSCAFIERYGIVD GIYRLSGVASNIQRLRHEFDSEHVPD LTKEPYVQDIHSVGLCKLYFRELPN PLLYQLYEKFSDAVSAATDEERLIKI HDVIQQLPPPHYRTLEFLMRHLSLL ADYCSITNMHAKNLAIVWAPNLLRS KQIESACFSGTAAFMEVRIQSVVVEF ILNHVDVLFSGRISMAMQEGAASLS RPKSLVSSPSTKLLTLEEAQARTQA QVNSPIVTENKYIEVGEGPAALQKGF HTIIEFPLERKRPQNKMKKSPVGSW RSFFNLGKSSSVSKRKLQRNESEPS EMKAMALKGGRAEGTLRSKSEESL TSLHAVDGDGSKLFRPRRPRSSDAL SASFNGEMLGNRCNSYDNLPHDNE SEEGGLLHIPALMSPHSAEDVDLS PPDIGVASLDFDPMSFQCSPPKAESE CLESGASFLDSPGYSKDKPSANKKD AETGSSQCQTPGSTASSEPVSPLOEK LSPFFTLDSLPTEDKSSKPSSTTEKV VYAFSPKIGRKLKSPSPMSISEPISVT LPPRVSEVIGTVSNTTAQNASSSTW DKCVEERDATNRSPTQIVKMKTNET VAQEAYESEVQPLDQVAEEVELPG KEDQSVSSSQSKAVASGQTQTGAVT HDPPQDSVPVSSVSLIPPPPPKNVA RMLALALAESAQCASTQSLKRPGTS QAGYTNYGDIAVATTEDNLSSYSYAV ALDKAYFQTRPAEQFHLQNNAPG NCDHPLPETTATGDPHTSNTTESGE QHHQVDLTGNQPHQAYLSGDPEKA RITSVPLDSEKSDDHVSFPEDQSGK NSMPTVSFLDQDQSPRFYSGDQPP SYLGASVDKLLHHPLEFADKSPTPPN

LPSDKIYPPSGSPEENTSTATMTYMT
TTPATAQMSTKEASWDVAEQPTTAD
FAAATLQRTHTRTNRPLPPPSQRSA
EQPPVVGQVQAATNIGLNNSHKVQG
VVPVPERPPEPRAMDDPASAFIDSG
AAAAQCPMATAVQPGLPEKVRD GAR
VPLLHLRAESVPAHPCGFAPLPPTR
MMESKMIAAIHSSSADATSSSNYHS
FVTASSTSVDDALPLPLPVPQPKHAS
QKTVYSSFARPDVTTEPFGPDNCLH
FNMTPNCOYR PQSVPPHHNKLEQH
QVYGARSEPPASMGLRYNTYVAPGR
NASGHHSKPCSRVEYVSSLSSSVRN
TCYPEDIPPYPTIRRVQSLHAPPSSMI
RSVPISRTEVPPDDEPAYCPRPLYQY
KPYQSSQARSDYHVTQLQPYFENGR
VHYRYSYSSSSSSSYSPDGALCDVD
AYGTVQLRPLHRLPNRDFAFYNPRL
QGKSLYSYAGLAPRPRANVTGYFSP
NDHNVVSMPPAADVKHTYTSWDLE
DMEKYRMQSIRRESRARQKVKG PV
MSQYDNMTPAVQDDLGGIYVIHLRS
KSDPGKTGLLSVAEGKESRHAAKAIS
PEGEDRFYRRHPEAEMDRAHHHGG
HGSTQPEKPSLPQKQSSLRSRKL PD
MGCSLPEHRAHQEASHRQFCESKN
GPPYPQGAGQLDYGSKGIPDTSEPV S
YHNSGVKYAASGQESLRLNHKEVRL
SKEMERPWVRQPSAPEKHSRDCYK
EEEHLTQSIVPPP K PERSHSLKLHHT
QNVERDPSVLYQYQPHGKRQSSVTV
VSQYDNLEDYHSLPQHQRGVFGGG
GMGTYVPPGFPHQSRTYATALGQG
AFLPAELSLQHPETQIHAE