

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane
P46940	IQGA1_HUMAN	Homo sapiens	Ras GTPase-activating-like protein IQGAP1	18.201546	S256;T435	S2;T172;S330;S1441;S1443	16408927;38665916;33214551;23301498;34019948;26853435;34725712;35008409;37217939;29351928	MSAADEV DGLGVARPHYGSVLDNE RLTAEEM DERRRRQNVAYEYLCHLEE AKRWMEACLGEDLPPTTELEEGLR NGVYLAKLGNFFSPKVVS LKKIYDRE QTRYKATGLHFRHTDNVIQWLNAM DEIGLPKIFYPETTTDIYDRKNMPCRY CIHALSLYLFKGLAPQIQDLYGKVD FTEEEINNMKTELEKYGIQMPAFSKI GGILANELSVDEAALHAAVIAINEAI DRRIPADTFAALKNPAMLVNLEEP LASTYQDILYQAKQDKMTNAKNRTE NSERERDVYEELLTQAEIQGNINKV NTFSALANIDLALAQGDALALFRALQ SPALGLRGLQQQNSDWYKQLLSDK QQKRQSGOTDPLQKEELQSGVDA NSAAQQYQRRLAVALINAAIQGV AEKTVLELMNPEAQLPQVYFFAADL YQKELATLQRQSPENLTHPELSVA VEMLSVALINRALESQDVTNVWQ LSSSVTGLTNIEEENCORYLDELK LKAQAHAENNEFITWNDIQACVDH VNLVVQEEHERILAIGLINEALDEGD AQKTLQALQIPAAKLEGLAEVAQHY QDTLIRAKREKAQEIQDESAVLWLD EIQGGIWQSNKDTQEAQKFBALGIFAI NEAVESGDVGTSLALRSPDVGLYG VIPECGETYHSDLAEAKKKLAVGD NNSKWWKHVWVGGYHHNLETQE GGWDEPPNFVQNSMQLSREEIQSSI SGVTAAYNREQLWLANEGLITRLQA RCRGYLVRRQEFRRSMNLFKKQIPAIT CIQSQRGKQKAYQDRLAYLRSH KDEVVKIQSLARMHQARKRYRDLQ YFRDHINDIHKIQAFIRANKARDYKT LINAEDPPMVVVRKFVHLLDQSDQD FQEELDLMKMREEVITLIRSNQOLE NDLNLMDIKIGLLVKNKITLQDVVS HSKKLTKNKEQLSDMMINKQKQ GLKALSKEKREKLEAYQHLLFYLLQT NPTYLAKLIFQMPQNKSTKFMDSVI FTLYNYASNQREEYLLRLFKTALQE EIKSKVDQIQEIVTGNPTVIKVVVVF NRGARGQNALRQILAPVVKEIMDDK SLNIKTDVPDIKSWVNQMESQTGE ASKLPYDVTPEQALAHAEVKTRLDSS IRNMRAVTDKFLSAIVSSVDKIPYGM RFIAKVLKDSLHEKFPDAGEDLLKI IGNLLYRYMNPVAVPDAFDIIDL GGQLTTDQRRNLGSIKMLQHAAS NKMFLGDNAHLSIINEYLSQSYQKF RRFFQTACDVPELQDKFNVDDEYSDL VTLTKPVIYISIGEIHNTHTLLDHDQD AIAPEHNDPIHELLDDLGEVPTIESLI GESSGNLNDPNKEALAKTEVSLTTL NKFDVPGDENAEAMDARTILLNTKRL IVDVIRFQPGETL TEILETPATSEQEA EHQRAMQRRRAIRDAKTPDKMKKSK SVKEDSNLTQEKKEKIQTGLKCLTE LGTVPKKNYQELINDIARDIRNQR YRORRKAELVKLQQTAAALNSKATF YGEQVDYKSYIKTCLDNLASKGKVS KKPREMKGKSKKISLKYTAARLHE KGVLEIEDLQVNFKNVIFEISPT EVGDFEVKAKFMGVQMETFMLHYQ DLLQLQYEGVAVMKLFDRAKVVVN LLIFLLNKKFYGK	True	True	4.733	5.0	1.845	1.799	1.689	5.0