

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ext reg
Q3UGY8	BIG3_MOUSE	Mus musculus	Brefeldin A-inhibited guanine nucleotide-exchange protein 3	25.573173	S13	S471;S628;S632;S1045;S1881;S1975;S1984;S2072;S2074;S2088;S2094;S2096	33300544;34418053	MEEILRKLQRDASGSKYKAIKESCT WALETLGGLDVTVVKIPPHLLREKCLL PLQALAESKNVKAQAHALAGMQKLL SEERFVSMETDSDKQLLNQILNAV KVTPSLNEDLQVEVMKVLCCITYTPT FDMNGSAVLKIAEVCIEITYTCSCHQ RSINTAVRATLSQMLGDLTLQLRQR QENTIENPDAPQEFRSQGLTVEALC DDVISVLAVLCEKLOASINDSQQLQL LYLECILSVLSSSSSMHLHRGFTDL IWKSLCPALVVILGNPIHDKITTSAAHS TSTSTSMESDSASLGVSDHGRGSGC SCTAPTLSGPVARTIYLLAAELVRLVG SVDSMKPVLQSLYHRVLLYPPQHR VEAIKIMKEILGSPQRLYDLGAPSSIE SEPRKRSISKRSKSHDLLKIMDGM TEACIKGGIEACYAAVSCVCTLLGAL DELSQKGLNDTQVQQLLRLEELR DGAESSRDSMEINEADFRWQRRVL SSEHTPWESGNERSPDISVTTDTG QTTLEGELGQTTPEDHKNGLKSPAI QEGKGTMGKVSEPEAIDQPDVVQRS HTVPPDITNFLSVDCTRTRSYGSRYS ESNFSVDDQDLRTEFDSCDQYSM AAEKDSGRSDVSDIGSDNCSLADEE QTPRDYIGHRSLRTAALSLLKLNQNE ADQHSARLFIQSLEGLLPRLLALSSV EEVDSALQNFASFCSGMMHSPGF DGGSSLSFQMLMNDLSYTAHCA LLNLKLSHGDYRKRPTVAPGMMK EFMKQVQTSGLVMVFQAWLEELY HQVLDNRNMLGEAGYWGSPEDNSLP LITMLTDIDGLESAIGGQLMASASV ESPFTQSRRLDDSTVAGVAFARYLV GCWKNLIDTLSTPLTGRMAGSSKGL AFILGAEGIKEQNQKERDAICMSLD GLRKAARLSCALGVAANCASALAQM AAASCVQEEKEERQSQEPSDALAQV KLKVEQKLEQMGKVQGVWLHTAHV LCMDAILSVGLEMGSHNPDWPHV FRVCEYVGTLEHTHFSDGIGSQPLTI HQPQKTSGSSGLLGEIEFKSSSQEQ SLEQGPSLNTAPVVQPHSIQELVREC SRGRTSDFRGGSLSGNSAAKVLSL STQADRLFDDATDKLNLALGGFLY QLKKASQSQLFHSVTDVYSLTMP GEVSTQDQKSALHLFRLGDAMLRI VRSKARPLLHVRCWLSLVAPHLVEA ACHKERHVSQKAVSFIHDILTEVLT WSEPPHFFNEALFRPFERIMQLEL CDEDVQDQVVTISIGELVEVCSAQIQS GWRPLFSALETVRSGNKSEVKEYLV GDYSMGKGQAPVDFVFEAFNLTDNI QVFANAATSYIMCLMKFVKGLGEVD CKEIGDCVPGAGATSTDCLPALDYL RRCSQLLAKIYKMLPKPIFLSGLAS LPRRLQEQASSEDGIESVLSDFDD DTGLIEVWILLEQLTAAVSNCPRH QPPTDLLFELLRDVTKTPGPGFGIY AVVHLLLPVMSLWLLRSHKDHYSW DVASANFKHAIGLSCELVEHIQSFL HSDIRYESMINTMLKDLFELLVVCV AKPTETISRVCSCIRYVLTAGPVFT EEMWRLACCALQDAFATLKPVKDL LGCFFHGGTEGFSGEGCQVRVAAPSS SPSAEAEYWRIRAMAQVFMMLDTQ CSPKTPNPNFDHAQSCQLIHELPHDE KPNGHAKKSVSFREIVVLSLHQVLL QNYDILLEEFVKGSPGEEKTVQVP DTKLAGFLRYISMQLAVIFDLLLLDS YRTAREFDTSPLGKCLLKKVSGIGGA ANLYRQSAMSFNIFYHALVCAVLTN QETITAEQVKVLFEEEEERSDSSSQ CSSEDEDIFEETAQVSPPRGKEKRO WRARLPSLSVQPVSNADWWVLVLR LHKLCMELCNHYIQMHLDLLESSLE EPLTFKSDPFFILPSFQSESTPSTGG FSGKNTPEDDRRHLESEPQSLRVG SGDMLMLPPSPKTEKKDPGRKKEW WESAGNKICTMAADKTIKLMTEYK	False	False	1.482	2.045	1.372	0.745	2.556	1.331	1.50

