

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P34756	FAB1_YEAST	Saccharomyces cerevisiae	1-phosphatidylinositol 3-phosphate 5-kinase FAB1	9.365641	NaN	S186;S1627;S1630;S1938;T1953	33229814	MSSEEPHASISFPDGS HVRSSTGT SSVNTIDATLSRPNYIKKPSLHIMST STTSTTTDLVTNPILSNISVPKISPPTS SSIATATSTSHVTGTASHSNIKANAN TSTSVNKKNLPTTSGRIPSSSTIKRYP SRYKPSHSLQLPIKNDNFKRSSIIYA SKSTVTAIPRNNRPISMQNSYARTP DSDHDDVGDEVSSIKSASSSLTASLS KSFLFAFYNNRKKDKTSNNGVLSKE YWMKDESSKECFSCGKTFNTFRRK HHCRCGQIFCSSCTLLIDGDRFGCH AKMRVCYNCYEHADTYEDSSDEEN DSTMQLNEPRSRSRSSNTNPYSH SHSHLHLISQDNHNGTDLHDPVAAT DNPQQQNEVYLLNDDDVQSIMTSG EDSKLFISTPPPPPKMAIPATKQGGG LEISFDSENDRALHYQDDNPGRHH HLDSVPTRYTIRDMNISHYDTNSN STLRPHYNTNSTITINNLNNTTSN NSNYNNTNSNSNINNPAAHSLRRSIF HYVSSNSVNKDSNNSSATPASSAQS SSILDPANRIIGNYAHRNYKFKFNYN SKGPSQQNDTANGNNDNNNNNNN NNNNNNNSASGIADNNNIPSDN GTTFTLDKKRNPLTKSKSTSAYLEY PLNEEDSSEDEGSMSIYVLNDDHK TDNPIRSMRNSTKSFQRAQASLQR MRFRRKSKSKHFPNNSKSSYRDLN FLTNPSTPNLLSVVSDDNLYDDSSPL QDKASSAASRLTDRKFSNSSGSNN NSNSNSNINTDPWKRIASISGFKLK KEKKRELNEVSLHMHALLKQLLN DQEISNLQEWITLLDGALRKVLRTIL NARDLNTLDFRQTYVKIKRISGGSPQ NSEYIDGVVFSKALPSKTMPRHLKN PRILLIMFPLEYQKNNNHFLSIESVF RQEREYLDKLVSRKSLHPDIIYVGA NVSGYALELLNDSGIVVQFNMKPQV IERIAKLTEADIAISVDKLATNIKMGE CETFVKSYYGNISKTYTFLRGCNP ELGGTILLRGDSLENLRKIKQVSEFM VYAFSLKLESSFFNDNFQIQLSTDVY LKRAESKKLQVFEQYFADFLIKFNN RILTVSPTVDFPIPFLEKARGLEKKL IERINQYESESDLDRQTQLNMLQGL ESTITKKHLGNLIKFLHEMEIENLEL EFQKRSRQWEVSYSSSQNLLGTGSH QSITVLYSMVSTKTATPCVGPQIVTID YFWWSDISIGQFIENVVGTARYPCQQ

GCNGLYLDHYRSYVHGSGKVDVLE
KFQTRLPKLKDII LTWSYCKKCGTST
PILQISEKTWNHSGKYLEVMFWSY
KDSVTGIGKCPHDFTKDHVKYFGYN
DLVVRLEYS DLEVHELITPPRKIKWK
PHIDIKLKV ELYYKILEKINNFYGSVL
SRLERIKLDSMTKDKVLSGQAKIHEL
KSNATEEQKLM LQDLDTFYADSPCD
QHLPLNLVIKSLYDKAVNWNSTFAIF
AKSYLPSETDISRITAKQLKKLFYDSS
RKDSEDKKS LHDEKAKTRKPEKNEL
PLEGLKDVEKPKIDSKNTTENRDRT
NEPQNAV TITTFKDDTPIIPTSGTSHL
TVTPSASSVSSSLTPQTEERPPISRSG
TGISMTHDKSTRPNIRKMSSDSSLC
GLASLANEYSKNNKVSKLATFFDQM
HFDALSKEFELE RERERLQLNKDY
QAIRLQTSTPIVEIYKNVKDAVDEPL
HSRSSGNLSSANVKTLEAPVGEHS
RANNCNPPNLDQNLETELENSISQ
WGENILNPSGKTTASTHLNSKPVVK
ETSENPKSIVRESDNSKSEPLPPVITT
TTVNKVESTPQPEKSLLMKTLNFW
ADRSAYLWKPLVYPTCPSEHIFTDSD
VIIREDEPSSLIAFCLSTSDYRNKMM
NLNVQQQQQQQTAEAAPAKTGGNS
GGTTQTGDPSVNISPSVSTTSHNKG
RDSEISSLVTTKEGLLNTPPIEGARD
RTPQESQTHSQANLDTLQELEKIMT
KKTATHLRYQFEGLTVMSCKIFFTE
HFDVFRKICDCQENFIQSLSRCVKW
DSNGGKSGSGFLKTLDDRFIKELSH
AELEAFIKFAPSYFEYMAQAMFHDL
PTTLAKVFGFYQIQVKSSISSSKSYK
MDVIIMENLFYEKKTTRIFDLKGSM
RNRHVEQTGKANEVLLDENMVEIYY
ESPIHVREYDKKLLRASVWNDTLFL
AKMNVMDYSLVIGIDNEGTYTLTVGII
DFIRFTWDDKLESWVKEKGLVGGGA
SVIKQPTVVTPROYKKRFREAMERYI
LMVPDPWYREGN