

| 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 | extracellular region |
|--------------|------------|--------------------------|--------------|--------------|---------------|--|----------|---|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|-----------------|----------------------|
| P38041 | BOB1_YEAST | Saccharomyces cerevisiae | Protein BOB1 | 24.475439 | NaN | S104;S106;S128;T151;T158;S209;S393;S412;S525;S528;S589;S590;S593;S644;S655;S735;T919 | 33229814 | MSLEGNTLGKGAKSFFPLYIAVNQYS KRMEDELNMKPGDKIKVITDDGEYN DGWYYGRNLRRTKEEGLYPVFTKRI AIEKPENLHKSPQESGNSGVKYGN LNDSASNIGKVSSHQQENRYTSLKS TMSDIDKALEELRSGSVEQEVSKSPT RVPEVSTPQLQDEQTLIQEKTRNEE NTTHDSLFSSTADLNLSSSELKNISK SNISTKSLEPSSSESVRQLDLKMAKS WSPEEVTDYFSLVGFQDSTCNKFKF HQVSGKILLELEHLEHLKEINSEFGI RFQIFKEIRNIKSAIDSSNKLDADYS TFAFENQAAQLMPAATVNRDEIQQQ ISSKCNKLSSESDRKSSTVTELR PSSVVVNPFKLHDPAEQILDMTEV PNLFADKDFESPRAPKPPSPSPV QPPQSPFNRYTNNNARFPQTTY PPKNKNPTVYNSGLIPNSSTSSDNST GKFKFPAMNGHDSNRKTTLTSATI PSINTVNTDESLPAISNISSNATSHH PNRNSVVYNNHKRTESGSSFVDLF NRISMLSPVKSSFDEEETKQPSKAS RAVFDSARRKSSYGHSDASLSEMK KHRRNSSILSFSSKQSNPTSPKQ TFTIDPAKMTSHRSQNSYSHARS QSYSHSRKHSVTSPLKTSLSPINSK SNIALAHSETPTSSNNKEAVSQPSE GKHKHKHKHKSKHKHKNSSSKDGS SEEKSKKLFSTKESFVGSKEFKRS PSELTQKSTKSILPRSNAKKQQTSAF TEGIRSITAKESMQTADCSGWMSSK GTGAMGTWKQRFFTLHGTRLSYFT NTNDEKERGLIDITAHRLPASDDD RLISLYAASLGKGKCYCFKLVPPQPGS KKGLTFTEPRVHYFAVENKSEMKA WLSAIIKATIDIDTSVPVISSYATPTIP LSKAQTLLEEARLQTLRDAEEEEG RDQFGWDDTQNKRNPNYPIEQDQF ETSDYLESSAFEYPGGRL | None | None | None | None | None | None | None | | |

0