

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P32873	BEM3_YEAST	Saccharomyces cerevisiae	GTPase-activating protein BEM3	9.365641	NaN	S254	33229814	<p>MTDNLTTTHGGSTTLELLAQYNDHR  SKKDKSIEHIEKGTCSGKERNPSYDE  IFTENIKLKLQVQEYETEIESLEKVID  MLQKNREASLEVVLQVQVQNDSDRS  YVNDQSFVLPPrSAERKAHIKSLNLP  IPTLSPPLQOGSDVALETSVTPTVPQI  GVTSNITSIRKHLQNMILNDEIEAN  SSFSSPKIINRSVSSPTKIHSEQLASP  AASVTYTTSRITIKSPNKGSKSPLQER  LRSPQNPNRMTAVINNHLHSPLKAS  TSNNLDELTESKSQQLTNDAIQKND  RVYSSITSSAYTTGTPTSAAKSPSSLL  EVKEGENKALGFSPASKEKLDDFTQ  LLDSSFGEEDLVNTDSKDPLSIKSTI  NESLPPPPAPPTFFSPTSSGNIKNST  PLSSHASPVLNKKDDNFGAQSASAK  NLKKPVLTSPLNLTSTKLTSSQNAS  LPPNPPVESSSKQKQLGETASIHSTN  TLNTFSSTPQGS�KTLRRPHASSVST  VKSVAQSLKSDIPLFVQPEDFGTIQIE  VLSTLYRDNEDDLSILIAIDRKSKE  MFKFSKSIHKVRELDVYMKSHVPDL  PLPTLPDRQLFQTLSPKVDTRKNIL  NQYYSIFSVPEFPKNVGLKIAQFIST  DTVMTPPMDDNVKDGSLLLRRPK  TLTGNSTWRVRYGILRDDVLFQFDK  NQLTETIKLRQSSIELIPNLPEDRFGT  RNGFLITEHKKSGLSTSTKYICTET  SKERELWLSAFSDYIDPSQSLSSSS  RNANDTDSASHLSAGTHHSKFGNA  TISATDTPSYVTDLTQEYNNNNNIN  SSNNIANSDGIDSNPSSHSNFLASS  SGNAEEEEKDSRRAKMRS�FPFKLT  GPASAMNHIGITISNDSPTSPTSII  KSPSKLMEVSSSSNSSTGPHVSTAI  FGSSLETCLRLSSHKYQNVYDLPSV  VYRCLEYLYKNRGIQEEGIFRLSGSS  TVIKTLQERFDKEYDVLCRYNESIE  AKDDEASPSLYGVNTVSGLLKLYLR  KLPHLLFGDEQFLSFKRVVDENHN  NPVQISLGFKELIESGLVPHANLSLM  YALFELLVRINENSKFNKMNLRLC  IVFSPTLNIPISMLQPFITDFACIFQG  GEPVKEEEREKVDIHIPQV</p>