

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasm meml
Q86U86	PB1_HUMAN	Homo sapiens	Protein polybromo-1	16.935769	S681	S10;S39;S131;T134;S178;S316;S319;S353;S355;S371;S375;S498;S509;S636;S648;S689;S948;S987;S1119;T1289;S1405;S1453	40596516;34019948;30379171	MGSKRRRATSPSSSVSGDFDDGHH SVSTPGPSRRRRRLSNLPTVDPIAVC HELYNTIRDYKDEOGRLLCELFIRAP KRRNQPDYEEVVSQPIDLMKIQQKL KMEEYDDVNLTLADFQLLFNNAKSY YKPDSPPEYKAACKLWDLYLRTNRF VQKGEADDEDDDEDGQDNQGTVTE GSSPAYLKEILEQLLEAIVVATNPSG RLISELFQKLPKSVQYPPDYAIIKEPI DLKTIARQIQNGSYKSIHAMAKDIDL LAKNAKTYNEPGSQVFKDANSIKKIF YMKKAIEIHHHEMAKSSLRMRTPSN LAAARLTGSPSHSKGSLGEERNPTSK YYRNKRAVQGGRLSAITMALQYQSE SEEDAALAAARYEEGESEAESITSM DVSNPFYQLYDTRVSCRNNQGGQLIA EPFYHLPSKKKYPDYQQIKMPISLQ QIRTKLKNQYETLDHLECDLNLMF ENAKRYNVPNSAIYKRVLKLQVVMQ AKKELARRDDIEDGDSMISSATSDT GSAKRKSKKNIRKQRMKILFNVVLE AREPGSGRRLCDLFMVKPSKKDYPD YYKIILEPMDLKHIEHNIRNDKYAGEE GMIEDMKLMFRNARHYNEEGSQVY NDAHILEKLLKEKRKELGPLPDDDD MASPKLKLSRKSGISPKKSKYMTPM QQKLEVVYEAVKNYTDKRGRRLSAI FLRLPSRSELPDYLLTKKPMDEMEKI RSHMMANKYQDIDSMVDFVMMF NNACTYNEPESLIYKDALVHLKVLLE TRRDLEGDEDSHPVNTLLIQELIH NLFVSVMSHQDDEGRCSYDSLAEIP AVDPNPNKPLTFDIIRKNVENNRY RRLDLFQEHMFVLEERARRMNRD SEIYEDAVELQQFFIKIRDELCKNGEI LLSPALSYTTKHLHNDVEKERKEKL PKEIEEDKLRKREKREAEKSEDSSG AAGLSGLHRTYSQDCSFKNSMYHV GDYVYVEPAEANLQPHIVCIERLWE DSAGEKWLYGCWFYRPNETFHLAT RKFLEKEVFKSDYYNKVPVSKILGKC VVMFVKEYFKLCPENFRDEDVFCV SRSYAKTKSFKKIKLWTPISSRVFV PRDVPLPVVRVASVFANADKGDDEK NTDNSEDRAEDNFNLEKEKEDVP VEMSNGEPGCHYFEQLHYNDMWL KVGDCVFIKSHGLVPRVGRIEKVV VRDGAAYFYGPFIHPEETEHEPTKM FYKKEVFLSNLEETCPMTCILGKCAV LSFKDFLSCRPTIEPENDILLCESRY NESDKQMKKFKGLKRFSLSAKVVD DEIYYFRKPIVPQKEPSLLEKKIQLL EAKFAELEGGDDIEEMGEEDSEVI EPPSLPQLQTLASELDLMPYTPPQS TPKSAGSAKKEGSKRKINMSGYILF SSEMRAVIKAQHPDYSGELSRVVG TEWRNLETAKKAEYEEAAKVAEQQ ERERAAQQQPSASPRAGTPVGALM GVVPPTPMGMLNQQTLVAVGMMG GYPPGLPPLQGPVDGLVSMGSMOPL HPGGPPPHLPPGVPLGPIPPGV MNQGVAPMVGTAPGGSPYGOQVG VLGPPGQAPPYYPGPHAGPPVIQQ PTPPMFVAPPKTRLLHSEAYLKYI EGLSAESNSISKWDQTLAARRRDVH LSKEQESRLPSHWLKSKAHTTMA DALWRLRDLMLRDTLNIRQAYNLE NV	True	False	1.594	5.0	False	False	False	False