

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	extracell region
Q9JKS6	PCLO_RAT	Rattus norvegicus	Protein piccolo	36.054081	NaN	S211;S231;S857;S869;T873;T1133;S1304;S1314;S1315;S1344;S1346;S1349;S1350;S1353;S1451;S1463;S1464;S1466;S1469;S1493;S1496;S1517;S1519;T1564;S1565;S1575;S1587;S1650;T1652;S1654;S1659;S1720;S1721;T1772;S1778;S1807;S1812;S1820;S1841;S2511;T3014;S3374;S3388;T3392;T3419;S3522;S3530;S3561;S3565;S3571;S3574;S3577;S3598;S3624;S3626;S3632;S3781;S4034;S4150;S4304;S4308;S4311;S4340;S4376;S4609;S4723	18683930;38843836	MGNEASLEGEGLPEGLAAAGAGG SGSALHPGIPAGMEADLSQLSEEER RQIAAVMSRAOGLPKGVSPPAAAES PSMHRKQELDSSQAPQPGKPPDP GRPTQPGLSKSRRTDTFRSEQKPLG RSPSTISLKEKSRRTDFKEEYKSSMM PGFFSDVNPLSAVSSVVNKFNPFDLI SDSEASQEETTKKQKVVOKEQKSE GMAKPPLQPPSPKPIPKOQGVKEV IQDSSPKSVSSQAEKVKPQAPGT GKPSQQSPAQTPAQASPGKPAVAQ PGSAKATVQQPGPAKSPAQAGTGK SPAQPPAKTPGQQAAGLEKTSSSQOP GPKSLAQTGPHGKFFLPGVVKSPAQQ PGTAKHPAQQPGPQTAAKVPGPTKT PAQQSGPGKTPAQQPGPTKPSQQPI PAKPQQQPVATKTQPPQSAFAKPP PQQPAPAKPQQQPTPAKPQQPPPT PAKPQQPPPTATKPPQPPPTATKPH HOQPLAKPSAQOQTKSISQTVTGR PLQPPPTAAQTPAQGLSKTICPLCN TTELLLHIPEKANFNTECTEQSTVCS LCGFNPNPHLTEIKEWLCLNCQMQ RALGGDLAAIPSSPQPTPKAATAPT ATASKSPVPSQQASPKKEPPSKQDSP KALESKKPPPEKPPPEKPPPEKPP PPLVKQPTLHGPTPATAPQLPVAEAL PEPAPKPEPSGPLPEQAKAPVGDVEP KQPKMTETRAIQSSSTTKPDILSSQ VQSQAVKTAASPLKTDKSAKPSQSFPP TGEKTPLDKAMPRPASDSKISIQP GPGSEKDPKHIDPIQKKDEPKKAQP KGSFKPETKPVKPGSPTPSGTRFTAG QAAPPSQPPKQEQSRRFSLNLGG ITDAPKSQPTTPOETVTKLFGFGAS IFSQASNLISTAGQQGPHPQTGPAAP SKQAPTPSQSPAAGPAKSTGQLPP APAKATAVKKKAKAAAENLESKPE QAPTAKKTEKDKKPPPAKVGKPPSE PEKAVPAHKPDKTTKPKPACPLCRTE LNLGSQEPNFNTECKNQVCNL CGFNPTPHLTEIQEWLCLNCQTORA ISGQLGDMGKMPPAPSGPKASMPMA PAEPSSQKTPGTQVKGKKKEAEGK TEAEKPVPEKETASIEKTPPMVTTDQ KLEESGKSKVSALPEKKPSEEEKA ISADKKERKPAEEKPPELEKPIPV DKKLPPEAKPLSSEGEKHEILKAHV QIPEEPTGKVAAGEEEEQPDSP PEALPGATPLTLPKAGEKERAVAQPQ AEGSSKDGQERSKEKTEKEEDKSD TSSSQPKSPQGLSDTYSSDGISGS LGEIPSLIPSEKDLLKGLKDSFSQ ESSPSSDLAKLESTVLSILEAQAST LVGEKAEKKTQPKISPEKPQDQK TQTASETLDTISEEEIKESQEKVSP KDDSEQGFPSRKEHKEKPELVDDL PRRASYDSVEDSSESENSPVVRRKR RTSIGSSSDYEKQEDSQSGSEED FIRKQIEMSADEADASGEDEEFIRS QLKEISVGVESQKREEAKGKGKVA GKRRRLTRKSTSFDDAGRRHSW HDEDETFDESPELKFRETQSQSE ELVVAGGGLLRRFTIENLSTIADKY SSESSQKKTILYFDEEPELEMESLTD SPEDRSRREGSSSLHASSFTPGTSPT SVSLDESDSDSPSHKKGESKQQRK ARHRSHGPLLPTIEDSSEEEELREE ELLKEQEKQRELEQQQRKSSSKSK KDKDELRAQRRRERKTPPSNLSPIE DASPTELRQAAEMEELHRSSCSEY SPSIESDPEGFEISPEKIEVQKVYL PAAVLSYPTDEQSVMQEGVQKAL KSAEEMYEEMMQKPHKYKAFPAAN ERDEVFEKEPLYGGMLIEDYIVESLV EDTYNGSVDGSLLTRQEEQNGFMQ QRGREQKVRLEQIYDDPMQKISDL QKEFYELSLHSVVPQEDIVSSSYIIP ESHEIVDLGSMVMSTSEKKLLDAD SAYEELMRRQVQVTDGSSPVQTTI	False	True	3.168	1.497	0.703	False	5.0	1.578	1.289

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 SEPSSESATSVPPSDTPSLTSSISSVCT
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