

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
Q9Y6V0	PCLO_HUMAN	Homo sapiens	Protein piccolo	36.182389	T615;S619;S2382;S2384;T2480;S2598;S2608;T2682;T2796;S2995;T3331;S3631;S3907;S4023	S906;S918;T922;S1356;S1366;S1367;S1396;S1398;S1401;S1402;S1405;S1516;S1517;S1519;S1522;S1546;S1549;S1570;S1572;T1617;S1618;S1628;S1640;S1703;T1705;S1707;S1712;S1773;S1774;T1825;S1831;S1860;S1865;S1873;S1894;S2562;T3069;S3443;T3447;T3474;S3577;S3585;S3615;S3619;S3625;S3628;S3631;S3652;S3678;S3680;S3686;S3835;S4088;S4204;S4358;S4362;S4365;S4394;S4430;S4664;S4778	28411811;28657654;29351928;29485866;30379171;20563614;39302247	MGNFEASLEGEGLPEGLAAAAAAGG GASGACGSPSHTAIPAGMEADLSOLS EEERRQIAAVMSRAQGLPKGVSPPA AAESPSMHRKQELDSSHPPKQSGRP PDPGRPAQPLSKSRTTDTFRSEQK LPGRSPTISLKEKSRITDLKEEHKS SMMPGFLSEVNALSAVSSVVKFN PFDLISDSEASQEEITTKKQKVQKE QKGPEGIKPLQOQPPIKPKOQP GRDPLQDGTTPKSISSSQPEKIKSQP PGTGKPIQGPTQTPQTDHAKLPLQR DASRPQTKQADIVRGESVKPLSPSP KPPIQOPTPGKPPAQPPGHEKSPQG PAKPPAQPSGLTKPLAQPGTVKPPV QPPGTTKPPAQPLGPAKPPAQQTGS EKPSSEQPGPKALAQPPGVGKTPAQ QPGPAKPTTQVGTGPKPLAQPGLO SPAKAPGPTKTPVQPPGPGKIPAQQA GPGKTSAAQQTGPTKPPSQLPGPAK PPQQPGPAKPPPPQPGSAKPPSQPP GSTKPPQPPGPAKPSPPQPGSTKP PSQQPGSAKPSAQPPSAKPSAQQS TKPVSTGSGKPLQPPTVSPSAKQPP SQGLPKTICPLCNTTELLLVHVEKAN FNTCTECQTTVCSLTCGFNPNPHLTE VKEWLCCLNCKMRAKGGDLAVPVS SPOPKLKTAPVTTTSAVSKSSPPQPP TSPKKDAAPKQDLSKAPEPKPPPLV KQFTLHGSPSAKAKQPEADSLSKP APPKEPSVPSEQDKAPVADDPKPKQ KMWKPTTDLVSSSSATTKPDISSKV QSQAEEKTTPPLKTDKAKPSQSFPT GEKVSFFDSKAIIPRASDSKIISHPGP SSESKGQKQVDPVQKKEPKKAQTK MSPKPAKMPKGSPTPPGPRPTAG QTVPTPQQSPKQEQSRRFSLNLGSI TDAPKSQPTTTPQETVTGKLFQFGASI FSQASNLISTAGQPGPHSQSGPGAP MKQAPAPSQPPTSQGPPKSTGQAPP APAKSIPVKKETKAPAAEKLEPKAEQ APTVKRTEKTKPPPIKDSKSLTAEF QKAVLPTKLEKSPKPESTCPLCKTEL NIGSKDPPNFNTCTECKNOVCNLCG FNPTPHLTEIQEWLCLNCQTRAIS GQLGDIRKMPPAPSGPKASMPVPT ESSSQKTAVPPQVKLVKKQEQEVKT EAEKVILEKVKETLSMEKIPPMVTTD KQEQESKLEKDKASALQEKKPLPEE KKLIPPEEKIRSEKPLLEKKPTPE DKLLPEAKTSAPEQKHDLKKSQV QIAEEKLEGRVAPKTVQEGKQPOTK MEGLPSGTQSLPKEDDKTTKTIKE QPOPPCTAKPDQVEPGKEKTEKEDD KSDTSSSQPKSPQGLSDTGYSSDGI SSSLGEIPSLIPTDEKDILKGLKDSF SQESSPSSPDLAKLESTVLSILEAQ ASTLADEKSEKKTQPHEVSPEQPKD QEKTSLSSETLEITISEEEIKESQEER KDTFKKDSQDIPSSKDHKEKSEFV DDITTRREPYDSVEESSESENSPVPQ RKRRTSVGSSSSDEYKQEDSQSGSE EEDFIRKQIEMSADEDAAGSEDEF IRNQLKEISSSTESQKKEETKGGKI TAGKRRRLTRKSSSTSIDAGRRHS WHDEDEAFDESPKLYRETKSQES EELVVTGGGLRRFKTIELNSTIADK YSAESSQKKTSLYFDEEPELEMESLT DSPEDRSRGEGLSSSLHASSFTPGTSP TSVSSLDSDSSPSHKKGESKQQR KARHRPHGPLLPTIEDSSEEEELREE EELLKEQEKQREIEQQQRKSSSKS KKDKDELRAQRRRERKTPPSNLSPI EDASPTIELRQAAMEELHRSSCSE YSPSIESDPEGFEISPEKIEVQKVYK LPTAVSLYSPTDEQSIMQKEGSQKAL KSAEEMYEEMMHKTHKYKAFPAAN ERDEVFEKEPLYGGMLIEDIYIESLV EDTYNGSVDGSLLTRQEEENGFMQ QKGREQKIRLSEQIYEDPMQKITDLQ KEFYELSLHSVVPQEDIVSSSFIPE	False	False	3.377	2.749	1.354

SHEIVDLGTMVSTEEERKLLDADA
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 EDMTESTMDFDRMPDASLTSSVLS
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