

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
Q9R0L6	PCM1_MOUSE	Mus musculus	Pericentriolar material 1 protein	29.989137	S44;S45;S384;S386;S435;S774;S777;T791;S792;S864	S65;S68;S69;S93;S110;S116;S119;S159;S370;S372;S384;S593;S644;T857;S859;S864;S867;S870;T875;S957;S974;S985;S988;S1182;S1185;S1228;S1254;S1257;S1259;S1260;S1315;S1317;T1466;S1571;S1695;S1729;S1766;S1769;S1777;S1783;S1959;S1978	30059200;36852467;34678516	MATGGGPFEEVMHDQDLPNWSND SVDDRLNNMEWGGQKKANRSSE KNKKKFGVADKRVNTAISPESSPG VGRRRTKIPHTFPHSRYMTQMSVPE QAELEKLRINRINFDLQDRSIGSDSQ GRATAANNKRQLSENKRPFNFLPM QINTNKSKDATALPKREMTTSAQC KELFASALSNDLLQNCQVSEEDGRG EPAMESSQIVSRVQIRDYITKASSM REDLVEKNERSANVERLTHLIEHLK EQEKSYMKFLQKILARDPQQEPMEE TENLKKQHDLKRLMLQQQQLRAL QGRQAALLALQHKAEQAIIVMDDSV VTETTGSLSGVSTSELNEELNDLIQ RFHNQLRDSQPPAVPDNRRQAESLS LTREISQSRNPSVSEHLPDEKVLFS KMRVLQEKKQKMDKLLGELHNLRD QHLNNSFFVPTSLQRSQDKRSSTV ALSAPVGFASAVNGEANSLISSVPCP ATSLVSNQSENEGHLPKAEKLOKL NEVQKRLNELRELVHYEQTSDMM TDAVNENTKDEETESEYDSEHENS EPVTNIRNPQVASTWNEVNTNSNT QCGSNNRDGRPVNSNCEINNRSA NIRALNMPPLDCRYNREGQRLHVA HGEDEEEVEEGVSGASLSRRSS LVDEAPEDEEFQKISRLMAAKEKL KQLQDLVAMVQDDDATQVVVPAAS NLDDFYAAEEDIKQNSNARENSN KIDTGVNEKTRKIFYEAKLQQQRE LKQLQEERKKLIEIQEKIQAQVQKAC DLQLSATSISSGPTKKYLPATSTPTV NENDSSTSKCVIDPEDSSVDNELW SDMRRHEMLREELRQRKQLEALM AEHQRRQGLAETSSPVAISLRSDGSE NLCTPQQRTEKTMATWGGSTQCA LDEGEDDGYLSEGVRTDEEEEEE QDASSNDNFPIYPPSMNQNYSNVKE TKTRWKSNNRPSADGNRYRPLAKTRQ QNISMQRQENLRWVSELSYIEEKEQ WQEQINQLKKQLDFSVNICQTLMO DQOTLSCLLQTLTGPYSVLPNSVAS PQVHLIMHQLNQCYPQLTWQQNNV QRLKQMLTELMRQONQHPEKPRSK ERGSASHPSSPNLFCPFSFPTQPV NLFNLPGFNTNFPFAPGMNFSPLFP SNFGDFSONVSTPTEQQQPLAQNPS GKTEYMAFPKPFESSSSLGAEKQRN QKQPEEEAENTKTPWLYDQEGGVE KPFKFTGFTESVEKATNSNRKNQPD TSRRRRQFDEESLESFSSMPDPIDPT TVTKTFKTRKASQAASLASKDKTPKS KSKRNSTQLKSRVKNIGYESASVSS TCEPKNRRNRHSAQTEEPVQAKLFS RKNHEQLEKIKYSRSAEISSSETGSD FSMFALRDTIYSEVATLISQNESRP HFLIELFHQLLNTDYLQRALYAL QDIVSRHISESDEREGENVKPVNSG TWWASNELTPSESLVTTDDETFKE NFERETHKVSEONDADNVSMVSVS SNFEPFATDDLGNVHLDQALARM REYERMKTETESHNMRCRCRVIED EDGAAAAATVSNSEETPIENHNHPQ PISDVSAPCPRIDTQQLDRQIKAIM KEVIPFLKEHMDEVCSQLLTSVRR MVLTLTQQNDESKEFVKFFHKQLGS ILQDSLAKFAGRKLKDCGEDLLVEIS EVLFNELAFFKLMQDLNNSIAVKQ RCKRKIEAAGVRQSYAKEAKRILEGD HGSPAGEIDDEDKDKDETETVKQTQ TSEVYDAKGPKNVRSVDSDQEEDEE SERCPVSINLSKAESQALTNYGSGED ENEDEEMEDFEESPDIQTSLOANT ETTEENEHDSQILQHDLEKTPESTN VPSDQEPSTKNDQDSSPVKPCYLNIL ENEQQLNSATHKDSLTTDSSKQPE PLPLPLAASETLVPRVKEVKSQETP ESSLAGSPDTEPVLVNDYEAESGNI SQSDEEDFVKVEDLPLKLTIVYSEEE LRKKMIEEEQKNHLSGEICEMQTEE	False	False	2.559	3.964	1.05

