

| UniprotKB ID | Entry name | organism     | full name   | oglcnacscore | oglcnac sites  | phosphorylation sites   | PMIDS  | sequence  |
|--------------|------------|--------------|-------------|--------------|----------------|---|--|---|
| O95613       | PCNT_HUMAN | Homo sapiens | Pericentrin | 9.093789     | T57;T345;T2439 | S44;S188;T191;S610;S682;S1245;S1653;S1712;S2044;S2177;S2192;S2225;S2226;S2327;S2352;S2355;S2477;S2486;S3302 | 30379171;31492838;29351928;34019948;23301498 | MEVEQEQRRRKVEAGRTKLAHFRQ<br>RKTKGDSSHSEKKTAKRKGSAVDAS<br>VQEESPVTKEDSALCGGDIKST<br>CDDTPDGAGGAFAAQPEDCDGK<br>EDLEQLQKQVNDHPPEQCGMFTV<br>SDHPPEQHGMFTVGDHPPEQRGMF<br>TVSDHPPEQHGMFTVSDHPPEQRG<br>MFTISDHQPEQRGMFTVSDHTPEQ<br>RGIFTISDHPAEQRGMFTKECEQEC<br>ELAITDLESGREDEAGLHQSQAVHG<br>LELEALRLSLSNMHTAQLELTQANL<br>QKEKETALTELREMLNSRRAQELAL<br>LQSRQQHELELLREQHAREKEEVVL<br>RCGQEAALKEKQLQSEMENAQIVK<br>TLKEDWESEKDLLENLRKELSAKH<br>QSEMEDLQNFQKELAEQRAELEKI<br>FQDKNQAERALRNLESHHQAIEKL<br>REDLQSEHGRCLEDFKFKESEKE<br>KQLELENLQASYEDLKAQSQEEIRR<br>LWSQLDSARTSRQELSELHEQLLAR<br>TSRVEDLEQLKQREKTQHESELEQL<br>RIYFEKCLRDAEKTYQEDLTLLQQL<br>QGAREDALLDSVEVGLSCVGLLEKP<br>EKGRKDHVDELEPERHKESLPRFQA<br>ELEESHRHQLEALESPLCIQHEGHV<br>SDRCCVETSALGHEWRLEPSEGHS<br>QELPWVHLQGVQDGDLEADTERAA<br>RVLGLETEHKVQLSLLQTELKEEIEL<br>LKIENRNLYGKLOHETRLKDDLEKV<br>KHNLIEDHQKELNNAKQKTELMKQ<br>EFQRKETDWKVMKEELQREAEKEL<br>TLMLELREKAESEKQTIINKFELRE<br>AEMRQLQDQAAQILDRLERSLTEQQ<br>GRLQQLQEDLTSDDALHCSQCGRGP<br>PTAQDGEALALHVKEDCALQLMLAR<br>SRFLEERKEITEKFSAEQDAFLQEAQ<br>EQHARELQLLQERHQQLLSVTAEL<br>EARHQAALGELTASLESKQGALLAA<br>RVAELQTKHAADLGALETRHLSLD<br>SLESCYLSEFQTIREEHRALELLRA<br>DFEEQLWKKDSLHQTLTQELEKLR<br>RKHEGELQSVRDHLRTEVSTELAGT<br>VAHELQGVHQGEFGSEKKTALHEK<br>EETLRLQSAQAQPFHQEESLSLQ<br>LQKKNHQVQQLKQVLSLSHEIEEC<br>RSELEVLQRRERENREGANLLSM<br>LKADVNLSSHARGALQDALRRLLGL<br>FGETLRAAVTLRSRIGERVGLCLDDA<br>GAGLALSTAPALEETWSDVALPELD<br>RTLSECAEMSSVAEISSHMRESFLM<br>SPESVRECEQPIRRVVFQSLSLAVDGL<br>MEMALDSSRQLEEARQIHSRFEKEF<br>SFKNEETAQVVRKHQELLECLKEES<br>AAKAEALALELHKTQGTLEGFKVETA<br>DLKEVLAGKEDSEHRLVLELESRR<br>QLQQAQEAALREECTRLWSRGE |

ATATDAEAREAALRKEVEDLTKEQS  
ETRKQAEKDRSALLSQMKILESELE  
EQLSQHRGCAKQAEAVTALEQQVAS  
LDKHLRNQRQFMDEQAAEREHERE  
EFQQEIQRLEGQLRQAAKQPWGP  
DSQQAPLDGEVELLQKLRKLEDEF  
NELAIQKESADRQVLMQEEIEKRLE  
EMNINIRKKVAQLQEEVEKQKNIVK  
GLEQDKEVLKKQMSLLLASTLQS  
TLDAGRCPEPPSGSPPEGPEIQLEVT  
QRALLRRESEVLDLKEQLEKMKGDL  
ESKNEEILHLNLKLDMONSQTAVSL  
RELEENTSLKVIYTRSSEIEELKATI  
ENLQENQKRLQKEKAEEIEQLHEVI  
EKLQHELMLMGPVVHEVSDSQAGSL  
QSELLCSQAGGPRGQALQGELEAAL  
EAKEALSRLADQERRHSQALEALQ  
QRLQGAEEAAELQLAELEARNVALRE  
AEVEDMASRIQEFEAALKAKEATIAE  
RNLEIDALNQRKAAHSAELEAVLLA  
LARIRRALEQQPLAAGAAPPQLWL  
RAQCARLSRQLQVLHQRFLRCQVEL  
DRRQARRATAHTRVPGAHPQPRMD  
GGAKAQVTGDVEASHDAALEPVVDP  
PQGDLPVLTLDAPLCKQEGVMS  
VLTVCQRQLQSELLVKNEMRLSLE  
DGGKQKEKVLKEDCQLPKVDLVAQVK  
QLQEKLNRLLYSMTFQNVDAADTKS  
LWPMASAHLLLESSWDDSCDGEEP  
DISPHIDTCDANTATGGVTDVIKNQA  
IDACDANTTPGGVTDVIKNWDSLIPD  
EMPDSPIQEKSECQDMSLSSPSTSVL  
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QGPGLLCSPGVSAALALQWAESEPP  
ADDHHVQRTAVEKDVEDFITTSFDS  
QETLSSPPGLEKADRSEKSDGSG  
FGARLSPGSGGPEAQTAGPVTPASIS  
GRFQPLPEAMKEKEVVRPKHVKALLQ  
MVRDESHQILALSEGLAPPSGEPHP  
PRKEDEIQDISLHGGKTQEVPTACPD  
WRGDLLQVVQEAFFEKEQEMQGVLE  
QRLSGSDLGGHSSLLERLEKIIREQ  
GDLQEKSLHLRPLDRSSLLSEIQAL  
RAQLRMTHLQNOEKLOHLRTALTS  
AEARGSQEHQLRRQVELLAYKVEQ  
EKCIAGDLQKTLSEEQEKANSVQKL  
LAAEQTVVRDLKSDLCESRQKSEQL  
SRSLCEVQQEVLQLRSMMLSSKENEL  
KAALQELESEQKGRALQSQLEEEQ  
LRHLQRESQSAKALEELRASLETQR  
AQSSRLCVALKHEQTAKDNLQKELR  
IEHSRCEALLAQERSQSELQKDLAA  
EKSRTLELSEALRHERLLTEQLSRT  
QEACVHQDTQAHHALLQKLKEEKS  
RVVDLQAMLEKVVQQALHSQQQLE  
AEAQKHCEALRREKEVSATLKSTVE  
ALHTQKRELRCSLEREREKPAWLQA  
ELEQSHPRLKEQGRKAARRSAEAR

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|--|--|--|--|--|--|--|---|
|  |  |  |  |  |  |  | QSPAAEQWRKWQRDKKLELEL<br>QRQRDLHKIKQLQQTVRDLESKDEV<br>PGSRLHLGSARRAAGSDADHLREQQ<br>RELEAMRQRLLSARLLTSFTSQAV<br>DRTVNDWTSSNEKAVMSLLHNTLEE<br>LKSDLRPTSSQKKMAAELQFQFVD<br>VLLKDNVSLTKALSTVTQEKLELSRA<br>VSKLEKLLKHHLQKGCSPSRSESA<br>WKPDETAPQSSLRRPDGRLPPAAS<br>EEAHTSNVKMEKLYLHYLRAESFRK<br>ALYQKKYLLLLIGGFQDSEQETLSM<br>IAHLGVFPSKAERKITSRPFTRFRTA<br>VRVIAILRLRFLVKKWQEVDRK GAL<br>AQQKAPRPGPRARQPQSPRTRESP<br>PTRDVPSGHTRDPARGRRLLLLAAASP<br>HSGGRATPSPNSRLERSLTASQDPE<br>HSLTEYIHHLEVIQQLGGVLPDSTS<br>KKSCHPMIKQ |
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