

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9Y520	PRC2C_HUMAN	Homo sapiens	Protein PRC2C	47.391828	S2;S779;S1233;S1280;S1282;S2013;S2021;S2061;S2149;T2155;T2166;S2175;S2186;T2188;T2191;T2192;S2194;S2195;S2196;T2200;T2203;T2211;T2221;T2229;S2233;S2235;T2237;S2238;T2242;T2243;S2245;T2247;S2260;S2268;T2271;S2272;T2273;T2279;S2282;S2284;S2286;S2289;S2330;T2331;T2332;T2349;S2354;S2356;S2380;S2382;T2400;S2409;S2421;T2424;S2425;S2446;S2454;S2461;S2462;S2469;S2477;S2479;S2482;S2486;T2488;S2531;T2583;S2589;S2592;S2633;T2644;T2673;S2680;T2681;T2684;S2685;S2686;T2691;S2692;T2693;S2694;T2717;T2721	S187;S191;S335;S395;S500;S779;S785;S801;S867;S878;S920;S929;S1242;S1246;S1248;S1249;S1263;T1265;T1267;S1544;T1965;S1983;S2013;S2105;S2143;S2260;T2673;T2682;S2686;S2694	32119511;34725712;35132862;23301498;34229054;32574038;22661428;28510447;31373491;21740066;30059200;20068230;35289036;33214551;29237092;30379171;34019948;35254053;20305658;28314751;32870666;37340703;27655845;28657654;34931806;35138101;27114449;30620550;31492838;29351928	MSEKSGQSTKAKDGKKYATLSLFNTYKGSLETQKTTARHGLQSLGKVGISRRMPPANLPSLKAENKQNDPNVNI VPKDGTGWASKQEQHHEEKTPEVPPAQPKPGVAAPPEVAPAPKSWASNKQGGQGDGIQVNSQFQEQEFPSSLQAAGDQEKKEKETNDDNYGPGPSLRPNV ACWRDGGKAAGSPSSSDQDEKLPGQDESTAGTSEQNDILKVVVEKRIACGPQAKLNGQQAALASQYRAMPPPYM FQQYPRMTYPLHGMRFPPSLSET NKGLRGRGPPPSWASEPERPSILSAS ELKELDKFDNLDAAEADGWAGAQM EVDYTEQLNFSDDDEQGSNSPKEN SEDQGSKASENNENKKETDEVSN TKSSSQIPAPQPSVAKVPYKGPSPFNQ ERGTSSHLPPPQLLAQQHPPPDRO AVPGRPGPFPSKQQVADEDEIWKQR RRQQSEISAAVERARRRREEERRM EEQRKAACAELKRLDEKLGILEKQ PSPEEIREREREREREKELEKEQE QEREKEREKDRERQKEKEKELEKE QEKQREMEKERKQEKELERQKE KEKELQKMKEQEKECELEKEREKLE EKIEPREPNLEPMVEKQESSENSCNK EEPVFTRODSNRSEKEATPVVHET EPESGSQPRPAVLSGYFKQFQKSLPP RFQRQQEQMKQQWQQQQQQQGVLPQTVPSPSSSTVPPPHRPLYQPM QPHPQHLASMGFDPRWLMMSYM DPRMMSGRPAMDIPPIHPGMIPPKP LMRRDQMEGSPNSSESFEHIARSAR DHAISLSEPRMLWGS DPYPHAEPQQ ATTPKATEEPEDVRSEAALDQEQITA AYSVEHNQLEAHPKADFIRESSEAQ VQKFLSRSVEDVRPHHTDANNQSA CFEAPDQKTL SAPQEERISAVESQPS RKRSVSHGSNHTQKPDEQRSEPSAG IPKVTSRCIDSKEPIERPEEKPKKEGF IRSSEGPKPEKVYKSKSETRWGPRPS SNRREEVND RPVRRSGPIKKPVL RD MKEEREQRKEKEGEKAEKVTEKVVV KPEKTEKKDLPPPPPPQPPAPIQPQ SVPPPIQPEAEKFPSTETATLAQKPS QDTEKPLEPVSTVQVEPAVKTVNOQ TMAAPVVKEEKQPEKVISKDLVIERP RPDSRPVAVKKESTLPPRTYWKEARE RDWFPDQGYRGRGRGEYYSRGRSY RGSYGRGRGRGRGHTRDYPQYRDN KPRAEHIPSGPLRQRESETRSESSD FEVVPKRRRQRGSETD TDSEIHESA SDKDSLKSKGLPKREERPENKKPKV PHSSFKPDNHVRIDNRLLEKPYVRD DDKAKPGFLPKGEPTRRGRGGTFRR GGRDPGGRPSRSTLRRPAYRDNQ WNPRQSEVPKPEDGEP RRHEQFIP IAADKRPPKFERKFDPARERPRRQRP TRPPRQDKPPFRRLREREAAKSN EVVAVPTNGTVNNVAQEPVNTLGDI SGNKTPDLSNQNSSDQANE EWETA SESSDFNERRERDEKKNADLNAQT VVKVGENVLPPKREIAKRSFSSQRPV

DRQNRGNNPPKSGRNFSGPRNE
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