

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrio
P48634	PRC2A_HUMAN	Homo sapiens	Protein PRC2A	16.999525	S1282;S1619;S1778;T1786;S1788;T1790;S1796;T2093;S2095;T2096	S18;S19;S30;S146;S166;S204;S342;S350;S363;S380;S383;S456;T610;S759;S761;S764;T807;S808;S908;S932;T997;S1004;T1083;S1085;S1089;S1092;T1094;S1106;S1110;T1120;S1147;S1219;S1306;S1310;T1323;S1325;S1328;T1347;T1353;S1384;S1386;S1525;S1778;S2036;T2076;S2082;S2113	38665916;34019948;28657654;33214551;30379171;23301498;39531497;40307207;30620550;20305658;32119511;40596516;40136647;35254053;39894887	MSDRSGPTAKGKDGKKYSSLNLFDTYKGSLSLEIQKPAVAPRRHGLQSLGKVAIARRMPPANLPSLKAENKGNPNVSLVPKDGTVGASKQEQSDPKSSDASTAQPPESQPLPASQTPASNQPKRPPA APENTPLVPSGVKSWAQASVTHGAHGDGGRASSLLSRFSREEFTLQAAGDQDKAAKERESAEQSSGPGPSLRPQNSTTWRDGGGRGPDLEGGPDSKLIHGHDPGRGLQPSGPPQFPYRGMMPPFMYPPYLPFPYGPQGPYRYPTPDGSRFRPVAGPRGSGPPMRLVEPVRPSPILKEDNLKEFDQLDQENDDGWAGAHEEVDTYKLFKFSDEEDGRDSDEEGAEGHRDSQSASGEERPPEADGKKGNSPNSEPPTPKTAWAETSRRPETEPGPPAPKPLPPPHRGPAGNWWPPGDYDPRGGPPCKPPAPEDEDEAWRQRRKQSSEISLAVERRRRREERERMQERRAACAEKLRLEKFGAPDKRLKAEPAAAPSTPAPPAPVPELPPAPPAPPASAPTEPEPEEPAQAPPAQSTPTPGVAAAPTIVSGGGSTSS TSSGSFEASVPEQLPSKEGPEPPEE VPPPTTTPPVKVEPKGDGIGPTRQPPSQGLGYPKYKSLPRFRQRRQQEQLLKQQQQHQWQQHQGSAPTPVPPSPPQVTLGAVPAPQAPPPPKALYPGALGRPPMPPMNFDPWMMIPPYVDPRLQGRPPLDFFYPPGVHPSGLVPRERSDGGSSSEPPDRHAPAMLRERGTTPVDPKLAWVGDVFTATPAEPLTSPLRQAADDDKGRMSETPPVPVPPPYLASYPGFENGA PGPPISRFLEEPGRPLPWPPGSDVAKIOTPPPKKEPPKEETAQLTGPEAGRKPARGVSGGGPPPPRRSRTETRWGPSPGSRRGIPPEEPGAPRRRAGPIKPPPTKVEELPPKPLEQGDETPKPPKPDPLKITKGLGGPKETPPNGNLSPAPLRRDYSYERVGPTSCRRGRGEYFARGRGFRCTYGGRRGARSREFRSYREFRGDDGRGGTGGPNHPPAPRGRTAS ETRSEGEYEEIPKRRRQRGSETGSE THESDLAPSDKEAPTKEGTLTQVPLAPPPGAPSPAPARFTARGGRVFTPRGVPSRRRGGGRPPPQVCPGWSPAKSLAPKKPPTGPLPPSKEPLKEKLIPGPLSPVARGGSGNSVGMEDGERPRRRRHGRAQQQDKPPFRRLKQERENAARGSEGKPSLTLPASAPGPEEALTTVTVAPAPRRAAAKSPDLNQN SDQANEWETASESSDFTSERRGDK EAPPVLLTPKAVGTPGGGGGAVPGISAMSRGDLRSQRAKDLKRSFSSQ RFGMERQNRPGPGKAGSSGSSSGGGGGPGGRTGPRGDKRSPWSPKNRSRPEERPPGLPLPPPPSSSAVFRLLDQVHNSNPAIQALQSSRQGSVTAPGGHPRHKPGLPOAPQGPSPRPPTRYEPQVNSGLSSDPHFEEPPPMVIRGVGTPRDSAGVSFPPKRRE RPPRKPELLQEESLPPPHSSGFLGSKPEGPGQAESRDGTALTPHIWNR LHTATSRKSYRPSMMEPWMEPLSPFEDVAGTEMSQSDSVDLSGDSQVSSGPCSRSSPDGGLKAAEGPPKRFPGSSPLNAVPCGPPGSEPPRRPPAPHDGDRKELPREQPLPPGPIGTERSQRDRGTGTEGPIRPSHRGPPVQFGTSDKDSDLRLVVGDSLKAEKELTASVTEAIPVSRDWELLPSAAAESAEPQSKNLD SGHCVPPEPSSSQRLYPEVFGYSA GPSSSQISGGAMDSQLHPNSGGFRPGTPSLHPYRSQPLYLPPGAPPSALLSGLALKGQFLDFSTMQATELGKLPAGVLYPPPSFLYSPAFCPSPLPDTSLLQVRQDLPSPSDFYSTPLQPGGQSGFLPSGAPAAQMLLPMVDSQLPVVNF GSLPPAPPAPPPLSLLPVGPAIQPP	True	False	4.383	4.512	False

