

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q96L91	EP400_HUMAN	Homo sapiens	E1A-binding protein p400	29.990194	T700;S701;S702;T703;S704;S705;S710;S717;T1488;T1492;T1493;S1495;T1526;S1527;S1530;S1532;S1540;S1543;S1547;T1624;T1627;T2604;T2605;S2608;T2615;S2624;S2631;T2638;T2646;S2686;T2689;T2691;S2696;T2699;T2700;T2707;S2708;T2710;S2712;T2716;T2717;T2720;T2724;S2728;S2734;T2737;T2877;T2878;T3019;T3023;T3024;S3027;T3081;T3094	S53;S135;S315;S321;S736;S755;S928;S941;T945;S1011;S1547;S1728;S1732;S2686;T2813	34725712;35132862;31637018;23301498;22661428;30059200;33214551;35289036;29237092;29351928;30379171;34019948;35254053;28314751;37340703;27655845;28657654;35138101;34846842;30620550;31492838;32574038	MHHGTGPNVQHQQLQSRACPGSE GEEQPAHPNPPSPAAPFAPSASPSA PQSPSYQIQQLMNRSPATGQNVNIT LQSVGPVVGNGQKITLAPLPLPSPTS PGFQFSAQPRRFEHGSFSYIQVTSPL SQQVQTQSPQSPGPGQALQNVRA GAPGPTGLGLCSSSFTGGFVDASVLV RQISLSPSSGGHFVFDGSGLTQIAQ GAQVQLQHPGTPITVRRRRPSQPHT QSGGTIHHLGPQSPAAAGGAGLQPL ASPSHITTANLPPQISSIIQQQLVQQQ QVLQGPPLPRPLGFERTPGVLLPGA GGAAGFGMTSPPPPTSPSRTAVPPG LSSLPLTSVGNVTGMKKVPKLEEIPP ASPEMAQMRKQCLDYHYQEMQALK EVFKEYLIELFFLQHFQGNMMDFLA FKKKHYAPLQAYLRQNDLDIEEEEE EEEEEEKSEVINDEVKVVVTGKDGQ TGTPVAIATQLPPKVSAAFSSQQQPF QQALAGSLVAGAGSTVETDLFKRQQ AMPSTGMAEQSKRPRLEVGHQGVV FQHPGADAGVPLQQLMPTAQGGMP PTPQAAQLAGQRQSQQQYDPSTGPP VQNAASLHTPLPQLPGRLLPAGVPT AALSSALQFAQQPVVEAQTQLQIPV KTQQPNVPIAPPSSQLPIPPSQPAQ LALHVPTPGKVQVQASQLSSLPQMV ASTRLPVDPAAPCPRPLPTSSTSSLA PVSGSGPGSPARSSPVNRPSSATN KALSPVTSRTPGVVASAPTQKQSPAQ NATSSQDSSQDTLLEQITLENQVHQ RIAELRKAGLWSQRRLPKLQEAPRP KSHWDYLLEEMQWMATDFAQERR WKVAAAKKLVRTVVRHHEEKQLRE ERGGKEEQSRLRRIAASAREIECFW SNIEQVVEIKLRVELEKRRKKALNLQ KVSRRGKELRPKGFDAEQESSLDSC MSGRRKASISLTDDEVDDEEETIEE EEANEGVVDHQTELSNLAKEAELPL LDLMKLYEGAFPLPSSQWPRPKPDGE DTSGEEDADDCPGDRESRKDLVLID SLFIMDQFKAERMNIGKPNAKDIA DVTAVAEAILPKGSARVTTSVKFNAP SLLYGALRDYQKIGLDWLAKLYRKN LNGILADEAGLGTQVQIIAFFAHLAC NEGNWGPLVVRSCNLIKWELEL KRWCPGLKILSYIGSHRELKAKRQE WAEPNSFHVCIITSYTQFFRGLTFT RVRWKCLVIDEMQRVKGMTERHWE AVFTLQSQRLLIDSPLHNTFLEL WTMVHFLVPGISRPYLSPLRAPSEE SQDYHKKVVIRLHRVTQPFILRRTRK DVEKQLTKKYEHLKCRLSNRQKAL YEDVILQPGTQEALKSGHFVNVLSIL VRLQRICNHPGLVEPRHPGSSYVAG PLEYPSASLILKALERDFWKEADLSM FDLIGLENKITRHEAELSKKKIPRKL MEEISTSAAPAARPAALKASRLFQ PVQYQKPEGRTVAFPSTHPPRTAA PTTASAAPQGPLRGRPIATFSANPE AKAAAAPFQTSQASAPRHQPASA SSTAASPAHPAKLRAQTQAQASTPG

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