

UniprotKB ID	Entry name	organism	full name	oglcnaescore	oglcnae sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
Q96L91	EP400_HUMAN	Homo sapiens	E1A-binding protein p400	25.457828	T700;S701;S702;T703;S704;S705;S710;S712;S717;T1488;T1492;T1493;S1495;T1526;S1527;S1530;S1532;S1540;S1543;S1547;T1624;T1627;T2604;T2605;S2608;T2615;T2623;S2624;S2631;T2638;T2646;S2686;T2689;T2691;S2696;T2699;T2700;T2707;S2708;T2710;S2712;T2716;T2717;T2720;T2724;S2728;S2734;T2737;T2875;T2877;T2878;S2920;T3019;T3023;T3024;S3027;T3081;T3094;T3119	S53;S135;S315;S321;S736;S755;S928;S941;T945;S1011;S1547;S1728;S1732;S2686;T2813	28657654;31637018;35132862;35254053;34846842;28314751;34725712;23301498;34019948;29237092;30059200;32574038;30379171;37340703;22661428;38665916;30620550;39534244;35289036;39302247;29351928;27655845;39531497;33214551;31492838;35138101	MHHGTGPQNVQHQLRSRACPGSE GEEQPAHPNPPSPAAPFAPSASP PQSPSYQIQQLMNRSPATGQNVNIT LQSVGPVVGNGQITLAPLPLPSP PGFQFSAQPRRFEHGSPSYIQVTSPL SQQVQTQSPQTQSPSPGQALQNVRA GAPGPGGLGCSSTGPFVDSVVLV ROISLSPSSGGHFVFDGSGLTQIAQ GAOVLQHPGTPTVTRRRRPSQPH QSGGTIHHLGPQSPAAAGGAGLQPL ASPSHITTANLPPQISSHQGLVQQQ QVLQGPPLPRPLGFERTPGVLLPGA GGAAGFGMTSPPPPTSPSRVAVPPG LSSLPLTSVGNMGKVKPKLEEIPP ASPEMAQMRKQCLDYHYQEMOALK EVFKEYLIELFLOHFQGNMMDFLA FKKKHYAPLQAYLRQNDLDIEEEEE EEEEEEKSEVINDEVKVVTKDGO TGTPVAIATQLPPKVSAAFSSQQQPF QOALAGSLVAGAGSTVETDLFKRQO AMPSTGMAEQSKRPRELVGHQGVV FQHPGADAGVPLQQLMPTAOGGMP PTPQAAQLAGQROSQOQYDPSTGPP VQNAASLHTPLPQLPGRLLPAGVPT AALSSALQFAQQPQVVEAQTQLQIPV KTQQPNVPIAPPSSQLPIPPSQPAQ LALHVPTPGKVQVQASQLSSLPQMV ASTRLPVDAPPCCRPLPTSSSTSLA PVSGSGPGSPARSSPVNRPSATN KALSPVTSRTPGVVASAPTQKQSPAQ NATSSQDSSQDTLQTEQITLENQVHQ RIAE LRKAGLWSQRRLLPKLQEA KSHWDYLLEEMQWMAFDFAQERR WKVAAAKKLVRTVVRHHEEKQLRE ERGGKEEQSRLRRIAASTAREIECFW SNIEQVVEIKLRVELEEKRRKALNLQ KVSRRGKELRPKGFDAEQESSLD MSGRRKASISLTDDEVDDEEETIE EEANEVVDHQTELSNLAKEAELPL LDLMLKLYEGAFPLPSSQWPRPKPDGE DTSGEEDADDCPGDRESRKDLVLID SLFIMDQFKAERMNIGKPNAKDIA DVTAVAEAILPKGSARVTTSVKFNAP SLLYGALRDYQKIGLDWLAKLYRKN LNGILADEAGLGKTQVHIAFFAHLAC NEGNWGPPLVVRSCNLIKWELEL KRWCPGLKILSYIGSHRELKAKRQE WAEPNSFHVCITSYQFFRGLTFT RVRWKCLVIDEMQRVKGMTERHWE AVFTLQSQRLLLDLSPHNTFLEL WTMVHFLVPGISRPLYSSPLRAPSEE SQDYHHKVVIRLHRVTQPFILRRTRR DVEKQLTKKYEHLKCRLSNRQKAL YEDVILQPGTQEALKSGHFVNVLSIL VRLQICNHPGLVEPRHPGSSYVAG PLEYPSASLILKALERDFWKEADLSM FDLIGLENKTRHEAELLKSKKIPRKL MEEISTSAAPAARPAAKLKASRLFQ PVQYQKPEGRTVAFPPSTHPPRTAA PTTASAAQGPLRGRPIATFSANPE AKAAAAPFQTSQASASAPRHQPASA SSTAASPAHPAKLRAQTTAQASTPG QPPPQPQAPSHAAGQSALPQRLVLP SQAQARLPSGEVVKIAQLASITGPQS RVAQPETPVTLQFQGSKFTLSHSOL RQLTAGQPLQLQGSVLQVQVAPGQPY LRAPGPVVMQTVSQAGAVHGALGSK PPAGGSPAPLTPQVGVPGRVAVNA LAVGEPGTASKPASPIGGPTQEEKTR LLKERLDQIYVNERRCSQAPVYGR DLLRICALPSHGRVQWRGSLDGRRG KEAGPAHSYTSSESPELMLTLCR CGESLQDVIDRVAFVIPPVVAAPPSL RVPRPPPLYSHRMRLRQGLREHAA PYFQQLROTTAPRLQFPELRLVQFD SGKLEALAILLOKLGKSEGRRLVLSQ MILMLDILEMFLNFHYLTYVRIDEN ASSEQRQELMRSFNDRRIFCAILST HSRTGINLVEADTVVFDNDLNPV MDAKAQEWCDRIGRCKDIHIYRLVS	True	False	1.901	5.0	1.264

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