

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
Q8CHI8	EP400_MOUSE	Mus musculus	E1A-binding protein p400	45.773785	T630;S643;S695;S699;S700;S709;S716;T2532;T2535;T2551;S2554;S2586;T2595;S2599;S2614;S2624;T2626;T2635;S2636;T2638;T2644;S2656;T2659;S2662;T2932;T2937;S2940;T3024	S52;S134;S315;S321;S735;S741;S754;T922;S923;S927;S940;T944;S1009;S1010;S1646;S1650;S2614	36852467;22645316;21606357;22517741;35822049	MHHGSGPQNVQHQLQRSRSFTGSE EEQPAHNPPLPPSPAAPFAPSASPSAP QSPGYQIQQLMSRSPVAGQNVNITL QNVGPPVGGNQITLAPLPLPNPTS PGFQFGAQRRFEHGSPSYQVTSPT MSQQVQTQSPTQSPSPGPGOTLQNV RAGAPGGLGICSNSTGGFVDASV LVROISSLSPSSGGHFVFEAPGLTQ MAQGAQVQLQHS GAPITVRRRLSQ PHAQSGGTIHHLGPQSPAAAGGTGL QPLASPNHITTAASLPPQISSIIQGQLI QQQQVVLQGGQPMNRSGLGFERTPGV LLPGVGGPSAFGMTSPPPPTSPSRTT MPPGLSSVPLTSMGSSGMKKVPKKL EEIPPASQEMAQMRKQCLDYHYKE MEALKEVFKEYLIELFFLQHLQGNM MDFLAFKKKHYAPLQAYLRQNDLDI EEEEEEEEEEGKSEVINDEVKVVV GKDGQTGTVAIATQLPPNVSAAFSS QQQPFQHQSLTGSLVVGPGSATEAD PFKRQQVMPPTQSKRPRLEVGHFG VVFQHPGVNAGVPLQQLMFTVQGG MPPTPQATQLTGQKQSQQYDPSTG PPVQNAASLHTPPPQLPARLPPASVP ATALPSTLQFSQQSQMVEASTQLQIP VKTQQLNAPIAPLPSQLPAPSSQPA QPALHVPMPGKAQMOTSQSSQTQ TVASTRPLDQAQPCQRSPTSSSS SLVPSGSGPGPSPARSSPVNRPSSA TNKALSPITSRSPGVAVSAPPKQSP AQNAASSQDGSQDKLAEQITLENQI HQRIADLRKEGLWSLRRLPKLQEAP RPKSHWDYLEEMQWMATDFAQE RRWKLAAAKLVRTVARHHEEKLR EERKKEEQSRLRRIAATTAREIEYF WSNIEQVVEIKLQVELEEKRKALN LQKVSRRGKESRLKGFDTSPHSLD LGISGRKRKASTSLDDEVEDEEETI EEEEEAHEGLVDHHTELTNLAKEAEL PLIDLMLKLYEGALPNFQWPOPEPD HEESSGEEDVEDCPSDRESRRDSVL IDSLFIMDQFKAARMSIGKSNTKDI TEVTAVAEAILPKGSARVTTAVKFS PSLLYGALRDYQKIGLDWLAKLYRK NLNGILADEAGLGKTVQIIAFFAHLA CNEGNWGHPLVVMRSCNILKWELE LKRWCPLKTLVYVSHRELKAKRQ EWTEPNFHCITSYKOFFRGYAFS RVHWKCLVDEMQRVKGMTERHW EAIFKLQSQQRLLIDVPLHNTFLEL WTMVHFLIPGISRPYLSFPLKAPNEE NQDYHMKMVRHLRVTQPFILRRTK RDVEKQLTRKYEHLKCRSSRQKA LYEDVILQPRTOEALKSGHFVSVLSV LTRLQICNHPGLVEPRVPCSSFAAG SLQYKSASLILRVLEREFWKETDLSI FDLIGLENKTRHEAELLCKKKVTRK LMEEVFASPPPSARPAAVLKASRLF QPVYQYQKPEGRTVAFSTHPPRMA NTNTSTATPQGVGRPPPIATFSANP DTKGGVVKIAQLASIAQPSRVAQP ETPVTLQFQGNKFTLSHSQRLQTA GQPLQOGSVLQIVSAPGQPYLRAPG PVMQTVSAGAVHSTLGSKPPTSG PSPAPLTPQVGVGRVAVSAMAVGE PGLASKPASPAAGPTQEEKSRLKER LDQIHFINERRCSQAPVYGRDLLRIC SLPGRRKRLCWSLDSNFGKPKGV NYDMSLSKSEGDLILTSQESLODV LGRVACVIPPVVATPPSLWVARPPSL YSSRLRALRQCLREHTGPYHRQLQ LTALRSLQFPELRLVQFDSGKLEALA ILLQKLKSEGRRLVLSQMVMLDLIL EMFLNFHYLYVRIDENANSEQRQE LMRSFNRRRIFCALLSTHSRATGI NLVEADTVVFDNDLNPVMDAKAQ EWCDRIGRCKDIHYRLVSGNSIEEK LLKNGTKDLIREVAAQGNDYMAFL TQRTIQELFEVYSPMDDTGFPVKA EFVVLQSEPSVSETIAPKIARPFIEAL	None	None	None	None	None

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