

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|-------------|--------------|--------------------------------|--------------|---------------|-----------------------|----------|---|
| B2RWS6 | EP300_MOUSE | Mus musculus | Histone acetyltransferase p300 | 15.818779 | S106 | S89;S500;S1037;S1725 | 36852467 | MAENVVEPGPPSAKRPKLSSPALSA SASDGTDFGSLFDLEHDLPELINST ELGLTNGGDISQLQTSLGIVQDAASK HKQSELLRSGSSPNLNMGVGGPG QAMASQAQQNSPGLSLINSMVKSP MAQTGLTSPNMIGSSGPNQGPQTQ SPAGMMNSPVNQPAMGMNTGMN AGMNPGLAAGNGQGIMPNOVMN GSIGAGRGRPNMQYPNAGMGNAGS LLTEPLQQGSPQMGGQPGLRGPQL KMGMMNNPSYGSPTQNSGQQIG ASGLGLQIQTKTVLPNNLSPFAMDK KAVPGGGMPMSGQQPTPSVQQPGL VTPVAAGMGSGAHTADPEKRKLIQQ QLVLLHAKKQRREQANGEVRQC NLPHCRTMKNVLNHMTHCQSGKS CQVAHCASSRQIISHWKNCTRHDPC VCLPLKNAGDKRNOQSILTGAPVGL GNPSSLGVGQQSTPSLSTVSQIDPSS IERAYAALGLPYQVNQIPPQPQVQAK NQQSQPSGQSPQGMRSVNNMSASP MGVNGGVGVQTPNLLSDSMLHSTI NSQNPMMSENAGVASLGPLPTAAQ PSSTGIRKQWHEDITQDLRNHLVHK LVQAIFPTDPAALKDRRMENLVAY ARKVEGDMYESANNRAEYHLLAE KIYKIQKELEKRRTRLQKQNMPLN APGMGPVPMNTGSNMGOQPTGMT TNGPVPDPSMIRGSVPNHMMPRMT PQPGLNQFGQMNMPQPPIGPRQS PLQHHGQLAQSGSLNPPMGYGRM QQASGQNQFLSQTQFTSQGMNVTN MPLAPSSGQAPVSAQMSSSSCPVN SPIMPPGSQGSHIHCTLPQQAHQN SPSPVPSRTPTPHHTPPSIGNQPPPA TAIPTVPTPPAIPPGPQPPSLHPSSR QTPTPPTHLPQVQPSLPAAPSADQS QQQPRSQQSTAVSVPTPTAPLLPPQP STPLSQPAVSIEGQVSNPPSTSSTEV NSQTIPEKQPSQEVKMEKMEVDKP EPADAQPEDTKEAKGEDVKVEPTM EERGPELKTGKEEEEQSTSATQS SPAPGQSKKIFKPEELRQALMPTLE ALYRQDPESLPFRQPVDPQLLGIPDY FDIVKSPMDLSTIKRKLDTGQYQEP WQYIDDIWLMFNNAWLYNRKTSRV YKYCSKLSEVFEQEIDPVMQSLGYC CGRKLEFSPQTLCCYGKQLCTIPRDA TYYSYQNRHYFCEKCFNEIQGESVS |

LGDDPSQPQTINKEQFSKRKNDTL
DPELFVECTECGRKMHQICVLHHEI
IWPSGFVCDGCLKKTARTRKENKLS
AKRLPSTRLGTFLENRVNDFLRRQN
HPESGEVTVRVVHASDKTVEVKPGM
KARFVDSGEMAESFPYRTKALFAFE
EIDGVDLCCFFGMHVQEYGSDCPPPN
QRRVYISYLDVHFFRPKCLRTAVYH
EILIGYLEYVKKLGYTTGHIWACPPSE
GDDYIFHCHPPDQKIPKPKRLQEWY
KKMLDKAVSERIVHDKDILKQATE
DRLTSAKELPYFEGDFWPNVLEESIK
ELEQEEEEERKREENTSNESTDVTKG
DSKNAKKNNKTSKNKSSLSRGN
KKKPGMPNVSNDLSQKLYATMEKH
KEVFFVIRLIACPAPNSLPPIVDPDPL
IPCDLMDGRDAFLTARDKHLEFSS
LRAQWSTMCMLEVELHTQSODRFV
YTCNECKHHVETRWHTVCEYDL
CITCYNTKNHDHKMEKLGGLDDE
SNNQAAATQSPGDSRRLSIQRCIQ
SLVHACQCRNANCSLPSCQKMKRV
VQHTKGCKRKTNGGCPICKQIALC
CYHAKHCQENKCPVPFCLNIKQKLR
QQQLQHRLQQAQMLRRRMASMQR
TGVAGQQQLPSPTPATPTTPTGQQ
PATPQTPQPPTSQPQTPPNMTP
YLPRTQTTGPVSQGKAPGQVTPPTPP
QTAQAPLPGPPAAVEMAMQIQRAA
ETQRQMAHVQIFORPIQHQMPPMS
PMAPMGMNPPPMARGPGGHLDPGI
GPAGMQQPWAQGGMPQPQQMQ
SGMPRPAMMSVAQHGQPLNMAPQ
PGLGQVGVSPKPGTVSQQALQNL
RTLRSPLQQQVLSILHANPQLL
AAFIKQRAAKYANPNPQPLPGQPGM
TQGQPLQPPTMPGQQGVHSPAL
QNMNPLQAGVQRAGLPQQQPQQQL
QPPMGAMSPQAQQMNMNHTMP
SQFRDILRRQMMQQQGAGPGIGPG
MANQFQQPQIGYPPQQQQQRM
QHHMQQMQQGNMGQMGQLPQAL
GAEAGASLQAYQORLLQQQMGSQA
QPNPMSPPQHMLPNQAQSPHLQ
QQIPNSLSNQVRSPQVPSPRPQSQ
PPHSSPSRMQPQSPHHVSPQTSS
PHPGLVAAQAANPMEQGHFASPDQ
NSMLSQLASNPGMANLHGASATDL
GLSSDNADLNSNLSQSTLDIH