	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	A0A1P8ARV7	A0A1P8ARV7_ARATH	Arabidopsis thaliana	histone acetyltransferase	27.144759	NaN	NaN	28154133	MNVQAHMSGQRSGQVPNQGTVPQ NNGNSQMQNLVGSNGAATAVTGAG AATGSGTGVRPSRNIVGAMDHDIMK LRQYMQTLVFNMLQQRQPSPADAA SKAKYMDVARRLEEGLFKMAVTKE DYMNRSTLESRITSLIKGRQINNYNQ RHANSSSVGTMIPTPGLSQTAGNMS NGYQHSSRNFSLGSGGSMTSMGAQ RSTAQMIPTPGFVNSVTNNNSGGFS AEPTIVPQSQQQQQRQHTGGQNSH MLSNHMAAGVRPDMQSKPSGAAN SSVNGDVGANEKIVDSGSSYTNASK KLQQGEGYSTTNPDPFDGAITSAGT GTKAHNINTASFQPVSRVNSSLSHQ QQFQQPPNRFQQQPNQIQQQQQQF LNQRKLKQQTPQQHRLISNDGLGKT QVDSDMVTKVKCEPGMENKSQAPQ SQASERFQLSQLQNQYQNSGEDCQ ADAQLLPVESQSDICTSLPQNSQQIQ QMMHPQNIGSDSSNSFSNLAVGVK SESSPQGQWPSKSQENTLMSNAISS GKHIQEDFRQRITGMDEAQPNNLTE GSVIGQNHTSTISESHNLQNSIGTTC RYGNVSHDPKFKNQQRWLLFLRHA RSCKPPGGRCQDQNCVTVQKLWSH MDNCADPQCLYPRCRHTKALIGHYK NCKDPRCPVCVPVKTYQQQANVRAL ARLKNESSAVGSVNRSVVSNDSLSA NAGAVSGTPRCADTLDNLQPSLKRL KVEQSFQPVVPKTESCKSSIVSTTEA DLSQDAERKDHRPLKSETMEVKVEI PDNSVQAGFGIKETKSEPFENVPKP KPVSEPGKHGLSGDSPKQENIKMKK EPGWPKKEPGCPKKEELVESPELTS KSRKPKIKGVSLTELFTPEQVREHIR GLRQWVGQSKAKAEKNQAMENSM SENSCQLCAVEKLTFEPPPIYCTPCG ARIKRNAMYYTVGGGETRHYFCIPCY NESRGDTILAEGTSMPKAKLEKKKN DEEIEESWVQCDKCQAWQHQICAL FNGRRNDGGQAEYTCPYCYVIDVEQ NERKPLLQSAVLGAKDLPRTILSDHI EQRLFKRLKQERTERARVQGTSYDE IPTVESLVVRVVSSVDKKLEVKSRFL EIFREDNFPTEFPYKSKVVLLFQKIE GVEVCLFGMYVQEFGSECSNPNQR RVYLSYLDSVKYFRPDIKSANGEALR TFVYHEILIGYLEYCKLRGFTSCYIWA CPPLKGEDYILYCHPEIQKTPKSDKL REWYLAMLRKAAKEGIVAETTNLYD HFFLQTGECRAKVTAARLPYFDGDY WPGAAEDIISQMSQEDDGRKGNKK GILKKPITKRALKASGQSDFSGNASK DLLLMHKLGETIHPMKEDFIMVHLQ HSCTHCCTLMVTGNRWVCSQCKDF QLCDGCYEAEQKREDRERHPVNQK DKHNIFPVEIADIPTDTKDRDEILESE FFDTRQAFLSLCQGNHYQYDTLRRA KHSSMMVLYHLHNPTAPAFVTTCN VCHLDIESGLGWRCEVCPDYDVCNA CYKKEGCINHPHKLTTHPSLADQNA QNKEARQLRVLQLRKMLDLLVHAS QCRSPVCLYPNCRKVKGLFRHGLRC KVRASGGCVLCKKMWYLLQLHARA CKESECDVPRCGDLKEHLRRLQQQS DSRRRAAVMEMMRQRAAEVAGTSG	None	None	None	None	None	None	None	None	None