| | UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochndrion | endoplasmic reticulum | g a |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0 | Q92794 | KAT6A_HUMAN | Homo sapiens | Histone acetyltransferase KAT6A | 22.533554 | S1772;S1774;T1778;S1779 | T369;S420;S473;S787;S812;T899;S941;S954;S974;S1089;S1090;S1113 | 34019948;29351928 | MVKLANPLYTEWILEAIKKVKKQKQ<br>RPSEERICNAVSSSHGLDRKTVLEQ<br>LELSVKDGTILKVSNKGLNSYKDPD<br>NPGRIALPKPRNHGKLDNKQNVDW<br>NKLIKRAVEGLAESGGSTLKSIERFL<br>KGQKDVSALFGGSAASGFHQQLRLA<br>IKRAIGHGRLLKDGPLYRLNTKATNV<br>DGKESCESLSCLPPVSLLPHEKDKP<br>VAEPIPICSFCLGTKEQNREKKPEELI<br>SCADCGNSGHPSCLKFSPELTVRVK<br>ALRWQCIECKTCSSCRDQGKNADN<br>MLFCDSCDRGFHMECCDPPLTRMP<br>KGMWICQICRPRKKGRKLLQKKAAQ<br>IKRRYTNPIGRPKNRLKKQNTVSKGP<br>FSKVRTGPGRGRKRKITLSSQSASSS<br>SEEGYLERIDGLDFCRDSNVSLKFN<br>KKTKGLIDGLTKFFTPSPDGRKARGE<br>VVDYSEQYRIRKRGNRKSSTSDWPT<br>DNQDGWDGKQENEERLFGSQEIMT<br>EKDMELFRDIQEQALQKVGVTGPPD<br>PQVRCPSVIEFGKYEIHTWYSSPYPQ<br>EYSRLPKLYLCEFCLKYMKSRTILQQ<br>HMKKCGWFHPPANEIYRKNNISVFE<br>VDGNVSTIYCQNLCLLAKLFLDHKT<br>LYYDVEPFLFYVLTQNDVKGCHLVG<br>YFSKEKHCQQKYNVSCIMILPQYQR<br>KGYGRFLIDFSYLLSKREGQAGSPEK<br>PLSDLGRLSYMAYWKSVILECLYHQ<br>NDKQISIKKLSKLTGICPQDITSTLHH<br>LRMLDFRSDQFVIIRREKLIQDHMA<br>KLQLNLRPVDVDPECLRWTPVIVSN<br>SVVSEEEEEEAEEGENEEPQCQERE<br>LEISVGKSVSHENKEQDSYSVESEK<br>KPEVMAPVSSTRLSKQVLPHDSLPA<br>NSQPSRRGRWGRKNRKTQERFGDK<br>DSKLLLEETSSAPQEQYGECGEKSE<br>ATQEQYTESEEQLVASEEQPSQDGK<br>PDLPKRRLSEGVEPWRGQLKKSPEA<br>LKCRLTEGSERLPRRYSEGDRAVLR<br>GFSESSEEEEEPESPRSSSPPILTKPT<br>LKRKKPFLHRRRRVRKRKHHNSSVV<br>TETISETTEVLDEPFEDSDSERPMPR<br>LEPTFEIDEEEEEEDENELFPREYFR<br>RLSSQDVLRCQSSSKRKSKDEEEDE<br>ESDDADDTPILKPVSLLRKRDVKNSP<br>LEPDTSTPLKKKKGWPKGKSRKPIH<br>WKKRPGRKPGFKLSREIMPVSTQAC<br>VIEPIVSIPKAGRKPKIQESEETVEPK<br>EDMPLPEERKEEEEMQAEAEEAEE<br>GEEEDAASSEVPAASPADSSNSPET<br>ETKEPEVEEEEEKPRVSEEQRQSEE<br>EQQELEEPEPEEEEDAAAETAQNDD<br>HDADDEDDGHLESTKKKELEEQPT<br>REDVKEEPGVQESFLDANMQKSRE<br>KIKDKEETELDSEEEQPSHDTSVVSE<br>QMAGSEDDHEEDSHTKEELIELKEE<br>EEIPHSELDLETVQAVQSLTQEESSE<br>HEGAYQDCEETLAACQTLQSYTQAD<br>EDPQMSMVEDCHASEHNSPISSVQ<br>SHPSQSVRSVSSPNVPALESGYTQIS<br>PEQGSLSAPSMQNMETSPMMDVPS<br>VSDHSQQVVDSGFSDLGSIESTTEN<br>YENPSSYDSTMGGSICGNSSSQSSC<br>SYGGLSSSSSLTQSSCVVTQQMASM<br>GSSCSMMQQSSVQPAANCSIKSPQS<br>CVVERPPSNQQQQPPPPPQQPQPP<br>PPQPQPAPQPPPPQQQPQQQPQPQP<br>QQPPPPPPPQQQPPLSQCSMNNSFT<br>PAPMIMEIPESGSTGNISIYERIPGDF<br>GAGSYSQPSATFSLAKLQQLTNTIM<br>DPHAMPYSHSPAVTSYATSVSLSNT<br>GLAQLAPSHPLAGTPQAQATMTPPP<br>NLASTTMNLTSPLLQCNMSATNIGI<br>PHTQRLQGQMPVKGHISIRSKSAPL<br>PSAAAHQQQLYGRSPSAVAMQAGPR<br>ALAVQRGMNMGVNLMPTPAYNVN<br>SMNMNTLNAMNSYRMTQPMMNS<br>SYHSNPAYMNQTAQYPMQMQMGM<br>MGSQAYTQQPMQPNPHGNMMYTG<br>PSHHSYMNAAGVPKQSLNGPYMRR | True | False | 4.553 | 5.0 | 1.861 | 1.304 | 2 |