

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	end reti
Q14AX6	CDK12_MOUSE	Mus musculus	Cyclin-dependent kinase 12	54.678456	T588;S589;T595;S597;T1359	T57;T73;S235;S248;S264;S273;S275;S300;S302;S309;S311;S317;S322;S324;S331;S332;S333;S337;S340;S342;S344;S382;S384;S399;S419;S422;T511;S610;S640;S677;S681;T688;S885;T889;S1049;S1079;T1240;T1242;T1240;T1242	22517741;22645316;21606357;40885482;36852467;40021952;40997131	MPNSERHGGKKDGGSGGASGTSQPS SGGGSSNSRERHRLVSKHKRHKSK HSKDVGLVTPEAASLGTIIKPLVEYD DISSDSDTFSDDTAFKSDRRRENEER RGTDRSDRLHRRHRHQHRRSRDLL KTKQTEKEKNQEVSKSGSMKDRVS GSSKRSVEGSDDYGAQLSKSGSKE SRSSKMHKEKTRKERELKSGYKDRS KSHRKRTPKSYKTVASPKRRSRSP HRKWSDDSSKQDDSPSGASYGQDYD LSPPRSHTSSNYDSYKSPGSTRRQ SISPPYKEPSAYQSSTRSPSPYRRQR SVSPYRRRSSHYSERSGSYGRSPSP YGRRRSSPFLSKRSLRSPLSRKS MKSRSRSPAYSRHSSSHKCRSGS RSRHSISPVRPLNSSLGAELSRKK KERAAAAAAKMDGKESKSSPIILPK KEKLEVKESGLESKKLPRSIKSEKST PDTELVTVAHNSNPEVKHCLDTGKVR LDENLQKHPAKDLKAQGTKDVKPVA PKEVIVTSETETSEKETLPLPITTS PPPLPATTPPPQTPPLPPLPAIPL QPPLPPPQPPFSQVPVSSSILPSSPH PRTSTLSSQTNQPPVQVSMKTQVSI TAAIPLHKTSTLPLPLPLLPGLDDD MDSPKETLPSKPAKKEKEQRTRHLL TDLPLPELPGGDPSPDSEPEKAITP PQQPYKRPKICCPRYGERRQTESD WGRKRCVDKFDIIGIEGTYGQVYKA KDKDTGELVALKKVRLDNEKEGFPI TAIREIKLRQLVHQSVMNMKEIVTD KQDALDFKDKGAFYLVFEYMDHD LMGLLESGLVHFSEDHKSFMKQL MEGLDYCHKKNFLHRDIKCSNILLN NSGQIKLADFLARLYNSESRPYT NKVITLWYRPELLLGEERYTPAIDV WSCGCGELFTKPIFQANLELAQL ELISRLCGSPCPAVWPDVIKLPYFNT MKPKKQYRRRLREEFSPFSAALDLL DHMLTLDPKRCTAEQTLQSDFLKD VELSKMAPPDLPHWQDCHLWSSK RRRQROSGIVIEDPPPSKASKETTS GTTAEPVKNNSPAPPQFAPVKAEPG PGDAVGLGDITQQLNQSELAVLLNL LQSQTDLSIPQMAQLLNHNSNPEMQ QOLEALNQSISALTEASSQQQDSESI APEESLKEVPSVPVLPPEAQITPEA SNTPADMONVLAULLSOLMKTQEP AGNLEENTNDKNSGPOGPRRTPTM PQEEAACPPHILPPEKRPPEPPGPP PPPPPPPLVEGDLSSAPQELNPAVTA ALLQLLSQPEAEPGHLPHHEHQALR PMEYSTRSHPNRTYGNTDGPETGFS SADTDERSSGALTESLVQTPVKNR TFSGSVSHLGSNSYQGTGSVQFPF DQDLRFTRVPLALHSVVGQPFKSE GNSNSVHAETKLQNYGELGPGTTG ANSSGTTLQWGGPAQSYGKPYRGAA RVLPRGGRGRGCVY	True	False	2.799	4.728	1.595	1.24