	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmi reticulum
0	Q3URK3	TET1_MOUSE	Mus musculus	Methylcytosine dioxygenase TET1	44.864767	T253;S270;S273;T277;T327;S533;T550;S724;T731;T740;S790;T792;T793;S794;S953;T956;S1055;S1136;T1327;S1328;S1342;S1721;T1728;S1729;S1966;S1981;T1982;T1984;S1995;T1997	S854	40155743;23729667;36852467;40128797;25568311	MSRSRPAKPSKSVKTKLQKKKDIQMKTKTSKQAVRHGASAKAVNPGKPKQLIKRRDGKKETEDKTPTPAPSFLTRAGAARMNRDRNQVLFQNPDSLTCNGFTMALRRTSLSWRLSQRPVVTPKPKKVPPSKKQCTHNIQDEPGVKHSENDSVPSQHATVSPGTENGEQNRCLVEGESQEITQSCPVFEERIEDTQSCISASGNLEAEISWPLEGTHCEELLSHQTSDNECTSPQECAPLPQRSTSEVTSQKNTSNQLADLSSQVESIKLSDPSPNPTGSDHNGFPDSSFRIVPELDLKTCMPLDESVYPTALIRFILAGSQPDVFDTKPQEKTLITTPEQVGSHPNQVLDATSVLGQAFSTLPLQWGFSGANLVQVEALGKGSDSPEDLGAITMLNQQETVAMDMDRNATPDLPIFLPKPPNTVATYSSPLLGPEPHSSTSCGLEVQGATPILTLDSGHTPQLPPNPESSSVPLVIAANGTRAEKQFGTSLFPAVPQGFTVAAENEVQHAPLDLTQGSQAAPSKLEGEISRVSITGSADVKATAMSMPVTQASTSSPPCNSTPPMVERRKRKACGVCEPCQQKANCGECTYCKNRKNSHQICKKRKCEVLKKKPEATSQAQVTKENKRPQREKKPKVLKTDFNNKPVNGPKSESMDCSRRGHGEEEQRLDLITHPLENVRKNAGGMTGIEVEKWAPNKKSHLAEGQVKGSCDANLTGVENPQPSEDDKQQTNPSPTFAQTIRNGMKNVHCLPTDTHLPLNKLNHEEFSKALGNNSSKLLTDPSNCKDAMSVTTSGGECDHLKGPRNTLLFQKPGLNCRSGAEPTIFNNHPNTHSAGSRPHPPEKVPNKEPKDGSPVQPSLLSLMKDRRLTLEQVVAIEALTQLSEAPSESSSPSKPEKDEEAHQKTASLLNSCKAILHSVRKDLQDPNVQGKGLHHDTVVFNGQNRTFKSPDSFATNQALIKSQGYPSSPTAEKKGAAGGRAPFDGFENSHPLPIESHNLENCSQVLSCDQNLSSHDPSCQDAPYSQIEEDVAAQLTQLASTINHINAEVRNAESTPESLVAKNTKQKHSQEKRMVHQKPPSSTQTKPSVPSAKPKKAQKKARATPHANKRKKKPPARSSQENDQKKQEQLAIEYSKMHDIWMSSKFQRFGQSSPRSFPVLLRNIPVFNQILKPVTQSKTPSQHNELFPPINQIKFTRNPELAKEKVKVEPSDSLPTCQFKTESGGQTFAEPADNSQGQPMVSVNQEAHPLPQSPPSNQCANIMAGAAQTQFHLGAQENLVHQIPPPTLPGTSPDTLLPDPASILRKGKVLHFDGITVVTEKREAQTSSNGPLGPTTDSAQSEFKESIMDLLSKPAKNLIAGLKEQEAAPCDCDGGTQKEKGPYYTHLGAGPSVAAVRELMETRFGQKGKAIRIEKIVFTGKEGKSSQGCPVAKWVIRRSGPEEKLICLVRERVDHHCSTAVIVVLILLWEGIPRLMADRLYKELTENLRSYSGHPTDRRCTLNKKRTCTCQGIDPKTCGASFSFGCSWSMYFNGCKFGRSENPRKFRLAPNYPLHNYYKRITGMSSEGSDVKTGWIIPDRKTLISREEKQLEKNLQELATVLAPLYKQMAPVAYQNQVEYEEVAGDCRLGNEEGRPFSGVTCCMDFCAHSHKDIHNMHNGSTVVCTLIRADGRDTNCPEDEQLHVLPLYRLADTDEFGSVEGMKAKIKSGAIQVNGPTRKRRLRFTEPVPRCGKRAKMKQNHNKSGSHNTKSFSSASSTSHLVKDESTDFCPLQASSAETSTCTYSKTASGGFAETSSILHCTMPSGAHSGANAAAGECTGTVQPAEVAAHPHQSLPTADSPVHAEPLTSPSEQLTSNQSNQQLPLLSNSQKLASCQVEDERHPEADEPQHPEDDNLPQLDEFWSDSEEIYADPSFGGVAIAPIHGSVLIECARKELHATTSLRSPKRGVPFRVSLVFYQHKSLNKPNHGFDINKIKCKCKKVTKKKPADRECPDVSPEANLSHQIPS	True	False	0.36	5.0	False	False

									RVASTLTRDNVVTVSPYSLTHVAGPYNRWV						