

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
A0A0G2JF55	A0A0G2JF55_MOUSE	Mus musculus	Methylcytosine dioxygenase TET	25.775171	NaN	NaN	34678516	MEQDRTHAEGTRLSPLIAPPSPIS HTEPLAVKLQNGSPLAERPHPEVNG DTKWQSSQSCYGISHMKGSSSHE SPHEDRGYSRCLQNGGKRTVSEPS LSGLHPNKILKLDQKAKGESNIFEES QERNHGKSSRQPNVSGLSDNGEV TSTTQESSGADAFPTRNYNGVEIQVL NEQEGEKGRSVTLKKNKIVLMPNGA TVSAHSEENTRGELLEKTQCYPCV SIAVQSTASHVNTPSSQAAIISHEIP QPSLTSAQINFSQTSSLQLPPEPAAAM VTKACDADNASKPAIVPGTCTPFQKA EHQOKSALDIGPSRAENKTIQGSME LFAEYYPPSSDRNLQASHGSSEQYS KQKETNGAYFRQSSKFPKDISIPTTV TPPSQSLAPRLVLPPLLEGKALND VALEEHHDYPNRSNRTLREKIDH QPKTSSSQSLNPSVHTPNPPLMLPE QHQNDCGSPSPEKSRKMSEYLMYY LPNHGHSGLQEHSYQLMGHREQE IPKDANGKQTQGSVQAAPGWIELKA PNLHEALHQTKRKDISLHVSLSQT GPVNMSSKQSTGNVNMPPGGFQRL PYLQKTAQPEQKAQMYQVQVNOGP SPGMGDQHLQFQKALYQECIPRTDP SSEAHQPAPSVQYHFQQRVNPSSD KHLSQATETQRLSGFLQHTPQTQA SOTPASQNSNFPOICQQQQQQLO RKNKEQMPQTFSHLQGSNDKQREG SCFGQIKVEESFCVGNQYSKSSNFQ THNNTQGGLEQVQINKNFPYSKIL TPNSSNLQILPSNDTHPACEREQAL HPVGSKTSNLQNMQYFPNNVTPNQ DVHRCFOEQAKPQOASSLOGKLD RSQGESAPPAAEAQAQRYLVHNEAK ALPVPQGGSQTTQTPPOKDTOKHAA LRWLLQKQEQQTQSQSPGHNQ MLRPIKTEPVSKPSSYRPLSPPOEN MSSRIKQEISSPSRDNGQPKSIETM EQHLKQFQLKSLCDYKALTKSOKH VKVPTDIAAESENHARAAEPQATK STDCSVLDDVSESDTPGEQSQNGKC EGCNPDKDEAPYYTHLGAQPDVAAI RTLMEERYGKGAIRIEKVITYGKE GKSSQGCPIAKWVYRRSSEEEKLLC LVRVRPNHTCETAVMVIAMLDWDGI PKLLASELYSELTDLGKCGICTNRR CSQNETKKKQSPSRNCCCQGENP ETCGASFSGCSWSMYNGCKFAR SKKPRKFRFHGAEPKEEERLGSHLQ NLATVIAPYKKLAPDAYNNQVEFEH QAPDCCLGLKEGRPFSGVTACLDFS AHSHRDQONMPNGSTVVVTLNRED NREVGAPEDEQFHVLPMYIAPED EFGSTEGQEKKIRMGSIQVLSFRR RRVIRIGELPKSCKKKAEPKAKTKK AARKRSSLENCSSRTEKKGSSHTK LMENASHMKQMTAQPLSGPVIRQ PPTLQRHLQGGQRFPQFPQPQPOQ TTPQFPQPQHIMPNGNSQSVGSHCS GSTSVYTRQPTPHSPYSSAHTSDIY GDTNHVNFYPTSSHASGSYLNPSNY MNPYLGLLNQNNQYAPFPYNGSVP VDNGSPFLGSYSQAQSRDLHRYPN QDHLTNQNLPIHTLHQQTFGDSSPS KLSYGNQNMQRDAFTTNTSLKPN VHHLATFSYPTPKMDSHFMGAAAS RSPYSHPHTDYKTEHHLPSHTIYSY TAAASGSSSSSHAFHNKENDNIANGL SRVLPGFNHDRTASAEQLLSLTGS SQEKQPEVSGQDAAAQVEIEYWSDS EHNFDPCIGGVAIAPTHGSILIECA KCEVHATTKVNDPDRNHPTRIISLV YRHKNLFLPKHCLALWEAKMAEKA RKEEECGKNGSDHVSQKNHGKQEK REPTGPQEPSYLRFIQSLAENTGSVT TDSTVTTSPYAFTQVTGPYNTFV	True	False	3.338	4.776	2.589	1.855	1.251	2.201	2.435