

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q4JK59	TET2_MOUSE	Mus musculus	Methylcytosine dioxygenase TET2	23.83078	T7;S15;S23;S26;T28;S57;S58;T95;S97;S134;S135;T165;T202;S204;T211;S290;S317;S346;S349;S350;S374;S376;T378;T379;T381;S384;S386;T514;S517;S545;S548;S552;T554;S561;S562;S565;T625;T711;S713;S736;S744;T776;S779;S805;T807;S808;S850;T912;T928;S932;T1428;S1434;T1595;T1604;S1613;S1615;S1619;T1631;T1645;S1647;T1651;S1663;T1672;S1694;S1696;S1697;S1698;S1735	S15;S23;S76;S97;S1036	25568311;36852467	MEQDRTHAEGTRLSPLFIAPPSPIS HTEPLAVKLQNGSPLAERPHPEVNG DTKWQSSQSCYGISHMKGSSSHE SPHEDRGYSRCLQNGGIKRTVSEPS LSGLHPNKILKLDQKAKGESDNIFEES QERNHGKSSRQPNVSGLSGSDNIEP TSTTQESSGADAFPTRNYNGVEIQVL NEQEGEKGRSVTLTKNKIVLMPNGA TVSAHSEENTRGELLEKTQCYPDCV SIAVQSTASHVNTTPSSQAIELSHEIP QPSL TSAINFQSSTSLQLPPEPAAM VTKACDADNASKPAIVPGTCTPFQKA EHQKKSALDIGPSRAENKTIQGSME LFAEYYPSSDRNLQASHGSSEQYS KQKETNGAYFRQSSKFPKDSISPTTV TPPSQSLAPRLVLQPPLEGKALND VALEEHHDYPNRSNRLLREGKIDH QPKTSSSLSLNPVHTPNPPLMLPE QHQNDCGSPSPEKSRKMSEYLMYY LPNHGHSGGLQEHSOYLMGHREQE IPKDANGKQTQGSVQAAPGWIELKA PNLHEALHQTKRKDISLHSLVLSQT GPVNMSSKQSTGNVNMPPGGFQRL PYLQKTAQPEQKAQMYQVQVNQGP SPGMGDQHLQFQKALYQECIPRTDP SSEAHQPAPSVQYHFQQRVNPSSD KHLSQQATETQRLSGFLQHTPQTQA SQT PASQNSNFPQICQQQQQQQLQ RKNKEQMPQTFSHLQGSNDKQREG SCFGQIKVEESFCVGNQYSKSSNFQ THNNTQGGLEQVQINKNFPYSKIL TPNSSNLQILPSNDTHPACEREQAL HPVGSKTSNLQNMQYFPNNVTPNQ DVHRCFQEQAKPQQASSLQGLKD RSQGESAPPAAEAAQQRVYLVHNEAK ALPVPEQGGSTQTPPKDTQKHAA LRWLLQKQEQQTQQSOPGHNQ MLRPIKTEPVSKPSSYRYPLSPPQEN MSSRIKQEISSPSRDNGQPKSIETM EQHLKQFQLKSLCDYKALTLKSQKH VKVPTDIQAAESENHARAAEPQATK STDCSVLDDVSESDTPGEQSQNGKC EGCNPDKDEAPYYTHLGAGPDVAI RTLMEERYGEKGAIRIEKVIYTGKE GKSSQGCPIAKWVYRRSSEEEKLLC LVRVRPNHTCETAVMVIAMLDGI PKLLASELYSELTDLGKCGICTNRR CSQNETRNCQGENPETCGASFS FGCSWSMYNGCKFARSKKPRKFR LHGAEPKEERLGSHLQNLATVIPI YKKLAPDAYNNQVEFEHQAPDCCLG LKEGRPFSGVTACLDFSAHSHRDQQ NMPNGSTVVTLNREDNREVGAKP EDEQFHVLPYIIAPEDEFGSTEGQ EKKIRMGSIQVLSFRRRRVIRIGELP

KSCCKKAEPKAKTKKAARKRSSLE
NCCSRTEKGGKSSSHTKLMENASHM
KQMTAQPOLSGPVIRQPPTLQRHLQ
QGQRPQQPQPQPQPQTTPQPQPQP
QHIMPGNSQSVGSHCSGSTS SVYTRQ
PTPHSPYPSSAHTSDIYGDTNHVNFY
PTSSHASGSYLNPSNYMNPYLGLLN
QNNQYAPFPYNGSVPVDNGSPFLGS
YSPQAQSRDLHRYPNQDHLTNQNL
PPIHTLHQQTFGDSPSKYLSYGNQN
MQRDAFTTNSTLKP NVHHLATFSPY
PTPKMDSHF MGAASRSPYSHPHTD
YKTSEHHLPSHTIYSYTA AASGSSSS
HAFHNKENDNIANGLSRVLP GFNH
DRTASAQELLYSLTGSSQEKQPEVS
GQDAAAVQIEIY WSDSEHNFQDPCI
GGVAIAPTHGSILIECAKCEVHATTK
VNDPDRNHPT RISLVLYRHKNLFLP
KHCLALWEAKMAEKARKEEECKGN
GSDHVSQKNHGKQEKREPTGPQEP
SYLRFIQSLAENTG SVTTDSTVTTSP
YAFTQVTGPYNTFV