

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extra-regi
O08550	KMT2B_MOUSE	Mus musculus	Histone-lysine N-methyltransferase 2B	24.992371	S2172	S113;S114;S118;S826;S849;S866;S941;S1037;S1040;S1098;S1101;S1926;S1932;T2064;T2079;S2286;S2346	36852467	MAAAAGGGSCPGGSARGRFPGRPRGSGGGGGRGGRGNGAERVRVALRRGGGAAGPGGAEPGEDTALLRLLGLRRGLRRLRLWAGARVQRGRGRGRGRGWGPNRGCMPPEESSDGESEEEEFQGFHSDDEDVAPSSLRSLRSQRGRAPRGRGRKHKTTPPLRDLADVTPVPPKAPTRKRGEEGTERMVQALTELLRRSQAPQPPRSRARAREPSTPRRSRGRPPGRPAGPCRKKQAVVLAEEAAVTIPKPEPPPPVVPVKNKAGSWKCKEGPQGGPGTPKRGQPPGRGGRRGRGRGRGLPLMIKFVSKAKVKVMGQLSQELESQGHGQRGESWQDAPQRKDGDEPERGSCRKKQEQKLEEEEEEEKEGEEKEEKDDNEDNNKQEEEEET ERAVAEEEEAMLAKEKEEAKLPSPLTPPPVSPPPPLPPPSTSPPPASPLPPVSPPPPLSPPPYPAPEKQEEESPPLVATCSRKRGRPPLTPSQAEREAAARSGPEGTLPSTPNPSTTTGSPLSDSPTVVPKSTTFLKNIRQFIMPVVSARSSRVIKTPRRFMDEDPPKPPKVEASIVRPPVATSPAPQEPVVPSSPPRVTPPSTPVLPPEKRRSILREPTFRWTSLTRELP PPPAPPAPSPPPAPATPSRRPLLLRAPQFTPSEAHLKIVESVLTPLPLGAL ETPEPELPPADDSPAEPEPRAVGRTNHLSLPRFVPVVTSPVKVEVPPHGAPALSEGQQLQLQPPQALQTQLLQALPPQQPQAQPPSPQHTPPLEKARVALGSLPLSGVEEKMFSLKRAKVQLFKIDQQQQKVAASMPSPAVQTEEAVGTVKQTPDRGCVRSEDESMEAKRDRASGPESPLQGPRIKHVCRHAVALGQARAMVPEDVPRLSALPLRDRQDLATEDTSSASETESVPSRSQREKVESAGPGGDSEPTGSTGALAHTPRRSLPSHHGKKMRMARCCHRCGLRVQDCGSCVNCCLKPKFGGPNTPKQCCVYRKCDKIEARKMERLAKKGRIVKTLLPWDSDESPEASGPPGPRRGAGAGGSREEVGATPGPEEQDSLLLQRKSARCVKQRPSYDVFEEDSDDEPGGPPAPRRRTPREHELPLVLEPEEQSRPKPTLQPVQLKARRRLDKDALAPGPFASFPNGWTGKQKSPDGVHRVVDVDFKEDCDLENVWLMGGLSVLTSVPGGPPMVCLLCASKGLHELVCQVCCDPFHPFCLAEAERPSPQHRDTWCCRRCKFCHVCGRKGRGSKHILLECERCRHAYHPACLGPSYPTRATRRRRHWICSACVRCCKSGATPGKNWDVEWSGDYSLCPRCTELYEKGNYPICTRCYEDNDYESKMMQCAQCQDHVWHAKCEGLSDEDEYILSGLPDSVLYTCGPCAGATQPRWREALSGALQGLRQVLQGLLSKRVAGPLLLCTCCGQDGKQLHPGPCDLQAVGKRFEGLYKSVHSFMEDVVAILMRHSEEGETPERRAGSOMKGLLLKLLSAFQWFDVADHPKYWRRSTRLPNGVLPNAVLPPLDHPVYAQWRQOESETPESGQPPGDPSAAFQSKDPAAFSLHDDPRQCALCLKYGDADSKEAGRLLYIGQNEWTHVNCIWSAEVFEEVDGSLKVNVAAVARGRQMRCELCLKPGATVGCCLSSCLSNFHFMCARASYCIFIQDDKVKVFCQKHTDLLDGKEIVTPDGFVLRVVYVDFEGINFKRKFLEGLPVDINVLIGSIRINSLGTLSDLSDCGRLFPYQCSRLYWSVTDARRRCWYRCRILEYRPPWGPREEPVHLEAAEENQTIHVSPTPSSDSDSLIPGDPVHHSPIQNLDPPLRTDSSNGPPPTPRSFSGARIKVPNYSRRRPLGGVSFGPLPSPGSPSSLTHHIPTVGDSDFPAPRRSRRPSPLATRPPPSRRRTSSPLRTSPQLRVPLSTVTAITPTSSELAPPDLAPSPLPPEEDLGPDFEDMEVVSGLSAA DLDFAAASLLGTEPFQEEIVAAGAVGS	None	None	None	None	None	None	None		

SQGGPGDSSEEEASPTTHYVHFPVT  
VMSGPALAPSSLAGAPRIQLDGVDD  
GTDSEAEAVQQPRGQGTTPSPGPGVG  
RGGVLGAAGDRAQPPELDPSEIVDF  
VLKNLGGPGEGAAGPREDSLPSAPP  
LANGSQPPQSLSTSPADPTRTFOWL  
PGAPGVRVLSLGPAPPEPKPATSKIL  
VNKLGQVFKMAGEGEPVAPPVKQP  
PLPPIIPTAPTSTWTLPPGLLSVLPV  
VGVGVVRPAPPPPPPLTLVFSGGPP  
SPPRQAIRVKRVSTFSGRSPVPPPN  
KTRPDEDEGESLEDAHHVPGISGSG  
FSRVRMKTPTVRGVLDLNNPGEQPE  
EESGPRPQDRCP LLPAEAPSQALD  
GSSDLLFESQWHHYSAGEASSSEEE  
PPSPEDKENQVPKRVGPHLRFEISS  
DDGFSVEAESLEVAWRTLIEKVQEA  
RGHARLRHLSFSGMSGARLLGIHH  
DAVIFLAEQLPGAQRQCQHYKFRYHQ  
QEGEQEEP LNPHGAARAEVYLKRC  
TFDMFNFLASQHRVLP EGATCDEEE  
DEVQLRSTRRATSLELPMAMRFRHL  
KKTSKAEAVGYRSAIHGRGLFCKRNI  
DAGEMVIEYSGIVIRSVLTDKREKFY  
DGKGIGCYMFRMDDFDVVDATMHG  
NAARFINHSCEPNCFSRVIHVEGQK  
HIVIFALRRILRGEELTYDYKFPIEDA  
SNKLCPCGAKRCRRFLN