

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus | plasm memb |
|--------------|-------------|--------------|---------------------------------------|--------------|---------------|---|-------------------|---|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|------------|
| P55200 | KMT2A_MOUSE | Mus musculus | Histone-lysine N-methyltransferase 2A | 38.939326 | S3045 | S134;S140;S151;S195;S516;S678;T837;S923;S1053;S1839;T1847;S1860;S2100;T2148;S2152;S2202;S2560;S2607;S2792;S2951;S3032;T3369;S3510;S3523 | 40997131;36852467 | MAHSCRWRFPARPGTTGGGGGGRR RGLGGAPRQRVPAALLPPGPQAGGG GPGAPPSPPAVAAAAAGSSGAGVPG GAAAAAASSSSSASSSSSSSSASSG PALLRVGPGFDAALQVSAIAGTNLRR FRAVFGESGGGGGSGEDEQFLGFGS DEEVVRSPTRSPSVKASPRKPRGRP RSGSDRNPAILSDPSVFSPLNKSETK SADKIKKDKSKSIEKKRGRPTTFPGV KIKITHGKDIAELTQGSKEDSLKKVK RTPSAMFQQATKIKKLRAGKLSPLKS KFKTGKLQIGRKGQVIVRRRGRPPST ERIKTPSGLLINSELEKPKQKVRKDK GTPPLTKEDKTVVROSPRRKPVRIIP SCKRTDIAIAKQLLQRAKKAQOKKIE KEAAQLQGRKVKTOVKNIROFIMPV VSAISSRIKTPRRFIEDYDPPMKI ARLESTPNRFSATS CGSSEKSSAAS QHSSQMSSDSRSSSPIDTTSDSQ ASEEIQALPEERSNTPVHTPLPISQ SPENESNDRRSRRYSMSERSFGSRA TKKLPTLQSAQQQTSSSPPPLLT PPPLQPASGISDHTPWLMPTIPLAS PFLPASAAPMQGKRKLSILREPTFRW TSLKHSRSEPQYFSSAKYAKEGLIRK PIFDNFRPPPLTPEDVGFASGFSASG TAASARLFSPLHSGTRFDIHKRSPI RAPRFTPEAHSRIFESVTLPSNRTS SGASSGVSNRKRKRVFSPRSEPR SPSHSMRTRSGRLSTSELSPLTPPSS VSSSLSIPVSLAASALNPTFTFPSS LTQSGESTEKNRARKQTSALAEFF SSNSPALFPWFTPGSQTEKGRKKDT APEELSKDRDADKSVKDKSRERDR EREKENKRESRKEKRRKGSIDIQSS ALYPVGRVSKKAVAGEDVGTSSAK KATGRKKSSLDGADVAVPTLGD TAVKAKILIKKGRGNLEKNNLDLGA APSLEKERTPCLSA PSSSTVKHSTSSI GSM LAQADKLPMTDKRVASLLKKA AQLCKIEKSKSLKQTDQPKAQQQES DSSETSVRGPRIKHVCRRAAVALGR KRAVFPDDMPTLSALPWEEREKILS SMGNDKSSVAGSEDAEPLAPPIKPI KPVTRNKAPQEPVVKGRSRRRCGQ CPGCQVPEDCGICTNCLDKPKFGGR NIKKQCKMRKCQNLQWMPKSKASL QKQTKAVKKEKSKTTEKESKES TAVKSPLEPAQKAAPPREEPAPKKS SSEPPRPVVEKSEEGGAPAPAPAP EPKQVSAPASRKSQVSPAAVVP QPPSTAPQKKEAPKAVSEPKKQPP PPEPGPEQSKQKVA PRPSIPVKQKP KDKEKPPVSKQENAGTLNILNPLS NGISSKQKIPADGVHRIRVDFKEDCE AENVWEMGGLGILTSVPIPRVVCFL CASSGHVEFVYQCVCCEPFHKFCLE ENERPLEDQLENWCCRRCKFCHVC GRQHATKQLECNKCRNSYHPEC LGPNYPTKPTKKKVVWICKCVRCK SCGSTTPGKGWDAQW SHDFSLCHD CAKLFAGNFCPLCDKCYDDDDYES KMMQCGKCDRWVHSKCESLSGTE DEMYEILSNLPESVAYTCVNCTERH PAEWRLALEKELQASLKQVLTALLN SRTTSHLLRYRQAAPPDNLNPETEE IPSRSSPEGDPVPLTEVSKQDEQQP LDLEGVKKRMDQGSYVSVLEFSDDI VKIIQAAINS DGGQPEIKKANSMVKS FFIRQMERYFPWFVSKSRFWEPN KVSNNSGMLPNAVLPPSLDHNAYQ WQEREESHTEQPPLMKKIIPAPK KGPGEPSPTPLHPPTPILSTDRSR EDSPELNPPPIDDNRQCALCLMYG DDSANDAGRLLYIQNEWTHVNCA LWSAEVFEDDDGSLKNVHMAVIRG KQLRCEFCQKPGATVGCCLTSCTSN YHFMCSRAKN CVFLDDKKVYQCRH RDLIKGEVVPENGFVFRRVFVDFE GISLRRKFLNGLEPENIHMMIGSMT | True | False | 3.145 | 5.0 | 2.059 | 1.473 | 1.57 | 1.886 |

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