

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	em ret
Q9UMN6	KMT2B_HUMAN	Homo sapiens	Histone-lysine N-methyltransferase 2B	20.761126	S1191;S1195;S2050;S2611	S113;S114;S118;S351;S821;S844;S861;S936;S1032;S1035;S1092;S1095;S1930;S1936;T2068;T2083;S2288;S2348	30379171;35289036;38253038	MAAAAGGGSCPGPGSARGRFPGRPRGAGGGGGGRGGRNGAERVRVALRRGGGATGPGAEPGEDTALLRLLGLRRGLRRLRRLWAGPRVQRGRGRGRGWGSPRGCVPEEESDGESDEE EFQGFHSDDEDVAPSSLRALSQRGRAPRGRGRKHKTTPPPRLADVAPTPPKTPARKRGEEGTERMVQALTELLRRAQAPQAPRSRACEPSTPRRSRGRPPGRPAGPCRKQAVVVAEAAVTIPKPEPPPPVVKHQGTSWKCKEPPGPGPPTPRRGQSSRGGRRGRGRGRGGGLPFVIKFSRAKKVKMGQLSGLSEGGQGGQHEESWQDVPQRRVSGGGGSPCWKKQEQKLDDEEEKK EEEKDKKEGEEERAAVEEMMPAAEKEEAKLPPPLTPPAPSPPLPPPSTSPPLCPPPPPVSPPLPSPPP PAQEEQEEPPVVPATCSRKRGRPLTPSQRAEREAARAGPEGTSPPTPTSTATGGPPEDSPTVAPKSTTFLKNI RQFIMPVVSARSSRVKTPRRFMDE DPPKPPKVEVSPVLRPPITSPVPQEPAPVSPPRAPTTPSTVPLPEKRRSILREPTFRWTSLTRELPPPPAPPPAPSPPPAPATSSRRPLLRAPQFTPSEAHLKIVESVLTTPPLGAPEAPEPEPPADDSPAEPERAVGRTNHLSLPRFAPVVTTPVKAEVSPHGAPALSNGPQTQAQLLQPLQALQTQLLQALPPPQQLQPPPPSQMPPELEKARIAGVGSPLSGVEEKMFSLKRAKVQLFKIDQQQQKVAASMPSPGGQMEEVAGAVKQISDRGPVRSDESVEAKRERPSGPESPVQGPRIKHVCRHAAVALGQARAMVPEDVPRLSALPLDRDQLATE DTSSASETESVPSRRRGKVEAAGP GGSEPTGSGGTLAHTPRRSLPSHHGKKMRMARCCHCRGCLRVQDCGSCVNCLDKPKFGGPNTKKQCCVYRKCDKIEARKMERLAKKGRITIVKTLPLWDSDESPEASPGPPGPRRGAGAGGPREEVVAHPGPEQDSSLQRKSARRVKQRPSYDIFEDSDDEPGGPPAPRRRTPRENELPLPEPEEQSRPRKPTLQVLQLKARRRLDKDALAPGPFASFNGWTGKQKSPDGVHRVRVDFKEDCDLENVWLMGGLSVLTSVPGGPPMVCLLCASKGLHELVCQVCCDPFHPFCLLEEAERLPLQHHDTWCCRRCKFCHVCGRKGRGSKHLEECERC RHAYHPACLGPSYPTRATKRKRHWICSACVCKSCGATPGKNWDVEWSGDYSLCPRCTQLYKGNYPICITRCYEDNDYESKMMQCAOCDHVVHAKCEGLSDE DYEILSGLPDSVLYTCGPCAGAAQPRWREALSGALQGGRLRQVLQGLSSKVVGPLLLCTQCGPDGKQLHPGPGCLQAVSQRFEFGHYKSVHFMEDMVGILMRHSEEGETPDRRAGGQMKGLLLKLLSAFGWFDADHPKYWRRSTRLPNGVLPNAVLPPLSDHVYAQWRQEPETPESGQPPGDPSAAFQKDPAAF SHLEDPRQCALCLKYGDADSKAAGRLLYIGQNEWTHVNCIWSAEVFEENDGSLKNVHAAVARGRQMRCELCLKPGATVGCCLSSCLSNFHFMCARASYCIFQDDKKVFCQKHTDLLDGKEIVNPDGFDVLRVYDFEGINFKRKFLTGLEPDAINVLIGSIRIDSLGTLSDLSDCERLFPYQCSRLYWSTVDARRRCWYRCRILEYRPWGPREEPAHLEAAEENQTIHSPAPSPPEPPGEDPPLDTPDLVPGAPERHSPIONLDPPLRPDSGSAPPPAPRSFSGARIKVFNYSRRLPLGGVSFGPLSPGSPSSLTHHIPTVGDPDFAPPPRRSRPSPLAPRPPSRWASPLKTSQLRVPPPTSVVLTALPTSGELAPPAPSPPPEDLGPDFEDMEVVSGLSADLDFASLLGTEPFQ	None	None	None	None	None	No

EEIVAAGAMGSSHGGPGDSSEESS
PTSRYIHFPVTVVSAPGLAPSATPGA
PRIQLDGVDDGTDSEAEAVQQPRG
QGTPPSGPGVVRAGVLGAADRARP
PEDLPSEIVDFVLKNLGGPGDGGAG
PREESLPPAPPLANGSQPSQGLTASP
ADPTRTFAWLPGAPGVRVLSLGPAP
EPPKPATSKIILVNKLGQVFKMAGE
GEPVPPPVKQPPPLPPTISPTAPTSWT
LPPGPLLGVLPVVGVVRPAPPPPPP
LTLVLSSGPASPPRQAIRVKRVSTFS
GRSPAPPYPYKAPRLDEDGEASEDTP
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LDRPGEPAGEESPGPLQERSPLLPLP
EDGPPQVPDGPDDLLESQWHHYS
GEASSSEEEPPSPDDKENQAPKRTG
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TLIEKVQEARGHARLRHLSFSGMSG
ARLLGIHHDVIFLAEQLPGAQRCO
HYKFRYHQGEGQEPLNPHGAA
RAEVYLRKCTFDMFNFLASQHRVLP
EGATCDEEDEVQLRSTRRATSLEL
PMAMRFRHLKKTSEAVGVYRSIAIH
GRGLFCKRNIDAGEMVIEYSGIVIRS
VLTDKREKFYDGKGIGCYMFRMDDF
DVVDATMHGNAARFINHSCEPNCF
SRVIHVEGQKHIVIFALRRILRGEELT
YDYKFPIEDASNKLPNCGAKRCRR
FLN