

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mit
O14686	KMT2D_HUMAN	Homo sapiens	Histone-lysine N-methyltransferase 2D	39.407771	S2402;S2405;T2487;S2488;T2699;S2719;T4772;S4822	S27;S744;S1151;T1195;S1249;T1267;S1270;S1606;S1671;S1820;S1834;T1843;T1865;S2239;T2240;S2260;S2274;S2309;S2311;S2342;S2640;S3130;T3197;S3199;S4215;S4359;S4738;S4822;S4849	35289036;28657654;39302247;31492838;30059200;23301498;39531497;40307207;30620550;35138101;34846842;29351928;32574038;39534244;35254053	MDSQKLAGEDKDKSEPAADGPAASE DPSATESDLPNPHVGEVSVLSSGSP LRQETPQDCSGGPRVRCALCNCGEP SLHGQRELRREFELPFDWPRCPVVSF GGSPGPNEAFLPSEDLSQLGFFPEGLT PAHLGEPGGSCWAHHWCAAWSAG VWGQEGPELGVDKAIFSGISQRCS HCTRLGASIPCRSPGCPRLYHFPCAT ASGSFLSMKTLQLLCPHSEGAAYL EEARCAVCEGPGELCDLFFCTSCGH HYHGACLDLTALTARKRAGWQCPEC KVCQACRKPNDKMLVCETCDKG YHTFCLKPPMEELPAHSWKCKACR VCRACGAGSAELNPSEWFENYSL CHRCHKAQGGQTIRSVAEQHTPVCS RFSPPPEGDTPTDEPDALYVACQGG PKGGHVTSMQPEKPGPLQCEAKPLG KAGVQLEPQLEAPLNEEMPLLPPE ESPLSPPEESPTSPPEASRLSPPE ELPASPLPEALHLSRPLEESPLSPPE EESPLSPPEESPFSPLEESPLSPPE SPPSPALETPLSPPEASPLSPPEES PLSPPEELPTSPPEASRLSPPEES PMSPPPEESPMSPPEASRLFPPEE SPLSPPEESPLSPPEASRLSPPEE SPMSPPPEESPMSPPEVSRPLPLV VSRLSPPEESPLSPPEESPTSPPE ASRLSPPEESPTSPPEESPASPPP EDSLMSLPLEESPLPLPEEPQLCPR SEGPHLSRPEEPHLSRPEEPHLS QAEPEHLSQPEEPCLCAVPEEPHL SPQAEGLHLSQPEELHLSQTEEP HLSPVVEEPCLSQPEESHLSQSE PCLSPRPEESHLSPELEKPLSPRPE KPPEEPGQCPEEPLFPFPGEP SPLLGEPALSEPGEPLSPLPEELPL PSGEPSPQLMPPDPLPPLSPHITA AAPPALSPGLEEYFPGAKGSDPES PLAAPILETPISPPPEANCTDEPVVPP MILLPPSPGSPVGPASPILMEPLPQC SPLLQHSVLPQNSPPSQCSPPALPLS VPSPLSPIGKVVGVSDAEELHEMET EKVSEPECPALEPSATSPPLSPMGDL SCPAPSPAPALDDFSGLGEDTAPLD GIDAPGSQPEPGQTPGSLASELKGSP VLLDPEELAPVTPMEVYPECKQTAG QGSPEEQUEEPRAVAPTPTLIKSD IVNEISNLSQGDASAFPGSEPLLS PDPEGGGSLSMELGVSTDVSPARDE GSLRLCTDSLPEPDDSLCDAGTAIS GGKAEGEKRRRSPARSRIKQGRS SSFPGRRRPRGGAGGRGRARLK STASSIETLVVADIDSSPSKEEEEEED DDTMONTVVLFSTDKFVLMQDMC VCGSFRGAEGHLLACSQCSCQYH PYCVNSKITKVMLLKGWRCVECIVC EVCQASDPSRLLCDDDISYHTY CLDPPLLTVPKGGWKCKWCVSCMQ CGAASPGFHCWQNSYTHCGPCAS LVTCPICHAPVVEEDLLIQCRHCER WMHAGCESLFTEDDVEQAADEGFD CVSCQYVVKPVAVAPPELVPMKV KEPEPQYFRFEGVWLTETGMALLRN LTMSPHLKRRQRRLGLPGEAGLE GSEPSDALGPDDKKDGLDTDELK GEGGVEHMECEIKLEGVSPDVEPG KEETEESKKRKRKPYRPGIGFMVR QRKSHTRTKKGPAAQAEVLSGGGQP DEVIPADLPAEGAVEQSLAEGDEK KQRRGRKSKLEDMFPAYLQEAFF GKELDLSRKALFAVGVGRPSFGLG TPKAKGDGGSERKELPTSQKDDGP DIAEESRGLGKADTPGPEGGVVK ASPVPSDPEKPGTPGEGMLSDDLDR STEELPKMESKDLQQLFKDVLGSR EQHLGCGTPGLEGSRTPLQRPFLQG GLPLGNLPSSSPMSYPGLCQSPFL DSRERGGFFSPEPGEPSDPTWGS TTPSTPTTTEGEGDGLSYNQRSQ RWEKDEELGQLSTISPVLYANINFPN	True	False	2.637	5.0	False

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