

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	37.553963	S2402;S2405;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	32574038;28657654;31492838;34846842;23301498;35138101;30620550;35289036;35254053;30059200;29351928	MDSQKLAGEDKDKSEPAADGPAASE DPSATESDLNPNHVGVEVSVLSSGSP LRQETPQDCSGGPPVRRCALCNCGEP SLHGQRELRRFELPFDWPRCPVVS GGSPGNEAVLPSEDLSQLGFFPEGLT PAHLGEPGGSCWAHHWCAAWSAG VWGQEGPELGVDKAIFSGISQRCS HCTRLGASIPCRSPGCPRLYHFPCAT ASGSFLSMKTLQLLCPHSEGAAYL EEARCAVCEGPGELCDLFFCTSCGH HYHGACLDLTALTARKRAGWQCPEC KVCQACRKPNDKMLVCETCDKG YHTFCLKPPMEELPAHSWKCKACR VCRACGAGSAELNPSEWFENYSL CHRCHKAQGGQTIRSVAEQHTPVCS RFSPPPEGDTPTDEPDALYVACQGG PKGGHVTSMQPEKPGPLQCEAKPLG KAGVQLEPQLEAPLNEEMPLLPPPE ESPLSPPEESPTSPPEASRLSPPE ELPASPLPEALHLSRPLEESPLSPPE EESPLSPPEESPFSPLEESPLSPPE SPPSPALETPLSPPEASPLSPPEES PLSPPEELPTSPPEASRLSPPEES PMSPPPEESPMSPPEASRLFPPEE SPLSPPEESPLSPPEASRLSPPEE SPMSPPPEESPMSPPEVSRPLPLV VSRLSPPEESPLSPPEESPTSPPE ASRLSPPEESPTSPPEESPASPPP EDSLMSLPLEESPLPLPEEPQLCPR SEGPLHSRPEEPHLSRPEEPHLS QAEPEHLSQPEEPLCAVPEEPHLS SPQAEGLHLSQPEELHLSQTEEP HLSPVPEECLSPQPEESHLSQSEE PCLSPRPEESHLSPELEKPLSRPE KPPEEPGQCPEEPLFPFPPGEP SPLLEPALSEPGEPLSPLPEELPLS PSGEPSPQLMPPDPLPPLSPHITA AAPPALSPGLELYPFGAKGSDPES PLAAPILETPISPPPEANCTDEPVVP MILLPPSPGSPVGPASPLMEPLPQC SPLLQHSVLPQNSPPSQCSPPALPLS VPSPLSPIGKVVGVSDAEELHEMET EKVSEPECPALEPSATSPPLSPMGDL SCPAPSPAPALDDFSGLGEDTAPLD GIDAPGSQPEPGQTPGSLASELKGSP VLLDPEELAPVTPMEVYPECKQTAG QGSPEEQUEEPRAVAPTPTLIKSD IVNEISNLSQGDASAFPGSEPLLS PDPEGGGSLSMELGVSTDVSPARDE GSLRLCTDSLPELDDSLCDAGTAIS GGKAEGEKRRRSPARSRIKQGRS SSFPGRRRPRGGAGGRGRARLK STASSIETLVVADIDSSPSKEEEEEED DDTMONTVVFSNTDKFVLMQDMC VCGSFRGAEGHLLACSQCSCQCYH PYCVNSKITKVMLLKGWRCVECIVC EVCQASDPSRLLCDDCDISYHTY CLDPPLLTVPKGGWKCKWCVSCMQ CGAASPGFHCWQNSYTHCGPCAS LVTCPICHAPVVEEDLLIQCRHCER WMHAGCESLFTEDDVEQAADEGFD CVSCQPVVVKPVAVAPPELVPMKV KEPEPQYFRFEGVWLTETGMALLRN LTMSPHLKRRQRRLGLPGEAGLE GSEPSDALGPDDKKDGLDTDELK GEGGVEHMECEIKLEGPVSPDVEPG KEETEESKKRKRKPYRPGIGGFMR QRKSHTRTKKGAQAQEVLSGDDGQP DEVIPADLPAEGAVEQSLAEGDEKK KQRRGRKSKLEDMFPAYLQEAFF GKELLDLSRKALFAVGVGRPSFGLG TPKAKGDGGSERKELPTSQKDDGP DIAEESRGLGKADTPGPEGGVVK ASPVPSDPEKPGTPGEGMLSDDLDR STEELPKMESKDLQQLFKDVLGSR EQHLGCGTPEGLSRTPLQRPFLQG GLPLGNLPSSSPMSYPGLCQSPFL DSRERGGFFSPEPGEPSDPTWTS TTPSTPTTTEGEGDGLSYNQRS RWEKDEELGQLSTISPVLYANINFPN	True	False	3.512	5.0	1.80

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