

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracell region
Q03112	MECOM_HUMAN	Homo sapiens	Histone-lysine N-methyltransferase MECOM	26.75988	NaN	S624;S726;S740;S1037;S1039	29485866	MRSKGRARKLATNNECVYGNYPEIP LEEMPDADGVASTPSLNIQPCSPA TSSEAFTPKEGSPYKAPIYIPDDIPIPA EFELRESNMPGAGLGIWTKRKIEVG EKFGPYVGEQRSNLKDPYSGWEILD EFYNVKFCIDASQPDVGSWLKYIRFA GCYDQHNLVACQINDQIFYRVVADI APGELLFLMKSEYPHETMAPDIH EEROYRCEDCDQLFESKAELADHQB FPCSTPHSAFMSVEDFQQKLESEN DLQEIHTIQECKECDQVFPDLQSLEK HMLSHTEEREYKCDQCPKAFNWKS NLIRHQMSHSDSGKHCECENCAKVF TDPSNLQRHIRSQHVGARAHACPEC GKTFATSSGLKQHKHHSVVKPFICE VCHKSYTQFSNLCRHKRMHADCR QIKCKDCGQMFSTTSSLNKHRRFCE GKNHFAAGFFGQGISLPGTPAMDK TSMVNMESHANPGLADYFGANRHPA GLTFPTAPGFSFSPGLFSPGLYHRP PLIPASSPVKGLSSTEQTNKSQSPLM THPQILPATQDILKALSKHPSVGDNK PVELQPERSSSEERPFEEKISDQSESSD LDDVSTPSGSDLETTSGSDLES DKEKFKENGMFKDKVSPQLNLASI NNKKEYSNHSIFSPLEEQTAVSGA VNDSIKAIASIAEKYFGSTGLVGLQD KKVGALPYPSMFPLPFFPAFSQSMY PFPDRDLRSLPLKMEPQSPGCEVKKL QKGSSSEPFDLTTKRKDEKPLTPVPS KPPVTPATSDQDPLDLSMGSRSRAS GTKLTEPRKNHVFSGGKGSNVE ASDGS LQHARPTPFMDPIRVEKR KLTDPLEALKEKYL RPSPGFLFHPQ MSAIENMAEKLESFSALKPEASELL QSVPSMFNFRAPPNALPENLLRKGK ERYTCRYCGKIFPRSANLRLRHTHT GEQPYRCKYCDRSFSISSNLQRHVR NIHNKEKPFKCHLCDRCFGQQTNL DRHLKKEHNGNMSGTATSSPHSEL ESTGAILDDKEDAYFTEIRNFIGNSN HGSQSPRNVEERMNGSHFKDEKAL VTSQNSDLLDEEVEDEVLLDEEDE DNDITGKTGKEPVTSNLHEGNPEDD YEETSALEMSCKTSPVRYKEEYYS GLSALDHIRHFTDSLKMRKMEDNQ YSEAE LSSFS TSHVPEELKQPLHRKS KSQAYAMMLS LSKESLHSTSHSSS NVVHSMARAAAESSAISISHV	True	False	4.566	5.0	1.87	1.199	0.966	1.693	1.714