

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extra regio
Q8CFT2	SET1B_MOUSE	Mus musculus	Histone-lysine N-methyltransferase SETD1B	25.775171	NaN	S977;S985;S1022;S1283;S1301;S1354;S1678;S1682	34678516	MENSHPHHHHQPPPQPGPSGERR NHHWRSYKLMIDPALKKGHHKLYR YDGHFSLAMSSNRPEIVEDPRVV GIWTKNKELELSVPKFKIDEFYVGPV PPKQVTFALKNNDNVRENFLRDMCK KYGEVEEVEILYNPKTKKHLGIAKVV FATVRGAKEAVOHLHSTSVMGNIH VELDTKGETRMRFYELLVTGRYTPQ TLPVGEFDAISPIVSETLQLSDALKRL KDGSLSAGCGSGSSSVTPNSGGTFF SQDTAYSSCRLDTPNSYQGQTPITPR LGTFFSQDSSYSRQPTPSYLSQDP TATFKARRHESKFTDAYNRRRHEHHY VHNSAVAGATAPFRGSSDLDFGTVG SSGTPFKAQSQDATTFAHTPPPAQT ATASGFKSAFSPYQTPAPPPPPPEE PTATAAFGSRDSEGEFRAPAPPLPP AEPFAKEKPGTPPGPPPPDSNSMEL GGRTFGWSPEPCDSPGTPTLESSP AGPEKPHDLSDSRIEMLLKEQRTKL PFLREQSDTEIQMEGSPISSSSSQL SPLSHFGTNSQPGFRGSPSSSRPSS TGLEDISPTPLPDSDEDEDLGLGLGP RPPPEPGPPDPMGLLGQTAEDVDL AGDRTPTSERMDEGQSSGEDMEI SDDEMPAPITSDADCKPMVVTGA GAVAAPNVLAPNLPPLPPGFPLPP PPPPPPQPGFPMPLPPPPPPPP AHPAVTVPPPLPAPPGVPPPIPLPL PPFPPLFPVMQVDMSHVLGGQWG GMPMSFQMOTQMSRLMTGQGAC PYPPFMAAAAAAASAGLQFVNLPPY RSPFSLNSGPGRGQHWPLPKFDP SVPPPGYIPRQEDPHKATVDGVLV LKELKAIMKRDINRKMVEVAVAFRAF DEWWDKKERMAKASLTPVKSGEHK DEDRPKPKDRIASCLLESWGKGEGL GYEGLGLGILRGAILRPSFKVKRKE PPDTASSGDQKRLRPSTSVDEEDEE SERERDRDIADAPCELTKRDPKSVG VRRRPRPLELDSGGEEDEKESLSA SSSSASSSSGSSTTSPSSASDKEE EDRESTEEEEEEEEEEEEEGP RSRISPSSSSSDKDEDDNEADS DGQIDSDIDDQGAPLSEASEKNDNGD SEEEETEISITTSKAPAESSSSSESSG SSEFESSSESSSSSEDEEEMTVP GVEEEEEEEEEEKETAMAAATVVA MAEESMPAGGQDFEQDRAEVPLG PRGPMRESLGTTEEVDIEAEDEVPE MQAPELEEPPLPMGARKLEGSPEPP EEPQNTQGDMLLSPPELARETEEA QLPSPPEHGPESDLMEPEPPMLS LPLQPLPPRLRPPSPPEPETPEP PKPPVLEPPPEHPPRTPGLCGSLA KSQSTETVPATPGGEPPLSGSSGSL LSSQVPGSPFSYSPSPGLSSGGLP RTPGRDFSTFTFPEPSGLLLLPVCP LPTGRRDERTGLASVLLTGLPLP LPLPLPLALPVVPLRAQPRPPQLP PLLATLAPCPTPIKRPGRRRSPPS MLSLDGLVLRPPGALGRDLLLLP GQPPAPIFSAHDPRAVTLDFRNTGI PAPPPPLPPQPPPPPPVESTKLPF KELDNQWPSEAIPPGRRDEVTEY VDLAKVRGWRPPKRRHEDLVAPS ASPEPSPQPLFRPRSEFEEMTILYDI WNGGIDEEDIRFLCVTYERLLQDDN GMDWLNIDLWVYHPSTLSSAKKK KREDGIREHVTGCARSEGFYIDKDD KLRYLNSRASSTDEPPMDTQMSIP AQPHASTRAGSERRSEQRLLSSFT GSCDSDLLKFNQLKFRKKLKFCKS HIHDWGLFAMEPIAADEMVIEWVQ NIRQVIADMREKRYEDEGIGSSYMF RVDHDIIDATKCGNFARFINHSCN PNCYAKVITVESQKKIVYSKQHINV NEEITYDYKFPIDVKIPCLCGSENC RGTLN	None	None	None	None	None	None	None		