	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellula region
0	Q3UHH1	ZSWM8_MOUSE	Mus musculus	Zinc finger SWIM domain-containing protein 8	25.810548	NaN	S36;S48;S53;S437;S564;T1141;S1155;S1158;S1162;S1270;S1831	29187734	MELMFAEWEDGERFSFEDSDRFEE DSLCSFISEAESLCQNWRGWRKQSA GPNSPTGGGGGGGSGGTRTRDGLVI PLVELSAKQVAFHIPFEVVEKVYPPV PEQLQLRIAFWSFPENEEDIRLYSCL ANGSADEFQRGDQLFRMRAVKDPL QIGFHLSATVVPPQMVPPKGAYNVA VMFDRCRVTSCSCTCGAGAKWCTH VVALCLFRIHNASAVCLRAPVSESLS RLQRDQLQKFAQYLISELPQQILPTA QRLLDELLSSQSTAINTVCGAPDPTA GPSASDQSTWYLDESTLTDNIKKTL HKFCGPSPVVFSDVNSMYLSSTEPP AAAEWACLLRPLRGREPEGVWNLLS IVREMFKRRDSNAAPLLEILTDQCLT YEQITGWWYSVRTSASHSSASGHTG RSNGQSEVAAHACASMCDEMVTLW RLAVLDPALSPQRRRELCAQLRQWQ LKVIENVKRGQHKKTLERLFPGFRP AVEACYFNWEEAYPLPGVTYSGTDR KLALCWARALPARPGASRSGGLEES RPRPLPTEPAVRPKEPGAKRKGLGE GISSQRGPRRLSAEGGDKALHKMGP SGGKAKVLGGTGSGGKSSAGSGSKR RLSSEDSSLEPDLAEMSLDDSSLAL GAEASTFGGFPESPPPCPSSVGSRGP STFLPEPPDTYEEDAGVYFSEGPEPP TASADHPGLLPGEVCTRDDLPSTDD SGSGLHKTKEAAPAVGEEDDDYQAY YLNAQDGAGGEEEKAEGGTGEEHD LFAGLKPLEQESRMEVLFACAEALH AHGYSNEASRLTVELAQDLLANPPD LKVEPPPAKGKKNKVSTSRQTWVAT NTLTKAAFLLTVLSERPEHHSLAFRV GMFALELQRPPASTKALEVKLAYQE SEVAALLKKIPRGPSEMSTIRCRAEE LREGTLCDYRPVLPLMLASFIFDVLC APVVSLTGSRPPSRNWTNEMPGDE ELGFEAAVAALGMKTTVSEAEHPLL CEGTRREKGDLALALMITYKDDQAK LKKILDKLLDRESQTHKPQTLSSFYS SSRPATANQRSPSKHGAPSAPGALQ PLTSSSAGPAQPGNVAGAGPGPTEG FTEKNVPESSPHSPCEGLPPEAALTP RPEGKVPSRLALGSRGGYNGRGWG SPGRPKKKHTGMASIDSSAPETTSD SSPTLSRRPLRGGWAPTSWGRGQDS DSISSSSSDSLGSSSSSGSRRASASG GARAKTVDVGRCYKGRRPESHAPHV PNQPSEAAAHFYFELAKTVLIKAGG NSSTSIFTHPSSSGGHQGPHRNLHL CAFEIGLYALGLHNFVSPNWLSRTY SSHVSWITGQAMEIGSAALTILVEC WDGHLTPPEVASLADRASRARDSN MVRAAAELALSCLPHAHALNPNEIQ RALVQCKEQDNLMLEKACMAVEEA AKGGGVYPEVLFEVAHQWFWLYEE TAGGSSTAREGATSCSGSGMRAAGE AGRGLPEGRGAPGTEPVTVAAAAVT AAATVVPVISVGSSLYPGPGLGHGHS PGLHPYTALQPHLPCSPQYLTHPAH PAHPMPHMPRPAVFPVPSSAYPQGV HPAFLGAQYPYSVTPPSLAATAVSFP VPSMAPITVHPYHTEPGLPLPTSVAL SSVHPASTFPAIQGASLPALTTQPSP LVSGGFPPPEEETHSQPVNPHSLHH LHAAYRVGMLALEMLGRRAHNDHP NNFSRSPPYTDDVKWLLGLAAKLGV NYVHQFCVGAAKGVLSPFVLQEIVM ETLQRLNPIHAHNHLRAPAFHQLVQ RCQQAYMQYIHHRLIHLTPADYDDF VNAIRSARSAFCLTPMGMMQFNDIL QNLKRSKQTKELWQRVSLEITTFSP	None	None	None	None	None	None	None	None	None