	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	pla me
0	A7E2V4	ZSWM8_HUMAN	Homo sapiens	Zinc finger SWIM domain-containing protein 8	9.722839	S514	S36;S48;S53;S437;S567;T1139;S1153;S1156;S1160;S1267;S1836	30379171;34019948;38665916	MELMFAEWEDGERFSFEDSDRFEE DSLCSFISEAESLCQNWRGWRKQSA GPNSPTGGGGGGGSGGTRMRDGLV IPLVELSAKQVAFHIPFEVVEKVYPPV PEQLQLRIAFWSFPENEEDIRLYSCL ANGSADEFQRGDQLFRMRAVKDPL QIGFHLSATVVPPQMVPPKGAYNVA VMFDRCRVTSCSCTCGAGAKWCTH VVALCLFRIHNASAVCLRAPVSESLS RLQRDQLQKFAQYLISELPQQILPTA QRLLDELLSSQSTAINTVCGAPDPTA GPSASDQSTWYLDESTLTDNIKKTL HKFCGPSPVVFSDVNSMYLSSTEPP AAAEWACLLRPLRGREPEGVWNLLS IVREMFKRRDSNAAPLLEILTDQCLT YEQITGWWYSVRTSASHSSASGHTG RSNGQSEVAAHACASMCDEMVTLW RLAVLDPALSPQRRRELCTQLRQWQ LKVIENVKRGQHKKTLERLFPGFRP AVEACYFNWEEAYPLPGVTYSGTDR KLALCWARALPSRPGASRSGGLEES RDRPRPLPTEPAVRPKEPGTKRKGL GEGVPSSQRGPRRLSAEGGDKALHK MGPGGGKAKALGGAGSGSKGSAGG GSKRRLSSEDSSLEPDLAEMSLDDS SLALGAEASTFGGFPESPPPCPLHGG SRGPSTFLPEPPDTYEEDGGVYFSEG PEPPTASVGPPGLLPGDVCTQDDLPS TDESGNGLPKTKEAAPAVGEEDDDY QAYYLNAQDGAGGEEEKAEGGAGE EHDLFAGLKPLEQESRMEVLFACAE ALHAHGYSSEASRLTVELAQDLLAN PPDLKVEPPPAKGKKNKVSTSRQTW VATNTLSKAAFLLTVLSERPEHHNL AFRVGMFALELQRPPASTKALEVKL AYQESEVAALLKKIPLGPSEMSTMR CRAEELREGTLCDYRPVLPLMLASFI FDVLCAPGSRPPSRNWNSETPGDEE LGFEAAVAALGMKTTVSEAEHPLLC EGTRREKGDLALALMITYKDDQAKL KKILDKLLDRESQTHKPQTLSSFYSS SRPTTASQRSPSKHGGPSAPGALQP LTSGSAGPAQPGSVAGAGPGPTEGF TEKNVPESSPHSPCEGLPSEAALTPR PEGKVPSRLALGSRGGYNGRGWGSP GRPKKKHTGMASIDSSAPETTSDSS PTLSRRPLRGGWAPTSWGRGQDSD SISSSSSDSLGSSSSSGSRRASASGG ARAKTVEVGRYKGRRPESHAPHVPN QPSEAAAHFYFELAKTVLIKAGGNSS TSIFTHPSSSGGHQGPHRNLHLCAF EIGLYALGLHNFVSPNWLSRTYSSH VSWITGQAMEIGSAALTILVECWDG HLTPPEVASLADRASRARDSNMVRA AAELALSCLPHAHALNPNEIQRALV QCKEQDNLMLEKACMAVEEAAKGG GVYPEVLFEVAHQWFWLYEQTAGG SSTAREGATSCSASGIRAGGEAGRG MPEGRGGPGTEPVTVAAAAVTAAAT VVPVISVGSSLYPGPGLGHGHSPGL HPYTALQPHLPCSPQYLTHPAHPAH PMPHMPRPAVFPVPSSAYPQGVHPA FLGAQYPYSVTPPSLAATAVSFPVPS MAPITVHPYHTEPGLPLPTSVACEL WGQGTVSSVHPASTFPAIQGASLPA LTTQPSPLVSGGFPPPEEETHSQPVN PHSLHHLHAAYRVGMLALEMLGRR AHNDHPNNFSRSPPYTDDVKWLLG LAAKLGVNYVHQFCVGAAKGVLSPF VLQEIVMETLQRLSPAHAHNHLRAP AFHQLVQRCQQAYMQYIHHRLIHLT PADYDDFVNAIRSARSAFCLTPMGM MQFNDILQNLKRSKQTKELWQRVS LEMATFSP	None	None	None	None	None	None	None	No