

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
Q5VUA4	ZN318_HUMAN	Homo sapiens	Zinc finger protein 318	20.488816	S866;T1328;T1333;S1334;T1341;T1342;T1693	S40;S79;S81;S136;S173;T205;S207;S214;S464;S472;S501;S527;T842;S1010;S1037;S1243;S1267;S1420;S1713;S1856;S1896;S1971;S2030;S2035;S2091;S2101;S2189;S2192;S2243	32574038;30379171;31492838;35132862;23301498;34019948;35254053;35289036;30059200;29237092;32119511;38665916	MYRSSARSSVSSHRPKDDGGGGPRSSGRSSSSSGPARRSSPPPPSGSSSRTPARRRPSPSGHRGRRASPSPPRGRVSPSPPRARRGSPSPRGRRLFPFGPAGFRGSSRSGESRADYARDGRGDHPGDSGSRRRSPGLCSDSLEKSLRITVGNDFHCVSTPERRRLSDRLGSPVDNLEDMDRDDLTDSDVFTRSSQCSRGLERYISQEEGPLSPFLGQLEDYRTKETFLHRSDYSPHISCHDELLRGTERNREKLLKGYISIRSEERSREAKRPRYDDTVKINSMGGDHPFSFTGTRNYRQRRRSPPRFLDPEFRELDLARRKREEEEEERSRSLSQELVVDGGGTGCSIPGLSGVLTASEPGYSLHRPEEVSVMKKSLIKKRIEVDIMEPSMQLESFSSSTSSQDHPLYSGHPSLPLSGAIAAFASEIENKGTMVETALKEPQGNLYQWGPLPGIPKDNSPLREKFGSFLCHKDNLDLKAEGPERHTDFLLPHERASQDGSFGRILSMLADSTSTQEKRRRSFPDIEDEEKFLYGDEEEDLKAESVVKPLGSSESEVMRQKASSLPSSAPAVKLESLEETNPEYAKIHDLLKTIGLDIGVAEISQLARTQERLHGKKPSLRSSADRRSSVDRYFSADHCSSVDHRFSADRCSSVDHCFSADRRSSDPHRLESREAHHSNTHSPEVSHPPPPSPVDPYLLTKNSPPFLKSDHPVGHISGPEVVGSGFQSSVAVRCMLPSAPSAPIRLPHTAALSQFHMPRASQFAAARIPPNYQGPAPFASFDAYRHYMAYAASRWPMYPTSQPSNHPVPEPHRIMPITKQATRSRPNLRVIFTVTPDKPKQKESLRGSIPAAQVPVQVSIPSLIRYNPEKISDEKNRASQKQKVIEREKLNKDREARQKKMYLRTLELERLHKQGEMLRKKRREKDGKDLLVEVSRQLQDNIMKDIAELRQEAEEAEKKQSELDKVAQILGINIFDKSQKSLSDSREPTKPGKAEKSKSPEKVSSFSNSSSNKESKVNNEKFRTKSPKPAESPOKATKQDQPTAAEYDAGNHWCKDCNTICGTMFDFFTMHNNKHTQTLDPYNRPWASKTQSEAKQDAIKRTDKITVPAKGSFVLPISGFYQCLEEFLDGDPISGEQHVKGHQHNEKYKKYVDENPLYEERRNLDRAQGLAVVLETERRRQSELKRKLEKPKKEKKEKKA KAVKEVKEDDKVSEKLEDQLEGRNSPEKAENKRNTGIKQLKEEVKESPTSSSFKFSWKKPEKEEEEKSSLVTPSISKEIILESSKDEKEDGKTEAGKAKPIKIKLSGKTVAHTSPWMPVVTSTQTKIRPNLPISTVLRKSCSATMSKPAPLNTFLSIKSSGTTAKPLPVVKESSADLLLPDIIKSAFGGEEVILKGSPEEKVVLAEKSEPSHLPKQILPPPPPPPPPPPPPPVPHPAAPSAAQANAILAPVKS NPVVSQTLSPGFVGNILNPVLPVAIMASAQPAAPSDETPAGVSESDRDQTLFVSVLRPPPLSSVFSEQAKKLEKRNSCLATANAKDLYDIFYSSGGKGA PETKGAPETKLSGGPLANGENSNLSRTKSSDTSSTPLNSSASQEEHLHQDEGLVAAPIVSNSEKPIAKTLVALGKWSVVEHVGPKSTGTYGFLQLPTRLCSQSRPYETITPKDTLAIWTSSTSFQSDTSRDISPEKSELDLGEPGPPGVEPPPQLLDIQCKESQKLVIEIHLRESVNDKESQELRKSEDCRESEIETNTELKERVKELSEGIVDEGVSTSIGPHSDDSNLNHGNRYMWEDEVKQPNLLMIDKEAEQSNKLMTGSETPSKVVIKLSPOACSFTKAKLDSFLSEARSLNPDQTPVKISAPELLLHSPARSAMCLTGSPEQGVSVVSEGLENSAPESARTSRYSRLKLLKRERSKDFQVKKIYELAVWDENKKRPETWESPEKPKTEALELQDVHPELTVTIESKALEDFEATDLKVEELTAGNLGDMPVDFCTTRVSPAHRSPTV	True	False	4.619	4.808	0.95

								LCQKVCEENSVP IGCNSSDPADFE PIPSFSGFPLD SPKTLVLD FETEGER NSPNPRSVRIP SPNILKTGLT ENVDR GLGGLEGTHQ ALDLAGGMPE EV KESQLDKQES LGLLEKTINS AGLGP SPCLPDLVDF VTRTSVQKDK LCSPL SEPGDPSKCS SLELGPLQLE ISNAST TEVAILQVDD DSDPLNLVKA PVRSR PPREQVIEDNM VPPQGMPEQET TVG AIQDHTESSVHN					
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