

UniprotKB ID	Entry name	organism	full name	oglcna score	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	gol
Q9WUU9	GANP_MOUSE	Mus musculus	Germinal-center associated nuclear protein	45.68119	S13;S18;T210;S211;S544;S547	S424;S502;S531;S550	22645316;40885482;36852467;34678516;39627609;40997131	MHPVNPFGGQOPSAFAVSSSTTGTG QTKSPFRFGQPSLFGQNSTPSSKSLA FSQVPSFATPSSGGSHSSSLPAFGLTQ TSSVGLFSSLESTPSFAATSSSSVPG NTAFSFKSTSSVGVFPFGATFGPETG EVAGSGFRKTEFKFKPLENAVFKPIP GPESEPEKTQSOISSGFFTFHPVGS GSGGLTPFSFPQVTNSSVTSSSFI KPVTSNTPAFASPLSNQNVVEEKRV STSAFGSSNSFSFTPTASPGSLGEP FPANKPSLRQCCEEAIQVEPLPTL MKGLKRKEDQDRSPRRHCHEAAED PDPLSRGDHPPDKRPVRLNRPGRGT LFGRTIQEVFKNKEAGRLGSKESK ESGFAEPGESDHAAVPGGSQSTMVP SRLPAVTKEEESRDEKEDSLRGKS VRQSKRREEWIYSLGGVSSLELTAIQ CKNIPDYLNDRAILEKHFSKIAKVQR VFTRRSKKLAVIHFFDHASAAALARKK GKGLHKDVFVFWHKKKISPSKLFPL KEKLGESQIEGIESPFQHSPLSKP IVRPAAGSLLSKSSPVKPSLLKMHQ FEADPFDSGSEGLGSCVSSLSTL IGTVADTSEEKYRLLDQRDRIMRQA RVKRTDLLKARAFVGTCPDMCPEKE RYLRETRSQLSVFEVVPGTQDQVHA AAVKEYSRSSADQEEPLPHELRSVA LSRTMDYLVTOIMDQKESLRDQWY DFVWNRTRGIRKIDITQQHLCDPLTV SLIEKCTRPHIHCAHFMCCEPMSSF DAKINNENMTKCLQSLKEMYQDLR NKGVFCASEAEFQGYNVLLNLNKG DILREVQOFHPDVRNSPEVNFVAVQA FAALNSNNFVRFKLVQASLYLAC LLHCYFNQIRKDALRALNVAYTVST QRSTVFPDGVVRLFRDSEETN FLNYHGLTVADGCVELNRSFALEPE GLCKARKSVFIGRKLTVSVGEVNG GPLPPVPRHTPVCSFNQNKYVGES LATELPSTORAGGDPAGGGRGDC EAEVDVPTLAVLPQPPASSATPALH VOPLAPAAAPSLQASTQPEVLLPKP APVYSDSDLVQVDELQEQALQVDC EEVSSAGAAYVAAALGVSNAAVEDLI TAATTGILRHVAAEEVSMERQLEE EKQRAEEERLKQERELMLTQLSEGL AAELTELTVTECVWETCSQELQSAV EIDQKRVARCEAVCAHLVDLFLA EEIFQTAKETLQELQCFCKYLQWR EAVAARKKFRQMRAPPAAPCCVDV NDRLQALVPSAECPIITEENLAKGLLD LGHAGKVGVSCTRLRRLRNKTAHQI KVQHFHQQLLRNAAWAPLDLPSIVS EHLPMKQKRRFWKLVVLDPVVEEQ TPESPGRILENWLKVKFTGDDSMVG DIGDNAGDIQTLVFNLSKGDQT VSVNVCIKVAHGTLSALDAVETQ KDLLGTSGLMLLLPPKVKSEEVAAE ELSWLSALLQLKQLQAKFPQPALP LVVLVPSRGDSAGRAVEDGLMLQD LVSAKLISDYVVEIPDSVNDLQGTVK VSGAVQWLISRCQALDLCCQTLVQ YVEDGISREFSRRFFHRRRRLASL PSQEPSTHILFNSVLQFLASVVSSEQ LCDISWPVMEFAEVGGSQLLPHLH WNSPEHLAWLKQAVLGFQLPQMDL PPPAPWLPVCSMVIQYTSQIPSSSQ TOPVLSQVENLLCRTYQKWKNSL SPGQELGPSVAEIPWDDIITLCINHK LRDWTPPRLPVTLEALSEDGQICVYF FKNLLRKYHVPLSWEQARMQTORE LQLSHGRSGMRSIHPPSTFTPTLLH VHQKGGKKEESGREGSLSTEDLLRG ASAEELLAQSLSSSLEEKENKRF DQLQQLWLSQDSQAFTESTRLPLYLP QTLVSPDSIKTQTMVKTSTSPQNSG TGKQLRFSEASGSSLTEKLLERLI QSSRAEEAASELHLSALLEMVD	True	False	3.099	5.0	1.327	0.872	Fal