

| UniprotKB ID | Entry name | organism | full name | oglcnaScore | oglcna sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion |
|--------------|-------------|--------------|-------------------------|-------------|---|--|--|--|---------------|---------------|---------|---------|---------------|
| 015014 | ZN609_HUMAN | Homo sapiens | Zinc finger protein 609 | 29.219845 | S626;S952;S1186;S1189;T1195;S1196;S1199 | S358;S361;S379;T381;S413;S433;S446;S452;S467;S470;S533;S576;S578;S743;T746;S758;S804;T823;S842;S846;S849;S1055 | 38665916;34019948;33214551;30059200;31492838;23301498;35289036;29237092;39531497;30620550;20068230;40596516;32574038;38253038;35254053 | MSLSSGASGGKGVNDANPVETYDSGD EWDICVGNLIIDLADLEKDDQKLE MSGSKVEGIPAPNAVATLPDNIKFVT PVPGPQKGEKSKSKRSKSGKDTSK PTPGTSLFTPSEGAASKKEVQGRSG DGANAGGLVAAIAPKGEKAAKASR SVAGSKKEKENSSSKSKKERSEGVG TCSEKDPGVLPVPLGGRGGQYDGS AGVDTGAVEPLGSIAIEPGAALNPLG TKPEPEGENECLLKKVKSEKME PVSTPAVLPIHLLVPVNNDISSPCE QIMVTRTSVGVNTCDVALATEPECL GPCEPGTSVNLEGIVWQETEDGMLV VNVTRNKTYVGTLLDCTRHWDWAP PRFCDSPSTDLEMRNRRGRGRMR PNSNTPVNETATASDSKGTSSNSKT RAGANSKGRGGSQNSSEHRPPASST SEDEVKASPPSANKRKNKPLSDMELN SSSEDSKSKRVRTNSMGSATGPLP GTKVEPTVLDNRNCPSPVLIDCPHPN CNKKYKHINGLKYHQAHHTDDDS KPEADGDSEYGEEPILHADLGSNG ASVSQKGSLSPARSATPKVRLVEPHS PSPSSKFSTKGLCKKLSGEGDIDL GALSNDGSDDGPSVMDETSNDADF SLERKCKMEKCKKPSLLKPEKIPSK SLKSARPIAIPPOQIYTFQTATFTA ASPGSSSGLTATVAQAMPNSPOLKPI QPKPTVMGEPFTVNPALPAKDKKK KDKKKKESKESPLTPGKVCRAE EGKSPRESSGDGMKMEGLLNGSS DPHQSRLASIKAEADKIYSFTDNAPS PSIGSSRLENTTPTQPLTPLHVVTQ NGAEASSVKTNSPAYSDISDAGEDG EGKVDVSKDAEQLVKEGAKTLF PPQPQSKDSPYYQGFESYSPSYAQS SPGALNPSSQAGVESQALKTKRDEE PESIEGKVNNDICEEKKPELSSSSQ PSVIQQRPNMYMOSLYYNQYAYVPP YGYSQSYHTHLLSTNTAYRQYEE QQRQSLQQRGVDKKAEMGLKE REAALEKEWKQKPSIPPTLTKAPSLT DLVKSGPGKAKEPGADPAKSVIIPKL DDSSKLPQAPEGLKVKLSDASHLS KEASEAKTGAECGRQAEMDPIWYR QEAEPBMWYVYPAKYSDIKSEDER WKEERDRKLKEERSRSDSVKPEDG KESTSSDKLPTSEESRLGSKPRPS VHVVPSSPLTQHQSYIPYMHGYSYS QSYDPNHPSYRSMVAVMMQNYPGS YLPSSYSFSPYGSKVS GGEDADKARA SPSVTCKSSSEKALDILQHASHYK SKSPTISDKTSQERDRGGCGVVG GCSVSVGGASGGERSVDRPRTSPSQ RLMSTHHHHHLLGYSLLPAQYNLP YAAGLSSTAIVASQQGSTPSLYPPRR | True | False | 1.664 | 5.0 | False |