

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|-------------|--------------|-------------------------------------|--------------|-------------------------------|---|--|---|
| Q96AY4 | TTC28_HUMAN | Homo sapiens | Tetratricopeptide repeat protein 28 | 18.156422 | S2190;S2201;S2202;T2203;S2246 | S28;S1590;S2104;S2224;S2251;S2393;S2398 | 37217939;31492838;35254053;30059200;29237092;37340703;30620550;35132862;30379171 | MEQSPPPAPEPTQGPTPARSRRRRE PESPPASAPIPLFGADTIGQRSPDGP VLSKAEFVEKVRQSNQACHDGDGFH TAIVLYNEALAVDPQNCILYSNRSAA YMKIQQYDKALDDAIKARLLNPKWP KAYFRQGVALQYLGRHADALAAFAS GLAQDPKSLQLLVGMVEAAMKSPM RDSLEPTYQQLQKMKLDKSPFVVVS VVGQELLTAGHHGASVVVLEAALKI GTCSLKLRGSVFSALSSAYWSLGNT EKSTGYMQDLDVAKTLGDQTGEC RAHGNLGSAFFSKGNYREALTNHR HQLVLAMKCLKDREAASSLSSLGHV YTAIGDYPNALASHKQCULLAKQSK DELSEARELGNMGAVVIAMGDFEN AVQCHEQHLKIAKDLGNKREEARAY SNLGSAYHYRRNFDKAMSYHNHYL ELAQELMEKAIEMRAYAGLGHAAARC MQDLERAKQYHEQQLGIAEDLKDR AAEGRASSNLGIIHQMKGDYDTALK LHKTHLCAQELSDYAAQGRAYGNM GNAYNALGMYDQAVKYHRQELQIS MEVNDRASQASTHGNLAVAYQALG AHDRALQHYQNHNLNIARELRDIQSE ARALSNLGNFHCGRGEYVQAAPYYE QYLRLAPDLQDMEGEGKVCCHNLGY AHYCLGNYQEAVKYEQDLALAKDL HDKLSQAKAYCNLGLAFKALLNFSK AEFCQKYLSSLAQSLNNSQAKFRAL GNLGDIFICKKDIINGAIKFYEQQLGL AHQVKDRRLEASAYAALGTAYRMIQ KYDKALGYHTQELEVYQELSDLPGE CRAHGHLAAVYMALGKYTMAFKCY EEQLDLGQKLDPSLEAQVYGNMGI TKMNMNVMEEAIGYFEQQLAMLQ QLSGNESVLDGRAYGNLGDICYEAL GDYEEAIKYEQYLSVAQSLNRMQD QAKAYRGLGNHRAMGSLQQALVC FEKRLVVAHELGEAFNKAQAYGELG SLHSQLGNYEQAISCLERQLNIARD MKDRALESDAACGLGGVYQGMGEY DTALQYHQDLQIAEETNNPTCQGR AYGNLGLTYESLGTFERAVVYQEQH LSIAAQMNDLAAKTVSYSSLGRTHH ALQNYSAVMYLOEGLRLAEQLGRR EDEAKIRHGLGLSLWASGNLEEAQH QLYRASALFETIRHEAQLSTDYKLSL FDLOTSSYQALQRVLVSLGHHDEAL AVAERGRTRAFADLLVERQTGQQDS DPYSPVTIDQILEMVNGQRGLVLYYS LAAGLYSWLLAPGAGIVKFHEHYL GENTVENSSDFQASSSVTLPTATGS ALEQHIASVREALGVESHYSRACASS ETESEAGDIMDQQFEEMNNKLSNV TDPTGFLRMVRRNLFNRSCQSM SLFSNTVSPTQDGTSSLPRRQSSFAK PPLRALYDLLIAPMEGGLMHSSGPV GRHRQLLVLLEGELYLIPFALLKGS SNEYLYERFGLLAVPSIRLSVQSKS HLRKNPPTYSSSTSMAAVIGNPKLPS AVMDRWLWGPMPSAEEEEAYMVSEL LGCQPLVGSVATKERVMSALTQAEC VHFATHISWKL SALVLTSPMDGNPA SSKSSFGHPYTIPESLRVQDDASDGE |

