

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|------------|--------------|-----------------|--------------|---------------|--|-------------------------------------|--|
| O08784 | TCOF_MOUSE | Mus musculus | Treacle protein | 27.465758 | S587 | S83;S85;S87;S88;T104;S151;S154;S169;T171;T324;S386;S413;S414;S433;S443;S590;S593;S662;S664;S669;S671;S760;S761;S765;S767;S794;S853;T860;T869;S1034;T1066;S1191;S1216;S1242;S1301;S1303 | 22645316;29187734;28528544;36852467 | MAEARKRRELLPLIYHLLQAGYVR AAREVKEQSGQKSFLTQPVTLLDIYT HWQQTSELGQKQKAEDDETLOAKK SRVSDPVSSSESSDQEKEEEAATER AKATPRPTPVNSATAALPSKVKEKGGK TKTANKTVNSVSHPGSGKTVVHLLS GKSPKKSAPLANTVLASETEEEGN AQALGPTAKSGTVSAGQSSSEDS SISSEDTDVEVKSPAKPAQAKASAAP AKDPPPARTAPGPTKLGNAVPTPAKPA RAAAAAAAAAVAAAAAAAAEESSE EDSDSEDEAPAGLPSQVKASGKGGPH VRADSVSAKGISGKGPILATPGKTGP AATQAKAERPEKDSSETSEDDSDSE DEMPVTVNTPQARTSGKSPRARGTS APAKESSQKGAPAVTPGKARPVAAQ AGKPEAKSSEESSESDSGETPAAATLT TSPAKVKPLGKSSQVRPVSTVTPGSS GKGANLPCPGKVGSAALRVQMVKK EDVSESSAELSDGPGSPAKAKAS LALPQKVRPVATQVKTDRGKGHSGS SEESSDSEEEAAPAASAAQAKPALEK QMKASSRKGTPASATGASTSSHCKA GAVTSSASLSPALAKGTQRSDVDSS SESESEGAAPSTPRVQKSGGKGLQ GKAALGQGVAPVHTQKTGPSVKAM AQEDSESLEEDSSSEEEDETPAQAT PLGRLPQAKANPPPTKTPPASASGKA VAAPTKGKPPVNPSTVSARGQRSVP AAGKAGAPATQAQKGPVAGTGEDSE SSSKEESDSEETPAQIKPVGKTSQV RAASAPAKESPCKGAHPGTPGKTGS SATQAQPGKTEDSDSSSEESDSDTE MPSAQAIKSPVSVNRNSSPAVPAPT PEGVQAVNTHKASGTTAQQSSSES EDGDEDLIPATQPSTYALRTSVTPA ALSRAASQPSKSEQSSRMPKGGKAK AAASAQTSSAVETLPMMPQSAPIQ PKATNKLGKSKLPEKQQLAPGYPKA PRSEDSSDTSEDEEDAKRPQMPK SAHRLDPDPSQKETVVEETPTESSE DEMVAQSLLSGYMTPLTVANSQ ASKATPRPDSNSLASSAPATKDNPD GKQKSKSQHAADTALPKTGRKEASS GSTPQKPKLKKSTSSSPAPTQTLPN SITQRLLQAWPLSEAQVQASVVKV LTELLEQERLKATEAIKESGKKSQKR KLSGDLEAGAPKNKKKKEQPVPRAS AVSPEKAPMTSKAKSKLDKGSAGGK GKSGPGPQGAKEKPDGELLGIKLES GEQSDPKSKSKKSLKSKKDKKKK EKKKGKSLAKDSASPIQKKKKKK KSAEPAV |

