

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus | plasma membrane | extrac region |
|--------------|-------------|--------------|--------------------------------|--------------|---------------|-----------------------|----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|-----------------|---------------|
| Q13772 | NCOA4_HUMAN | Homo sapiens | Nuclear receptor coactivator 4 | 25.212942 | T277;S456 | NaN | 30379171;29485866;29237092 | MNTFQDQSGSSSNREPLLRCS DAR RDLELAIGVLR AEQQIKDNLREVKA QIHSCISRHLECLRSREVWLYEQVD LIYQLKEETLQQQAQQLYSLLGQFN CLTHQLECTQNKDLANQVSVCLERL GSLTLKPEDSTVLLFEADTITLRQTIT TFGSLKTIQIPEHLM AHASSANIGPF LEKRGCSMPEQKSASGIVAVPFSE WLLGSKPASGYQAPYIPSTDPODWL TQKQTL ENSQTSSRACNFFN NVGG NLKGL ENWLLKSEKSSYQKCNSHS TTSSFSIEMEKVGDQELPDQDEMDL SDWLVT PQESHKLRKPENGSRETSE KFLLFQSYNVNDWL VKTDSCTNC QGNQPKGVEIENLGNL KCLNDHLE AKKPLSTPSMVTEDWL VQNHQDPC KVEEVCRAN EPCTSF AECVCDENCE KEALYK WLLKKEGKDKNGMPVEPK PEPEKHKDSLNMWLCPRKEVIEQTK APKAMTPSRIADSFQVIKNSPLSEWL IRPPYKEGSPKEVPGTEDRAGKQKFK SPMNTSWCSFN TADWVLP GK KMG NLSQLSSGEDKWLLR KKAQEVLLNS PLQEEHNFPDPHYGLPAVCDL FACM QLKVDKEKWL YRTPLQM | True | False | 3.341 | 4.688 | 2.823 | 1.973 | 2.366 | 2.263 | 3.086 |