

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus |
|--------------|------------|--------------|-----------|--------------|---------------|---|--|---|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|
| Q86YZ3 | HORN_HUMAN | Homo sapiens | Hornerin | 19.355858 | NaN | S659;S661;S890;S993;S1008;S1463;S1478;S1712;S1714;S1829;S1831;S1933;S1948;S2299;S2301;S2403;S2418;S2652;S2654 | 34229054;38665916;34019948;26374642;39990658;37217939;26853435;23271734;28510447 | MPKLLQGVTVIDVFYQYATQHGEYD TLNKAELKELLENEFHQILKNPNP DVTVDIILQSLDRDHNNKVVDFTEYLL MIFKLVQARNKIIGKDYCQVSGSKLR DDTHQHQQEETEKEENKROESS FSHSSWSAGENDSYSRNVKSLKP GTESISRRLSFQRDFSGQHNNSYSGQ SSSYGEQNSDSHQSSGRGQCGSGS GQSPNYGQHSGSGQSSSNDTHGS GSGQSSGFSQHKSSSGQSSGYSQH GSGSGHSSGYQHGSRSRGSRRGE RHRSSSSSSSYGQHGSRSRQSLGH GRQGSRSRQSPSHVRHGS SGHSS SHGQHSGSSYSYRGRHYESGSGQT SGFGOHESGSGQSSGYKHS GSG HSSSQGQHGSTSGQASSGQHGSS SRQSSSYGQHEASRHSRSGRQHS GSGQSPGHGQRGSGSGQSPSSGQH GTGFRSSSSGYPVSGSGYSSGFGH HSSSEHSSGYTQHGSGSGHSSGH GQHGSRSGQSSRGERQGSAGSSSS YGQHGSGSRQSLGHSRHSRSGSGQS PSPSRGRHESGSRQSSSYGPHGYGS GRSSSRGPIESGSGHSSGLGHQESR SGQSSGYGQHGSSSGHSSHTHGQHG STSGQSSSCGQHGATSGQSSSHGQ HSGSSSQSSRYGQSGSGQSPSRG RHGDFGHSYSGQHGSGSGWSSS NGPHGSVSGQSSGFGHKS GSGQSS GYSQHSGSSHSSGYRKHGSRSGQ SSRSEQHGSSSGLSSSYGQHGSGSH QSSGHGRQGS SGHSPSRVRHGS SGHSSSHGQHGSGTSCSSSCGHYES GSGQASGFGQHEGSGGQYSQHGS ASGHFSSQGRHGSTSGQSSSGQH DSSSGQSSSYGQHEASHHASGRG RHGSGSGQSPGHGQRGSGSGQSPS YGRHSGSGSRSSSGRHS GSGSGQS GFGHSSSGQSSGYTQHGSGSGHS SSYEQHGSRSGQSSRSEQHGSSSGS SSSYGQHGSGSRQSLGHGQHGSGS GQSPSPSRGRHSGSGQSSSYGPYR SGSGWSSSRGPIESGSGHSSGLGH RESRSGQSSGYGQHGSSSGHSSHT GQHGSTSGQSSSCGQHGASSGQSS SHGQHGSGSSQSSGYGRQGS SGQ SPGHGQRGSGSRQSPSYGRHSGSGS GRSSSSGQHGSGLGESSGFGHHES SSGQSSSYQHSGSGHSSGYGQH GSRSGQSSRGERHSGSSGSSHYGQ HGSGSRQSSGHGRQGS SGHSPSR GRHSGSLGHSSSHGQHGSGSGRSS SRGPYESSRSGHSSVFGQHEGSGHS SAYSQHSGSGGHFCSGQGHGSTSG QSSTFDQEGSSTGQSSSYGHRCSGS SQSSGYGRHGAGSGQSPSRGRHGS GSGHSSSYGQHGSGSGWSSSSGRH GSGSGQSSGFGHHESSSWQSSGCT QHSGSGHSSSYEQHGSRSGQSSR GERHSSSGSSSYGQHGSGSRQSL GHGQHGSGSGQSPSPSRGRHSGSGS QSSSYSPYCGSGCWSSSRGPYESG SSHSSGLGHRESRSGQSSGYGQHG SSSGHSSHTGQHGSTSGQSSSCGQ HGASSGQSSSHGQHGSGSSQSSGY GRQGS SGQSPGHGQRGSGSRQSP SYGRHSGSGRSSSGQHGSGLGES SGFGHHESSSGQSSSYQHSGSGS HSSGYGQHGSRSGQSSRGERHGS SRSSRYGQHGSGSRQSSGHGRQ SGSGQSPSRGRHSGSLGHSSSHGQ HGSGSRSSSRGPYESRSGHSSVFG QHESGSGHSSAYSQHSGSGGHFCS QGQHGSTSGQSSSTFDQEGSSTGQSS SHGQHGSGSSQSSSYGQGS SGQ SPSRGRHSGSGHSSSYGQHGSGS GWSSSSGRHSGSGQSSGFGHHES SSWQSSGYTQHGSGSGHSSSYEQH GSRSGQSSRGEQHGSSSGSSSYGQ HGSGSRQSLGHGQHGSGSGQSPSP | True | True | 2.376 | 4.347 | 1.837 | False | 0.188 |

SRGRHGSGSGQSSSYGPGYSGSGW
SSSRGPYESGSGHSSGLGHRESRSG
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