| | UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochndrion | endoplasmic reticulum | golgi apparatus | plasma membrane | extracellular region |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | Q9UP79 | ATS8_HUMAN | Homo sapiens | A disintegrin and metalloproteinase with thrombospondin motifs 8 | 22.903221 | T714 | NaN | 38253038 | MLPAPAAPRWPPLLLLLLLLLPLARG<br>APARPAAGGQASELVVPTRLPGSAG<br>ELALHLSAFGKGFVLRLAPDDSFLAP<br>EFKIERLGGSGRATGGERGLRGCFF<br>SGTVNGEPESLAAVSLCRGLSGSFLL<br>DGEEFTIQPQGAGGSLAQPHRLQRW<br>GPAGARPLPRGPEWEVETGEGQRQ<br>ERGDHQEDSEEESQEEEAEGASEPP<br>PPLGATSRTKRFVSEARFVETLLVAD<br>ASMAAFYGADLQNHILTLMSVAARI<br>YKHPSIKNSINLMVVKVLIVEDEKW<br>GPEVSDNGGLTLRNFCNWQRRFNQ<br>PSDRHPEHYDTAILLTRQNFCGQEG<br>LCDTLGVADIGTICDPNKSCSVIEDE<br>GLQAAHTLAHELGHVLSMPHDDSK<br>PCTRLFGPMGKHHVMAPLFVHLNQ<br>TLPWSPCSAMYLTELLDGGHGDCLL<br>DAPAAALPLPTGLPGRMALYQLDQQ<br>CRQIFGPDFRHCPNTSAQDVCAQLW<br>CHTDGAEPLCHTKNGSLPWADGTP<br>CGPGHLCSEGSCLPEEEVERPKPVA<br>DGGWAPWGPWGECSRTCGGGVQF<br>SHRECKDPEPQNGGRYCLGRRAKY<br>QSCHTEECPPDGKSFREQQCEKYNA<br>YNYTDMDGNLLQWVPKYAGVSPRD<br>RCKLFCRARGRSEFKVFEAKVIDGTL<br>CGPETLAICVRGQCVKAGCDHVVDS<br>PRKLDKCGVCGGKGNSCRKVSGSLT<br>PTNYGYNDIVTIPAGATNIDVKQRSH<br>PGVQNDGNYLALKTADGQYLLNGN<br>LAISAIEQDILVKGTILKYSGSIATLER<br>LQSFRPLPEPLTVQLLTVPGEVFPPK<br>VKYTFFVPNDVDFSMQSSKERATTN<br>IIQPLLHAQWVLGDWSECSSTCGAG<br>WQRRTVECRDPSGQASATCNKALK<br>PEDAKPCESQLCPL | False | False | 0.979 | 1.478 | 1.183 | 1.056 | 0.864 | 2.343 | 4.221 |