| | 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** | O15440 | MRP5_HUMAN | Homo sapiens | ATP-binding cassette sub-family C member 5 | 22.903221 | S485 | S14;S19;S60;S505;S509;T513 | 38253038 | MKDIDIGKEYIIPSPGYRSVRERTSTS<br>GTHRDREDSKFRRTRPLECQDALET<br>AARAEGLSLDASMHSQLRILDEEHP<br>KGKYHHGLSALKPIRTTSKHQHPVD<br>NAGLFSCMTFSWLSSLARVAHKKG<br>ELSMEDVWSLSKHESSDVNCRRLE<br>RLWQEELNEVGPDAASLRRVVWIFC<br>RTRLILSIVCLMITQLAGFSGPAFMV<br>KHLLEYTQATESNLQYSLLLVLGLLL<br>TEIVRSWSLALTWALNYRTGVRLRG<br>AILTMAFKKILKLKNIKEKSLGELINI<br>CSNDGQRMFEAAAVGSLLAGGPVV<br>AILGMIYNVIILGPTGFLGSAVFILFYP<br>AMMFASRLTAYFRRKCVAATDERVQ<br>KMNEVLTYIKFIKMYAWVKAFSQSV<br>QKIREEERRILEKAGYFQSITVGVAPI<br>VVVIASVVTFSVHMTLGFDLTAAQAF<br>TVVTVFNSMTFALKVTPFSVKSLSEA<br>SVAVDRFKSLFLMEEVHMIKNKPAS<br>PHIKIEMKNATLAWDSSHSSIQNSP<br>KLTPKMKKDKRASRGKKEKVRQLQ<br>RTEHQAVLAEQKGHLLLDSDERPSP<br>EEEEGKHIHLGHLRLQRTLHSIDLEI<br>QEGKLVGICGSVGSGKTSLISAILGQ<br>MTLLEGSIAISGTFAYVAQQAWILNA<br>TLRDNILFGKEYDEERYNSVLNSCC<br>LRPDLAILPSSDLTEIGERGANLSGG<br>QRQRISLARALYSDRSIYILDDPLSAL<br>DAHVGNHIFNSAIRKHLKSKTVLFV<br>THQLQYLVDCDEVIFMKEGCITERG<br>THEELMNLNGDYATIFNNLLLGETP<br>PVEINSKKETSGSQKKSQDKGPKTG<br>SVKKEKAVKPEEGQLVQLEEKGQGS<br>VPWSVYGVYIQAAGGPLAFLVIMALF<br>MLNVGSTAFSTWWLSYWIKQGSGN<br>TTVTRGNETSVSDSMKDNPHMQYY<br>ASIYALSMAVMLILKAIRGVVFVKGT<br>LRASSRLHDELFRRILRSPMKFFDTT<br>PTGRILNRFSKDMDEVDVRLPFQAE<br>MFIQNVILVFFCVGMIAGVFPWFLV<br>AVGPLVILFSVLHIVSRVLIRELKRLD<br>NITQSPFLSHITSSIQGLATIHAYNKG<br>QEFLHRYQELLDDNQAPFFLFTCAM<br>RWLAVRLDLISIALITTTGLMIVLMH<br>GQIPPAYAGLAISYAVQLTGLFQFTV<br>RLASETEARFTSVERINHYIKTLSLEA<br>PARIKNKAPSPDWPQEGEVTFENAE<br>MRYRENLPLVLKKVSFTIKPKEKIGI<br>VGRTGSGKSSLGMALFRLVELSGGC<br>IKIDGVRISDIGLADLRSKLSIIPQEPV<br>LFSGTVRSNLDPFNQYTEDQIWDAL<br>ERTHMKECIAQLPLKLESEVMENGD<br>NFSVGERQLLCIARALLRHCKILILD<br>EATAAMDTETDLLIQETIREAFADCT<br>MLTIAHRLHTVLGSDRIMVLAQGQV<br>VEFDTPSVLLSNDSSRFYAMFAAAE<br>NKVAVKG | None | None | None | None | None | None | None | None | None |