| | 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 | extrace region |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | Q6P158 | DHX57_HUMAN | Homo sapiens | Putative ATP-dependent RNA helicase DHX57 | 23.693478 | T739;S747 | S127;S132;S475;S477;S480 | 28510447;38253038 | MSSSVRRKGKPGKGGGKGSSRGGR<br>GGRSHASKSHGSGGGGGGGGGGGG<br>GNRKASSRIWDDGDDFCIFSESRRP<br>SRPSNSNISKGESRPKWKPKAKVPL<br>QTLHMTSENQEKVKALLRDLQEQD<br>ADAGSERGLSGEEEDDEPDCCNDE<br>RYWPAGQEPSLVPDLDPLEYAGLAS<br>VEPYVPEFTVSPFAVQKLSRYGFNTE<br>RCQAVLRMCDGDVGASLEHLLTQC<br>FSETFGERMKISEAVNQISLDECME<br>QRQEEAFALKSICGEKFIERIQNRVW<br>TIGLELEYLTSRFRKSKPKESTKNVQ<br>ENSLEICKFYLKGNCKFGSKCRFKH<br>EVPPNQIVGRIERSVDDSHLNAIEDA<br>SFLYELEIRFSKDHKYPYQAPLVAFY<br>STNENLPLACRLHISEFLYDKALTFA<br>ETSEPVVYSLITLLEEESEIVKLLTNT<br>HHKYSDPPVNFLPVPSRTRINNPAC<br>HKTVIPNNSFVSNQIPEVEKASESEE<br>SDEDDGPAPVIVENESYVNLKKKISK<br>RYDWQAKSVHAENGKICKQFRMKQ<br>ASRQFQSILQERQSLPAWEERETILN<br>LLRKHQVVVISGMTGCGKTTQIPQFI<br>LDDSLNGPPEKVANIICTQPRRISAIS<br>VAERVAKERAERVGLTVGYQIRLESV<br>KSSATRLLYCTTGVLLRRLEGDTALQ<br>GVSHIIVDEVHERTEESDFLLLVLKD<br>IVSQRPGLQVILMSATLNAELFSDYF<br>NSCPVITIPGRTFPVDQFFLEDAIAVT<br>RYVLQDGSPYMRSMKQISKEKLKAR<br>RNRTAFEEVEEDLRLSLHLQDQDSV<br>KDAVPDQQLDFKQLLARYKGVSKSV<br>IKTMSIMDFEKVNLELIEALLEWIVD<br>GKHSYPPGAILVFLPGLAEIKMLYEQ<br>LQSNSLFNNRRSNRCVIHPLHSSLS<br>SEEQQAVFVKPPAGVTKIIISTNIAET<br>SITIDDVVYVIDSGKMKEKRYDASKG<br>MESLEDTFVSQANALQRKGRAGRV<br>ASGVCFHLFTSHHYNHQLLKQQLPE<br>IQRVPLEQLCLRIKILEMFSAHNLQS<br>VFSRLIEPPHTDSLRASKIRLRDLGA<br>LTPDERLTPLGYHLASLPVDVRIGKL<br>MLFGSIFRCLDPALTIAASLAFKSPF<br>VSPWDKKEEANQKKLEFAFANSDYL<br>ALLQAYKGWQLSTKEGVRASYNYCR<br>QNFLSGRVLQEMASLKRQFTELLSD<br>IGFAREGLRAREIEKRAQGGDGVLD<br>ATGEEANSNAENPKLISAMLCAALY<br>PNVVQVKSPEGKFQKTSTGAVRMQP<br>KSAELKFVTKNDGYVHIHPSSVNYQ<br>VRHFDSPYLLYHEKIKTSRVFIRDCS<br>MVSVYPLVLFGGGQVNVQLQRGEF<br>VVSLDDGWIRFVAASHQVAELVKEL<br>RCELDQLLQDKIKNPSIDLCTCPRGS<br>RIISTIVKLVTTQ | None | None | None | None | None | None | None | None | None |