| | 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 | ex re |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | Q9ULL0 | K1210_HUMAN | Homo sapiens | Acrosomal protein KIAA1210 | 20.111456 | T1127;S1136;S1137;T1708 | NaN | 30379171;29351928 | MRAGWTPRGFSAFHASLLPGRHPYL<br>AHLGPRDRGARIGSRAYSQGCCSCL<br>WLTYKGKKEGSTKGELGPAAVTDLE<br>IPSYSRGFLPCTPRFPTTWCRGPGCF<br>CGTAVIAGNLGDLARIVGPSHHASQ<br>LLLLQEQDSGNHPTMAESLSEISDS<br>LDVLEAGDEGKKKCKFKALKSFFVK<br>KKEKEAEDTQEEEMLELSLSSSNINI<br>SSLQPVRENQPTKARAKSSMGSKAL<br>SHDSIFMLGPEPERSASKMFPSMDP<br>QRGRPQQRSHISRTLPKPRSKVPGV<br>VSGAMSGAVLQNVPTSAVWVAGPKI<br>TENPPSRRRRLSIIPPVIQPEIISKNLV<br>EISLDDESPKNPQKKALPHKSLTATQ<br>SFSELSSGPDCSQSLTAFATLASTSS<br>TQLPIGFSTPATTQGCLDSSAARHK<br>MTLNPRKQKKNLQVIIRGLPVWFSH<br>FQGILEGSLQCVTQTLETPNLDEPLP<br>VEPKEEEPNLPLVSEEEKSITKPKEI<br>NEKKLGMDSADSSSQKQNNKTEMY<br>DKKTTDQAPNTDASRSQGYPMSAAY<br>GRRWRRKGASVSGLSGCEFKGRSLK<br>QSSEGYGLGDRAGSSPTNKTARNVP<br>FSHLSLEKDNMEQPTTSQPETTTPQ<br>GLLSDKDDMGRRNAGIDFGSRKASA<br>AQPIPENMDNSMVSDPQPYHEDAA<br>SGAEKTEARASLSLMVESLSTTQEE<br>AILSVAAEAQVFMNPSHIQLEDQEA<br>FSFDLQKAQSKMESAQDVQTICKEK<br>PSGNVHQTFTASVLGMTSTTAKGDV<br>YAKTLPPRSLFQSSRKPDAEEVSSDS<br>ENIPEEGDGSEELAHGHSSQSLGKF<br>EDEQEVFSESKSFVEDLSSSEEELDL<br>RCLSQALEEPEDAEVFTESSSYVEKY<br>NTSDDCSSSEEDLPLRHPAQALGKP<br>KNQQEVSSASNNTPEEQNDFMQQL<br>PSRCPSQPIMNPTVQQQVPTSSVGT<br>SIKQSDSVEPIPPRHPFQPWVNPKVE<br>QEVSSSPKSMAVEESISMKPLPPKLL<br>CQPLMNPKVQQNMFSGSEDIAVER<br>VISVEPLLPRYSPQSLTDPQIRQISES<br>TAVEEGTYVEPLPPRCLSQPSERPKF<br>LDSMSTSAEWSSPVAPTPSKYTSPP<br>WVTPKFEELYQLSAHPESTTVEEDIS<br>KEQLLPRHLSQLTVGNKVQQLSSNF<br>ERAAIEADISGSPLPPQYATQFLKRS<br>KVQEMTSRLEKMAVEGTSNKSPIPR<br>RPTQSFVKFMAQQIFSESSALKRGS<br>DVAPLPPNLPSKSLSKPEVKHQVFS<br>DSGSANPKGGISSKMLPMKHPLQSL<br>GRPEDPQKVFSYSERAPGKCSSFKE<br>QLSPRQLSQALRKPEYEQKVSPVSAS<br>SPKEWRNSKKQLPPKHSSQASDRSK<br>FQPQMSSKGPVNVPVKQSSGEKHLP<br>SSSPFQQQVHSSSVNAAARRSVFES<br>NSDNWFLGRDEAFAIKTKKFSQGSK<br>NPIKSIPAPATKPGKFTIAPVRQTSTS<br>GGIYSKKEDLESGDGNNNQHANLS<br>NQDDVEKLFGVRLKRAPPSQKYKSE<br>KQDNFTQLASVPSGPISSSVGRGHKI<br>RSTSQGLLDAAGNLTKISYVADKQQ<br>SRPKSESMAKKQPACKTPGKPAGQQ<br>SDYAVSEPVWITMAKQKQKSFKAHI<br>SVKELKTKSNAGADAETKEPKYEGA<br>GSANENQPKKMFTSSVHKQEKTAQ<br>MKPPKPTKSVGFEAQKILQVPAMEK<br>ETKRSSTLPAKFQNPVEPIEPVWFSL<br>ARKKAKAWSHMAEITQ | None | None | None | None | None | None | None | None | No |