| | 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** | P06102 | NOT3_YEAST | Saccharomyces cerevisiae | General negative regulator of transcription subunit 3 | 24.475439 | NaN | S303;S307;S322;S446;S450;S565;S569;T571;S657 | 33229814 | MAHRKLQQEVDRVFKKINEGLEIFN<br>SYYERHESCTNNPSQKDKLESDLKR<br>EVKKLQRLREQIKSWQSSPDIKDKD<br>SLLDYRRSVEIAMEKYKAVEKASKEK<br>AYSNISLKKSETLDPQERERRDISEY<br>LSQMIDELERQYDSLQVEIDKLLLLN<br>KKKKTSSTTNDEKKEQYKRFQARYR<br>WHQQQMELALRLLANEELDPQDVK<br>NVQDDINYFVESNQDPDFVEDETIY<br>DGLNLQSNEAIAHEVAQYFASQNAE<br>DNNTSDANESLQDISKLSKKEQRKL<br>EREAKKAAKLAAKNATGAAIPVAGPS<br>STPSPVIPVADASKETERSPSSSPIHN<br>ATKPEEAVKTSIKSPRSSADNLLPSL<br>QKSPSSATPETPTNVHTHIHQTPNGI<br>TGATTLKPATLPAKPAGELKWAVAAS<br>QAVEKDRKVTSASSTISNTSTKTPTT<br>AAATTTSSNANSRIGSALNTPKLSTS<br>SLSLQPDNTGASSSAATAAAVLAAGA<br>AAVHQNNQAFYRNMSSSHHPLVSL<br>ATNPKSEHEVATTVNQNGPENTTKK<br>VMEQKEEESPEERNKLQVPTFGVFD<br>DDFESDRDSETEPEEEEQPSTPKYLS<br>LEQREAKTNEIKKEFVSDFETLLLPS<br>GVQEFIMSSELYNSQIESKITYKRSR<br>DMCEISRLVEVPQGVNPPSPLDAFR<br>STQQWDVMRCSLRDIIIGSERLKED<br>SSSIYAKILENFRTLEMFSLFYNYYF<br>AITPLEREIAYKILNERDWKVSKDGT<br>MWFLRQGEVKFFNEICEVGDYKIFK<br>LDDWTVIDKINFRLDYSFLQPPVDTA<br>SEVRDVSVDNNNVNDQSNVTLEQQ<br>KQEISHGKQLLKQLKQGKISV | None | None | None | None | None | None | None | None | None |