

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	er
Q71F56	MD13L_HUMAN	Homo sapiens	Mediator of RNA polymerase II transcription subunit 13-like	18.9764	T1735	S553;S560;S817;S826;S923;S2083	37217939;38253038	MTAAANVWVANGASLEDCHSNLFSL AELTGKWRRYNFGGHGDCGPIISAP AQDDPILLSFIRCLQANLLCVRWRD VKPDCRELWIFWWGDEPNLVGVIIH HELQVVEEGLWENGLSYECRTLLFK AIHNLLERCLMDKNFVRIGKWFVRP YEKDEKPVNKSEHLSCAFTFFLHGE SNVCTSVEIAQHQPYYLINEEHIHMA QSSPAPFOVLVSPYGLNGTLTGQAY KMSDPATRKLIIEEWQYFPMVLKPK EESKEEDELGYDDDFPVAVEVIVGG VRMVYPSAFVLISQNDIPVQSVASA GGHIAVGQQGLGSVKDPSNCGMPL TPPTSPEQAILGESGGMQSAASHLV SQDGGMITMHSKRSKIPKLNHNH MVHRVWKECILNRTQSKRSQMSTP TLEEEFASNPAWDFVDPTQRVSCS CSRHKLLKRCVAVGNRPPTVVSQPGF SAGPSSSSSLPPPASSKHKTAERQEK GDKLQKRPLPFHHRPSVAEELCME QDTPGQKLAGLIDSSLEVSRRKYD KQMAVPSRNTSKQMNLPMDSPH SPISPLPPTLSPQPRQETESLDPPSV PVNPALYGNLELQQLSTLDDRTVL VGQRLPLMAEVSETALYCGIRPSNP ESSEKWWHSYRLPPSDDAEFRPEL QGERCDAKMEVNSESTALQRLLAQ PNKRFKIWQDKPQQLPLHFLDPLP LSQQPGDSLGEVNDPYTFEDGDIKIY FTANKKCKQGTEDKSLKKNKSEDF GTDKDVTPGHSTPVPDGKNAMSIFS SATKTDVQRDAAAGRAGSSSLTQVT DLAPSLHDLNIFDNDSDDELGAVS PALRSSKMPAVGTEDRPLGKDGRAA VPYPTVADLQRMFPTPPSLEQHPA FSPVMNYKDGISSETVTALGMMESP MVS MVSTQLTEFKMEVEDGLGSPK PEEIKDFSYHKVPSFQPFVGSMMFA PLKMLPSHCLLPLKIPDAFLFRPSWA IPPKIEQLMPPAATFIRDGYNVPS VGLADPDYLNTPQMNTPTVTLNSAA PASNSGAGVLPSPATPRFSVPTPRTP RTPRTPRGGGTASGQGSVKYDSTDQ GSPASTPSTTRPLNSVEPATMQPIPE AHSLYVTLLSDSVMNIFKDRNFDSC CICACNMNIKADVGLYIPDSSNED QYRCTCGFSAIMNRKLGYSGLFLE DELDIFGKNSDIGQAAERLMMMCQS TFLPQVEGTTKPOEPPISLLLLLQNO HTQPFASLNFLDYISSNRRQTLPCVS WSYDRVQADNNDYWTECFNALEQG RQYVDNPTGGKVDEALVRSATVHS WPHSNVLDISMLSSQDVVRMLLSL QPFLQDAIQKRTGRTWENIQHVQG PLTWQQFHKMAGRGTYGSEESPEP LPIPTLLVGYDKDFLTISPFSLPFWER LLLDPYGGHRDVAYIVVCPENEALLE GAKTFFRDL SAVYEMCRLGQHKPIC KVL RDGIMRVGKTVAQKLTDELVSE WFNQPWSGEENDNHSRLKLYAQVC RHHLPYLATLQLDSSLLIPPKYQTP PAAAQQAATPGNAGPLAPNGSAAPP AGSAFNPTSNSSTNPAASSASGSS VPPVSSASAPGISQISTSSSGFSGS VGGQNPSTGGISADRTQGNIGCGGD TDPGQSSSQSQDQGESVTERERIGI PTEPDSADSHAHPPAVVIYMDPFTY AAEEDSTSGNFWLLSLMRCYTEML DNLPEHMRNSFILQIVPCQYMLQT MKDEQVFIQYLKSMASFVYCQCR PLPTQIHIKSLTGFGPAASIEMTLKN PERPSPILYSPFFILAPIKDKQTELG ETFGEASQKYNVLFVGYCLSHDQR WLLASCTDLHGELLETCVVNIALPN RSRRSKVSARKIGLQKLWEWCIGIV QMTSLPWRVVIGRLGRLGHGELKD WSILLGECSLQTISSKLDVCRMCGI SAADSPSILSACL VAMEPQGSFVVM PDAVTMGSVFGRSTALNMQSSQLN TPQDASCTHILVFFPSTIQVAPANY	True	False	1.78	4.623	1.099	1.4	1.423	0.788	

