	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	e r
0	Q9UHV7	MED13_HUMAN	Homo sapiens	Mediator of RNA polymerase II transcription subunit 13	5.295773	S225;S227;T229;T336;S1247	S395;S500;S504;S530;S537;S826;S890;S1029	34725712;38665916;34019948;33214551;30379171;40596516;38253038	MSASFVPNGASLEDCHCNLFCLADL TGIKWKKYVWQGPTSAPILFPVTEED PILSSFSRCLKADVLGVWRRDQRPG RRELWIFWWGEDPSFADLIHHDLSE EEDGVWENGLSYECRTLLFKAVHN LLERCLMNRNFVRIGKWFVKPYEKD EKPINKSEHLSCSFTFFLHGDSNVC TSVEINQHQPVYLLSEEHITLAQQSN SPFQVILCPFGLNGTLTGQAFKMSD SATKKLIGEWKQFYPISCCLKEMSEE KQEDMDWEDDSLAAVEVLVAGVRM IYPACFVLVPQSDIPTPSPVGSTHCSS SCLGVHQVPASTRDPAMSSVTLTPP TSPEEVQTVDPQSVQKWVKFSSVSD GFNSDSTSHHGGKIPRKLANHVVDR VWQECNMNRAQNKRKYSASSGGLC EEATAAKVASWDFVEATQRTNCSCL RHKNLKSRNAGQQGQAPSLGQQQQ ILPKHKTNEKQEKSEKPQKRPLTPF HHRVSVSDDVGMDADSASQRLVISA PDSQVRFSNIRTNDVAKTPQMHGTE MANSPQPPPLSPHPCDVVDEGVTKT PSTPQSQHFYQMPTPDPLVPSKPME DRIDSLSQSFPPQYQEAVEPTVYVGT AVNLEEDEANIAWKYYKFPKKKDVE FLPPQLPSDKFKDDPVGPFGQESVT SVTELMVQCKKPLKVSDELVQQYQI KNQCLSAIASDAEQEPKIDPYAFVEG DEEFLFPDKKDRQNSEREAGKKHK VEDGTSSVTVLSHEEDAMSLFSPSIK QDAPRPTSHARPPSTSLIYDSDLAVS YTDLDNLFNSDEDELTPGSKKSANG SDDKASCKESKTGNLDPLSCISTADL HKMYPTPPSLEQHIMGFSPMNMNN KEYGSMDTTPGGTVLEGNSSSIGAQ FKIEVDEGFCSPKPSEIKDFSYVYKP ENCQILVGCSMFAPLKTLPSQYLPPI KLPEECIYRQSWTVGKLELLSSGPS MPFIKEGDGSNMDQEYGTAYTPQT HTSFGMPPSSAPPSNSGAGILPSPST PRFPTPRTPRTPRTPRGAGGPASAQG SVKYENSDLYSPASTPSTCRPLNSVE PATVPSIPEAHSLYVNLILSESVMNL FKDCNFDSCCICVCNMNIKGADVGV YIPDPTQEAQYRCTCGFSAVMNRKF GNNSGLFLEDELDIIGRNTDCGKEA EKRFEALRATSAEHVNGGLKESEKL SDDLILLLQDQCTNLFSPFGAADQD PFPKSGVISNWVRVEERDCCNDCYL ALEHGRQFMDNMSGGKVDEALVKS SCLHPWSKRNDVSMQCSQDILRML LSLQPVLQDAIQKKRTVRPWGVQGP LTWQQFHKMAGRGSYGTDESPEPL PIPTFLLGYDYDYLVLSPFALPYWER LMLEPYGSQRDIAYVVLCPENEALL NGAKSFFRDLTAIYESCRLGQHRPV SRLLTDGIMRVGSTASKKLSEKLVAE WFSQAADGNNEAFSKLKLYAQVCR YDLGPYLASLPLDSSLLSQPNLVAPT SQSLITPPQMTNTGNANTPSATLAS AASSTMTVTSGVAISTSVATANSTLT TASTSSSSSSNLNSGVSSNKLPSFPP FGSMNSNAAGSMSTQANTVQSGQL GGQQTSALQTAGISGESSSLPTQPHP DVSESTMDRDKVGIPTDGDSHAVTY PPAIVVYIIDPFTYENTDESTNSSSVW TLGLLRCFLEMVQTLPPHIKSTVSVQ IIPCQYLLQPVKHEDREIYPQHLKSL AFSAFTQCRRPLPTSTNVKTLTGFGP GLAMETALRSPDRPECIRLYAPPFIL APVKDKQTELGETFGEAGQKYNVLF VGYCLSHDQRWILASCTDLYGELLE TCIINIDVPNRARRKKSSARKFGLQK LWEWCLGLVQMSSLPWRVVIGRLG RIGHGELKDWSCLLSRRNLQSLSKR LKDMCRMCGISAADSPSILSACLVA MEPQGSFVIMPDSVSTGSVFGRSTT LNMQTSQLNTPQDTSCTHILVFPTS ASVQVASATYTTENLDLAFNPNNDG ADGMGIFDLLDTGDDLDPDIINILPA	True	False	1.172	5.0	0.719	0

									SPTGSPVHSPGSHYPHGGDAGKGQS TDRLLSTEPHEEVPNILQQPLALGYF VSTAKAGPLPDWFWSACPQAQYQCP LFLKASLHLHVPSVQSDELLHSKHS HPLDSNQTSDVLRFVLEQYNALSWL TCDPATQDRRSCLPIHFVVLNQLYN FIMNML					