

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	extracellular region		
Q8TEP8	CE192_HUMAN	Homo sapiens	Centrosomal protein of 192 kDa	26.873146	S791	S812;S1755;S2098;S2110	40136647;30379171	MEDFRGIAEESFPSFLTNSLFGNSGILENVTLSNNLGLPVAVSTLARDRSSTDNRYPDIQASYLVEGRFVSPGSSSPG SQSDAEPRERLQLSFQDDDSISRKK SYVESQRLSNALSKQALQMETAGP EEEPAGATESLQGDQDLFNRAASPLEQ AQDSPIDFHLQSWMNNKEPKIVVLD AGKHFEDKTLKSDLSTLLENEKLI LPTSLEDDSDDDIDEMFYDDHLEA YFEQLAIPGMIYEDLEGPEPPEKGFK LPTNGLRQANENGLNCKFQSENN SSLISLDSHSETTHKESEESQVICL PGTNSIGTGDSRRYTDGMLPFSSG TWGTEKEIENLKGIVPDLNSECASK DVLVKTLRaidvKLNsdNFHDANAN RGGFDLTDpvKQGAECPhQnKTVL HMDGCLDTETPTVSIQENVDVASLK PISDSGINFTDAIWSPTCERRTCECH ESIEKNKDKTDLPQSVVYQNEEGRW VTDLAYYTSFNKQNLNLSLDEMNE DFRSGSEAFDLIAQDEEFNKHEHQ FIQEEENIDAHNSTVALGDTSWGATI NYSLLRKSrstSDLDKDDASYLRLSL GEFFAQRSEALGCLGGNNVkrPsf GYFIRSPekRePIALIRKSDVSRGNLE KEMAHLNHDLYSGDLNEQSAQLS EGSITLQVEAVESTSQVDENDVTLTA DKGKTEDTFFMSNKPQRyKDKLPDS GDSMLRISTIASAIAEASVNTDPSQL AAMIKALSNKTRDKTFQEDeKQkDY SHVRHFLPNdleKSNgsNALDMEK YLkKTEVSRyESALENfSRASMSDT WDLsLPKEQTQDIHPVdLSATSVS VRAPEENTAaIVyVENGESEnQESF RTINSSNSVTNrenNSAVdVKTCSI DNKLQDVGNDEKATSISTPsdSYSS VRNPRITSLCLLKDCeEIRDnRENQ RQNECVSEISnSEKHvTFENHRIVS PKNSDLKNTSPEHGGRGSEDEQESF RPSTSPLSHSSPSEISGTSSSGCALE SFGSAAQQQPpCEQELsPLVcSPA GVSRLTYVSEPESSyPTTATDDALE D RkSDITSELSTTHIQGSPAALeERAME KLREKVPFQNRGKGTLSIIQnNSDT RKATETTSLSSKPEYVKPDRfRWskD PSSKSGNLLETSEVGWTSNPEELDPI RLALLGKSGLSCOVGSATSHpVscQ EPIDEDQRISPKDKSTAGREFSGQVS HQTTSENQCTPIPSSTVHSSVADMQ NMPAAVHALLTQPSLSAAPFAQRyL GTLPSTGSTTLpQHAGNATVCGFS GGLPYPAVAGEPVQNSVAVGICLGS NIGSGWMGTSSLCNPYSNTLNQNL LSTTKPFVPVsvGTnCGIEPwDSGVT SGLGSVRVPEELKLPHACCVGIASQT LLSVLNPTDRWLQVSIgVLSISVNGE KVDLSTYRCLVfKNKAIRPHATEEIK VLFIPSPGvFRCTfSVASwPCSDA ETIVQAEALASTVTLTAIAESpVIEVE TEKkDVLDFGDLTYGGWkALpLkLI NRTHATVPiRLIINANAVAWRCtTfS KESVRAPVEVAPCADVVTRLAGPSVV NHMMPASyDGDPEFLMIWVLFHS PKKQISSDILDsAEeFSakVDIEVDS PNPtPVLRSVSLRARAGIARIHAPRD LQTMHFLAKVASSRkQHLpLKNAG NIEVYLDIKVPEQGSHFsvDPKnlLL KPGEeHEVIVSfTPKdPEACEERIKI FVQPFGPQYEVVLKGEVISSGSKPLS PGPCLDIPsILSNKQFLAWGGVPLGR TQLQKLALRNNSASTQHOLLRLIRG QDQDCFQLQNTFGSEQRlTSNCEIR IHPKEDIFISVLFAPTRLScMLARLEI KQLGNRSQPgIKFTIPLSGYGGTSNL ILEGVKLSDSYmVTVNGLVPGKES KIVfSVrNTGSRAAFVKAGVfKDSQ KKVLLDPKVLRIFPDKFVLKERTQEN VTLIYNPSDRGINNKATeLSTVYLF GGDEISRQYRRALLHKPEMIKQILP EHSVLQnINfVEAFQDELLVTEVYD	True	False	4.508	2.203	False	False	False	False	False	False	False

LPQRPNDVQLFYGSMCKIILSVIGEF
RDCISSREFLQPSKASLESTSDLGA
SGKHGGNVSLDVLVKGPGQSPLLS
RAARPLDQLASEEPWTVLPEHLILV
APSPCDMAKTGRFQIVNNSVRLLR
ELCWP AHCLTVTPQHGCVAPESKLO
ILVSPNSSLSTKQSMFPWSGLIYIHC
DDGQKIVKVQIREDLTQVELLTRLT
SKPFGILSPVSEPSVSHLVKPMTRPP
STKVEIRNKSITFPITTEPGETSESCLE
LENHGTTDVKWHLSSLAPPYVKGVD
ESGDVFRATYAAFRCSPISGLLESHG
IQKVSITFLPRGRGDYAQFWDVECH
PLKEPHMKHTLRFQLSGQSIEAENE
PENACLSTSLIKIDHLVKPRRQAVS
EASARIPEQLDVTARGVYAPEDVYRF
RPTSVGESRTLKVNLRNNSFITHSLK
FLSPREPFYVKHISKYSLRAQHYNM
PVQFKPKSAGKFEALLVIQTDEGKSI
AIRLIGEALGKN