

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P48415	SEC16_YEAST	Saccharomyces cerevisiae	COPII coat assembly protein SEC16	9.365641	NaN	S28;S73;S144;S313;S472;S483;T595;S607;S660;S663;S665;S674;S678;S681;S701;S704;S706;S759;S762;S765;S768;S843;S1511;S1515;S1578;S1602;S1603;S1611;S1617;S1778;S1875;S1973;S1986;S1992;T2049;S2130	33229814	MTPEAKKRKNQKKLQKQKKAEE KAASHSEEPLELPSTINSSFNDDSV NRTESDIASKSDVPPVSSSTNISPAN ETQLEIPDTQELHHKLLNDSQDQHI TADSNLDPNSIVEHDSVITQTKPA MSQEYEETA AHLSSRNPSLDVVAGE LHNNNEHTQKIAVSAVEEDSFNEEE GENHDSIISSLN DATPSQYNHFLPS DGNLLSPELSSGDTPTHNVPLGTKD NEINDDEYCN DKEISLNANNVLPDE LSKEEDERL KLETHVSTEEKQDIAD QETAENLFTSSTEPSENKIRNSGDD TSMLFQDDESDQKVPWEEDVKKDF HNENTNNTQESAPNTDDRDKGYEG NEALKKSECTAADERSYSEETSEDI FHGHDKQVVEGQNDFTGKNIENES QKLMGEGNHKLPLSAEADIIEPGKDI QDQAE DLFTQSSGDLGEVLPWESTD KNADVTSK SQEKHEDLFAASGNDE KLPWEVSDGEVSSGKTENSMQTST EKIAEQKFSFLENDDLLDDDD SFL ASSEEDTVPNTDNTNLTSKPVEE KKASRYKPIIEEEAGMRQEQVHFTN TTGIVTPQQFHGLTKTGLGTPNQV SVPNIVSPKPPVVKDNRSNFKINEEK KKS DAYDFPLEIIESSKKGHAKPVA VPTQRF GSGNSFSSLDKPIPQSRKGS NNSNRPPVIPLGTQEPRSSRTNSAIS QSPVNYAFP NPYKIQQLQQA PQSG MPLPNTNIPPPALKVETT VSAPPIRA RGVSNASV GSSASFGARHATQYGLN NGVPPVSPY GQATINLPTANKYAPVS PTVQQKQYPSV VQNLGASAVNTPNF VKTHRGHTSSISYTPNQNEHASRY APNYQQSYQVPYTSQP VGPVAGNSS YQSQRSSYAVP MMPQAQTSASIQP HANIQPPTGILPLAPLRPLDPLQAAT NLQPRASNITAA NSLPLANLPLAENI LPEIITHRATSSVAPPRQENNP IKIDN EALLRRQFP IFWWSAANKV VYAVPPI PDQSQYMISSSIVQEIKVTPIDQIIKP NDMLKSFPGPLGSAK LKKDLTKW METTIKSISENESSTD MTIWQ LLEM KLNDKVNWKNISKLLYNSDELLMYL SQPFPNGDMIPNAYRLDINCQMRVL AFLQTGNHDEALRLALSKRDYAIALL VGS LMGKDRWSEVIQKYL YEGFTAG PNDQKELAHFLLLIFQV FVGNSKMA IKSFYTNNETSQWASENWKSIVA AV

LINIPENNEDPLLIPPVVLEFLIEFGIF  
LTKKGLTAAASTLFIIGNVPLSNEPV  
MADSDVIFESIGNMNTFESILWDEIY  
EYIFSYPDPKFKGFSSILPQKIYHASLL  
QEQGLNSLGTKYTDYLSSSVRKLPK  
KDILTINLTRELSEVASRLSESNTGW  
LAKPKLSSVWGQLDKSFNKYIGGDD  
IDALNKKNDKKKVFDFGFTPGSSANS  
STVDLTQTFTPFQAQVTSQSYVDTTA  
LLHNAHNVPSHVLHSHKPSNVSKGL  
VEANLPYTHRIGDSLQSPQRIHNT  
QFAAAEPQMASLRRVRTDQHTNEK  
ALKSQQILEKKSTAYTPQFGQNHSV  
PMEKSNSNVPSLFADFPAPPKLGTV  
PSNYVSSPDLVRRRESIISTGSEFLPPP  
KIGVPTKANSSQGSMLYSPSVEALPI  
DPVVPQVHETGYNDFGNKHSQKSM  
PEDESHTSHDNSNADQNTLKDSDAD  
VTDETMIEGPGFNDVKNLLPMEP  
NHQPTSTVNPIQTISDDIQPILQTNV  
EVRGTDASKMENSLSIENERSSEE  
QPENISKSASSAYLPSTGGLSLENRP  
LTQDENSISQSTYLPAGSISMEA  
KPISQVQDVPRNVNNAKASKLVEQH  
MAPPKPKSTDATKMNYSPYVPQSTA  
ASADGDESTILKTSPAIYARTHQAHA  
SNPSQYFPLVNQANETASFELSEST  
SQAQSNNGNVAENRFSPIKKAEVVE  
KDTFQPTIRKASTNQYRAFKPLESDA  
DKYNDVIEDESDDDNMSTDEAKNR  
KEEKNVNMKKETKPSNKDIDDKS  
NGWFGWLKDTGDKKVYKAKLGHK  
NTLYYDEKLRWVNKDATEEEKQKI  
IESSAPPPPIVKRKDGPKTKPRSG  
PINNSLPPVHATSVIPNPNPITGEPLPI  
KTSPSPPTGPNPNNSPSPSSPISRISG  
VNLTSKKANGLDDLLSLAGGPKPAS  
TRRKKKTARGYVNVMDNIQ