

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P40477	NU159_YEAST	Saccharomyces cerevisiae	Nucleoporin NUP159	9.365641	NaN	S404;S657;S724;S735;S745;T803;S805;S819;S889;S940	33229814	MSSLKDEVPTETSEDGFKFLGQKQ ILPSFNEKLPFASLQNLDISNSKSLF VAASGSKAVVGELQLLRDHITSdstp LTFKWEKEIPDVIFVCFHGDQVLVST RNALYSLDLEELSEFRTVTSFEKPVF QLKNVNTLVILNSVNDLSALDLRT KSTKQLAQNVTSFDVTNSQLAVLLK DRSFQSAWRNGEMEKQFEFSLPS ELEEPLVEEYSPLSVTILSPQDFLAVF GNVISETDDEVSYDQKMYIIKHIDGS ASFQETFDITPPFGQIVRFPYMYKVT LSGLIEPDANVNVLASSCSSEVSIWD SKQVIEPSQDSERAVLPiseETDKDT NPIGVAVDVVTSGTILEPCSGVDTIER LPLVYILNNEGSLQIVGLFHVAIKS GHYSINLESLEHEKSLSPtSEKIPIAG QEQUEKKKNNESSKALSENPFtsAN TSGFTFLKTQAAAANSLQSQSSSTFG APSGSSAFKIDLPSVSTSTGVASS EQDATDPASAKPVFGKPAFGAIAKEP STSEYAFGKPSFGAPSGSGKSSVES PASGSFAFGKPSFGTPSFGSGNSSVEP PASGSFAFGKPSFGTPSFGSGNSSAEP PASGSFAFGKPSFGTSAFGTASSNET NSGSIFGKAAGSSSFAPANNELFG SNFTISKPTVDSPKEVDSTSPFPSSG DQSEDESKSDVDSSTPFGTkPNTS TKPKTNAFDGSSSFSGGFSKALES VGSDDTTFKFGTQASPFSSQLGNKSP FSSFTKDDTENGSLSKGSTSEINDD NEEHESNGPNVSGNDLTDSTVEQT SSTRLPETPSDEDGEVVEEEAQKSPI GKLTETIKKSANIDMAGLKNPVFGN HVKAKSESPFSAFATNITKPSSTTPA FSFGNSTMKNsNTSTVSPMEEADT KETSEKGPITLKSVENPFLPAKEERT GESSKKDHNDDPKdGYVSGSEISVR TSESAFDTTANEEIPKSQDVNNHEK SETDPKYSQHAVVDHDNKSKEMNE TSKNNERSGQPNHGVQGDGIALKK DNEKENFDSNMAIKQFEDHQSSSE DASEKDSRQSSEVKESDDNMSLNS DRDESISESYDKLEDINTDELPHGGE AFKAREVSASADFDVQTSLEDNYAE SGIQTDLSESSKENEVQTDaIPVKHN STQTVKKEAVDNGLQTEPVETCNFS VQTFEGDENYLAEQCKPKQLKEYYT SAKVSNIpFVSQNSTLRLIESTFQTV EAeFTVLMENIRNMDTFFTDQSSIP

								LVKRTVRSINNLYTWRIPEAEILLNIQ NNIKCEQMQITNANIQDLKEKVTDY VRKDIAQITEDVANAKEEYFLMHF DDASSGYVKDLSTHQFRMQKTLRQ KLFDVSAKINHTEELLNILKLFTVKN KRLDDNPLVAKLAKESLARDGLLKEI KLLREQVSRQLQLEEKGKKASSFDAS SSITKDMKGFKVVEVGLAMNTKKQI GDFFKNLNMAK
--	--	--	--	--	--	--	--	--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------