

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q80U93	NU214_MOUSE	Mus musculus	Nuclear pore complex protein Nup214	44.729812	S492;T494;S504;S506;S507;S513;T515;S527;T539;S540;T585;S589;S590;S595;T597;S598;T612;S614;T621;S626;S627;T648;S1049;S1051;S1056;S1057;S1060;T1064;S1089;T1091;S1109;T1124;S1136;S1152;T1156;S1167;T1204;S1210;T1313;T1314;S1316;S1336;S1337;S1362;S1529;T1537;T1556;T1557;S1573;T1574;T1580;S1899;T1908;T1924;S1980;T1996	S30;T416;S421;S430;S433;T437;S645;S651;S660;S672;S754;S930;S960;S964;S979;T1027;S1029;S1051;S1062;S1139;T1156;T1162;S1187;T1324;S1365;S1980	36064721;27669760;22645316;22517741;36852467;33300544;21606357;34887587;35822049;30059200;23443134;34678516;29125738	MGDEMDAMIPEREMKDFQFRALKK VRIFDGSPEELPKERSVLTISNKYGM LFAGGTNGLNVFPPTKSLLIQNKPGD DPNKIVDTIQGLNVPMKFPVHLLAL SCDSLTLTSLACMMSSEYGSIAFFDVR TFSNQAKPLKRPFTYHKVSNDSAGM VNDMKWNPTVPSMVAVCLADGSIS VLQVTDVVKVCATLPPSTGVTCVCW SPKKGQLAVGKQNGTVVQYLPQLQE KKVIPCPFFYEDHPVRLDVLWIGT YVFTIVYAGADGTLETCPDVMALLP KKEEKHPEIFVNFMEPCYSSCTERQ HHYLSYIEEWDLVLAASAASTEVSI LARQNDQTNWESWLEDSSRAELP VTDKSDDSLPMGVAIDYTNNEVEVTIN EETLPPAPVLLLLSTDGVLCPFYMI NQNPQVRSLIKTLLELISTEGERQPKS SGSFPGTSSPQAPQNLDPATASSP LPPVSAAPTSTFFMPSAAGSPSVFSF GPSSFKSSASVTGEPPLYPTGSDSSR AAPGSGTSTFSFAPPSKGLASTPAV APVATSAAPFTFGFKPTLESTPMSST PNTGMKPSFPPSASSVKVNLNEKFT AVASSAPVHSSTSTPSVLPFSSSPKP TASGPLSHPTPLPASSSMLPKSSVS PSPAAGRSTQTPASSAPSTGOKSPRV NPPVPKSGSSQAKALQPPVTEKQRP QWKSDPVLGIGEEIAHFQKELEE LKARTAKACLQVGTSEEMKMLRTES DDLHTFLFEIRETTESLHGDISTLKT TLLEGFAGVEEAREQHGRNHDSGYL HLLYKRPLDPKSEAQLQEIRRLHQYV KFAVQDVNDVLDLEWDRHLEQKKR QRRRLIVPERETLFNTLANNREIINQQ RKRLNQLVDSLQQLRLYNHTAPWSL PSALSTQSNHSFSDLECLLKTIE SHTKPSRVPVQKLSPAKQAQLRNFL AKRKTTPVVRSTAPASLSRASFQRY YEDLDEGSSASSVAQPLEGEDARPT CTSVAQPLEGEDAQPICKEEEAVVPV PRHAPVVRTPSIQPSLLPQSMPPFAKP HLIHSSSPAVMSSAVSTSAKVIPOG ADSTMLATKTVKHGAPGPSHTVAAP QAAAAAALRRQMASQAPAMSTLTES TLKTVPQVVNVQELRSNPSPPSAAM GSAVQHSAAKTPHAVLTPVANSQAK QGSLINSFKPSGPTAASCQLSSGDKA VGQGTAKTESAATSTPSAAGQLNKP FSFASPFTFTFGTITPTSSSFTATPG AGPPTKEPTQLEAFSFGGGGKPFSE AIPGNPATGATSAPSTSVTAASLED SAPSSSKPAAPPETTSSASSKLETPP SKLGELLFPSSLAGETLGSFSGLRVG QAEDSTKPVSKASSTNLAGAQPAPK SGVSFPNTSVLQKPVPAVTSVSPA PAAPASALNVSTSSSATVFGSVPLT SAGPPGLISFGGAALASSKASFSFGN QQTSSSTASSATPTSTSVAPSLPASF PTLSFGGLLSSPSASSLPVSSGKSTE EAAPPVDPKSDSSEVSATTPSLPVQ PQSTQASLQTSDPVKKEPVLVQTTDS SPSRPASSASFVASTESMPVTLGAPD

