

| UniprotKB ID | Entry name  | organism     | full name                           | oglcnacscore | oglcnac sites                                      | phosphorylation sites                                                                                                                       | PMIDS                                                                   | sequence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|--------------|-------------|--------------|-------------------------------------|--------------|----------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Q80U93       | NU214_MOUSE | Mus musculus | Nuclear pore complex protein Nup214 | 36.994326    | S504;S507;S513;S1049;T1091;S1337;S1362;T1557;S1899 | 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 | 22645316;30059200;33300544;23443134;27669760;22517741;21606357;29125738 | MGDEMDAMIPEREMKDFQFRALKK<br>VRIFDSPEELPKERSVLTISNKYGM<br>LFAGGTNGLNVFPTKSLLIQNKPGD<br>DPNKIVDTIQGLNVPMKFFPVHLLAL<br>SCDSLTLTSLACMMSSEYGSIAFFDVR<br>TFSNQAKPLKRPFTYHKVSNDSAGM<br>VNDMKWNPTVPSMVAVCLADGSIS<br>VLQVTDVVKVCATLPPSTGVTCVCW<br>SPKQKQLAVGKQNGTVVQYLPQLQE<br>KKVIPCPFFYESDHPVRLDVLWIGT<br>YVFTIVYAGADGTLETCPDVMALLP<br>KKEEKHPEIFVNFMEPCYSSCTERQ<br>HHYLSYIEEWDLVLAASAASTEVSI<br>LARQNDQTNWESWLEDSRRAELP<br>VTDKSDDSLPMGVAIDYTNNEVEVTIN<br>EETLPPAPVLLLLSTDGVLCPFYMI<br>NQNPQVRSLIKTLLELISTEGERQPKS<br>SGSFPGTPSSPQAPQNLDPATASSP<br>LPPVSAAPTSTFFMPSAAGSPSVFSF<br>GPSSFKSSASVTGEPPLYPTGSDSSR<br>AAPGSGTSTFSFAPPSKGLASTPAV<br>APVATSAAPFTFGFKPTLESTPMSST<br>PNTGMKPSFPPSASVVKVNLNEKFT<br>AVASSAPVHSSTSTPSVLPFSSSPKP<br>TASGPLSHPTLPASSSSMPLKSSVS<br>PSPAAGRSTQTAPSSAPSTGOKSPRV<br>NPPVPKSGSSQAKALQPPVTEKQRP<br>QWKDSDPVLGIGEEIAHFQKELEE<br>LAKARTAKACLQVGTSEEMKMLRTES<br>DDLHTFLFEIRETTESLHGDISTLKT<br>TLLEGFAGVEEAREQHGRNHDSGYL<br>HLLYKRPLDPKSEAQLQEIRRLHQYV<br>KFAVQDVNDVLDLEWDRHLEQKKR<br>QRRRLIVPERETLFNTLANNREIINQQ<br>RKRLNQLVDSLQQLRLYNHTAPWSL<br>PSALSTQSNHSFSDLECLLKTIE<br>SHTKPSRVPVPGKLSPAKQAQLRNFL<br>AKRKTTPVVRSTAPASLSRASFQRY<br>YEDLDEGSSASSVAQPLEGEDARPT<br>CTSVAQPLEGEDAQPICKEEEAVVPV<br>PRHAPVVRTPSIQPSLLPQSMPPFAKP<br>HLIHSSSPAVMSSAVSTSAKVIPOG<br>ADSTMLATKTVKHGAPGPSHTVAAP<br>QAAAAAALRRQMASQAPAMSTLTES<br>TLKTVPQVVNVQELRSNPPSAAM<br>GSAVQHSAAKTPHAVLTPVANSQAK<br>QGSLINSFKPSGPTAASCQLSSGDKA<br>VGQGTAKTESAATSTPSAAGQLNKP<br>FSFASPGTFTFGTITPTSSSFTATPG<br>AGPPTKEPTQLEAFSFGGGGKPFSE<br>AIPGNPATGATSAPSTSVTAASLED<br>SAPSSSKPAAPPETTSSASSKLETPP<br>SKLGELLFPSSLAGETLGSFSGLRVG<br>QAEDSTKPVSKASSTNLAGAQPAPK<br>SGVSPNTSVLGPVEPAVTSVSPA<br>PAAPASALNVSTSSSATVFGSVPLT<br>SAGPPGLISFGGAALASSKASFSFGN<br>QQTSSSTASSATPTSTSVAPSLPASF<br>PTLSFGGLLSSPSASSLPVSSGKSTE<br>EAAPPVDPKSDSSEVSATTPSLPVQ<br>PQSTQASLQTSDPVKKEPVLVQTTDS<br>SPSRPASSASFVASTESMPVTLGAPD |

