

Nuclear pore complex protein Nup153 Recombinant Protein | NUP153 recombinant protein

Recombinant Human Nuclear pore complex protein Nup153

CATALOG # AAA113207	HOST E Coli or Yeast or Baculovirus or Mammalian Cell
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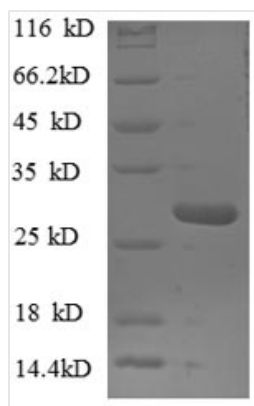
PRODUCT SYNONYMS

Nuclear pore complex protein Nup153; Recombinant Human Nuclear pore complex protein Nup153; 153 kDa nucleoporin; Nucleoporin Nup153; NUP153 recombinant protein

PRODUCT SPECIFICATIONS

Host	E Coli or Yeast or Baculovirus or Mammalian Cell
Purity/Purification	Greater or equal to 85% purity as determined by SDS-PAGE.
Form/Format	Lyophilized or liquid (Format to be determined during the manufacturing process)
Sequence Positions	657-880aa; Partial
Sequence	KAGSSWQCDT CLLQNKVTDN KCIACQAAKL SPRDTAKQTG IETPNKSGKT TLSASGTGFG DKFKPVIQGW DCDTCLVQNK PEAIKCVACE TPKPGTCVKR ALTLTVSES AETMTASSSS CTVTGTGLGF GDKFKRPIGS WECSVCCVSN NAEDNKCVCSC MSEKPGSSVP ASSSSTVPVS LPSGGSLGLE KFKKPEGSWD CELCLVQNKA DSTKCLACES AKPG
Sequence Length	1,506
Preparation and Storage	Store at -20 degree C, for extended storage, conserve at -20 degree C or -80 degree C.

IMAGES



SDS-PAGE

ADDITIONAL INFORMATION

Related Product Information for NUP153 recombinant protein	Component of the nuclear pore complex (NPC), a complex required for the trafficking across the nuclear envelope. Functions as a scaffolding element in the nuclear phase of the NPC essential for normal nucleocytoplasmic transport of proteins and mRNAs. Involved in the quality control and retention of unspliced mRNAs in the nucleus; in association with TPR, regulates the nuclear export of unspliced mRNA species bearing constitutive transport element (CTE) in a NXF1- and KHDRBS1-independent manner. Mediates TPR anchoring to the nuclear membrane at NPC. The repeat-containing domain may be involved in anchoring other components of the NPC to the pore membrane. Possible DNA-binding subunit of the nuclear pore complex (NPC).
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References

Sequence analysis of a cDNA encoding a human nuclear pore complex protein, hnup153. *McMorrow I., Bastos R., Horton H., Burke B. Biochim. Biophys. Acta* 1217:219-223(1994) Complete sequencing and characterization of 21,243 full-length human cDNAs. *Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S. *Nat. Genet.* 36:40-45(2004) Preparation of a set of expression-ready clones of mammalian long cDNAs encoding large proteins by the ORF trap cloning method. *Nakajima D., Saito K., Yamakawa H., Kikuno R.F., Nakayama M., Ohara R., Okazaki N., Koga H., Nagase T., Ohara O.* The DNA sequence and analysis of human chromosome 6. *Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L., Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E., Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R., Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S., Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J., Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P., Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y., Burford D.C., Burrill W., Burton J., Carder C., Carter N.P., Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V., Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J., Culley K.M., Dhami P., Davies J., Dunn M., Earthrowl M.E., Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A., Frankland J., French L., Garner P., Garnett J., Ghori M.J., Gilby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M., Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S., Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R., Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E., Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A., Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C., Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M., Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M., Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K., McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T., Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R., Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W., Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M., Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L., Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J., Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B., Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L., Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W., Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A., Durbin R.M., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S. *Nature* 425:805-811(2003) Bienvenut W.V., Dozynkiewicz M., Norman J.C. Submitted (MAR-2009) to UniProtKB Exportin-5, a novel karyopherin, mediates nuclear export of double-stranded RNA binding proteins. *Brownawell A.M., Macara I.G.J. Cell Biol.* 156:53-64(2002) Tpr is localized within the nuclear basket of the pore complex and has a role in nuclear protein export. *Frosst P., Guan T., Subauste C., Hahn K., Gerace L.J. Cell Biol.* 156:617-630(2002) Direct interaction with nup153 mediates binding of Tpr to the periphery of the nuclear pore complex. *Hase M.E., Cordes V.C. Mol. Biol. Cell* 14:1923-1940(2003) Nucleoporins as components of the nuclear pore complex core structure and Tpr as the architectural element of the nuclear basket. *Krull S., Thyberg J., Bjorkroth B., Rackwitz H.R., Cordes V.C. Mol. Biol. Cell* 15:4261-4277(2004) Global, in vivo, and site-specific phosphorylation dynamics in signaling networks. *Olsen J.V., Blagoev B., Gnäd F., Macek B., Kumar C., Mortensen P., Mann M. Cell* 127:635-648(2006) A probability-based approach for high-throughput protein phosphorylation analysis and site localization. *Beausoleil S.A., Villen J., Gerber S.A., Rush J., Gygi S.P. Nat. Biotechnol.* 24:1285-1292(2006) Combining protein-based IMAC, peptide-based IMAC, and MudPIT for efficient phosphoproteomic analysis. *Cantin G.T., Yi W., Lu B., Park S.K., Xu T., Lee J.-D., Yates J.R. III. J. Proteome Res.* 7:1346-1351(2008) Kinase-selective enrichment enables quantitative phosphoproteomics of the kinome across the cell cycle. *Daub H., Olsen J.V., Bairlein M., Gnäd F., Oppermann F.S., Korner J., Greff Z., Keri G., Stemmann O., Mann M. Mol. Cell* 31:438-448(2008) A quantitative atlas of mitotic phosphorylation. *Dephoure N., Zhou C., Villen J., Beausoleil S.A., Bakalarski C.E., Elledge S.J., Gygi S.P. Proc. Natl. Acad. Sci. U.S.A.* 105:10762-10767(2008) Lys-N and trypsin cover complementary parts of the phosphoproteome in a refined SCX-based approach. *Gauci S., Helbig A.O., Slijper M., Krijgsveld J., Heck A.J., Mohammed S. Anal. Chem.* 81:4493-4501(2009) Integrase interacts with nucleoporin NUP153 to mediate the nuclear import of human immunodeficiency virus type 1. *Woodward C.L., Prakobwanakit S., Mosessian S., Chow S.A. J. Virol.* 83:6522-6533(2009) Quantitative phosphoproteomic analysis of T cell receptor signaling reveals system-wide modulation of protein-protein interactions. *Mayya V., Lundgren D.H., Hwang S.-I., Rezaul K., Wu L., Eng J.K., Rodionov V., Han D.K. Sci. Signal.* 2:RA46-RA46(2009) Lysine acetylation targets protein complexes and co-regulates major cellular functions. *Choudhary C., Kumar C., Gnäd F., Nielsen M.L., Rehman M., Walther T.C., Olsen J.V., Mann M. Science* 325:834-840(2009) Protein Tpr is required for establishing nuclear pore-associated zones of heterochromatin exclusion. *Krull S., Dorries J., Boysen B., Reidenbach S., Magnusius L., Nordner H., Thyberg J., Cordes V.C. EMBO J.* 29:1659-1673(2010) Nucleoporin translocated promoter region (Tpr) associates with dynein complex, preventing chromosome lagging formation during mitosis. *Nakano H.,***

NCBI AND UNIPROT INFORMATION

NCBI GI #	503774352
NCBI GeneID	9972
NCBI Accession #	NP_001265138.1
NCBI GenBank Nucleotide #	NM_001278209.1
UniProt Accession #	P49790; Q4LE47; Q5T9I7; Q7Z743; B4DIK2; E7EPX5; F6QR24
Molecular Weight	27.3 kDa
NCBI Official Full Name	nuclear pore complex protein Nup153 isoform 1
NCBI Official Synonym Full Names	nucleoporin 153kDa
NCBI Official Symbol	NUP153
NCBI Official Synonym Symbols	N153; HNUP153
NCBI Protein Information	nuclear pore complex protein Nup153
UniProt Protein Name	Nuclear pore complex protein Nup153
UniProt Gene Name	NUP153
UniProt Entry Name	NU153_HUMAN

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