

Nuclear pore membrane glycoprotein 210 (NUP210) Recombinant Protein | NUP210 recombinant protein

Recombinant Human Nuclear pore membrane glycoprotein 210 (NUP210), partial

CATALOG # AAA114257	HOST E Coli or Yeast or Baculovirus or Mammalian Cell
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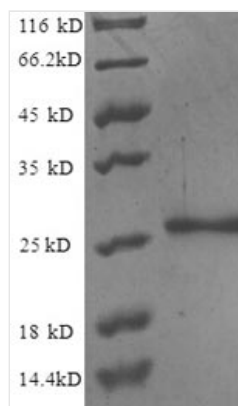
PRODUCT SYNONYMS

Nuclear pore membrane glycoprotein 210 (NUP210); Recombinant Human Nuclear pore membrane glycoprotein 210 (NUP210); partial; Nuclear envelope pore membrane protein POM 210; POM210; Nucleoporin Nup210; Pore membrane protein of 210 kDa; NUP210 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	28-238. Partial
Sequence	LNIPKVLLPF TRATRVNFTL EASEGCRYWL STRPEVASIE PLGLDEQQCS QKAVVQARLT QPARLTSIIF AEDITTGQVL RCDAIVDLIH DIQIVSTTRE LYLEDSPLEL KIQALDSEGN TFSTLAGLVF EWTIVKDSEA DRFSDSHNAL RILTFLESTY IPPSYISEME KAAKQGDITL VSGMKTGSSK LKARIQEAVY KNVRPAEVRL L
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 NUP210 recombinant protein	Nucleoporin essential for nuclear pore assembly and fusion, nuclear pore spacing, as well as structural integrity.
Product Categories/Family for NUP210 recombinant protein	Transport

References

The DNA sequence, annotation and analysis of human chromosome 3. Muzny D.M., Scherer S.E., Kaul R., Wang J., Yu J., Sudbrak R., Buhay C.J., Chen R., Cree A., Ding Y., Dugan-Rocha S., Gill R., Gunaratne P., Harris R.A., Hawes A.C., Hernandez J., Hodgson A.V., Hume J., Jackson A., Khan Z.M., Kovar-Smith C., Lewis L.R., Lozado R.J., Metzker M.L., Milosavljevic A., Miner G.R., Morgan M.B., Nazareth L.V., Scott G., Sodergren E., Song X.-Z., Steffen D., Wei S., Wheeler D.A., Wright M.W., Worley K.C., Yuan Y., Zhang Z., Adams C.Q., Ansari-Lari M.A., Ayele M., Brown M.J., Chen G., Chen Z., Clendenning J., Clerc-Blankenburg K.P., Chen R., Chen Z., Davis C., Delgado O., Dinh H.H., Dong W., Draper H., Ernst S., Fu G., Gonzalez-Garay M.L., Garcia D.K., Gillett W., Gu J., Hao B., Haugen E., Havlak P., He X., Hennig S., Hu S., Huang W., Jackson L.R., Jacob L.S., Kelly S.H., Kube M., Levy R., Li Z., Liu B., Liu J., Liu W., Lu J., Maheshwari M., Nguyen B.-V., Okwuonu G.O., Palmeiri A., Pasternak S., Perez L.M., Phelps K.A., Plopper F.J., Qiang B., Raymond C., Rodriguez R., Saenphimmachak C., Santibanez J., Shen H., Shen Y., Subramanian S., Tabor P.E., Verduzco D., Waldron L., Wang J., Wang J., Wang Q., Williams G.A., Wong G.K.-S., Yao Z., Zhang J., Zhang X., Zhao G., Zhou J., Zhou Y., Nelson D., Lehrach H., Reinhardt R., Naylor S.L., Yang H., Olson M., Weinstock G., Gibbs R.A. *Nature* 440:1194-1198(2006) 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) Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro. Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O. *DNA Res.* 5:355-364(1998) Signal sequence and keyword trap in silico for selection of full-length human cDNAs encoding secretion or membrane proteins from oligo-capped cDNA libraries. Otsuki T., Ota T., Nishikawa T., Hayashi K., Suzuki Y., Yamamoto J., Wakamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S., Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Nagai K., Sugano S., Isogai T. *DNA Res.* 12:117-126(2005) The full-ORF clone resource of the German cDNA consortium. Bechtel S., Rosenfelder H., Duda A., Schmidt C.P., Ernst U., Wellenreuther R., Mehrle A., Schuster C., Bahr A., Bloecker H., Heubner D., Hoerlein A., Michel G., Wedler H., Koehrer K., Ottenwaelter B., Poustka A., Wiemann S., Schupp I. *BMC Genomics* 8:399-399(2007) The 210-kD nuclear envelope polypeptide recognized by human autoantibodies in primary biliary cirrhosis is the major glycoprotein of the nuclear pore. Courvalin J.-C., Lassoued K., Bartrik E., Blobel G., Wozniak R.W.J. *Clin. Invest.* 86:279-285(1990) Nuclear pore protein gp210 is essential for viability in HeLa cells and *Caenorhabditis elegans*. Cohen M., Feinstein N., Wilson K.L., Gruenbaum Y. *Mol. Biol. Cell* 14:4230-4237(2003) 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) Glycoproteomics analysis of human liver tissue by combination of multiple enzyme digestion and hydrazide chemistry. Chen R., Jiang X., Sun D., Han G., Wang F., Ye M., Wang L., Zou H.J. *Proteome Res.* 8:651-661(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) Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. Olsen J.V., Vermeulen M., Santamaria A., Kumar C., Miller M.L., Jensen L.J., Gnad F., Cox J., Jensen T.S., Nigg E.A., Brunak S., Mann M. *Sci. Signal.* 3:RA3-RA3(2010) Initial characterization of the human central proteome. Burkard T.R., Planyavsky M., Kaupe I., Breitwieser F.P., Buerckstuemmmer T., Bennett K.L., Superti-Furga G., Colinge J. *BMC Syst. Biol.* 5:17-17(2011) System-wide temporal characterization of the proteome and phosphoproteome of human embryonic stem cell differentiation. Rigbolt K.T., Prokhorova T.A., Akimov V., Henningsen J., Johansen P.T., Kratchmarova I., Kassem M., Mann M., Olsen J.V., Blagoev B. *Sci. Signal.* 4:RS3-RS3(2011) An enzyme assisted RP-RPLC approach for in-depth analysis of human liver phosphoproteome. Bian Y., Song C., Cheng K., Dong M., Wang F., Huang J., Sun D., Wang L., Ye M., Zou H.J. *Proteomics* 96:253-262(2014) Detection and validation of non-synonymous coding SNPs from orthogonal analysis of shotgun proteomics data. Bunger M.K., Cargile B.J., Sevinsky J.R., Deyanova E., Yates N.A., Hendrickson R.C., Stephenson J.L. Jr. *J. Proteome Res.* 6:2331-2340(2007)

NCBI AND UNIPROT INFORMATION

NCBI GI #	27477134
NCBI GeneID	23225
NCBI Accession #	NP_079199.2
NCBI GenBank Nucleotide #	NM_024923.3
UniProt Accession #	Q8TEM1; O94980; Q6NXG6; Q8NBJ1; Q9H6C8; Q9UFP3; A6NN56
Molecular Weight	27.6 kDa
NCBI Official Full Name	nuclear pore membrane glycoprotein 210
NCBI Official Synonym Full Names	nucleoporin 210kDa
NCBI Official Symbol	NUP210
NCBI Official Synonym Symbols	GP210; POM210
NCBI Protein Information	nuclear pore membrane glycoprotein 210
UniProt Protein Name	Nuclear pore membrane glycoprotein 210
UniProt Gene Name	NUP210
UniProt Synonym Gene Names	KIAA0906; Nuclear pore protein gp210; POM210
UniProt Entry Name	PO210_HUMAN

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AAA Biotech | Tel: +1 (619) 604-9440 | Fax: +1 (619) 604-9441 | contact@aaabiotech.com
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