

# **Product datasheet**

Decorintion

# Recombinant Human KPNA5 protein (Tagged) ab199581

Description		
Product name	Recombinant Human KPNA5 protein (Tagged)	
Purity	> 90 % SDS-PAGE. ab199581 was refolded usin chromatographically purified.	g a unique temperature shift inclusion body refolding technology and
Expression system	Escherichia coli	
Accession	<u>015131</u>	
Protein length	Full length protein	
Animal free	No	
Nature	Recombinant	
Species	Human	
Sequence		<ul> <li>MASMTGGQQMGRGHHHHHHGNLYFQGGEFDAMASPGK</li> <li>DNYRMKSYKNKAL</li> <li>NPQEMRRRREEEGIQLRKQKREEQLFKRRNVYLPRNDES</li> <li>MLESPIQDPDI</li> <li>SSTVPIPEEEVVTTDMVQMIFSNNADQQLTATQKFRKLLS</li> <li>KEPNPPIDQV</li> <li>IQKPGVVQRFVKFLERNENCTLQFEAAWALTNIASGTFLHT</li> <li>KVVIETGAV</li> <li>PIFIKLLNSEHEDVQEQAVWALGNIAGDNAECRDFVLNCEI</li> <li>LPPLLELLT</li> <li>NSNRLTTTRNAVWALSNLCRGKNPPPNFSKVSPCLNVLS</li> <li>RLLFSSDPDVL</li> <li>ADVCWALSYLSDGPNDKIQAVIDSGVCRRLVELLMHNDY</li> <li>KVVSPALRAVG</li> <li>NIVTGDDIQTQVILNCSALPCLLHLLSSPKESIRKEACWTVS</li> <li>NITAGNRA</li> <li>QIQAVIDANIFPVLIEILQKAEFRTRKEAAWAITNATSGGTPE</li> <li>QIRYLVA</li> <li>LGCIKPLCDLLTVMDSKIVQVALNGLENILRLGEQESKQNGI</li> <li>GINPYCAL</li> <li>IEEAYGLDKIEFLQSHENQEIYQKAFDLIEHYFGVEEDDPSI</li> <li>VPQVDENQ QQFIFQQQEAPMDGFQL</li> </ul>
Predicted molecular weight	64 kDa including tags	VFQVDLNQQQFIFQQQEAFINDOFQL

Additional sequence information Constructed with a small T7-His-TEV cleavage site Tag (29 amino acids) fusion at the N-terminal.

### Specifications

Our <u>Abpromise guarantee</u> covers the use of ab199581 in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Applications	SDS-PAGE
Form	Liquid
Preparation and Storage	
Stability and Storage	Shipped at 4°C. Store at +4°C short term (1-2 weeks). Upon delivery aliquot. Store at -80°C. Avoid freeze / thaw cycle.
	рН: 8.00
	Constituent: 0.32% Tris HCI
	Contains NaCl, KCl, EDTA, Sucrose, DTT.

#### **General Info**

Function	Functions in nuclear protein import as an adapter protein for nuclear receptor KPNB1. Binds specifically and directly to substrates containing either a simple or bipartite NLS motif. Docking of the importin/substrate complex to the nuclear pore complex (NPC) is mediated by KPNB1 through binding to nucleoporin FxFG repeats and the complex is subsequently translocated through the pore by an energy requiring, Ran-dependent mechanism. At the nucleoplasmic side of the NPC, Ran binds to importin-beta and the three components separate and importin-alpha and -beta are re-exported from the nucleus to the cytoplasm where GTP hydrolysis releases Ran from importin. The directionality of nuclear import is thought to be conferred by an asymmetric distribution of the GTP- and GDP-bound forms of Ran between the cytoplasm and nucleus. Mediates nuclear import of STAT1 homodimers and STAT1/STAT2 heterodimers by recognizing non-classical NLSs of STAT1 and STAT2 through ARM repeats 8-9. Recognizes influenza A virus nucleoprotein through ARM repeat 7-9 In vitro, mediates the nuclear import of human cytomegalovirus UL84 by recognizing a non-classical NLS.
Tissue specificity	Testis.
Sequence similarities	Belongs to the importin alpha family. Contains 10 ARM repeats. Contains 1 IBB domain.
Domain	Consists of an N-terminal hydrophilic region, a hydrophobic central region composed of 10 repeats, and a short hydrophilic C-terminus. The N-terminal hydrophilic region contains the importin beta binding domain (IBB domain), which is sufficient for binding importin beta and essential for nuclear protein import. The IBB domain is thought to act as an intrasteric autoregulatory sequence by interacting with the internal autoinhibitory NLS. Binding of KPNB1 probably overlaps the internal NLS and contributes to a high affinity for cytoplasmic NLS-containing cargo substrates. After dissociation of the importin/substrate complex in the nucleus the internal autohibitory NLS contributes to a low affinity for nuclear NLS-containing proteins.

The major and minor NLS binding sites are mainly involved in recognition of simple or bipartite NLS motifs. Structurally located within in a helical surface groove they contain several conserved Trp and Asn residues of the corresponding third helices (H3) of ARM repeats which mainly contribute to binding.

#### **Cellular localization**

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