

# Nucleoporin POM152 - P39685 (PO152\_YEAST)

## Protein Feature View of PDB entries mapped to a UniProtKB sequence

Number of PDB entries for P39685: 0

### Function

Functions as a component of the nuclear pore complex (NPC). NPC components, collectively referred to as nucleoporins (NUPs), can play the role of both NPC structural components and of docking or interaction partners for transiently associated nuclear transport factors. POM152 is important for the de novo assembly of NPCs. (data source: UniProt )

### Subunit structure

The nuclear pore complex (NPC) constitutes the exclusive means of nucleocytoplasmic transport. NPCs allow the passive diffusion of ions and small molecules and the active, nuclear transport receptor-mediated bidirectional transport of macromolecules such as proteins, RNAs, ribonucleoparticles (RNPs), and ribosomal subunits across the nuclear envelope. The 55-60 MDa NPC is composed of at least 31 different subunits: ASM4, CDC31, GLE1, GLE2, NDC1, NIC96, NSP1, NUP1, NUP2, NUP100, NUP116, NUP120, NUP133, NUP145, NUP157, NUP159, NUP170, NUP188, NUP192, NUP42, NUP49, NUP53, NUP57, NUP60, NUP82, NUP84, NUP85, POM152, POM34, SEH1 and SEC1. Due to its 8-fold rotational symmetry, all subunits are present with 8 copies or multiples thereof. Interacts with NUP188. (data source: UniProt )

P39685 - *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) 0 ▾

UniProtKB: P39685


Length:1337

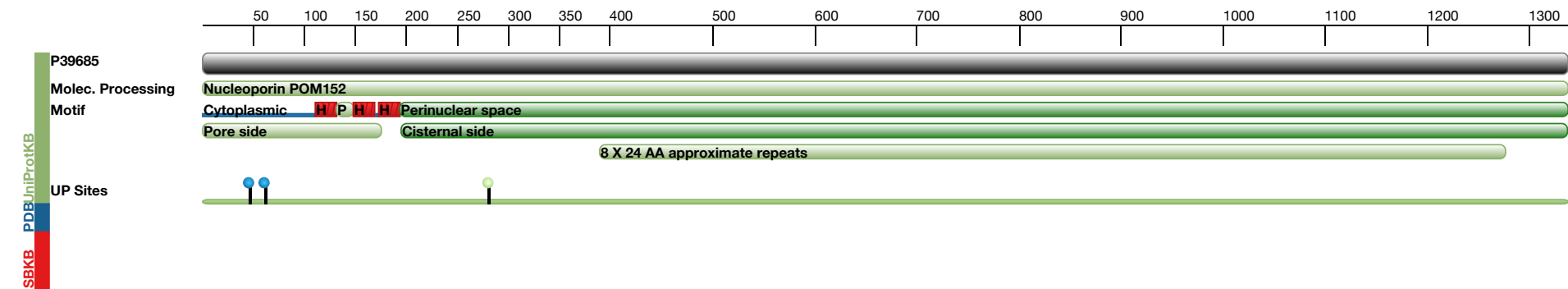
Organism (common name): Baker's yeast

MOPED

Other Gene names: POM152 YMR129W YM9553.05

Action ▾

 Full screen



Export

Display Options

Zoom	min	max
Showing all PDB entries	<div>Show All</div>	
Sort by	<div>Alignment Length</div>	
Color by	<div>Alignment Length</div>	

Legend

The Protein Feature View requires a browser that supports SVG (Scalable Vector Graphics). Mouse over tracks and labels for more information.

Data origin/color codes

The vertical color bar on the left side indicates data provenance.

- Data in green originates from UniProtKB
- Data in yellow originates from Pfam, by interacting with the HMMER3 web site
- Data in purple originates from Phosphosite
- Data in orange originates from the SCOP (version 1.75) and SCOPe (version 2.04) classifications.
- Data in grey has been calculated using BioJava. Protein disorder predictions are based on JRONN (Troshin, P. and Barton, G. J. unpublished), a Java implementation of RONN
  - Red: potentially disorderd region
  - Blue: probably ordered region.

Hydropathy has been calculated using a sliding window of 15 residues and summing up scores from standard hydrophobicity tables.

- Red: hydrophobic

- Blue: hydrophilic.

Data in lilac represent the genomic exon structure projected onto the UniProt sequence.

Data in blue originates from PDB

- Secstruc: Secondary structure projected from representative PDB entries onto the UniProt sequence.

Data in red indicates combined ranges of Homology Models from SBKB and the Protein Model Portal

The PDB to UniProt mapping is based on the data provided by the EBI SIFTS project. See also Velankar et al., Nucleic Acids Research 33, D262-265 (2005).

Organism icons generated by flaticon.com under CC BY. The authors are: Freepik, Icons8, OCHA, Scott de Jonge.

The RCSB PDB is funded by a grant (DBI-1338415) from the National Science Foundation, the National Institutes of Health, and the US Department of Energy.