

4XMM

Structure of the yeast coat nucleoporin complex, space group C2

DOI: 10.2210/pdb4xmm/pdb

Classification: <u>Transport Protein / Immune System</u> **Deposited**: 2015-01-14 **Released**: 2015-03-25

Deposition author(s): Stuwe, T., Correia, A.R., Lin, D.H., Paduch, M., Lu, V.T., Kossiakoff, A.A., Hoelz, A.

Organism: Saccharomyces cerevisiae | Homo sapiens

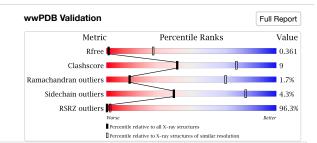
Expression System: Escherichia coli

Structural Biology Knowledgebase: 4XMM (28 models >19 annotations)

Experimental Data Snapshot

Method: X-RAY DIFFRACTION

Resolution: 7.38 Å R-Value Free: 0.353 R-Value Work: 0.330



Protein Symmetry: Asymmetric (View in 3D)

Protein Staichiometry: Hetero 8-mer - ABCDEFGH

Biological assembly 1 assigned by authors and generated by PISA (software)

Macromolecule Content

• Unique protein chains: 8

Literature

Nuclear pores. Architecture of the nuclear pore complex coat.

Stuwe, T., Correia, A.R., Lin, D.H., Paduch, M., Lu, V.T., Kossiakoff, A.A., Hoelz, A.

(2015) Science 347: 1148-1152

PubMed: 25745173

DOI: 10.1126/science.aaa4136

Primary Citation of Related Structures: 4XMM 4XMN

PubMed Abstract:

The nuclear pore complex (NPC) constitutes the sole gateway for bidirectional nucleocytoplasmic transport. Despite half a century of structural characterization, the architecture of the NPC remains unknown. Here we present the crystal structure of a reconstituted ~400-kilodalton coat nucleoporin complex (CNC) from Saccharomyces cerevisiae at a 7.4 angstrom resolution. The crystal structure revealed a curved Y-shaped architecture and the molecular details of the coat nucleoporin interactions forming the central "triskelion" of the Y. A structural comparison of the yeast CNC with an electron microscopy reconstruction of its human counterpart suggested the evolutionary conservation of the elucidated architecture. Moreover, 32 copies of the CNC crystal structure docked readily into a cryoelectron tomographic reconstruction of the fully assembled human NPC, thereby accounting for ~16 megadalton of its mass.

Organizational Affiliation:

Division of Chemistry and Chemical Engineering, California Institute of Technology, 1200 East California Boulevard, Pasadena, CA 91125, USA. These authors contributed equally to this work.

Macromolecules

Classification: Transport Protein / Immune System

Total Structure Weight: 454643.61

Total Structure Weight: 454643.61 🛡						
Macromolecule Entities						
Molecule	Chains	Length	Organism	Details		
Protein transport protein SEC13	А	297	Saccharomyces cerevisiae	SEC13 Gene View ANU3 YLR208W L8167.4		
Nucleoporin NUP145	В	652	Saccharomyces cerevisiae	EC#: 3.4.21 [IUBMB]		
				NUP145 RAT10 YGL092W		
Nucleoporin SEH1	С	349	Saccharomyces cerevisiae	SEH1 YGL100W		
Nucleoporin NUP85	D	715	Saccharomyces cerevisiae	NUP85 Gene View RAT9 YJR042W J1624		

Show All 8 Protein Entities

Experimental Data & Validation

Experimental Data

Method: X-RAY DIFFRACTION

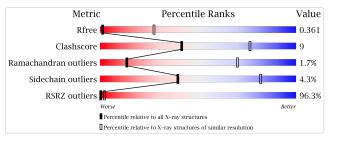
Resolution: 7.38 Å R-Value Free: 0.353 R-Value Work: 0.330 Space Group: <u>C 1 2 1</u>

Unit Cell:

Length (Å)	Angle (°)
a = 210.65	$\alpha = 90.00$
b = 186.30	$\beta = 100.85$
c = 199.57	γ = 90.00

Structure Validation

View Full Validation Report or Ramachandran Plots



Entry History

Deposition Data

Deposited Date: 2015-01-14 Released Date: 2015-03-25

Deposition author(s): Stuwe, T., Correia, A.R., Lin, D.H., Paduch, M., Lu, V.T., Kossiakoff,

A.A., Hoelz, A.

Revision History 9

• 2016-02-03

Type: Citation | Details: Citation

• 2015-04-01

Type: Entry title | Details: Entry title

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.

2 of 2 2/27/2016 8:08 AM