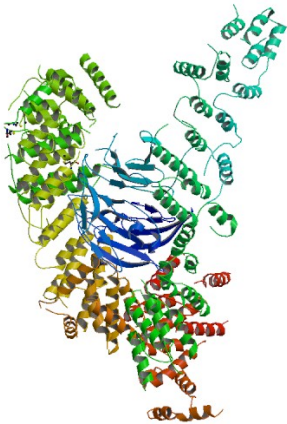


Biological Assembly 1 ⓘ



Protein Symmetry: Asymmetric (View in 3D)

Protein Stoichiometry: Hetero 3-mer - ABC

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

4YCZ

Y-COMPLEX HUB (NUP85-NUP120-NUP145C-SEC13 COMPLEX) FROM M. THERMOPHILA (A.K.A. T. HETEROHALLICA)

DOI: 10.2210/pdb4ycz/pdb

Classification: **STRUCTURAL PROTEIN**

Deposited: 2015-02-20 Released: 2015-04-01

Deposition author(s): [Kelley, K.](#), [Knockenbauer, K.E.](#), [Schwartz, T.U.](#)

Organism: [Myceliophthora thermophila](#)

Expression System: Escherichia coli, Escherichia coli, Escherichia coli, Escherichia coli, Escherichia coli

Structural Biology Knowledgebase: 4YCZ

Experimental Data Snapshot

Method: X-RAY DIFFRACTION

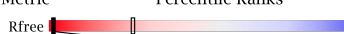



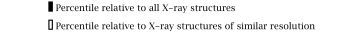
Resolution: 4.1 Å

R-Value Free: 0.358

R-Value Work: 0.319

wwPDB Validation

Full Report

Metric	Percentile Ranks	Value
Rfree		0.357
Clashscore		8
Ramachandran outliers		1.1%
Sidechain outliers		1.0%
RSRZ outliers		5.6%

Worse

Better

■ Percentile relative to all X-ray structures

▨ Percentile relative to X-ray structures of similar resolution

Literature

Atomic structure of the Y complex of the nuclear pore.

[Kelley, K.](#), [Knockenbauer, K.E.](#), [Kabachinski, G.](#), [Schwartz, T.U.](#)

(2015) Nat.Struct.Mol.Biol. **22**: 425-431

PubMed: 25822992

DOI: 10.1038/nsmb.2998

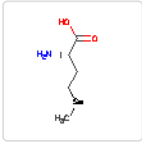
PubMed Abstract:

The nuclear pore complex (NPC) is the principal gateway for transport into and out of the nucleus. Selectivity is achieved through the hydrogel-like core of the NPC. The structural integrity of the NPC depends on ~15 architectural proteins, which are organized in distinct subcomplexes to form the >40-MDa ring-like structure. Here we present the 4.1-Å crystal structure of a heterotetrameric core element ('hub') of the Y complex, the essential NPC building block, from *Myceliophthora thermophila*. Using the hub structure together with known Y-complex fragments, we built the entire ~0.5-MDa Y complex. Our data reveal that the conserved core of the Y complex has six rather than seven members. Evolutionarily distant Y-complex assemblies share a conserved core that is very similar in shape and dimension, thus suggesting that there are closely related architectural codes for constructing the NPC in all eukaryotes.

Organizational Affiliation:

Department of Biology, Massachusetts Institute of Technology (MIT), Cambridge, Massachusetts USA.

Macromolecules				
Classification: STRUCTURAL PROTEIN				
Total Structure Weight: 234482.60 ⓘ				
Macromolecule Entities				
Molecule	Chains	Length	Organism	Details
Fusion Protein of Sec13 and Nup145C	A	876	Myceliophthora thermophila	Gene Name(s): MYCTH_2306744 MYCTH_2306912
Nup85	B	933	Myceliophthora thermophila	Gene Name(s): MYCTH_2059413
Nup120	C	313	Myceliophthora thermophila	Gene Name(s): MYCTH_2296711

Modified Residues 1 Unique					
ID	Chains	Type	Formula	2D Diagram	Parent
MSE	B	L-PEPTIDE LINKING	C ₅ H ₁₁ N O ₂ Se		MET

Experimental Data & Validation

Experimental Data

Method: X-RAY DIFFRACTION

Resolution: 4.1 Å

R-Value Free: 0.358

R-Value Work: 0.319

Space Group: **C 1 2 1**

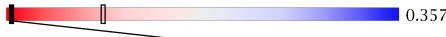
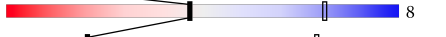
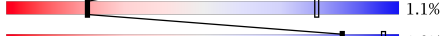
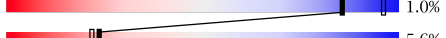

Diffraction Data DOI: 10.15785/SBGRID/175

Unit Cell:

Length (Å)	Angle (°)
a = 104.98	α = 90.00
b = 212.02	β = 107.21
c = 170.64	γ = 90.00

Structure Validation

View Full Validation Report or Ramachandran Plots

Metric	Percentile Ranks	Value
Rfree		0.357
Clashscore		8
Ramachandran outliers		1.1%
Sidechain outliers		1.0%
RSRZ outliers		5.6%

Worse

Better

■ Percentile relative to all X-ray structures

□ Percentile relative to X-ray structures of similar resolution

Entry History

Deposition Data

Deposited Date: 2015-02-20

Released Date: 2015-04-01

Deposition author(s): Kelley, K., Knockenhauer, K.E., Schwartz, T.U.

Revision History ⓘ

• 2015-05-27

Type: Citation | Details: Citation

• 2015-04-22

Type: Citation | Details: Citation

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