wwPDB EM Validation Summary Report (i)

May 4, 2024 – 06:11 pm BST

PDB ID	:	5NVS
EMDB ID	:	EMD-3703
Title	:	Human cytoplasmic dynein-1 tail in the twisted N-terminus state
Authors	:	Zhang, K.; Foster, H.E.; Carter, A.P.
Deposited on	:	2017-05-04
Resolution	:	8.40 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 8.40 Å.

There are no overall percentile quality scores available for this entry.

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition (i)

There are 13 unique types of molecules in this entry. The entry contains 20072 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called dynein heavy chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	932	4654	2790	932	932	0	0

- Molecule 2 is a protein called dynein intermediate chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	D	350	1723	1023	350	350	0	0
2	C	350	1723	1023	350	350	0	0

- Molecule 3 is a protein called dynein heavy chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	B	893	4459	2673	893	893	0	0

- Molecule 4 is a protein called dynein light intermediate chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	F	298	1496	890	303	303	5	0

- Molecule 5 is a protein called dynein light intermediate chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	E	295	1459	869	295	295	0	0

- Molecule 6 is a protein called N-terminal dimerization domain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	2	125	625	375	125	125	0	0

- Molecule 7 is a protein called N-terminal dimerization domain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	1	124	620	372	124	124	0	0

- Molecule 8 is a protein called LC8.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	I	85	421	251	85	85	0	0
8	J	85	421	251	85	85	0	0

- Molecule 9 is a protein called Tctex.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	K	103	507	301	103	103	0	0

- Molecule 10 is a protein called Tctex.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	L	104	513	305	104	104	0	0

- Molecule 11 is a protein called intermediate chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	M	27	134	80	27	27	0	0

- Molecule 12 is a protein called intermediate chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	N	29	143	85	29	29	0	0

- Molecule 13 is a protein called Robl.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	R	120	587	347	120	120	0	0
			Total	C	N	O		
13	S	120	587	347	120	120	0	0

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	187830	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	1.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

There are no ligands in this entry.

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	B	28
1	A	27
6	2	7
7	1	7
4	F	3
2	D	3
2	C	3
5	E	3

The worst 5 of 81 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1161:UNK	C	1190:UNK	N	65.65
1	B	1161:UNK	C	1190:UNK	N	65.10
1	A	1354:UNK	C	1356:UNK	N	52.82
1	B	1354:UNK	C	1356:UNK	N	52.47
1	A	1389:UNK	C	1391:UNK	N	50.96

5 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-3703. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections (i)

This section was not generated.

5.2 Central slices (i)

This section was not generated.

5.3 Largest variance slices (i)

This section was not generated.

5.4 Orthogonal standard-deviation projections (False-color) (i)

This section was not generated.

5.5 Orthogonal surface views (i)

This section was not generated.

5.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

6 Map analysis (i)

This section contains the results of statistical analysis of the map.

6.1 Map-value distribution (i)

This section was not generated.

6.2 Volume estimate versus contour level (i)

This section was not generated.

6.3 Rotationally averaged power spectrum (i)

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

7 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

8 Map-model fit (i)

This section was not generated.