



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 02:28 AM UTC

PDB ID : 8TO0 / pdb_00008to0
EMDB ID : EMD-41431
Title : 48-nm repeating structure of doublets from mouse sperm flagella
Authors : Chen, Z.; Shiozak, M.; Hass, K.M.; Skinner, W.; Zhao, S.; Guo, C.; Polacco, B.J.; Yu, Z.; Krogan, N.J.; Kaake, R.M.; Vale, R.D.; Agard, D.A.
Deposited on : 2023-08-02
Resolution : 7.70 Å(reported)

This is a Full wwPDB EM Validation 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.70 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 35 unique types of molecules in this entry. The entry contains 673884 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 Cilia- and flagella-associated protein 95.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	40	Total	C	N	O	0	0
			160	80	40	40		
1	7	113	Total	C	N	O	0	0
			452	226	113	113		

- Molecule 2 is a protein called Tektin-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	L	334	Total	C	N	O	0	0
			1336	668	334	334		
2	M	32	Total	C	N	O	0	0
			128	64	32	32		
2	I	222	Total	C	N	O	0	0
			888	444	222	222		
2	J	396	Total	C	N	O	0	0
			1584	792	396	396		
2	K	393	Total	C	N	O	0	0
			1572	786	393	393		

- Molecule 3 is a protein called Detyrosinated tubulin alpha-1A chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	N	438	Total	C	N	O	0	0
			1752	876	438	438		
3	P	440	Total	C	N	O	0	0
			1760	880	440	440		
3	R	435	Total	C	N	O	0	0
			1740	870	435	435		
3	T	440	Total	C	N	O	0	0
			1760	880	440	440		
3	V	440	Total	C	N	O	0	0
			1760	880	440	440		
3	X	440	Total	C	N	O	0	0
			1760	880	440	440		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	Z	439	Total	C	N	O	0	0
			1756	878	439	439		
3	n	430	Total	C	N	O	0	0
			1720	860	430	430		
3	p	440	Total	C	N	O	0	0
			1760	880	440	440		
3	r	433	Total	C	N	O	0	0
			1732	866	433	433		
3	t	440	Total	C	N	O	0	0
			1760	880	440	440		
3	v	430	Total	C	N	O	0	0
			1720	860	430	430		
3	x	439	Total	C	N	O	0	0
			1756	878	439	439		
3	z	430	Total	C	N	O	0	0
			1720	860	430	430		
3	BQ	425	Total	C	N	O	0	0
			1700	850	425	425		
3	BS	426	Total	C	N	O	0	0
			1704	852	426	426		
3	BU	427	Total	C	N	O	0	0
			1708	854	427	427		
3	BW	424	Total	C	N	O	0	0
			1696	848	424	424		
3	BY	429	Total	C	N	O	0	0
			1716	858	429	429		
3	AW	439	Total	C	N	O	0	0
			1756	878	439	439		
3	AY	439	Total	C	N	O	0	0
			1756	878	439	439		
3	Aj	399	Total	C	N	O	0	0
			1596	798	399	399		
3	Al	429	Total	C	N	O	0	0
			1716	858	429	429		
3	An	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Ap	431	Total	C	N	O	0	0
			1724	862	431	431		
3	Ar	429	Total	C	N	O	0	0
			1716	858	429	429		
3	At	430	Total	C	N	O	0	0
			1720	860	430	430		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	Av	430	Total	C	N	O	0	0
			1720	860	430	430		
3	A5	439	Total	C	N	O	0	0
			1756	878	439	439		
3	A7	441	Total	C	N	O	0	0
			1764	882	441	441		
3	A9	437	Total	C	N	O	0	0
			1748	874	437	437		
3	BA	436	Total	C	N	O	0	0
			1744	872	436	436		
3	BC	440	Total	C	N	O	0	0
			1760	880	440	440		
3	BE	428	Total	C	N	O	0	0
			1712	856	428	428		
3	BO	431	Total	C	N	O	0	0
			1724	862	431	431		
3	CX	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Cc	432	Total	C	N	O	0	0
			1728	864	432	432		
3	Ce	431	Total	C	N	O	0	0
			1724	862	431	431		
3	Cg	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Ci	428	Total	C	N	O	0	0
			1712	856	428	428		
3	Bc	440	Total	C	N	O	0	0
			1760	880	440	440		
3	Be	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Bg	440	Total	C	N	O	0	0
			1760	880	440	440		
3	Bi	429	Total	C	N	O	0	0
			1716	858	429	429		
3	Bk	429	Total	C	N	O	0	0
			1716	858	429	429		
3	Bm	439	Total	C	N	O	0	0
			1756	878	439	439		
3	Br	427	Total	C	N	O	0	0
			1708	854	427	427		
3	Bt	430	Total	C	N	O	0	0
			1720	860	430	430		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	Bv	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Bx	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Bz	431	Total	C	N	O	0	0
			1724	862	431	431		
3	B2	429	Total	C	N	O	0	0
			1716	858	429	429		
3	B4	386	Total	C	N	O	0	0
			1544	772	386	386		
3	B8	429	Total	C	N	O	0	0
			1716	858	429	429		
3	B0	432	Total	C	N	O	0	0
			1728	864	432	432		
3	CB	440	Total	C	N	O	0	0
			1760	880	440	440		
3	CD	432	Total	C	N	O	0	0
			1728	864	432	432		
3	CF	440	Total	C	N	O	0	0
			1760	880	440	440		
3	CH	431	Total	C	N	O	0	0
			1724	862	431	431		
3	CJ	427	Total	C	N	O	0	0
			1708	854	427	427		
3	CN	432	Total	C	N	O	0	0
			1728	864	432	432		
3	CP	430	Total	C	N	O	0	0
			1720	860	430	430		
3	CR	428	Total	C	N	O	0	0
			1712	856	428	428		
3	CT	429	Total	C	N	O	0	0
			1716	858	429	429		
3	CV	440	Total	C	N	O	0	0
			1760	880	440	440		
3	Dj	432	Total	C	N	O	0	0
			1728	864	432	432		
3	Dl	431	Total	C	N	O	0	0
			1724	862	431	431		
3	Dp	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Dr	432	Total	C	N	O	0	0
			1728	864	432	432		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	Ck	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Cm	432	Total	C	N	O	0	0
			1728	864	432	432		
3	Co	408	Total	C	N	O	0	0
			1632	816	408	408		
3	Cs	440	Total	C	N	O	0	0
			1760	880	440	440		
3	Cu	440	Total	C	N	O	0	0
			1760	880	440	440		
3	Cw	440	Total	C	N	O	0	0
			1760	880	440	440		
3	Cy	440	Total	C	N	O	0	0
			1760	880	440	440		
3	C1	440	Total	C	N	O	0	0
			1760	880	440	440		
3	C3	431	Total	C	N	O	0	0
			1724	862	431	431		
3	C8	439	Total	C	N	O	0	0
			1756	878	439	439		
3	C0	429	Total	C	N	O	0	0
			1716	858	429	429		
3	DB	430	Total	C	N	O	0	0
			1720	860	430	430		
3	DD	431	Total	C	N	O	0	0
			1724	862	431	431		
3	DF	440	Total	C	N	O	0	0
			1760	880	440	440		
3	DH	431	Total	C	N	O	0	0
			1724	862	431	431		
3	DM	430	Total	C	N	O	0	0
			1720	860	430	430		
3	DO	429	Total	C	N	O	0	0
			1716	858	429	429		
3	DQ	430	Total	C	N	O	0	0
			1720	860	430	430		
3	DS	432	Total	C	N	O	0	0
			1728	864	432	432		
3	DU	432	Total	C	N	O	0	0
			1728	864	432	432		
3	DW	430	Total	C	N	O	0	0
			1720	860	430	430		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	Db	428	Total	C	N	O	0	0
			1712	856	428	428		
3	Dd	429	Total	C	N	O	0	0
			1716	858	429	429		
3	Df	433	Total	C	N	O	0	0
			1732	866	433	433		
3	Dh	433	Total	C	N	O	0	0
			1732	866	433	433		
3	Es	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Eu	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Ew	432	Total	C	N	O	0	0
			1728	864	432	432		
3	Ey	430	Total	C	N	O	0	0
			1720	860	430	430		
3	E3	433	Total	C	N	O	0	0
			1732	866	433	433		
3	Dt	431	Total	C	N	O	0	0
			1724	862	431	431		
3	Dv	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Dx	427	Total	C	N	O	0	0
			1708	854	427	427		
3	Dz	430	Total	C	N	O	0	0
			1720	860	430	430		
3	D2	430	Total	C	N	O	0	0
			1720	860	430	430		
3	D5	431	Total	C	N	O	0	0
			1724	862	431	431		
3	D7	430	Total	C	N	O	0	0
			1720	860	430	430		
3	D9	430	Total	C	N	O	0	0
			1720	860	430	430		
3	EA	431	Total	C	N	O	0	0
			1724	862	431	431		
3	EC	429	Total	C	N	O	0	0
			1716	858	429	429		
3	EE	431	Total	C	N	O	0	0
			1724	862	431	431		
3	EG	431	Total	C	N	O	0	0
			1724	862	431	431		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	EJ	429	Total	C	N	O	0	0
			1716	858	429	429		
3	EL	432	Total	C	N	O	0	0
			1728	864	432	432		
3	EN	428	Total	C	N	O	0	0
			1712	856	428	428		
3	EP	430	Total	C	N	O	0	0
			1720	860	430	430		
3	ER	431	Total	C	N	O	0	0
			1724	862	431	431		
3	ET	431	Total	C	N	O	0	0
			1724	862	431	431		
3	EV	428	Total	C	N	O	0	0
			1712	856	428	428		
3	EY	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Ea	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Ec	431	Total	C	N	O	0	0
			1724	862	431	431		
3	Ee	431	Total	C	N	O	0	0
			1724	862	431	431		
3	Eg	427	Total	C	N	O	0	0
			1708	854	427	427		
3	Ei	432	Total	C	N	O	0	0
			1728	864	432	432		
3	Ek	431	Total	C	N	O	0	0
			1724	862	431	431		
3	Eo	430	Total	C	N	O	0	0
			1720	860	430	430		
3	Eq	432	Total	C	N	O	0	0
			1728	864	432	432		
3	E5	432	Total	C	N	O	0	0
			1728	864	432	432		
3	AM	438	Total	C	N	O	0	0
			1752	876	438	438		
3	E7	433	Total	C	N	O	0	0
			1732	866	433	433		
3	E9	433	Total	C	N	O	0	0
			1732	866	433	433		
3	FA	433	Total	C	N	O	0	0
			1732	866	433	433		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	FC	431	Total	C	N	O	0	0
			1724	862	431	431		
3	FG	440	Total	C	N	O	0	0
			1760	880	440	440		
3	FI	433	Total	C	N	O	0	0
			1732	866	433	433		
3	FK	440	Total	C	N	O	0	0
			1760	880	440	440		
3	FM	433	Total	C	N	O	0	0
			1732	866	433	433		
3	FO	440	Total	C	N	O	0	0
			1760	880	440	440		
3	FQ	430	Total	C	N	O	0	0
			1720	860	430	430		
3	FU	440	Total	C	N	O	0	0
			1760	880	440	440		
3	FW	431	Total	C	N	O	0	0
			1724	862	431	431		
3	FY	439	Total	C	N	O	0	0
			1756	878	439	439		
3	Fa	431	Total	C	N	O	0	0
			1724	862	431	431		
3	Fc	438	Total	C	N	O	0	0
			1752	876	438	438		
3	Fe	431	Total	C	N	O	0	0
			1724	862	431	431		
3	AO	438	Total	C	N	O	0	0
			1752	876	438	438		
3	AQ	438	Total	C	N	O	0	0
			1752	876	438	438		
3	AS	439	Total	C	N	O	0	0
			1756	878	439	439		
3	AU	439	Total	C	N	O	0	0
			1756	878	439	439		

- Molecule 4 is a protein called Tubulin beta-4B chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	O	436	Total	C	N	O	0	0
			1744	872	436	436		
4	Q	436	Total	C	N	O	0	0
			1744	872	436	436		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	S	436	Total	C	N	O	0	0
			1744	872	436	436		
4	U	436	Total	C	N	O	0	0
			1744	872	436	436		
4	W	436	Total	C	N	O	0	0
			1744	872	436	436		
4	Y	435	Total	C	N	O	0	0
			1740	870	435	435		
4	o	427	Total	C	N	O	0	0
			1708	854	427	427		
4	q	427	Total	C	N	O	0	0
			1708	854	427	427		
4	s	427	Total	C	N	O	0	0
			1708	854	427	427		
4	u	427	Total	C	N	O	0	0
			1708	854	427	427		
4	w	427	Total	C	N	O	0	0
			1708	854	427	427		
4	y	425	Total	C	N	O	0	0
			1700	850	425	425		
4	BR	426	Total	C	N	O	0	0
			1704	852	426	426		
4	BT	426	Total	C	N	O	0	0
			1704	852	426	426		
4	BV	426	Total	C	N	O	0	0
			1704	852	426	426		
4	BX	425	Total	C	N	O	0	0
			1700	850	425	425		
4	BZ	427	Total	C	N	O	0	0
			1708	854	427	427		
4	AV	427	Total	C	N	O	0	0
			1708	854	427	427		
4	AX	425	Total	C	N	O	0	0
			1700	850	425	425		
4	Ak	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Am	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Ao	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Aq	426	Total	C	N	O	0	0
			1704	852	426	426		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	As	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Au	425	Total	C	N	O	0	0
			1700	850	425	425		
4	Aw	387	Total	C	N	O	0	0
			1548	774	387	387		
4	A4	426	Total	C	N	O	0	0
			1704	852	426	426		
4	A6	426	Total	C	N	O	0	0
			1704	852	426	426		
4	A8	426	Total	C	N	O	0	0
			1704	852	426	426		
4	A0	427	Total	C	N	O	0	0
			1708	854	427	427		
4	BB	426	Total	C	N	O	0	0
			1704	852	426	426		
4	BD	425	Total	C	N	O	0	0
			1700	850	425	425		
4	BF	426	Total	C	N	O	0	0
			1704	852	426	426		
4	BN	426	Total	C	N	O	0	0
			1704	852	426	426		
4	BP	427	Total	C	N	O	0	0
			1708	854	427	427		
4	CY	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Cb	403	Total	C	N	O	0	0
			1612	806	403	403		
4	Cd	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Cf	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Ch	429	Total	C	N	O	0	0
			1716	858	429	429		
4	Bb	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Bd	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Bf	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Bh	427	Total	C	N	O	0	0
			1708	854	427	427		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	Bj	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Bl	425	Total	C	N	O	0	0
			1700	850	425	425		
4	Bn	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Bs	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Bu	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Bw	427	Total	C	N	O	0	0
			1708	854	427	427		
4	By	427	Total	C	N	O	0	0
			1708	854	427	427		
4	B1	425	Total	C	N	O	0	0
			1700	850	425	425		
4	B3	427	Total	C	N	O	0	0
			1708	854	427	427		
4	B7	369	Total	C	N	O	0	0
			1476	738	369	369		
4	B9	427	Total	C	N	O	0	0
			1708	854	427	427		
4	CA	427	Total	C	N	O	0	0
			1708	854	427	427		
4	CC	427	Total	C	N	O	0	0
			1708	854	427	427		
4	CE	427	Total	C	N	O	0	0
			1708	854	427	427		
4	CG	426	Total	C	N	O	0	0
			1704	852	426	426		
4	CI	428	Total	C	N	O	0	0
			1712	856	428	428		
4	CM	426	Total	C	N	O	0	0
			1704	852	426	426		
4	CO	427	Total	C	N	O	0	0
			1708	854	427	427		
4	CQ	426	Total	C	N	O	0	0
			1704	852	426	426		
4	CS	426	Total	C	N	O	0	0
			1704	852	426	426		
4	CU	426	Total	C	N	O	0	0
			1704	852	426	426		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	CW	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Di	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Dk	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Dm	424	Total	C	N	O	0	0
			1696	848	424	424		
4	Dq	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Ds	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Cj	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Cl	429	Total	C	N	O	0	0
			1716	858	429	429		
4	Cn	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Cr	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Ct	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Cv	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Cx	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Cz	427	Total	C	N	O	0	0
			1708	854	427	427		
4	C2	426	Total	C	N	O	0	0
			1704	852	426	426		
4	C4	427	Total	C	N	O	0	0
			1708	854	427	427		
4	C7	426	Total	C	N	O	0	0
			1704	852	426	426		
4	C9	426	Total	C	N	O	0	0
			1704	852	426	426		
4	DA	427	Total	C	N	O	0	0
			1708	854	427	427		
4	DC	427	Total	C	N	O	0	0
			1708	854	427	427		
4	DE	426	Total	C	N	O	0	0
			1704	852	426	426		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	DG	426	Total	C	N	O	0	0
			1704	852	426	426		
4	DI	426	Total	C	N	O	0	0
			1704	852	426	426		
4	DL	427	Total	C	N	O	0	0
			1708	854	427	427		
4	DN	427	Total	C	N	O	0	0
			1708	854	427	427		
4	DP	427	Total	C	N	O	0	0
			1708	854	427	427		
4	DR	427	Total	C	N	O	0	0
			1708	854	427	427		
4	DT	427	Total	C	N	O	0	0
			1708	854	427	427		
4	DV	427	Total	C	N	O	0	0
			1708	854	427	427		
4	DX	425	Total	C	N	O	0	0
			1700	850	425	425		
4	Dc	425	Total	C	N	O	0	0
			1700	850	425	425		
4	De	424	Total	C	N	O	0	0
			1696	848	424	424		
4	Dg	425	Total	C	N	O	0	0
			1700	850	425	425		
4	Er	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Et	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Ev	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Ex	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Du	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Dw	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Dy	427	Total	C	N	O	0	0
			1708	854	427	427		
4	D1	425	Total	C	N	O	0	0
			1700	850	425	425		
4	D6	427	Total	C	N	O	0	0
			1708	854	427	427		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	D8	427	Total	C	N	O	0	0
			1708	854	427	427		
4	D0	428	Total	C	N	O	0	0
			1712	856	428	428		
4	EB	427	Total	C	N	O	0	0
			1708	854	427	427		
4	ED	427	Total	C	N	O	0	0
			1708	854	427	427		
4	EF	426	Total	C	N	O	0	0
			1704	852	426	426		
4	EK	427	Total	C	N	O	0	0
			1708	854	427	427		
4	EM	427	Total	C	N	O	0	0
			1708	854	427	427		
4	EO	427	Total	C	N	O	0	0
			1708	854	427	427		
4	EQ	427	Total	C	N	O	0	0
			1708	854	427	427		
4	ES	427	Total	C	N	O	0	0
			1708	854	427	427		
4	EU	426	Total	C	N	O	0	0
			1704	852	426	426		
4	EZ	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Eb	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Ed	428	Total	C	N	O	0	0
			1712	856	428	428		
4	Ef	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Eh	427	Total	C	N	O	0	0
			1708	854	427	427		
4	Ej	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Ep	427	Total	C	N	O	0	0
			1708	854	427	427		
4	E4	427	Total	C	N	O	0	0
			1708	854	427	427		
4	E6	427	Total	C	N	O	0	0
			1708	854	427	427		
4	E8	428	Total	C	N	O	0	0
			1712	856	428	428		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	E0	427	Total	C	N	O	0	0
			1708	854	427	427		
4	FB	426	Total	C	N	O	0	0
			1704	852	426	426		
4	FD	427	Total	C	N	O	0	0
			1708	854	427	427		
4	FH	427	Total	C	N	O	0	0
			1708	854	427	427		
4	FJ	427	Total	C	N	O	0	0
			1708	854	427	427		
4	FL	427	Total	C	N	O	0	0
			1708	854	427	427		
4	FN	427	Total	C	N	O	0	0
			1708	854	427	427		
4	FP	426	Total	C	N	O	0	0
			1704	852	426	426		
4	FR	427	Total	C	N	O	0	0
			1708	854	427	427		
4	FV	427	Total	C	N	O	0	0
			1708	854	427	427		
4	FX	426	Total	C	N	O	0	0
			1704	852	426	426		
4	AN	426	Total	C	N	O	0	0
			1704	852	426	426		
4	FZ	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Fb	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Fd	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Ff	426	Total	C	N	O	0	0
			1704	852	426	426		
4	AP	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Bq	426	Total	C	N	O	0	0
			1704	852	426	426		
4	Da	411	Total	C	N	O	0	0
			1644	822	411	411		
4	En	427	Total	C	N	O	0	0
			1708	854	427	427		
4	E2	428	Total	C	N	O	0	0
			1712	856	428	428		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	FF	427	Total	C	N	O	0	0
			1708	854	427	427		
4	FT	427	Total	C	N	O	0	0
			1708	854	427	427		
4	AR	427	Total	C	N	O	0	0
			1708	854	427	427		
4	AT	427	Total	C	N	O	0	0
			1708	854	427	427		

- Molecule 5 is a protein called Tektin-2.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	b	191	Total	C	N	O	0	0
			764	382	191	191		
5	e	416	Total	C	N	O	0	0
			1664	832	416	416		
5	f	416	Total	C	N	O	0	0
			1664	832	416	416		
5	g	383	Total	C	N	O	0	0
			1532	766	383	383		
5	h	48	Total	C	N	O	0	0
			192	96	48	48		
5	i	51	Total	C	N	O	0	0
			204	102	51	51		
5	j	358	Total	C	N	O	0	0
			1432	716	358	358		
5	k	414	Total	C	N	O	0	0
			1656	828	414	414		
5	l	403	Total	C	N	O	0	0
			1612	806	403	403		
5	m	191	Total	C	N	O	0	0
			764	382	191	191		

- Molecule 6 is a protein called EF-hand domain-containing family member B.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	1	141	Total	C	N	O	0	0
			564	282	141	141		
6	2	190	Total	C	N	O	0	0
			760	380	190	190		

- Molecule 7 is a protein called Tektin-3.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	AC	31	Total	C	N	O	0	0
			124	62	31	31		
7	AD	334	Total	C	N	O	0	0
			1336	668	334	334		
7	AE	394	Total	C	N	O	0	0
			1576	788	394	394		
7	AF	394	Total	C	N	O	0	0
			1576	788	394	394		
7	AG	215	Total	C	N	O	0	0
			860	430	215	215		
7	AH	113	Total	C	N	O	0	0
			452	226	113	113		
7	AI	385	Total	C	N	O	0	0
			1540	770	385	385		
7	AJ	413	Total	C	N	O	0	0
			1652	826	413	413		
7	AK	407	Total	C	N	O	0	0
			1628	814	407	407		
7	BI	139	Total	C	N	O	0	0
			556	278	139	139		
7	BJ	421	Total	C	N	O	0	0
			1684	842	421	421		
7	BK	421	Total	C	N	O	0	0
			1684	842	421	421		
7	BL	378	Total	C	N	O	0	0
			1512	756	378	378		
7	BM	99	Total	C	N	O	0	0
			396	198	99	99		
7	AL	112	Total	C	N	O	0	0
			448	224	112	112		

- Molecule 8 is a protein called Meiosis-specific nuclear structural protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	a	354	Total	C	N	O	0	0
			1416	708	354	354		
8	A	170	Total	C	N	O	0	0
			680	340	170	170		

- Molecule 9 is a protein called Tektin-4.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	Aa	292	Total	C	N	O	0	0
			1168	584	292	292		

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Mol	Chain	Residues	Atoms				AltConf	Trace
9	Ab	425	Total	C	N	O	0	0
			1700	850	425	425		
9	Ac	425	Total	C	N	O	0	0
			1700	850	425	425		
9	Ad	316	Total	C	N	O	0	0
			1264	632	316	316		
9	Af	314	Total	C	N	O	0	0
			1256	628	314	314		
9	Ag	414	Total	C	N	O	0	0
			1656	828	414	414		
9	Ah	413	Total	C	N	O	0	0
			1652	826	413	413		
9	Ai	291	Total	C	N	O	0	0
			1164	582	291	291		

- Molecule 10 is a protein called Cilia- and flagella-associated protein 53.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	3	306	Total	C	N	O	0	0
			1224	612	306	306		
10	4	201	Total	C	N	O	0	0
			804	402	201	201		

- Molecule 11 is a protein called Tektin bundle-interacting protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	Az	68	Total	C	N	O	0	0
			272	136	68	68		
11	A1	127	Total	C	N	O	0	0
			508	254	127	127		
11	A2	144	Total	C	N	O	0	0
			576	288	144	144		
11	A3	144	Total	C	N	O	0	0
			576	288	144	144		

- Molecule 12 is a protein called Cilia- and flagella-associated protein 141.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	AB	87	Total	C	N	O	0	0
			348	174	87	87		

- Molecule 13 is a protein called Nucleoside diphosphate kinase 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	5	358	Total	C	N	O	0	0
			1432	716	358	358		
13	6	358	Total	C	N	O	0	0
			1432	716	358	358		

- Molecule 14 is a protein called Protein FAM166B.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	B6	152	Total	C	N	O	0	0
			608	304	152	152		
14	CL	152	Total	C	N	O	0	0
			608	304	152	152		
14	Ca	152	Total	C	N	O	0	0
			608	304	152	152		
14	Cq	152	Total	C	N	O	0	0
			608	304	152	152		
14	C6	152	Total	C	N	O	0	0
			608	304	152	152		
14	DK	155	Total	C	N	O	0	0
			620	310	155	155		

- Molecule 15 is a protein called Sperm-associated antigen 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	AZ	147	Total	C	N	O	0	0
			588	294	147	147		

- Molecule 16 is a protein called RIB43A-like with coiled-coils protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	Do	373	Total	C	N	O	0	0
			1492	746	373	373		
16	DZ	33	Total	C	N	O	0	0
			132	66	33	33		
16	D4	39	Total	C	N	O	0	0
			156	78	39	39		
16	EI	222	Total	C	N	O	0	0
			888	444	222	222		
16	EX	170	Total	C	N	O	0	0
			680	340	170	170		

- Molecule 17 is a protein called Cilia- and flagella-associated protein 107.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	8	188	Total	C	N	O	0	0
			752	376	188	188		
17	9	32	Total	C	N	O	0	0
			128	64	32	32		

- Molecule 18 is a protein called Cilia- and flagella-associated protein 161.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Ay	251	Total	C	N	O	0	0
			1004	502	251	251		
18	BH	251	Total	C	N	O	0	0
			1004	502	251	251		

- Molecule 19 is a protein called EF-hand domain-containing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	E1	442	Total	C	N	O	0	0
			1768	884	442	442		
19	Em	442	Total	C	N	O	0	0
			1768	884	442	442		
19	FE	442	Total	C	N	O	0	0
			1768	884	442	442		

- Molecule 20 is a protein called Sperm acrosome-associated protein 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	F1	150	Total	C	N	O	0	0
			600	300	150	150		
20	F2	150	Total	C	N	O	0	0
			600	300	150	150		
20	F3	150	Total	C	N	O	0	0
			600	300	150	150		
20	F4	150	Total	C	N	O	0	0
			600	300	150	150		
20	F5	150	Total	C	N	O	0	0
			600	300	150	150		
20	F6	150	Total	C	N	O	0	0
			600	300	150	150		
20	F7	149	Total	C	N	O	0	0
			596	298	149	149		
20	F8	150	Total	C	N	O	0	0
			600	300	150	150		

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Mol	Chain	Residues	Atoms				AltConf	Trace
20	F9	150	Total 600	C 300	N 150	O 150	0	0
20	F0	150	Total 600	C 300	N 150	O 150	0	0
20	GA	148	Total 592	C 296	N 148	O 148	0	0
20	GB	150	Total 600	C 300	N 150	O 150	0	0
20	GC	150	Total 600	C 300	N 150	O 150	0	0
20	GD	148	Total 592	C 296	N 148	O 148	0	0
20	GE	150	Total 600	C 300	N 150	O 150	0	0
20	GF	146	Total 584	C 292	N 146	O 146	0	0
20	GG	145	Total 580	C 290	N 145	O 145	0	0
20	GH	150	Total 600	C 300	N 150	O 150	0	0
20	GI	150	Total 600	C 300	N 150	O 150	0	0
20	GJ	149	Total 596	C 298	N 149	O 149	0	0
20	GK	149	Total 596	C 298	N 149	O 149	0	0
20	GL	150	Total 600	C 300	N 150	O 150	0	0
20	GM	150	Total 600	C 300	N 150	O 150	0	0
20	GN	150	Total 600	C 300	N 150	O 150	0	0
20	GO	149	Total 596	C 298	N 149	O 149	0	0
20	GP	149	Total 596	C 298	N 149	O 149	0	0
20	GQ	152	Total 608	C 304	N 152	O 152	0	0

- Molecule 21 is a protein called EF-hand domain-containing family member C2.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Fg	636	Total	C	N	O	0	0
			2544	1272	636	636		
21	FS	553	Total	C	N	O	0	0
			2212	1106	553	553		
21	Fo	636	Total	C	N	O	0	0
			2544	1272	636	636		
21	Fv	449	Total	C	N	O	0	0
			1796	898	449	449		

- Molecule 22 is a protein called Cilia- and flagella-associated protein 20.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	Fh	184	Total	C	N	O	0	0
			736	368	184	184		
22	Fi	184	Total	C	N	O	0	0
			736	368	184	184		
22	Fj	184	Total	C	N	O	0	0
			736	368	184	184		
22	Fk	184	Total	C	N	O	0	0
			736	368	184	184		
22	Fl	184	Total	C	N	O	0	0
			736	368	184	184		
22	Fm	184	Total	C	N	O	0	0
			736	368	184	184		
22	Fn	184	Total	C	N	O	0	0
			736	368	184	184		

- Molecule 23 is a protein called Parkin coregulated gene protein homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	Fp	219	Total	C	N	O	0	0
			876	438	219	219		
23	Fq	219	Total	C	N	O	0	0
			876	438	219	219		
23	Fr	219	Total	C	N	O	0	0
			876	438	219	219		
23	Fs	219	Total	C	N	O	0	0
			876	438	219	219		
23	Ft	219	Total	C	N	O	0	0
			876	438	219	219		

- Molecule 24 is a protein called Dual specificity protein phosphatase 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Fx	185	Total	C	N	O	0	0
			740	370	185	185		
24	Fy	185	Total	C	N	O	0	0
			740	370	185	185		
24	Fz	185	Total	C	N	O	0	0
			740	370	185	185		

- Molecule 25 is a protein called Piercer of microtubule wall 2 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	G	71	Total	C	N	O	0	0
			284	142	71	71		

- Molecule 26 is a protein called Tektin-5.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	GR	274	Total	C	N	O	0	0
			1096	548	274	274		
26	GS	274	Total	C	N	O	0	0
			1096	548	274	274		
26	GT	274	Total	C	N	O	0	0
			1096	548	274	274		
26	GU	171	Total	C	N	O	0	0
			684	342	171	171		
26	GV	244	Total	C	N	O	0	0
			976	488	244	244		
26	GW	349	Total	C	N	O	0	0
			1396	698	349	349		
26	GX	346	Total	C	N	O	0	0
			1384	692	346	346		
26	GY	288	Total	C	N	O	0	0
			1152	576	288	288		
26	GZ	23	Total	C	N	O	0	0
			92	46	23	23		
26	Ga	114	Total	C	N	O	0	0
			456	228	114	114		
26	Gb	342	Total	C	N	O	0	0
			1368	684	342	342		
26	Gc	333	Total	C	N	O	0	0
			1332	666	333	333		
26	Gd	327	Total	C	N	O	0	0
			1308	654	327	327		
26	Ge	58	Total	C	N	O	0	0
			232	116	58	58		

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Mol	Chain	Residues	Atoms				AltConf	Trace
26	z0	270	Total	C	N	O	0	0
			1080	540	270	270		
26	z1	268	Total	C	N	O	0	0
			1072	536	268	268		
26	z3	254	Total	C	N	O	0	0
			1016	508	254	254		
26	z4	184	Total	C	N	O	0	0
			736	368	184	184		
26	Gf	29	Total	C	N	O	0	0
			116	58	29	29		
26	Gg	292	Total	C	N	O	0	0
			1168	584	292	292		
26	Gh	320	Total	C	N	O	0	0
			1280	640	320	320		
26	Gi	321	Total	C	N	O	0	0
			1284	642	321	321		
26	Gj	190	Total	C	N	O	0	0
			760	380	190	190		

- Molecule 27 is a protein called Cilia- and flagella-associated protein 45.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	B	57	Total	C	N	O	0	0
			228	114	57	57		
27	AA	327	Total	C	N	O	0	0
			1308	654	327	327		
27	c	48	Total	C	N	O	0	0
			192	96	48	48		
27	Ax	215	Total	C	N	O	0	0
			860	430	215	215		
27	d	238	Total	C	N	O	0	0
			952	476	238	238		

- Molecule 28 is a protein called Cilia- and flagella-associated protein 52.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	BG	605	Total	C	N	O	0	0
			2420	1210	605	605		
28	Ba	605	Total	C	N	O	0	0
			2420	1210	605	605		
28	Bo	605	Total	C	N	O	0	0
			2420	1210	605	605		

- Molecule 29 is a protein called Enkurin.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	B5	142	Total	C	N	O	0	0
			568	284	142	142		
29	CK	229	Total	C	N	O	0	0
			916	458	229	229		
29	CZ	229	Total	C	N	O	0	0
			916	458	229	229		
29	Cp	229	Total	C	N	O	0	0
			916	458	229	229		

- Molecule 30 is a protein called Protein Flattop.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	C5	114	Total	C	N	O	0	0
			456	228	114	114		
30	DJ	113	Total	C	N	O	0	0
			452	226	113	113		
30	DY	118	Total	C	N	O	0	0
			472	236	118	118		

- Molecule 31 is a protein called Cilia- and flagella- associated protein 210.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	Dn	378	Total	C	N	O	0	0
			1512	756	378	378		
31	D3	100	Total	C	N	O	0	0
			400	200	100	100		

- Molecule 32 is a protein called Cilia- and flagella-associated protein 276.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	EH	77	Total	C	N	O	0	0
			308	154	77	77		
32	EW	77	Total	C	N	O	0	0
			308	154	77	77		
32	El	79	Total	C	N	O	0	0
			316	158	79	79		

- Molecule 33 is a protein called EF-hand calcium-binding domain-containing protein 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Ez	178	Total	C	N	O	0	0
			712	356	178	178		

- Molecule 34 is a protein called Coiled-coil domain-containing protein 105.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	C	173	Total	C	N	O	0	0
			692	346	173	173		
34	D	302	Total	C	N	O	0	0
			1208	604	302	302		
34	E	302	Total	C	N	O	0	0
			1208	604	302	302		
34	F	282	Total	C	N	O	0	0
			1128	564	282	282		
34	H	9	Total	C	N	O	0	0
			36	18	9	9		

- Molecule 35 is a protein called Piercer of microtubule wall 1 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	Fw	76	Total	C	N	O	0	0
			304	152	76	76		

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

3 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	12848	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 ($e^-/\text{\AA}^2$)	100	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	6000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k 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 oligosaccharides 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

There are no chain breaks in this entry.

5 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-41431. 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 ⓘ

This section was not generated.

5.2 Central slices ⓘ

This section was not generated.

5.3 Largest variance slices ⓘ

This section was not generated.

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

This section was not generated.

5.5 Orthogonal surface views ⓘ

This section was not generated.

5.6 Mask visualisation ⓘ

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

6 Map analysis ⓘ

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

6.1 Map-value distribution ⓘ

This section was not generated.

6.2 Volume estimate versus contour level ⓘ

This section was not generated.

6.3 Rotationally averaged power spectrum ⓘ

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

7 Fourier-Shell correlation ⓘ

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

8 Map-model fit

This section was not generated.