



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 09:21 PM UTC

PDB ID : 5ADX / pdb_00005adx
EMDB ID : EMD-2856
Title : CryoEM structure of dynactin complex at 4.0 angstrom resolution
Authors : Zhang, K.; Urnavicius, L.; Diamant, A.G.; Motz, C.; Schlage, M.A.; Yu, M.;
Patel, N.A.; Robinson, C.V.; Carter, A.P.
Deposited on : 2015-08-24
Resolution : 4.00 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 ⓘ 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:

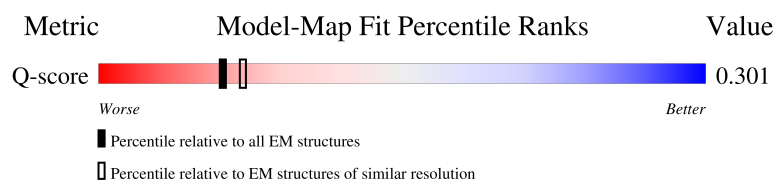
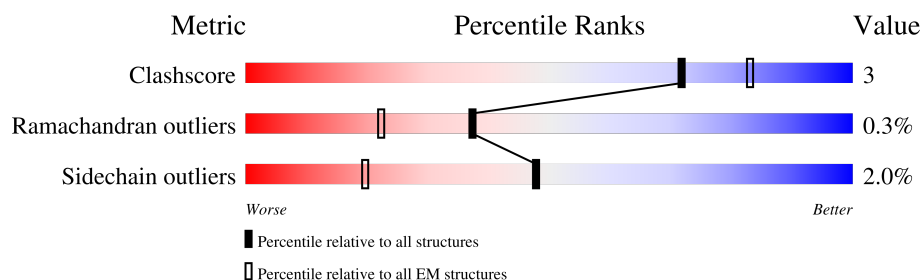
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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

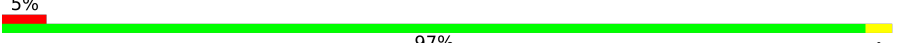
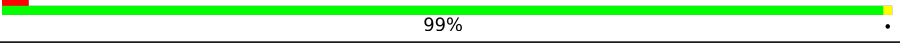
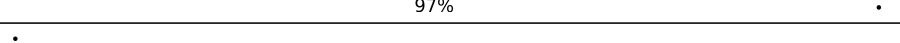
The reported resolution of this entry is 4.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



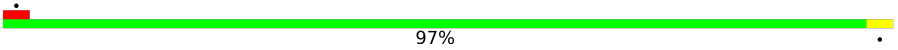
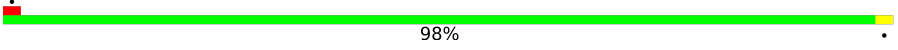
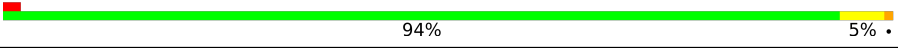
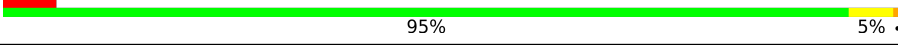
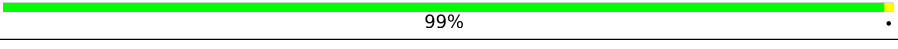
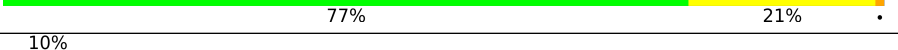
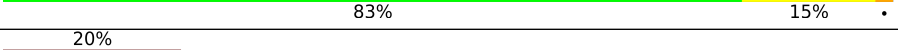
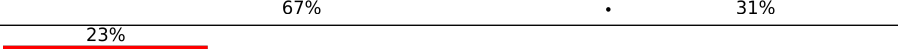
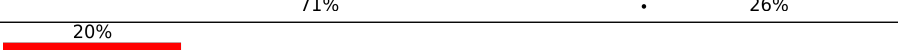
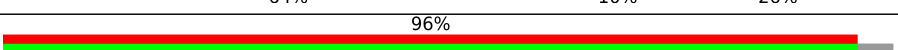
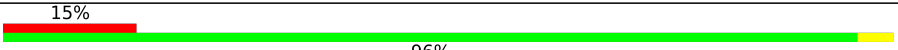
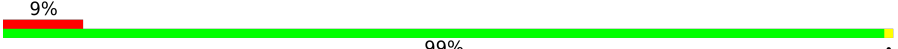
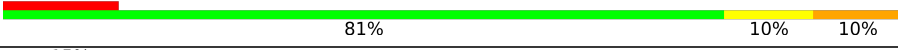
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7587 (3.50 - 4.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	370	 5% 97%
1	B	370	 1% 99%
1	C	370	 1% 97%
1	D	370	 1% 98%

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Mol	Chain	Length	Quality of chain
1	E	370	
1	F	370	
1	G	370	
1	I	370	
2	H	370	
3	J	417	
4	K	275	
5	L	270	
6	M	824	
7	N	818	
8	O	88	
8	P	88	
9	Q	91	
9	R	91	
10	U	190	
11	V	165	
12	Y	243	
13	Z	419	
13	z	419	
14	a	48	
15	b	71	
16	c	31	
17	d	20	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 49392 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 ACTIN RELATED PROTEIN 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	370	Total	C	N	O	S	0	0
			2957	1893	509	545	10		
1	B	370	Total	C	N	O	S	0	0
			2957	1893	509	545	10		
1	C	370	Total	C	N	O	S	0	0
			2957	1893	509	545	10		
1	D	370	Total	C	N	O	S	0	0
			2957	1893	509	545	10		
1	E	370	Total	C	N	O	S	0	0
			2957	1893	509	545	10		
1	F	370	Total	C	N	O	S	0	0
			2957	1893	509	545	10		
1	G	370	Total	C	N	O	S	0	0
			2957	1893	509	545	10		
1	I	370	Total	C	N	O	S	0	0
			2957	1893	509	545	10		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	97	GLU	ASP	conflict	UNP F2Z5G5
B	97	GLU	ASP	conflict	UNP F2Z5G5
C	97	GLU	ASP	conflict	UNP F2Z5G5
D	97	GLU	ASP	conflict	UNP F2Z5G5
E	97	GLU	ASP	conflict	UNP F2Z5G5
F	97	GLU	ASP	conflict	UNP F2Z5G5
G	97	GLU	ASP	conflict	UNP F2Z5G5
I	97	GLU	ASP	conflict	UNP F2Z5G5

- Molecule 2 is a protein called ACTIN, CYTOPLASMIC 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	370	Total	C	N	O	S	0	0
			2885	1827	486	550	22		

- Molecule 3 is a protein called ACTIN RELATED PROTEIN 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	369	Total	C	N	O	S	0	0
			2879	1857	486	520	16		

- Molecule 4 is a protein called CAPPING PROTEIN (ACTIN FILAMENT) MUSCLE Z-LINE, ALPHA 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	275	Total	C	N	O	S	0	0
			2242	1415	393	429	5		

- Molecule 5 is a protein called F-ACTIN CAPPING PROTEIN BETA SUBUNIT VARIANT II.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	270	Total	C	N	O	S	0	0
			2137	1333	373	420	11		

- Molecule 6 is a protein called DYNAMACTIN SUBUNIT 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	M	571	Total	C	N	O	0	0
			2855	1713	571	571		

- Molecule 7 is a protein called DYNAMACTIN SUBUNIT 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	N	602	Total	C	N	O	0	0
			3010	1806	602	602		

- Molecule 8 is a protein called DYNAMACTIN SUBUNIT 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	O	65	Total	C	N	O	0	0
			323	193	65	65		
8	P	65	Total	C	N	O	0	0
			323	193	65	65		

- Molecule 9 is a protein called DYNAMACTIN SUBUNIT 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	Q	87	Total	C	N	O	0	0
			435	261	87	87		
9	R	87	Total	C	N	O	0	0
			435	261	87	87		

- Molecule 10 is a protein called DYNAMACTIN 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	U	169	Total	C	N	O	0	0
			831	493	169	169		

- Molecule 11 is a protein called DYNAMACTIN SUBUNIT 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	V	165	Total	C	N	O	0	0
			812	482	165	165		

- Molecule 12 is a protein called DYNAMACTIN SUBUNIT 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	Y	243	Total	C	N	O	0	0
			1215	729	243	243		

- Molecule 13 is a protein called DYNAMACTIN SUBUNIT 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	Z	419	Total	C	N	O	0	0
			2095	1257	419	419		
13	z	419	Total	C	N	O	0	0
			2095	1257	419	419		

- Molecule 14 is a protein called DYNAMACTIN SUBUNIT 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	a	48	Total	C	N	O	S	0	0
			341	216	58	66	1		

- Molecule 15 is a protein called DYNAMACTIN SUBUNIT 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	b	71	Total	C	N	O	S	0	0
			517	324	93	99	1		

- Molecule 16 is a protein called DYNACTIN SUBUNIT 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	c	31	Total	C	N	O	S	0	0
			179	112	34	32	1		

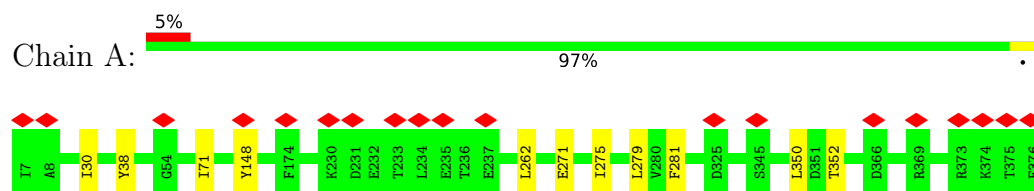
- Molecule 17 is a protein called DYNACTIN SUBUNIT 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	d	20	Total	C	N	O	S	0	0
			127	80	23	23	1		

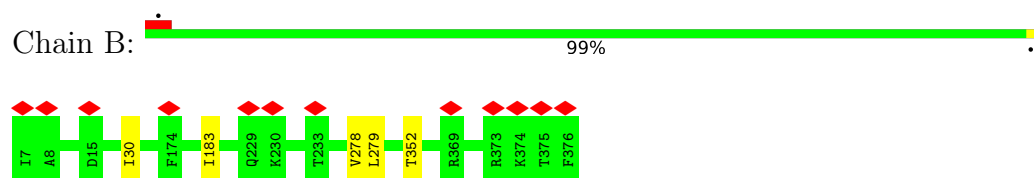
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

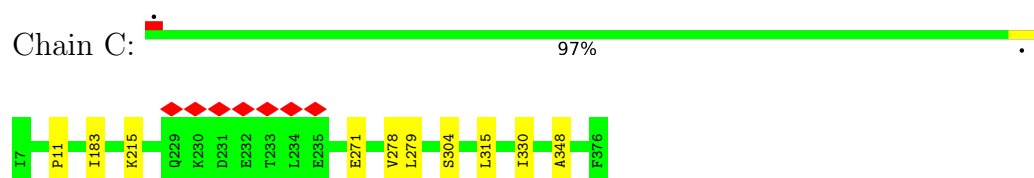
- Molecule 1: ACTIN RELATED PROTEIN 1



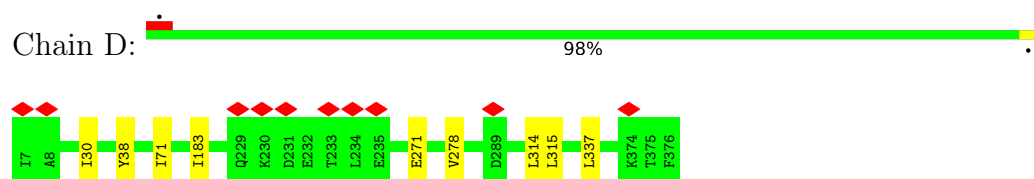
- Molecule 1: ACTIN RELATED PROTEIN 1



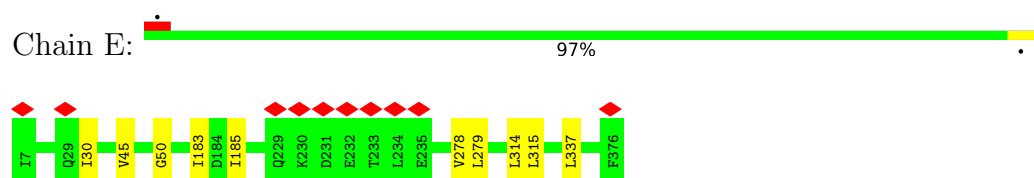
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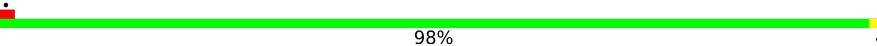
- Molecule 1: ACTIN RELATED PROTEIN 1

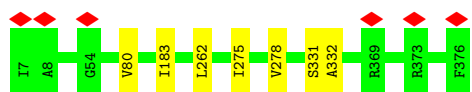


- Molecule 1: ACTIN RELATED PROTEIN 1

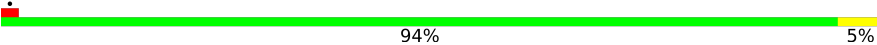


- Molecule 1: ACTIN RELATED PROTEIN 1

Chain F:  98%

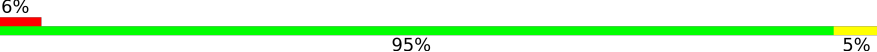


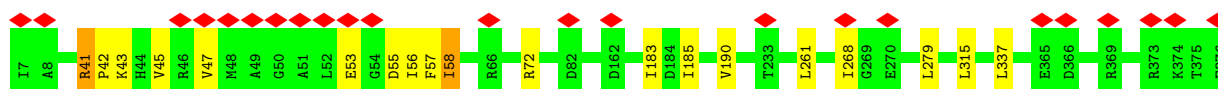
- Molecule 1: ACTIN RELATED PROTEIN 1

Chain G:  94% 5%

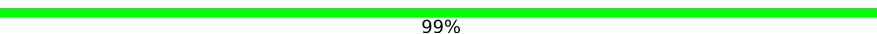


- Molecule 1: ACTIN RELATED PROTEIN 1

Chain I:  6% 95% 5%



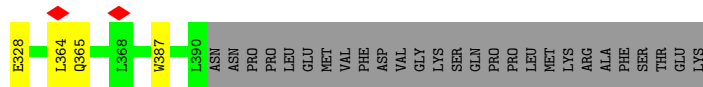
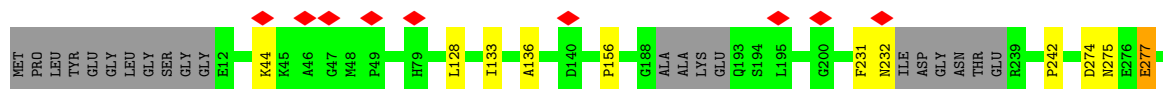
- Molecule 2: ACTIN, CYTOPLASMIC 1

Chain H:  99%



- Molecule 3: ACTIN RELATED PROTEIN 11

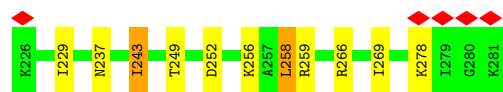
Chain J:  85% 12%



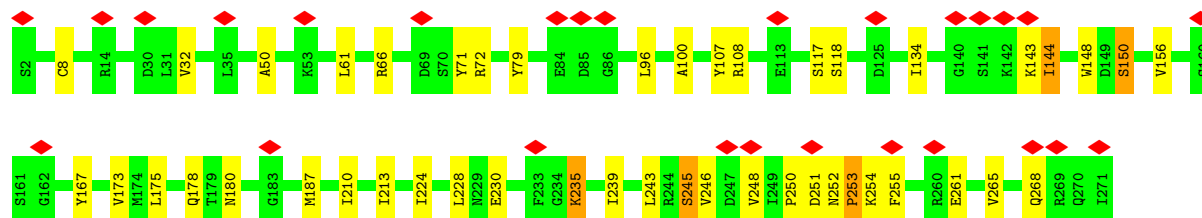
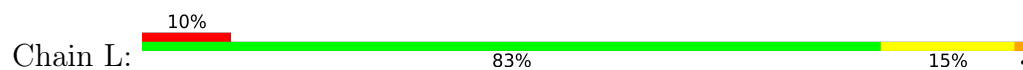
- Molecule 4: CAPPING PROTEIN (ACTIN FILAMENT) MUSCLE Z-LINE, ALPHA 1

Chain K:  14% 77% 21%

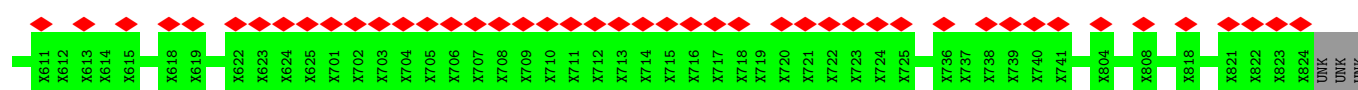
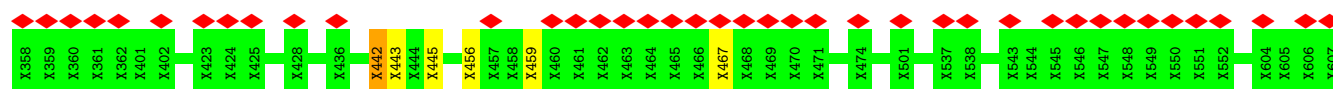
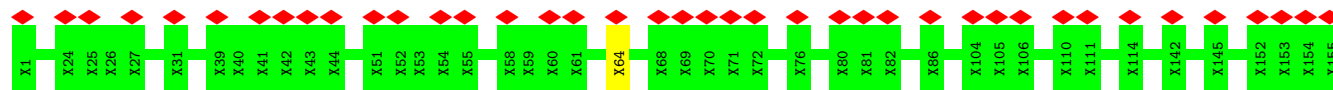




- Molecule 5: F-ACTIN CAPPING PROTEIN BETA SUBUNIT VARIANT II

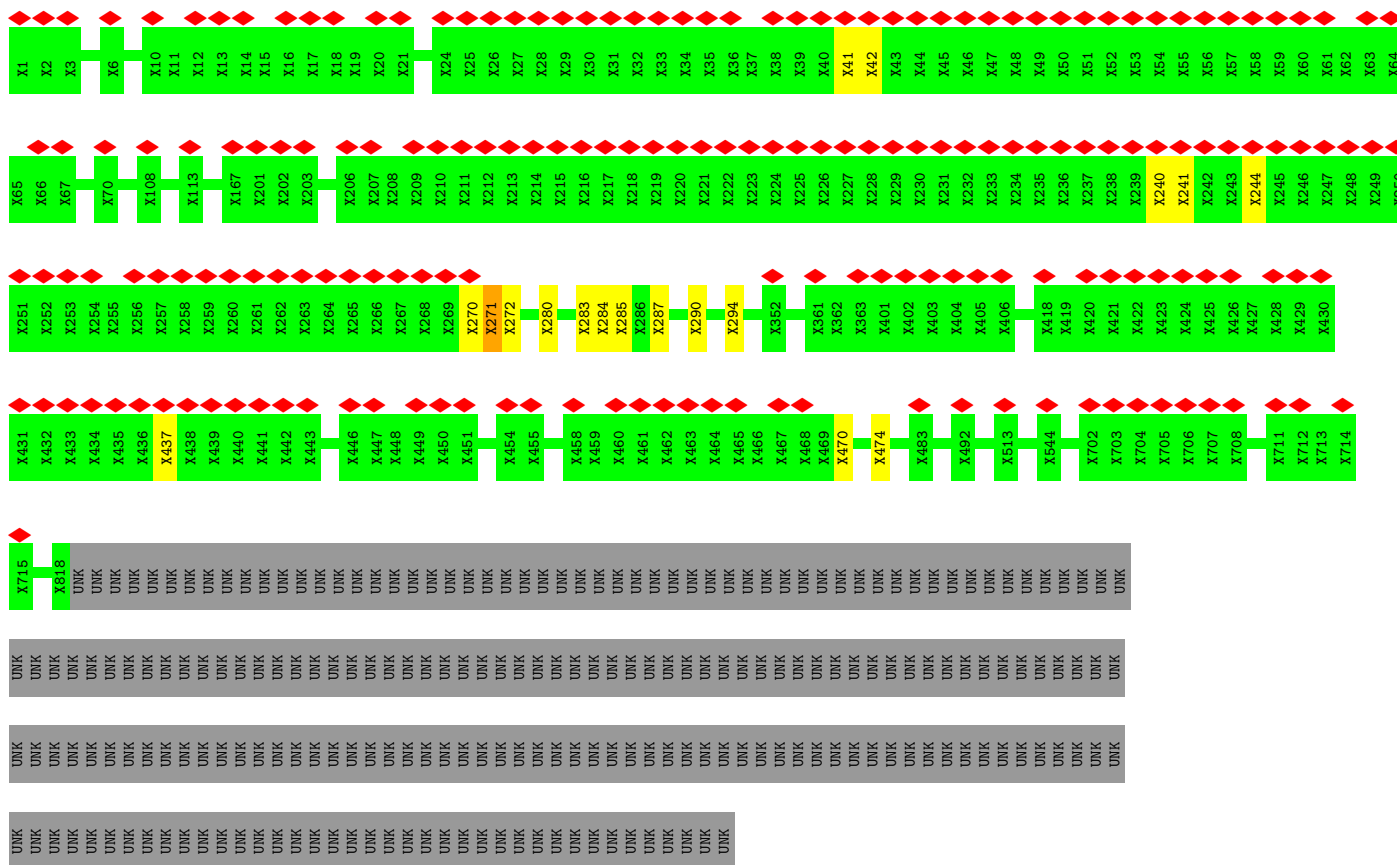


- Molecule 6: DYNAMACTIN SUBUNIT 2

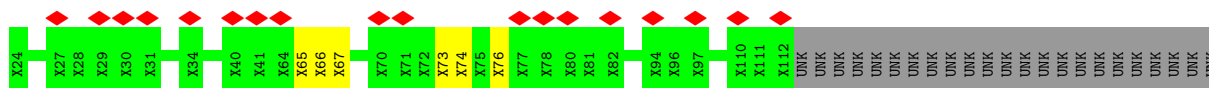


- Molecule 7: DYNAMACTIN SUBUNIT 2

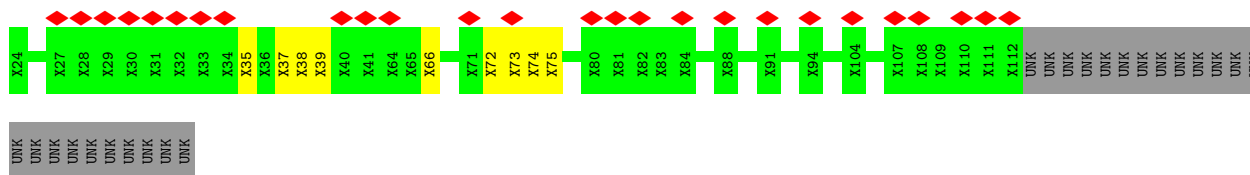




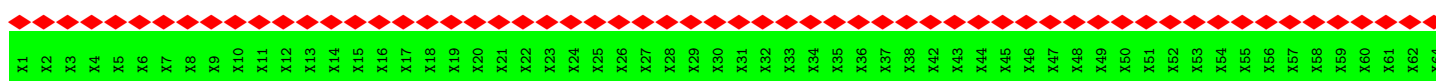
• Molecule 8: DYNACTIN SUBUNIT 3

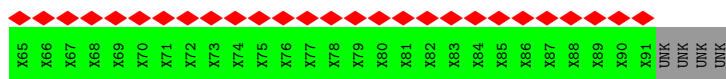


• Molecule 8: DYNACTIN SUBUNIT 3

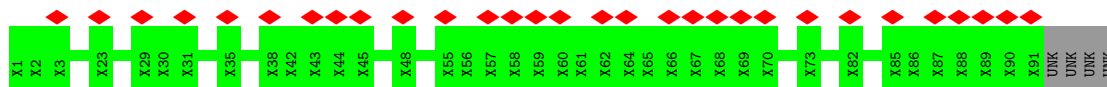


• Molecule 9: DYNACTIN SUBUNIT 2

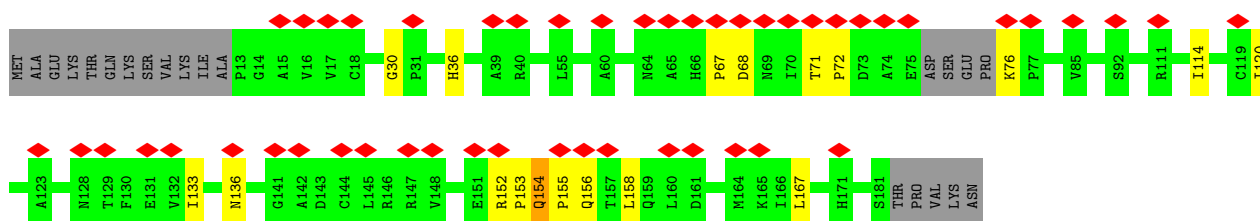
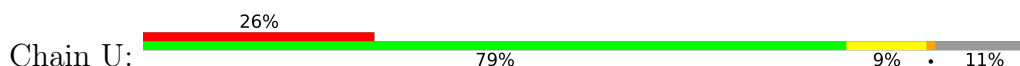




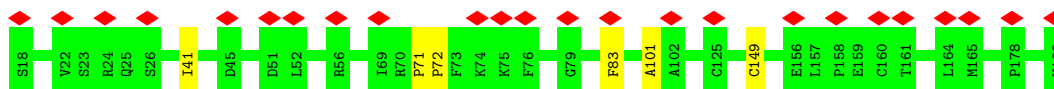
• Molecule 9: DYNACTIN SUBUNIT 2



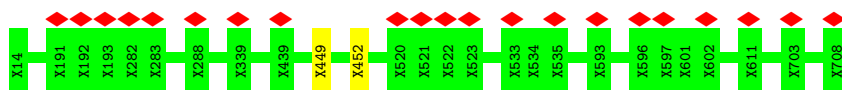
• Molecule 10: DYNACTIN 5



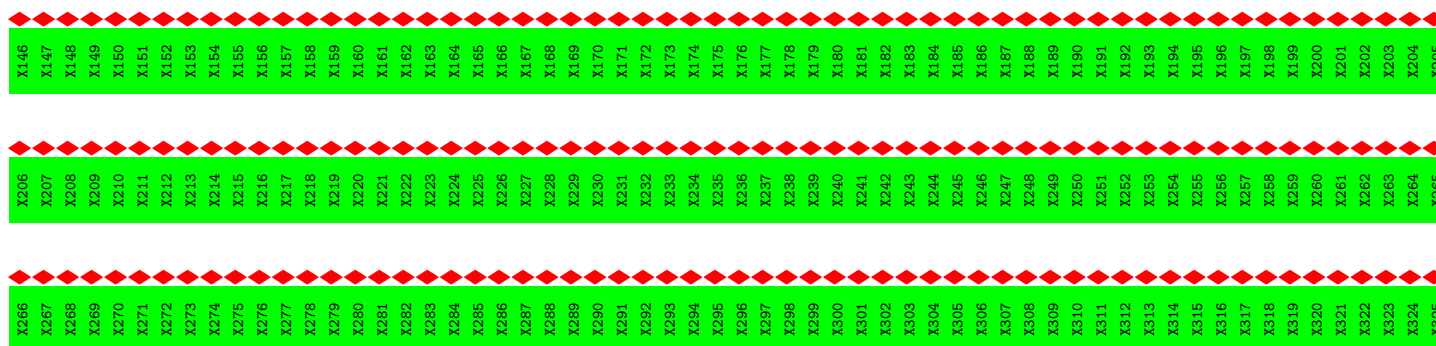
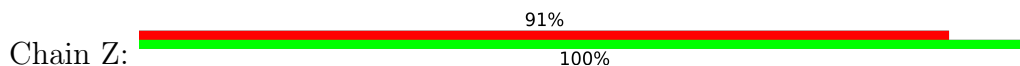
• Molecule 11: DYNACTIN SUBUNIT 6

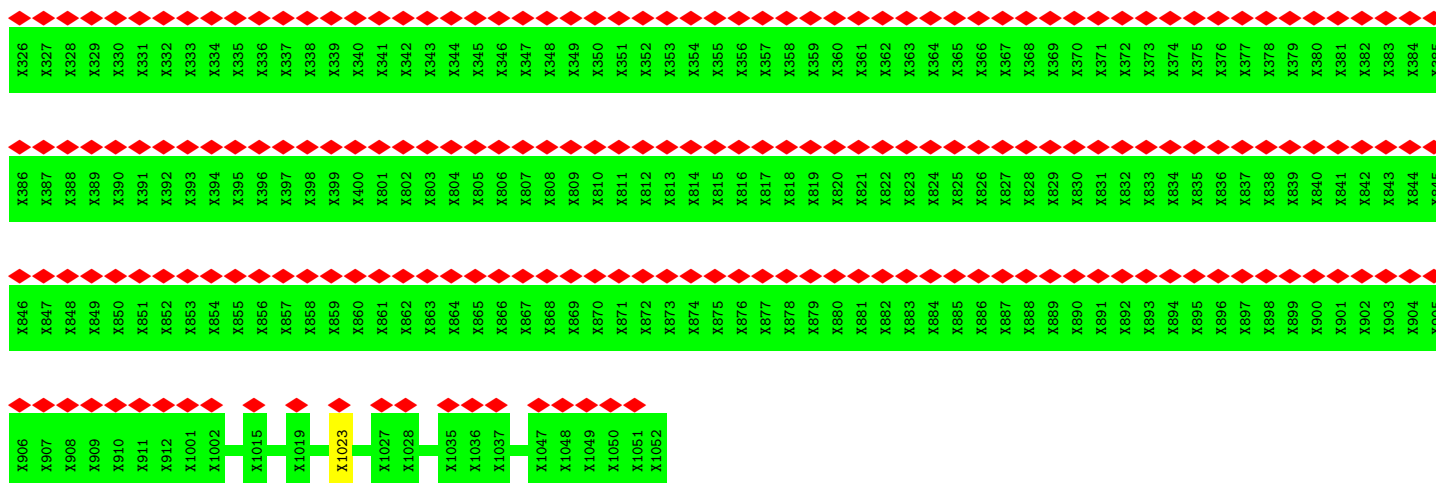


• Molecule 12: DYNACTIN SUBUNIT 2

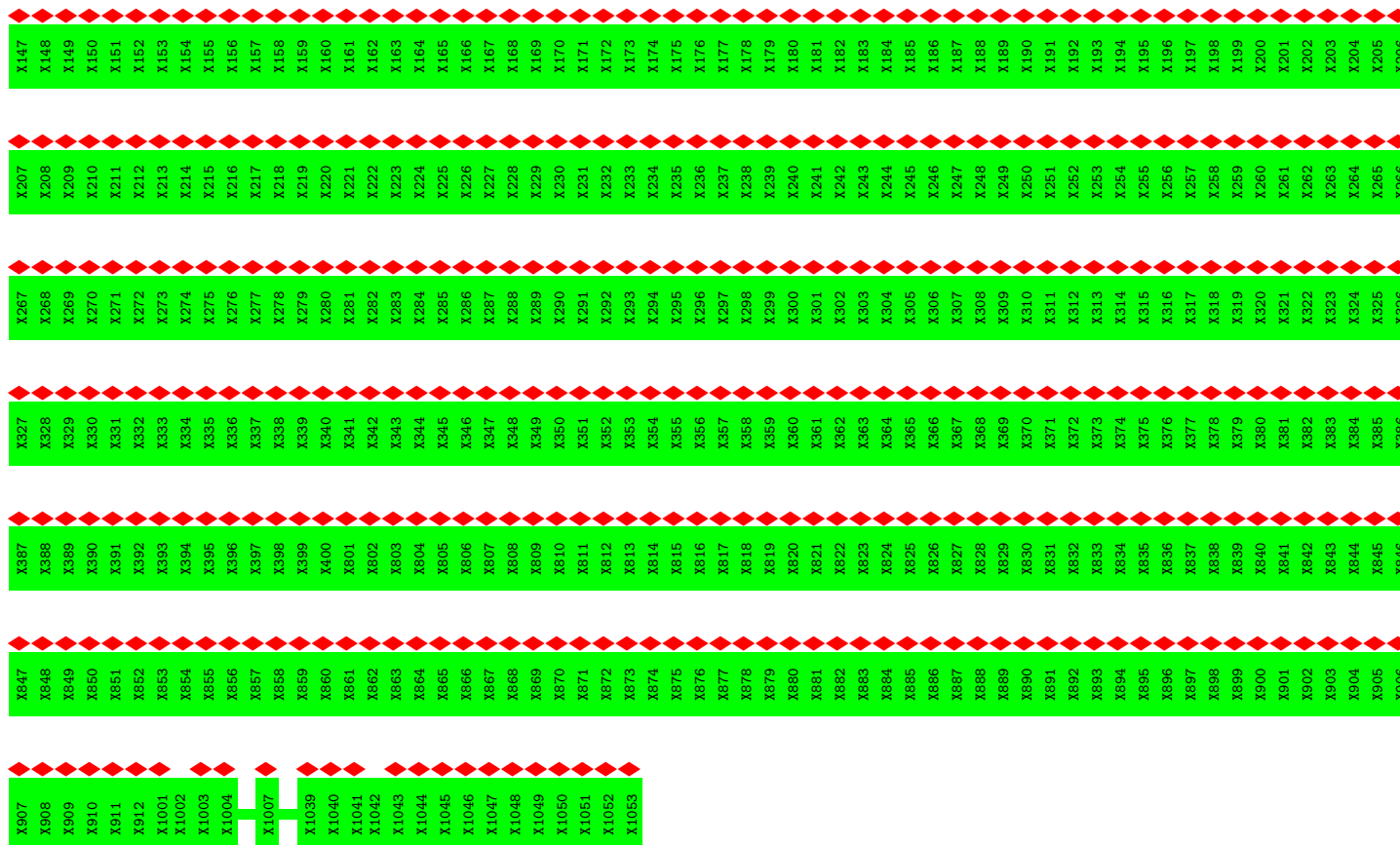


• Molecule 13: DYNACTIN SUBUNIT 2

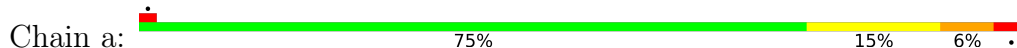


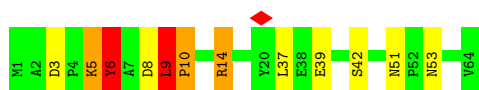


• Molecule 13: DYNAMACTIN SUBUNIT 2



• Molecule 14: DYNAMACTIN SUBUNIT 2

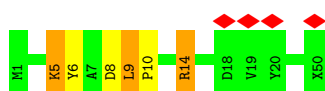
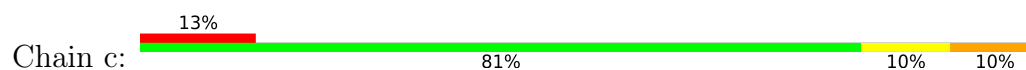




• Molecule 15: DYNAMICTIN SUBUNIT 2



• Molecule 16: DYNAMICTIN SUBUNIT 2



• Molecule 17: DYNAMICTIN SUBUNIT 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	115044	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.504	Depositor
Minimum map value	-0.212	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.088	Depositor
Map size ($\text{\AA}$)	578.88, 578.88, 578.88	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.54	0/3026	0.77	0/4086
1	B	0.55	0/3026	0.76	0/4086
1	C	0.55	0/3026	0.77	0/4086
1	D	0.54	0/3026	0.76	0/4086
1	E	0.55	0/3026	0.77	0/4086
1	F	0.55	0/3026	0.76	0/4086
1	G	0.55	0/3026	0.77	0/4086
1	I	0.55	0/3026	0.79	2/4086 (0.0%)
2	H	0.55	0/2948	0.77	0/3991
3	J	0.57	0/2939	0.81	1/3987 (0.0%)
4	K	0.57	0/2294	0.84	0/3106
5	L	0.55	0/2173	0.80	1/2935 (0.0%)
10	U	0.51	0/830	1.20	14/1152 (1.2%)
11	V	0.52	0/811	1.23	6/1126 (0.5%)
14	a	0.76	2/347 (0.6%)	1.05	4/473 (0.8%)
15	b	0.67	0/525	0.96	2/708 (0.3%)
16	c	0.72	0/127	1.14	1/175 (0.6%)
17	d	0.69	0/130	0.98	0/179
All	All	0.55	2/37332 (0.0%)	0.81	31/50520 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	1
6	M	0	1
7	N	0	2
All	All	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	a	9	LEU	C-N	5.24	1.41	1.34
14	a	10	PRO	N-CD	5.12	1.54	1.47

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	V	83	PHE	CA-C-N	9.65	131.90	119.84
11	V	83	PHE	C-N-CA	9.65	131.90	119.84
11	V	71	PRO	CA-C-N	9.58	128.93	118.97
11	V	71	PRO	C-N-CA	9.58	128.93	118.97
5	L	253	PRO	CA-N-CD	-9.25	99.05	112.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	375	THR	Peptide
6	M	442	UNK	Peptide
7	N	270	UNK	Peptide
7	N	271	UNK	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2957	0	2952	7	0
1	B	2957	0	2952	2	0
1	C	2957	0	2952	2	0
1	D	2957	0	2952	3	0
1	E	2957	0	2952	7	0
1	F	2957	0	2952	3	0
1	G	2957	0	2952	28	0
1	I	2957	0	2952	28	0
2	H	2885	0	2856	2	0
3	J	2879	0	2969	18	0
4	K	2242	0	2169	73	0
5	L	2137	0	2122	75	0
6	M	2855	0	585	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	N	3010	0	619	13	0
8	O	323	0	76	3	0
8	P	323	0	77	10	0
9	Q	435	0	93	0	0
9	R	435	0	93	0	0
10	U	831	0	374	7	0
11	V	812	0	344	1	0
12	Y	1215	0	286	2	0
13	Z	2095	0	429	1	0
13	z	2095	0	427	0	0
14	a	341	0	310	8	0
15	b	517	0	490	52	0
16	c	179	0	116	4	0
17	d	127	0	103	6	0
All	All	49392	0	38154	299	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 299 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:b:66:THR:HG21	15:b:83:TYR:CD1	1.44	1.52
5:L:251:ASP:CG	5:L:255:PHE:HE2	1.36	1.33
5:L:251:ASP:O	5:L:255:PHE:CD2	1.94	1.20
1:G:183:ILE:HD11	1:G:278:VAL:CG2	1.72	1.19
5:L:253:PRO:HD2	5:L:254:LYS:H	1.08	1.17

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	368/370 (100%)	350 (95%)	18 (5%)	0	100	100
1	B	368/370 (100%)	348 (95%)	20 (5%)	0	100	100
1	C	368/370 (100%)	347 (94%)	21 (6%)	0	100	100
1	D	368/370 (100%)	347 (94%)	21 (6%)	0	100	100
1	E	368/370 (100%)	346 (94%)	22 (6%)	0	100	100
1	F	368/370 (100%)	341 (93%)	27 (7%)	0	100	100
1	G	368/370 (100%)	344 (94%)	24 (6%)	0	100	100
1	I	368/370 (100%)	347 (94%)	21 (6%)	0	100	100
2	H	368/370 (100%)	350 (95%)	18 (5%)	0	100	100
3	J	363/417 (87%)	331 (91%)	31 (8%)	1 (0%)	36	70
4	K	273/275 (99%)	258 (94%)	15 (6%)	0	100	100
5	L	268/270 (99%)	257 (96%)	11 (4%)	0	100	100
10	U	167/190 (88%)	145 (87%)	16 (10%)	6 (4%)	2	23
11	V	163/165 (99%)	146 (90%)	16 (10%)	1 (1%)	21	57
14	a	44/48 (92%)	40 (91%)	3 (7%)	1 (2%)	5	31
15	b	67/71 (94%)	58 (87%)	8 (12%)	1 (2%)	8	38
16	c	18/31 (58%)	16 (89%)	1 (6%)	1 (6%)	1	17
17	d	18/20 (90%)	15 (83%)	1 (6%)	2 (11%)	0	6
All	All	4693/4817 (97%)	4386 (94%)	294 (6%)	13 (0%)	37	70

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	U	67	PRO
10	U	72	PRO
10	U	154	GLN
14	a	9	LEU
15	b	9	LEU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	318/318 (100%)	316 (99%)	2 (1%)	78	81
1	B	318/318 (100%)	314 (99%)	4 (1%)	61	72
1	C	318/318 (100%)	312 (98%)	6 (2%)	50	67
1	D	318/318 (100%)	313 (98%)	5 (2%)	55	70
1	E	318/318 (100%)	313 (98%)	5 (2%)	55	70
1	F	318/318 (100%)	315 (99%)	3 (1%)	70	76
1	G	318/318 (100%)	312 (98%)	6 (2%)	50	67
1	I	318/318 (100%)	314 (99%)	4 (1%)	61	72
2	H	313/313 (100%)	313 (100%)	0	100	100
3	J	322/363 (89%)	318 (99%)	4 (1%)	63	73
4	K	245/245 (100%)	238 (97%)	7 (3%)	37	58
5	L	242/242 (100%)	236 (98%)	6 (2%)	42	62
14	a	31/41 (76%)	24 (77%)	7 (23%)	1	6
15	b	49/60 (82%)	37 (76%)	12 (24%)	1	5
16	c	7/16 (44%)	5 (71%)	2 (29%)	0	3
17	d	8/16 (50%)	7 (88%)	1 (12%)	4	20
All	All	3761/3840 (98%)	3687 (98%)	74 (2%)	48	66

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	a	51	ASN
16	c	6	TYR
15	b	6	TYR
15	b	53	ASN
1	F	278	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
5	L	209	HIS
5	L	264	GLN
15	b	47	HIS
1	G	37	ASN
1	F	77	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
12	Y	12
7	N	5
6	M	5
8	O	3
8	P	3
13	Z	2
9	Q	2
9	R	2
13	z	2
16	c	1
14	a	1
15	b	1

The worst 5 of 39 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	N	363:UNK	C	401:UNK	N	98.24
1	N	167:UNK	C	201:UNK	N	96.90
1	M	166:UNK	C	201:UNK	N	95.47
1	M	362:UNK	C	401:UNK	N	81.15
1	M	625:UNK	C	701:UNK	N	68.30

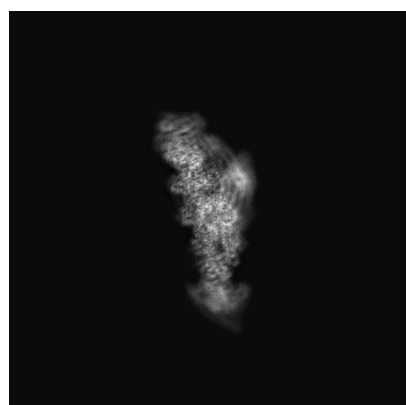
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2856. These allow visual inspection of the internal detail of the map and identification of artifacts.

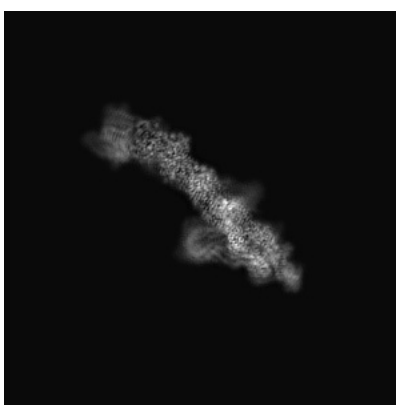
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

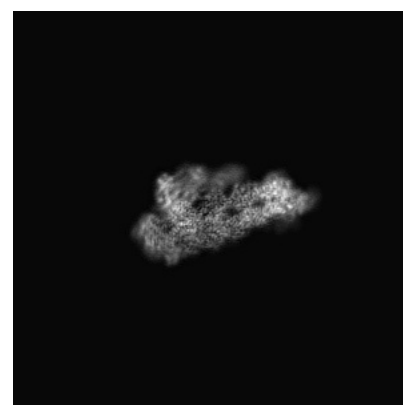
6.1.1 Primary map



X



Y

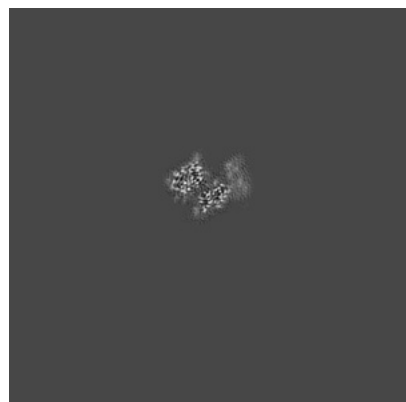


Z

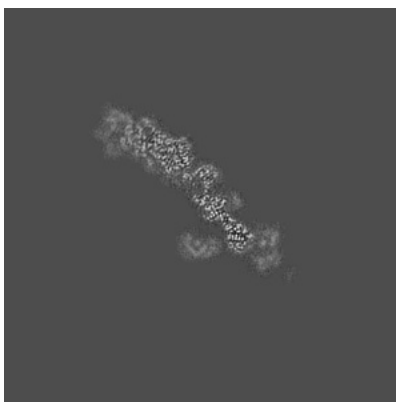
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

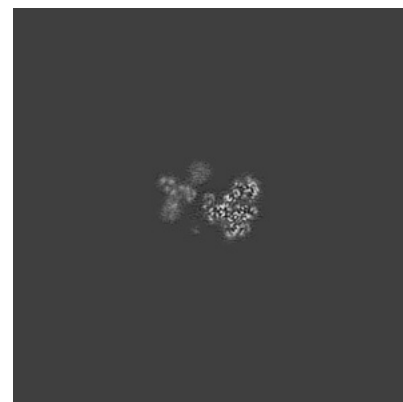
6.2.1 Primary map



X Index: 216



Y Index: 216



Z Index: 216

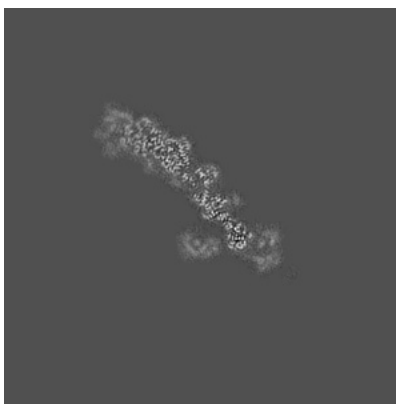
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

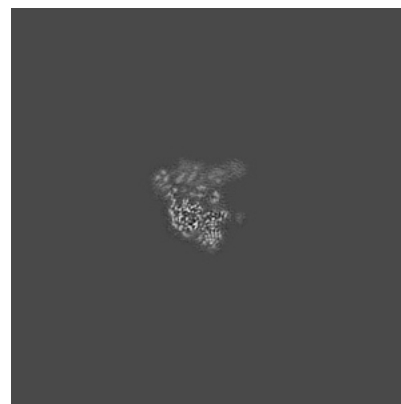
6.3.1 Primary map



X Index: 176



Y Index: 217

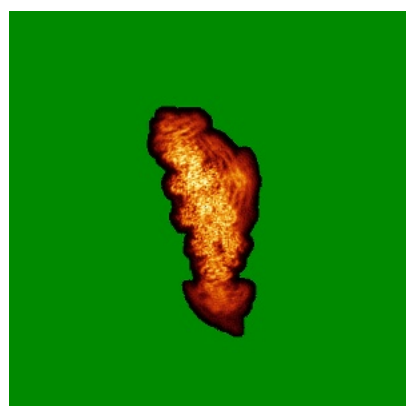


Z Index: 244

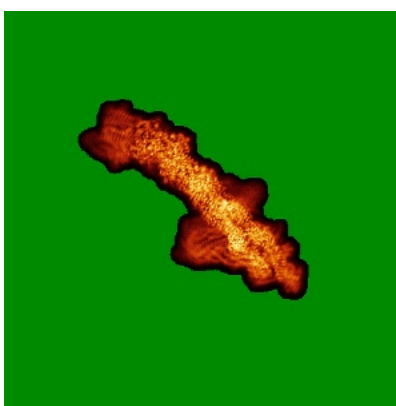
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

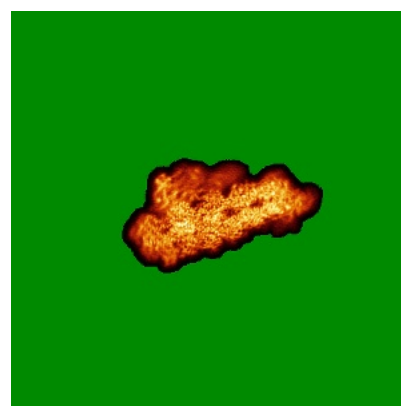
6.4.1 Primary map



X



Y

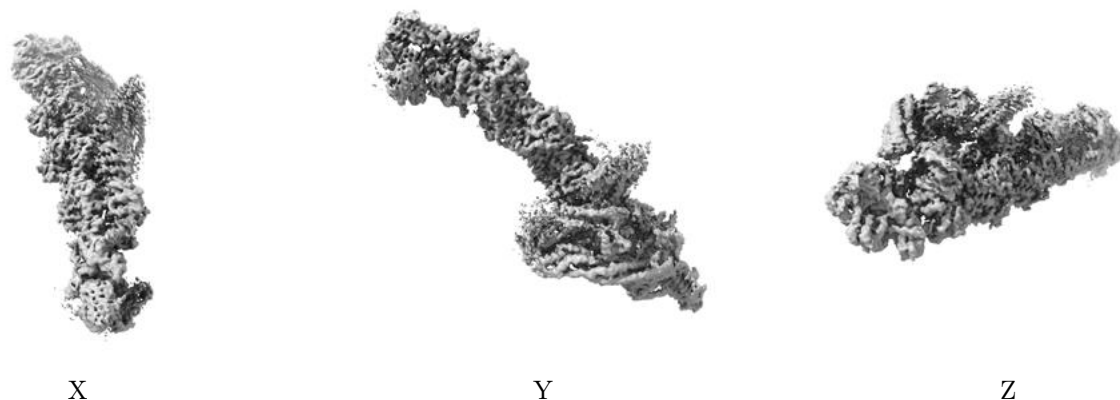


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.088. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

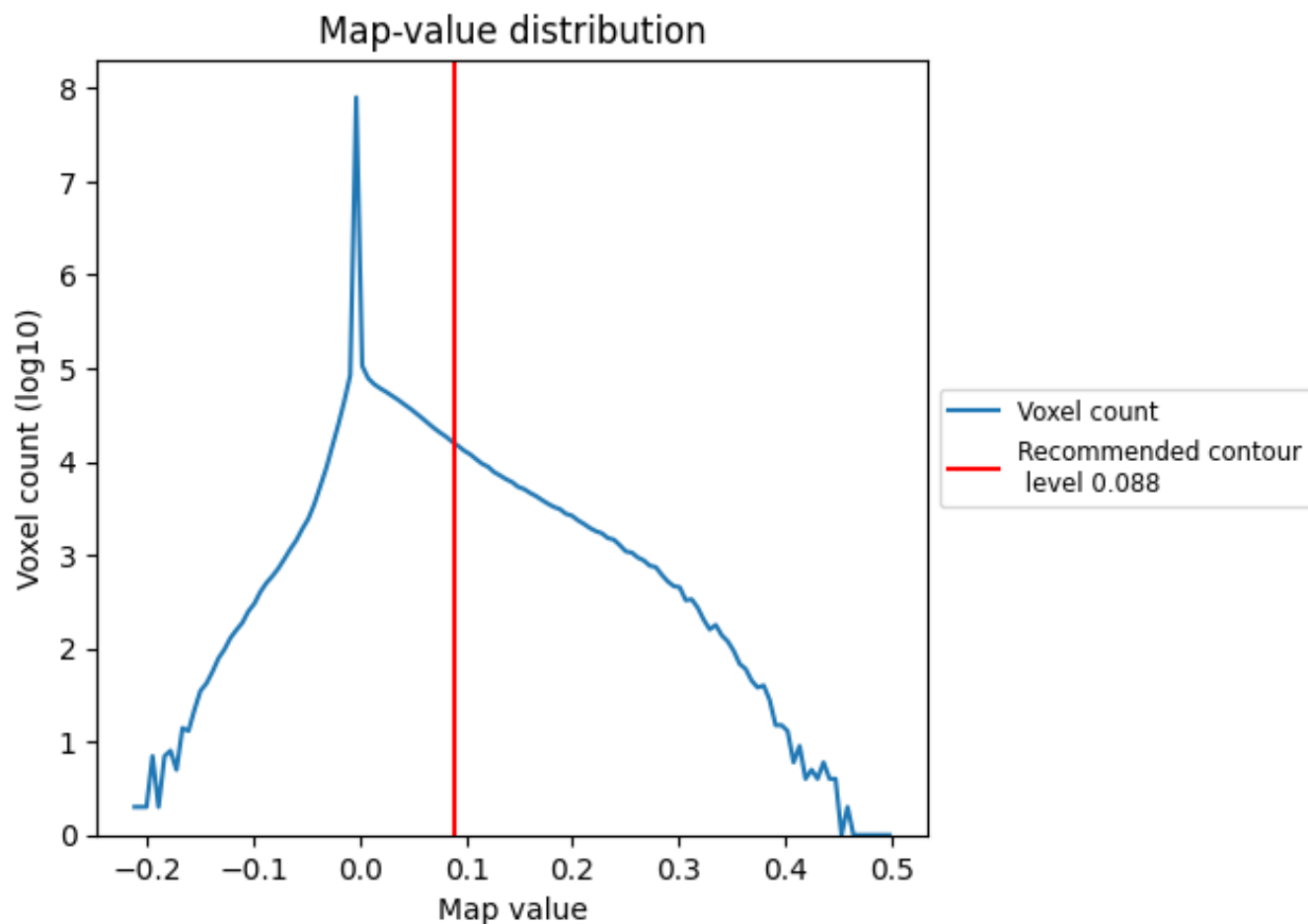
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

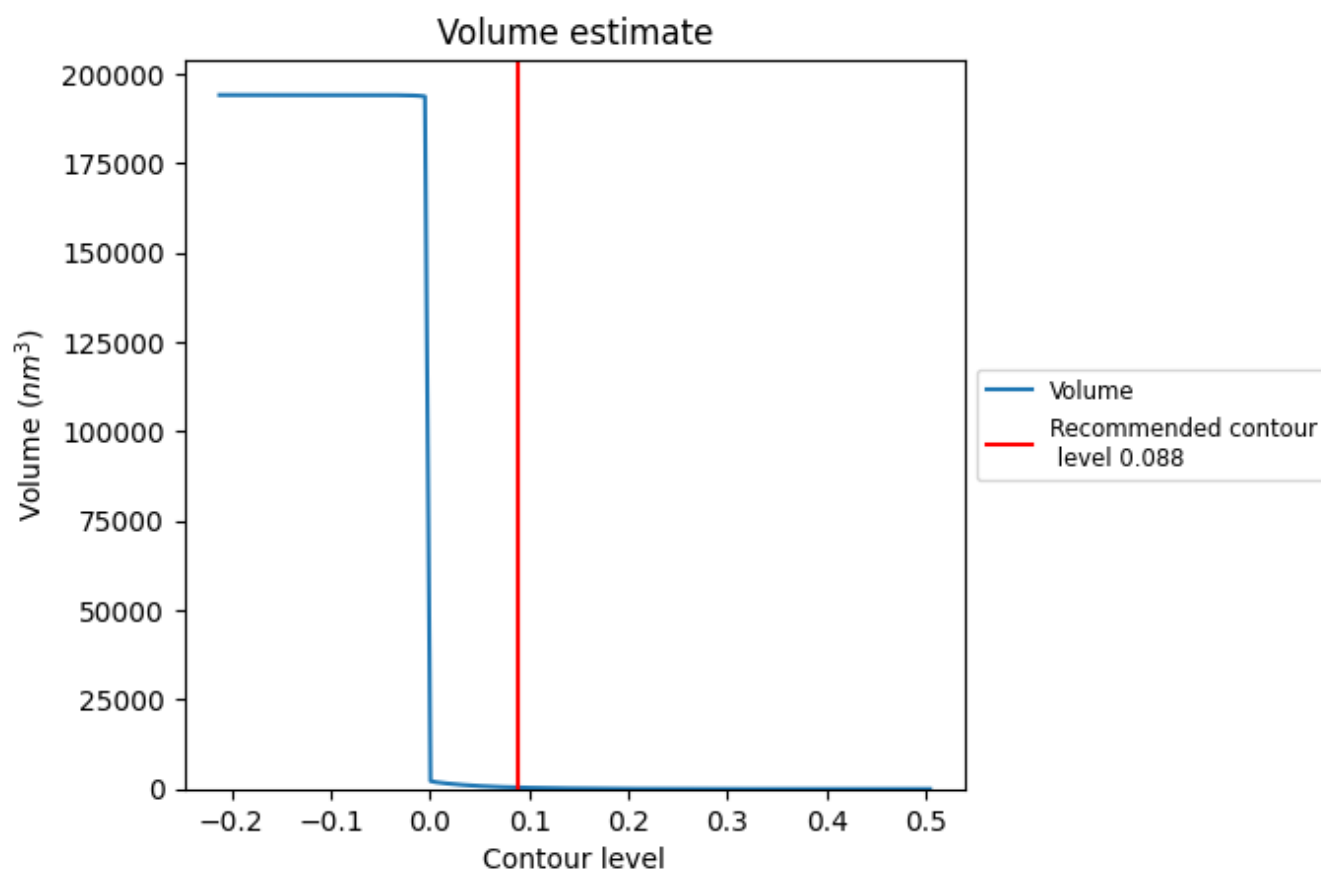
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

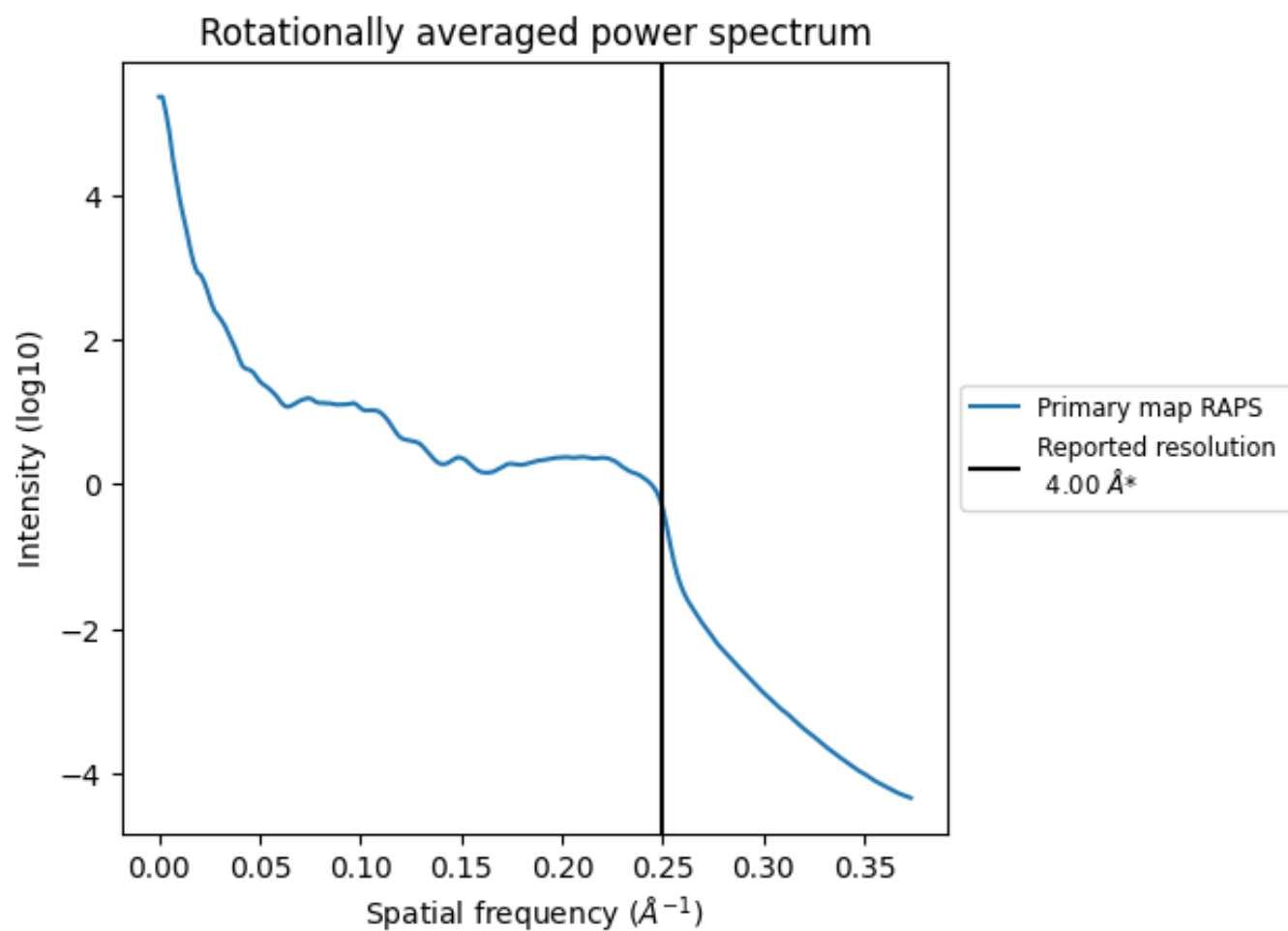
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 412 nm^3 ; this corresponds to an approximate mass of 372 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

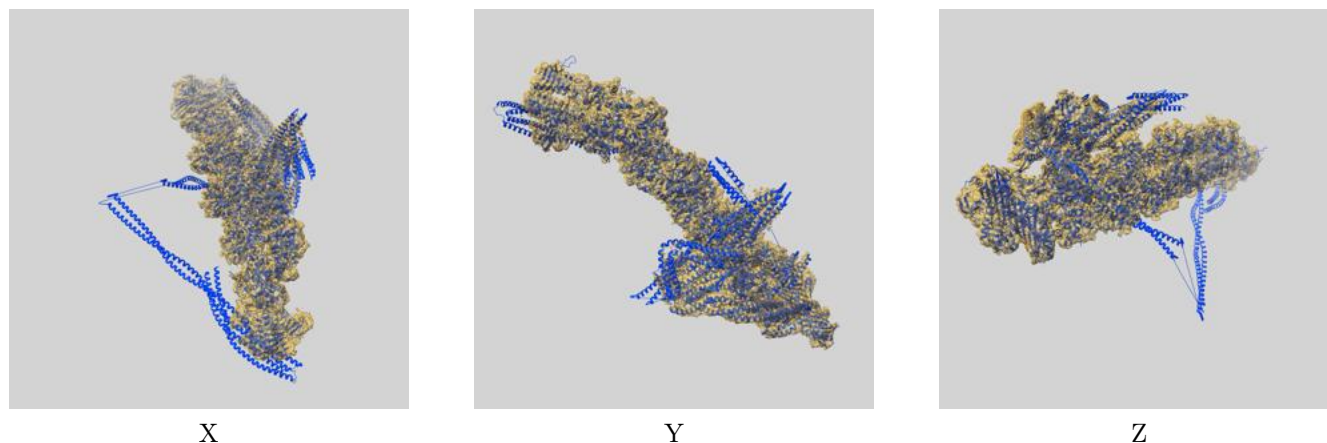
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

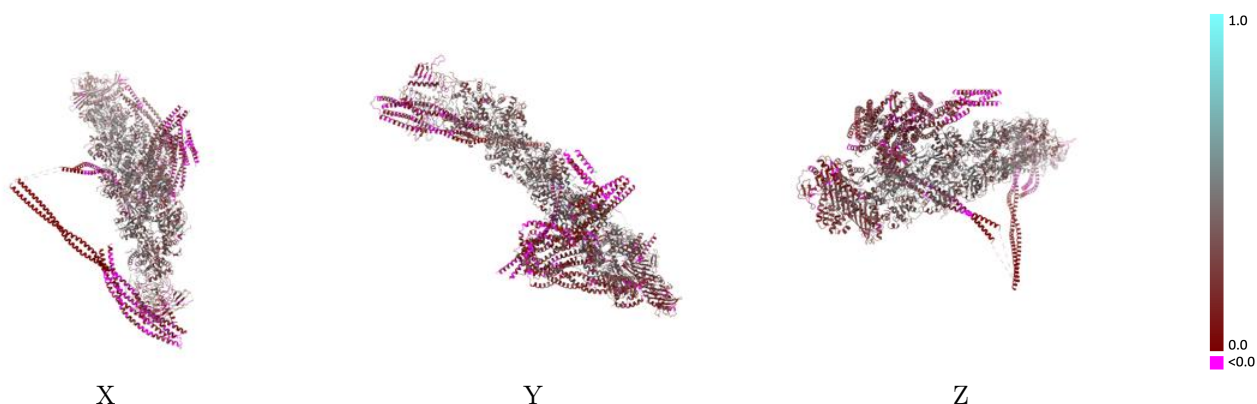
This section contains information regarding the fit between EMDB map EMD-2856 and PDB model 5ADX. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



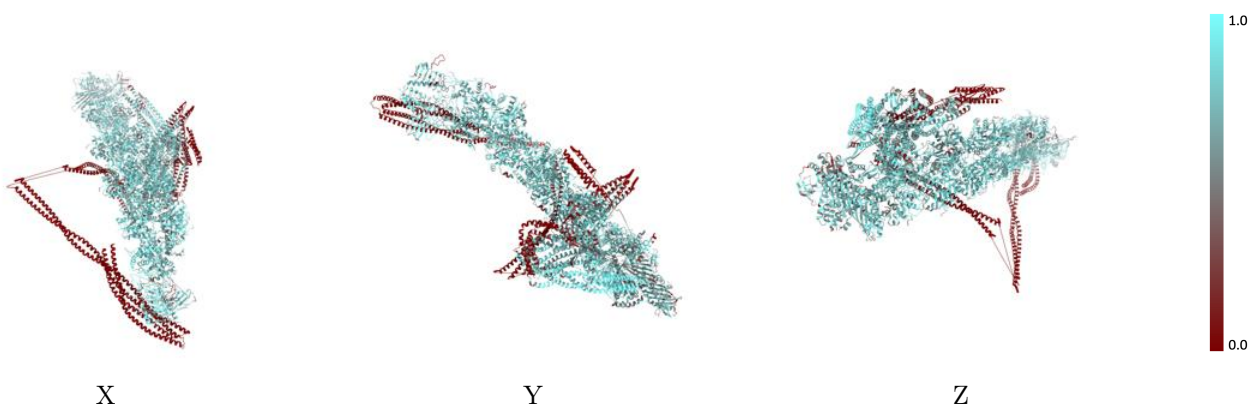
The images above show the 3D surface view of the map at the recommended contour level 0.088 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



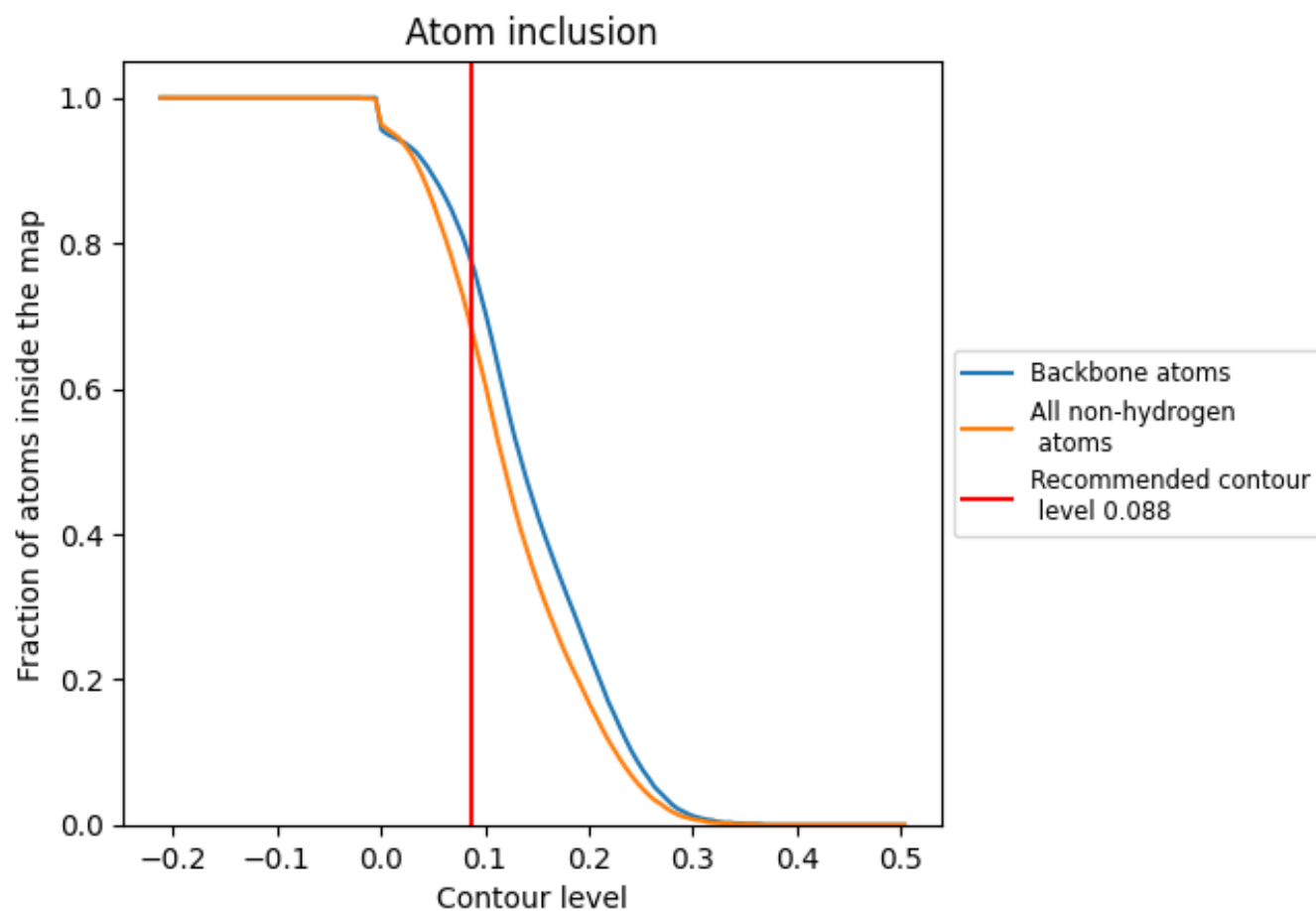
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.088).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.088) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6770	 0.3010
A	 0.7400	 0.3410
B	 0.7730	 0.3850
C	 0.8010	 0.4250
D	 0.7890	 0.3850
E	 0.7780	 0.3980
F	 0.7960	 0.3920
G	 0.7940	 0.3940
H	 0.8130	 0.4040
I	 0.7410	 0.3400
J	 0.7440	 0.3500
K	 0.6430	 0.2180
L	 0.6780	 0.2480
M	 0.6430	 0.1610
N	 0.6430	 0.1930
O	 0.6970	 0.1830
P	 0.5910	 0.1690
Q	 0.0000	 -0.0110
R	 0.6020	 0.2040
U	 0.6190	 0.1900
V	 0.7460	 0.2670
Y	 0.8310	 0.3290
Z	 0.0860	 0.0570
a	 0.7600	 0.4040
b	 0.7130	 0.3490
c	 0.7560	 0.3760
d	 0.6690	 0.3020
z	 0.0760	 0.0360

