



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:30 PM UTC

PDB ID : 4UUK / pdb_00004uuk
EMDB ID : EMD-2701
Title : Human dynamin 1 K44A superconstricted polymer stabilized with GTP strand 2
Authors : Sundborger, A.C.; Fang, S.; Heymann, J.A.; Ray, P.; Chappie, J.S.; Hinshaw, J.E.
Deposited on : 2014-07-29
Resolution : 12.50 Å (reported)
Based on initial models : 3SNH, 1DYN, 3ZYC

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

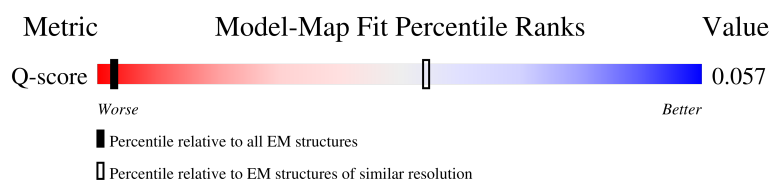
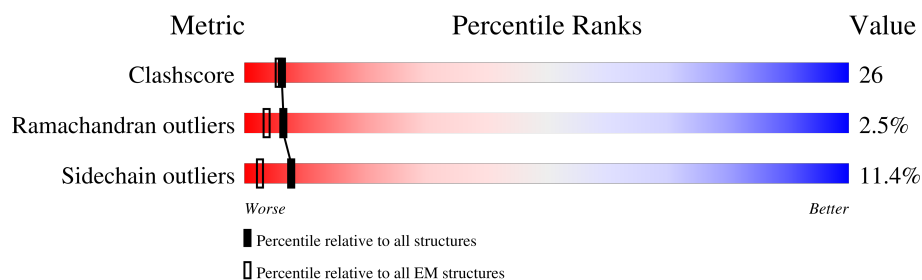
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 12.50 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	96 (12.00 - 13.00)

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	864	
1	D	864	
1	G	864	
1	K	864	

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Mol	Chain	Length	Quality of chain
2	B	864	8%7%6%.76%
2	C	864	6%5%..87%
2	E	864	7%9%5%.76%
2	F	864	6%5%..87%
2	H	864	6%5%..87%
2	I	864	8%8%5%.76%
2	J	864	7%9%5%.76%
2	L	864	6%5%..87%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 21116 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 DYNAMIN-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	329	Total	C	N	O	S	0	0
			2567	1615	453	489	10		
1	D	337	Total	C	N	O	S	0	0
			2643	1664	466	503	10		
1	G	329	Total	C	N	O	S	0	0
			2567	1615	453	489	10		
1	K	337	Total	C	N	O	S	0	0
			2643	1664	466	503	10		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	744	ASN	ASP	variant	UNP Q05193
D	744	ASN	ASP	variant	UNP Q05193
G	744	ASN	ASP	variant	UNP Q05193
K	744	ASN	ASP	variant	UNP Q05193

- Molecule 2 is a protein called DYNAMIN-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	208	Total	C	N	O	S	0	0
			1728	1097	304	313	14		
2	C	113	Total	C	N	O	S	0	0
			946	609	158	175	4		
2	E	208	Total	C	N	O	S	0	0
			1728	1097	304	313	14		
2	F	113	Total	C	N	O	S	0	0
			946	609	158	175	4		
2	H	113	Total	C	N	O	S	0	0
			946	609	158	175	4		
2	I	208	Total	C	N	O	S	0	0
			1728	1097	304	313	14		
2	J	208	Total	C	N	O	S	0	0
			1728	1097	304	313	14		

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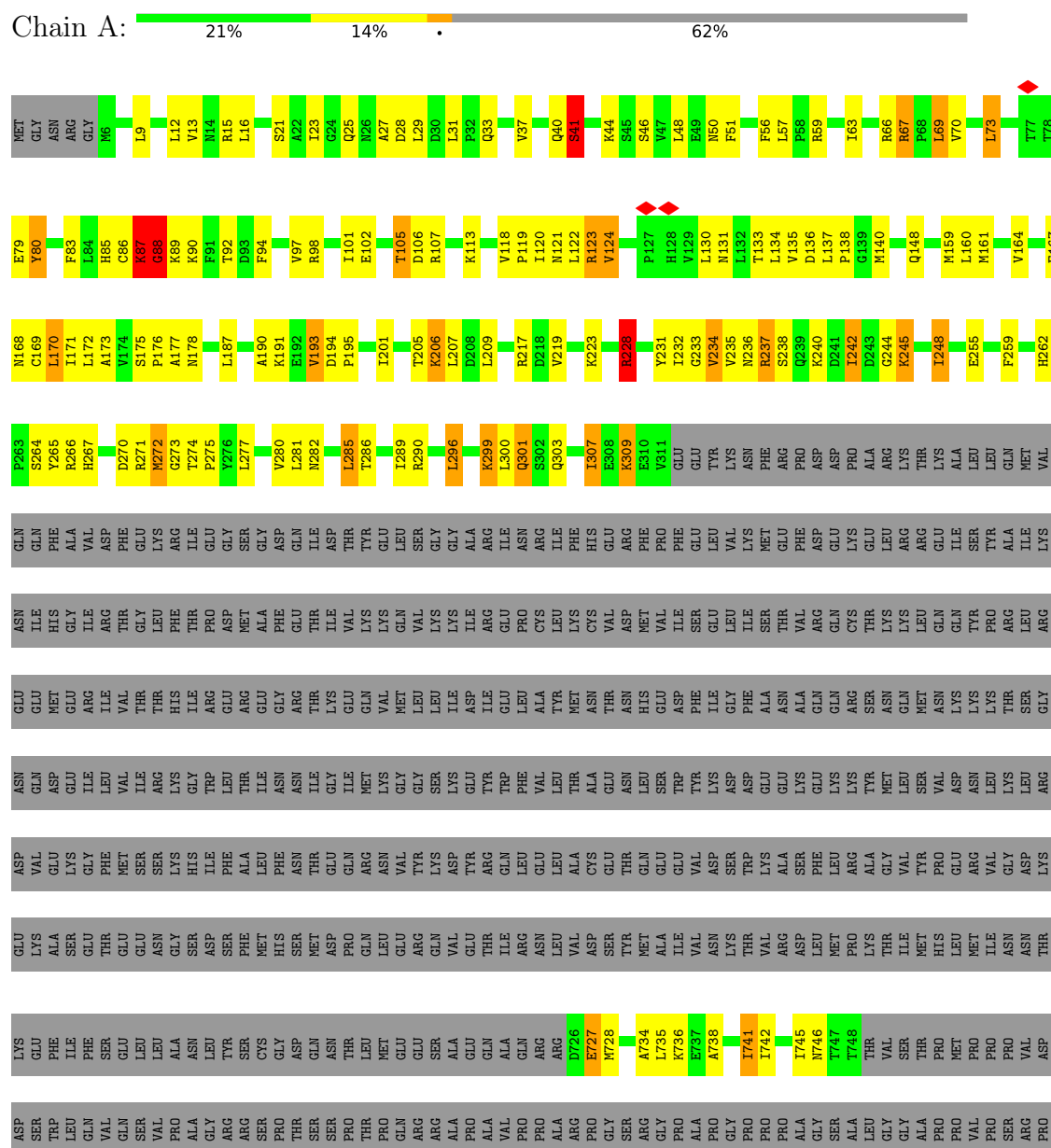
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	113	Total	C	N	O	S	0	0
			946	609	158	175	4		

3 Residue-property plots

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.

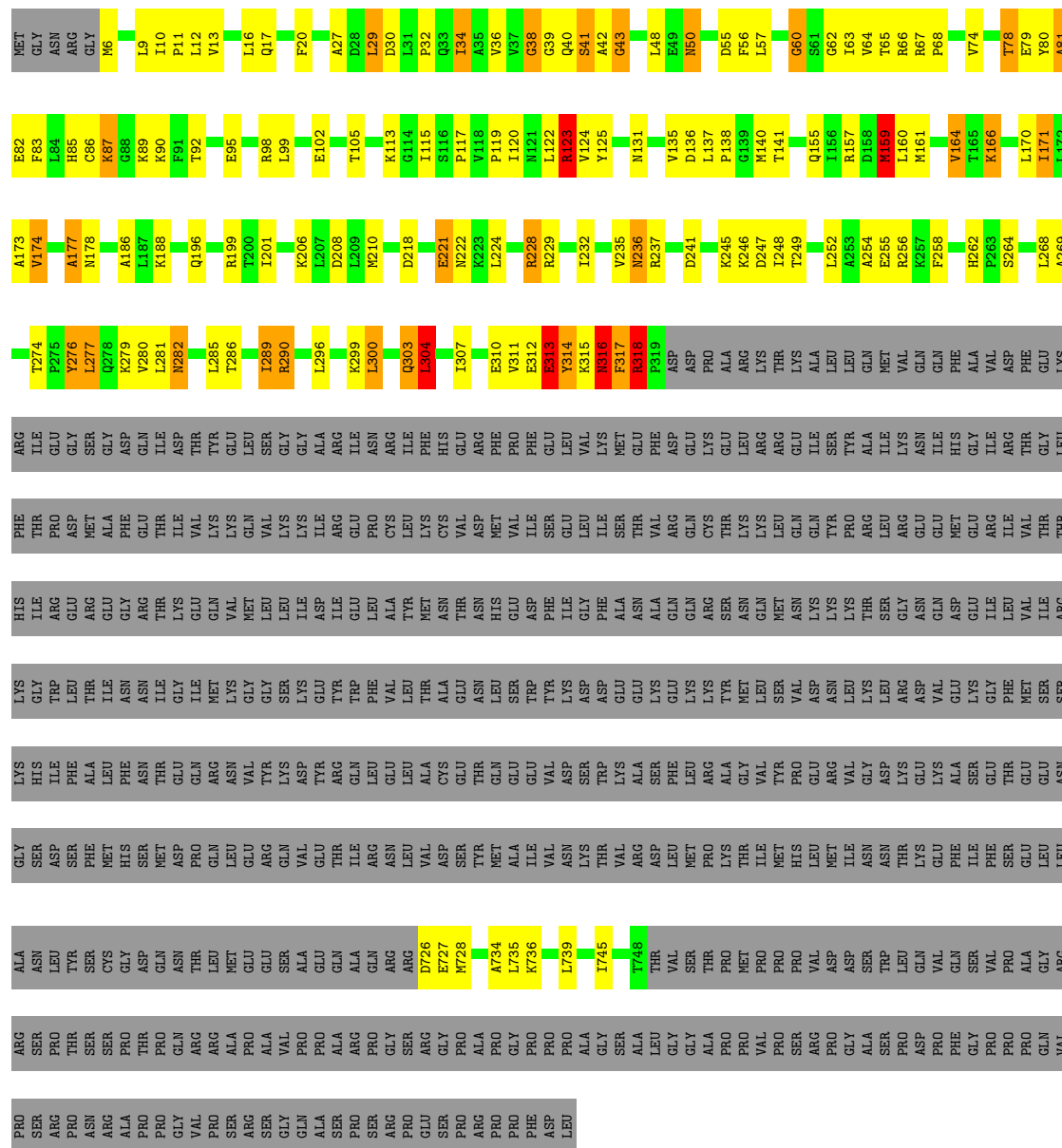
• Molecule 1: DYNAMIN-1



GLY
ALA
SER
ASN
PRO
ARG
ASP
GLY
PRO
PHE
GLY
PRO
PRO
PRO
PRO
GLN
VAL
PRO
SER
ARG
PRO
ASN
ARG
ALA
PRO
PRO
GLY
VAL
PRO
SER
ARG
GLY
GLN
ALA
SER
PRO
SER
ARG
GLU
SER
PRO
ARG
PHE
ASP
LEU

• Molecule 1: DYNAMIN-1

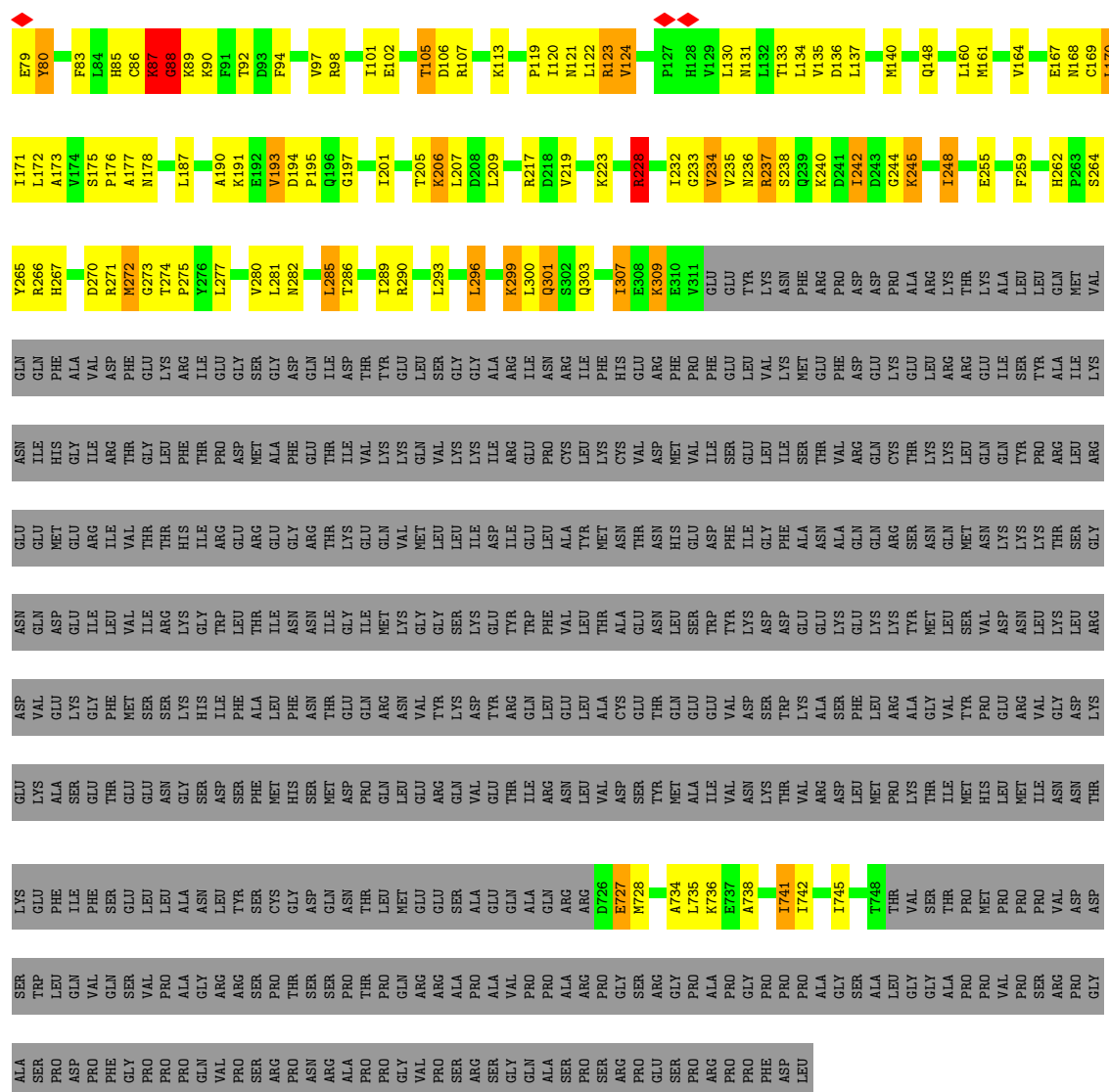
Chain D: 22% 13% . . 61%



• Molecule 1: DYNAMIN-1

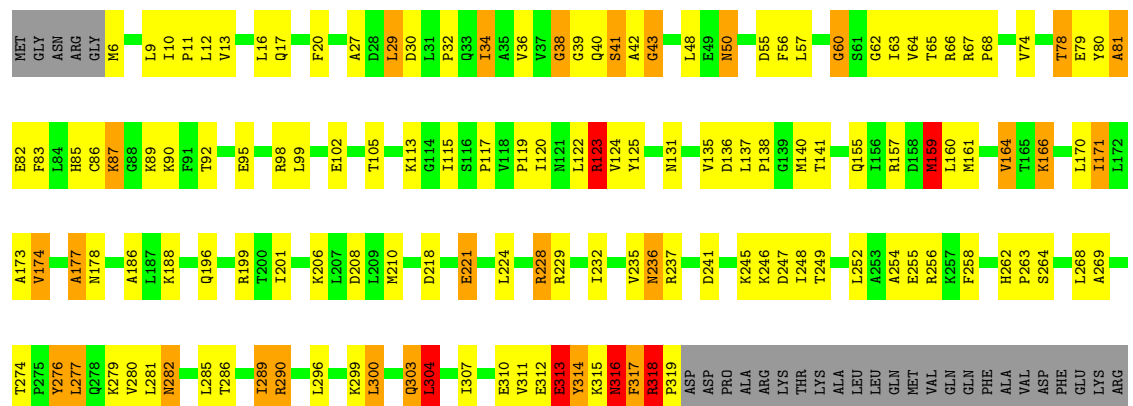
Chain G: 21% 14% . 62%

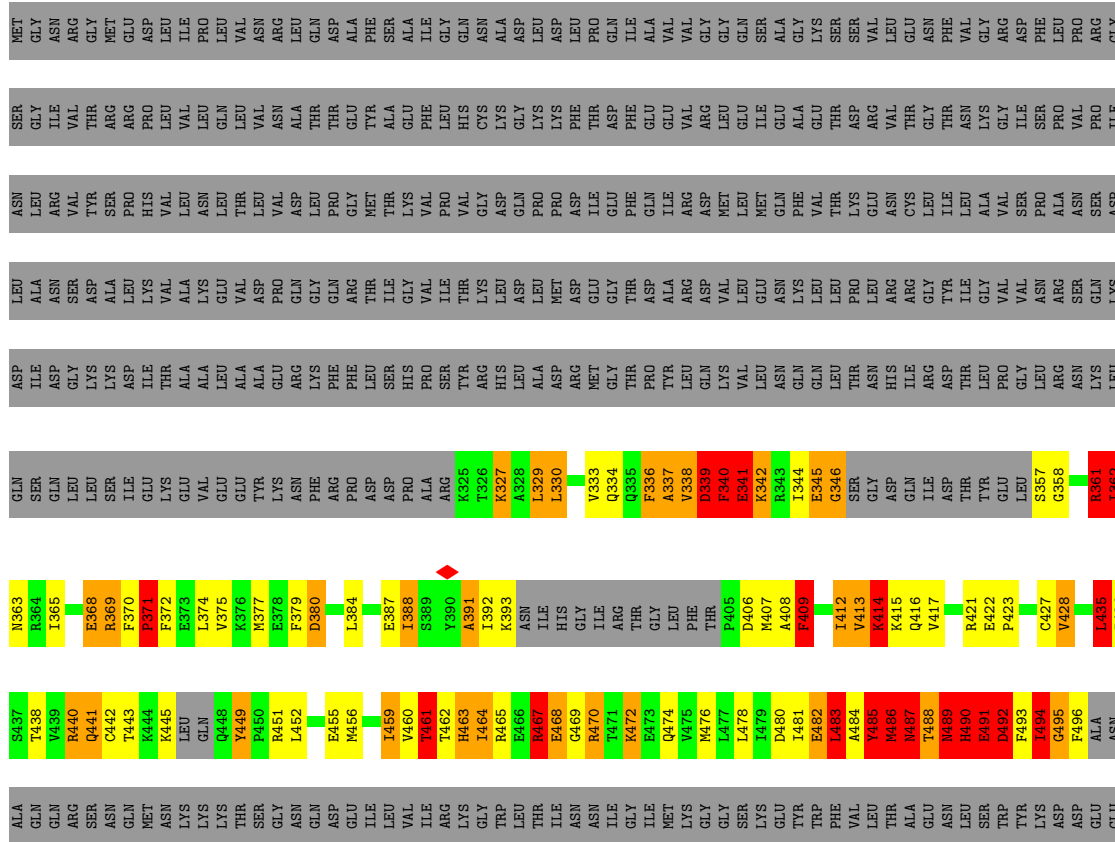




• Molecule 1: DYNAMIN-1

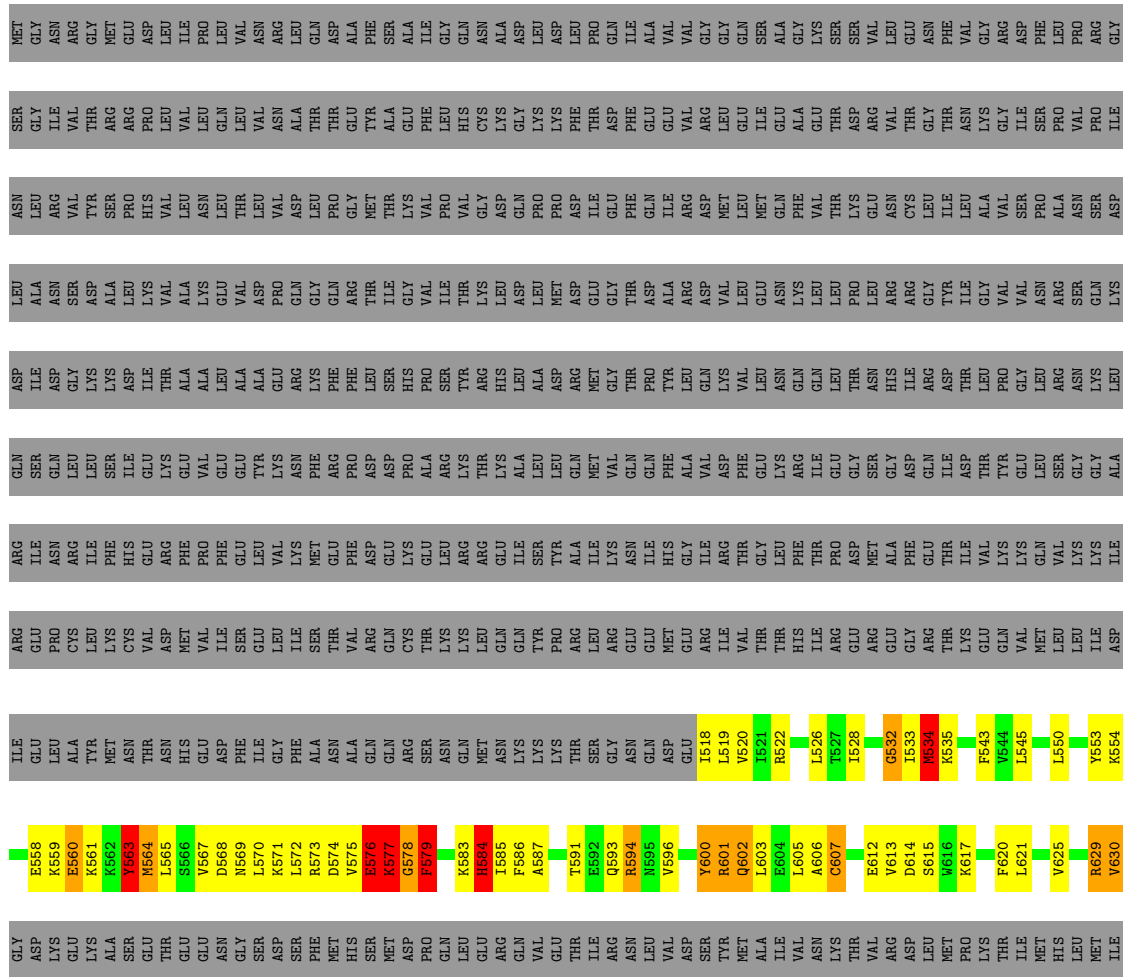
Chain K: 22% 13% • • 61%





LEU

Chain C: 6% 5% 2% 87%

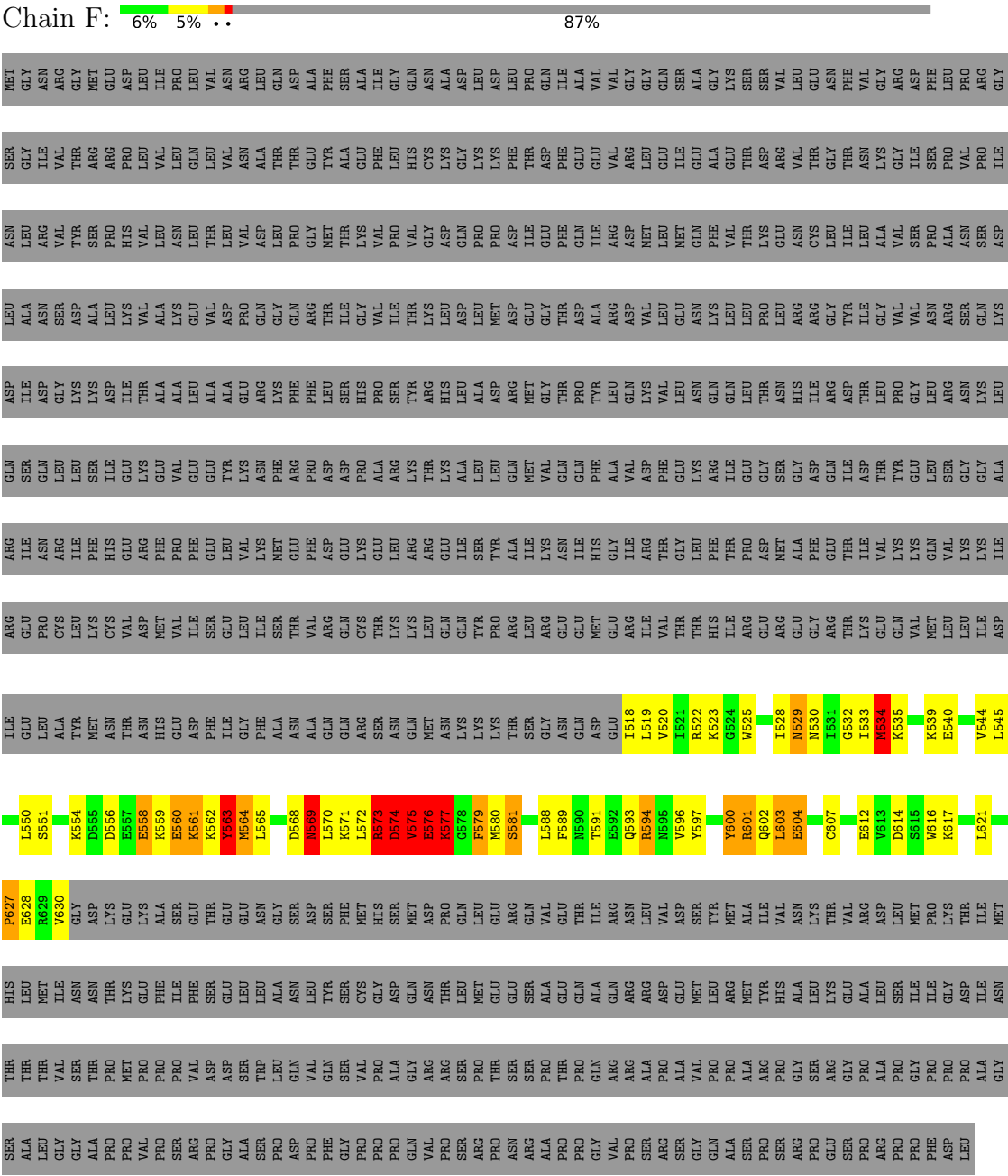


- Molecule 2: DYNAMIN-1

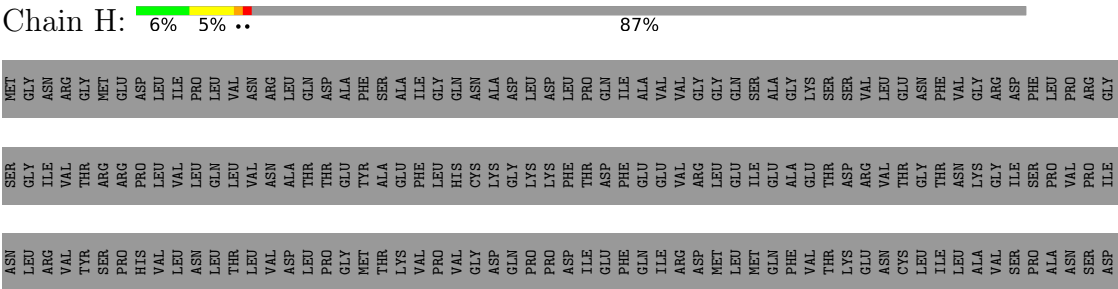
Chain E: 7% 9% 5% . 76%

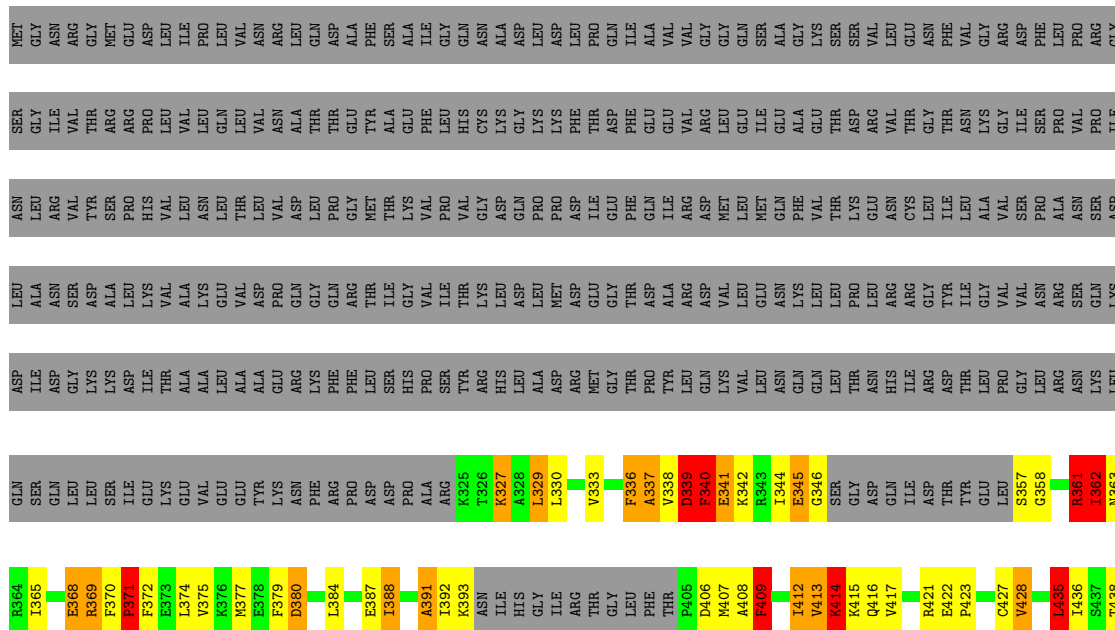
[illegible]

- Molecule 2: DYNAMIN-1



● Molecule 2: DYNAMIN-1









ALA	GLY	SER	ALA	LEU	GLY	GLY	ALA	PRO	PRO	VAL	PRO	SER	ARG	PRO	GLY	ALA	SER	PRO	ASP	PRO	PHE	GLY	PRO	PRO	PRO	GLN	VAL	PRO	SER	ARG	PRO	ASN	ARG	ALA	PRO	PRO	GLY	VAL	PRO	SER	SER	GLY	GLN	ALA	SER	PRO	SER	ARG	PRO	GLU	SER	PRO	ARG	PRO	PHE	ASP	LEU
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4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	7525	Depositor
Resolution determination method	Not provided	
CTF correction method	INDIVIDUAL IMAGES	Depositor
Microscope	FEI/PHILIPS CM300FEG/HE	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	49000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	18.352	Depositor
Minimum map value	-18.065	Depositor
Average map value	0.361	Depositor
Map value standard deviation	3.624	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	510.0, 510.0, 510.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.55, 2.55, 2.55	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	1.06	6/2604 (0.2%)	1.76	88/3524 (2.5%)
1	D	1.26	14/2683 (0.5%)	2.06	112/3630 (3.1%)
1	G	1.06	7/2604 (0.3%)	1.76	88/3524 (2.5%)
1	K	1.26	14/2683 (0.5%)	2.06	112/3630 (3.1%)
2	B	1.86	31/1748 (1.8%)	3.16	156/2331 (6.7%)
2	C	1.20	11/966 (1.1%)	2.15	54/1298 (4.2%)
2	E	2.01	50/1748 (2.9%)	3.30	186/2331 (8.0%)
2	F	1.74	21/966 (2.2%)	2.60	80/1298 (6.2%)
2	H	1.20	11/966 (1.1%)	2.15	53/1298 (4.1%)
2	I	1.86	31/1748 (1.8%)	3.16	156/2331 (6.7%)
2	J	2.01	50/1748 (2.9%)	3.29	184/2331 (7.9%)
2	L	1.74	21/966 (2.2%)	2.60	80/1298 (6.2%)
All	All	1.51	267/21430 (1.2%)	2.50	1349/28824 (4.7%)

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	A	1	11
1	D	0	14
1	G	1	12
1	K	0	14
2	B	5	40
2	C	4	9
2	E	10	36
2	F	7	10
2	H	4	9
2	I	5	39
2	J	10	36
2	L	7	10
All	All	54	240

The worst 5 of 267 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	492	ASP	C-O	-22.46	0.95	1.24
2	B	492	ASP	C-O	-22.46	0.95	1.24
2	E	492	ASP	C-O	-22.01	0.96	1.24
2	J	492	ASP	C-O	-22.00	0.96	1.24
2	E	490	HIS	CG-CD2	-19.26	1.14	1.35

The worst 5 of 1349 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	489	ASN	O-C-N	-36.81	73.63	122.59
2	I	489	ASN	O-C-N	-36.79	73.66	122.59
2	J	490	HIS	ND1-CG-CD2	-31.84	74.26	106.10
2	E	490	HIS	ND1-CG-CD2	-31.83	74.27	106.10
2	E	491	GLU	O-C-N	-29.54	83.49	122.19

5 of 54 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	726	ASP	CA
2	B	339	ASP	CA
2	B	442	CYS	CA
2	B	489	ASN	CA
2	B	490	HIS	CA

5 of 240 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	105	THR	Mainchain
1	A	123	ARG	Sidechain
1	A	28	ASP	Mainchain
1	A	41	SER	Mainchain
1	A	50	ASN	Sidechain

5.2 Too-close contacts [i](#)

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	2567	0	2629	80	0
1	D	2643	0	2693	169	0
1	G	2567	0	2629	76	0
1	K	2643	0	2693	173	0
2	B	1728	0	1780	205	0
2	C	946	0	939	29	0
2	E	1728	0	1780	294	0
2	F	946	0	938	29	0
2	H	946	0	939	29	0
2	I	1728	0	1780	103	0
2	J	1728	0	1780	197	0
2	L	946	0	938	27	0
All	All	21116	0	21518	1106	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 26.

The worst 5 of 1106 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)
2:J:491:GLU:CB	2:J:491:GLU:CA	1.74	1.58
2:E:491:GLU:CB	2:E:491:GLU:CA	1.74	1.57
2:B:338:VAL:HG13	2:E:687:HIS:CE1	1.40	1.54
2:B:463:HIS:HE1	2:E:334:GLN:CD	1.19	1.46
2:J:453:ARG:HG2	1:K:318:ARG:N	1.17	1.44

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	325/864 (38%)	313 (96%)	10 (3%)	2 (1%)	21 59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	333/864 (38%)	317 (95%)	14 (4%)	2 (1%)	21	59
1	G	325/864 (38%)	313 (96%)	10 (3%)	2 (1%)	21	59
1	K	333/864 (38%)	317 (95%)	14 (4%)	2 (1%)	21	59
2	B	196/864 (23%)	165 (84%)	22 (11%)	9 (5%)	2	17
2	C	111/864 (13%)	93 (84%)	13 (12%)	5 (4%)	2	17
2	E	196/864 (23%)	161 (82%)	27 (14%)	8 (4%)	2	18
2	F	111/864 (13%)	93 (84%)	12 (11%)	6 (5%)	1	15
2	H	111/864 (13%)	93 (84%)	13 (12%)	5 (4%)	2	17
2	I	196/864 (23%)	165 (84%)	22 (11%)	9 (5%)	2	17
2	J	196/864 (23%)	161 (82%)	27 (14%)	8 (4%)	2	18
2	L	111/864 (13%)	93 (84%)	12 (11%)	6 (5%)	1	15
All	All	2544/10368 (24%)	2284 (90%)	196 (8%)	64 (2%)	6	26

5 of 64 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	88	GLY
2	B	489	ASN
2	B	490	HIS
2	B	492	ASP
2	C	534	MET

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	287/761 (38%)	272 (95%)	15 (5%)	21	42
1	D	295/761 (39%)	282 (96%)	13 (4%)	25	47
1	G	287/761 (38%)	272 (95%)	15 (5%)	21	42
1	K	295/761 (39%)	282 (96%)	13 (4%)	25	47
2	B	194/761 (26%)	150 (77%)	44 (23%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	102/761 (13%)	94 (92%)	8 (8%)	11	32
2	E	194/761 (26%)	153 (79%)	41 (21%)	1	6
2	F	102/761 (13%)	89 (87%)	13 (13%)	4	16
2	H	102/761 (13%)	94 (92%)	8 (8%)	11	32
2	I	194/761 (26%)	150 (77%)	44 (23%)	1	6
2	J	194/761 (26%)	153 (79%)	41 (21%)	1	6
2	L	102/761 (13%)	89 (87%)	13 (13%)	4	16
All	All	2348/9132 (26%)	2080 (89%)	268 (11%)	8	18

5 of 268 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	J	664	ASN
2	J	692	ASN
2	L	569	ASN
2	E	451	ARG
2	E	445	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
2	J	692	ASN
1	K	25	GLN
1	K	155	GLN
1	D	148	GLN
1	D	131	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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
1	D	1
1	K	1
2	B	1
2	I	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	316:ASN	C	317:PHE	N	1.18
1	K	316:ASN	C	317:PHE	N	1.18
1	B	489:ASN	C	490:HIS	N	1.17
1	I	489:ASN	C	490:HIS	N	1.17

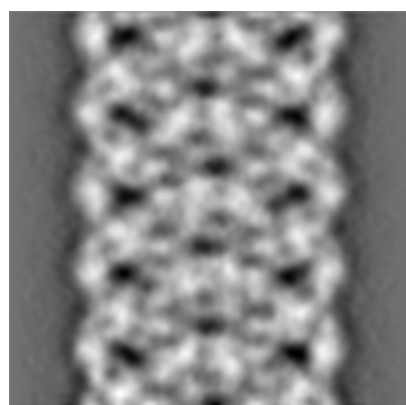
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2701. These allow visual inspection of the internal detail of the map and identification of artifacts.

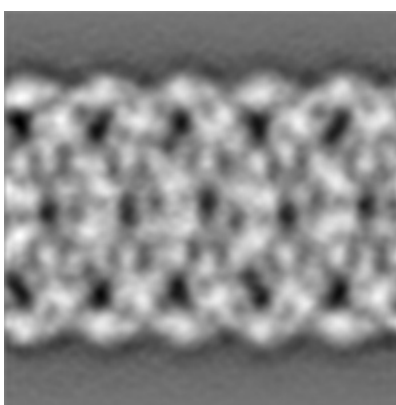
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

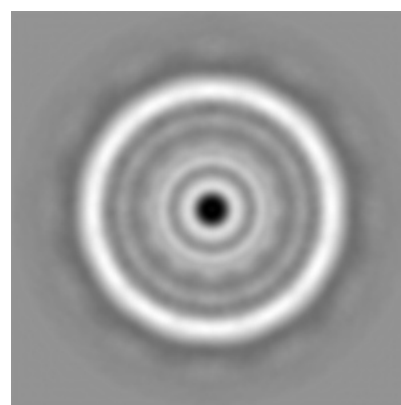
6.1.1 Primary map



X



Y

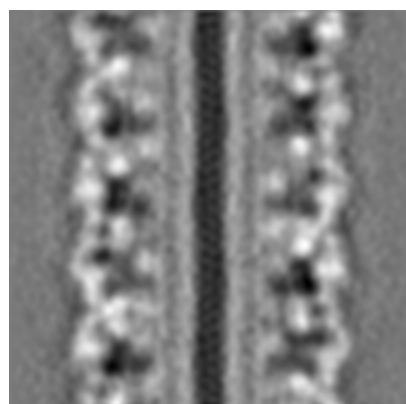


Z

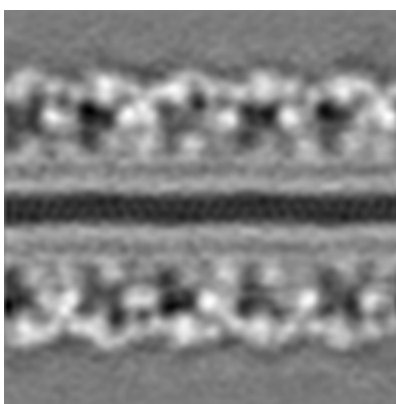
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 100



Y Index: 100

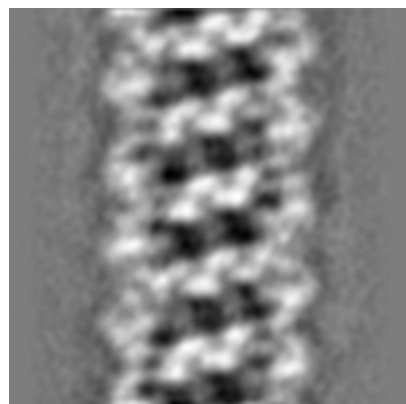


Z Index: 100

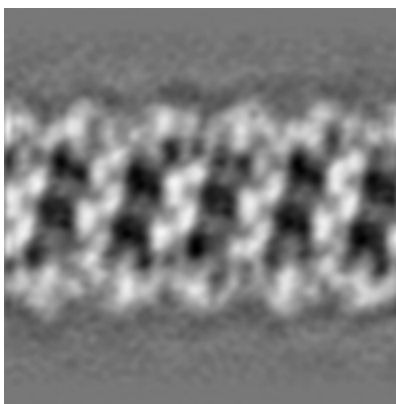
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 145



Y Index: 55

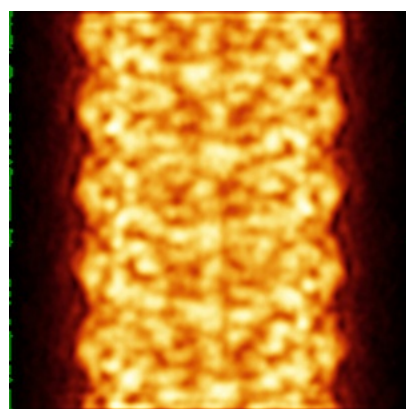


Z Index: 197

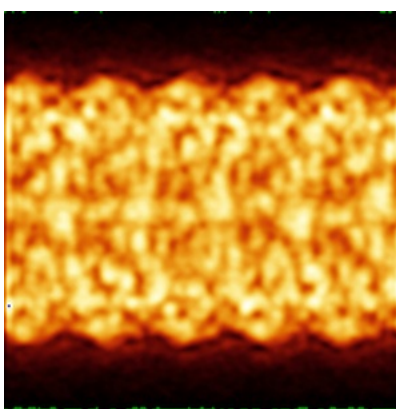
The images above show the largest variance slices of the map in three orthogonal directions.

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

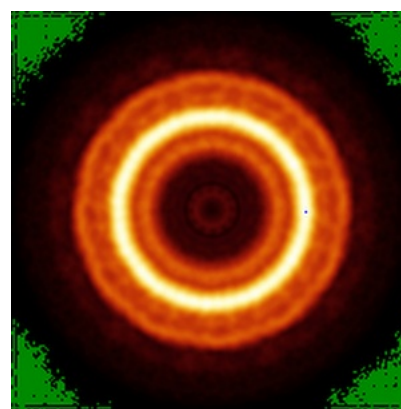
6.4.1 Primary map



X



Y

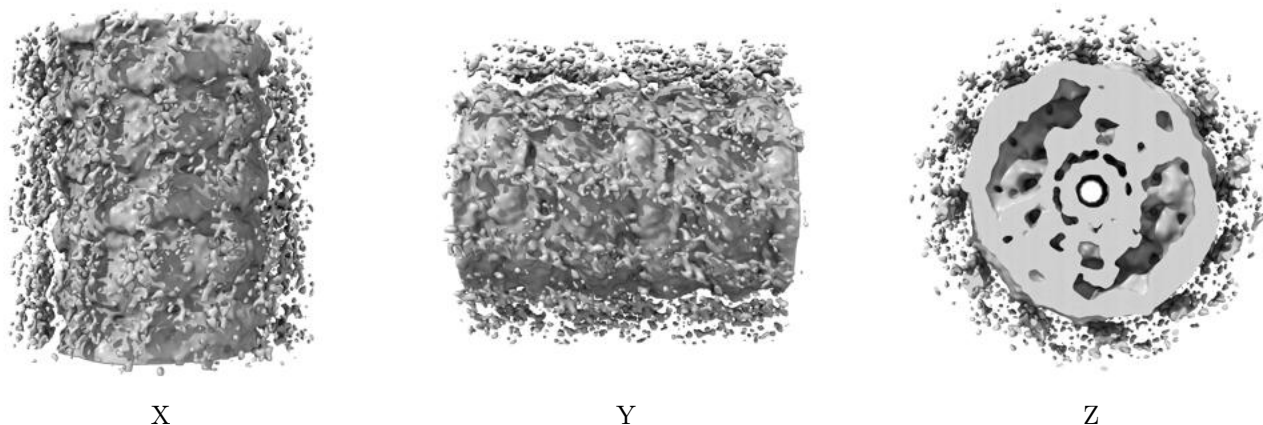


Z

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 0.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

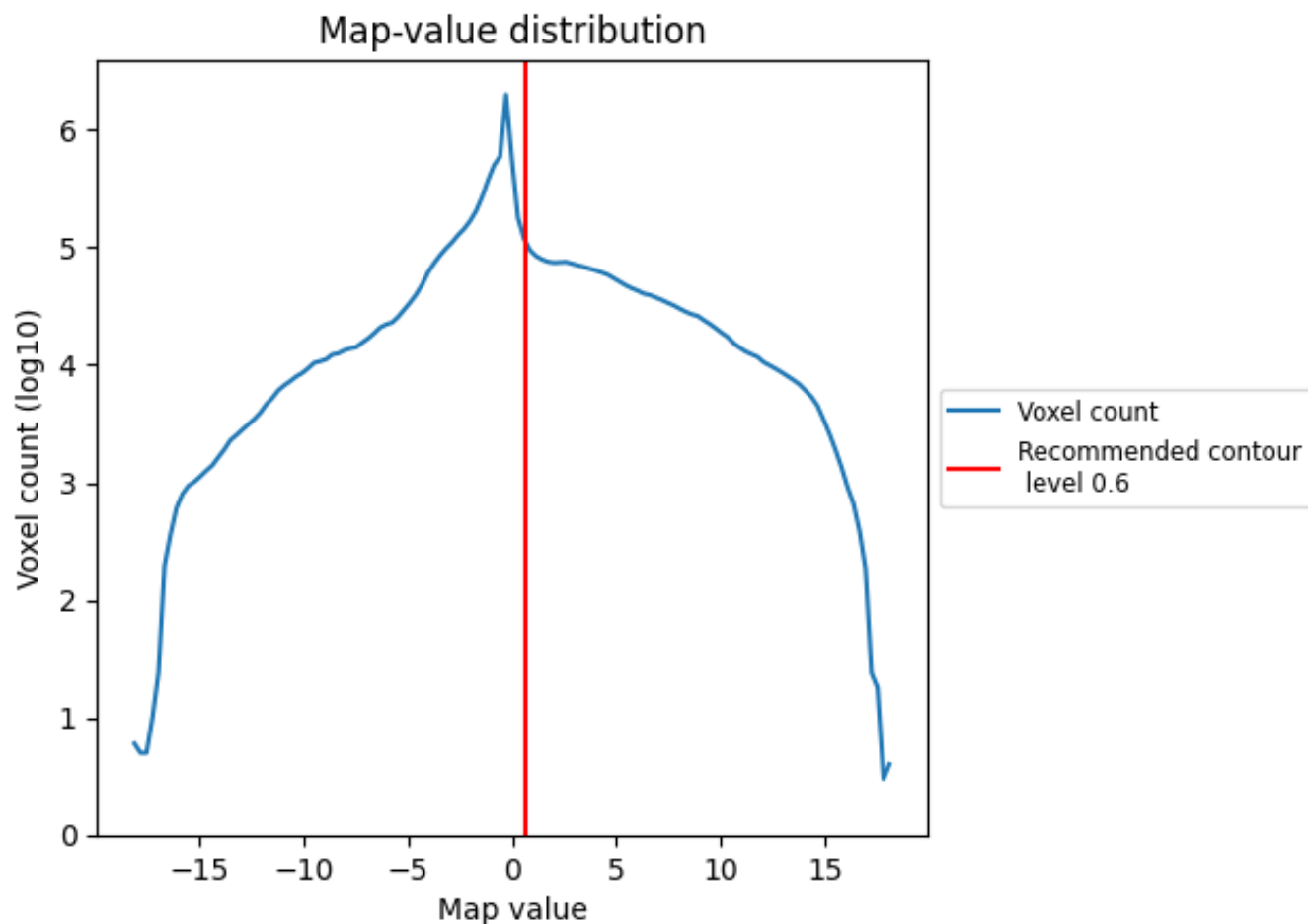
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

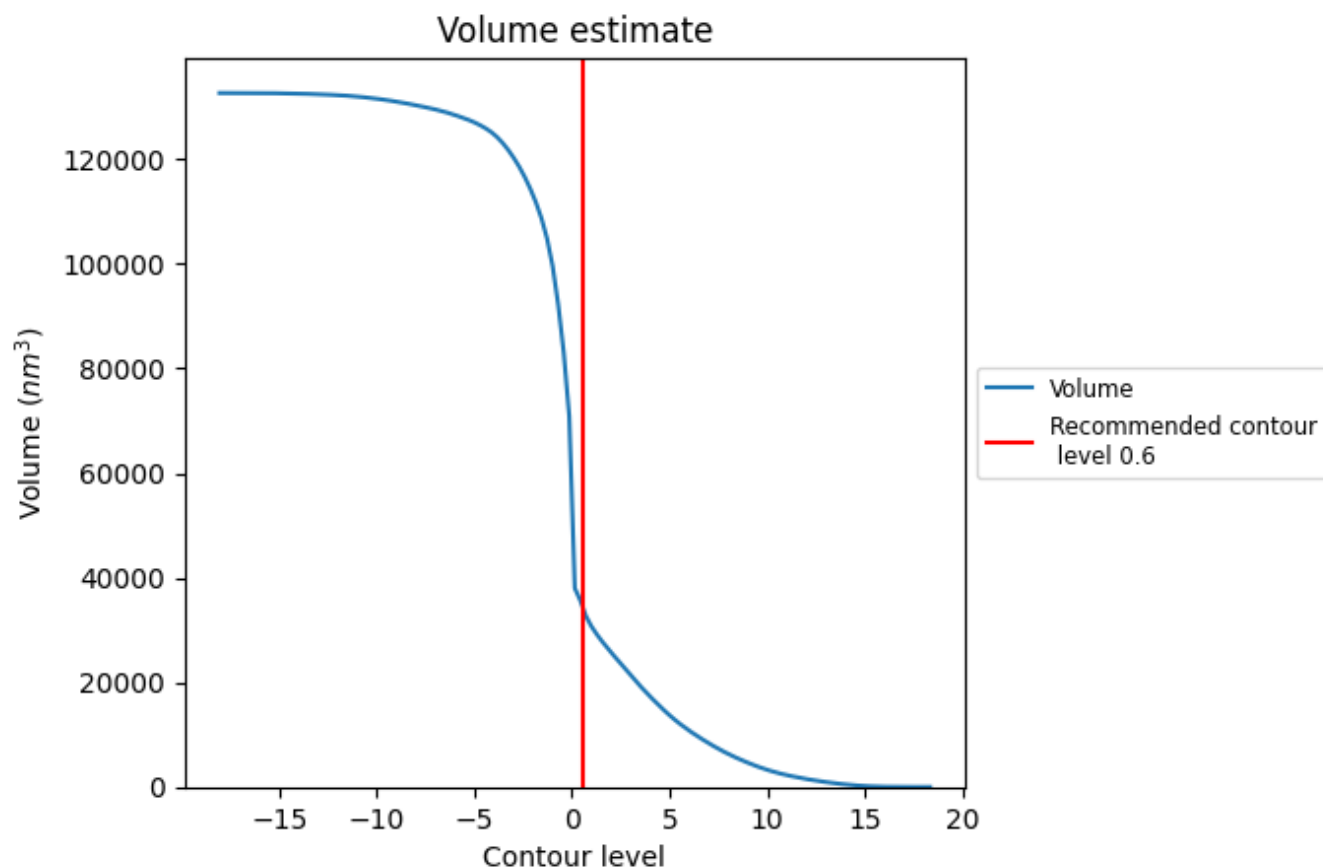
This section contains the results of statistical analysis of the map.

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.

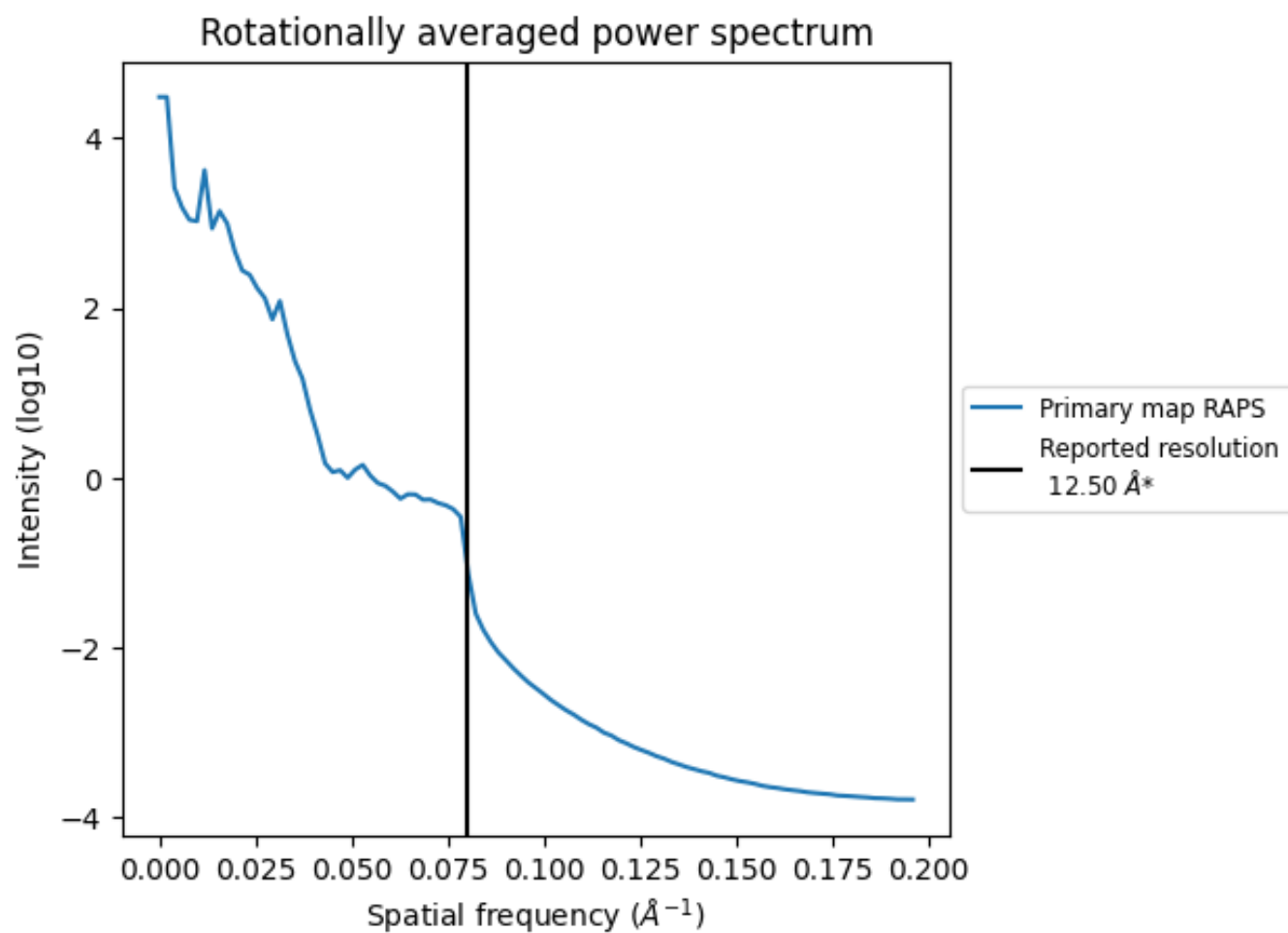
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 33840 nm^3 ; this corresponds to an approximate mass of 30569 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.080 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-2701 and PDB model 4UUK. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

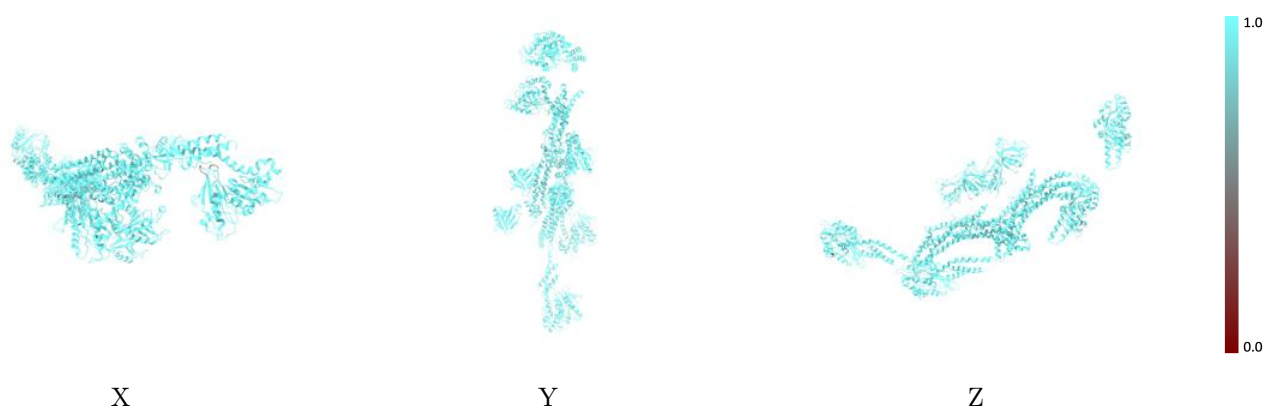
This section was not generated.

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



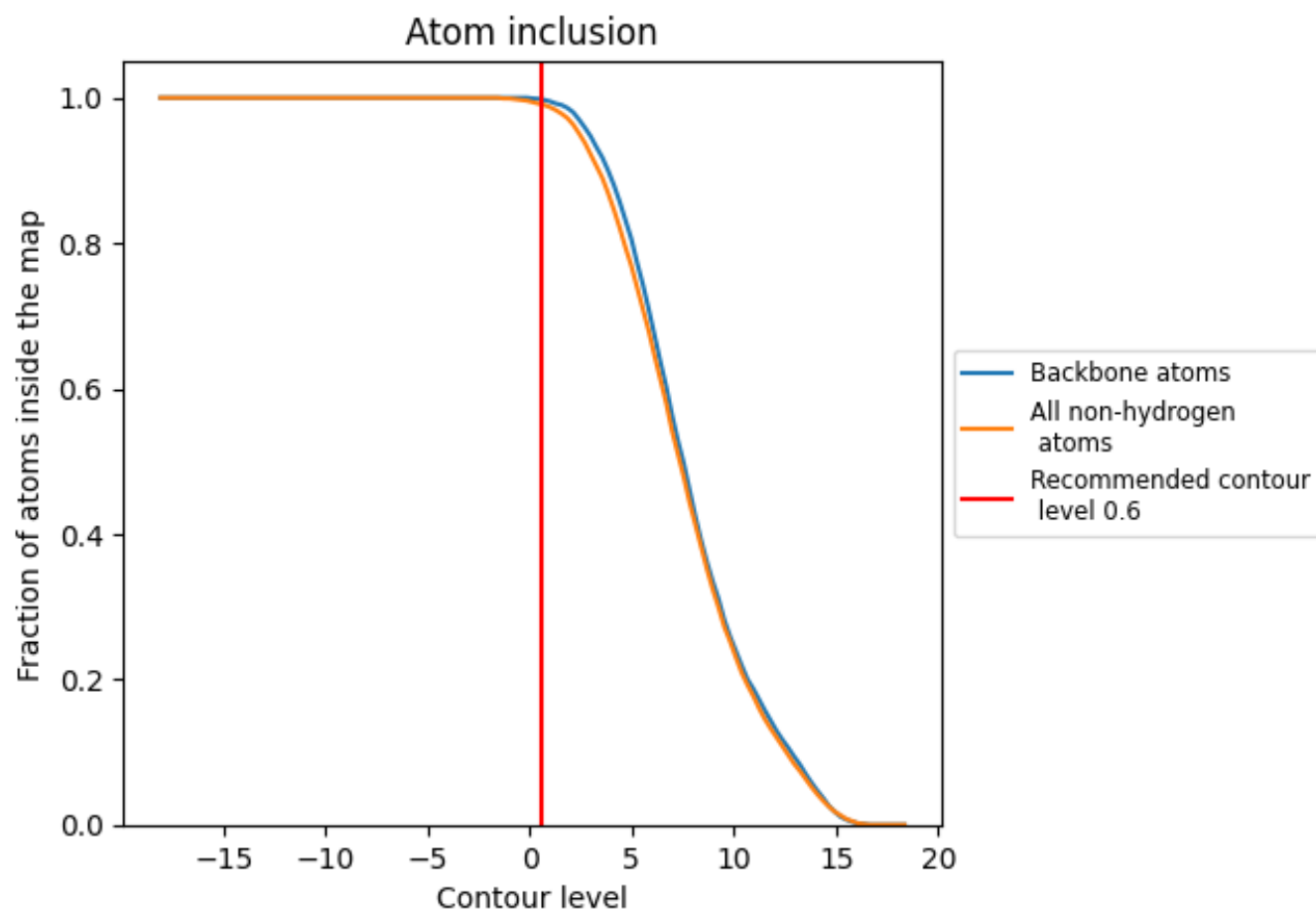
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 99% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9910	0.0570
A	0.9880	0.0550
B	0.9890	0.0420
C	0.9810	0.0730
D	0.9960	0.0570
E	0.9940	0.0620
F	0.9910	0.0590
G	0.9870	0.0550
H	0.9820	0.0730
I	0.9910	0.0410
J	0.9940	0.0640
K	0.9960	0.0570
L	0.9920	0.0570

1.0

0.0

<0.0