



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 01:20 AM UTC

PDB ID : 7NHT / pdb_00007nht
EMDB ID : EMD-12341
Title : Akirin2 bound human proteasome
Authors : Singh, K.; Brunner, H.; Grishkovskaya, I.; de Almeida, M.; Hinterndorfer, M.; Zuber, J.; Haselbach, D.
Deposited on : 2021-02-11
Resolution : 3.20 Å(reported)
Based on initial model : 5LE5

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:

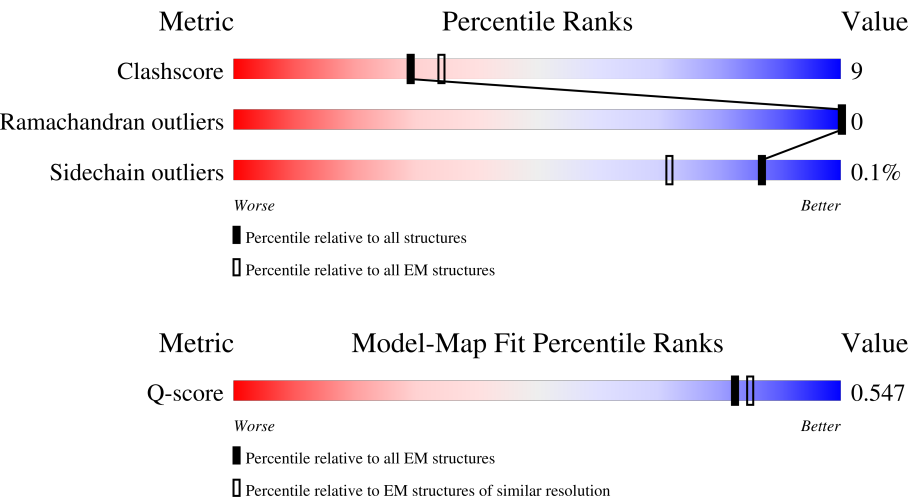
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	234	75% 24% .
2	B	261	74% 20% • 5%
3	C	248	75% 21% .
4	D	241	77% 23%

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Mol	Chain	Length	Quality of chain
5	E	263	
6	F	255	
7	G	246	
8	H	277	
9	I	205	
10	J	201	
11	K	263	
12	L	241	
13	M	264	
14	N	239	
15	c	203	
15	d	203	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 24915 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 Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	231	Total	C	N	O	S	0	0
			1799	1151	306	336	6		

- Molecule 2 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	248	Total	C	N	O	S	0	0
			1945	1228	334	373	10		

- Molecule 3 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	237	Total	C	N	O	S	0	0
			1846	1160	328	353	5		

- Molecule 4 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	241	Total	C	N	O	S	0	0
			1841	1157	303	369	12		

- Molecule 5 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	236	Total	C	N	O	S	0	0
			1846	1159	332	345	10		

- Molecule 6 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	242	Total	C	N	O	S	0	0
			1889	1199	323	356	11		

- Molecule 7 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	242	Total	C	N	O	S	0	0
			1882	1194	314	361	13		

- Molecule 8 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	220	Total	C	N	O	S	0	0
			1659	1044	283	320	12		

- Molecule 9 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	204	Total	C	N	O	S	0	0
			1591	1013	265	294	19		

- Molecule 10 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	196	Total	C	N	O	S	0	0
			1561	1001	264	287	9		

- Molecule 11 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	201	Total	C	N	O	S	0	0
			1555	980	273	293	9		

- Molecule 12 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	213	Total	C	N	O	S	0	0
			1650	1044	283	313	10		

- Molecule 13 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	216	Total	C	N	O	S	0	0
			1687	1064	291	320	12		

- Molecule 14 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	203	Total	C	N	O	S	0	0
			1517	952	259	294	12		

- Molecule 15 is a protein called Akirin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	c	48	Total	C	N	O	S	0	0
			332	207	60	64	1		
15	d	44	Total	C	N	O	S	0	0
			312	195	56	60	1		

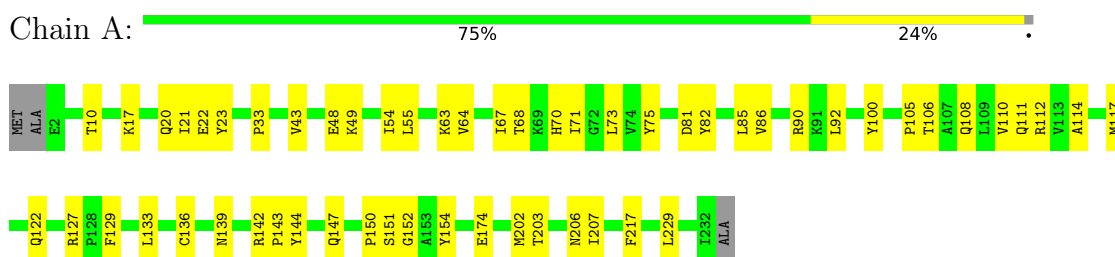
- Molecule 16 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
16	G	1	Total	K	0
			1	1	
16	L	1	Total	K	0
			1	1	
16	N	1	Total	K	0
			1	1	

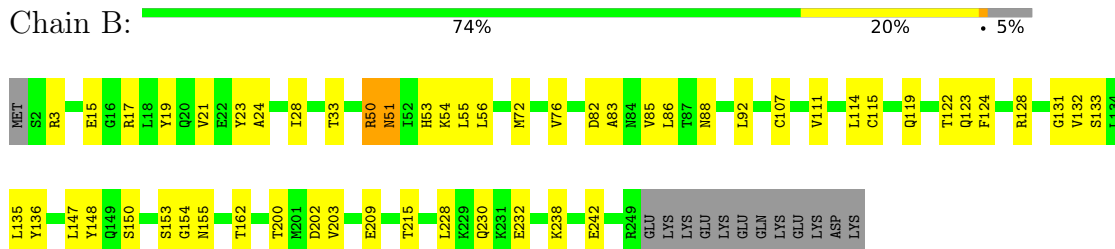
3 Residue-property plots [i](#)

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.

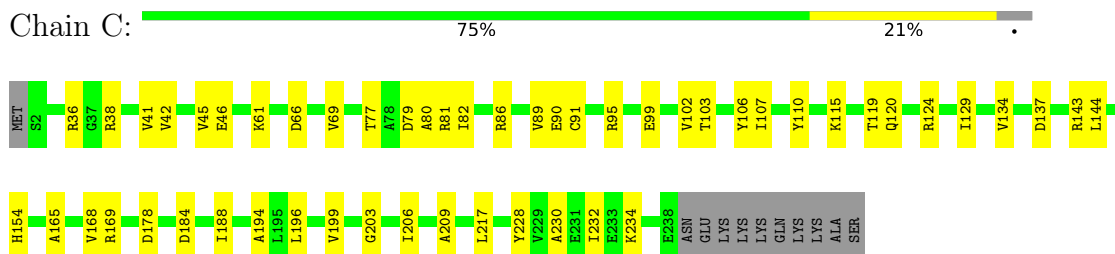
• Molecule 1: Proteasome subunit alpha type-2



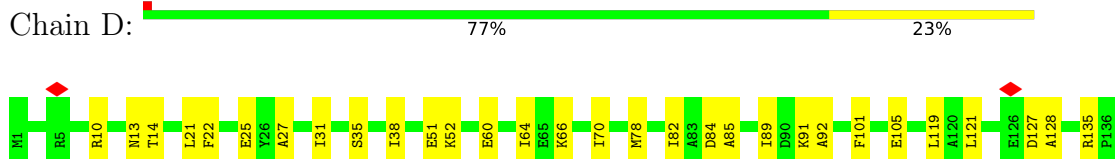
• Molecule 2: Proteasome subunit alpha type-4

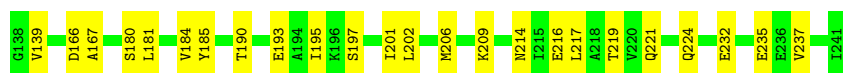


• Molecule 3: Proteasome subunit alpha type-7



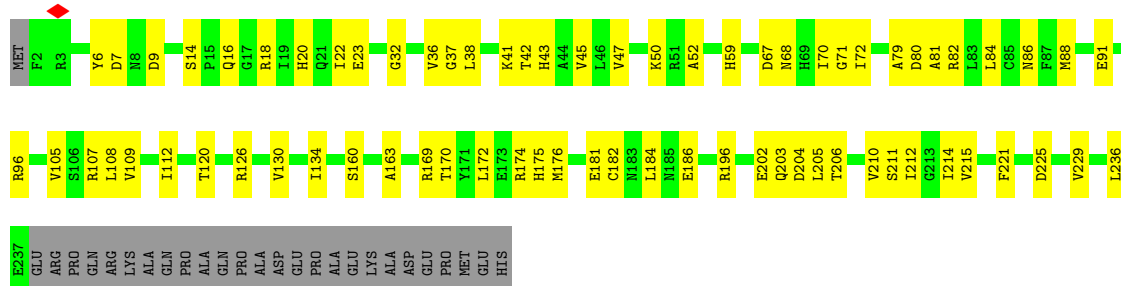
• Molecule 4: Proteasome subunit alpha type-5





• Molecule 5: Proteasome subunit alpha type-1

Chain E: 63% 27% 10%



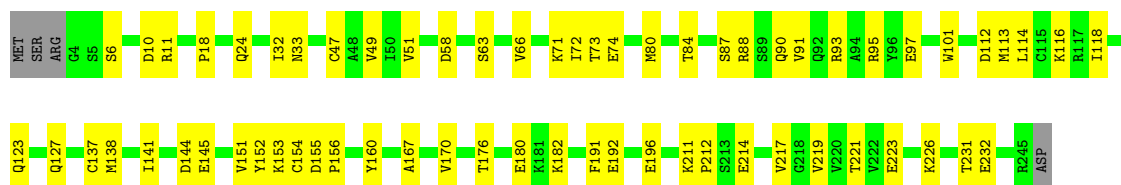
• Molecule 6: Proteasome subunit alpha type-3

Chain F: 71% 24% 5%



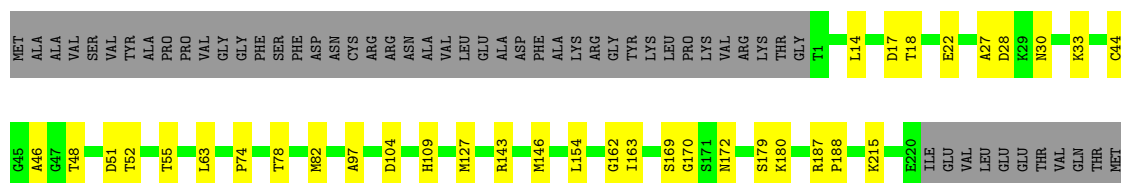
• Molecule 7: Proteasome subunit alpha type-6

Chain G: 72% 26% 2%



• Molecule 8: Proteasome subunit beta type-7

Chain H: 67% 13% 21%



ASP
THR
SER

• Molecule 9: Proteasome subunit beta type-3

Chain I:  76% 23%



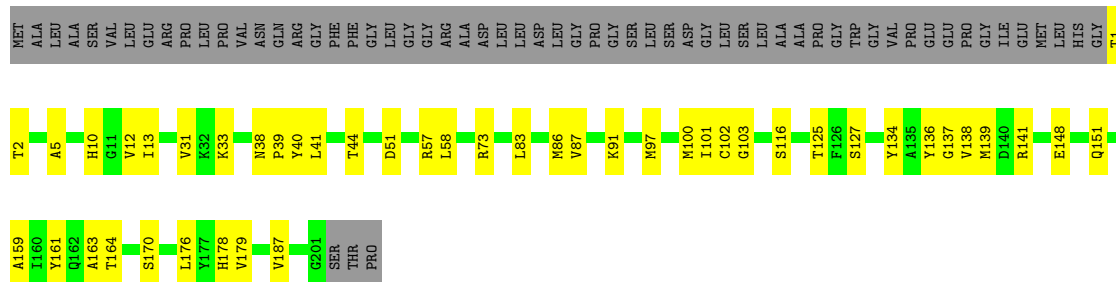
• Molecule 10: Proteasome subunit beta type-2

Chain J:  85% 13%



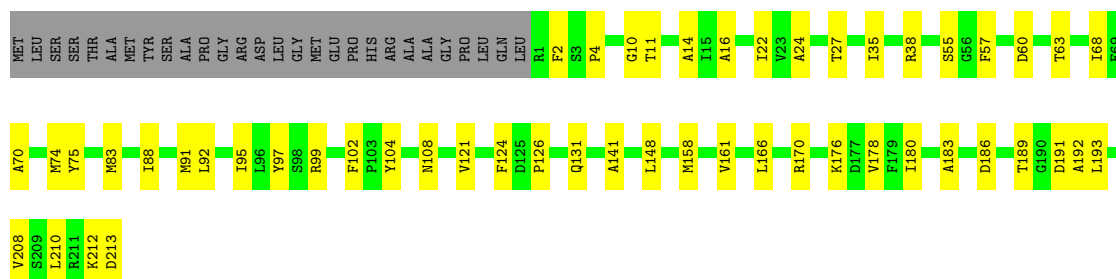
• Molecule 11: Proteasome subunit beta type-5

Chain K:  59% 17% 24%



• Molecule 12: Proteasome subunit beta type-1

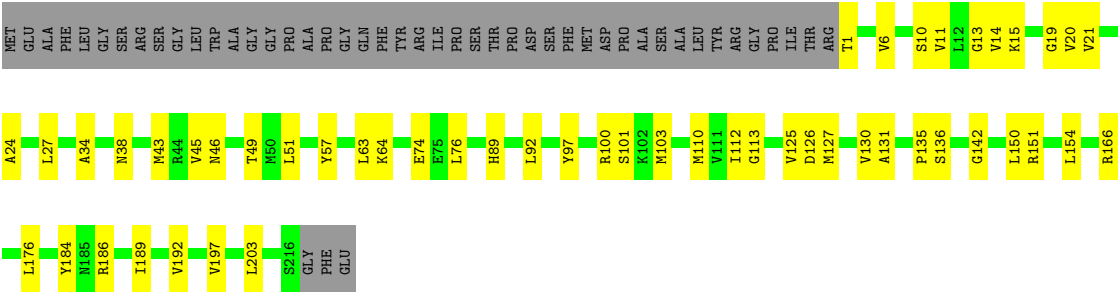
Chain L:  67% 22% 12%



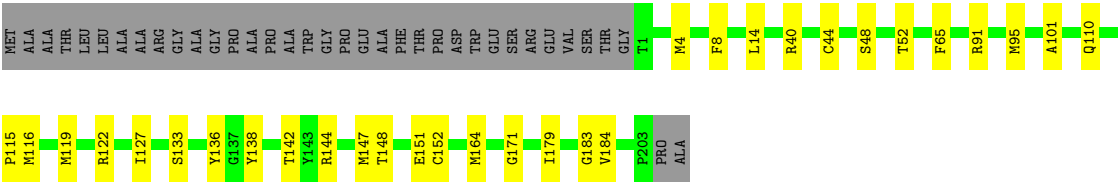
• Molecule 13: Proteasome subunit beta type-4

Chain M:  62% 20% 18%

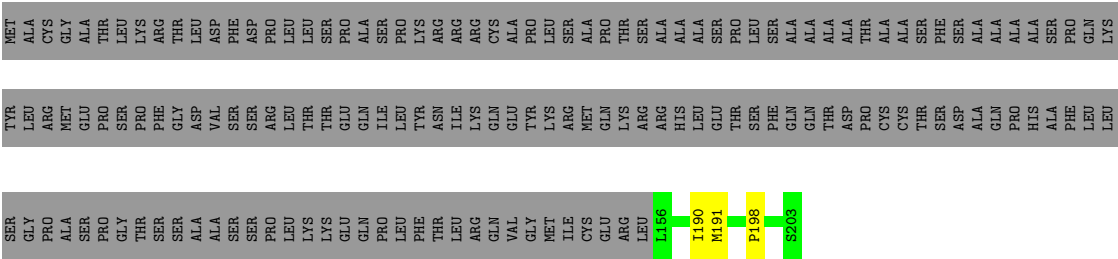




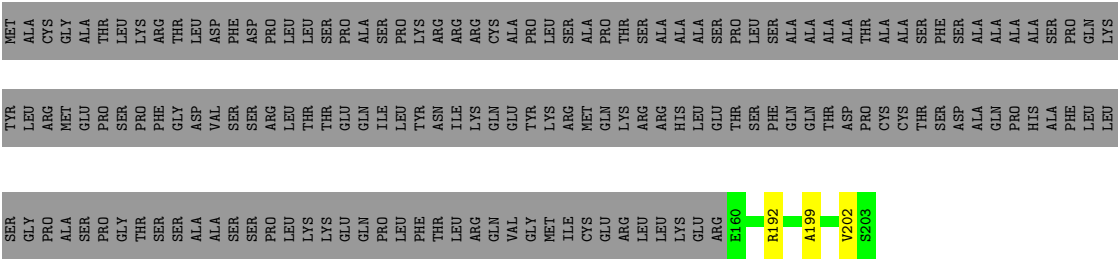
● Molecule 14: Proteasome subunit beta type-6



● Molecule 15: Akirin-2



● Molecule 15: Akirin-2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	37447	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 ($e^-/\text{\AA}^2$)	33	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.719	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	381.59998, 381.59998, 381.59998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:
K

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	0.21	0/1838	0.35	0/2490
2	B	0.24	0/1975	0.43	0/2663
3	C	0.25	0/1872	0.43	0/2530
4	D	0.20	0/1870	0.35	0/2528
5	E	0.22	0/1881	0.43	0/2544
6	F	0.23	0/1924	0.42	0/2591
7	G	0.22	0/1916	0.37	0/2591
8	H	0.20	0/1686	0.36	0/2282
9	I	0.22	0/1620	0.39	0/2184
10	J	0.22	0/1593	0.35	0/2156
11	K	0.22	0/1586	0.37	0/2142
12	L	0.22	0/1680	0.41	0/2264
13	M	0.22	0/1720	0.37	0/2328
14	N	0.22	0/1544	0.36	0/2092
15	c	0.14	0/338	0.34	0/459
15	d	0.12	0/318	0.27	0/431
All	All	0.22	0/25361	0.39	0/34275

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1799	0	1793	43	0
2	B	1945	0	1951	43	0
3	C	1846	0	1853	33	0
4	D	1841	0	1814	42	0
5	E	1846	0	1824	48	0
6	F	1889	0	1878	44	0
7	G	1882	0	1881	46	0
8	H	1659	0	1681	22	0
9	I	1591	0	1612	34	0
10	J	1561	0	1558	21	0
11	K	1555	0	1517	30	0
12	L	1650	0	1645	39	0
13	M	1687	0	1666	40	0
14	N	1517	0	1490	20	0
15	c	332	0	250	3	0
15	d	312	0	242	2	0
16	G	1	0	0	0	0
16	L	1	0	0	0	0
16	N	1	0	0	0	0
All	All	24915	0	24655	461	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 9.

The worst 5 of 461 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:B:136:TYR:HE1	2:B:150:SER:HG	0.97	0.91
7:G:231:THR:HG22	7:G:232:GLU:H	1.40	0.86
8:H:163:ILE:HG12	8:H:170:GLY:HA2	1.58	0.85
7:G:231:THR:HG22	7:G:232:GLU:N	1.93	0.84
4:D:121:LEU:HD12	5:E:79:ALA:HB3	1.67	0.77

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	229/234 (98%)	224 (98%)	5 (2%)	0	100	100
2	B	246/261 (94%)	242 (98%)	4 (2%)	0	100	100
3	C	235/248 (95%)	230 (98%)	5 (2%)	0	100	100
4	D	239/241 (99%)	230 (96%)	9 (4%)	0	100	100
5	E	234/263 (89%)	225 (96%)	9 (4%)	0	100	100
6	F	240/255 (94%)	234 (98%)	6 (2%)	0	100	100
7	G	240/246 (98%)	232 (97%)	8 (3%)	0	100	100
8	H	218/277 (79%)	213 (98%)	5 (2%)	0	100	100
9	I	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
10	J	194/201 (96%)	189 (97%)	5 (3%)	0	100	100
11	K	199/263 (76%)	194 (98%)	5 (2%)	0	100	100
12	L	211/241 (88%)	206 (98%)	5 (2%)	0	100	100
13	M	214/264 (81%)	207 (97%)	7 (3%)	0	100	100
14	N	201/239 (84%)	195 (97%)	6 (3%)	0	100	100
15	c	46/203 (23%)	44 (96%)	2 (4%)	0	100	100
15	d	42/203 (21%)	42 (100%)	0	0	100	100
All	All	3190/3844 (83%)	3101 (97%)	89 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	188/191 (98%)	188 (100%)	0	100	100
2	B	206/221 (93%)	204 (99%)	2 (1%)	68	80
3	C	195/211 (92%)	194 (100%)	1 (0%)	81	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	201/203 (99%)	201 (100%)	0	100	100
5	E	198/224 (88%)	198 (100%)	0	100	100
6	F	198/212 (93%)	198 (100%)	0	100	100
7	G	205/210 (98%)	205 (100%)	0	100	100
8	H	181/228 (79%)	181 (100%)	0	100	100
9	I	173/174 (99%)	173 (100%)	0	100	100
10	J	165/171 (96%)	165 (100%)	0	100	100
11	K	155/202 (77%)	155 (100%)	0	100	100
12	L	177/199 (89%)	177 (100%)	0	100	100
13	M	179/215 (83%)	179 (100%)	0	100	100
14	N	157/181 (87%)	157 (100%)	0	100	100
15	c	23/171 (14%)	23 (100%)	0	100	100
15	d	23/171 (14%)	23 (100%)	0	100	100
All	All	2624/3184 (82%)	2621 (100%)	3 (0%)	87	91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	50	ARG
2	B	51	ASN
3	C	99	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	90	GLN
9	I	6	ASN
7	G	24	GLN
10	J	186	ASN
3	C	68	ASN

5.3.3 RNA ⓘ

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](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

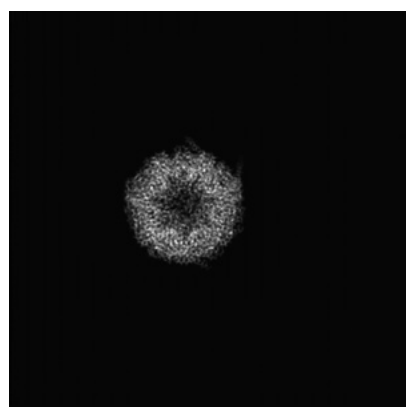
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12341. These allow visual inspection of the internal detail of the map and identification of artifacts.

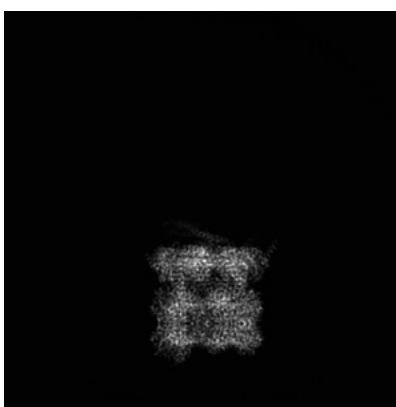
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

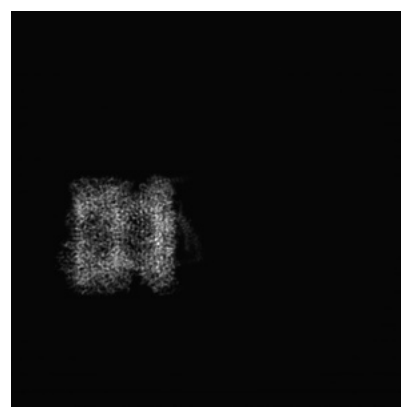
6.1.1 Primary map



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: 180



Y Index: 180



Z Index: 180

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: 131



Y Index: 180

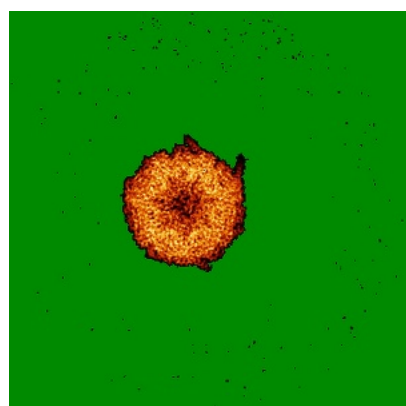


Z Index: 159

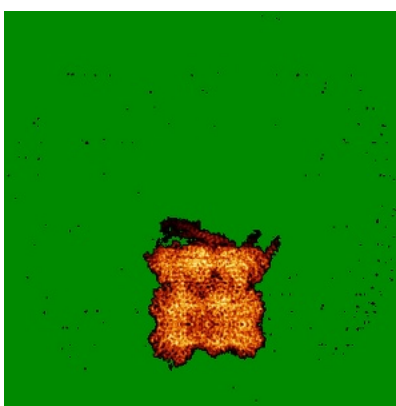
The images above show the largest variance slices of the map in three orthogonal directions.

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

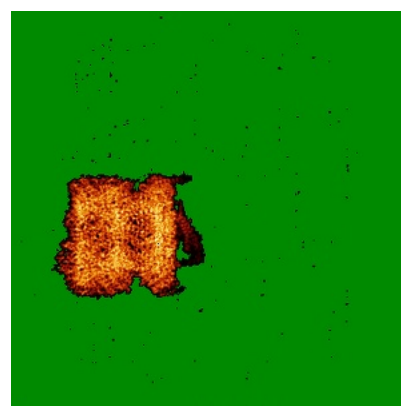
6.4.1 Primary map



X



Y

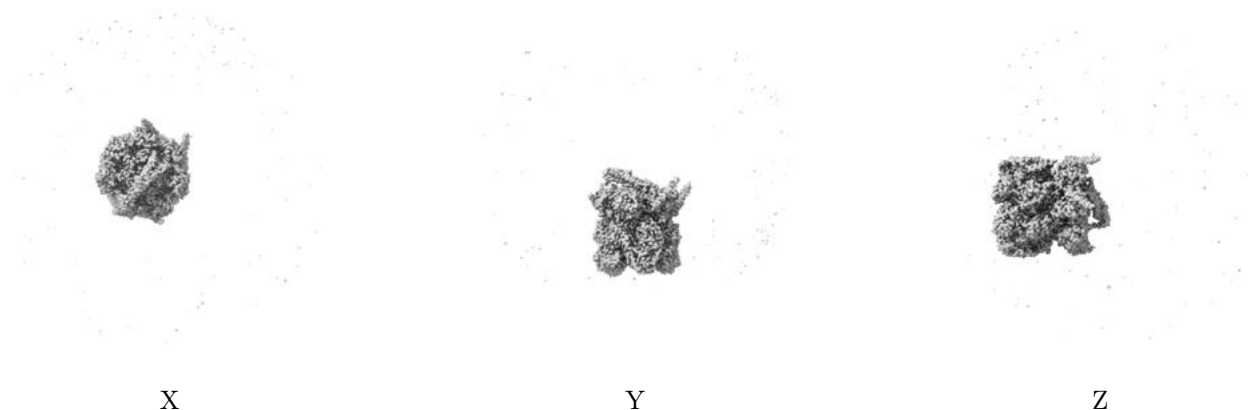


Z

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

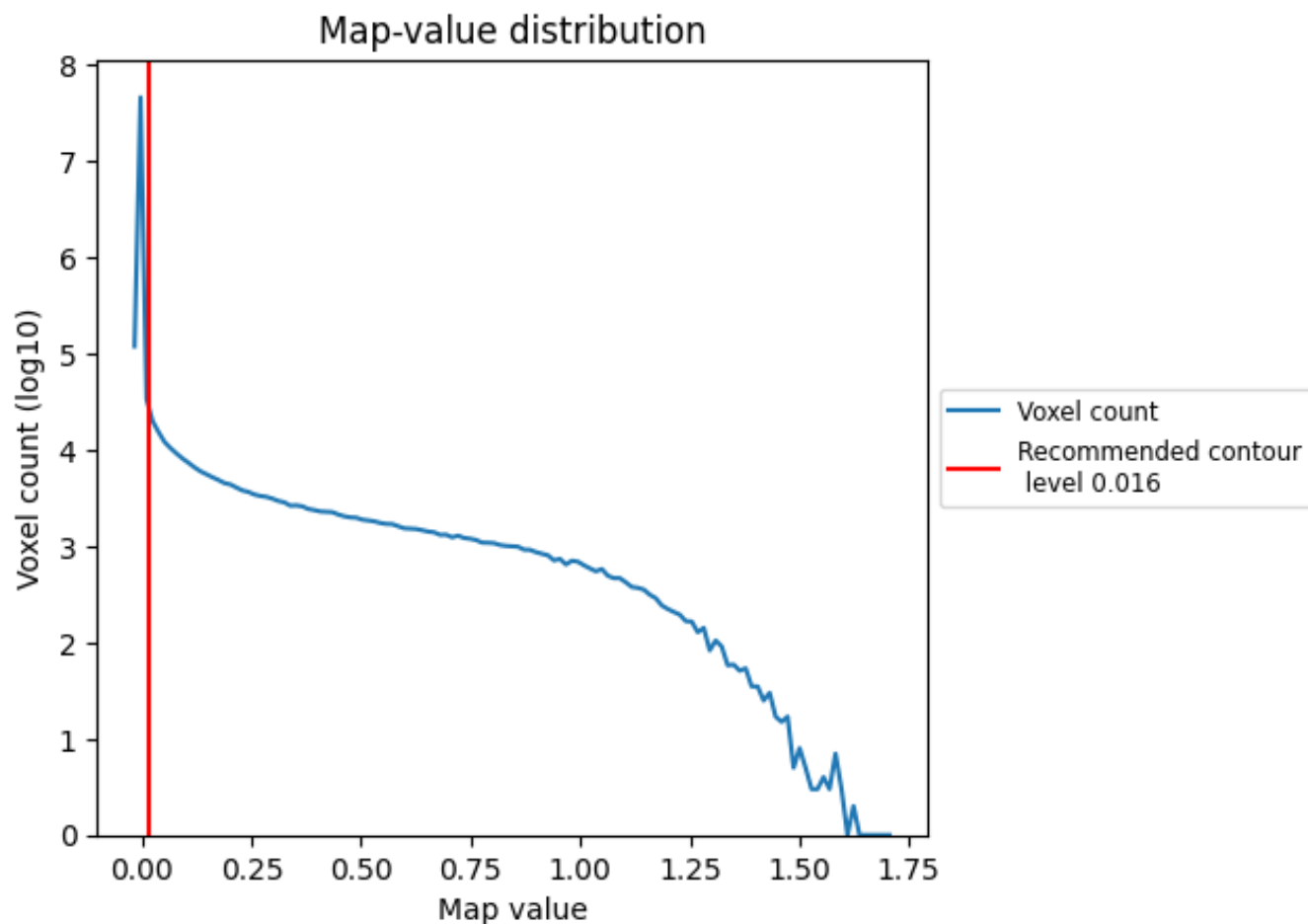
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

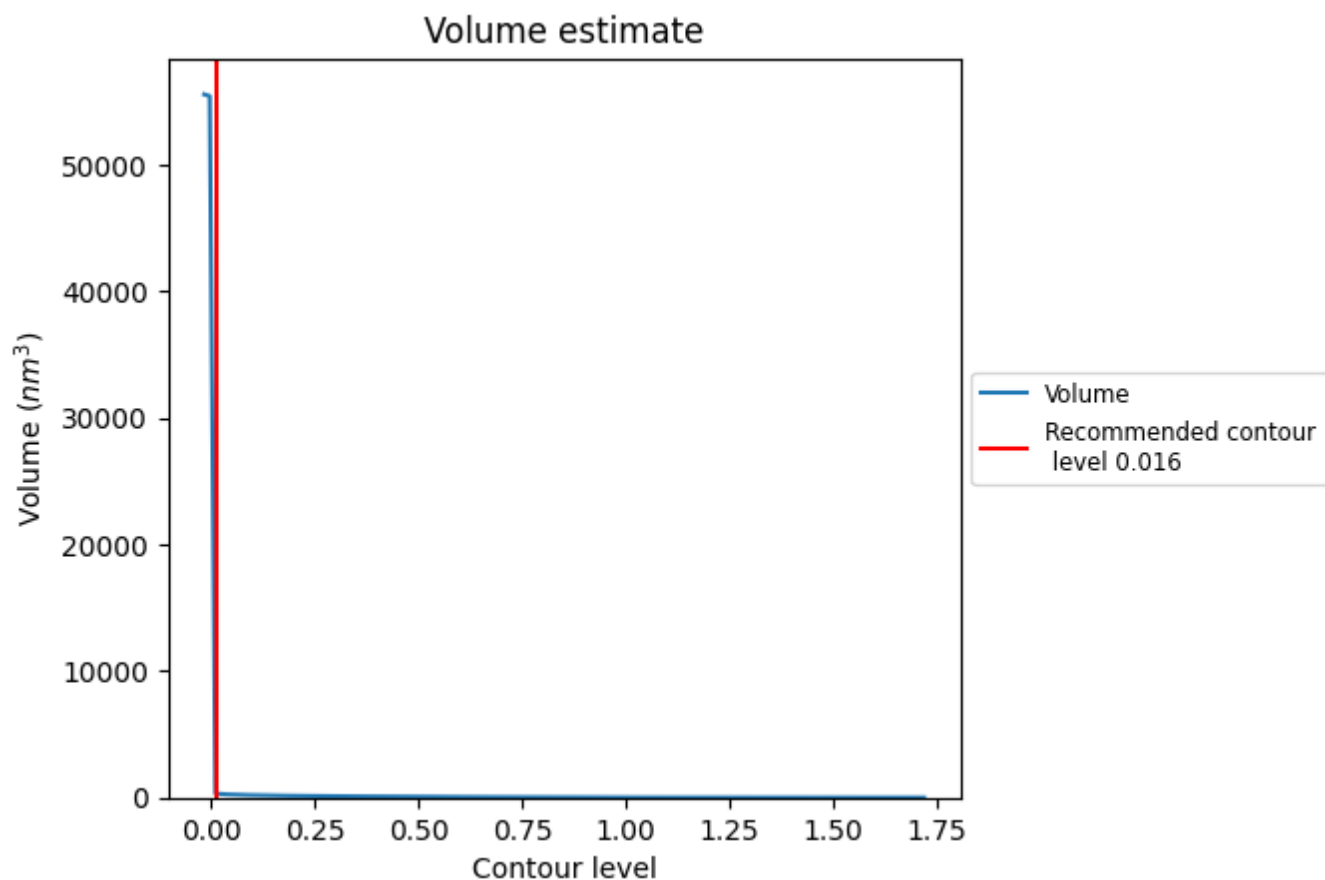
This section contains the results of statistical analysis of the map.

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.

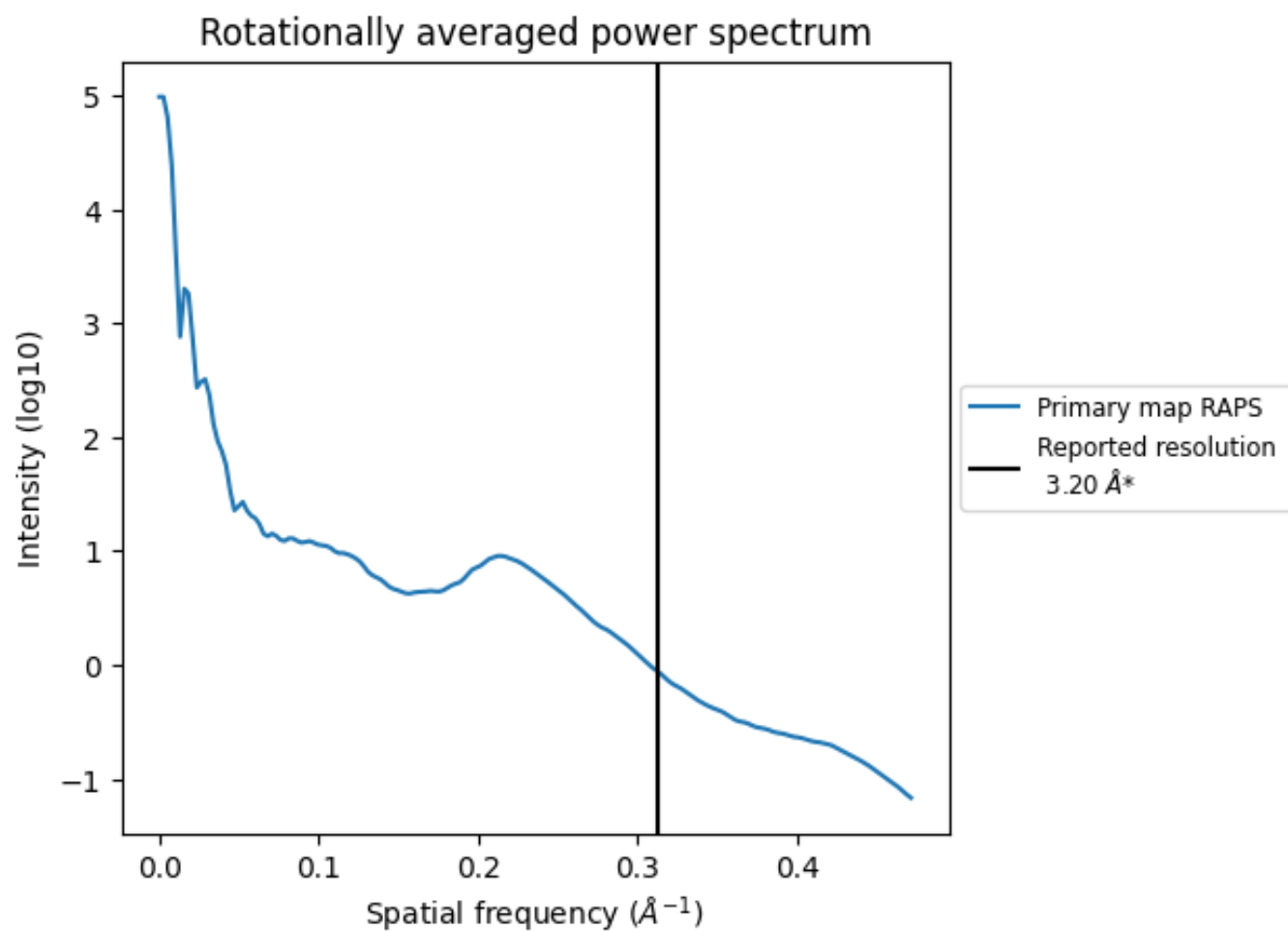
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 302 nm^3 ; this corresponds to an approximate mass of 273 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 0.312 Å⁻¹

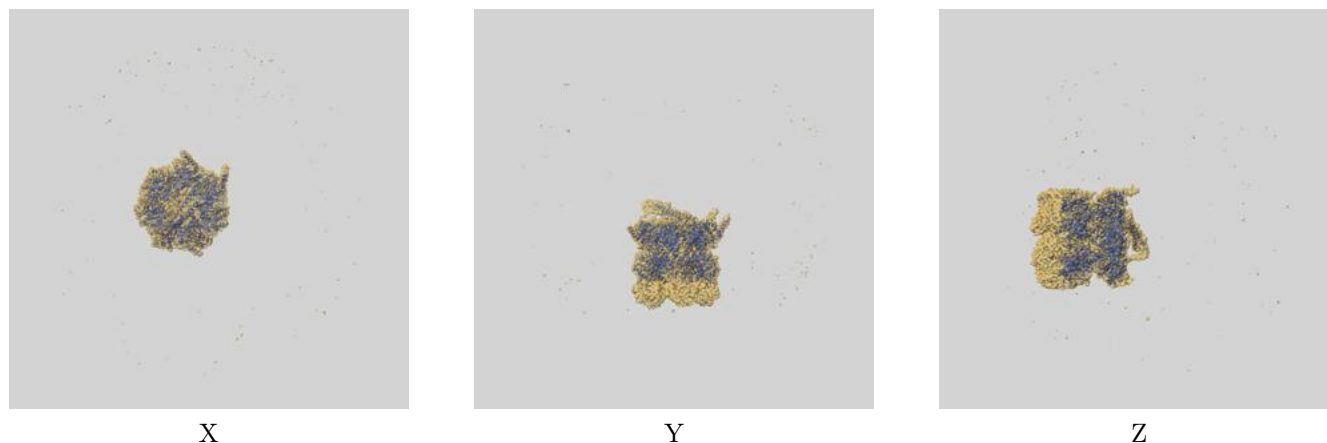
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

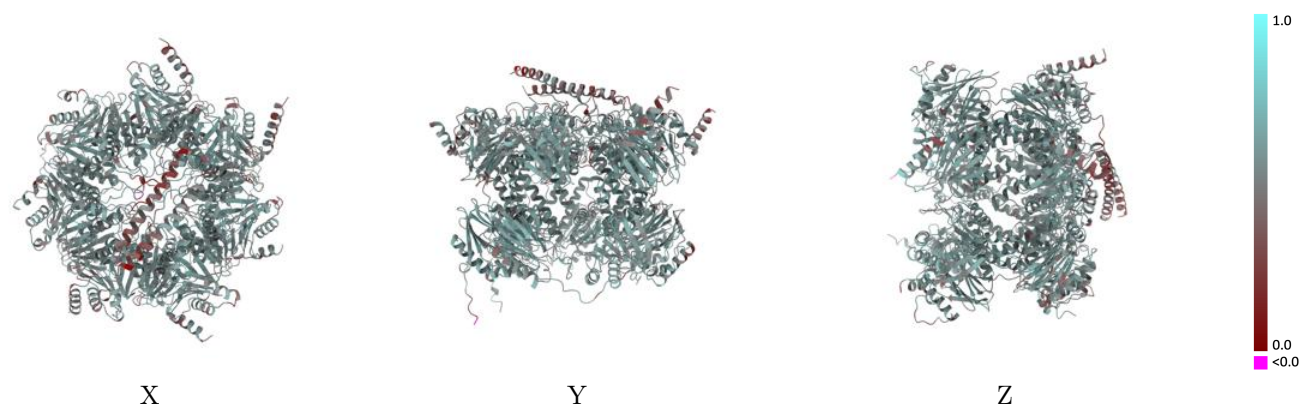
This section contains information regarding the fit between EMDB map EMD-12341 and PDB model 7NHT. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



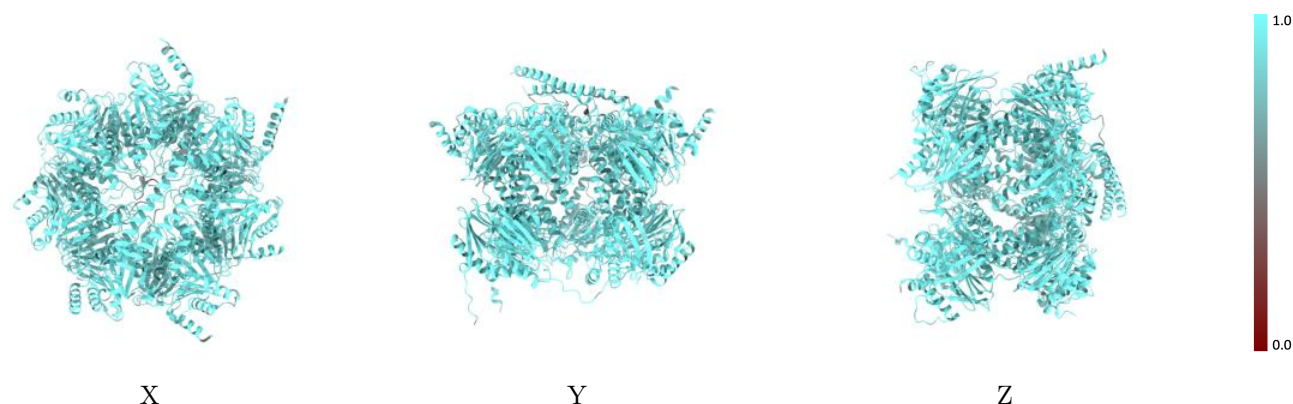
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



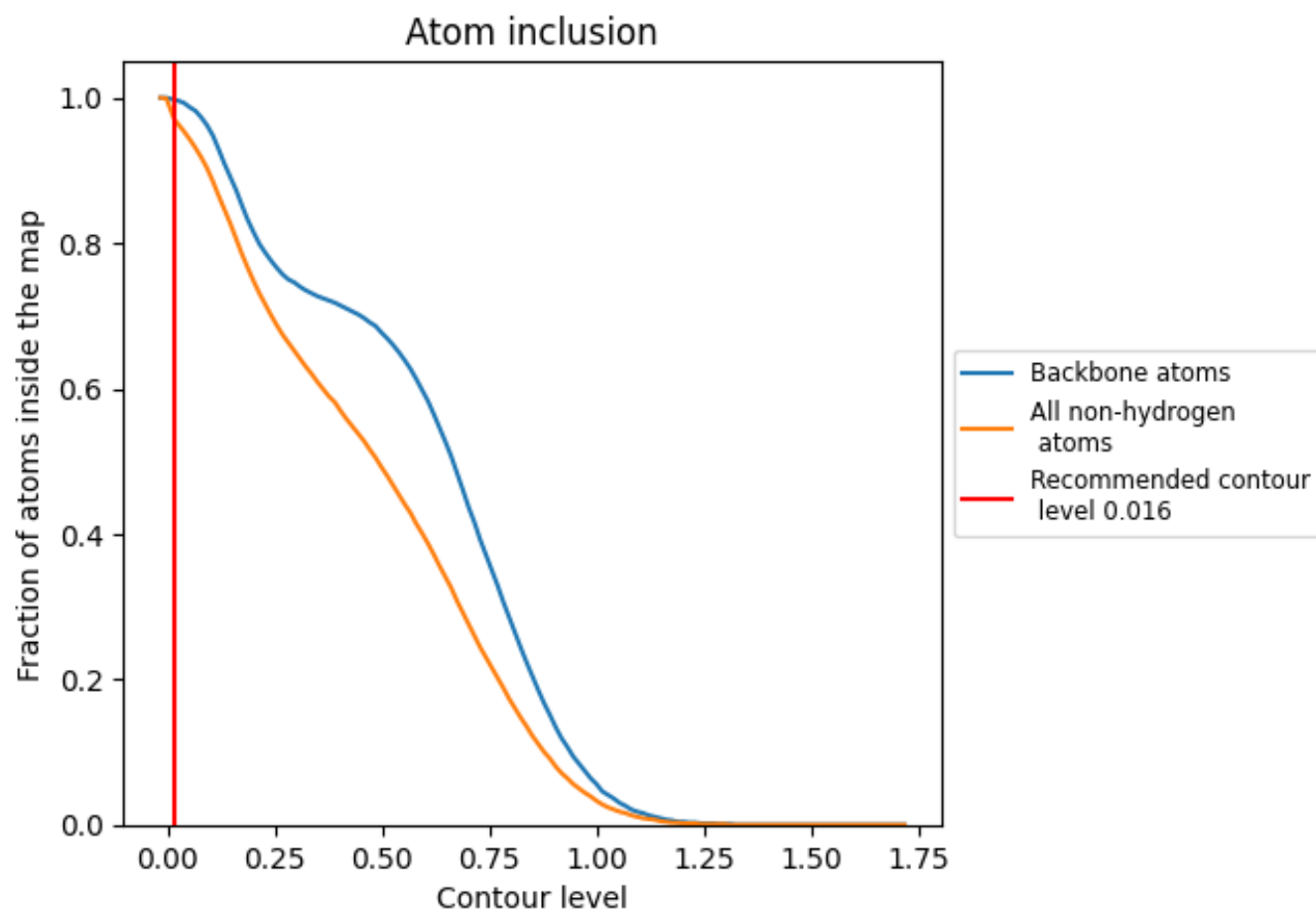
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.016).

9.4 Atom inclusion ⓘ



At the recommended contour level, 100% of all backbone atoms, 97% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9700	0.5470
A	0.9720	0.5520
B	0.9640	0.5430
C	0.9620	0.5390
D	0.9540	0.5310
E	0.9680	0.5430
F	0.9640	0.5400
G	0.9670	0.5450
H	0.9790	0.5610
I	0.9830	0.5680
J	0.9760	0.5580
K	0.9840	0.5640
L	0.9810	0.5590
M	0.9780	0.5670
N	0.9720	0.5610
c	0.9290	0.3970
d	0.9080	0.3580

1.0

0.0

<0.0