wwPDB EM Validation Summary Report (i)

Mar 2, 2024 – 10:18 AM EST

PDB ID	:	5VHR
EMDB ID	:	EMD-8683
Title	:	Conformational Landscape of the p28-Bound Human Proteasome Regulatory Particle
Authors	:	Lu, Y.; Wu, J.; Dong, Y.; Chen, S.; Sun, S.; Ma, Y.B.; Ouyang, Q.; Finley, D.; Kirschner, M.W.; Mao, Y.
Deposited on	:	2017-04-13
Resolution	:	7.70 Å(reported)

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

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

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

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

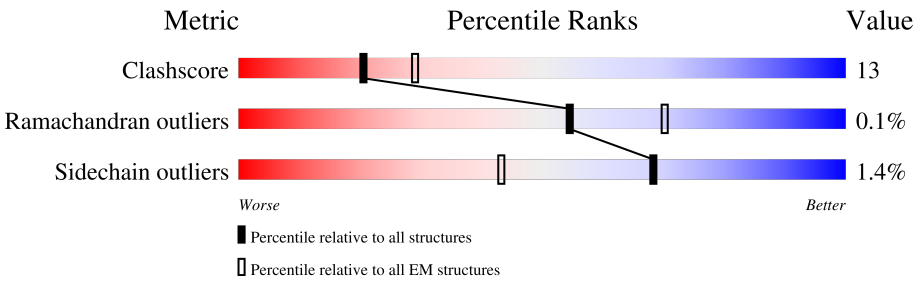
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 7.70 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	G	223	26% 69% 20% 11%
2	A	266	22% 70% 27% •
3	B	267	19% 70% 17% 13%
4	D	262	37% 68% 22% 10%
5	E	262	25% 58% 22% 20%
6	F	267	17% 64% 30% 6%
7	C	266	39% 65% 24% • 9%
8	f	848	10% 79% • 19%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 18057 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 26S proteasome non-ATPase regulatory subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	G	199	1516	945	266	297	8	0	0

- Molecule 2 is a protein called 26S proteasome regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	258	2022	1271	365	371	15	0	0

- Molecule 3 is a protein called 26S proteasome regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	233	1843	1163	318	354	8	0	0

- Molecule 4 is a protein called 26S proteasome regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	236	1873	1184	332	348	9	0	0

- Molecule 5 is a protein called 26S proteasome regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	210	1644	1032	294	306	12	0	0

- Molecule 6 is a protein called 26S proteasome regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	252	1965	1232	348	371	14	0	0

- Molecule 7 is a protein called 26S proteasome regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	C	242	1890	1190	337	350	13	0	0

- Molecule 8 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

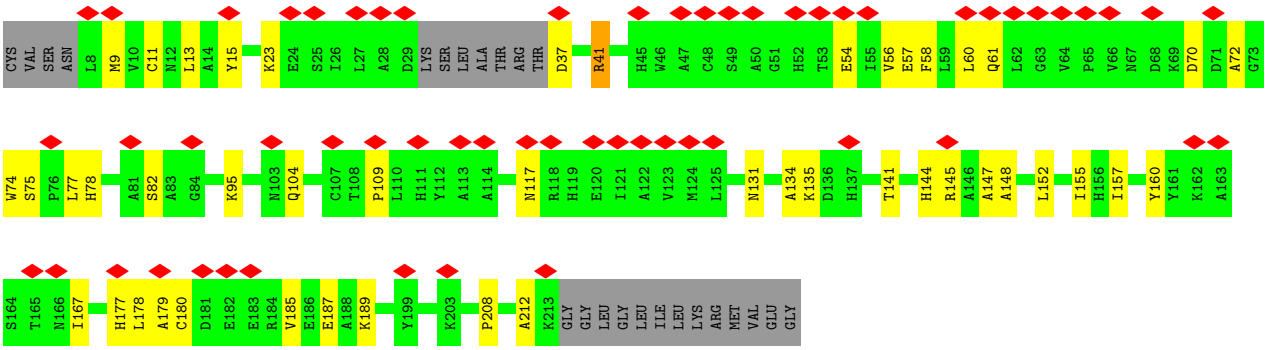
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	f	686	5304	3335	901	1033	35	0	0

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.

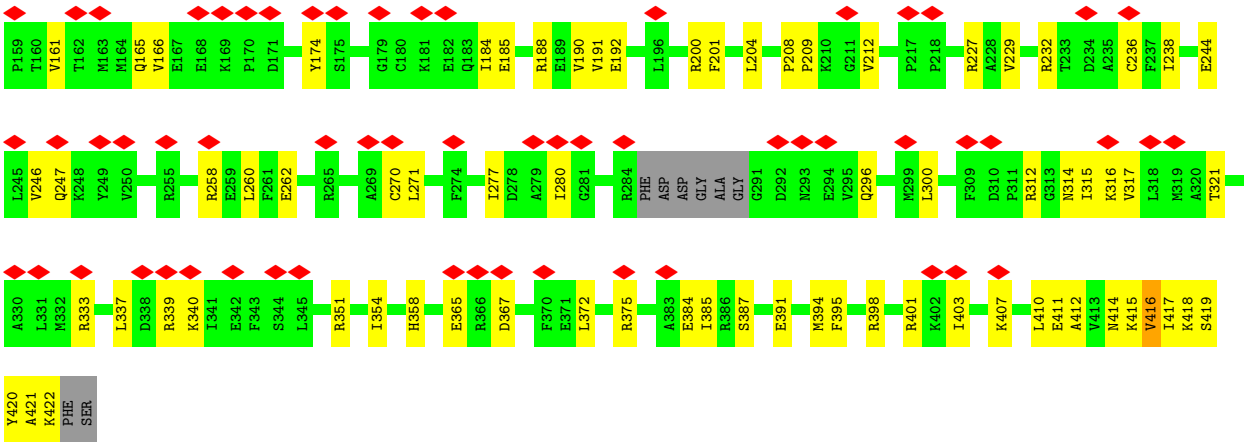
• Molecule 1: 26S proteasome non-ATPase regulatory subunit 10

Chain G: 26% 69% 20% 11%



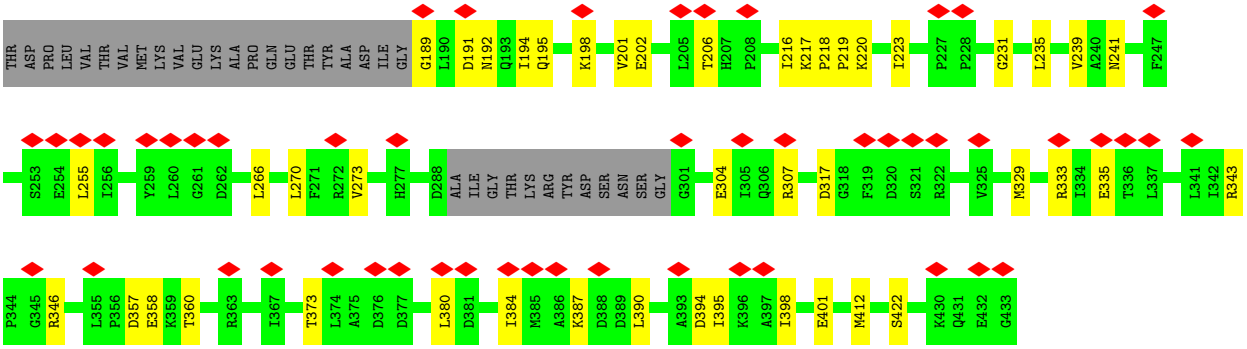
• Molecule 2: 26S proteasome regulatory subunit 7

Chain A: 22% 70% 27%



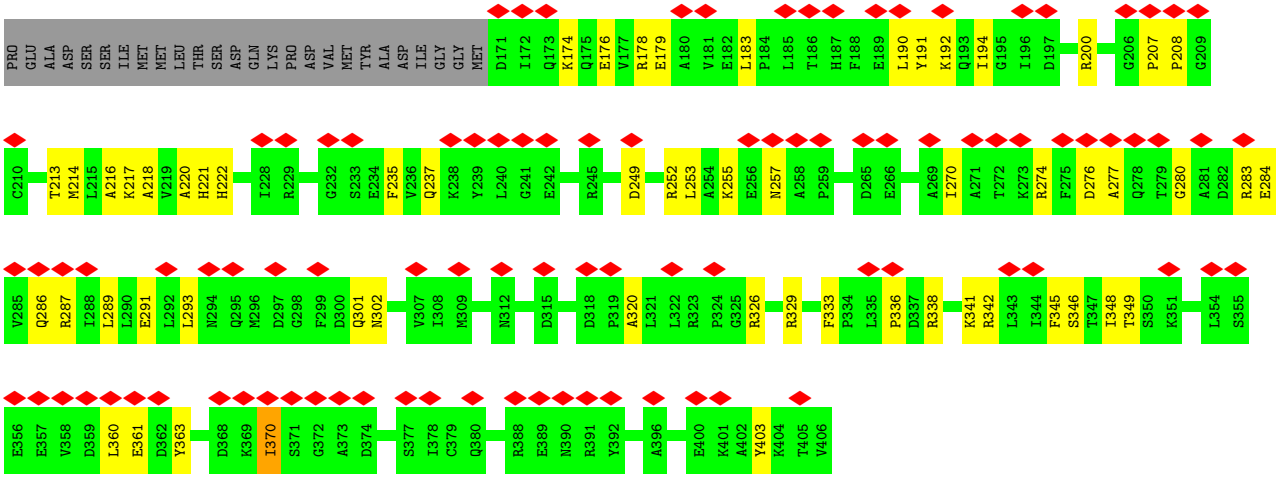
• Molecule 3: 26S proteasome regulatory subunit 4

Chain B: 19% 70% 17% 13%



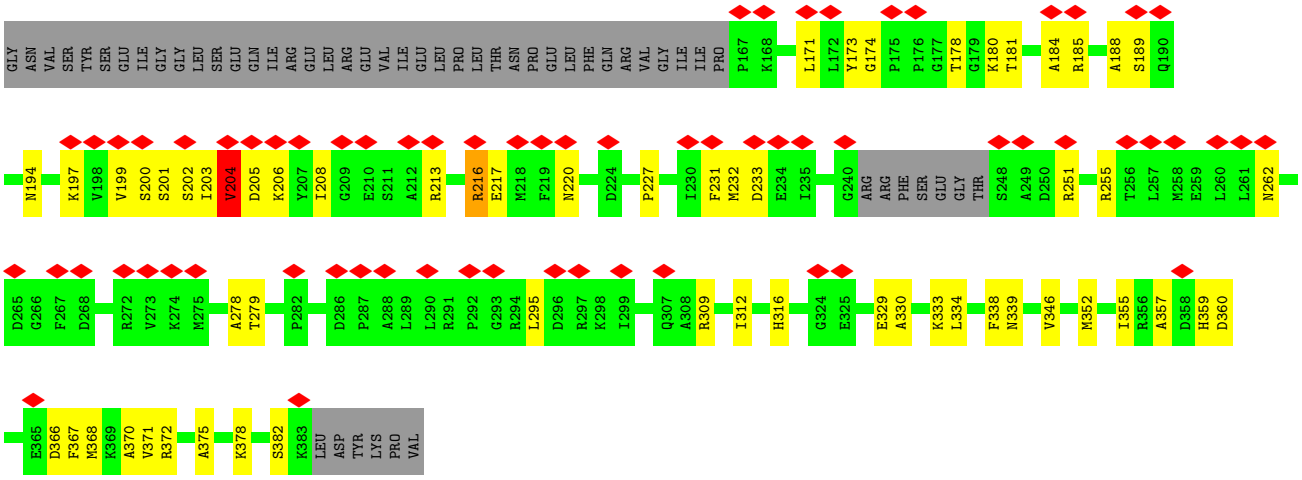
• Molecule 4: 26S proteasome regulatory subunit 6B

Chain D:



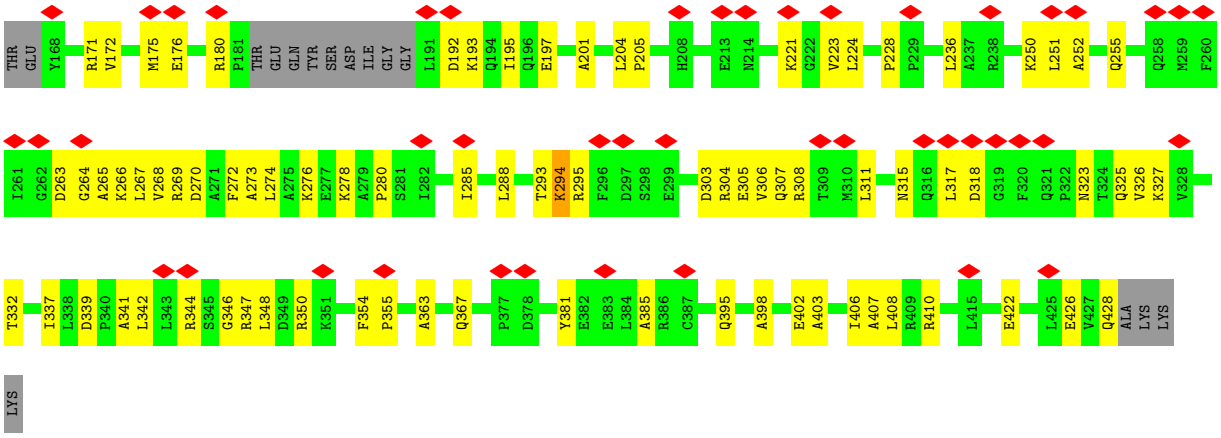
• Molecule 5: 26S proteasome regulatory subunit 10B

Chain E:



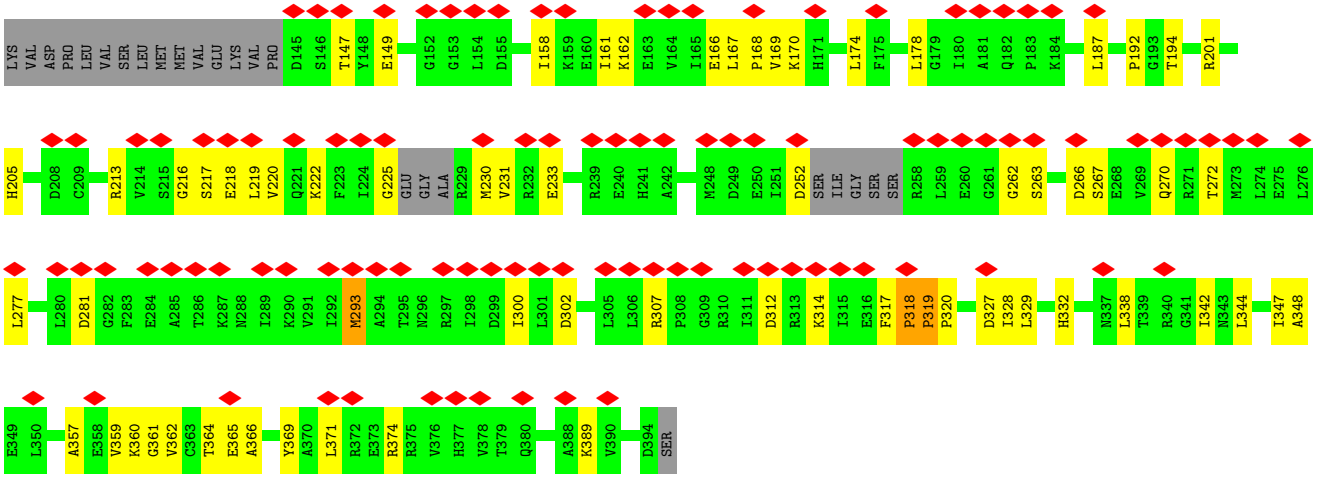
• Molecule 6: 26S proteasome regulatory subunit 6A

Chain F:



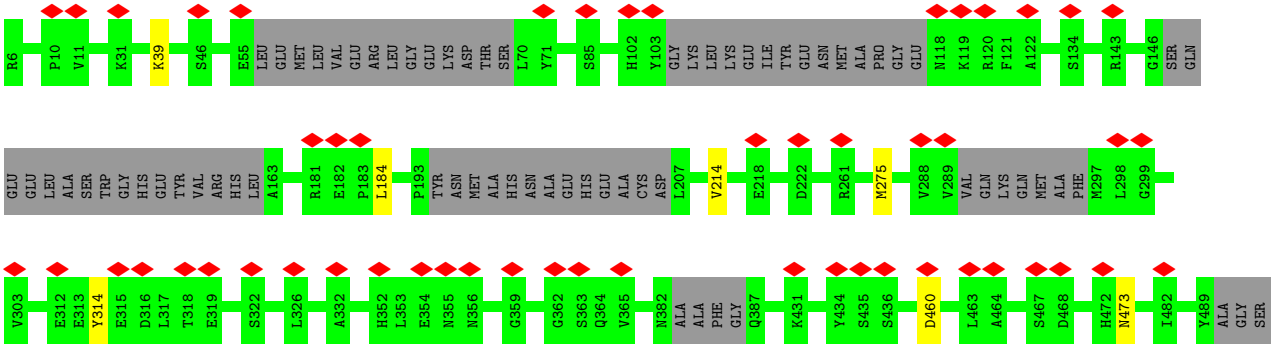
- Molecule 7: 26S proteasome regulatory subunit 8

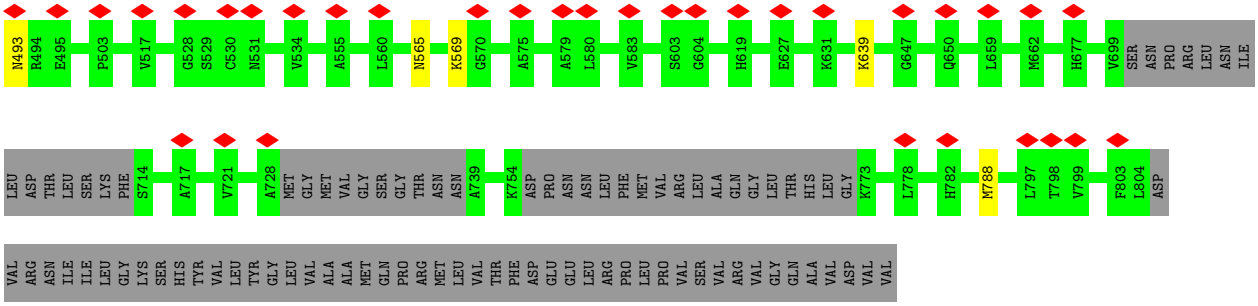
Chain C:



- Molecule 8: 26S proteasome non-ATPase regulatory subunit 2

Chain f:




N493 R494 E495 P503 V517 G528 S529 C530 N531 V534 A555 L560 N565 K569 G570 A575 A579 L580 V583 S603 G604 H619 E627 K631 K639 G647 Q650 L659 M662 H677 V699 SER ASN PRO ARG LEU ASN ILE

LEU ASP THR LEU SER LYS PHE S714 A717 V721 A728 MET GLY MET VAL GLY SER GLY THR ASN ASN A739 K754 ASP PRO ASN ASN LEU PHE MET VAL ARG LEU ALA GLN GLY LEU THR HIS LEU GLY K773 L778 H782 M788 L797 T798 V799 F803 L804 ASP

VAL ARG ASN ILE ILE LEU GLY LYS SER HIS TYR VAL LEU TYR GLY LEU VAL VAL ALA ALA MET GLN PRO ARG MET LEU VAL THR PHE ASP GLU GLU LEU ARG PRO LEU PRO VAL SER VAL ARG VAL GLY GLN ALA VAL ASP VAL VAL

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14464	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.019	Depositor
Minimum map value	-0.006	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	309.6, 309.6, 309.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	G	0.23	0/1540	0.37	0/2084
2	A	0.24	0/2052	0.42	0/2759
3	B	0.23	0/1868	0.41	0/2513
4	D	0.24	0/1903	0.41	0/2568
5	E	0.23	0/1669	0.40	0/2244
6	F	0.23	0/1992	0.41	0/2682
7	C	0.23	0/1915	0.42	0/2570
8	f	0.23	0/5377	0.42	0/7248
All	All	0.23	0/18316	0.41	0/24668

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 (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	G	1516	0	1499	29	0
2	A	2022	0	2079	48	0
3	B	1843	0	1895	29	0
4	D	1873	0	1912	46	0
5	E	1644	0	1667	53	0
6	F	1965	0	2000	63	0
7	C	1890	0	1948	54	0
8	f	5304	0	5315	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	18057	0	18315	301	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 13.

The worst 5 of 301 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)
5:E:216:ARG:O	5:E:220:ASN:HB2	1.64	0.96
7:C:318:PRO:HB2	7:C:319:PRO:HD3	1.46	0.94
5:E:330:ALA:O	5:E:334:LEU:HB2	1.69	0.92
5:E:367:PHE:O	5:E:371:VAL:HB	1.71	0.90
2:A:161:VAL:O	2:A:165:GLN:HB2	1.70	0.90

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	G	195/223 (87%)	191 (98%)	4 (2%)	0	100	100
2	A	254/266 (96%)	230 (91%)	24 (9%)	0	100	100
3	B	229/267 (86%)	216 (94%)	13 (6%)	0	100	100
4	D	234/262 (89%)	224 (96%)	10 (4%)	0	100	100
5	E	206/262 (79%)	185 (90%)	20 (10%)	1 (0%)	29	69
6	F	248/267 (93%)	233 (94%)	15 (6%)	0	100	100
7	C	236/266 (89%)	222 (94%)	12 (5%)	2 (1%)	19	60
8	f	664/848 (78%)	598 (90%)	66 (10%)	0	100	100
All	All	2266/2661 (85%)	2099 (93%)	164 (7%)	3 (0%)	54	86

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	C	318	PRO
7	C	319	PRO
5	E	204	VAL

5.3.2 Protein sidechains (i)

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	G	159/178 (89%)	156 (98%)	3 (2%)	57 75
2	A	219/224 (98%)	218 (100%)	1 (0%)	88 93
3	B	203/231 (88%)	203 (100%)	0	100 100
4	D	202/224 (90%)	200 (99%)	2 (1%)	76 86
5	E	178/225 (79%)	175 (98%)	3 (2%)	60 78
6	F	210/222 (95%)	207 (99%)	3 (1%)	67 80
7	C	204/225 (91%)	201 (98%)	3 (2%)	65 80
8	f	579/714 (81%)	567 (98%)	12 (2%)	53 72
All	All	1954/2243 (87%)	1927 (99%)	27 (1%)	68 80

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	C	293	MET
8	f	214	VAL
8	f	569	LYS
8	f	184	LEU
8	f	275	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
8	f	493	ASN
8	f	475	ASN

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Mol	Chain	Res	Type
5	E	345	ASN
8	f	382	ASN
5	E	316	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 monosaccharides 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)

There are no chain breaks in this entry.

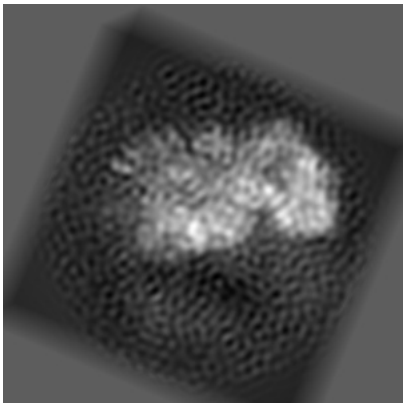
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-8683. These allow visual inspection of the internal detail of the map and identification of artifacts.

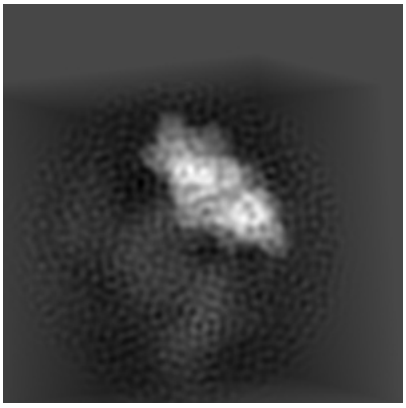
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

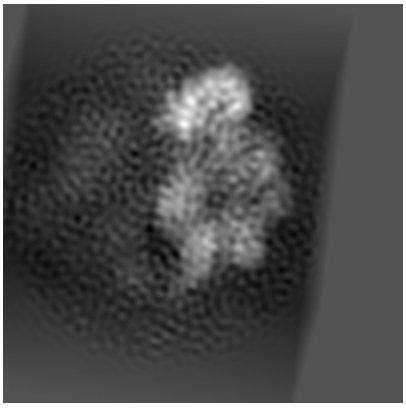
6.1.1 Primary map



X



Y

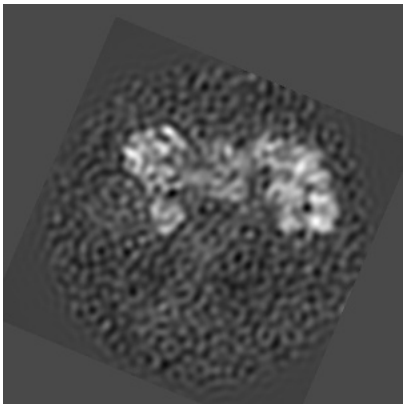


Z

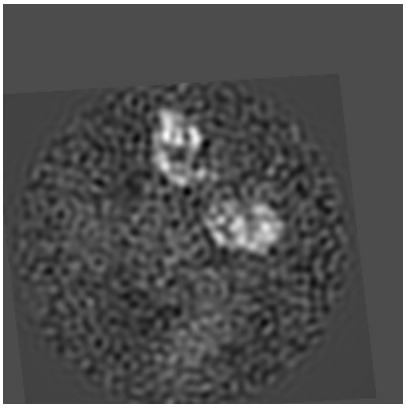
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

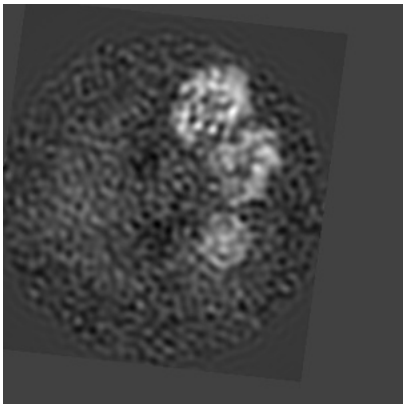
6.2.1 Primary map



X Index: 180



Y Index: 180

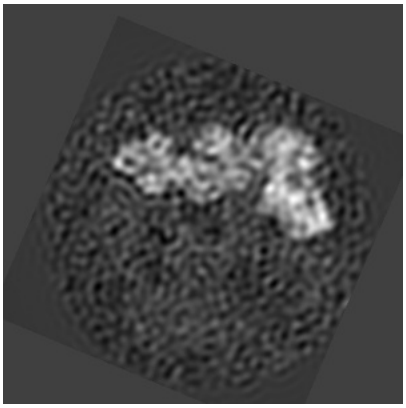


Z Index: 180

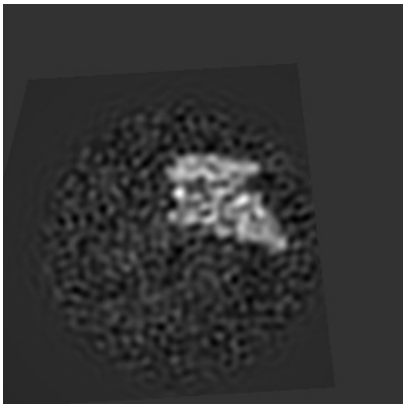
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

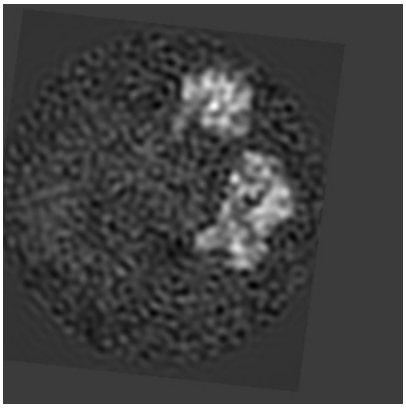
6.3.1 Primary map



X Index: 165



Y Index: 267

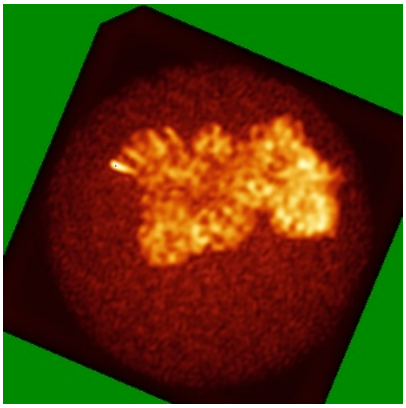


Z Index: 158

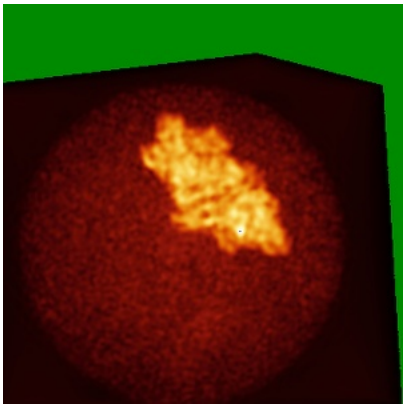
The images above show the largest variance slices of the map in three orthogonal directions.

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

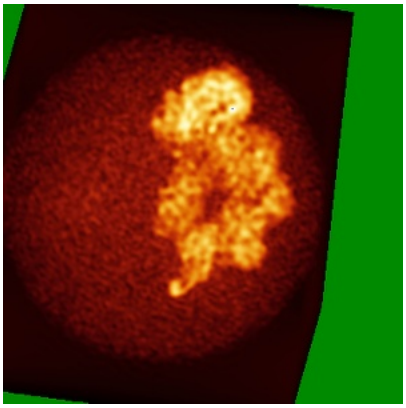
6.4.1 Primary map



X



Y

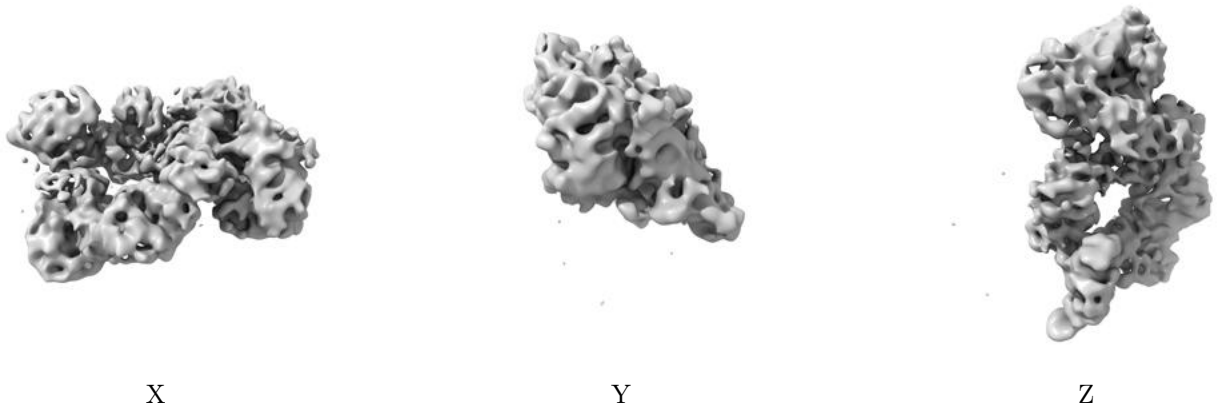


Z

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

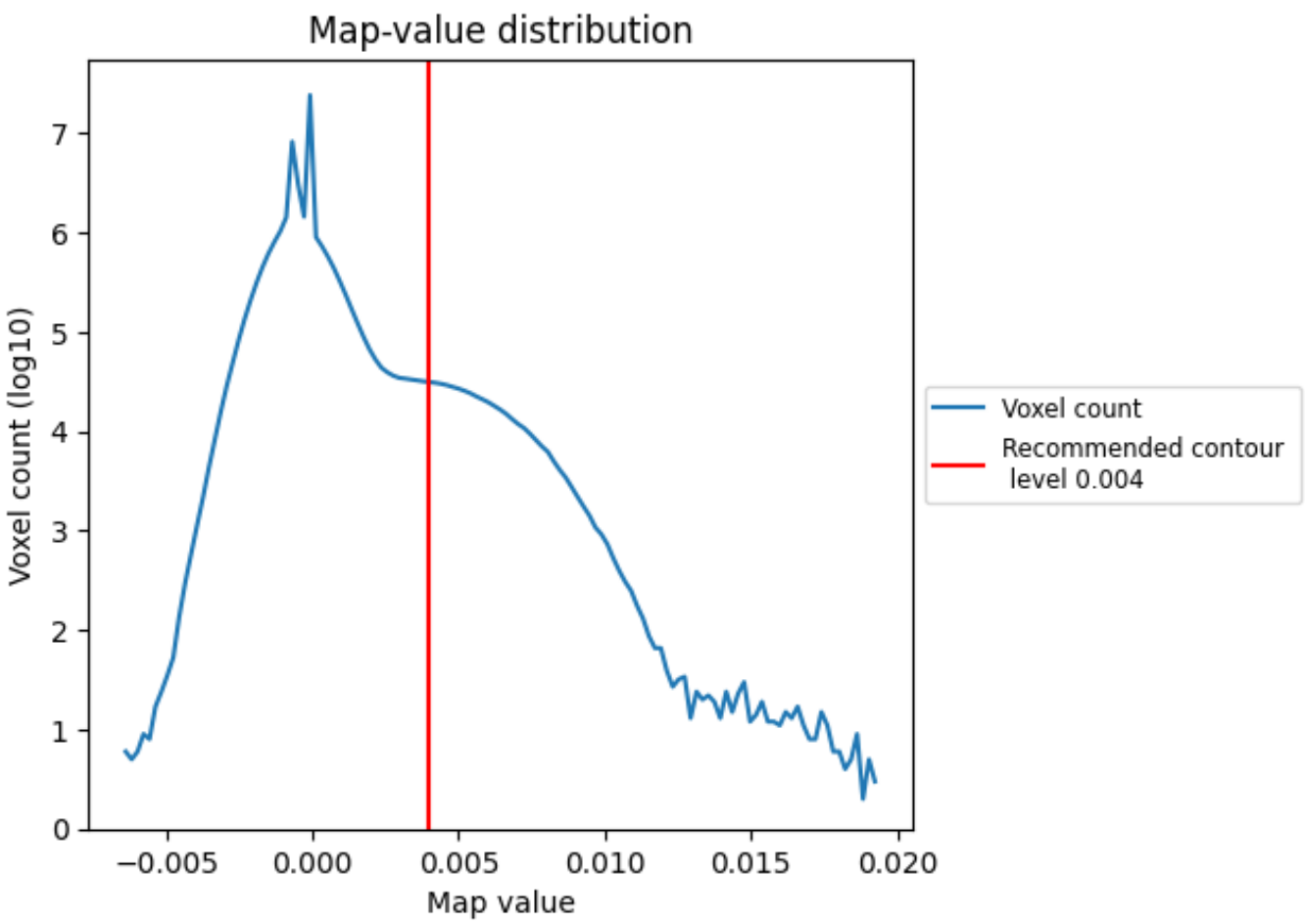
6.6 Mask visualisation (i)

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

7 Map analysis (i)

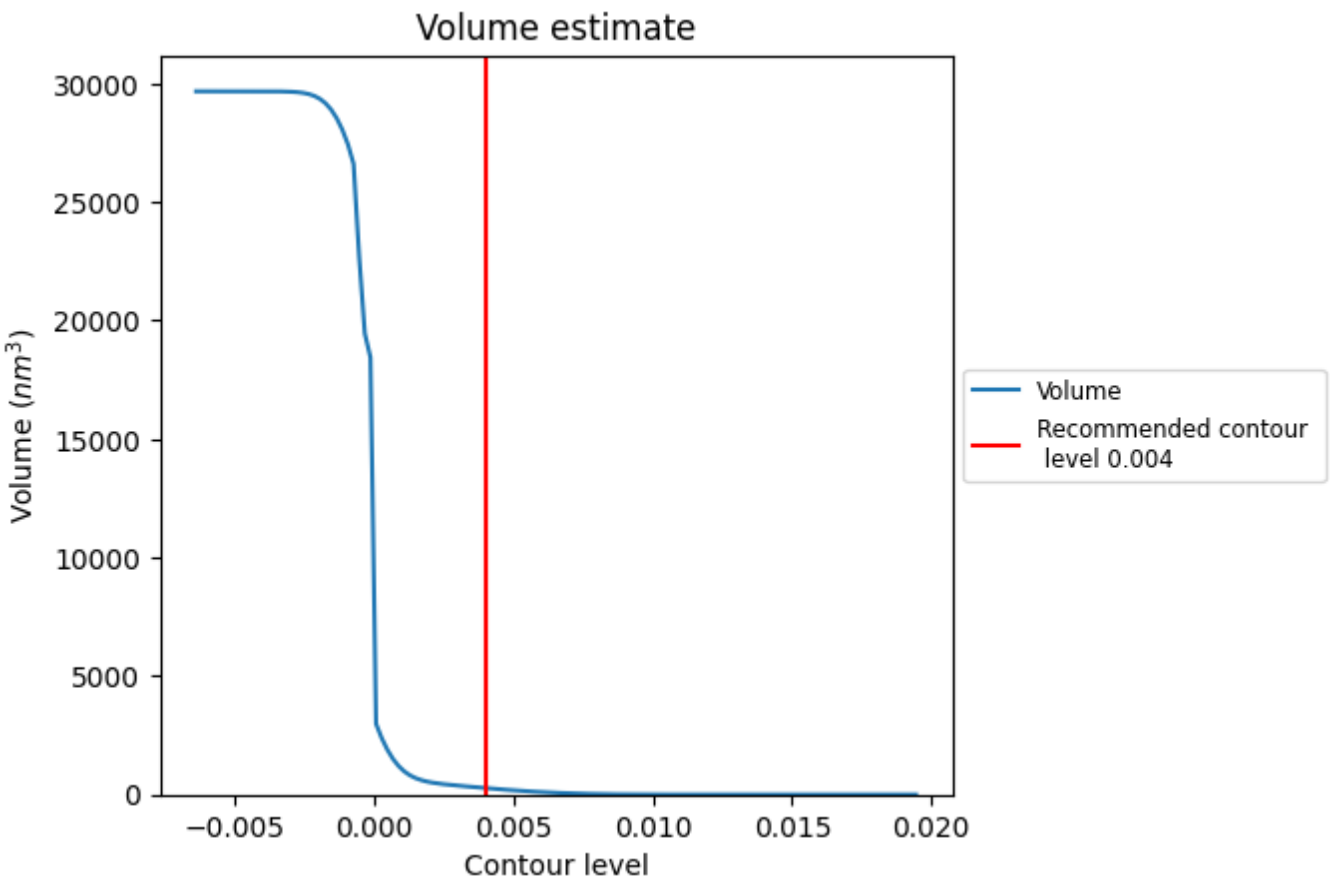
This section contains the results of statistical analysis of the map.

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.

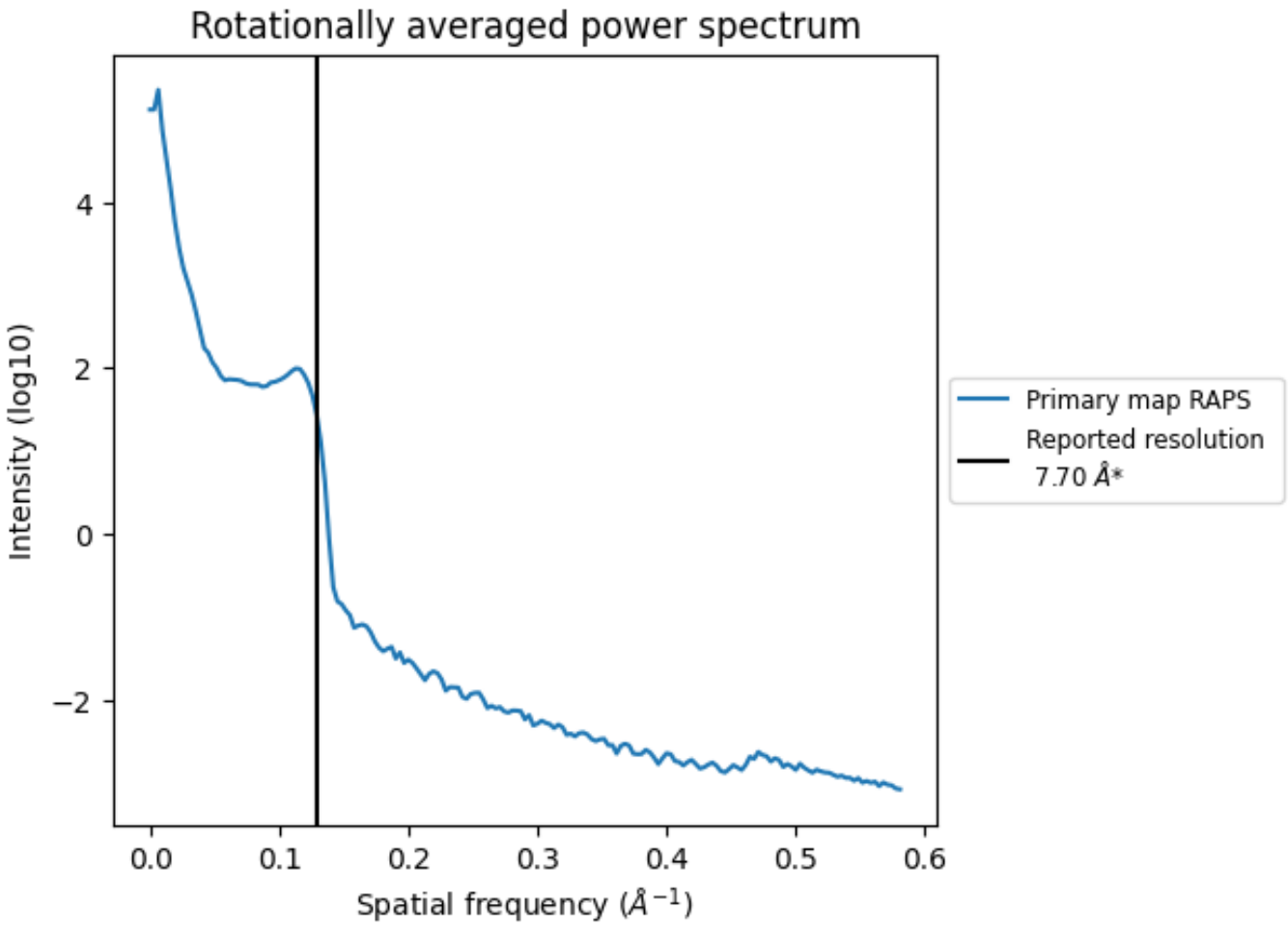
7.2 Volume estimate (i)



The volume at the recommended contour level is 274 nm^3; this corresponds to an approximate mass of 247 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 0.130 Å^{-1}

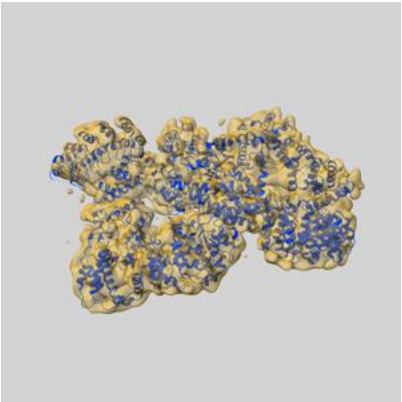
8 Fourier-Shell correlation (i)

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

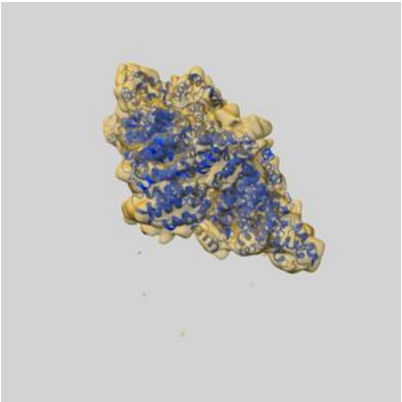
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-8683 and PDB model 5VHR. Per-residue inclusion information can be found in section 3 on page 5.

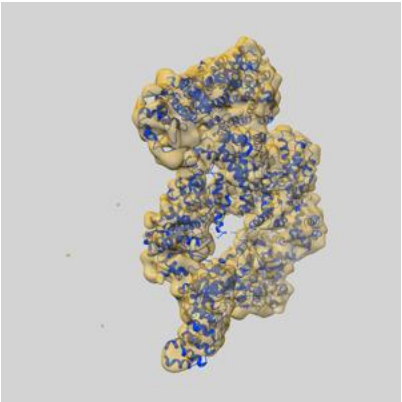
9.1 Map-model overlay (i)



X



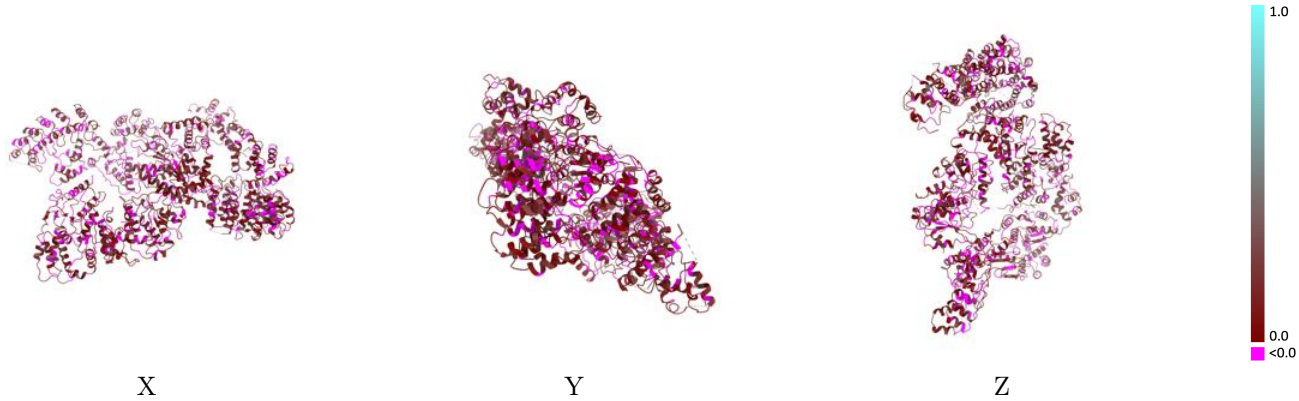
Y



Z

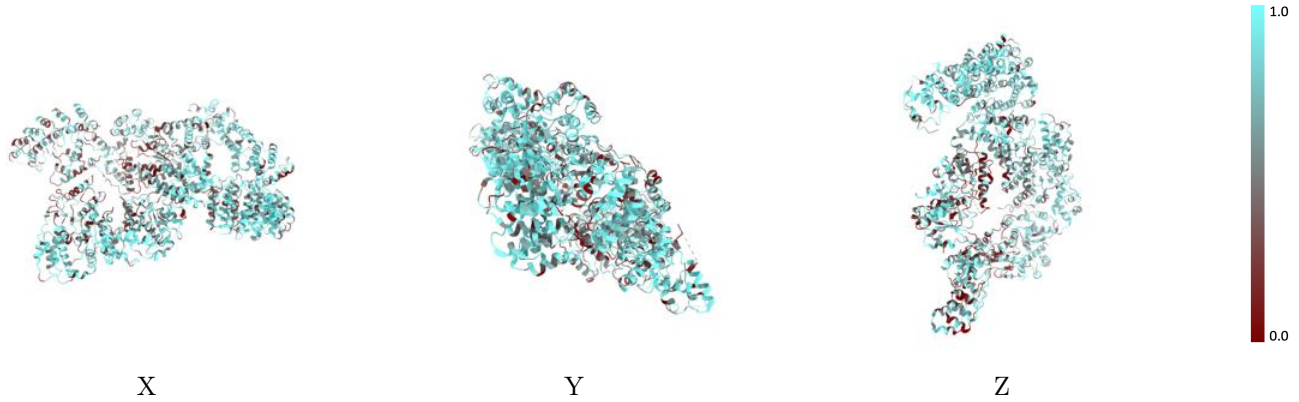
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



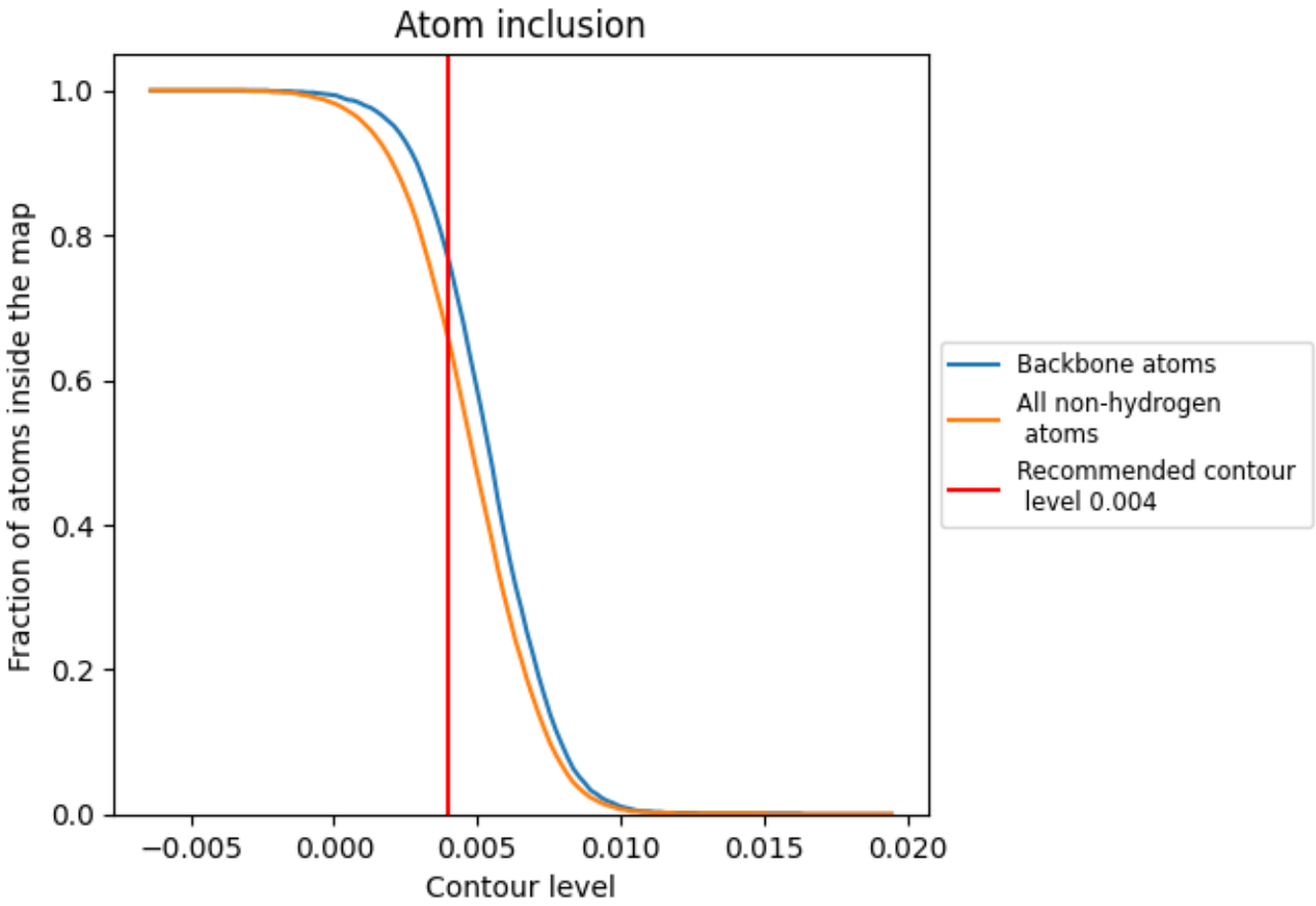
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.004).

9.4 Atom inclusion (i)



At the recommended contour level, 77% of all backbone atoms, 66% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6550	0.0920
A	0.6650	0.1040
B	0.6440	0.1070
C	0.5100	0.0870
D	0.5130	0.0600
E	0.5980	0.0770
F	0.7150	0.1010
G	0.5870	0.0860
f	0.7720	0.0990