wwPDB EM Validation Summary Report (i)

Nov 21, 2022 – 10:03 PM EST

PDB ID	:	3J47
EMDB ID	:	EMD-2165
Title	:	Formation of an intricate helical bundle dictates the assembly of the 26S proteasome lid
Authors	:	Estrin, E.; Lopez-Blanco, J.R.; Chacon, P.; Martin, A.
Deposited on	:	2013-06-27
Resolution	:	7.40 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:

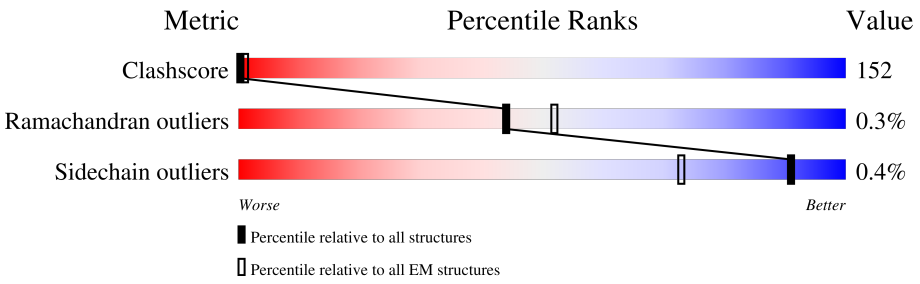
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

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 7.40 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	V	69	30%; 33%, 55%, • 9%
2	U	121	13%; 37%, 38%, 25%
3	O	28	14%; 64%, 36%
4	P	34	12%; 62%, 38%
5	Q	25	56%; 28%, 72%
6	R	26	38%; 58%, 42%
7	S	24	50%; 29%, 67%, •
8	T	17	47%; 71%, 29%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 2498 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 regulatory subunit RPN11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	V	63	509	313	83	112	1	0	0

- Molecule 2 is a protein called 26S proteasome regulatory subunit RPN8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	U	91	742	474	129	138	1	0	0

- Molecule 3 is a protein called 26S proteasome regulatory subunit RPN9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	O	28	232	143	43	44	2	0	0

- Molecule 4 is a protein called 26S proteasome regulatory subunit RPN5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	P	34	279	176	47	55	1	0	0

- Molecule 5 is a protein called 26S proteasome regulatory subunit RPN6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	Q	25	192	122	30	40	0	0

- Molecule 6 is a protein called 26S proteasome regulatory subunit RPN7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	R	26	203	130	38	35	0	0

- Molecule 7 is a protein called 26S proteasome regulatory subunit RPN3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	S	24	206	130	34	42	0	0

- Molecule 8 is a protein called 26S proteasome regulatory subunit RPN12.

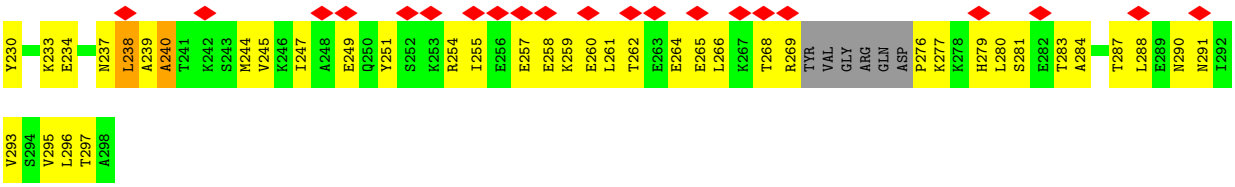
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	T	17	135	85	21	28	1	0	0

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.

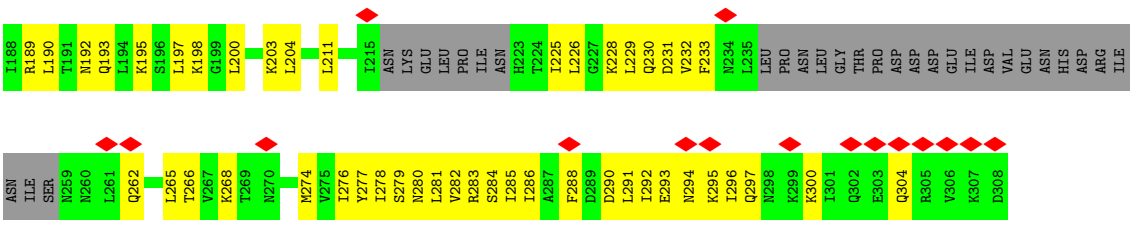
• Molecule 1: 26S proteasome regulatory subunit RPN11

Chain V:



• Molecule 2: 26S proteasome regulatory subunit RPN8

Chain U:

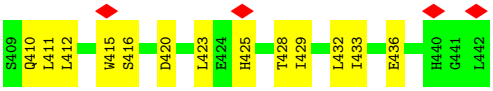


• Molecule 3: 26S proteasome regulatory subunit RPN9

Chain O:

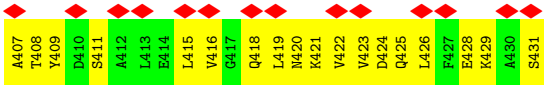
• Molecule 4: 26S proteasome regulatory subunit RPN5

Chain P:



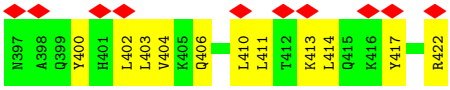
• Molecule 5: 26S proteasome regulatory subunit RPN6

Chain Q:



- Molecule 6: 26S proteasome regulatory subunit RPN7

Chain R:

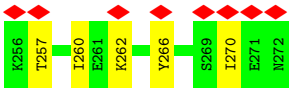


- Molecule 7: 26S proteasome regulatory subunit RPN3

Chain S:

- Molecule 8: 26S proteasome regulatory subunit RPN12

Chain T:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	2464694	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	150000	Depositor
Image detector	TVIPS TEMCAM-F816 (8k x 8k)	Depositor
Maximum map value	6.526	Depositor
Minimum map value	-4.591	Depositor
Average map value	0.014	Depositor
Map value standard deviation	0.200	Depositor
Recommended contour level	1.28	Depositor
Map size (Å)	557.2, 557.2, 557.2	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.99, 1.99, 1.99	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	V	1.06	3/511 (0.6%)	1.09	2/682 (0.3%)
2	U	0.46	0/744	0.90	0/995
3	O	0.76	1/233 (0.4%)	1.06	1/307 (0.3%)
4	P	0.53	0/284	0.92	0/384
5	Q	0.86	1/193 (0.5%)	0.90	0/260
6	R	0.48	0/205	0.90	0/274
7	S	1.29	1/210 (0.5%)	0.96	0/283
8	T	0.50	0/135	0.84	0/180
All	All	0.78	6/2515 (0.2%)	0.96	3/3365 (0.1%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	S	457	PRO	N-CD	15.78	1.70	1.47
1	V	239	ALA	N-CA	-14.14	1.18	1.46
1	V	276	PRO	N-CD	11.48	1.64	1.47
5	Q	407	ALA	N-CA	-7.42	1.31	1.46
1	V	238	LEU	C-N	7.04	1.50	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	V	238	LEU	O-C-N	-5.45	113.98	122.70
1	V	240	ALA	CB-CA-C	5.17	117.85	110.10
3	O	373	TRP	CG-CD2-CE3	-5.09	129.32	133.90

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	V	509	0	499	244	0
2	U	742	0	787	488	0
3	O	232	0	236	126	0
4	P	279	0	266	130	0
5	Q	192	0	187	142	0
6	R	203	0	211	84	0
7	S	206	0	185	179	0
8	T	135	0	137	56	0
All	All	2498	0	2508	762	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 152.

The worst 5 of 762 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)
6:R:422:ARG:HH21	7:S:474:GLU:CG	1.02	1.66
2:U:288:PHE:CD1	7:S:471:LEU:HG	1.23	1.65
1:V:264:GLU:CB	1:V:280:LEU:HB2	1.23	1.61
2:U:288:PHE:CZ	7:S:471:LEU:HD11	1.27	1.61
2:U:233:PHE:CG	3:O:369:ARG:HD2	1.08	1.60

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	V	59/69 (86%)	57 (97%)	1 (2%)	1 (2%)	9	42
2	U	85/121 (70%)	83 (98%)	2 (2%)	0	100	100
3	O	26/28 (93%)	26 (100%)	0	0	100	100
4	P	32/34 (94%)	32 (100%)	0	0	100	100
5	Q	23/25 (92%)	23 (100%)	0	0	100	100
6	R	24/26 (92%)	24 (100%)	0	0	100	100
7	S	22/24 (92%)	22 (100%)	0	0	100	100
8	T	15/17 (88%)	15 (100%)	0	0	100	100
All	All	286/344 (83%)	282 (99%)	3 (1%)	1 (0%)	44	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	V	247	ILE

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	V	58/63 (92%)	57 (98%)	1 (2%)	60	78
2	U	87/116 (75%)	87 (100%)	0	100	100
3	O	25/25 (100%)	25 (100%)	0	100	100
4	P	32/32 (100%)	32 (100%)	0	100	100
5	Q	21/21 (100%)	21 (100%)	0	100	100
6	R	20/20 (100%)	20 (100%)	0	100	100
7	S	23/23 (100%)	23 (100%)	0	100	100
8	T	15/15 (100%)	15 (100%)	0	100	100
All	All	281/315 (89%)	280 (100%)	1 (0%)	91	94

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	V	249	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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.

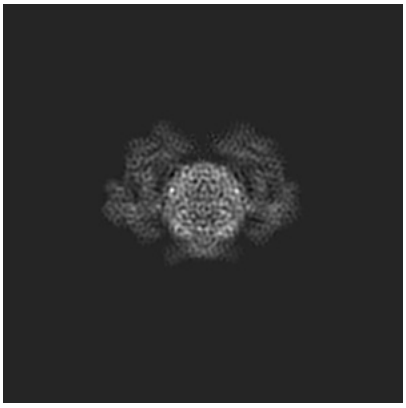
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-2165. These allow visual inspection of the internal detail of the map and identification of artifacts.

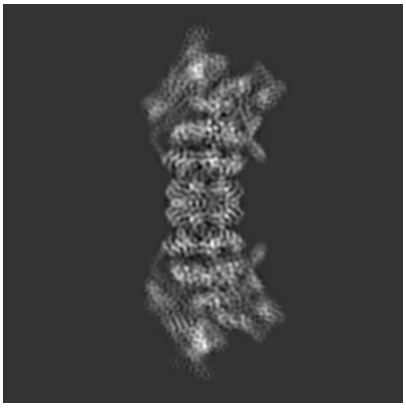
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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: 140

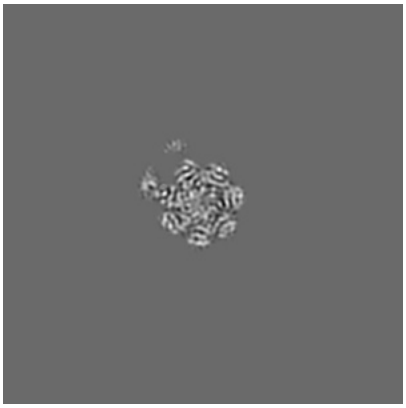
Y Index: 140

Z Index: 140

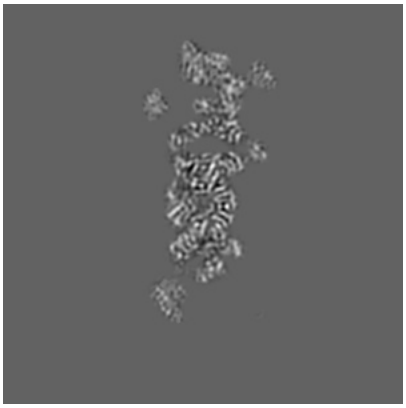
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 169



Y Index: 126

Z Index: 150

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 1.28. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

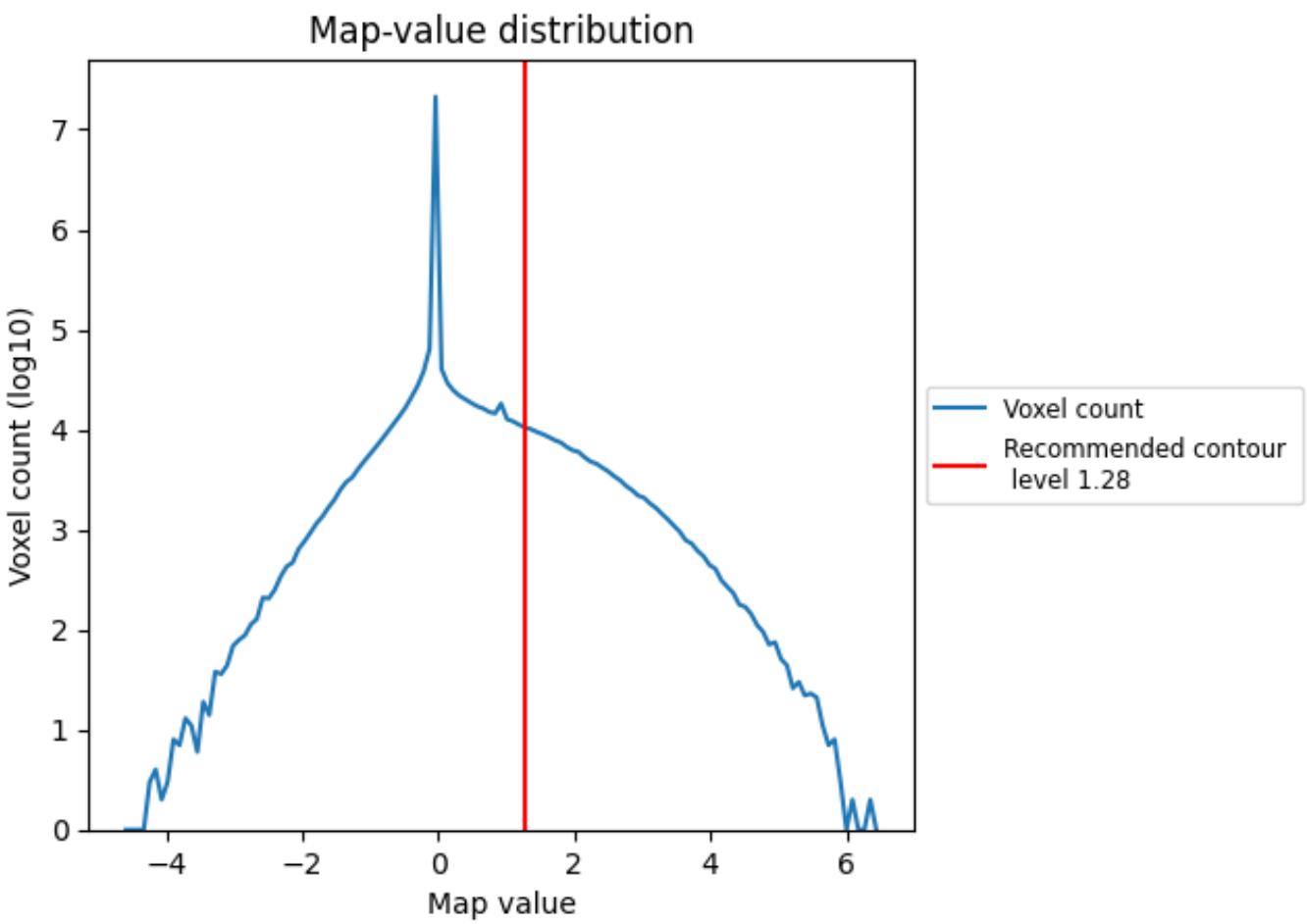
6.5 Mask visualisation (i)

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

7 Map analysis (i)

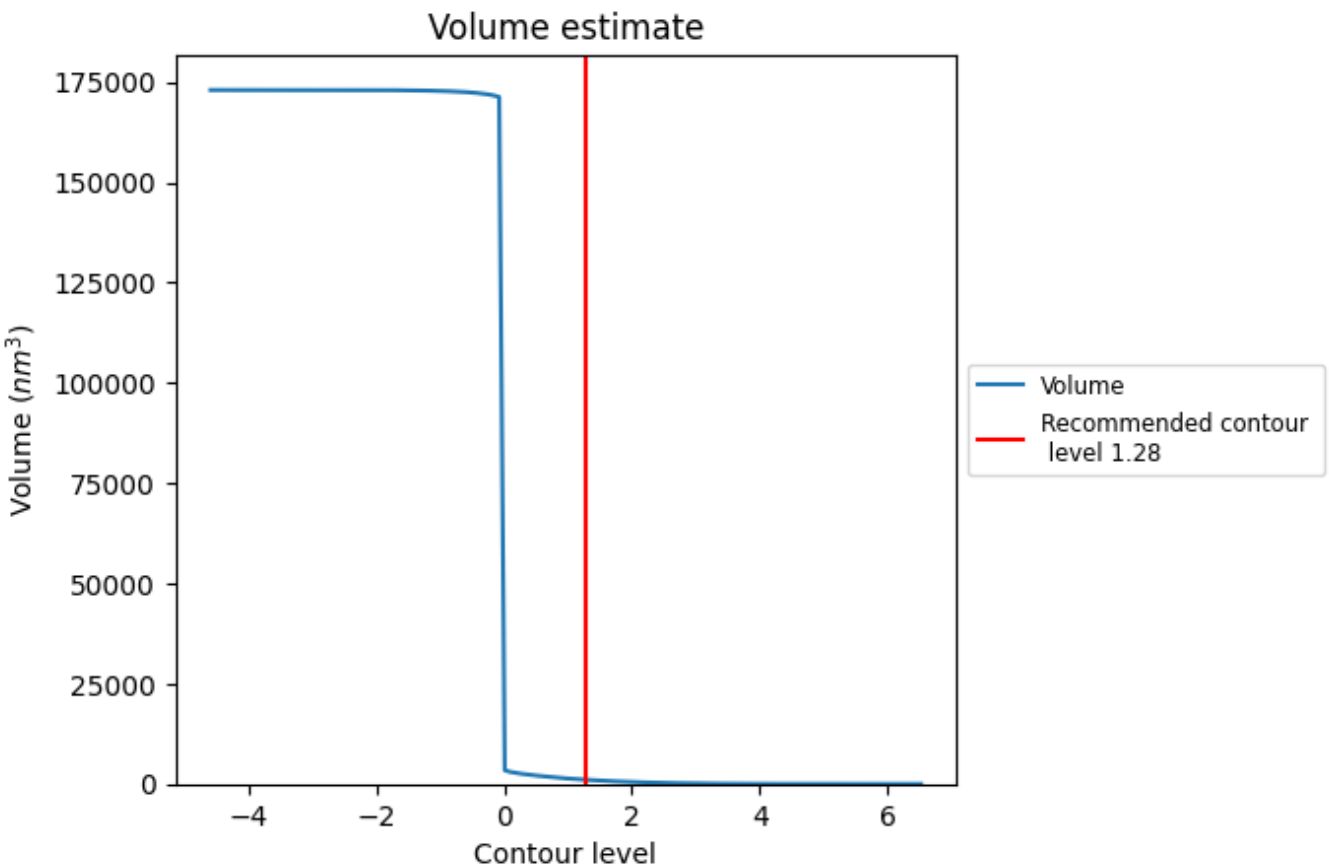
This section contains the results of statistical analysis of the map.

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.

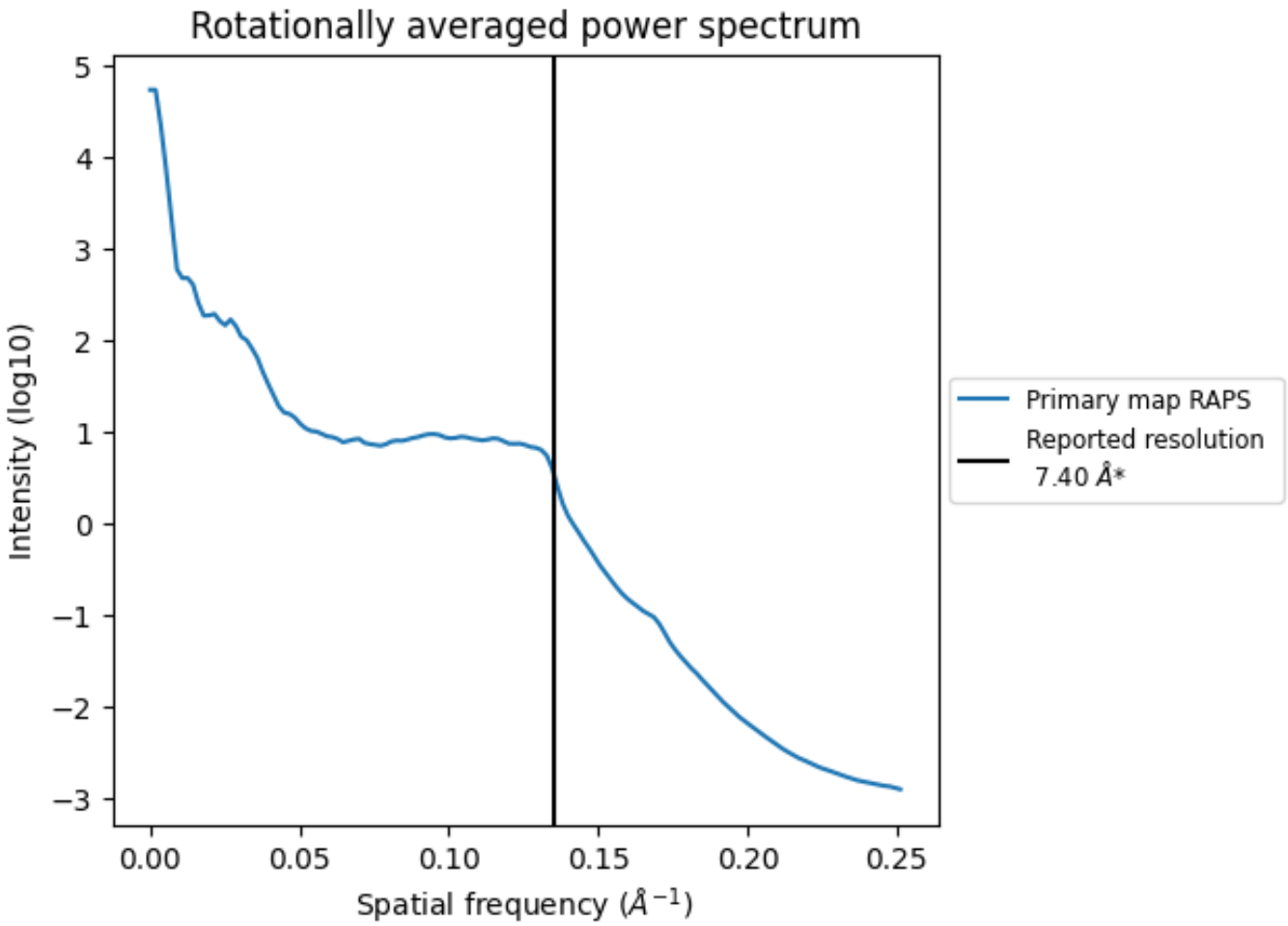
7.2 Volume estimate (i)



The volume at the recommended contour level is 1051 nm^3; this corresponds to an approximate mass of 950 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 0.135 Å^{-1}

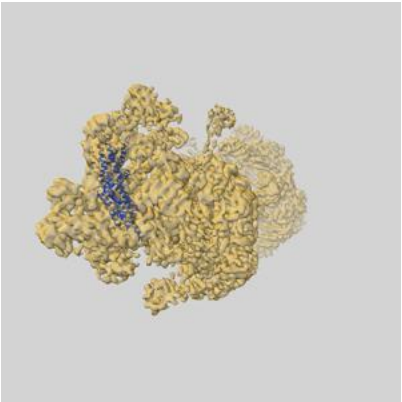
8 Fourier-Shell correlation (i)

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

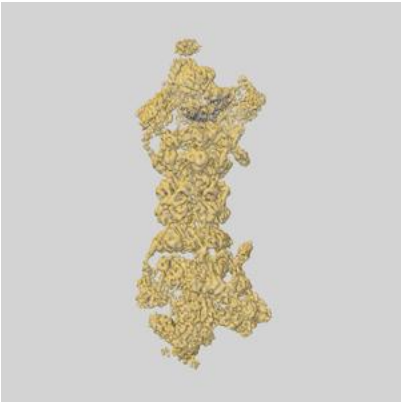
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-2165 and PDB model 3J47. Per-residue inclusion information can be found in section 3 on page 5.

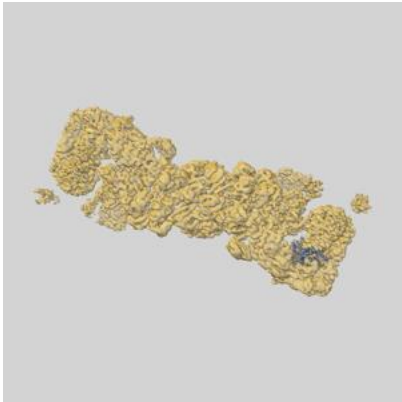
9.1 Map-model overlay (i)



X



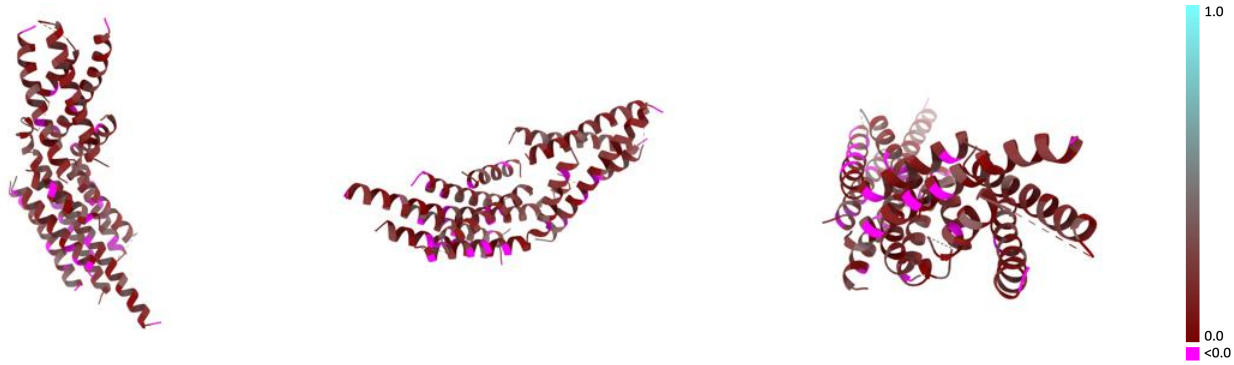
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.28 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.

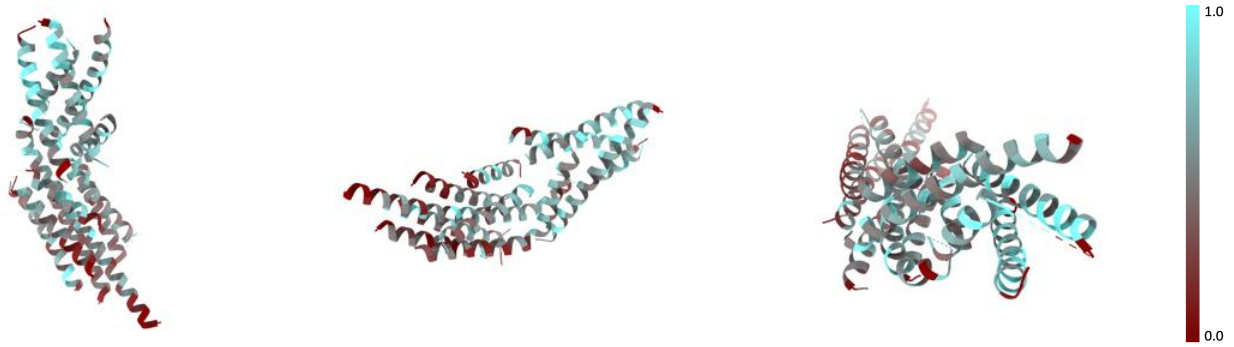
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

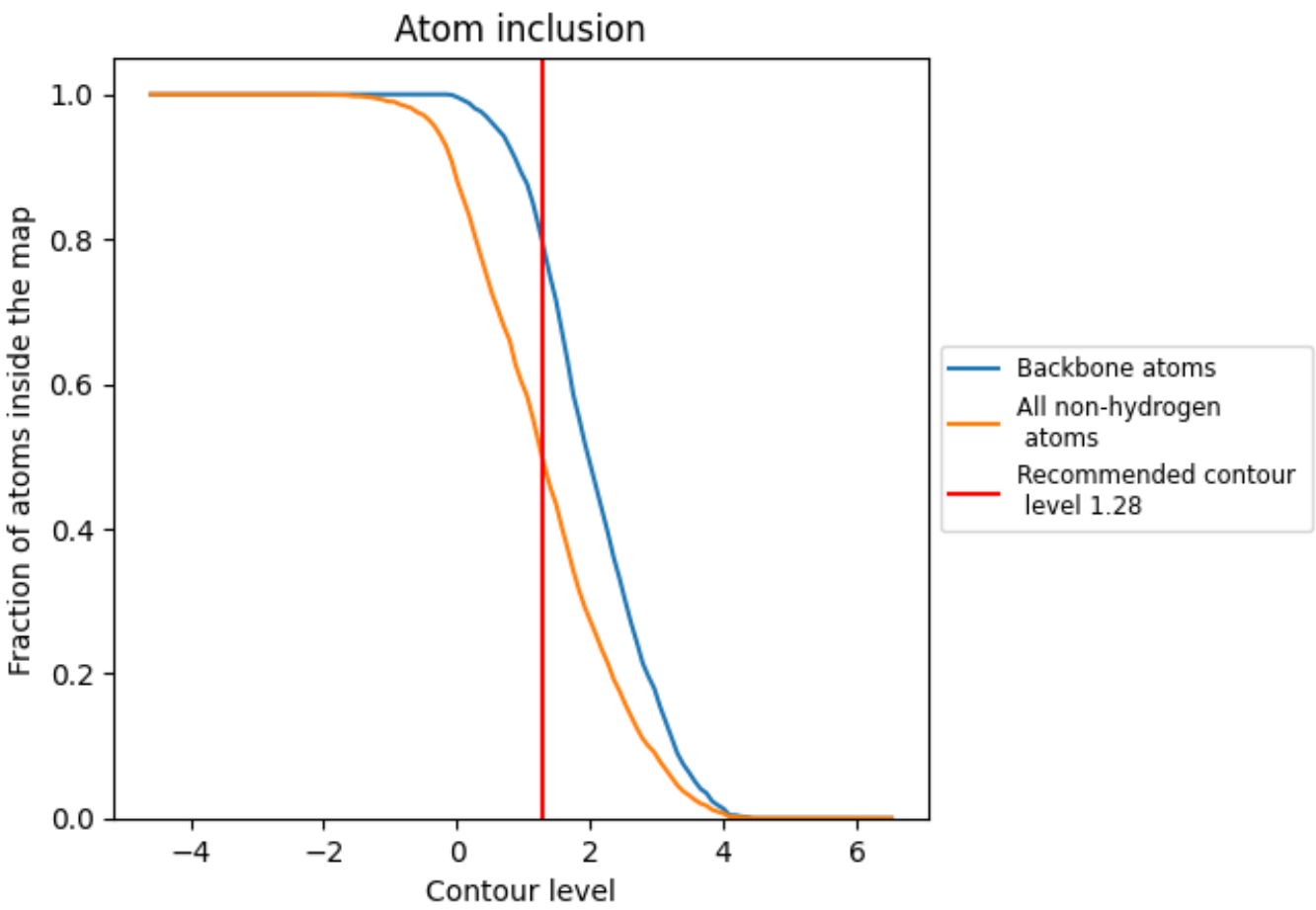
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (1.28).

9.4 Atom inclusion (i)



At the recommended contour level, 80% of all backbone atoms, 50% 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 (1.28) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4990	0.1310
O	0.6432	0.1580
P	0.5683	0.1170
Q	0.3246	0.1170
R	0.4523	0.1310
S	0.3547	0.1040
T	0.4179	0.1260
U	0.5640	0.1370
V	0.4652	0.1330