



wwPDB EM Validation Summary Report ⓘ

Nov 5, 2022 – 09:58 AM EDT

PDB ID : 5VHM
EMDB ID : EMD-8678
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 : 8.30 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.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) : 2.31.2

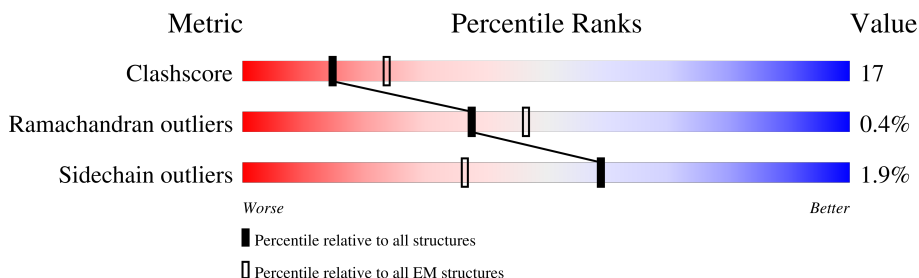
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.30 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 $\leq 5\%$. 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	G	223	
2	A	266	
3	B	266	
4	D	262	
5	E	262	
6	F	267	
7	C	266	
8	f	848	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 17595 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
1	G	210	Total	C	N	O	S	0	0
			1596	992	282	313	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	258	Total	C	N	O	S	0	0
			2023	1274	362	372	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	232	Total	C	N	O	S	0	0
			1834	1160	316	350	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	220	Total	C	N	O	S	0	0
			1734	1093	309	323	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	209	Total	C	N	O	S	0	0
			1642	1030	296	304	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	219	Total	C	N	O	S	0	0
			1682	1053	299	318	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	229	Total	C	N	O	S	0	0
			1780	1115	322	331	12		

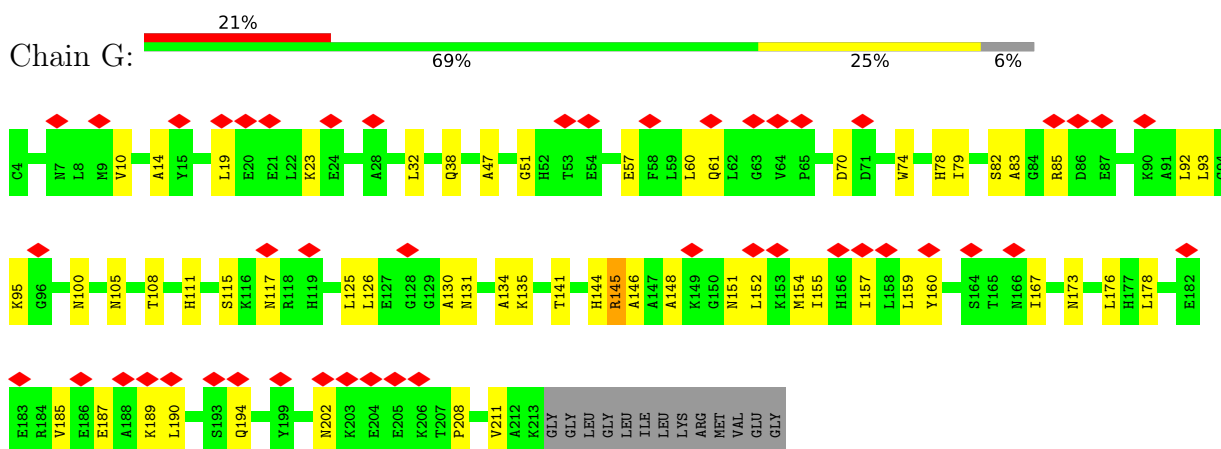
- Molecule 8 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

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

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.

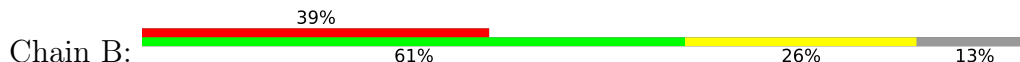
- Molecule 1: 26S proteasome non-ATPase regulatory subunit 10

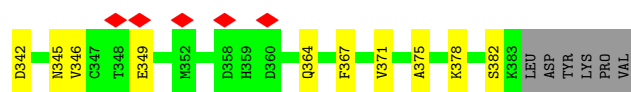


- Molecule 2: 26S proteasome regulatory subunit 7

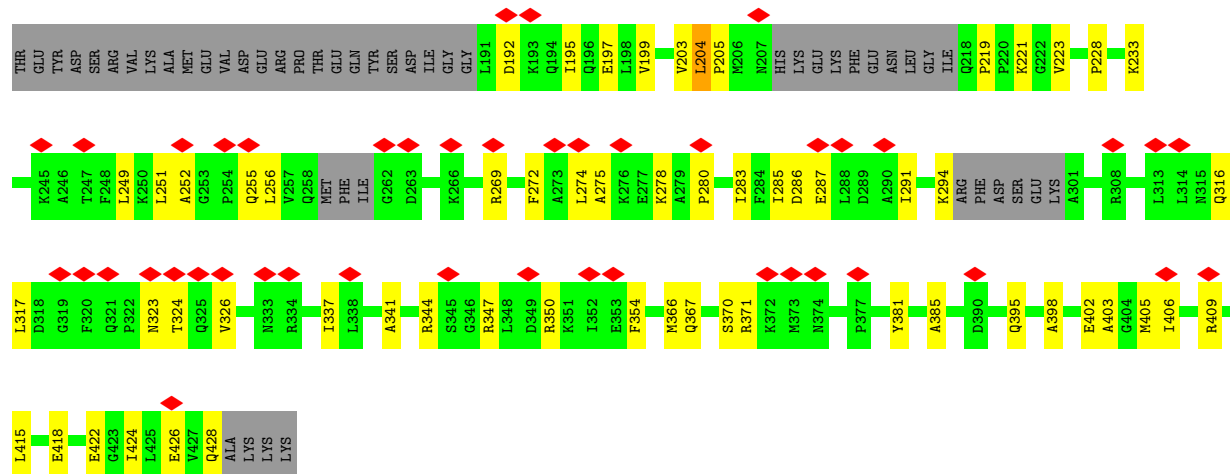


- Molecule 3: 26S proteasome regulatory subunit 4

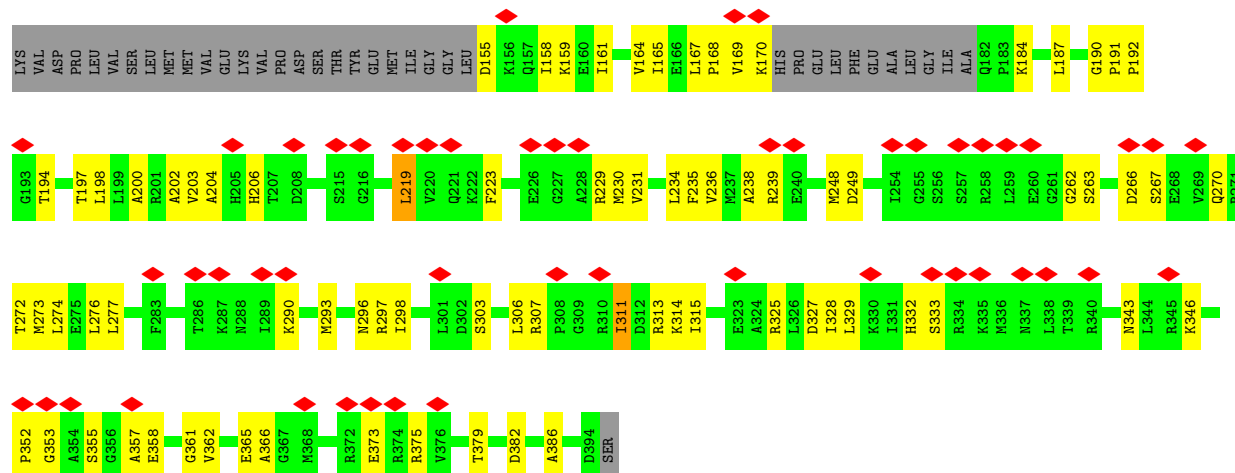




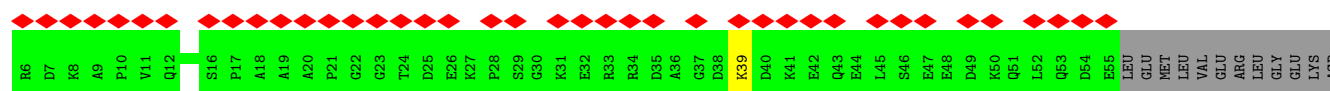
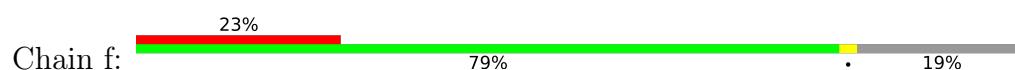
• Molecule 6: 26S proteasome regulatory subunit 6A



• Molecule 7: 26S proteasome regulatory subunit 8



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



THR	SER	L70	Y71	R72	F73	A74	L75	L78	R79	R83	T86	T87	S88	M89	T90	S91	V92	P93	K94	P95	L96	K97	F98	L99	R100	P101	H102	Y103	GLY	LYS	LEU	LYS	ILE	TYR	GLU	ASN	MET	ALA	PRO	GLY	GLU	N118	K119	A122	A123	D124	I125	I126	S127	V128	L129	A130	M131	T132	
E136	R137	E138	C139	L140	K141	Y142	R143	L144	V145	G146	SER	GLN	GLU	LEU	ALA	SER	TRP	GLY	HIS	GLU	TYR	VAL	ARG	HIS	LEU	G164	A167	K168	E169	E182	P183	L184	V192	P193	TYR	ASN	MET	ALA	HIS	ASN	ALA	GLU	HIS	GLU	ALA	CYS	L207	E218	I221						
C230	L231	T234	V237	N238	Y239	F259	M275	D287	V288	V289	VAL	GLN	GLN	MET	PHE	M297	L307	E312	D316	N323	V324	Q325	L326	F330	L331	A332	L333	A334	R335	E336	L337	E341	P345	D346	H352	L353	E354	N355	N356	G359	S363	Q364													
V365	D366	S367	A368	A373	F376	N382	ALA	ALA	PHE	GLY	Q387	D388	K389	L390	G395	N396	Y400	K401	D438	D460	A464	Y469	V470	N473	Y489	ALA	GLY	SER	N493	R494	E495	T499	L502	P503	S536	H543	A555	N565	K569	G570	E571														
A572	I573	I576	L577	P586	L594	V597	C598	A599	Y600	A601	G602	S603	G604	N605	E618	H619	D636	K637	D638	K639	A642	G647	V652	M662	G663	E664	E665	I666	G667	A668	E669	M670	A671	F675	R680	Y681	G682	E683	P684	S698	V699	SER	ASN	PRO	ARG	LEU									
ASN	ILE	LEU	ASP	THR	LEU	SER	LYS	PHE	S714	H715	D718	P719	I726	F727	A728	MET	GLY	MET	VAL	GLY	SER	GLY	THR	ASN	A739	R740	L745	K754	ASP	PRO	ASN	ASN	LEU	PHE	MET	MET	VAL	THR	ASP	GLU	GLU	LEU	ARG	PRO	LEU	PRO	VAL	K773	T777	L778	C779	P780	Y781	H782	
S783	D784	R785	Q786	L787	M788	A794	L797	V801	S802	F803	L804	ASP	VAL	ARG	ASN	ILE	ILE	LEU	GLY	LYS	SER	HIS	TYR	VAL	LEU	TYR	GLY	LEU	VAL	ALA	ALA	MET	GLN	PRO	ARG	MET	LEU	VAL	THR	ASP	GLU	GLU	LEU	ARG	PRO	LEU	PRO	VAL	SER	VAL	ARG	VAL	GLY	GLN	ALA
VAL	ASP	VAL	VAL	VAL																																																			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11082	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 ($e^-/\text{\AA}^2$)	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	0.009	Depositor
Minimum map value	-0.005	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.003	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	0/1621	0.38	0/2195
2	A	0.23	0/2054	0.44	0/2762
3	B	0.24	0/1859	0.42	0/2502
4	D	0.24	0/1759	0.44	0/2372
5	E	0.23	0/1666	0.40	0/2239
6	F	0.24	0/1701	0.41	0/2292
7	C	0.23	0/1801	0.43	1/2413 (0.0%)
8	f	0.24	0/5377	0.44	0/7248
All	All	0.24	0/17838	0.43	1/24023 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	352	PRO	C-N-CA	6.09	135.08	122.30

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	1596	0	1586	40	0
2	A	2023	0	2075	67	0
3	B	1834	0	1894	55	0
4	D	1734	0	1774	81	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1642	0	1667	41	0
6	F	1682	0	1722	39	0
7	C	1780	0	1843	59	0
8	f	5304	0	5315	0	0
All	All	17595	0	17876	373	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 17.

The worst 5 of 373 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)
4:D:335:LEU:O	4:D:341:LYS:HE2	1.62	0.99
6:F:274:LEU:O	6:F:278:LYS:HB3	1.65	0.96
4:D:171:ASP:N	4:D:347:THR:HG1	1.63	0.95
4:D:174:LYS:O	4:D:178:ARG:HB2	1.66	0.94
4:D:334:PRO:HB2	4:D:344:ILE:HB	1.50	0.94

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	208/223 (93%)	204 (98%)	4 (2%)	0	100	100
2	A	254/266 (96%)	222 (87%)	32 (13%)	0	100	100
3	B	228/266 (86%)	209 (92%)	18 (8%)	1 (0%)	34	72
4	D	214/262 (82%)	196 (92%)	16 (8%)	2 (1%)	17	57
5	E	205/262 (78%)	183 (89%)	21 (10%)	1 (0%)	29	69
6	F	211/267 (79%)	197 (93%)	14 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
7	C	223/266 (84%)	209 (94%)	13 (6%)	1 (0%)	34 72
8	f	664/848 (78%)	595 (90%)	65 (10%)	4 (1%)	25 66
All	All	2207/2660 (83%)	2015 (91%)	183 (8%)	9 (0%)	38 72

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	334	PRO
8	f	336	GLU
5	E	272	ARG
7	C	353	GLY
8	f	334	ALA

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	G	169/178 (95%)	167 (99%)	2 (1%)	71 83
2	A	220/224 (98%)	216 (98%)	4 (2%)	59 77
3	B	202/231 (87%)	200 (99%)	2 (1%)	76 86
4	D	188/224 (84%)	181 (96%)	7 (4%)	34 58
5	E	177/225 (79%)	175 (99%)	2 (1%)	73 84
6	F	179/222 (81%)	177 (99%)	2 (1%)	73 84
7	C	193/225 (86%)	189 (98%)	4 (2%)	53 72
8	f	579/714 (81%)	565 (98%)	14 (2%)	49 69
All	All	1907/2243 (85%)	1870 (98%)	37 (2%)	59 75

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	f	460	ASP
8	f	745	LEU

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Mol	Chain	Res	Type
8	f	473	ASN
8	f	569	LYS
4	D	304	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
6	F	428	GLN
8	f	180	GLN
7	C	377	HIS
8	f	213	GLN
3	B	193	GLN

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
7	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	307:ARG	C	308:PRO	N	3.65

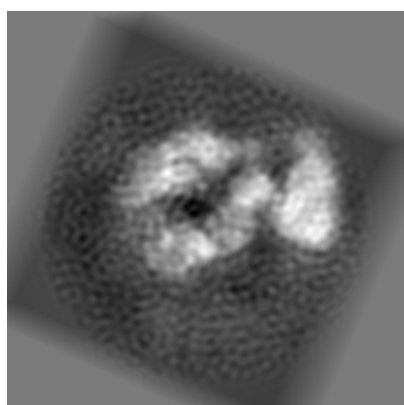
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8678. These allow visual inspection of the internal detail of the map and identification of artifacts.

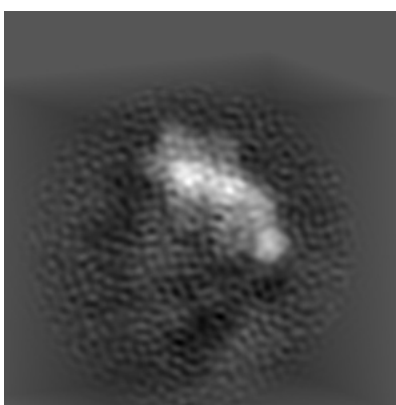
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

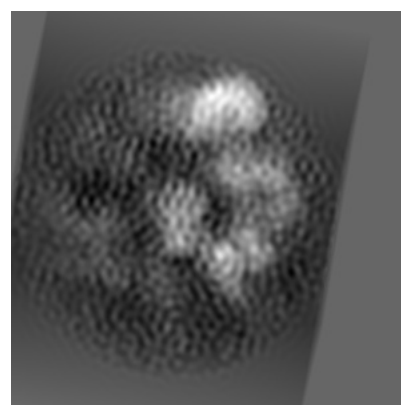
6.1.1 Primary map



X



Y

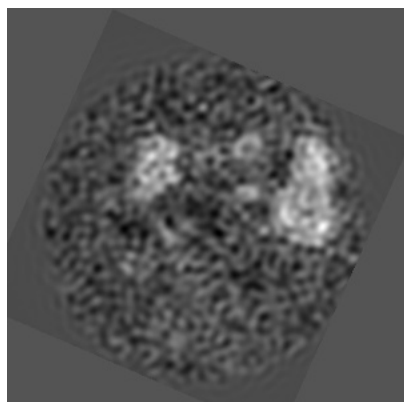


Z

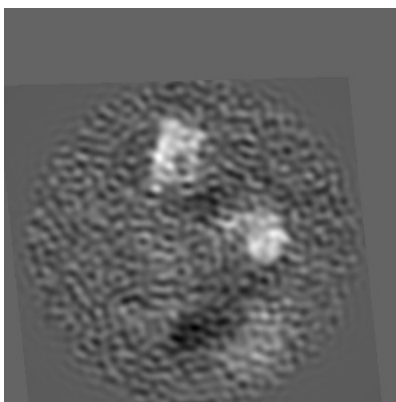
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

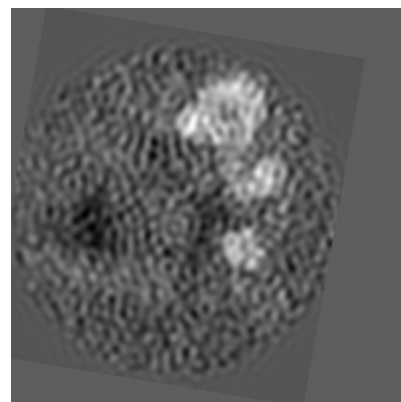
6.2.1 Primary map



X Index: 180



Y Index: 180

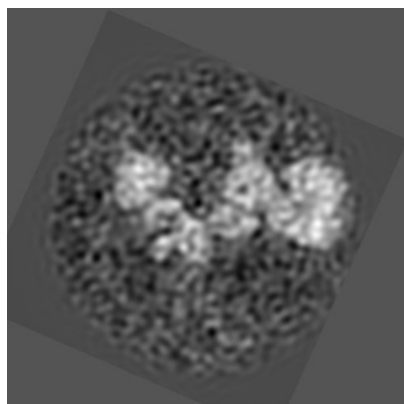


Z Index: 180

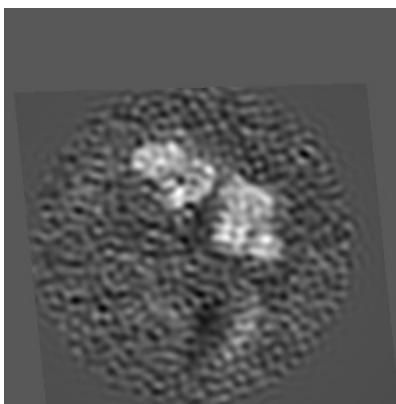
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

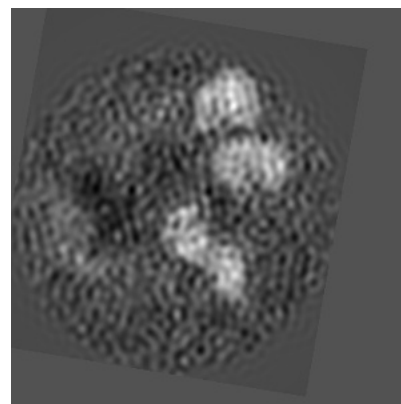
6.3.1 Primary map



X Index: 203



Y Index: 144

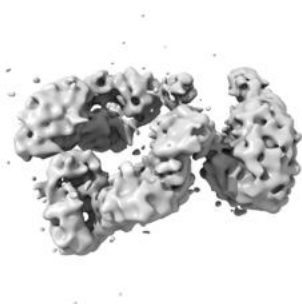


Z Index: 201

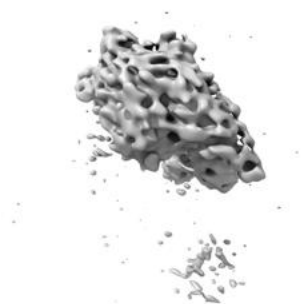
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

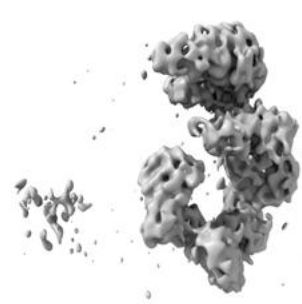
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

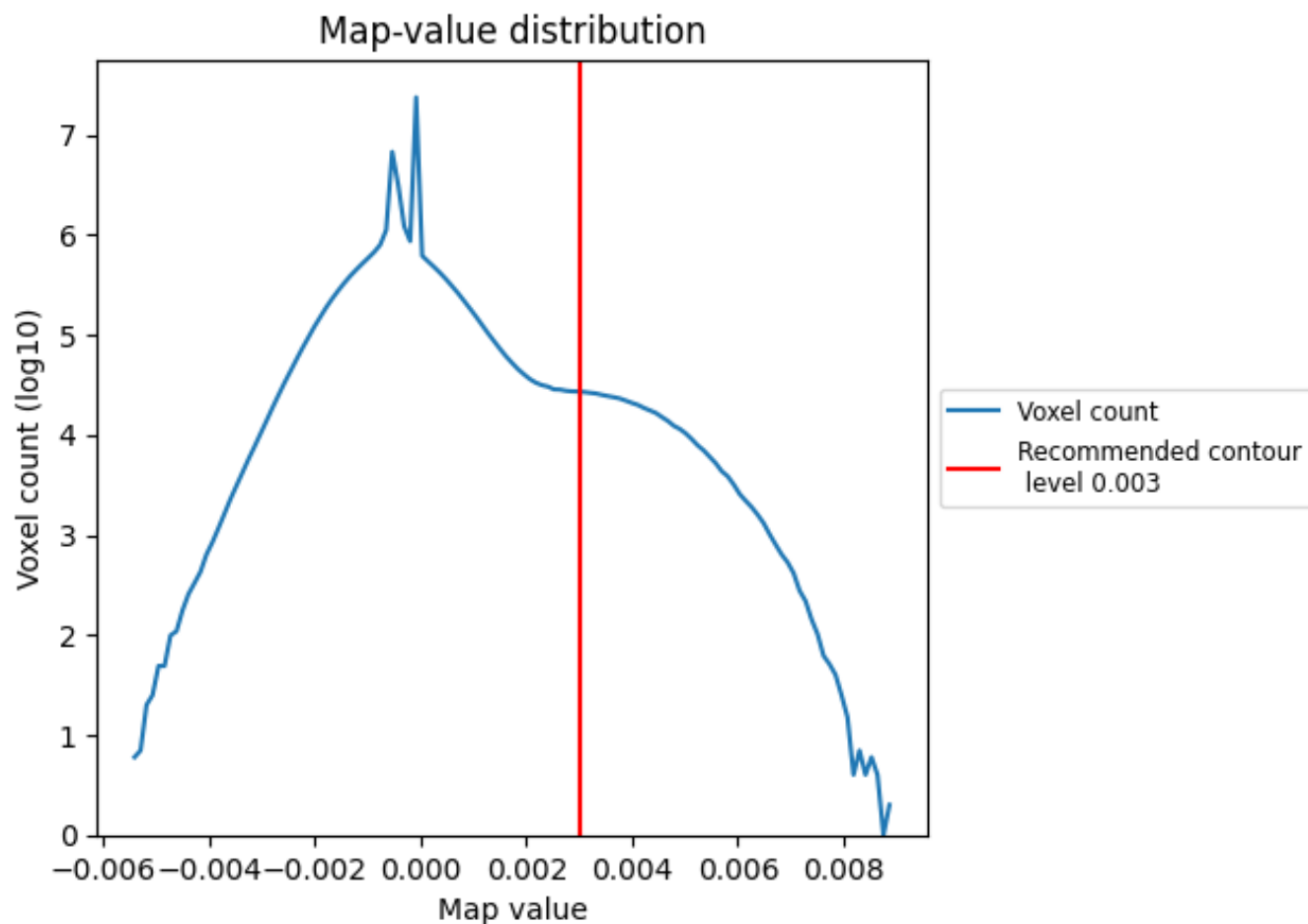
6.5 Mask visualisation

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

7 Map analysis [i](#)

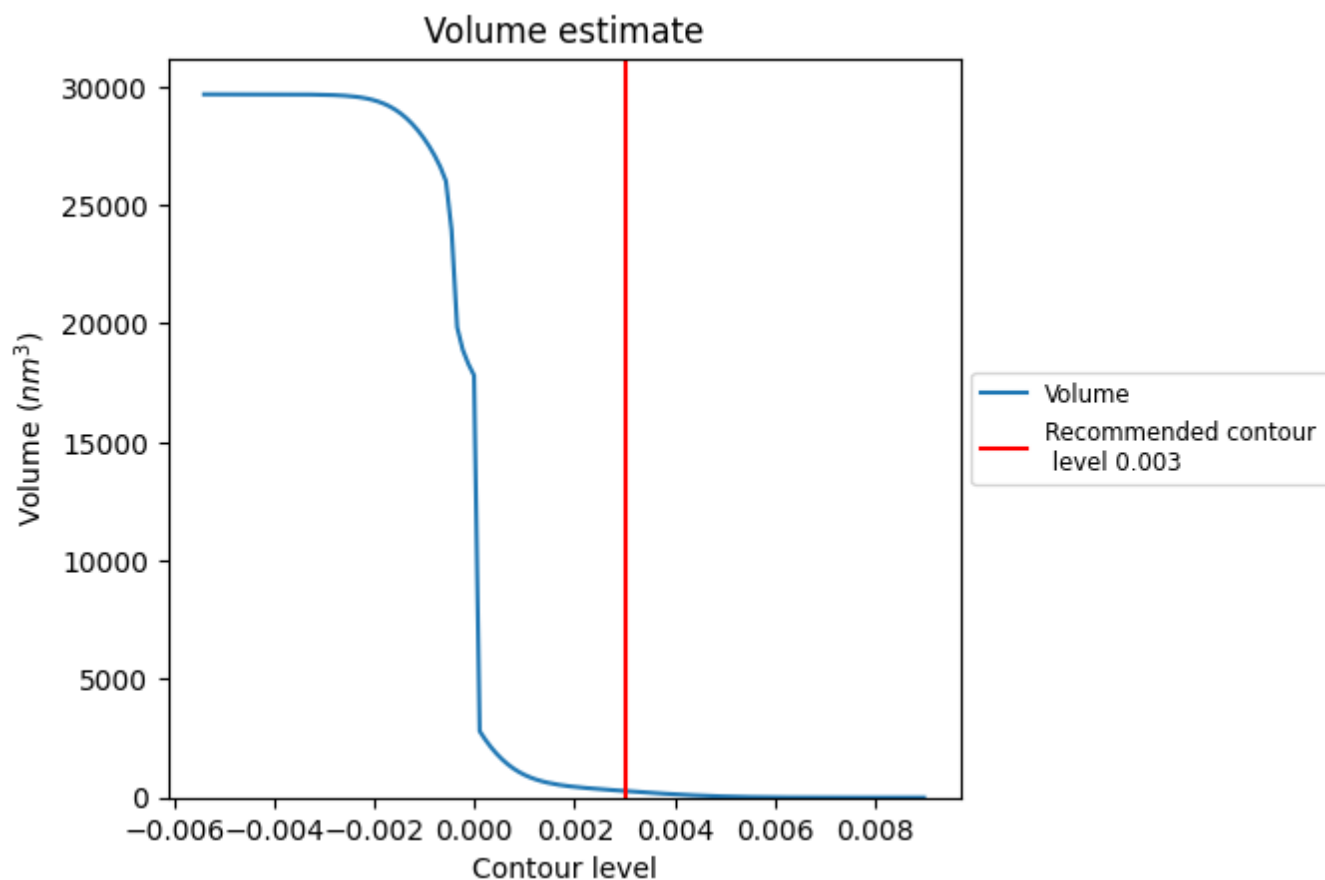
This section contains the results of statistical analysis of the map.

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.

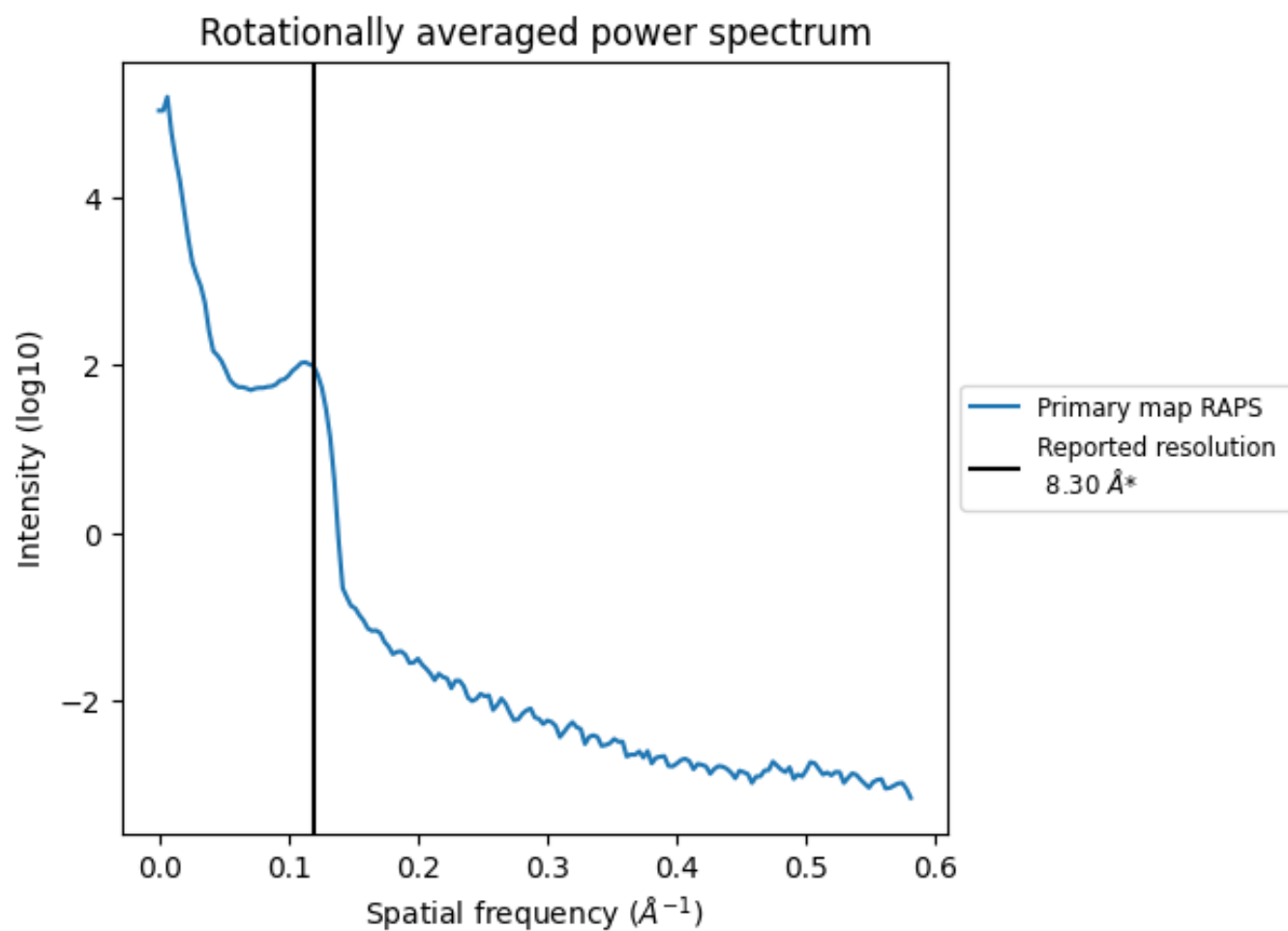
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 277 nm³; this corresponds to an approximate mass of 251 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 0.120 Å⁻¹

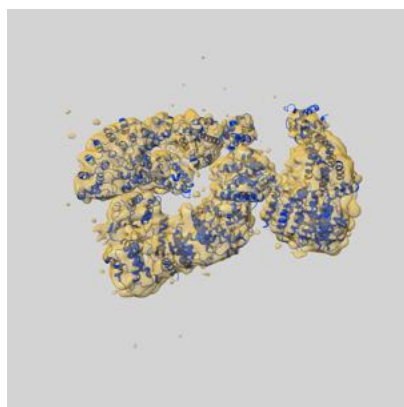
8 Fourier-Shell correlation

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

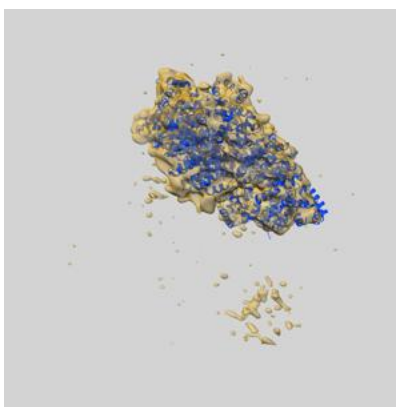
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8678 and PDB model 5VHM. Per-residue inclusion information can be found in section [3](#) on page [5](#).

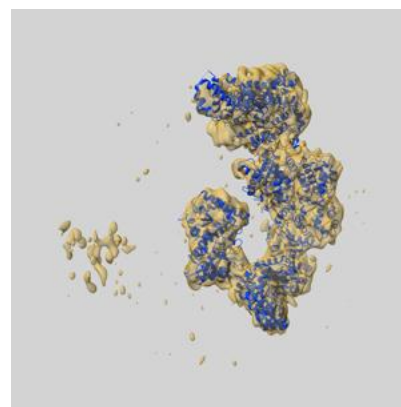
9.1 Map-model overlay [i](#)



X



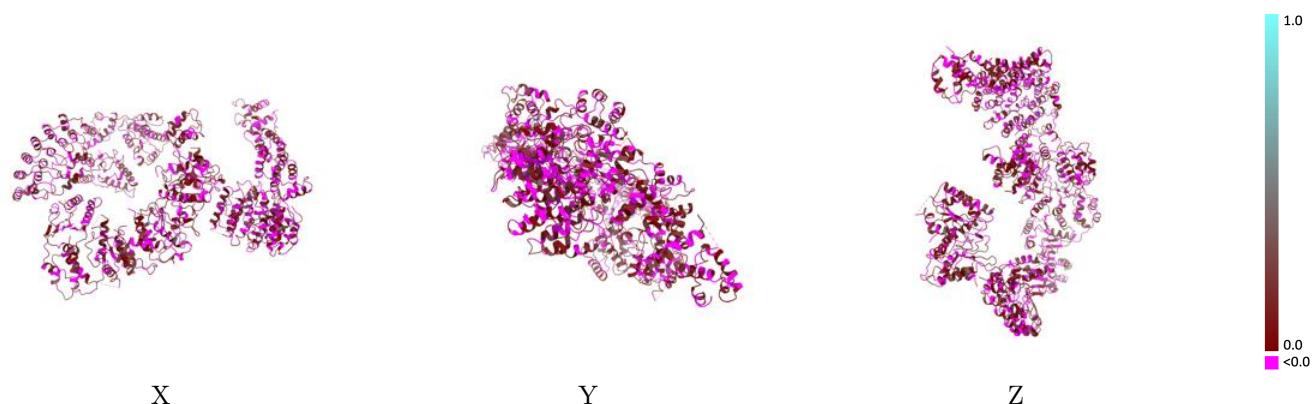
Y



Z

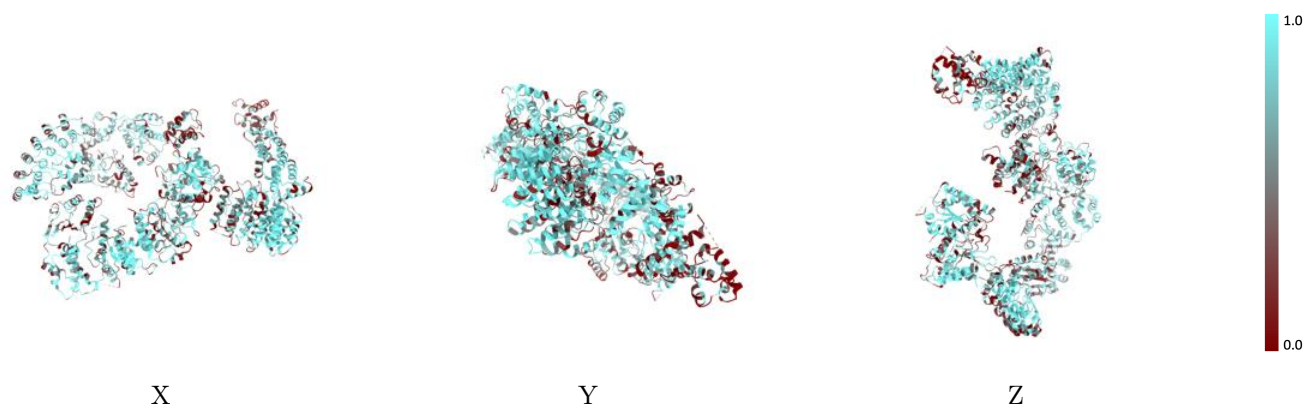
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



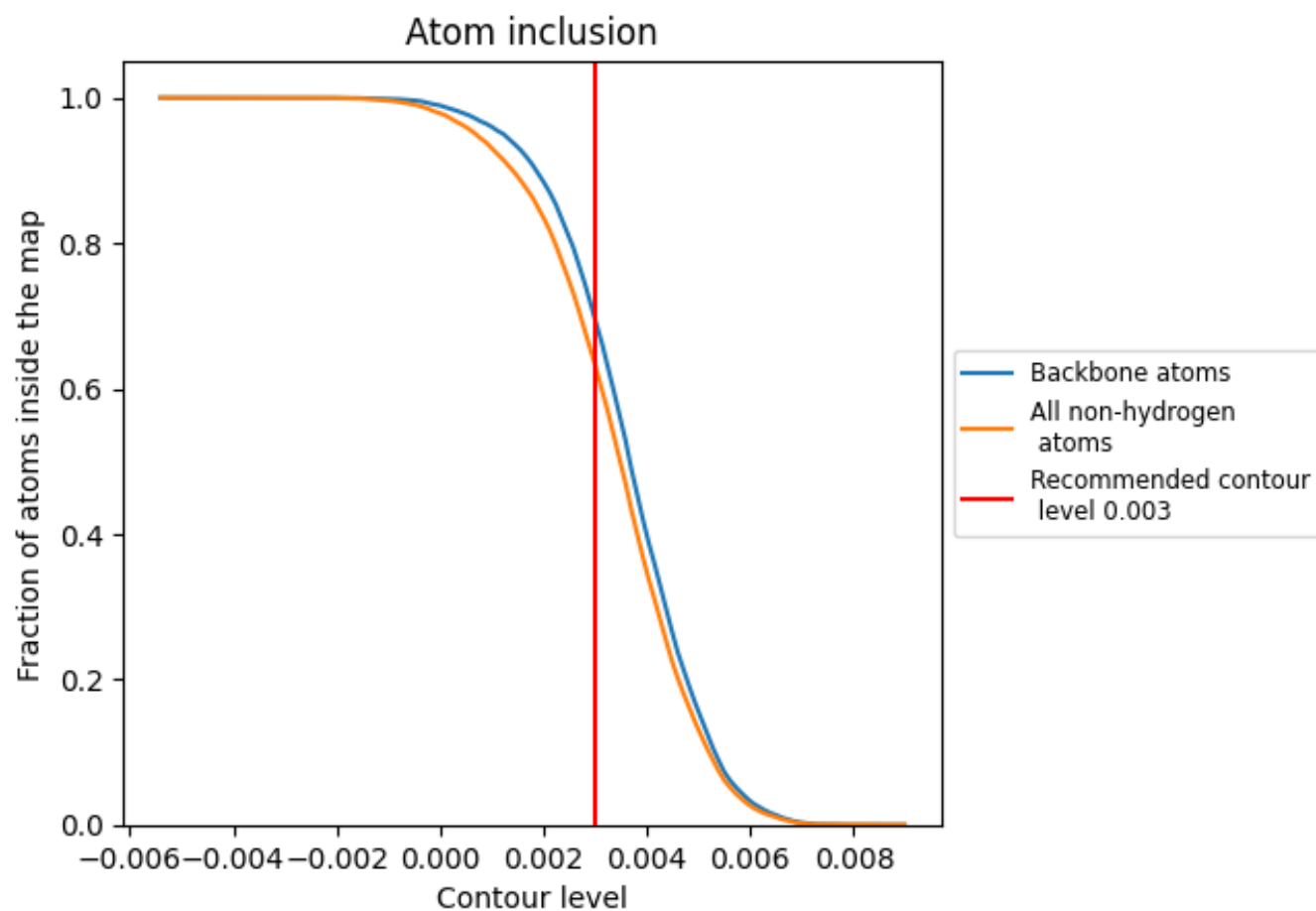
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.003).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 63% 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 (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6314	<div></div> 0.0600
A	<div></div> 0.5942	<div></div> 0.0630
B	<div></div> 0.4892	<div></div> 0.0660
C	<div></div> 0.6889	<div></div> 0.0830
D	<div></div> 0.5735	<div></div> 0.0760
E	<div></div> 0.5990	<div></div> 0.0780
F	<div></div> 0.7075	<div></div> 0.0790
G	<div></div> 0.7056	<div></div> 0.0570
f	<div></div> 0.6576	<div></div> 0.0330

1.0

0.0

<0.0