



Full wwPDB EM Validation Report ⓘ

Jun 26, 2023 – 10:36 AM EDT

PDB ID : 8FZ5
EMDB ID : EMD-29603
Title : The PI31-free Bovine 20S proteasome
Authors : Hsu, H.-C.; Li, H.
Deposited on : 2023-01-27
Resolution : 2.23 Å (reported)
Based on initial model : 1IRU

This is a Full wwPDB EM Validation 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:

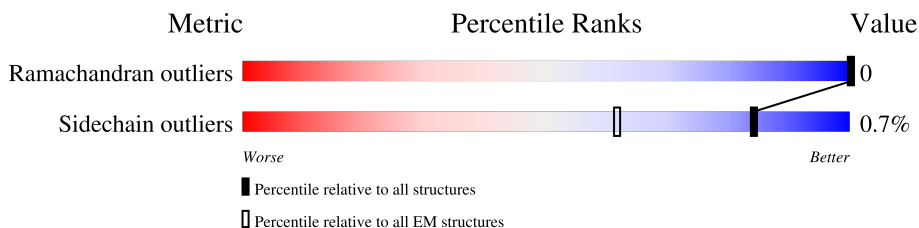
EMDB validation analysis : 0.0.1.dev50
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.33

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 2.23 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.



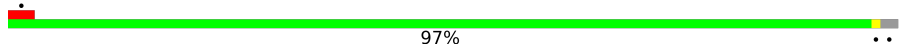

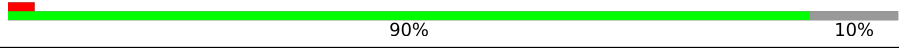
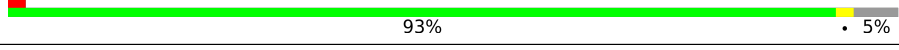
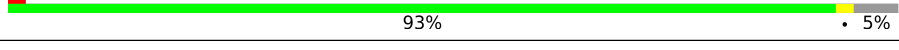


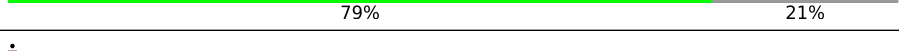
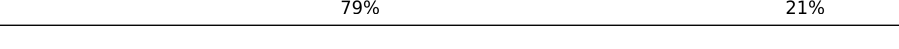
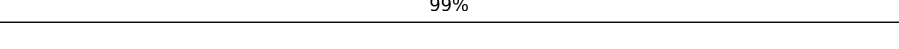
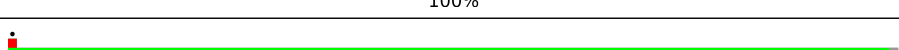
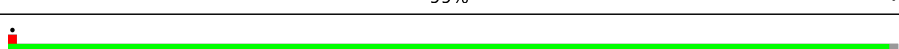


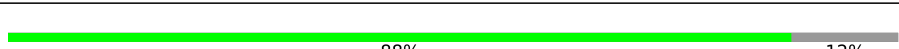




Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	A	246	5% 99%
1	O	246	5% 98%
2	B	234	1% 100%
2	P	234	1% 100%
3	C	261	6% 96%
3	Q	261	6% 96%
4	D	248	8% 98%
4	R	248	8% 98%
5	E	241	1% 97%

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Mol	Chain	Length	Quality of chain
5	S	241	 97%
6	F	263	 90% 10%
6	T	263	 90% 10%
7	G	255	 93% 5%
7	U	255	 93% 5%
8	H	239	 85% 15%
8	V	239	 85% 15%
9	I	277	 79% 21%
9	W	277	 79% 21%
10	J	205	 99%
10	X	205	 100%
11	K	201	 99%
11	Y	201	 99%
12	L	263	 76% 24%
12	Z	263	 76% 24%
13	M	241	 88% 12%
13	a	241	 88% 12%
14	N	264	 81% 19%
14	b	264	 81% 19%

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 48892 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-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	245	Total	C	N	O	S	0	0
			1911	1211	321	365	14		
1	O	245	Total	C	N	O	S	0	0
			1911	1211	321	365	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	233	Total	C	N	O	S	0	0
			1820	1163	308	342	7		
2	P	233	Total	C	N	O	S	0	0
			1820	1163	308	342	7		

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	251	Total	C	N	O	S	0	0
			1979	1250	340	378	11		
3	Q	251	Total	C	N	O	S	0	0
			1979	1250	340	378	11		

- Molecule 4 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	243	Total	C	N	O	S	0	0
			1922	1208	340	369	5		
4	R	243	Total	C	N	O	S	0	0
			1922	1208	340	369	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	236	1805	1133	297	364	11	0	0
5	S	236	1805	1133	297	364	11	0	0

- Molecule 6 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	238	1873	1172	337	353	11	0	0
6	T	238	1873	1172	337	353	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	241	1888	1196	322	359	11	0	0
7	U	241	1888	1196	322	359	11	0	0

- Molecule 8 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	202	1519	955	258	294	12	0	0
8	V	202	1519	955	258	294	12	0	0

- Molecule 9 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	220	1660	1045	283	320	12	0	0
9	W	220	1660	1045	283	320	12	0	0

- Molecule 10 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	204	1594	1015	265	295	19	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	X	204	Total	C	N	O	S	0	0
			1594	1015	265	295	19		

- Molecule 11 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	199	Total	C	N	O	S	0	0
			1602	1028	272	294	8		
11	Y	199	Total	C	N	O	S	0	0
			1602	1028	272	294	8		

- Molecule 12 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	201	Total	C	N	O	S	0	0
			1557	980	272	296	9		
12	Z	201	Total	C	N	O	S	0	0
			1557	980	272	296	9		

- Molecule 13 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	213	Total	C	N	O	S	0	0
			1645	1042	282	311	10		
13	a	213	Total	C	N	O	S	0	0
			1645	1042	282	311	10		

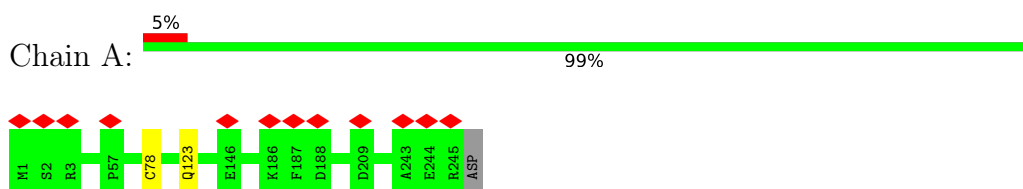
- Molecule 14 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	214	Total	C	N	O	S	0	0
			1671	1056	287	316	12		
14	b	214	Total	C	N	O	S	0	0
			1671	1056	287	316	12		

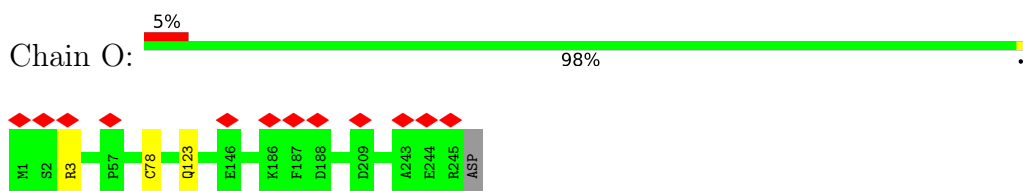
3 Residue-property plots [i](#)

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.

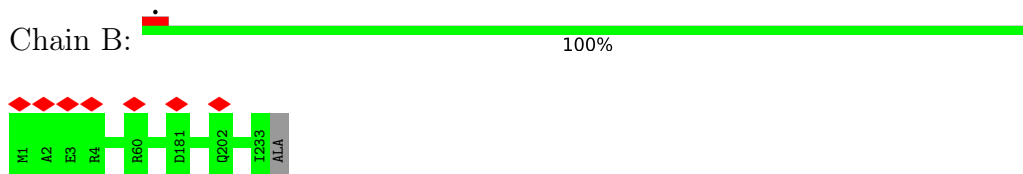
- Molecule 1: Proteasome subunit alpha type-6



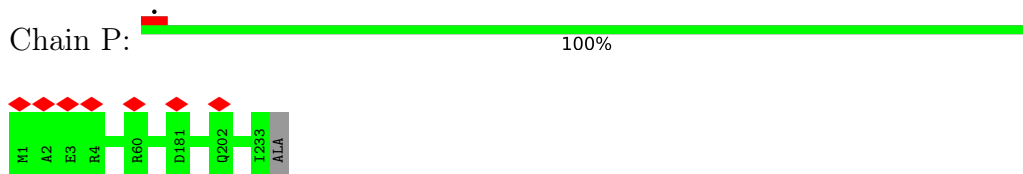
- Molecule 1: Proteasome subunit alpha type-6



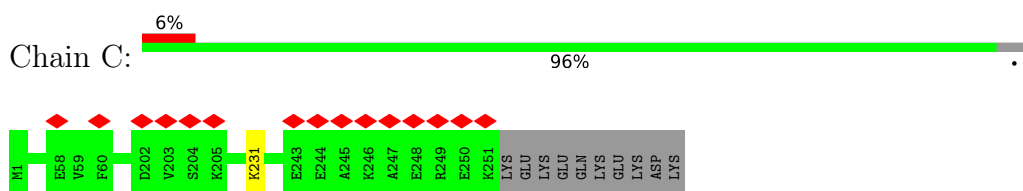
- Molecule 2: Proteasome subunit alpha type-2



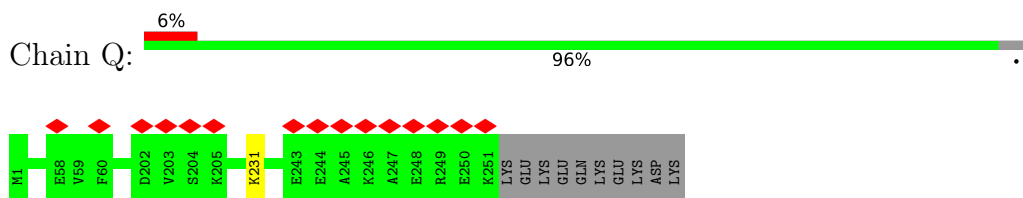
- Molecule 2: Proteasome subunit alpha type-2



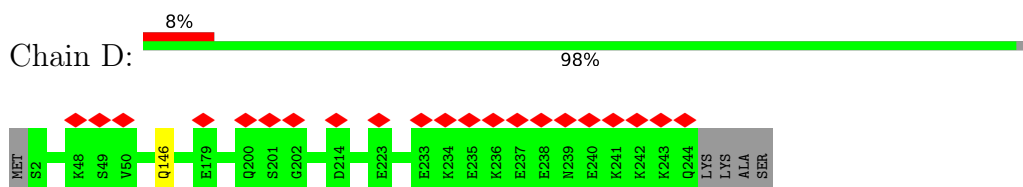
- Molecule 3: Proteasome subunit alpha type-4



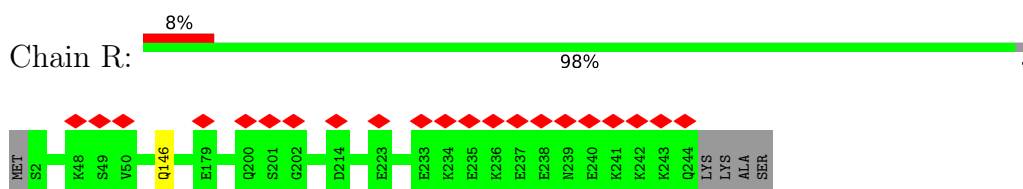
- Molecule 3: Proteasome subunit alpha type-4



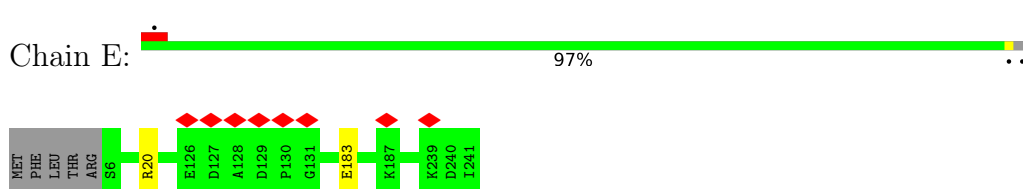
- Molecule 4: Proteasome subunit alpha type-7



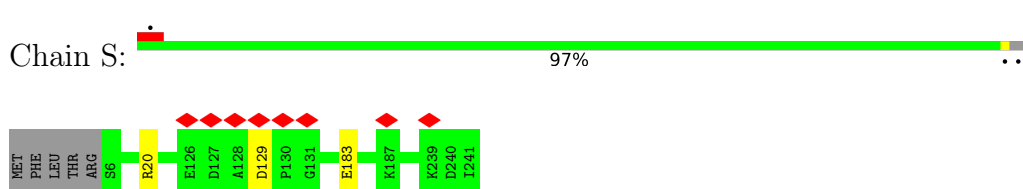
- Molecule 4: Proteasome subunit alpha type-7



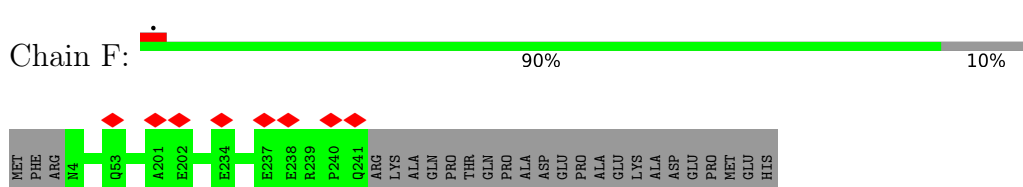
- Molecule 5: Proteasome subunit alpha type-5



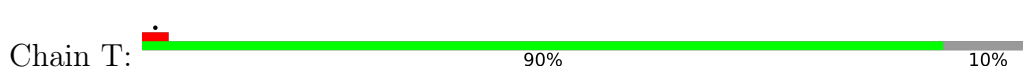
- Molecule 5: Proteasome subunit alpha type-5

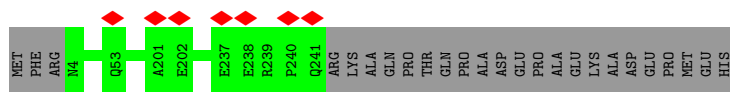


- Molecule 6: Proteasome subunit alpha type-1

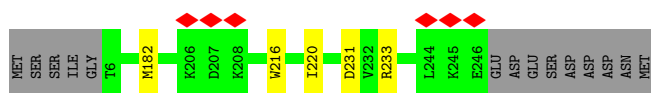


- Molecule 6: Proteasome subunit alpha type-1

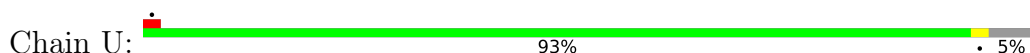




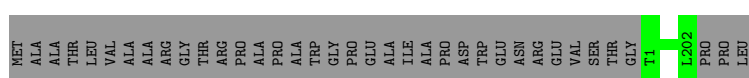
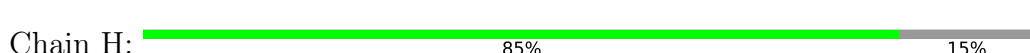
• Molecule 7: Proteasome subunit alpha type-3



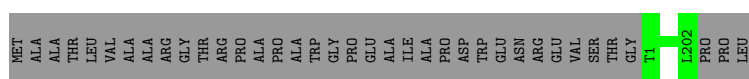
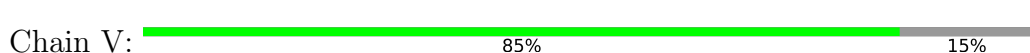
• Molecule 7: Proteasome subunit alpha type-3



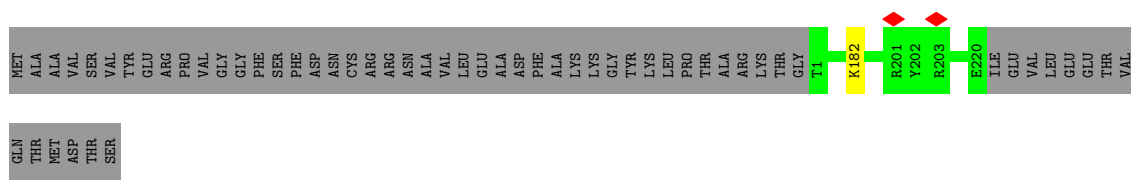
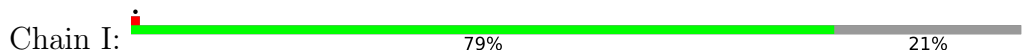
• Molecule 8: Proteasome subunit beta type-6



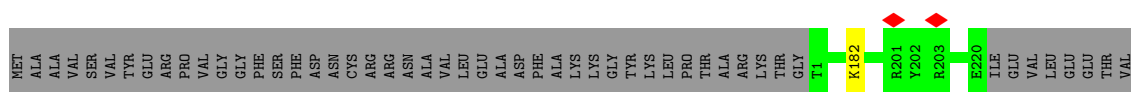
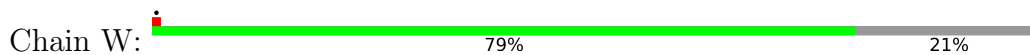
• Molecule 8: Proteasome subunit beta type-6



• Molecule 9: Proteasome subunit beta type-7

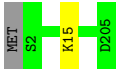


• Molecule 9: Proteasome subunit beta type-7





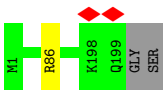
• Molecule 10: Proteasome subunit beta type-3



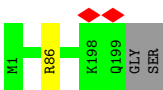
• Molecule 10: Proteasome subunit beta type-3



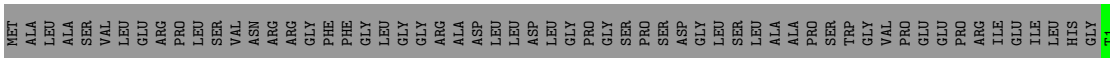
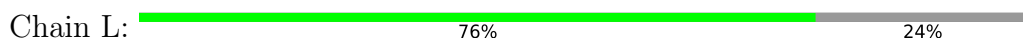
• Molecule 11: Proteasome subunit beta type-2



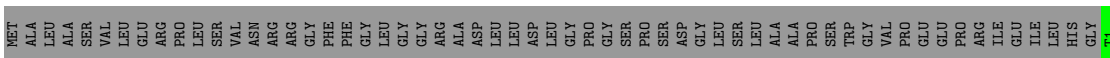
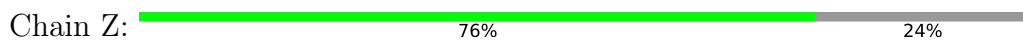
• Molecule 11: Proteasome subunit beta type-2




• Molecule 12: Proteasome subunit beta type-5

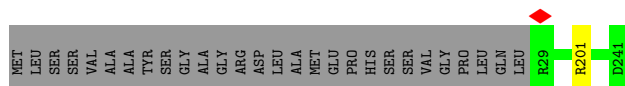


• Molecule 12: Proteasome subunit beta type-5




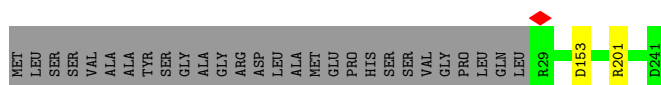
- Molecule 13: Proteasome subunit beta type-1

Chain M:  88% 12%




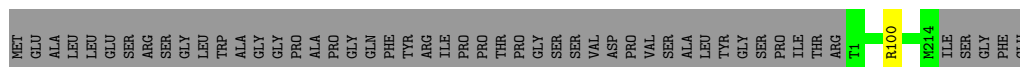
- Molecule 13: Proteasome subunit beta type-1

Chain a:  88% 12%




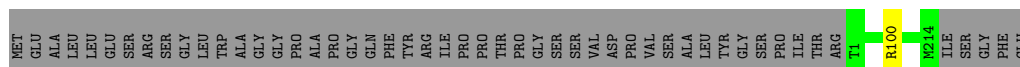
- Molecule 14: Proteasome subunit beta type-4

Chain N:  81% 19%



- Molecule 14: Proteasome subunit beta type-4

Chain b:  81% 19%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	675686	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.124	Depositor
Minimum map value	-1.526	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.130	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	291.456, 291.456, 291.456	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.828, 0.828, 0.828	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	A	0.32	0/1945	0.50	0/2627
1	O	0.32	0/1945	0.50	0/2627
2	B	0.34	0/1859	0.50	0/2517
2	P	0.34	0/1859	0.50	0/2517
3	C	0.31	0/2009	0.52	0/2704
3	Q	0.31	0/2009	0.51	0/2704
4	D	0.31	0/1949	0.51	0/2627
4	R	0.31	0/1949	0.51	0/2627
5	E	0.30	0/1833	0.48	0/2475
5	S	0.30	0/1833	0.48	0/2475
6	F	0.31	0/1908	0.53	0/2579
6	T	0.31	0/1908	0.53	0/2579
7	G	0.34	0/1923	0.50	0/2590
7	U	0.34	0/1923	0.50	0/2590
8	H	0.33	0/1547	0.54	0/2097
8	V	0.33	0/1547	0.54	0/2097
9	I	0.31	0/1687	0.52	0/2280
9	W	0.31	0/1687	0.52	0/2280
10	J	0.31	0/1623	0.53	0/2188
10	X	0.31	0/1623	0.53	0/2188
11	K	0.34	0/1636	0.53	0/2213
11	Y	0.34	0/1636	0.53	0/2213
12	L	0.34	0/1588	0.56	0/2144
12	Z	0.34	0/1588	0.55	0/2144
13	M	0.32	0/1676	0.53	0/2258
13	a	0.32	0/1676	0.53	0/2258
14	N	0.33	0/1704	0.55	0/2305
14	b	0.33	0/1704	0.55	0/2305
All	All	0.32	0/49774	0.52	0/67208

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](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	A	243/246 (99%)	242 (100%)	1 (0%)	0	100	100
1	O	243/246 (99%)	241 (99%)	2 (1%)	0	100	100
2	B	231/234 (99%)	228 (99%)	3 (1%)	0	100	100
2	P	231/234 (99%)	228 (99%)	3 (1%)	0	100	100
3	C	249/261 (95%)	245 (98%)	4 (2%)	0	100	100
3	Q	249/261 (95%)	245 (98%)	4 (2%)	0	100	100
4	D	241/248 (97%)	238 (99%)	3 (1%)	0	100	100
4	R	241/248 (97%)	238 (99%)	3 (1%)	0	100	100
5	E	234/241 (97%)	229 (98%)	5 (2%)	0	100	100
5	S	234/241 (97%)	231 (99%)	3 (1%)	0	100	100
6	F	236/263 (90%)	232 (98%)	4 (2%)	0	100	100
6	T	236/263 (90%)	232 (98%)	4 (2%)	0	100	100
7	G	239/255 (94%)	236 (99%)	3 (1%)	0	100	100
7	U	239/255 (94%)	236 (99%)	3 (1%)	0	100	100
8	H	200/239 (84%)	199 (100%)	1 (0%)	0	100	100
8	V	200/239 (84%)	199 (100%)	1 (0%)	0	100	100
9	I	218/277 (79%)	215 (99%)	3 (1%)	0	100	100
9	W	218/277 (79%)	215 (99%)	3 (1%)	0	100	100
10	J	202/205 (98%)	198 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	X	202/205 (98%)	198 (98%)	4 (2%)	0	100	100
11	K	197/201 (98%)	193 (98%)	4 (2%)	0	100	100
11	Y	197/201 (98%)	193 (98%)	4 (2%)	0	100	100
12	L	199/263 (76%)	196 (98%)	3 (2%)	0	100	100
12	Z	199/263 (76%)	196 (98%)	3 (2%)	0	100	100
13	M	211/241 (88%)	210 (100%)	1 (0%)	0	100	100
13	a	211/241 (88%)	210 (100%)	1 (0%)	0	100	100
14	N	212/264 (80%)	207 (98%)	5 (2%)	0	100	100
14	b	212/264 (80%)	207 (98%)	5 (2%)	0	100	100
All	All	6224/6876 (90%)	6137 (99%)	87 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	A	209/210 (100%)	207 (99%)	2 (1%)	76	82
1	O	209/210 (100%)	206 (99%)	3 (1%)	67	74
2	B	191/191 (100%)	191 (100%)	0	100	100
2	P	191/191 (100%)	191 (100%)	0	100	100
3	C	211/221 (96%)	210 (100%)	1 (0%)	88	92
3	Q	211/221 (96%)	210 (100%)	1 (0%)	88	92
4	D	207/211 (98%)	206 (100%)	1 (0%)	88	92
4	R	207/211 (98%)	206 (100%)	1 (0%)	88	92
5	E	198/203 (98%)	196 (99%)	2 (1%)	76	82
5	S	198/203 (98%)	195 (98%)	3 (2%)	65	72
6	F	204/225 (91%)	204 (100%)	0	100	100
6	T	204/225 (91%)	204 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	199/212 (94%)	194 (98%)	5 (2%)	47	54
7	U	199/212 (94%)	194 (98%)	5 (2%)	47	54
8	H	158/184 (86%)	158 (100%)	0	100	100
8	V	158/184 (86%)	158 (100%)	0	100	100
9	I	181/228 (79%)	180 (99%)	1 (1%)	86	90
9	W	181/228 (79%)	180 (99%)	1 (1%)	86	90
10	J	174/175 (99%)	173 (99%)	1 (1%)	86	90
10	X	174/175 (99%)	174 (100%)	0	100	100
11	K	170/171 (99%)	169 (99%)	1 (1%)	86	90
11	Y	170/171 (99%)	169 (99%)	1 (1%)	86	90
12	L	157/205 (77%)	157 (100%)	0	100	100
12	Z	157/205 (77%)	157 (100%)	0	100	100
13	M	177/198 (89%)	176 (99%)	1 (1%)	86	90
13	a	177/198 (89%)	175 (99%)	2 (1%)	73	80
14	N	176/215 (82%)	175 (99%)	1 (1%)	86	90
14	b	176/215 (82%)	175 (99%)	1 (1%)	86	90
All	All	5224/5698 (92%)	5190 (99%)	34 (1%)	84	88

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	CYS
1	A	123	GLN
3	C	231	LYS
4	D	146	GLN
5	E	20	ARG
5	E	183	GLU
7	G	182	MET
7	G	216	TRP
7	G	220	ILE
7	G	231	ASP
7	G	233	ARG
9	I	182	LYS
10	J	15	LYS
11	K	86	ARG
13	M	201	ARG

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Mol	Chain	Res	Type
14	N	100	ARG
1	O	3	ARG
1	O	78	CYS
1	O	123	GLN
3	Q	231	LYS
4	R	146	GLN
5	S	20	ARG
5	S	129	ASP
5	S	183	GLU
7	U	182	MET
7	U	216	TRP
7	U	220	ILE
7	U	231	ASP
7	U	233	ARG
9	W	182	LYS
11	Y	86	ARG
13	a	153	ASP
13	a	201	ARG
14	b	100	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	GLN
1	O	123	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](#)

There are no chain breaks in this entry.

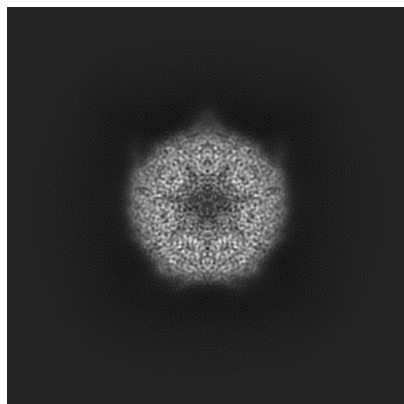
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29603. These allow visual inspection of the internal detail of the map and identification of artifacts.

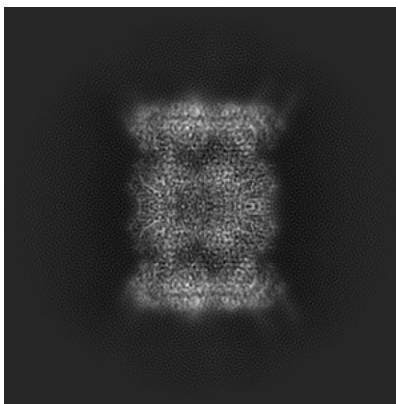
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

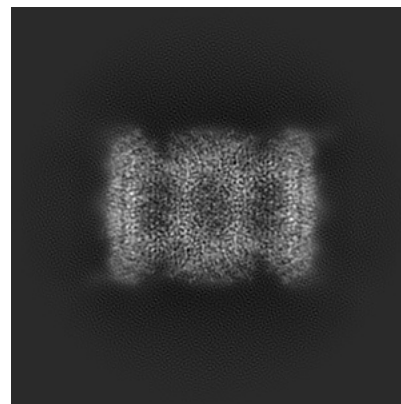
6.1.1 Primary map



X

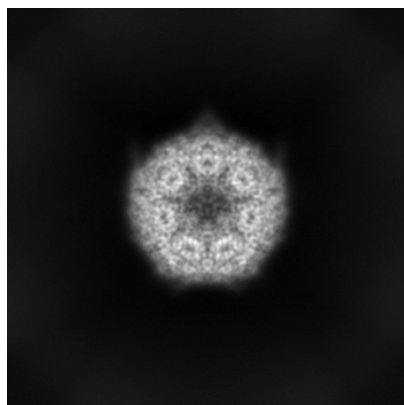


Y

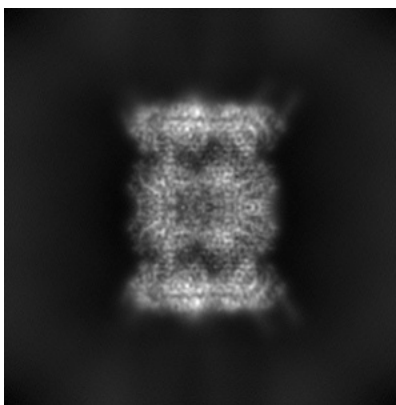


Z

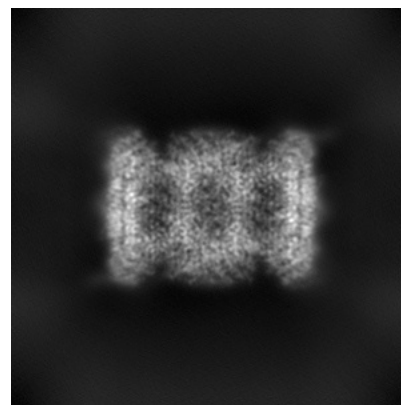
6.1.2 Raw map



X



Y

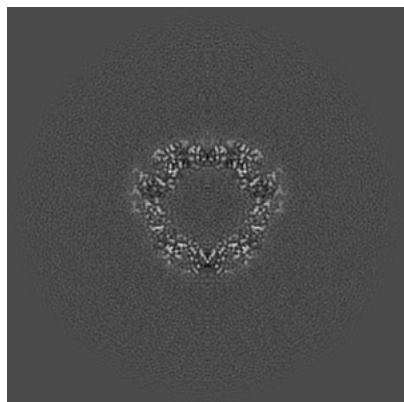


Z

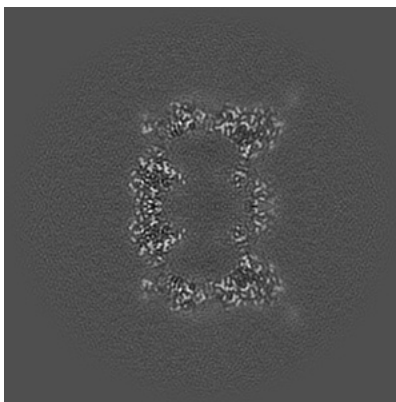
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

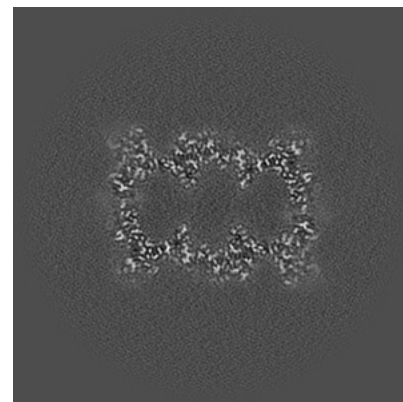
6.2.1 Primary map



X Index: 176

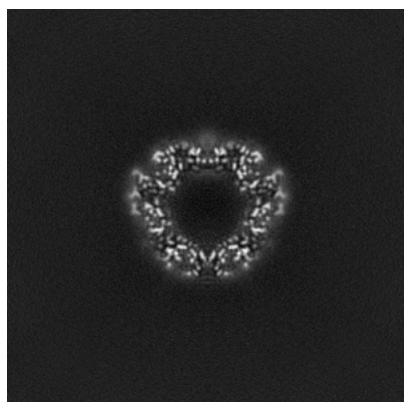


Y Index: 176

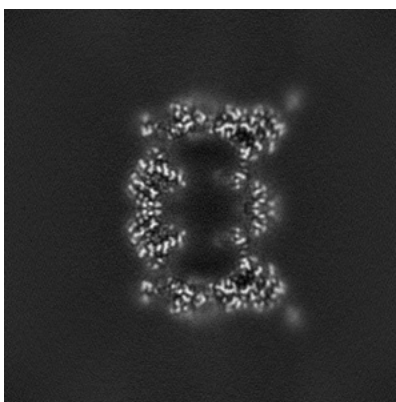


Z Index: 176

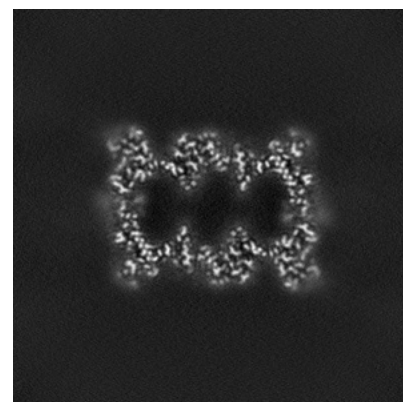
6.2.2 Raw map



X Index: 176



Y Index: 176

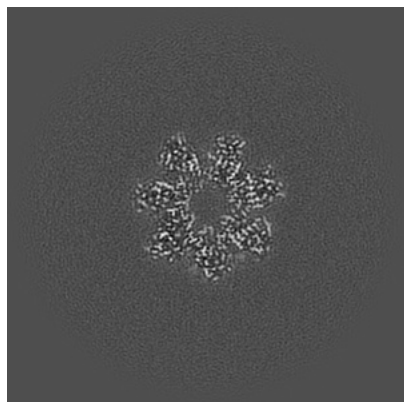


Z Index: 176

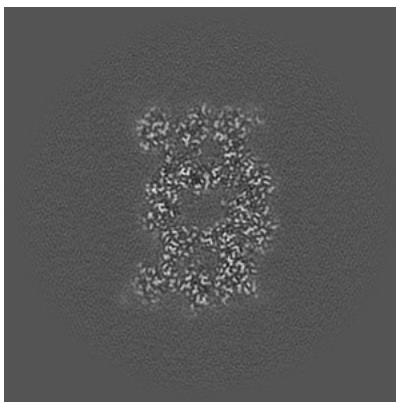
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

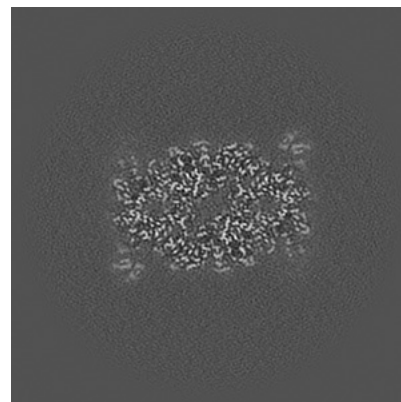
6.3.1 Primary map



X Index: 199

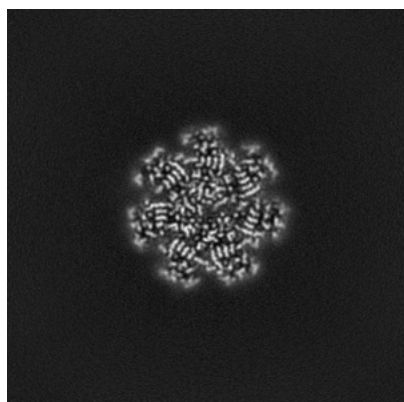


Y Index: 148

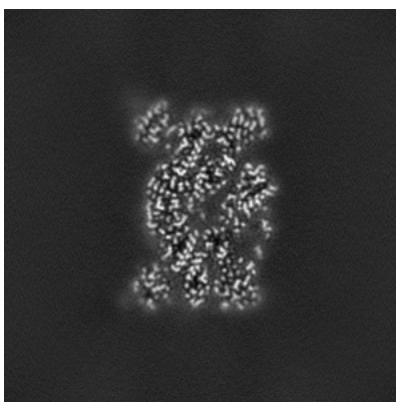


Z Index: 145

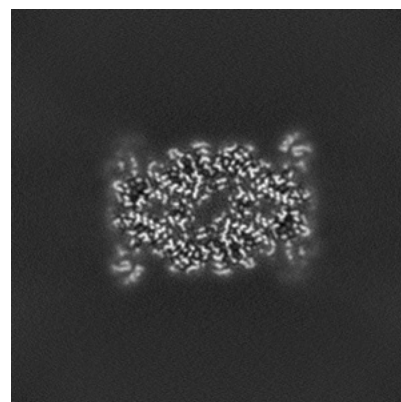
6.3.2 Raw map



X Index: 107



Y Index: 143

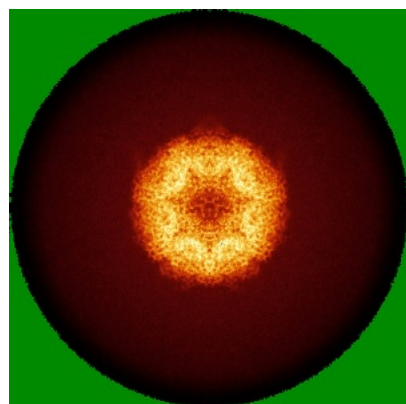


Z Index: 145

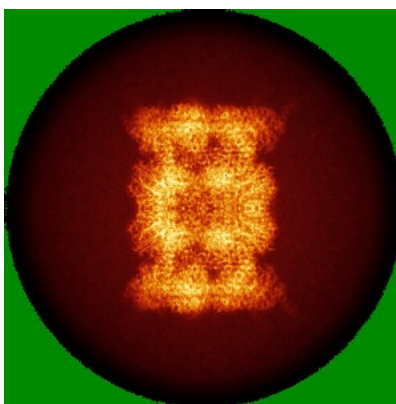
The images above show the largest variance slices of the map in three orthogonal directions.

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

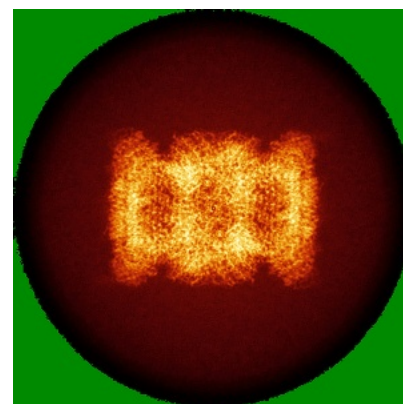
6.4.1 Primary map



X

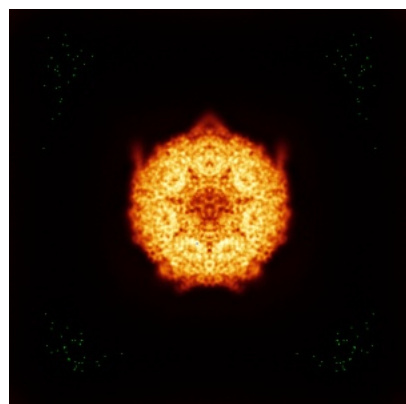


Y

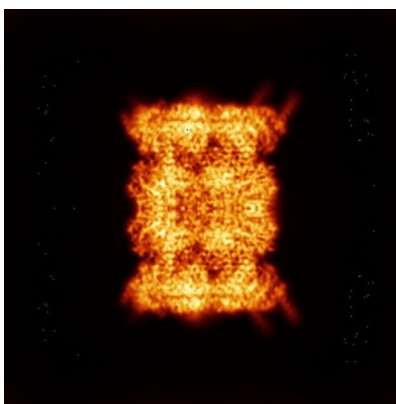


Z

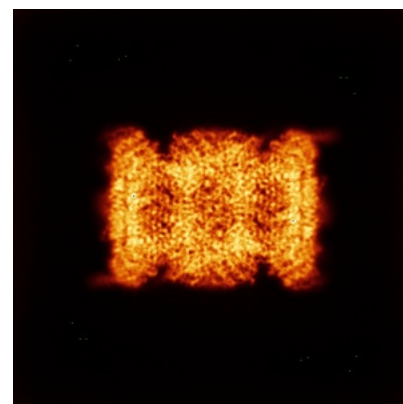
6.4.2 Raw map



X



Y

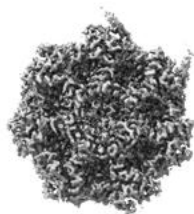


Z

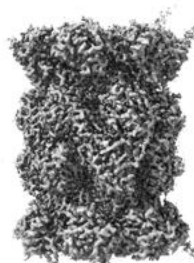
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

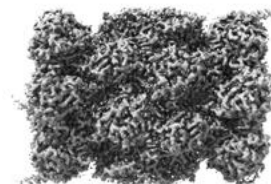
6.5.1 Primary map



X



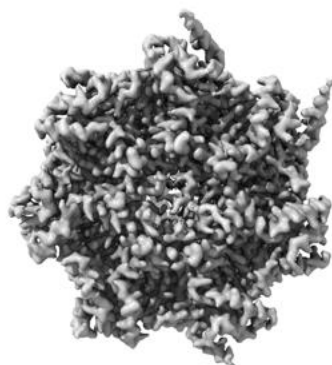
Y



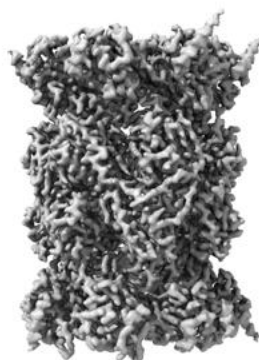
Z

The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

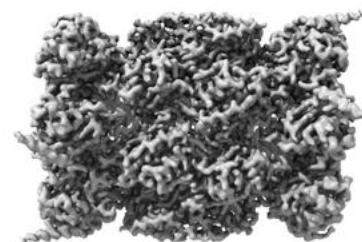
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

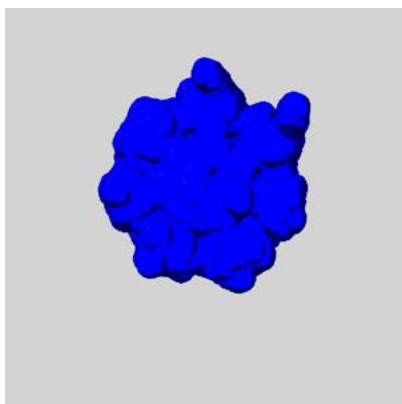
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

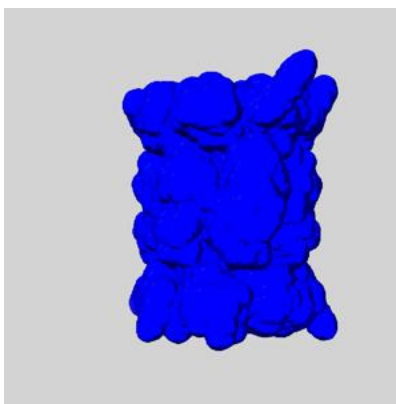
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

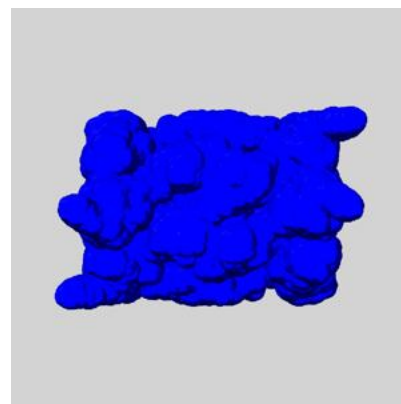
6.6.1 emd_29603_msk_1.map [i](#)



X



Y

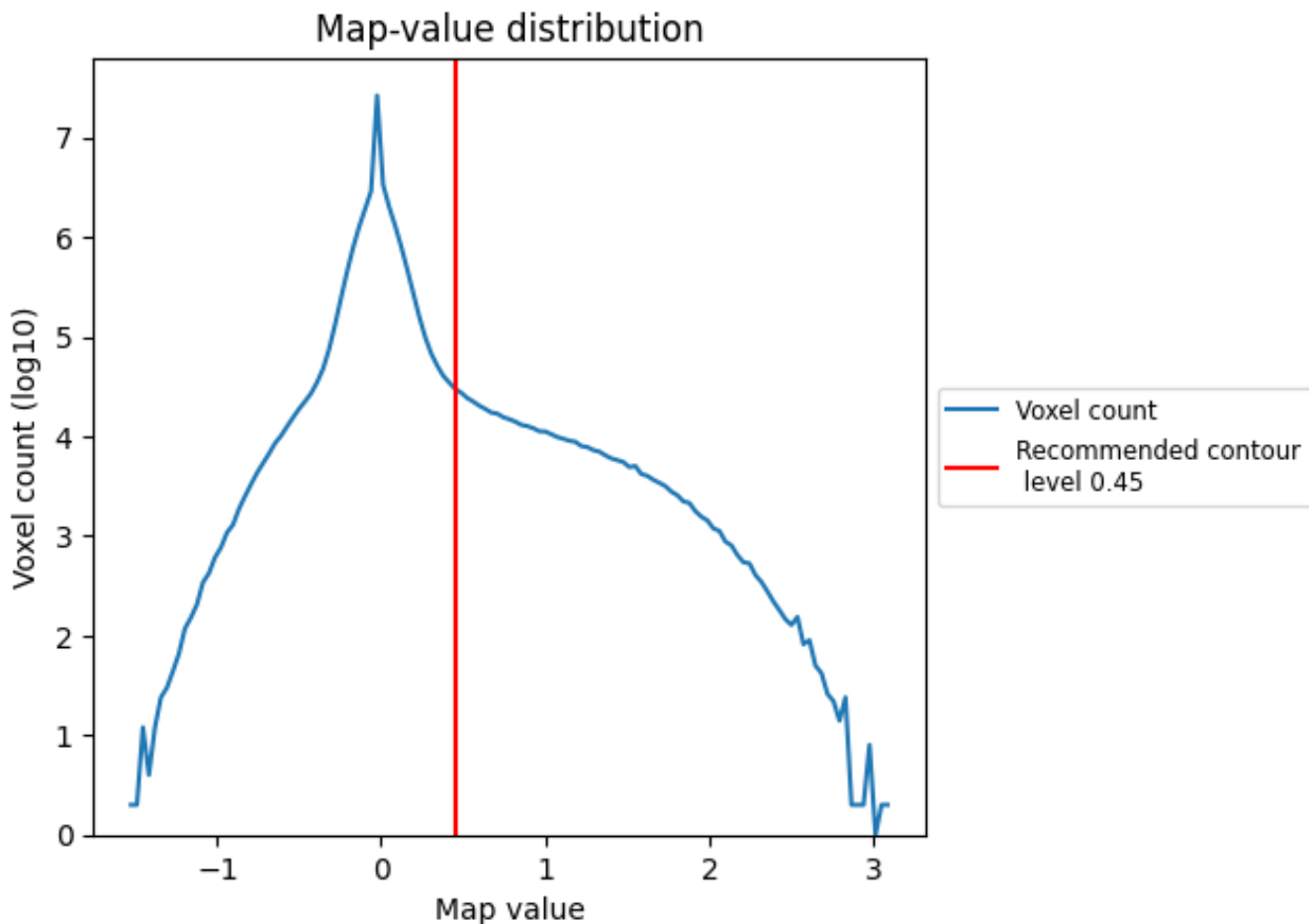


Z

7 Map analysis [i](#)

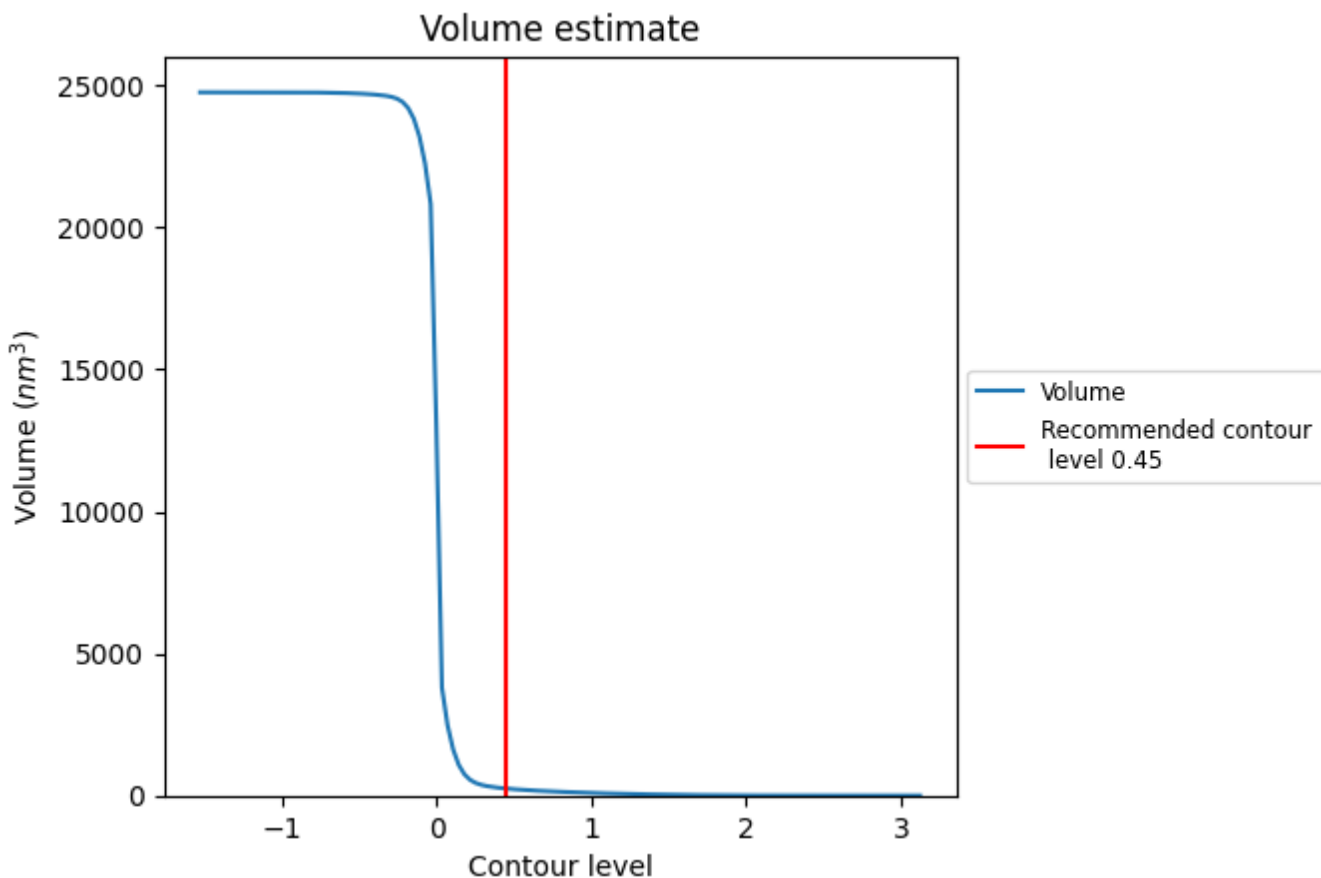
This section contains the results of statistical analysis of the map.

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.

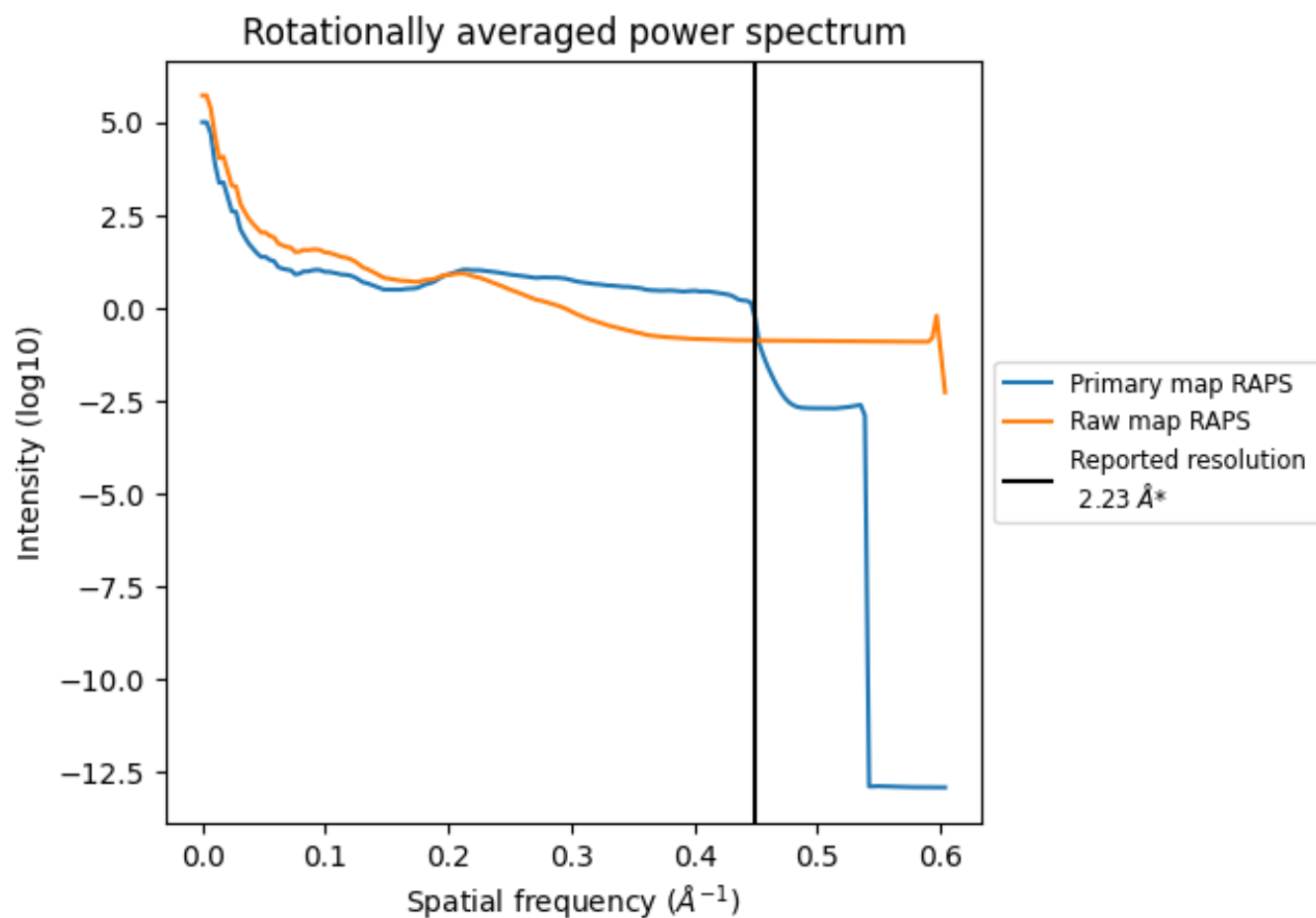
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 248 nm³; this corresponds to an approximate mass of 224 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](#)

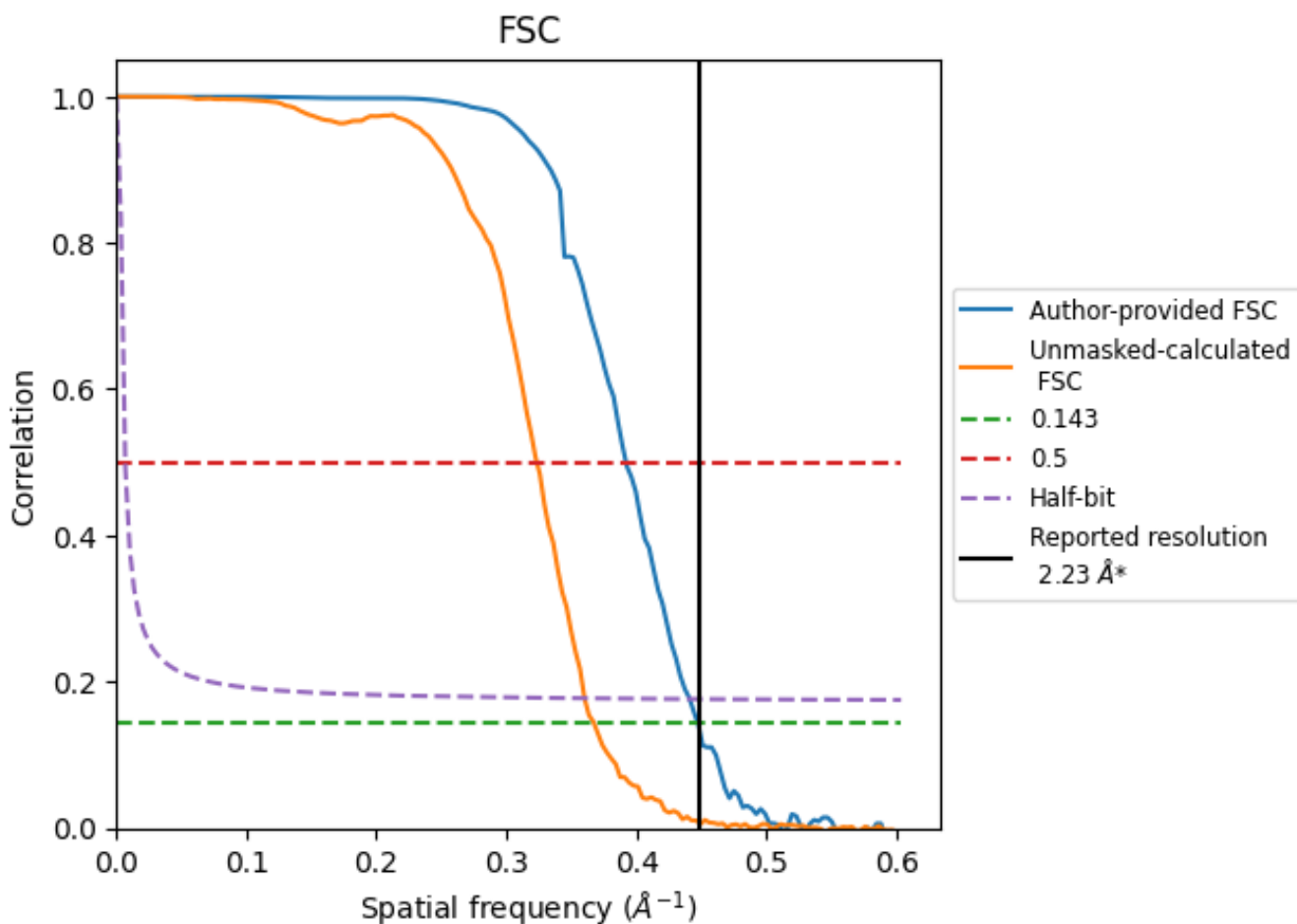


*Reported resolution corresponds to spatial frequency of 0.448 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.448 \AA^{-1}

8.2 Resolution estimates

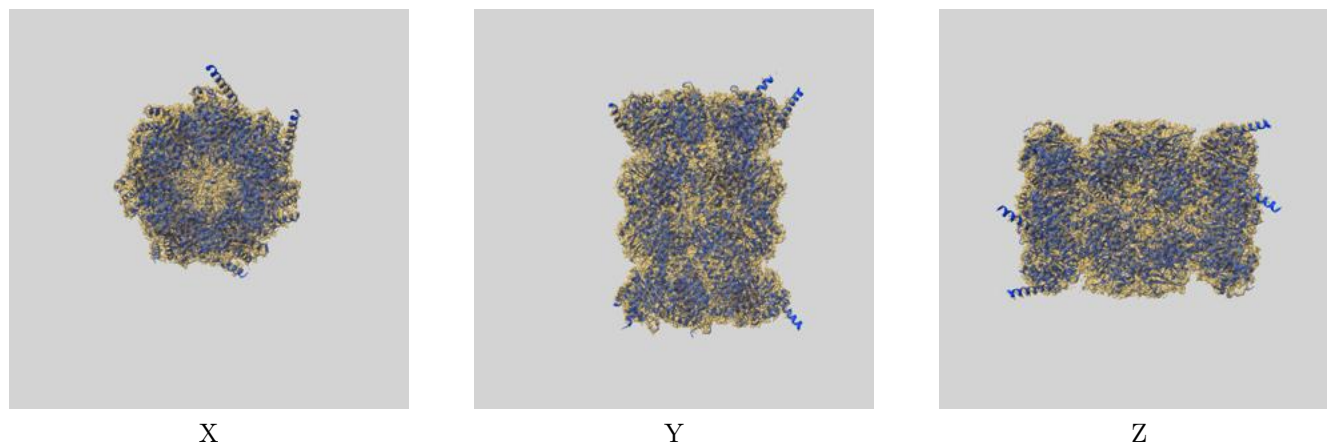
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.23	-	-
Author-provided FSC curve	2.23	2.55	2.27
Unmasked-calculated*	2.72	3.09	2.78

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.72 differs from the reported value 2.23 by more than 10 %

9 Map-model fit [i](#)

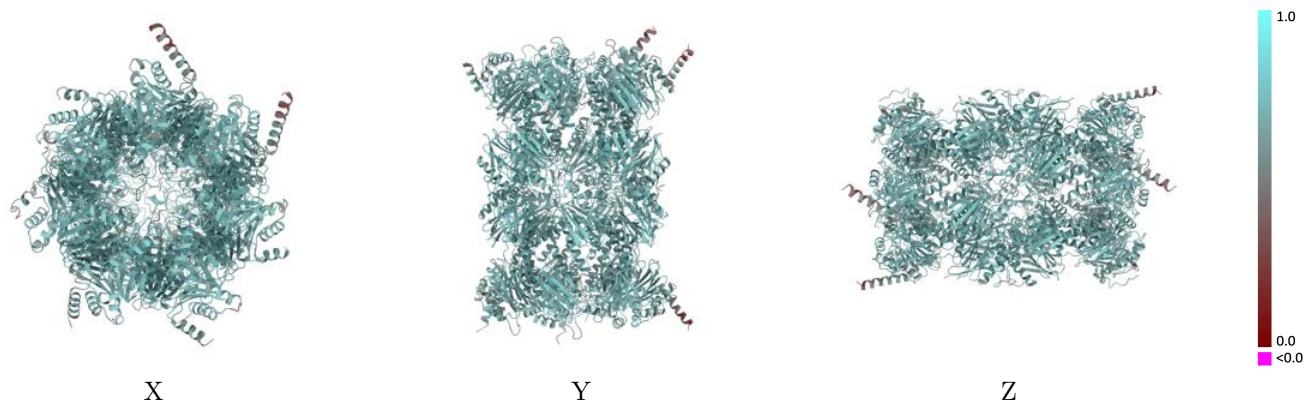
This section contains information regarding the fit between EMDB map EMD-29603 and PDB model 8FZ5. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



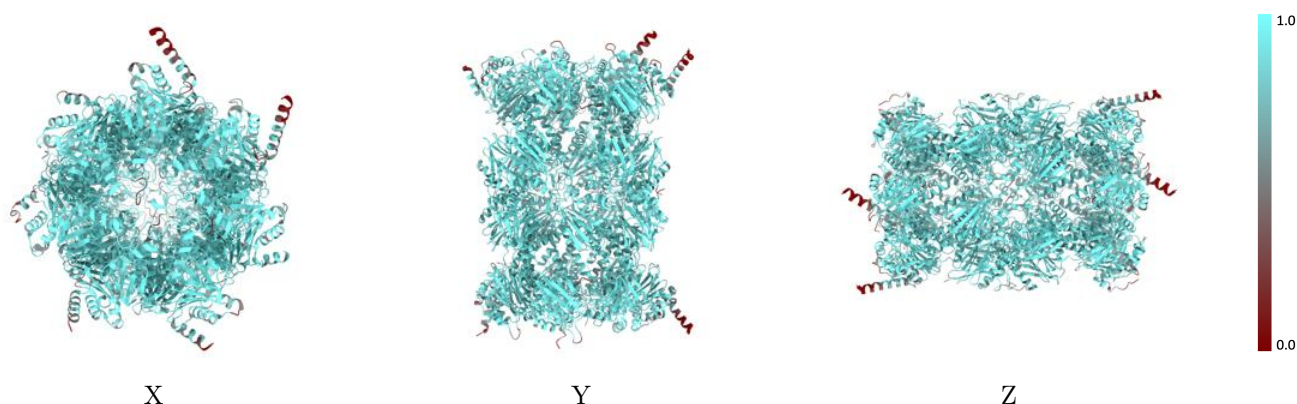
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



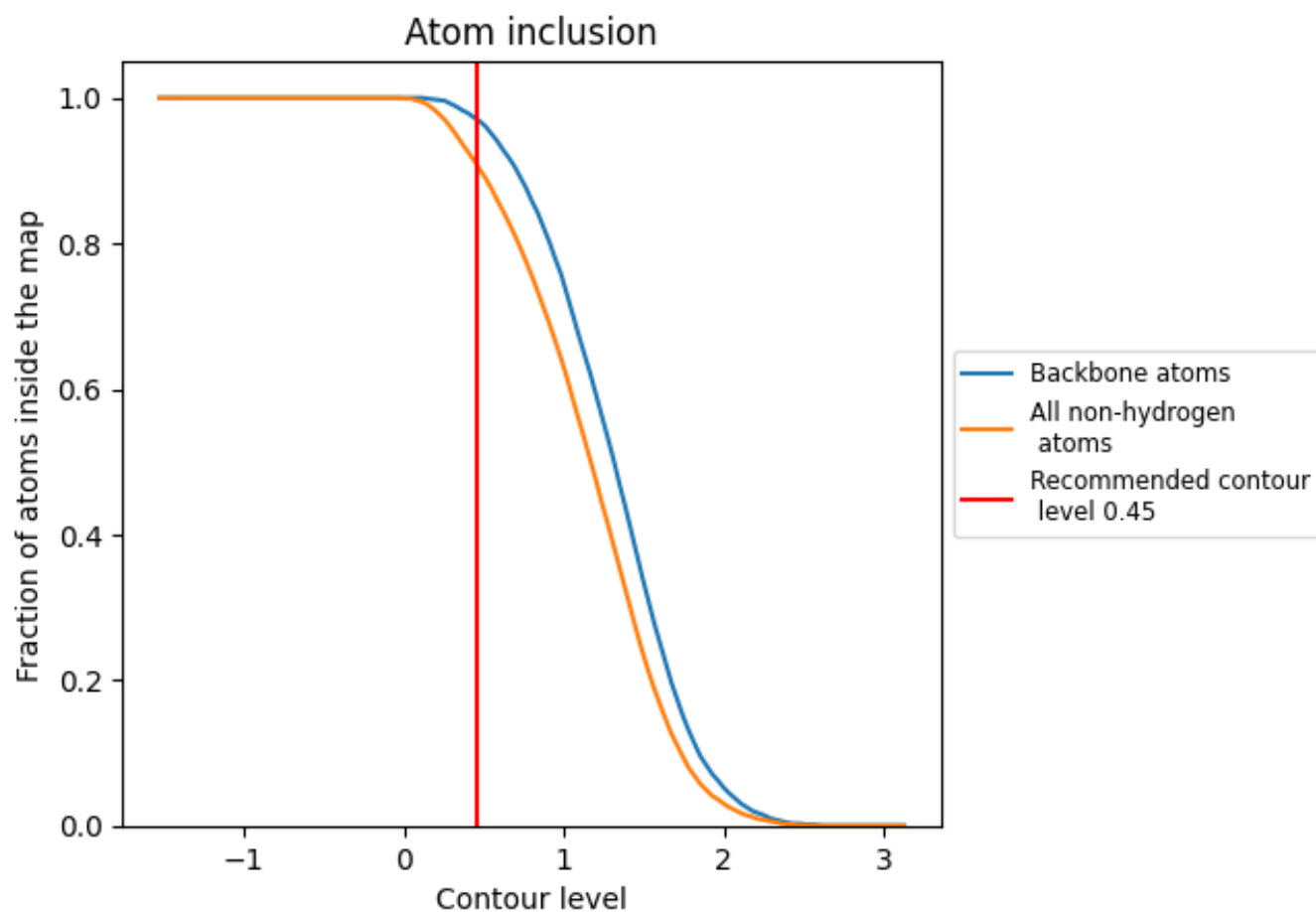
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).



























































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 91% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9100	 0.6920
A	 0.8720	 0.6790
B	 0.9020	 0.6860
C	 0.8570	 0.6650
D	 0.8390	 0.6550
E	 0.8830	 0.6760
F	 0.8930	 0.6780
G	 0.8850	 0.6770
H	 0.9550	 0.7210
I	 0.9430	 0.7110
J	 0.9520	 0.7150
K	 0.9460	 0.7130
L	 0.9670	 0.7180
M	 0.9390	 0.7080
N	 0.9530	 0.7190
O	 0.8700	 0.6750
P	 0.9020	 0.6860
Q	 0.8570	 0.6650
R	 0.8390	 0.6530
S	 0.8790	 0.6740
T	 0.8980	 0.6790
U	 0.8860	 0.6790
V	 0.9540	 0.7200
W	 0.9440	 0.7110
X	 0.9530	 0.7150
Y	 0.9440	 0.7130
Z	 0.9680	 0.7180
a	 0.9390	 0.7080
b	 0.9530	 0.7170

