



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 08:38 PM UTC

PDB ID : 7QVE / pdb_00007qve
EMDB ID : EMD-14175
Title : Spinach 20S proteasome
Authors : Kandolf, S.; Grishkovskaya, I.; Meinhart, A.; Haselbach, D.
Deposited on : 2022-01-21
Resolution : 3.30 Å(reported)
Based on initial model : 6MSB

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

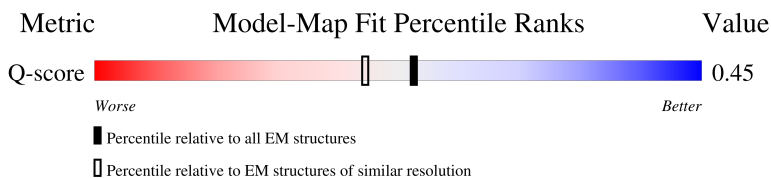
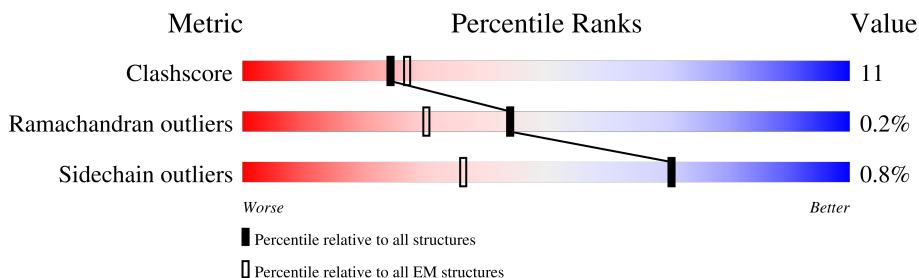
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.



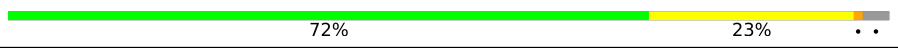
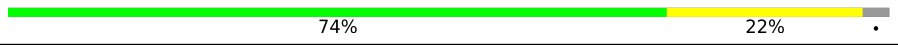
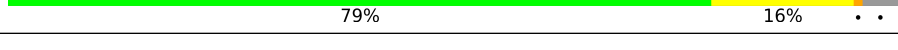
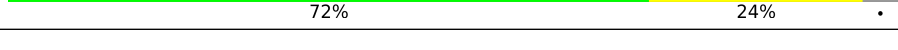
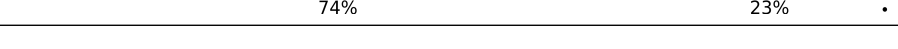
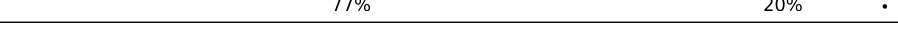
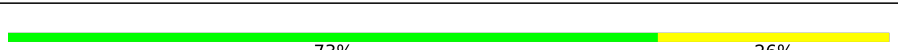
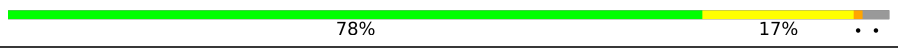
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	C	235	
1	i	235	
2	D	250	
2	j	250	

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Mol	Chain	Length	Quality of chain
3	E	247	
3	k	247	
4	F	237	
4	l	237	
5	G	274	
5	m	274	
6	X	249	
6	n	249	
7	B	246	
7	h	246	
8	a	236	
8	o	236	
9	b	274	
9	p	274	
10	c	204	
10	q	204	
11	d	209	
11	r	209	
12	e	272	
12	s	272	
13	f	223	
13	t	223	
14	g	240	
14	u	240	

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 48322 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	i	229	Total	C	N	O	S	0	0
			1754	1117	291	342	4		
1	C	229	Total	C	N	O	S	0	0
			1754	1117	291	342	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	j	249	Total	C	N	O	S	0	0
			1920	1209	322	380	9		
2	D	249	Total	C	N	O	S	0	0
			1920	1209	322	380	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	k	240	Total	C	N	O	S	0	0
			1845	1157	327	358	3		
3	E	240	Total	C	N	O	S	0	0
			1845	1157	327	358	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	l	230	Total	C	N	O	S	0	0
			1763	1104	294	357	8		
4	F	230	Total	C	N	O	S	0	0
			1763	1104	294	357	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	m	231	Total	C	N	O	S	0	0
			1794	1129	312	345	8		
5	G	231	Total	C	N	O	S	0	0
			1794	1129	312	345	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	n	239	Total	C	N	O	S	0	0
			1842	1164	320	347	11		
6	X	239	Total	C	N	O	S	0	0
			1842	1164	320	347	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	238	Total	C	N	O	S	0	0
			1861	1180	319	356	6		
7	h	238	Total	C	N	O	S	0	0
			1861	1180	319	356	6		

- Molecule 8 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	o	212	Total	C	N	O	S	0	0
			1617	1024	273	317	3		
8	a	212	Total	C	N	O	S	0	0
			1617	1024	273	317	3		

- Molecule 9 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	p	220	Total	C	N	O	S	0	0
			1648	1033	286	320	9		
9	b	220	Total	C	N	O	S	0	0
			1648	1033	286	320	9		

- Molecule 10 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	q	203	Total	C	N	O	S	0	0
			1593	1010	269	303	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	c	203	Total	C	N	O	S	0	0
			1593	1010	269	303	11		

- Molecule 11 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	r	196	Total	C	N	O	S	0	0
			1524	972	260	284	8		
11	d	196	Total	C	N	O	S	0	0
			1524	972	260	284	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	s	203	Total	C	N	O	S	0	0
			1553	985	270	288	10		
12	e	203	Total	C	N	O	S	0	0
			1553	985	270	288	10		

- Molecule 13 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	t	217	Total	C	N	O	S	0	0
			1695	1074	286	325	10		
13	f	217	Total	C	N	O	S	0	0
			1695	1074	286	325	10		

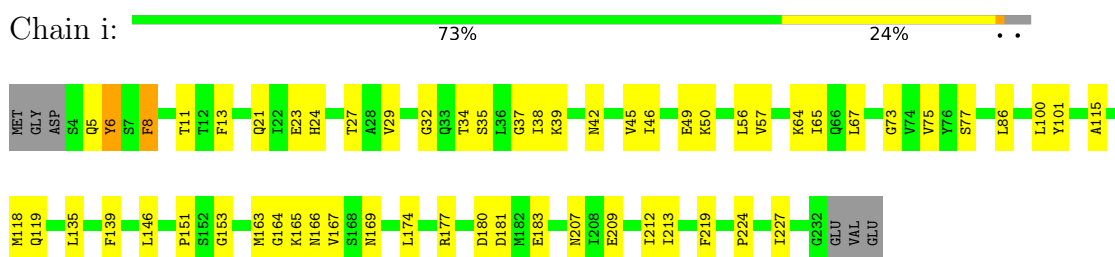
- Molecule 14 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	u	221	Total	C	N	O	S	0	0
			1752	1120	300	326	6		
14	g	221	Total	C	N	O	S	0	0
			1752	1120	300	326	6		

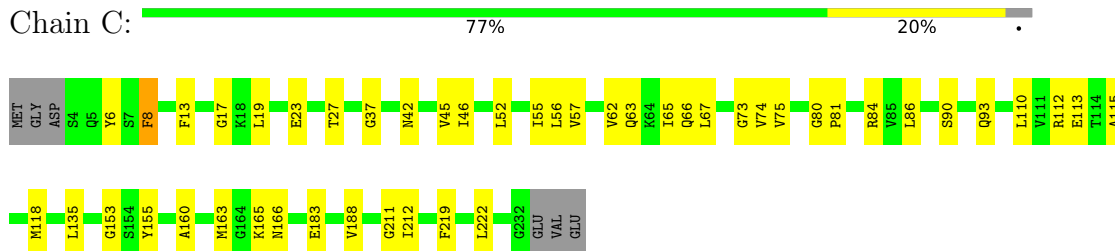
3 Residue-property plots

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.

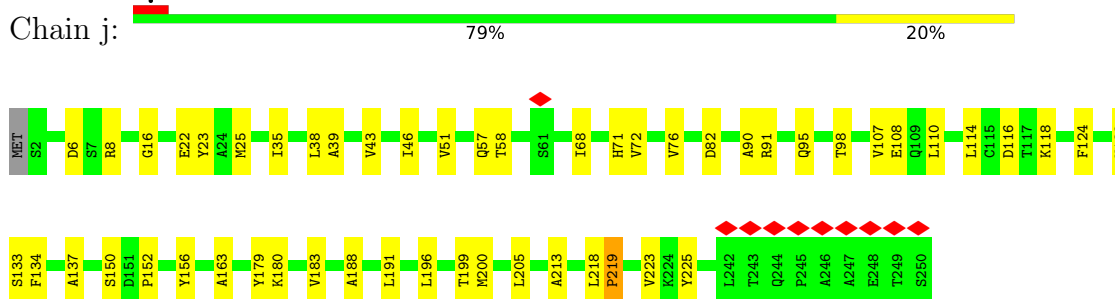
- Molecule 1: Proteasome subunit alpha type



- Molecule 1: Proteasome subunit alpha type

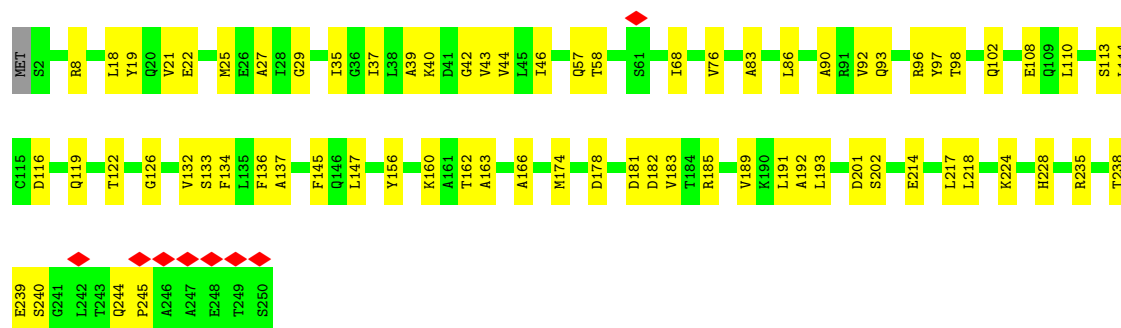


- Molecule 2: Proteasome subunit alpha type



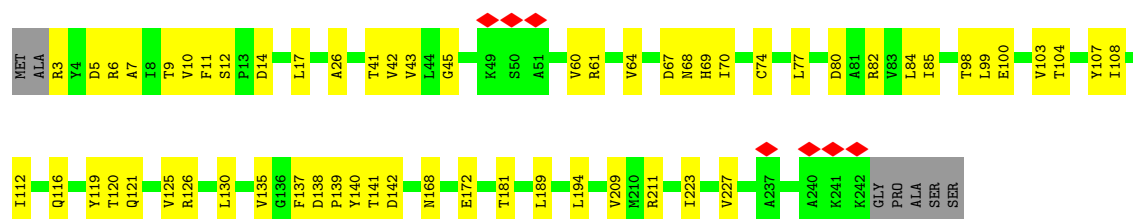
- Molecule 2: Proteasome subunit alpha type





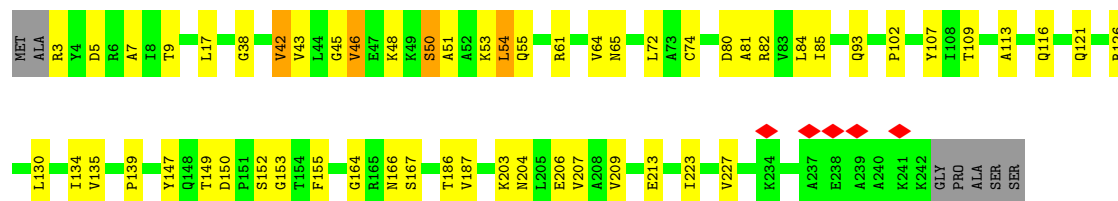
- Molecule 3: Proteasome subunit alpha type

Chain k: 73% 24%



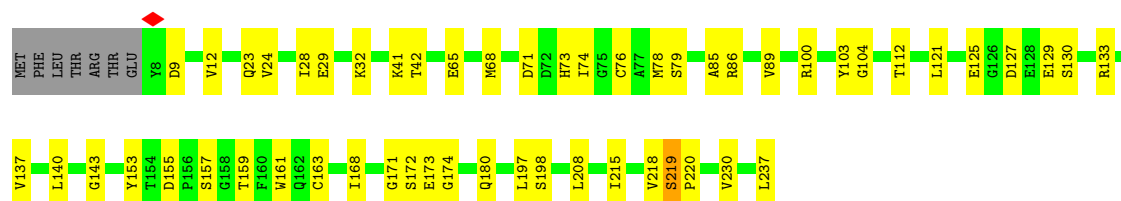
- Molecule 3: Proteasome subunit alpha type

Chain E: 74% 21%



- Molecule 4: Proteasome subunit alpha type

Chain I: 74% 22%



- Molecule 4: Proteasome subunit alpha type

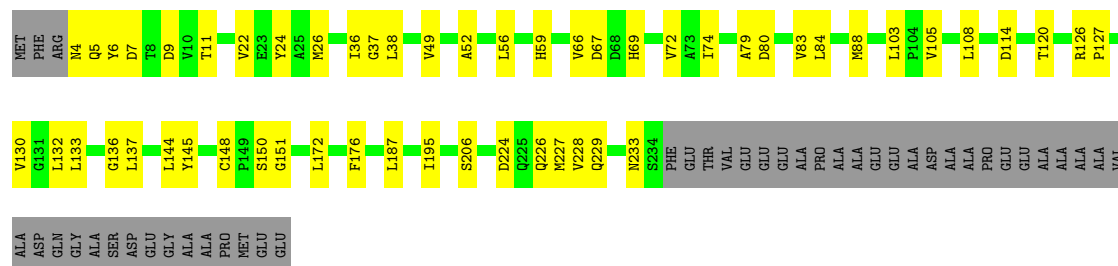
Chain F: 72% 23%





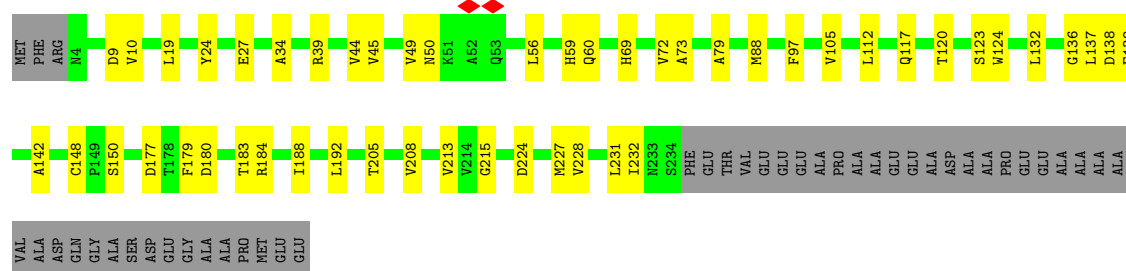
• Molecule 5: Proteasome subunit alpha type

Chain m: 65% 20% 16%



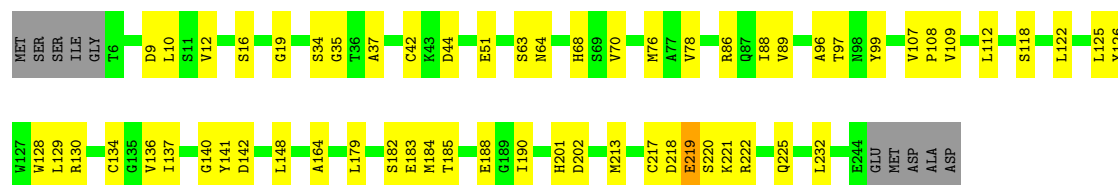
• Molecule 5: Proteasome subunit alpha type

Chain G: 66% 18% 16%



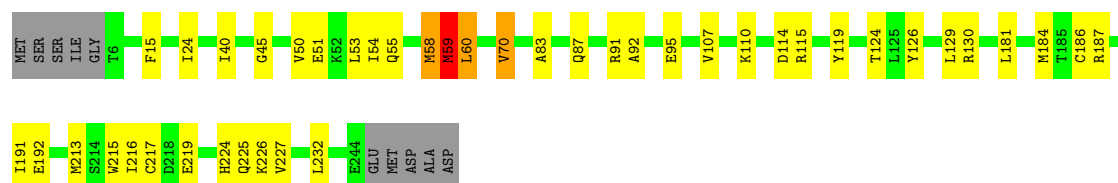
• Molecule 6: Proteasome subunit alpha type-3

Chain n: 72% 24% 4%



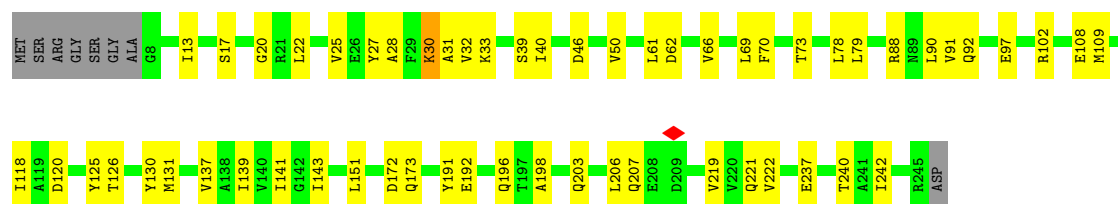
• Molecule 6: Proteasome subunit alpha type-3

Chain X: 79% 16% 5%



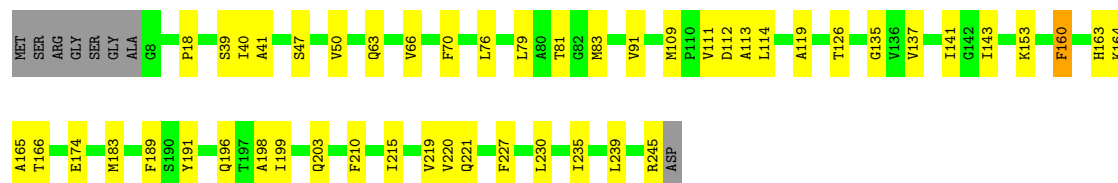
• Molecule 7: Proteasome subunit alpha type

Chain B:  74% 23% .



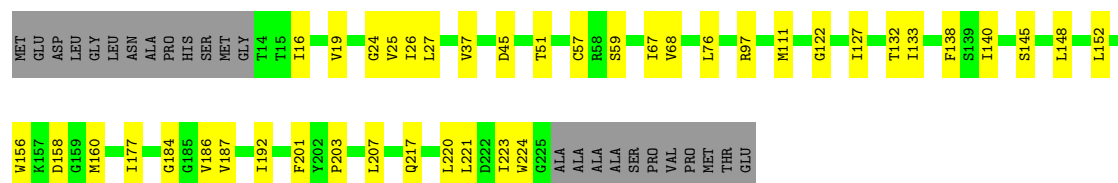
- Molecule 7: Proteasome subunit alpha type

Chain h:  77% 20% .



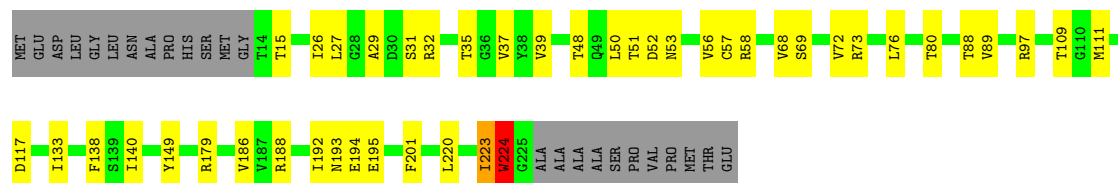
- Molecule 8: Proteasome subunit beta

Chain o:  72% 17% 10%



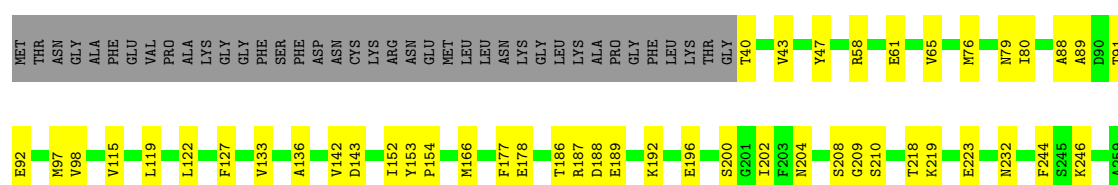
- Molecule 8: Proteasome subunit beta

Chain a:  71% 18% 10%



- Molecule 9: Proteasome subunit beta

Chain p:  63% 17% 20%



GLN
ARG
ALA
VAL
THR
GLU
ARG
GLY
ASP
ALA
MET
GLU
GLU

• Molecule 9: Proteasome subunit beta

Chain b:  62% 18% 20%

MET THR ASN GLY ALA PHE THR GLU VAL PRO ARG GLY LYS ASP ALA MET LEU LEU ASN GLY LEU LYS LYS ALA PRO GLY PHE LEU LYS THR GLY
T40 V43 Q44 D56 T57 R58 V65 K72 M76 Y81 A85 G86 T87

D90 T91 V94 V98 L102 H105 T109 R114 A118 L119 H125 V133 S134 A135 A136 D143 V144 I152 Y153 P154 T165 M166 F177 E178 R182 E189 I198 G209 S210 N211 V212 D213 V214 T217 T218 V222 R226 N227 R234

T235 Y236 T237 T248 E249 V250 T253 T256 A259 GLN ARG ALA VAL THR GLU ARG GLY ASP MET LEU GLU
T235 Y236 T237 T248 E249 V250 T253 T256 A259 GLN ARG ALA VAL THR GLU ARG GLY ASP MET LEU GLU

• Molecule 10: Proteasome subunit beta

Chain q:  73% 26%

MET S2 E5 M14 V15 I20 D25 R26 R27 V30 Q31 Q33 T34 T35 A36 T37 D38 B41 T45 L49 F50 G55 S58 F69 R70 H71 K72 L73 M82 K83 P84 E85 T86 F87 L90 V91 P107 G111 I120 G121 M123 M124

S125 K129 E130 L131 D134 F135 V136 E150 Y153 V166 S167 Q168 V174 D175 R176 D177 C178 G181 V189 R202 M203 D204

• Molecule 10: Proteasome subunit beta

Chain c:  75% 24%

MET S2 V12 I20 G23 S24 D25 R26 R27 L28 G29 V30 Q31 T34 I42 H46 L49 R70 H71 K72 L73 Y74 Q75 L76 R77 E78 D81 M82 A88 I94 A110 D114 P118 T122 M123 D124 S125 L131 D134 F135 V136 V137

M152 Y153 K154 P155 D156 M157 E158 P159 E160 F161 L162 F163 E164 S167 Q168 L179 S180 G181 H185 E196 D204

• Molecule 11: Proteasome subunit beta

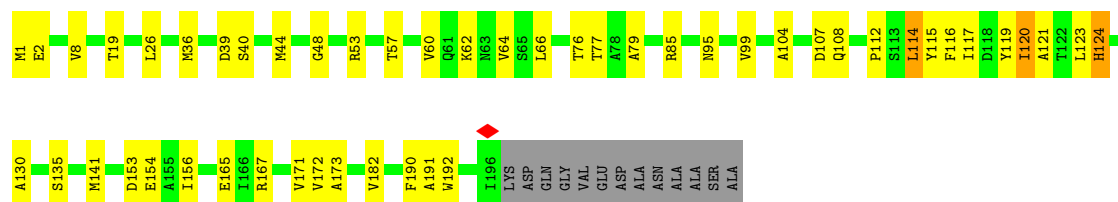
Chain r:  74% 20% 6%

H1 M10 G11 A21 V22 V27 H28 K29 T30 K37 L38 L43 M44 E49 D52 Q61 V64 F116 I117 D118 Y119 I120 A121 T122 L123 H124 K125 V126 D127 R128 A129 A130 F131 Y136 M141 M142 D143 Y146 S151 E154 R167 V171 V172

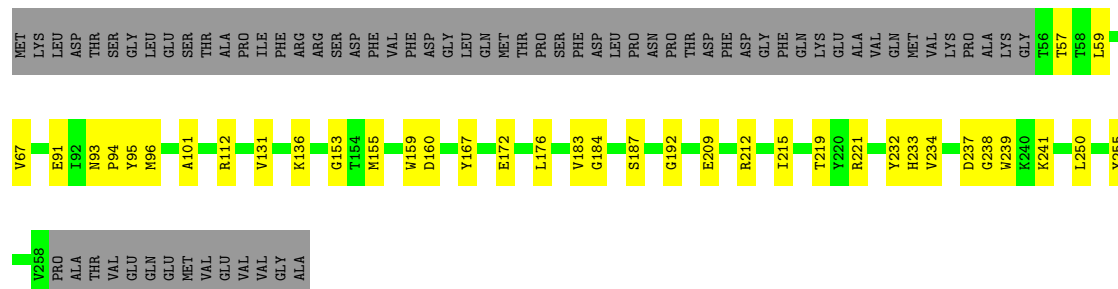
A173 P174 P175 V182 W192 R193 Q194 S195 I196 LYS ASP GLN GLY VAL GLU ASP ALA ASN ALA ALA SER ALA

• Molecule 11: Proteasome subunit beta

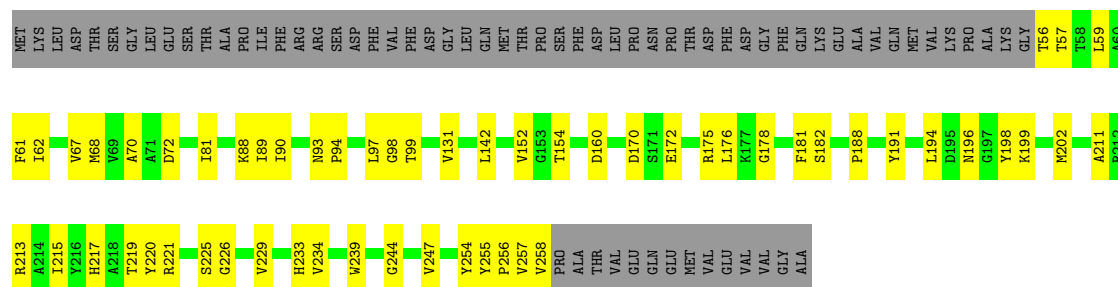
Chain d:  70% 22% 6%



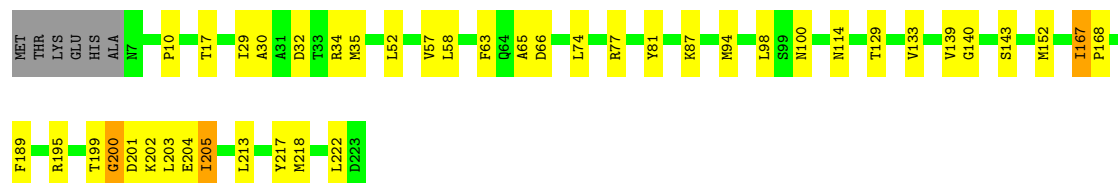
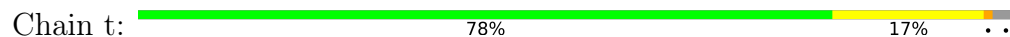
• Molecule 12: Proteasome subunit beta type-5



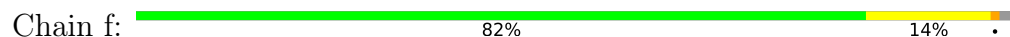
• Molecule 12: Proteasome subunit beta type-5



• Molecule 13: Proteasome subunit beta

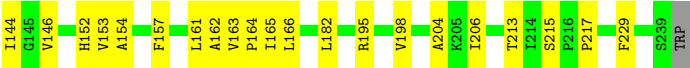


• Molecule 13: Proteasome subunit beta

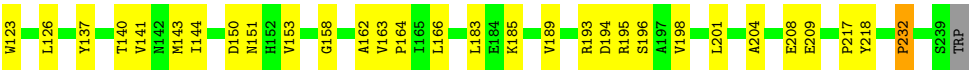
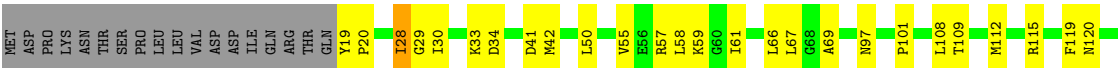




● Molecule 14: Proteasome subunit beta



● Molecule 14: Proteasome subunit beta



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	951422	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 ($e^-/\text{\AA}^2$)	80, 50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k), FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.932	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.0168	Depositor
Map size (Å)	541.696, 541.696, 541.696	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2311273, 1.2311273, 1.2311273	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	C	0.35	0/1785	0.45	2/2414 (0.1%)
1	i	0.36	0/1785	0.50	1/2414 (0.0%)
2	D	0.33	0/1953	0.40	0/2640
2	j	0.40	0/1953	0.52	0/2640
3	E	0.45	0/1870	0.60	1/2526 (0.0%)
3	k	0.35	0/1870	0.45	0/2526
4	F	0.49	0/1794	0.71	3/2428 (0.1%)
4	l	0.55	0/1794	0.62	0/2428
5	G	0.37	0/1827	0.45	0/2470
5	m	0.46	0/1827	0.55	0/2470
6	X	0.40	0/1876	0.55	1/2529 (0.0%)
6	n	0.41	0/1876	0.57	1/2529 (0.0%)
7	B	0.49	0/1897	0.68	3/2565 (0.1%)
7	h	0.48	0/1897	0.61	1/2565 (0.0%)
8	a	0.58	1/1648 (0.1%)	0.64	0/2238
8	o	0.58	0/1648	0.71	0/2238
9	b	0.59	0/1679	0.75	1/2282 (0.0%)
9	p	0.51	0/1679	0.66	0/2282
10	c	0.52	0/1624	0.64	1/2189 (0.0%)
10	q	0.55	0/1624	0.82	1/2189 (0.0%)
11	d	0.54	0/1553	0.72	3/2099 (0.1%)
11	r	0.49	0/1553	0.58	0/2099
12	e	0.49	0/1589	0.59	1/2146 (0.0%)
12	s	0.45	0/1589	0.53	1/2146 (0.0%)
13	f	0.58	0/1730	0.70	1/2340 (0.0%)
13	t	0.57	0/1730	0.66	2/2340 (0.1%)
14	g	0.54	0/1792	0.70	1/2422 (0.0%)
14	u	0.49	0/1792	0.55	0/2422
All	All	0.48	1/49234 (0.0%)	0.61	25/66576 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	a	31	SER	CA-CB	-7.25	1.47	1.53

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	s	255	TYR	CB-CA-C	8.72	119.72	110.65
4	F	70	ILE	N-CA-C	-7.21	103.94	111.58
12	e	255	TYR	CB-CA-C	7.10	118.03	110.65
4	F	123	PHE	CA-CB-CG	6.25	120.05	113.80
7	B	30	LYS	CA-C-N	6.20	130.12	120.82

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	C	1754	0	1775	30	0
1	i	1754	0	1775	43	0
2	D	1920	0	1910	52	0
2	j	1920	0	1910	41	0
3	E	1845	0	1872	53	0
3	k	1845	0	1872	44	0
4	F	1763	0	1728	58	0
4	l	1763	0	1728	48	0
5	G	1794	0	1769	41	0
5	m	1794	0	1769	42	0
6	X	1842	0	1847	39	0
6	n	1842	0	1847	42	0
7	B	1861	0	1848	48	0
7	h	1861	0	1848	35	0
8	a	1617	0	1594	39	0
8	o	1617	0	1594	34	0
9	b	1648	0	1640	38	0
9	p	1648	0	1640	38	0
10	c	1593	0	1570	37	0
10	q	1593	0	1570	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	d	1524	0	1520	34	0
11	r	1524	0	1520	35	0
12	e	1553	0	1518	46	0
12	s	1553	0	1518	27	0
13	f	1695	0	1665	29	0
13	t	1695	0	1665	32	0
14	g	1752	0	1732	44	0
14	u	1752	0	1732	50	0
All	All	48322	0	47976	1034	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 11.

The worst 5 of 1034 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:m:6:TYR:OH	6:n:9:ASP:OD2	1.61	1.15
14:u:213:THR:HG22	8:a:224:TRP:CZ2	1.81	1.15
3:E:50:SER:CB	3:E:53:LYS:HD3	1.79	1.11
4:F:78:MET:HB3	4:F:139:LEU:CD2	1.87	1.03
3:E:50:SER:HB3	3:E:53:LYS:HD3	1.38	1.03

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	C	227/235 (97%)	219 (96%)	8 (4%)	0	100	100
1	i	227/235 (97%)	214 (94%)	13 (6%)	0	100	100
2	D	247/250 (99%)	238 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	j	247/250 (99%)	234 (95%)	13 (5%)	0	100	100
3	E	238/247 (96%)	228 (96%)	9 (4%)	1 (0%)	30	60
3	k	238/247 (96%)	230 (97%)	8 (3%)	0	100	100
4	F	228/237 (96%)	213 (93%)	15 (7%)	0	100	100
4	l	228/237 (96%)	216 (95%)	11 (5%)	1 (0%)	30	60
5	G	229/274 (84%)	220 (96%)	9 (4%)	0	100	100
5	m	229/274 (84%)	218 (95%)	11 (5%)	0	100	100
6	X	237/249 (95%)	219 (92%)	17 (7%)	1 (0%)	30	60
6	n	237/249 (95%)	220 (93%)	17 (7%)	0	100	100
7	B	236/246 (96%)	225 (95%)	11 (5%)	0	100	100
7	h	236/246 (96%)	224 (95%)	12 (5%)	0	100	100
8	a	210/236 (89%)	191 (91%)	17 (8%)	2 (1%)	12	40
8	o	210/236 (89%)	196 (93%)	13 (6%)	1 (0%)	24	55
9	b	218/274 (80%)	199 (91%)	18 (8%)	1 (0%)	24	55
9	p	218/274 (80%)	205 (94%)	12 (6%)	1 (0%)	24	55
10	c	201/204 (98%)	184 (92%)	16 (8%)	1 (0%)	24	55
10	q	201/204 (98%)	178 (89%)	22 (11%)	1 (0%)	24	55
11	d	194/209 (93%)	179 (92%)	15 (8%)	0	100	100
11	r	194/209 (93%)	181 (93%)	13 (7%)	0	100	100
12	e	201/272 (74%)	193 (96%)	8 (4%)	0	100	100
12	s	201/272 (74%)	192 (96%)	9 (4%)	0	100	100
13	f	215/223 (96%)	198 (92%)	17 (8%)	0	100	100
13	t	215/223 (96%)	201 (94%)	13 (6%)	1 (0%)	24	55
14	g	219/240 (91%)	202 (92%)	17 (8%)	0	100	100
14	u	219/240 (91%)	198 (90%)	21 (10%)	0	100	100
All	All	6200/6792 (91%)	5815 (94%)	374 (6%)	11 (0%)	44	71

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	t	201	ASP
10	c	160	GLU
4	l	219	SER

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Mol	Chain	Res	Type
8	a	224	TRP
9	p	210	SER

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	C	192/197 (98%)	192 (100%)	0	100	100
1	i	192/197 (98%)	191 (100%)	1 (0%)	81	83
2	D	208/209 (100%)	208 (100%)	0	100	100
2	j	208/209 (100%)	206 (99%)	2 (1%)	68	76
3	E	194/198 (98%)	190 (98%)	4 (2%)	47	67
3	k	194/198 (98%)	194 (100%)	0	100	100
4	F	194/201 (96%)	191 (98%)	3 (2%)	57	72
4	l	194/201 (96%)	194 (100%)	0	100	100
5	G	193/220 (88%)	193 (100%)	0	100	100
5	m	193/220 (88%)	193 (100%)	0	100	100
6	X	191/199 (96%)	188 (98%)	3 (2%)	55	72
6	n	191/199 (96%)	191 (100%)	0	100	100
7	B	199/204 (98%)	199 (100%)	0	100	100
7	h	199/204 (98%)	198 (100%)	1 (0%)	81	83
8	a	171/188 (91%)	167 (98%)	4 (2%)	44	66
8	o	171/188 (91%)	168 (98%)	3 (2%)	51	70
9	b	180/222 (81%)	176 (98%)	4 (2%)	45	66
9	p	180/222 (81%)	180 (100%)	0	100	100
10	c	171/172 (99%)	168 (98%)	3 (2%)	51	70
10	q	171/172 (99%)	170 (99%)	1 (1%)	78	81
11	d	160/168 (95%)	156 (98%)	4 (2%)	42	64
11	r	160/168 (95%)	160 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	e	158/217 (73%)	158 (100%)	0	100	100
12	s	158/217 (73%)	158 (100%)	0	100	100
13	f	181/186 (97%)	178 (98%)	3 (2%)	53	71
13	t	181/186 (97%)	179 (99%)	2 (1%)	65	76
14	g	186/205 (91%)	185 (100%)	1 (0%)	81	83
14	u	186/205 (91%)	186 (100%)	0	100	100
All	All	5156/5572 (92%)	5117 (99%)	39 (1%)	70	79

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	c	155	PRO
13	f	162	PRO
10	c	158	GLU
11	d	120	ILE
14	g	28	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
14	u	159	ASN
9	b	228	HIS
14	u	202	GLN
8	a	103	ASN
10	c	40	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides 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-14175. These allow visual inspection of the internal detail of the map and identification of artifacts.

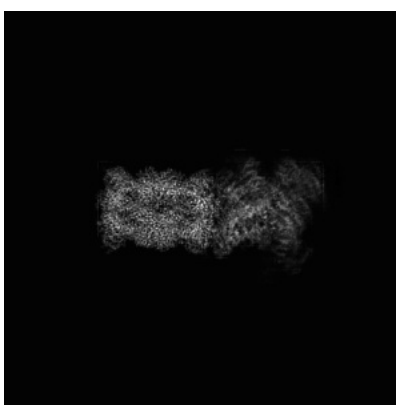
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

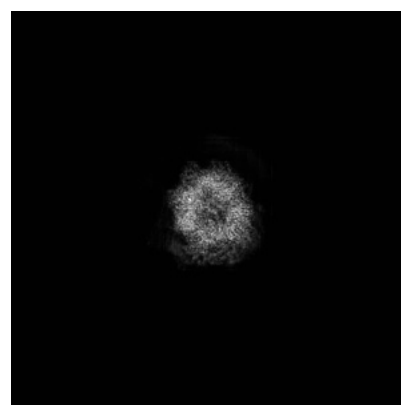
6.1.1 Primary map



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: 220



Y Index: 220



Z Index: 220

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

6.3 Largest variance slices [i](#)

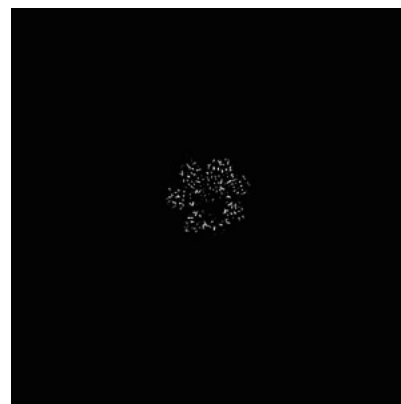
6.3.1 Primary map



X Index: 199



Y Index: 200



Z Index: 210

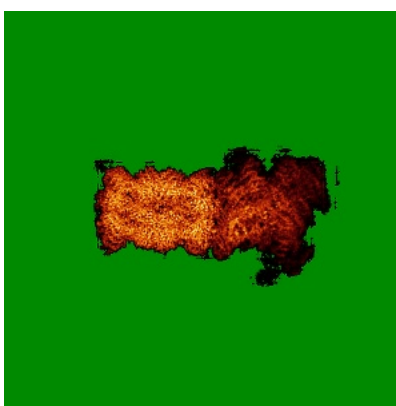
The images above show the largest variance slices of the map in three orthogonal directions.

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

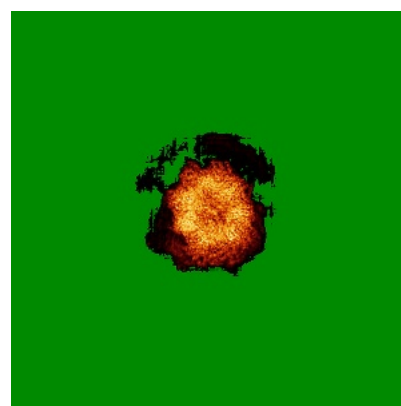
6.4.1 Primary map



X



Y

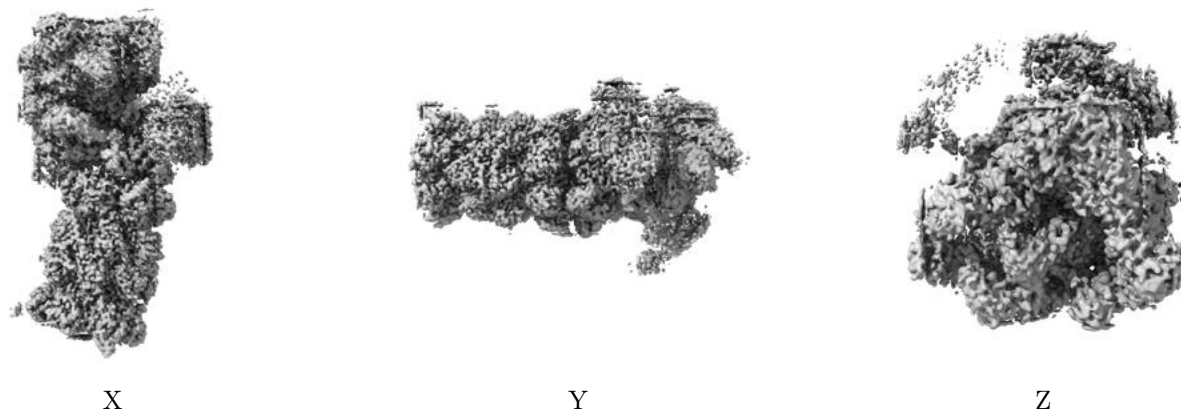


Z

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 0.0168. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

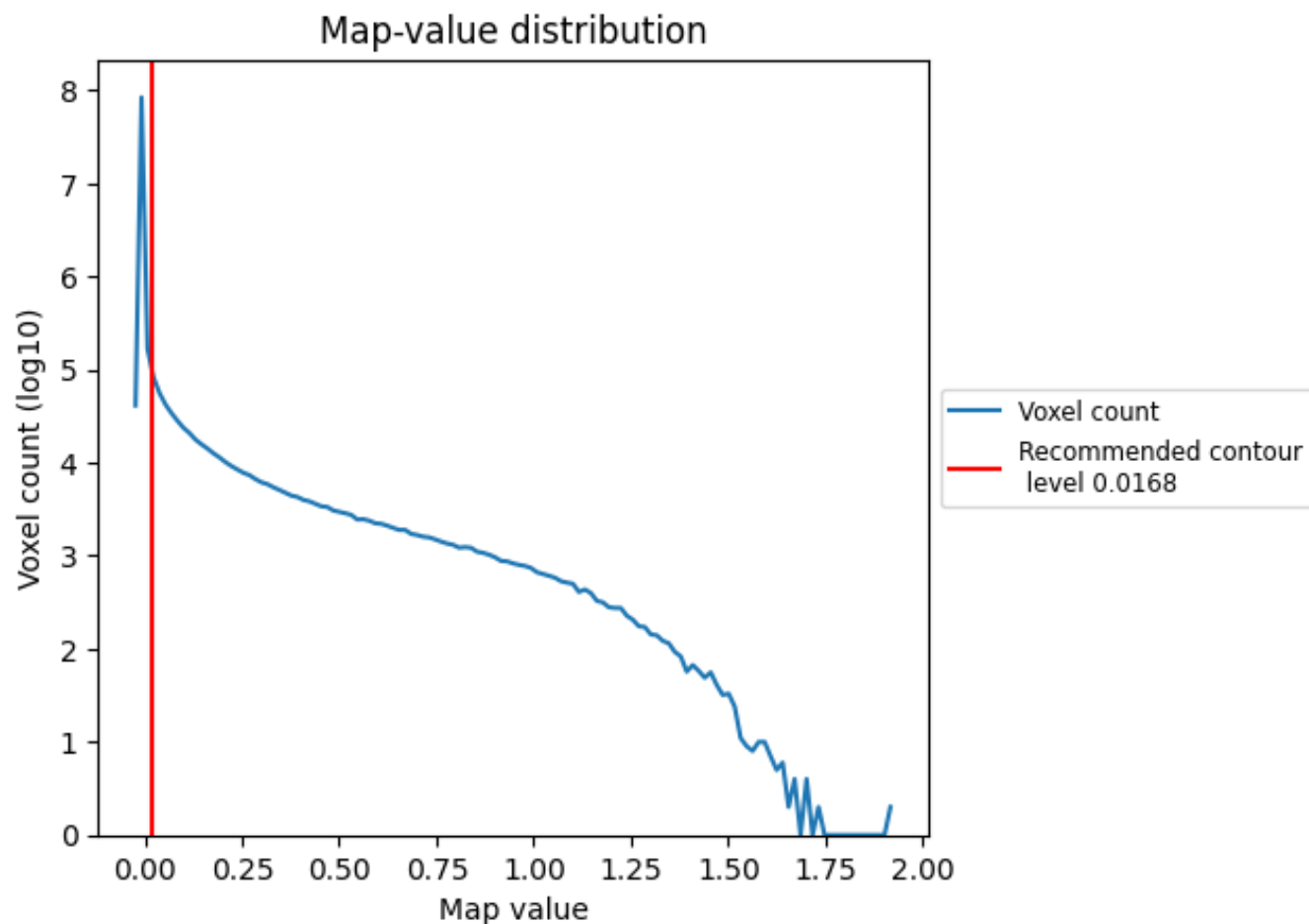
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

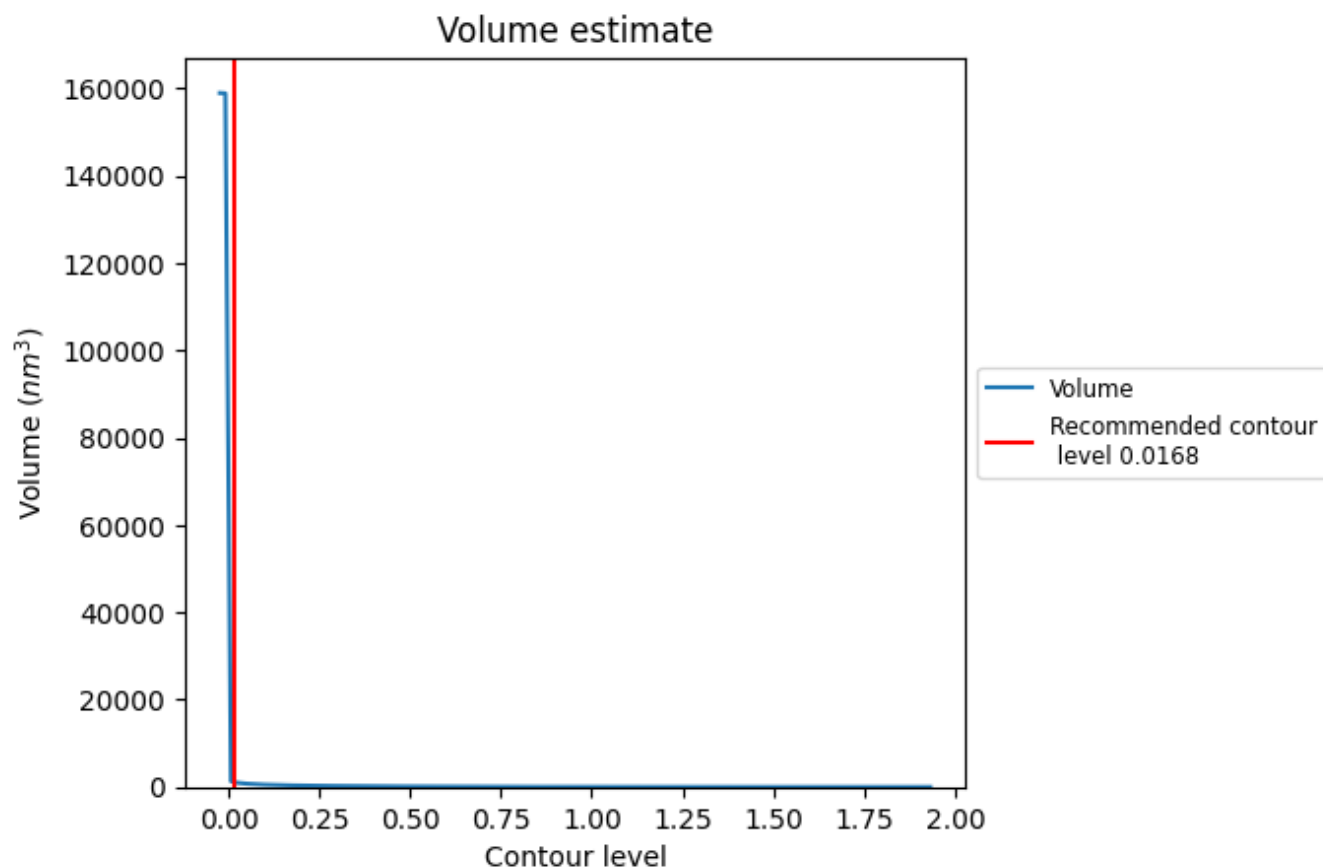
This section contains the results of statistical analysis of the map.

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.

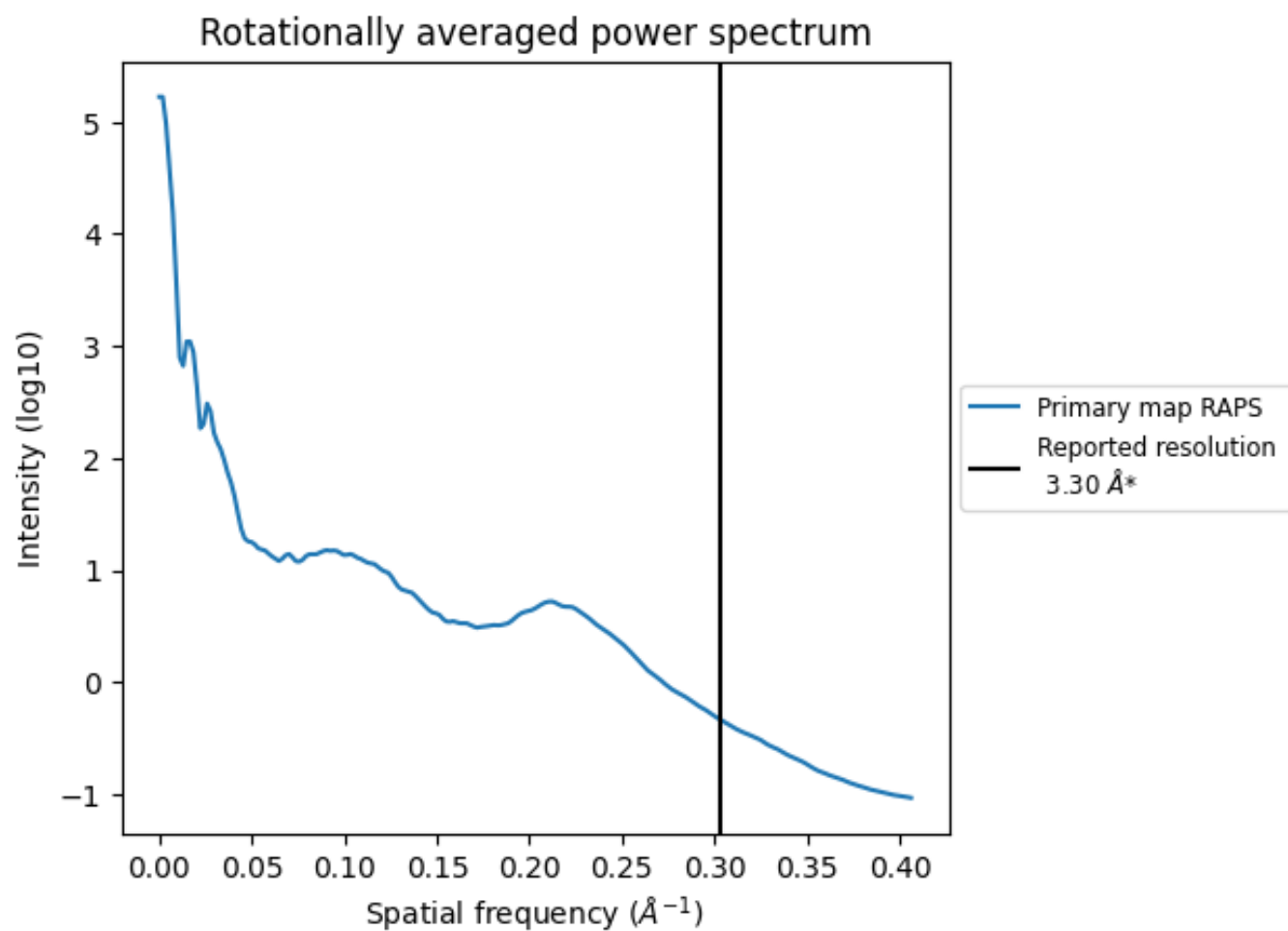
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1112 nm^3 ; this corresponds to an approximate mass of 1004 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 0.303 Å⁻¹

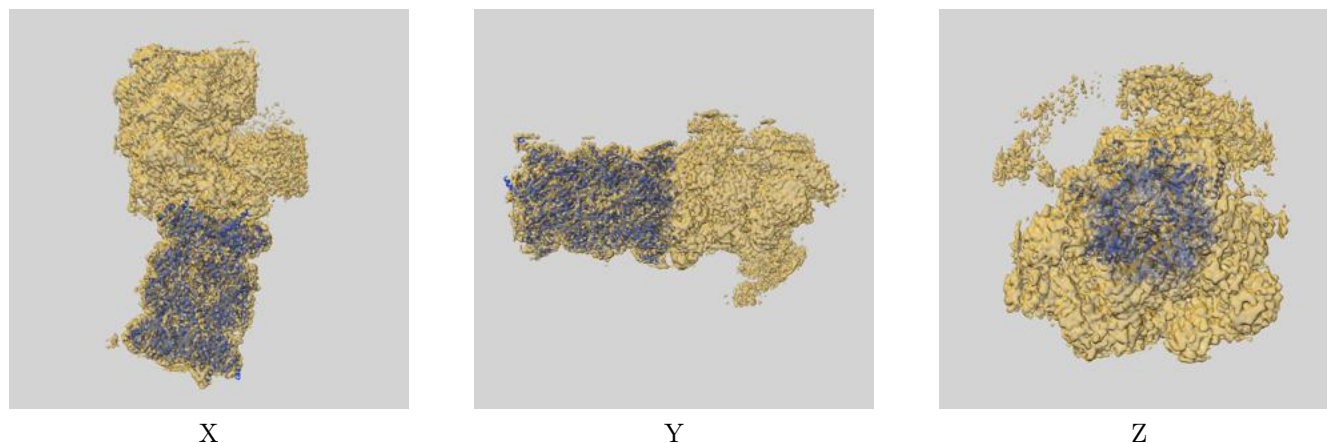
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

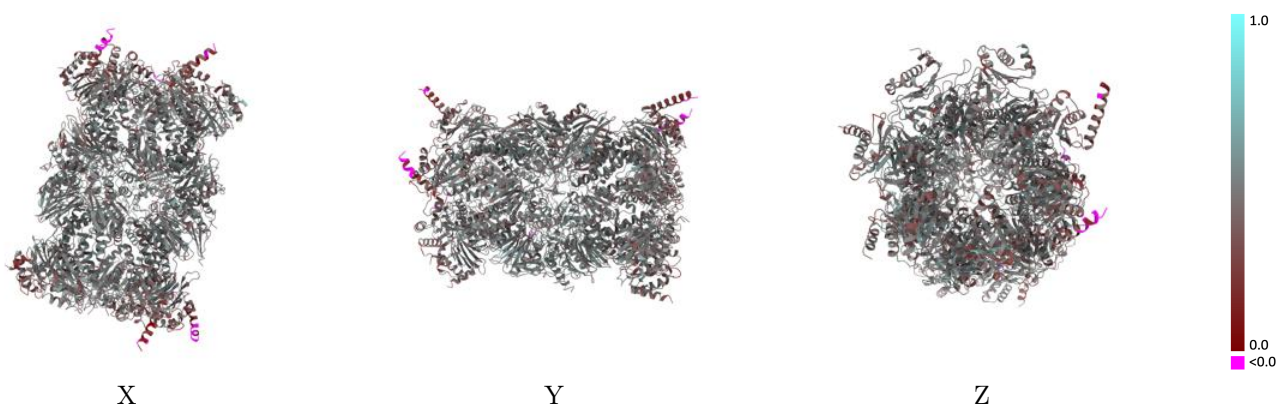
This section contains information regarding the fit between EMDB map EMD-14175 and PDB model 7QVE. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



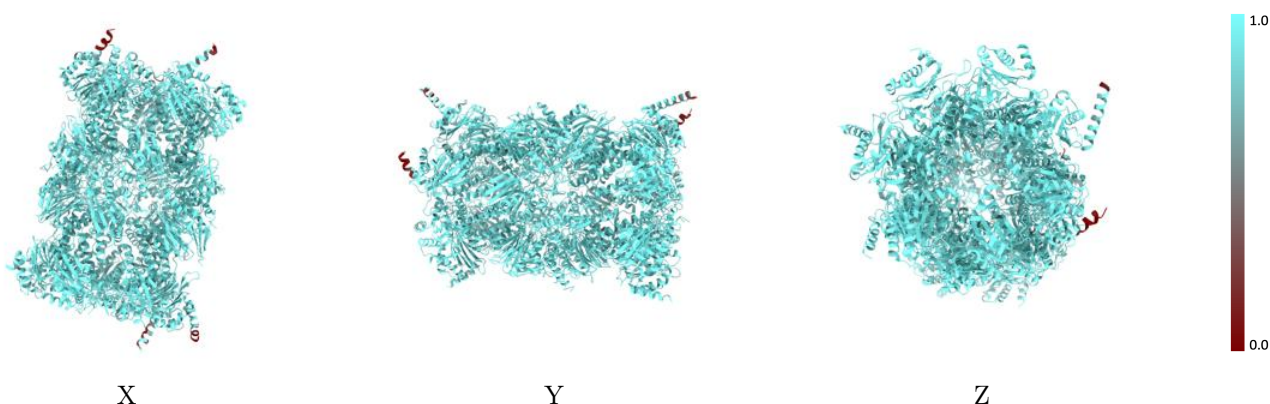
The images above show the 3D surface view of the map at the recommended contour level 0.0168 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



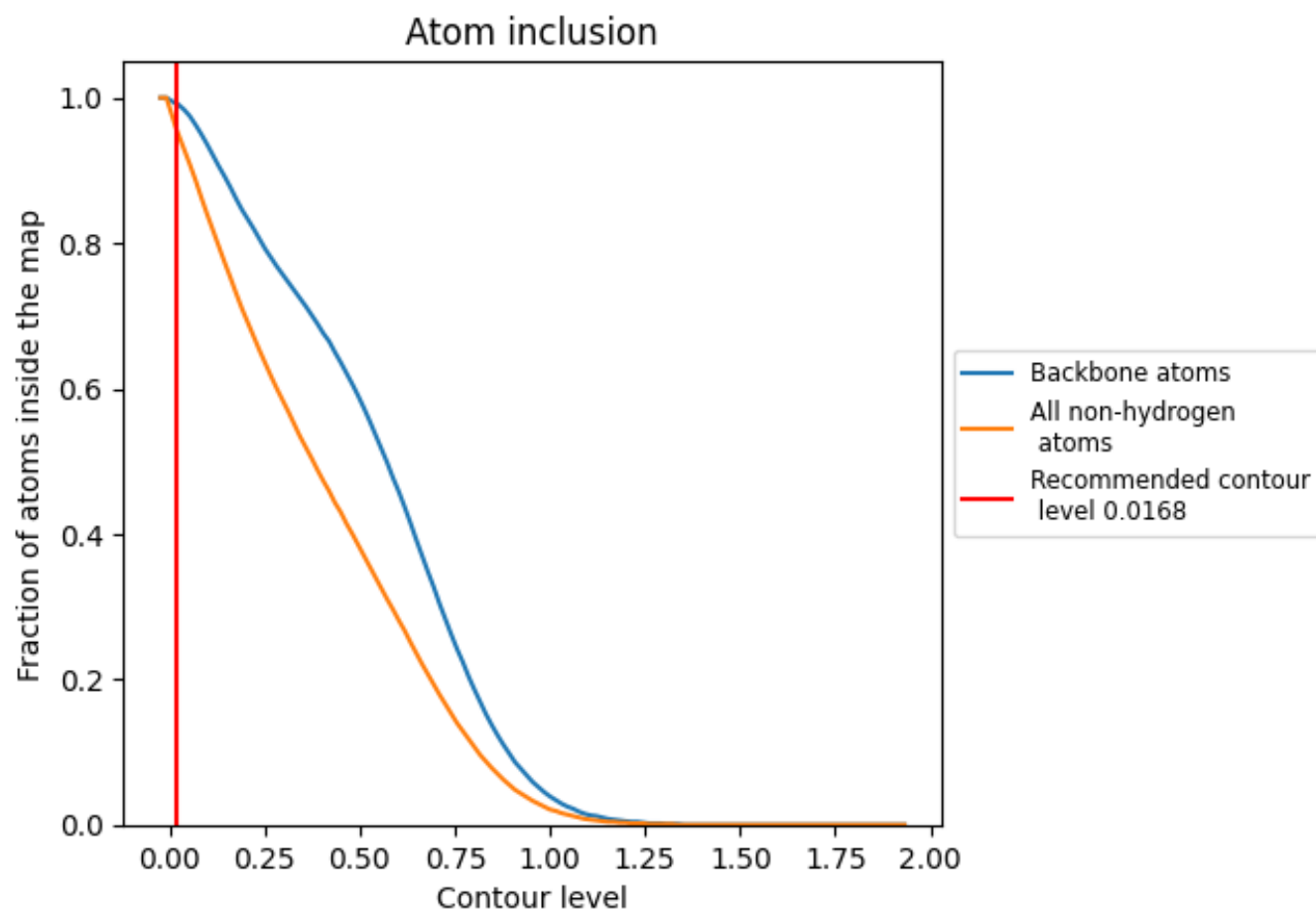
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0168).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 96% 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 (0.0168) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9590	 0.4500
B	 0.9570	 0.4350
C	 0.9580	 0.4350
D	 0.9230	 0.4040
E	 0.9170	 0.4070
F	 0.9570	 0.4510
G	 0.9490	 0.4270
X	 0.9440	 0.4180
a	 0.9810	 0.4990
b	 0.9620	 0.4690
c	 0.9800	 0.4730
d	 0.9670	 0.4660
e	 0.9820	 0.4710
f	 0.9770	 0.4830
g	 0.9780	 0.4930
h	 0.9570	 0.4390
i	 0.9430	 0.4100
j	 0.8980	 0.3880
k	 0.9250	 0.4070
l	 0.9620	 0.4410
m	 0.9700	 0.4550
n	 0.9560	 0.4460
o	 0.9860	 0.4890
p	 0.9640	 0.4580
q	 0.9710	 0.4670
r	 0.9740	 0.4640
s	 0.9800	 0.4690
t	 0.9840	 0.4840
u	 0.9790	 0.4860

