



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 10:19 AM UTC

PDB ID : 8CXB / pdb_00008cxb
EMDB ID : EMD-24276
Title : Human PA28-20S (PA28-4a3b)
Authors : Zhao, J.; Makhija, S.; Huang, B.; Cheng, Y.
Deposited on : 2022-05-20
Resolution : 2.90 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:

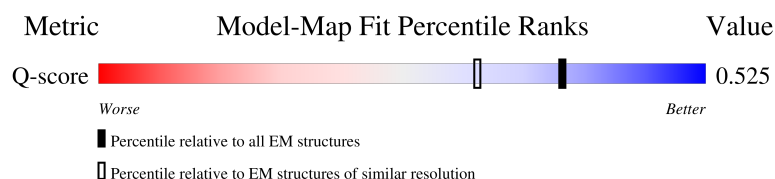
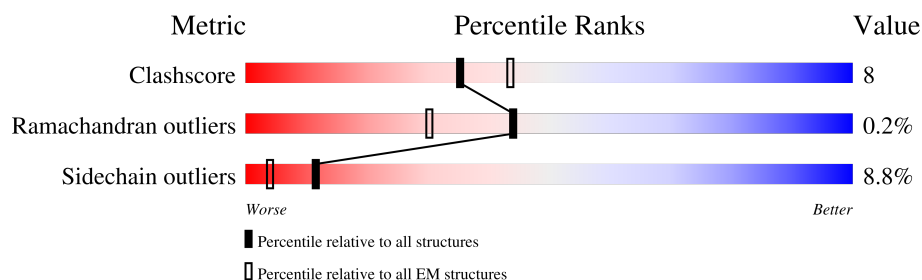
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.90 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	13054 (2.40 - 3.40)

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	239	
1	e	239	
1	g	239	
2	d	249	

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Mol	Chain	Length	Quality of chain
2	f	249	
2	h	249	
2	i	249	
3	A	234	
3	O	234	
4	B	261	
4	P	261	
5	C	248	
5	Q	248	
6	D	241	
6	R	241	
7	E	263	
7	S	263	
8	F	255	
8	T	255	
9	G	246	
9	U	246	
10	H	277	
10	V	277	
11	I	205	
11	W	205	
12	J	201	
12	X	201	
13	K	263	
13	Y	263	

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Mol	Chain	Length	Quality of chain
14	L	241	 64% 21% • 12%
14	Z	241	 64% 21% • 12%
15	M	264	 57% 22% • 19%
15	a	264	 64% 14% • 19%
16	N	239	 70% 14% • 15%
16	b	239	 68% 15% • 15%

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 57967 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 activator complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	c	214	Total	C	N	O	S	0	0
			1666	1080	281	301	4		
1	e	213	Total	C	N	O	S	0	0
			1661	1077	280	300	4		
1	g	214	Total	C	N	O	S	0	0
			1666	1080	281	301	4		

- Molecule 2 is a protein called Proteasome activator complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	d	211	Total	C	N	O	S	0	0
			1634	1054	281	295	4		
2	f	204	Total	C	N	O	S	0	0
			1590	1025	274	287	4		
2	h	211	Total	C	N	O	S	0	0
			1636	1058	283	289	6		
2	i	211	Total	C	N	O	S	0	0
			1630	1053	282	289	6		

- Molecule 3 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	229	Total	C	N	O	S	0	0
			1696	1101	294	295	6		
3	O	229	Total	C	N	O	S	0	0
			1678	1089	290	293	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	249	Total	C	N	O	S	0	0
			1793	1146	318	319	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	251	Total	C	N	O	S	0	0
			1843	1174	328	331	10		

- Molecule 5 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	235	Total	C	N	O	S	0	0
			1703	1082	314	302	5		
5	Q	236	Total	C	N	O	S	0	0
			1723	1095	320	303	5		

- Molecule 6 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	241	Total	C	N	O	S	0	0
			1751	1116	301	322	12		
6	R	235	Total	C	N	O	S	0	0
			1693	1076	292	314	11		

- Molecule 7 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	239	Total	C	N	O	S	0	0
			1810	1144	331	324	11		
7	S	237	Total	C	N	O	S	0	0
			1759	1119	329	301	10		

- Molecule 8 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	240	Total	C	N	O	S	0	0
			1785	1145	313	316	11		
8	T	239	Total	C	N	O	S	0	0
			1784	1143	314	317	10		

- Molecule 9 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	239	Total	C	N	O	S	0	0
			1769	1133	305	319	12		
9	U	242	Total	C	N	O	S	0	0
			1789	1146	307	323	13		

- Molecule 10 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	222	Total	C	N	O	S	0	0
			1609	1023	276	299	11		
10	V	222	Total	C	N	O	S	0	0
			1612	1023	274	304	11		

- Molecule 11 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	204	Total	C	N	O	S	0	0
			1564	1003	264	278	19		
11	W	204	Total	C	N	O	S	0	0
			1559	1000	264	277	18		

- Molecule 12 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	197	Total	C	N	O	S	0	0
			1544	998	265	272	9		
12	X	196	Total	C	N	O	S	0	0
			1535	990	264	273	8		

- Molecule 13 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	200	Total	C	N	O	S	0	0
			1525	968	273	275	9		
13	Y	200	Total	C	N	O	S	0	0
			1532	970	272	281	9		

- Molecule 14 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	213	Total	C	N	O	S	0	0
			1599	1022	279	288	10		
14	Z	213	Total	C	N	O	S	0	0
			1593	1022	281	280	10		

- Molecule 15 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	215	Total	C	N	O	S	0	0
			1643	1043	289	299	12		
15	a	215	Total	C	N	O	S	0	0
			1624	1034	288	290	12		

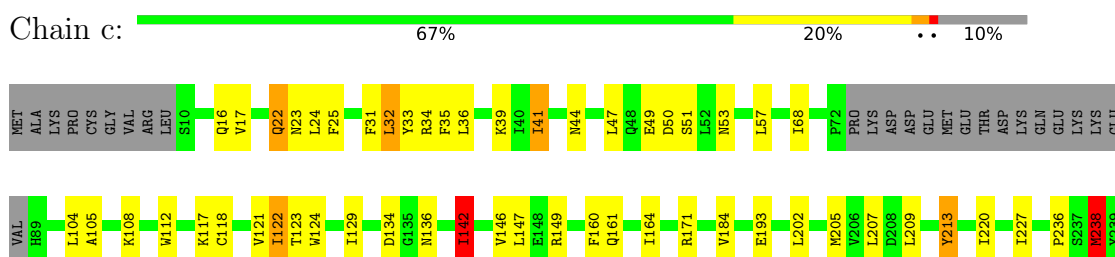
- Molecule 16 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	202	Total	C	N	O	S	0	0
			1491	939	258	282	12		
16	b	202	Total	C	N	O	S	0	0
			1478	934	258	274	12		

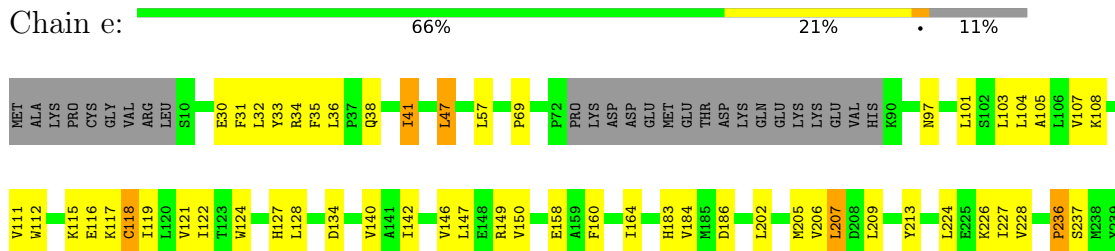
3 Residue-property plots [i](#)

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.

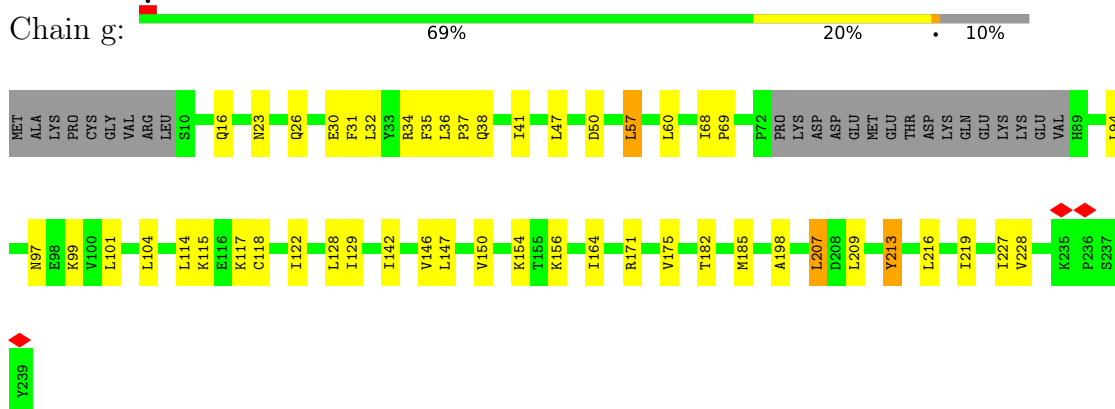
- Molecule 1: Proteasome activator complex subunit 2



- Molecule 1: Proteasome activator complex subunit 2

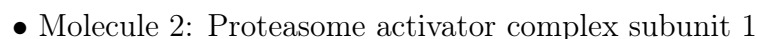


- Molecule 1: Proteasome activator complex subunit 2

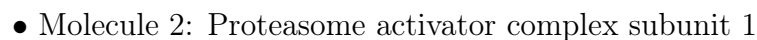


- Molecule 2: Proteasome activator complex subunit 1

15%



18%



15%

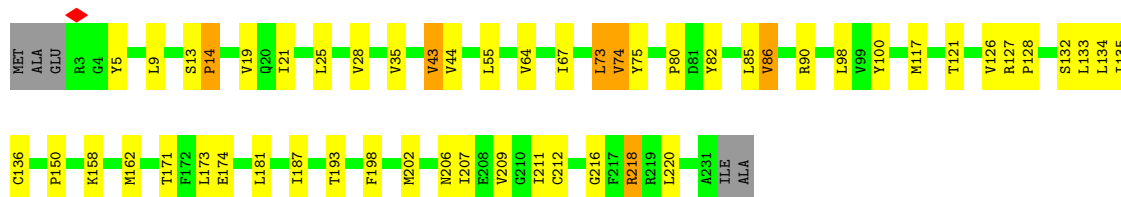


15%



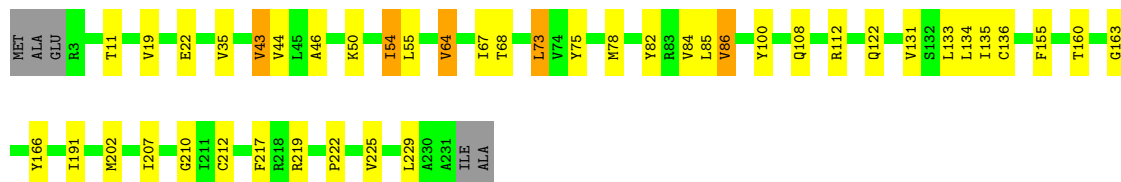
• Molecule 3: Proteasome subunit alpha type-2

Chain A: 75% 20% • •



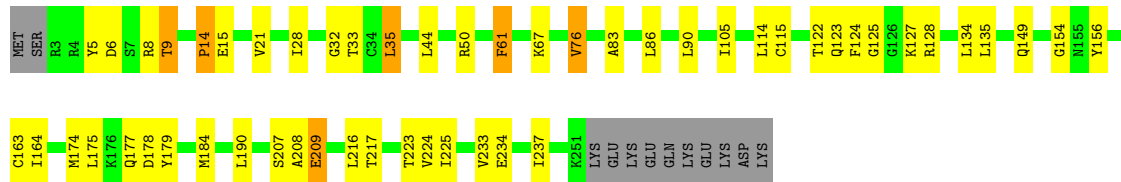
• Molecule 3: Proteasome subunit alpha type-2

Chain O: 79% 16% • •



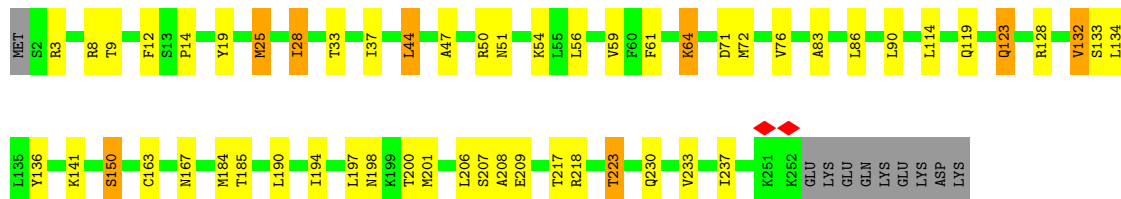
• Molecule 4: Proteasome subunit alpha type-4

Chain B: 75% 18% • 5%



• Molecule 4: Proteasome subunit alpha type-4

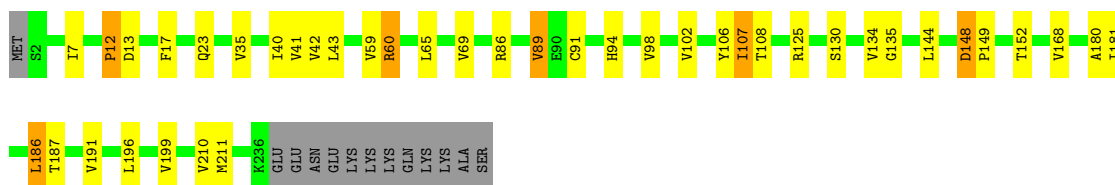
Chain P: 75% 18% • •



• Molecule 5: Proteasome subunit alpha type-7

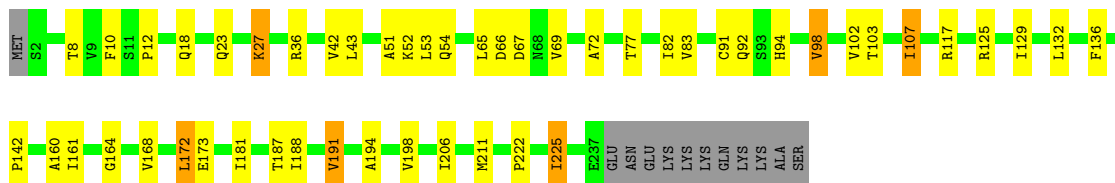
Chain C: 78% 14% • 5%





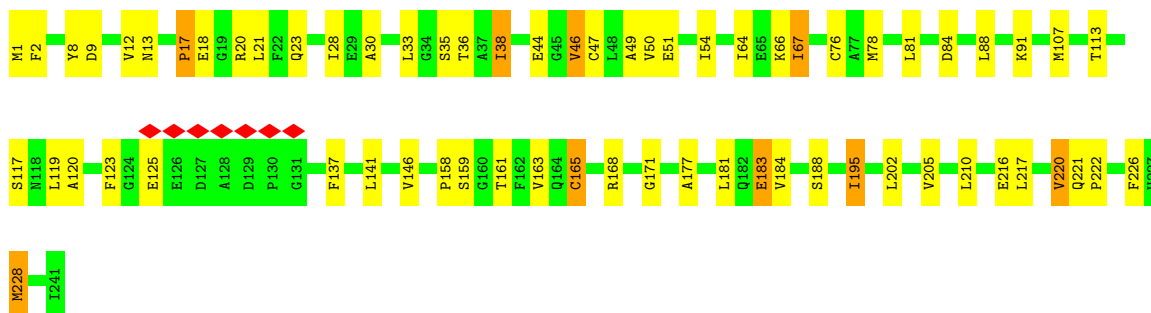
• Molecule 5: Proteasome subunit alpha type-7

Chain Q: 75% 18% 5%



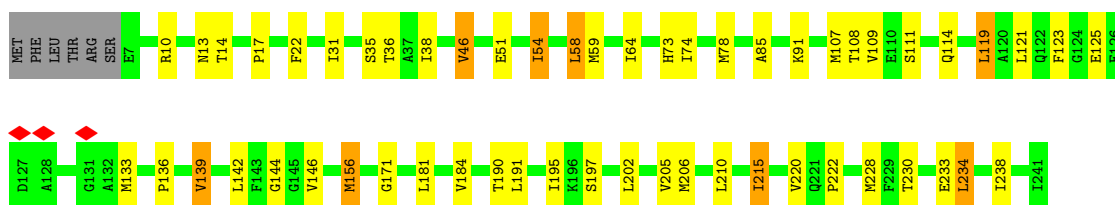
• Molecule 6: Proteasome subunit alpha type-5

Chain D: 73% 24% 3%



• Molecule 6: Proteasome subunit alpha type-5

Chain R: 75% 20% 5%



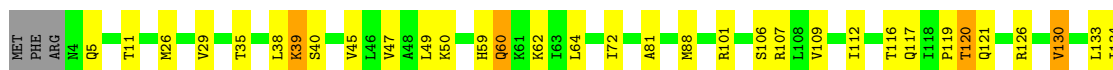
• Molecule 7: Proteasome subunit alpha type-1

Chain E: 71% 17% 9%

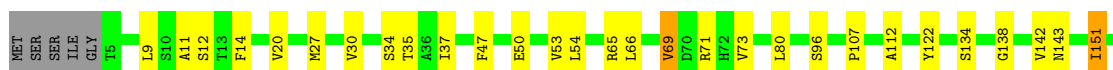
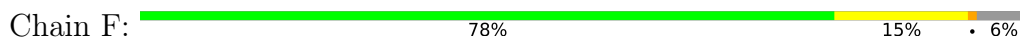




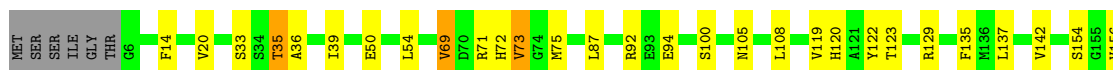
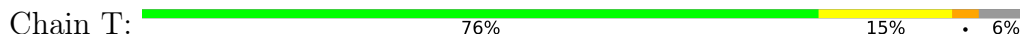
- Molecule 7: Proteasome subunit alpha type-1



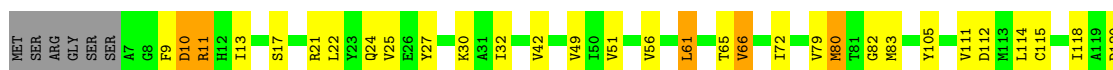
- Molecule 8: Proteasome subunit alpha type-3



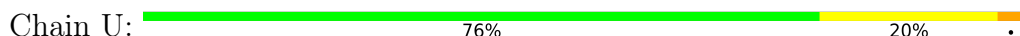
- Molecule 8: Proteasome subunit alpha type-3



- Molecule 9: Proteasome subunit alpha type-6

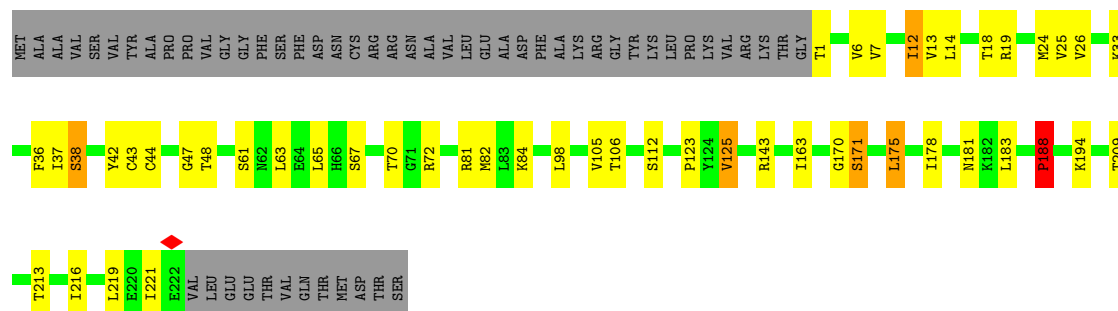


- Molecule 9: Proteasome subunit alpha type-6

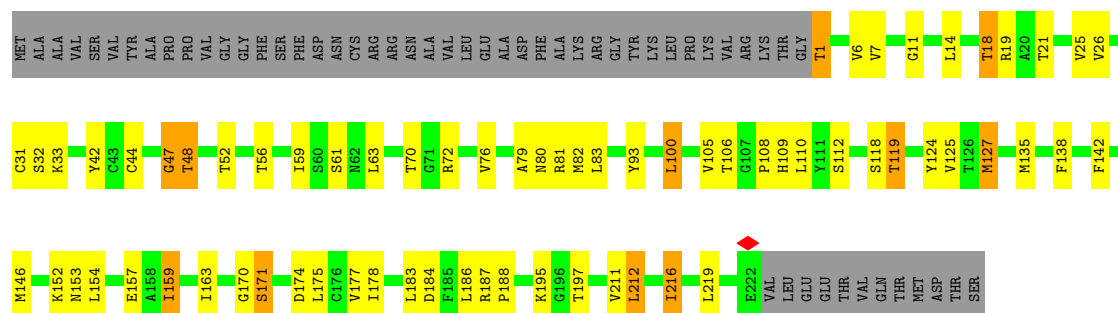




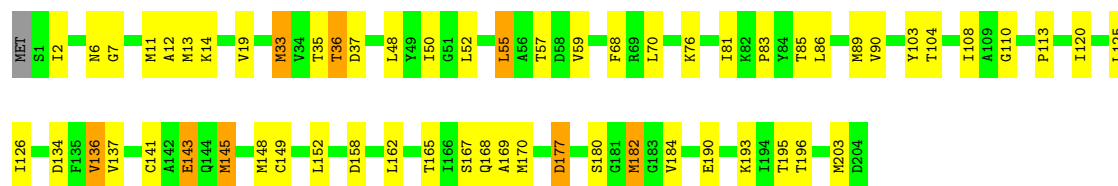
• Molecule 10: Proteasome subunit beta type-7



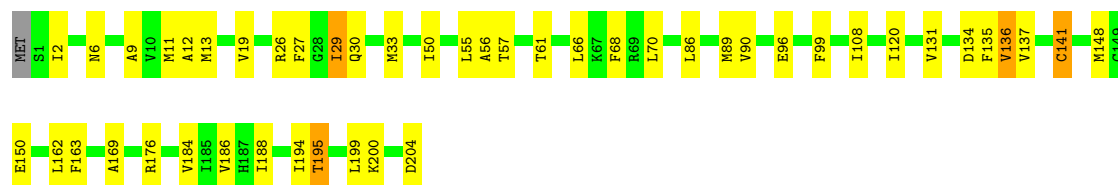
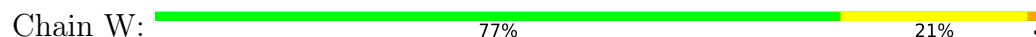
• Molecule 10: Proteasome subunit beta type-7



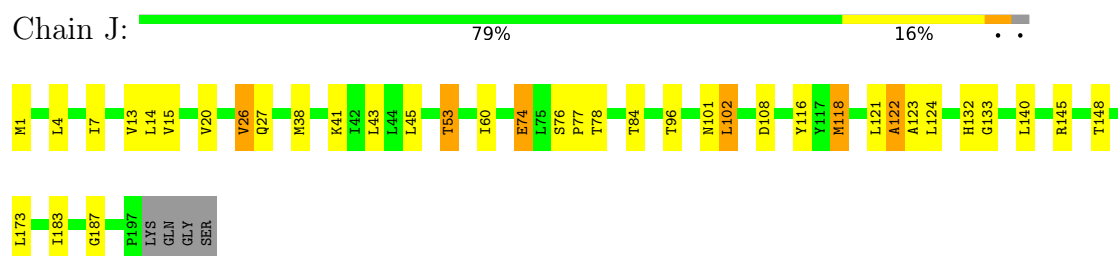
• Molecule 11: Proteasome subunit beta type-3



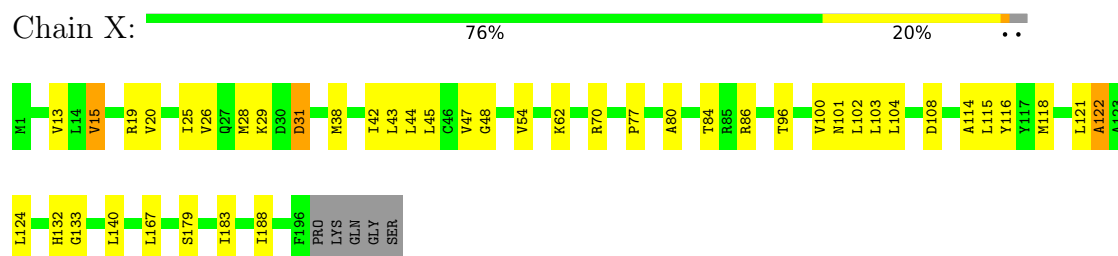
• Molecule 11: Proteasome subunit beta type-3



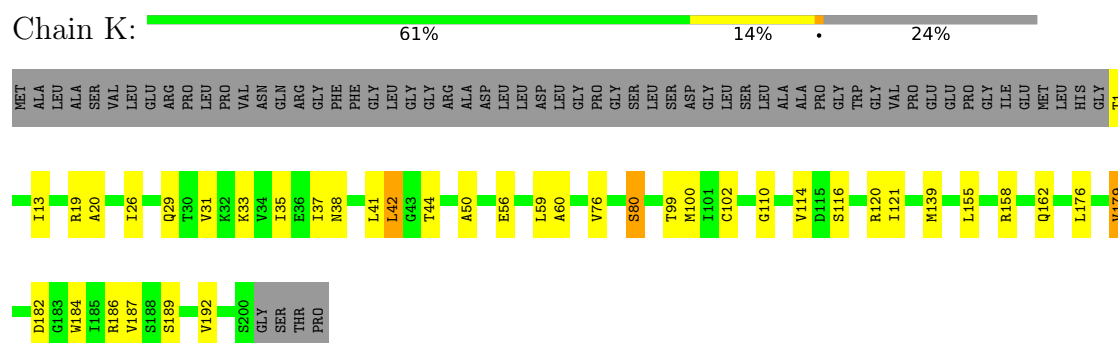
- Molecule 12: Proteasome subunit beta type-2



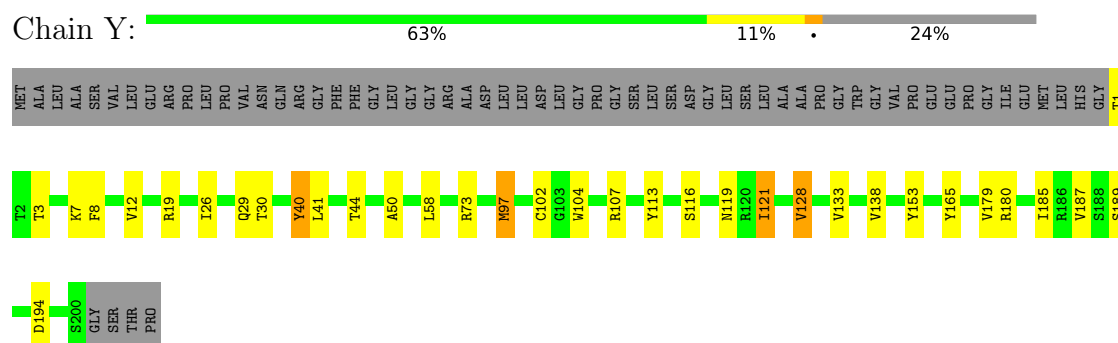
- Molecule 12: Proteasome subunit beta type-2



- Molecule 13: Proteasome subunit beta type-5

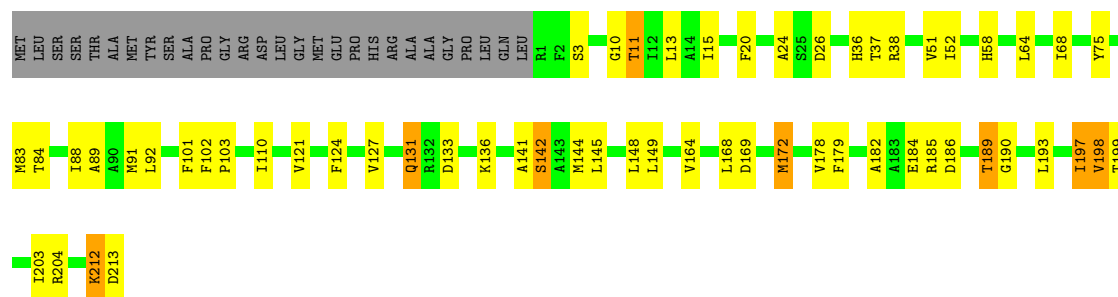


- Molecule 13: Proteasome subunit beta type-5

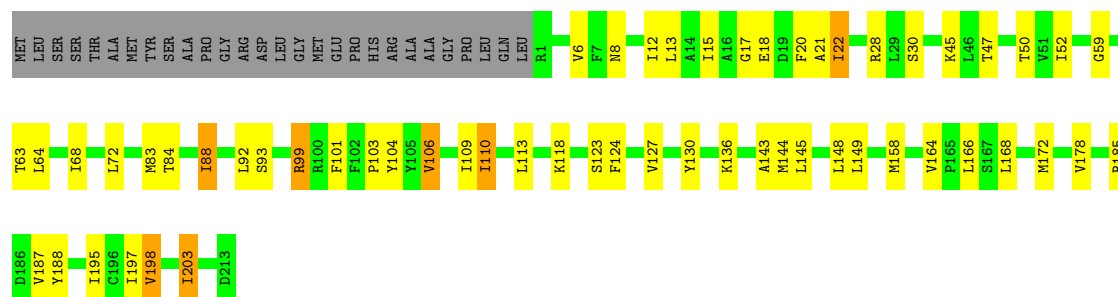


- Molecule 14: Proteasome subunit beta type-1

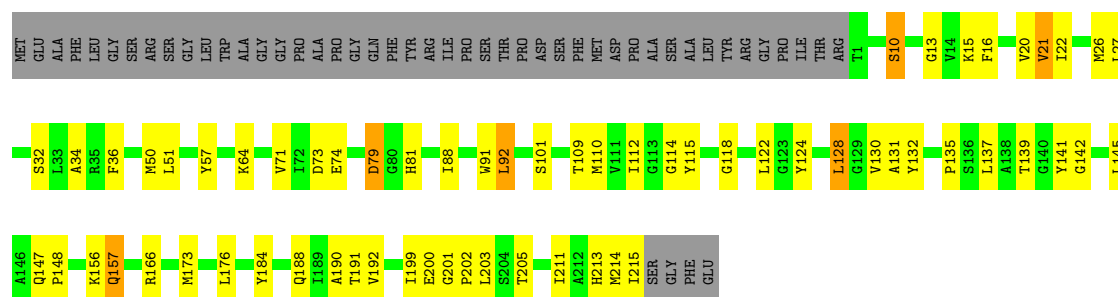




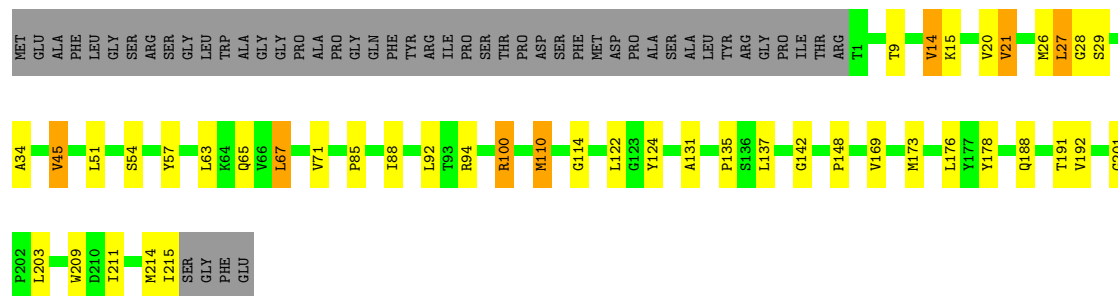
• Molecule 14: Proteasome subunit beta type-1



• Molecule 15: Proteasome subunit beta type-4



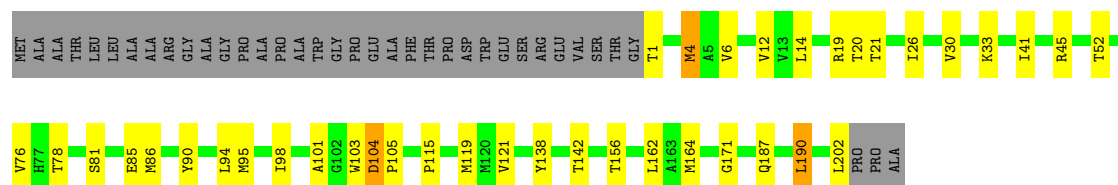
• Molecule 15: Proteasome subunit beta type-4



• Molecule 16: Proteasome subunit beta type-6

[illegible]

Chain b: 68% 15% 15%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	135937	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	26.106	Depositor
Minimum map value	-10.669	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	4	Depositor
Map size (Å)	388.992, 388.992, 388.992	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2156, 1.2156, 1.2156	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.81	0/1700	1.43	6/2310 (0.3%)
1	e	0.81	0/1695	1.45	5/2303 (0.2%)
1	g	0.82	0/1700	1.42	4/2310 (0.2%)
2	d	0.80	0/1665	1.49	7/2258 (0.3%)
2	f	0.81	0/1620	1.47	3/2196 (0.1%)
2	h	0.79	0/1667	1.47	6/2258 (0.3%)
2	i	0.80	0/1661	1.45	6/2251 (0.3%)
3	A	0.95	0/1735	1.46	5/2362 (0.2%)
3	O	0.93	0/1717	1.39	0/2339
4	B	0.91	0/1821	1.50	9/2477 (0.4%)
4	P	0.90	0/1872	1.44	5/2541 (0.2%)
5	C	0.93	0/1729	1.50	4/2356 (0.2%)
5	Q	0.89	0/1749	1.46	3/2380 (0.1%)
6	D	0.97	0/1780	1.47	7/2417 (0.3%)
6	R	0.91	0/1720	1.41	3/2336 (0.1%)
7	E	0.95	1/1845 (0.1%)	1.43	4/2504 (0.2%)
7	S	0.94	0/1794	1.46	5/2437 (0.2%)
8	F	0.94	0/1820	1.42	3/2464 (0.1%)
8	T	0.93	0/1819	1.41	4/2463 (0.2%)
9	G	0.95	0/1802	1.49	8/2449 (0.3%)
9	U	0.91	1/1823 (0.1%)	1.43	3/2478 (0.1%)
10	H	0.97	1/1636 (0.1%)	1.51	5/2223 (0.2%)
10	V	0.97	0/1639	1.46	3/2228 (0.1%)
11	I	0.92	0/1593	1.47	5/2149 (0.2%)
11	W	0.94	0/1588	1.46	5/2144 (0.2%)
12	J	0.93	0/1577	1.41	2/2138 (0.1%)
12	X	0.94	0/1567	1.41	2/2124 (0.1%)
13	K	0.95	0/1556	1.44	2/2104 (0.1%)
13	Y	0.93	1/1563 (0.1%)	1.43	2/2115 (0.1%)
14	L	0.98	0/1629	1.48	7/2201 (0.3%)
14	Z	0.96	0/1623	1.46	5/2192 (0.2%)
15	M	0.94	0/1676	1.47	7/2272 (0.3%)
15	a	0.97	0/1657	1.44	3/2250 (0.1%)
16	N	0.99	0/1517	1.43	0/2056

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	b	0.98	0/1504	1.45	3/2038 (0.1%)
All	All	0.92	4/59059 (0.0%)	1.45	151/80123 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	E	127	PRO	C-O	-5.36	1.17	1.23
13	Y	189	SER	CA-CB	-5.36	1.48	1.53
10	H	38	SER	CA-CB	-5.09	1.47	1.54
9	U	133	PRO	C-O	-5.06	1.17	1.23

The worst 5 of 151 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	c	238	MET	N-CA-C	-11.12	98.40	113.30
5	C	12	PRO	N-CA-C	-10.69	94.46	111.14
6	D	17	PRO	N-CA-C	-9.82	95.83	111.14
4	B	14	PRO	N-CA-C	-9.70	96.02	111.14
14	L	103	PRO	N-CA-C	9.60	125.81	111.41

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	1666	0	1655	35	0
1	e	1661	0	1653	27	0
1	g	1666	0	1655	27	0
2	d	1634	0	1625	36	0
2	f	1590	0	1594	30	0
2	h	1636	0	1652	31	0
2	i	1630	0	1634	33	0
3	A	1696	0	1647	30	0
3	O	1678	0	1616	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1793	0	1704	25	0
4	P	1843	0	1780	38	0
5	C	1703	0	1616	17	0
5	Q	1723	0	1659	30	0
6	D	1751	0	1707	35	0
6	R	1693	0	1629	29	0
7	E	1810	0	1759	31	0
7	S	1759	0	1711	32	0
8	F	1785	0	1717	17	0
8	T	1784	0	1718	26	0
9	G	1769	0	1730	26	0
9	U	1789	0	1743	32	0
10	H	1609	0	1609	23	0
10	V	1612	0	1602	51	0
11	I	1564	0	1587	30	0
11	W	1559	0	1575	26	0
12	J	1544	0	1537	19	0
12	X	1535	0	1527	25	0
13	K	1525	0	1490	20	0
13	Y	1532	0	1483	10	0
14	L	1599	0	1582	31	0
14	Z	1593	0	1595	34	0
15	M	1643	0	1611	40	0
15	a	1624	0	1585	27	0
16	N	1491	0	1458	21	0
16	b	1478	0	1448	24	0
All	All	57967	0	56893	903	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 8.

The worst 5 of 903 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)
2:h:122:LYS:HG3	2:i:210:ARG:HD3	1.52	0.92
10:V:42:TYR:CE1	10:V:183:LEU:HD11	2.09	0.88
10:V:216:ILE:HD12	10:V:216:ILE:N	1.90	0.86
9:U:103:TYR:O	10:V:81:ARG:HD3	1.74	0.86
5:Q:27:LYS:NZ	5:Q:27:LYS:HB3	1.91	0.85

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	210/239 (88%)	209 (100%)	1 (0%)	0	100	100
1	e	209/239 (87%)	206 (99%)	2 (1%)	1 (0%)	24	54
1	g	210/239 (88%)	210 (100%)	0	0	100	100
2	d	207/249 (83%)	204 (99%)	3 (1%)	0	100	100
2	f	200/249 (80%)	197 (98%)	3 (2%)	0	100	100
2	h	207/249 (83%)	204 (99%)	2 (1%)	1 (0%)	24	54
2	i	207/249 (83%)	205 (99%)	2 (1%)	0	100	100
3	A	227/234 (97%)	224 (99%)	3 (1%)	0	100	100
3	O	227/234 (97%)	226 (100%)	1 (0%)	0	100	100
4	B	247/261 (95%)	241 (98%)	6 (2%)	0	100	100
4	P	249/261 (95%)	245 (98%)	3 (1%)	1 (0%)	30	59
5	C	233/248 (94%)	230 (99%)	3 (1%)	0	100	100
5	Q	234/248 (94%)	232 (99%)	2 (1%)	0	100	100
6	D	239/241 (99%)	231 (97%)	8 (3%)	0	100	100
6	R	233/241 (97%)	232 (100%)	1 (0%)	0	100	100
7	E	237/263 (90%)	233 (98%)	4 (2%)	0	100	100
7	S	235/263 (89%)	230 (98%)	5 (2%)	0	100	100
8	F	238/255 (93%)	238 (100%)	0	0	100	100
8	T	237/255 (93%)	236 (100%)	1 (0%)	0	100	100
9	G	237/246 (96%)	232 (98%)	4 (2%)	1 (0%)	30	59
9	U	240/246 (98%)	239 (100%)	1 (0%)	0	100	100
10	H	220/277 (79%)	215 (98%)	3 (1%)	2 (1%)	14	41
10	V	220/277 (79%)	217 (99%)	1 (0%)	2 (1%)	14	41
11	I	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
11	W	202/205 (98%)	198 (98%)	3 (2%)	1 (0%)	24	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	J	195/201 (97%)	191 (98%)	3 (2%)	1 (0%)	24	54
12	X	194/201 (96%)	189 (97%)	4 (2%)	1 (0%)	24	54
13	K	198/263 (75%)	196 (99%)	2 (1%)	0	100	100
13	Y	198/263 (75%)	196 (99%)	2 (1%)	0	100	100
14	L	211/241 (88%)	209 (99%)	2 (1%)	0	100	100
14	Z	211/241 (88%)	208 (99%)	3 (1%)	0	100	100
15	M	213/264 (81%)	209 (98%)	3 (1%)	1 (0%)	24	54
15	a	213/264 (81%)	205 (96%)	7 (3%)	1 (0%)	24	54
16	N	200/239 (84%)	196 (98%)	4 (2%)	0	100	100
16	b	200/239 (84%)	197 (98%)	3 (2%)	0	100	100
All	All	7640/8589 (89%)	7527 (98%)	100 (1%)	13 (0%)	44	72

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	e	236	PRO
10	H	171	SER
10	H	188	PRO
10	V	171	SER
2	h	247	MET

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	172/212 (81%)	159 (92%)	13 (8%)	12	36
1	e	172/212 (81%)	159 (92%)	13 (8%)	12	36
1	g	172/212 (81%)	162 (94%)	10 (6%)	18	49
2	d	168/224 (75%)	157 (94%)	11 (6%)	15	44
2	f	166/224 (74%)	149 (90%)	17 (10%)	7	23
2	h	170/224 (76%)	156 (92%)	14 (8%)	10	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	i	168/224 (75%)	147 (88%)	21 (12%)	4	15
3	A	158/191 (83%)	143 (90%)	15 (10%)	8	26
3	O	155/191 (81%)	143 (92%)	12 (8%)	12	35
4	B	159/221 (72%)	143 (90%)	16 (10%)	7	24
4	P	171/221 (77%)	158 (92%)	13 (8%)	12	36
5	C	152/211 (72%)	137 (90%)	15 (10%)	7	24
5	Q	157/211 (74%)	142 (90%)	15 (10%)	8	26
6	D	173/203 (85%)	155 (90%)	18 (10%)	7	23
6	R	164/203 (81%)	148 (90%)	16 (10%)	7	25
7	E	181/224 (81%)	169 (93%)	12 (7%)	15	43
7	S	169/224 (75%)	156 (92%)	13 (8%)	12	35
8	F	167/212 (79%)	149 (89%)	18 (11%)	6	21
8	T	168/212 (79%)	154 (92%)	14 (8%)	10	32
9	G	175/210 (83%)	156 (89%)	19 (11%)	6	20
9	U	177/210 (84%)	160 (90%)	17 (10%)	8	26
10	H	165/228 (72%)	145 (88%)	20 (12%)	5	16
10	V	166/228 (73%)	146 (88%)	20 (12%)	5	16
11	I	164/174 (94%)	141 (86%)	23 (14%)	3	11
11	W	162/174 (93%)	149 (92%)	13 (8%)	11	34
12	J	156/171 (91%)	144 (92%)	12 (8%)	12	35
12	X	156/171 (91%)	148 (95%)	8 (5%)	21	53
13	K	146/202 (72%)	133 (91%)	13 (9%)	9	28
13	Y	147/202 (73%)	129 (88%)	18 (12%)	5	16
14	L	161/199 (81%)	149 (92%)	12 (8%)	12	37
14	Z	160/199 (80%)	147 (92%)	13 (8%)	11	33
15	M	166/215 (77%)	157 (95%)	9 (5%)	20	51
15	a	160/215 (74%)	145 (91%)	15 (9%)	8	26
16	N	149/181 (82%)	141 (95%)	8 (5%)	20	51
16	b	145/181 (80%)	136 (94%)	9 (6%)	16	46
All	All	5717/7216 (79%)	5212 (91%)	505 (9%)	11	29

5 of 505 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	K	121	ILE
15	a	67	LEU
4	P	190	LEU
15	a	27	LEU
2	h	248	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 109 such sidechains are listed below:

Mol	Chain	Res	Type
4	P	230	GLN
10	V	80	ASN
2	i	147	ASN
5	Q	54	GLN
7	S	68	ASN

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 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.

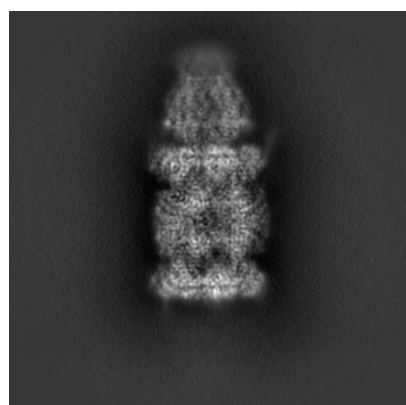
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24276. These allow visual inspection of the internal detail of the map and identification of artifacts.

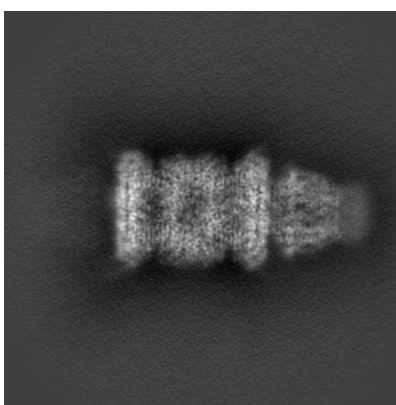
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

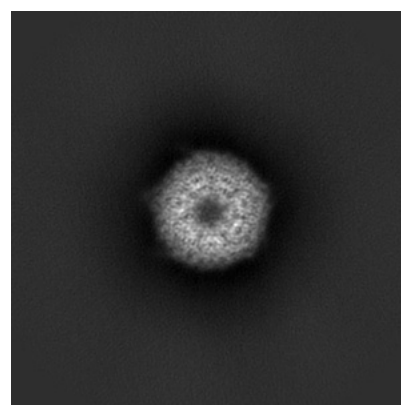
6.1.1 Primary map



X



Y

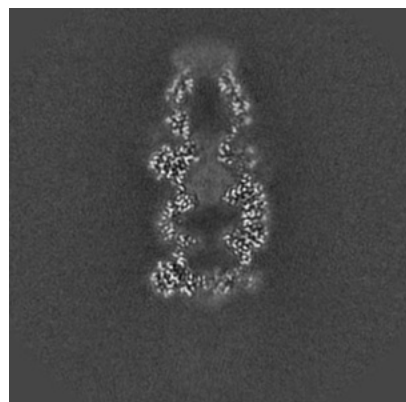


Z

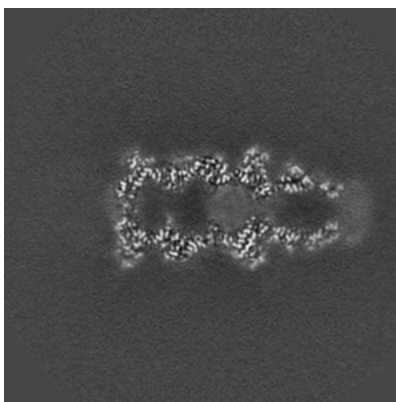
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

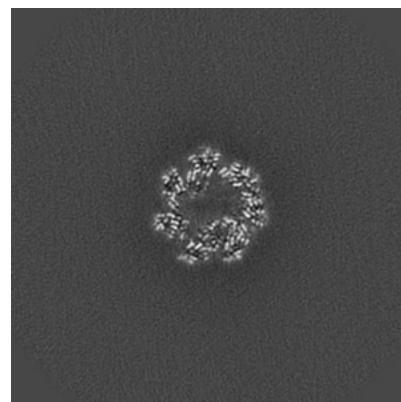
6.2.1 Primary map



X Index: 160



Y Index: 160

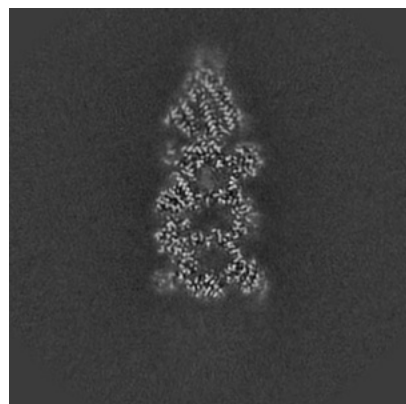


Z Index: 160

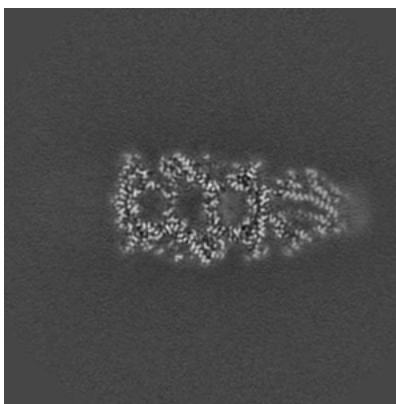
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

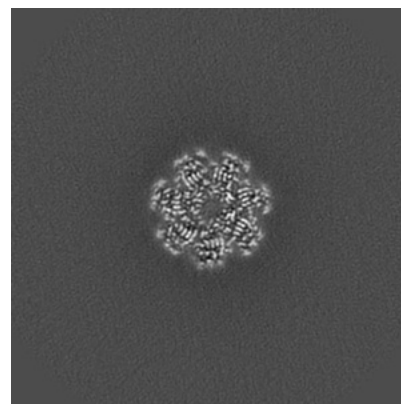
6.3.1 Primary map



X Index: 176



Y Index: 145

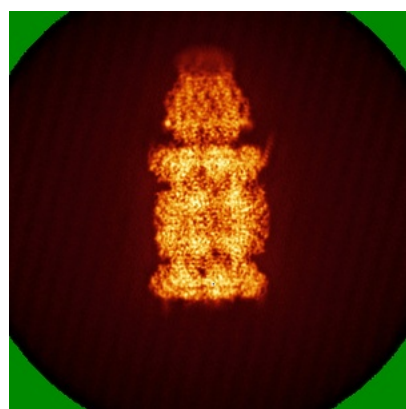


Z Index: 197

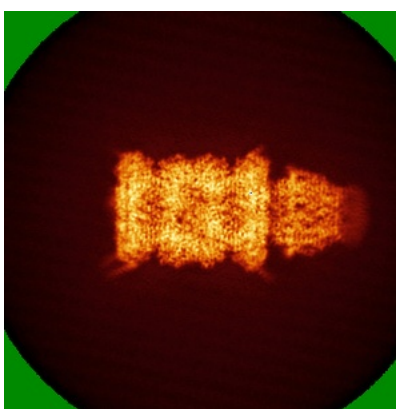
The images above show the largest variance slices of the map in three orthogonal directions.

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

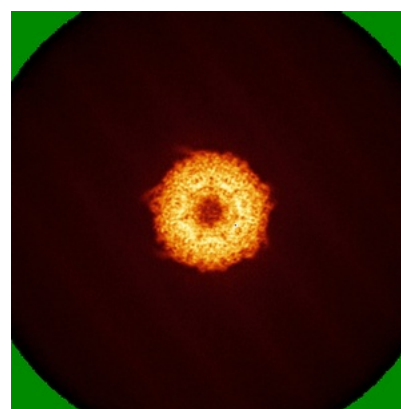
6.4.1 Primary map



X



Y

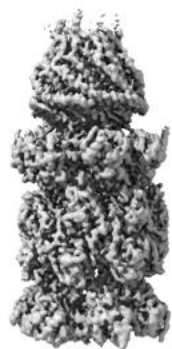


Z

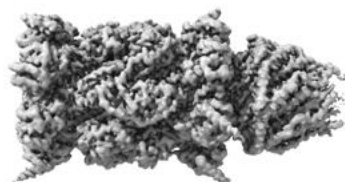
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 4.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

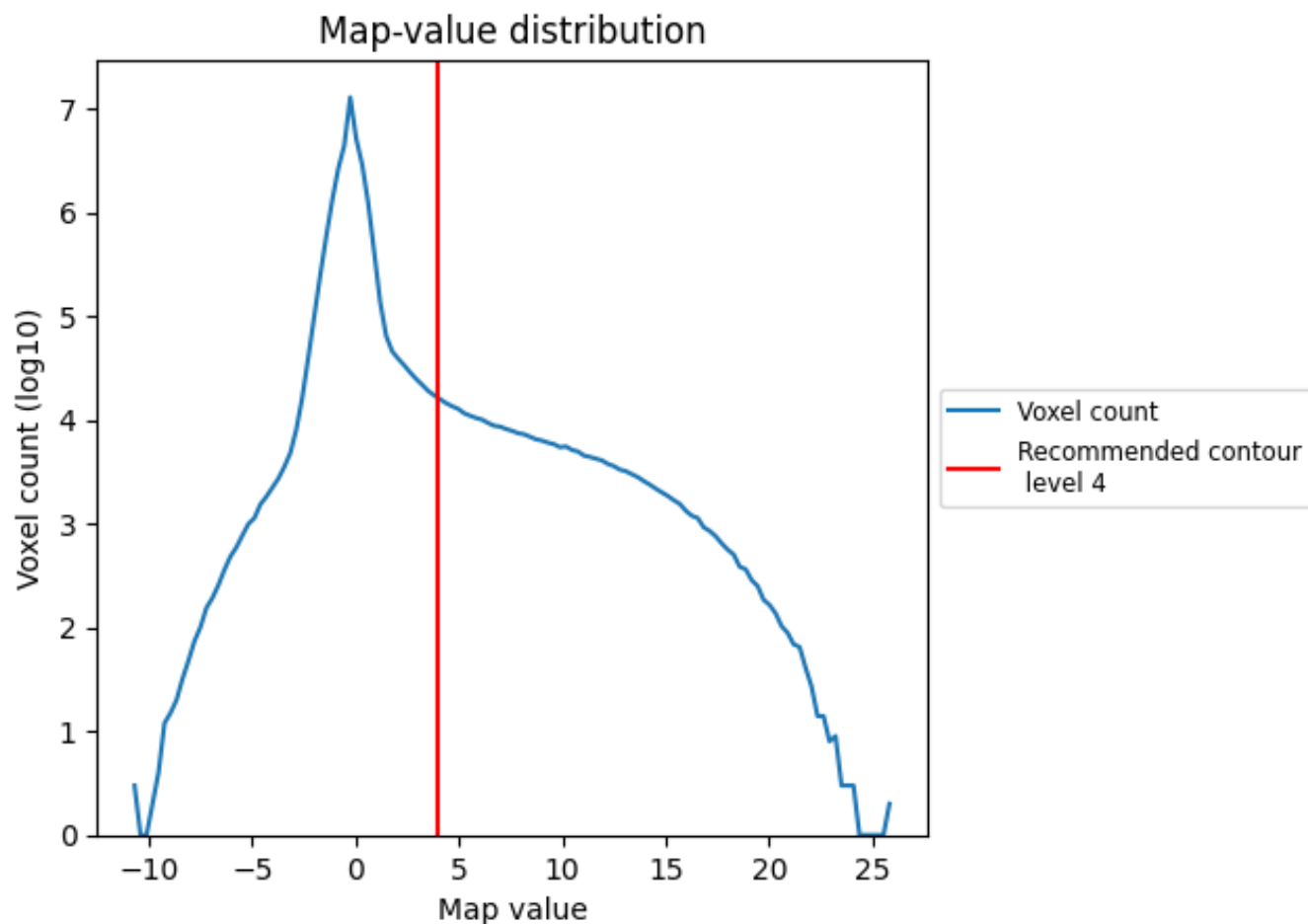
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

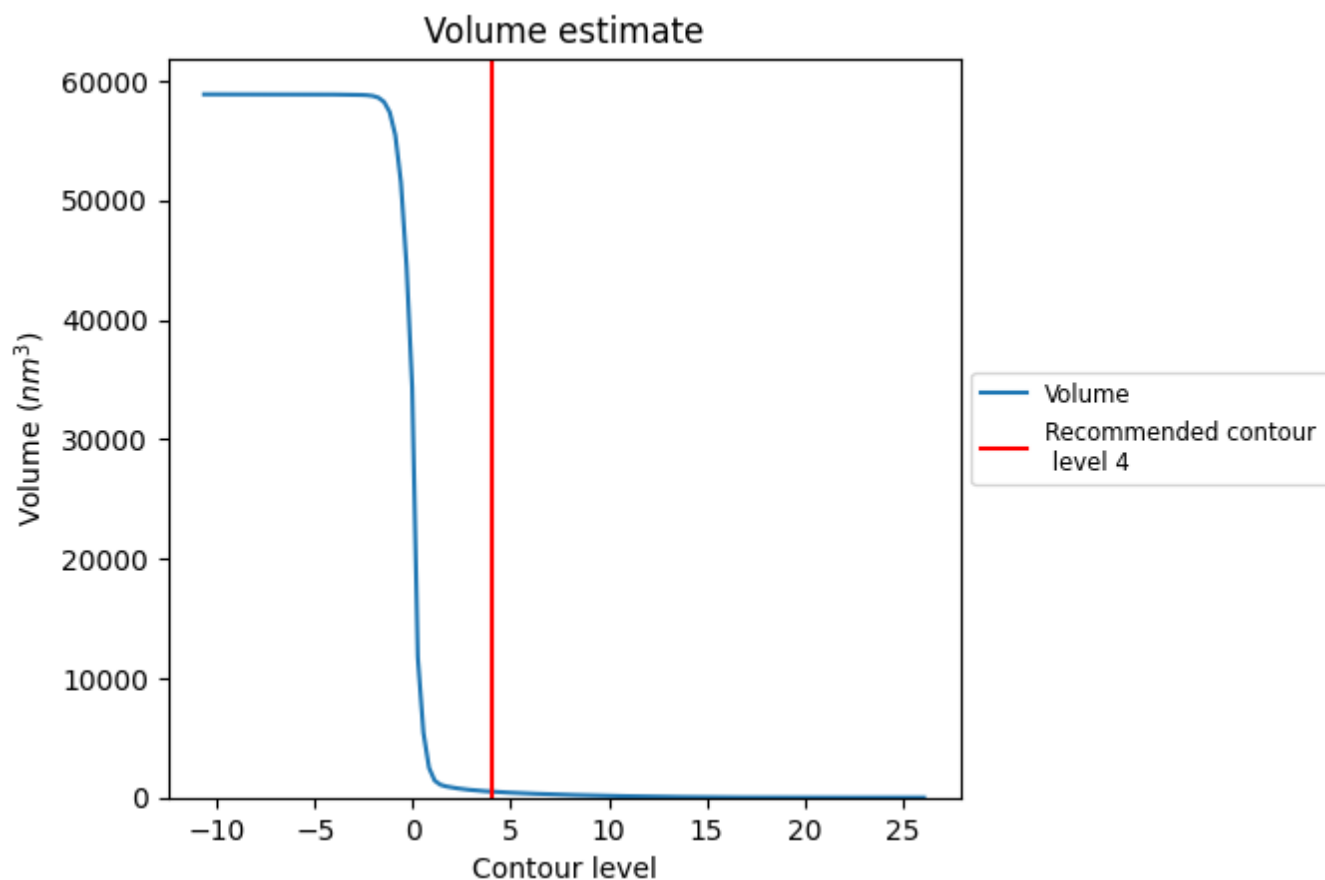
This section contains the results of statistical analysis of the map.

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.

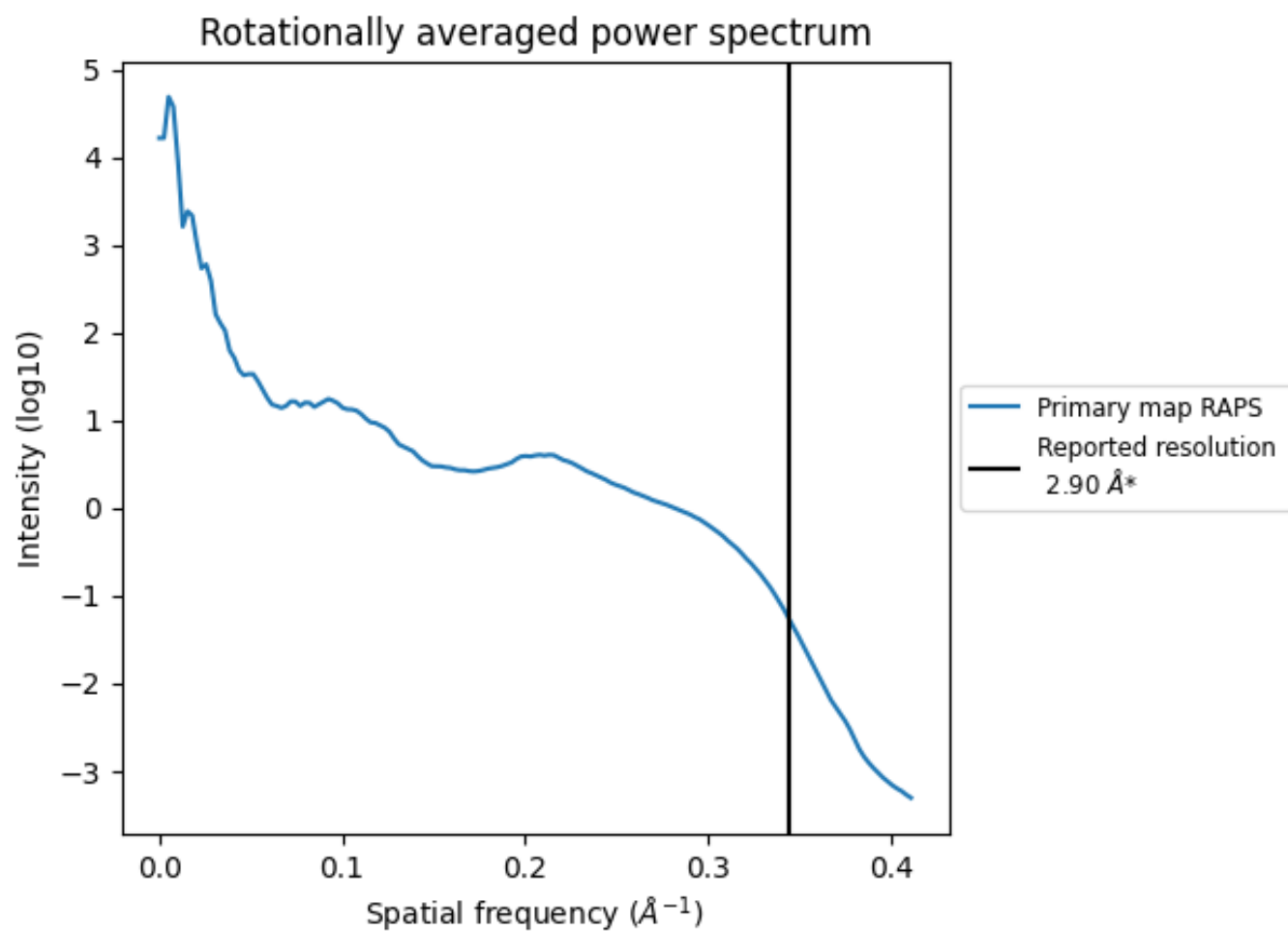
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 499 nm³; this corresponds to an approximate mass of 451 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 ⓘ

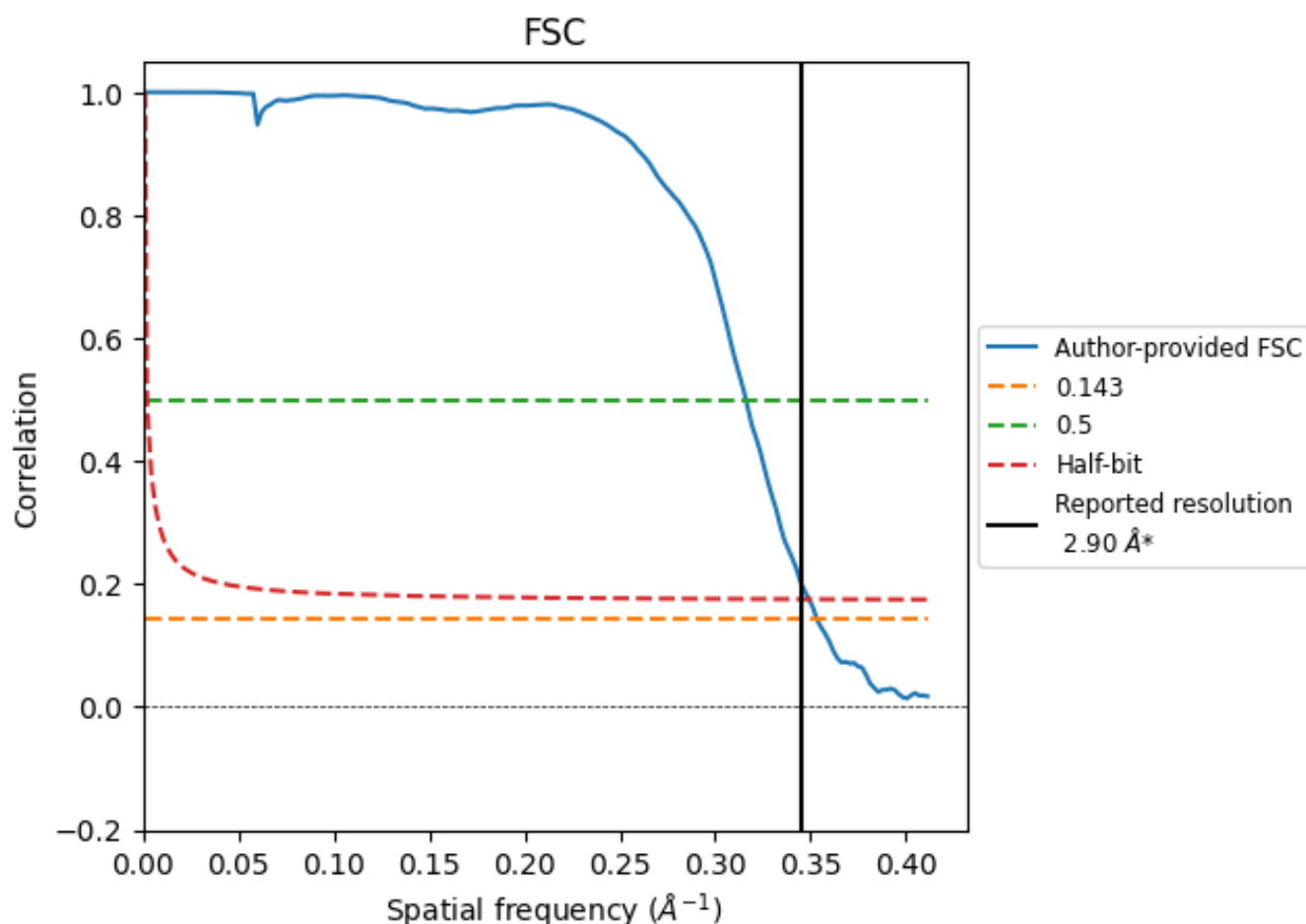


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

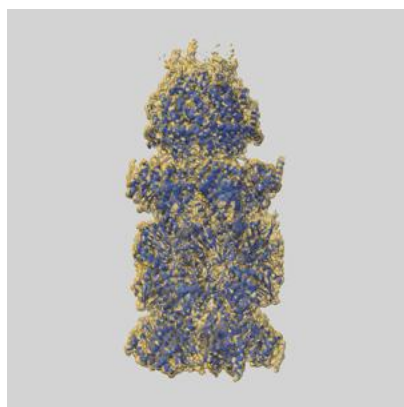
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.83	3.16	2.86
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

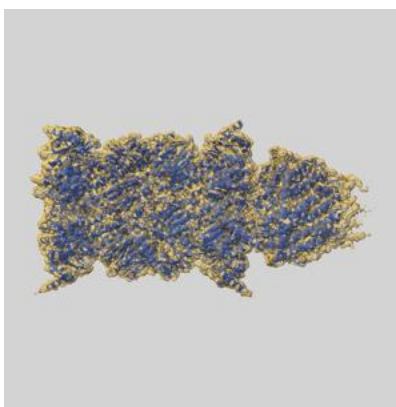
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24276 and PDB model 8CXB. Per-residue inclusion information can be found in section [3](#) on page [9](#).

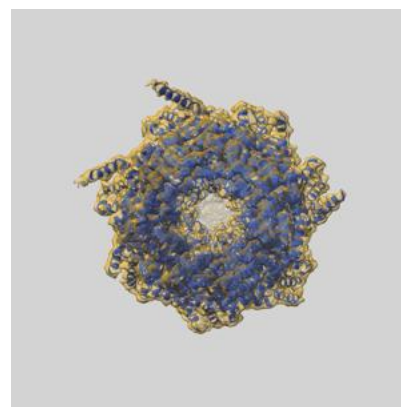
9.1 Map-model overlay [i](#)



X



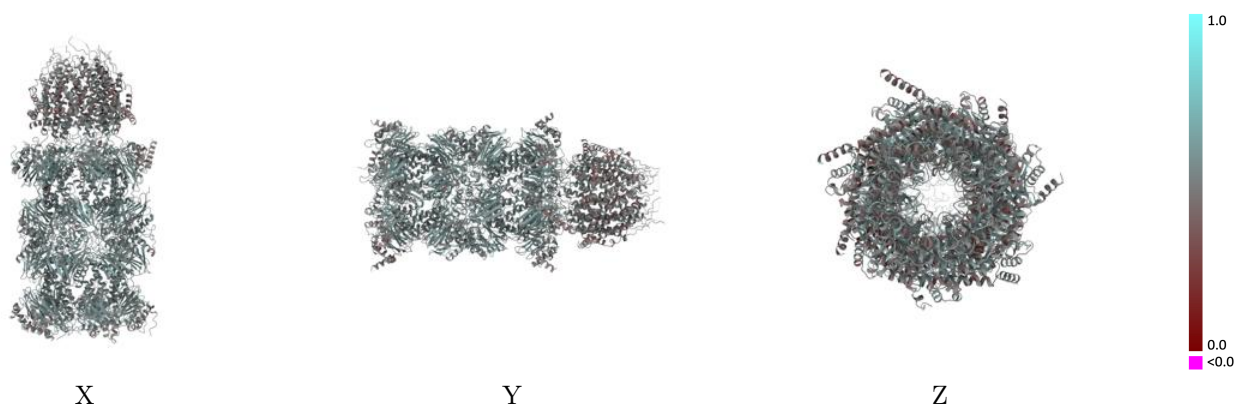
Y



Z

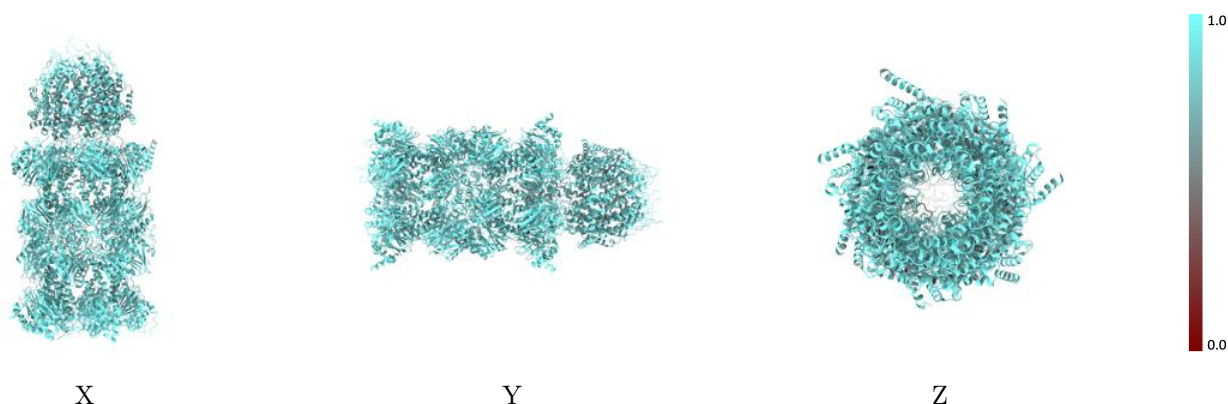
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



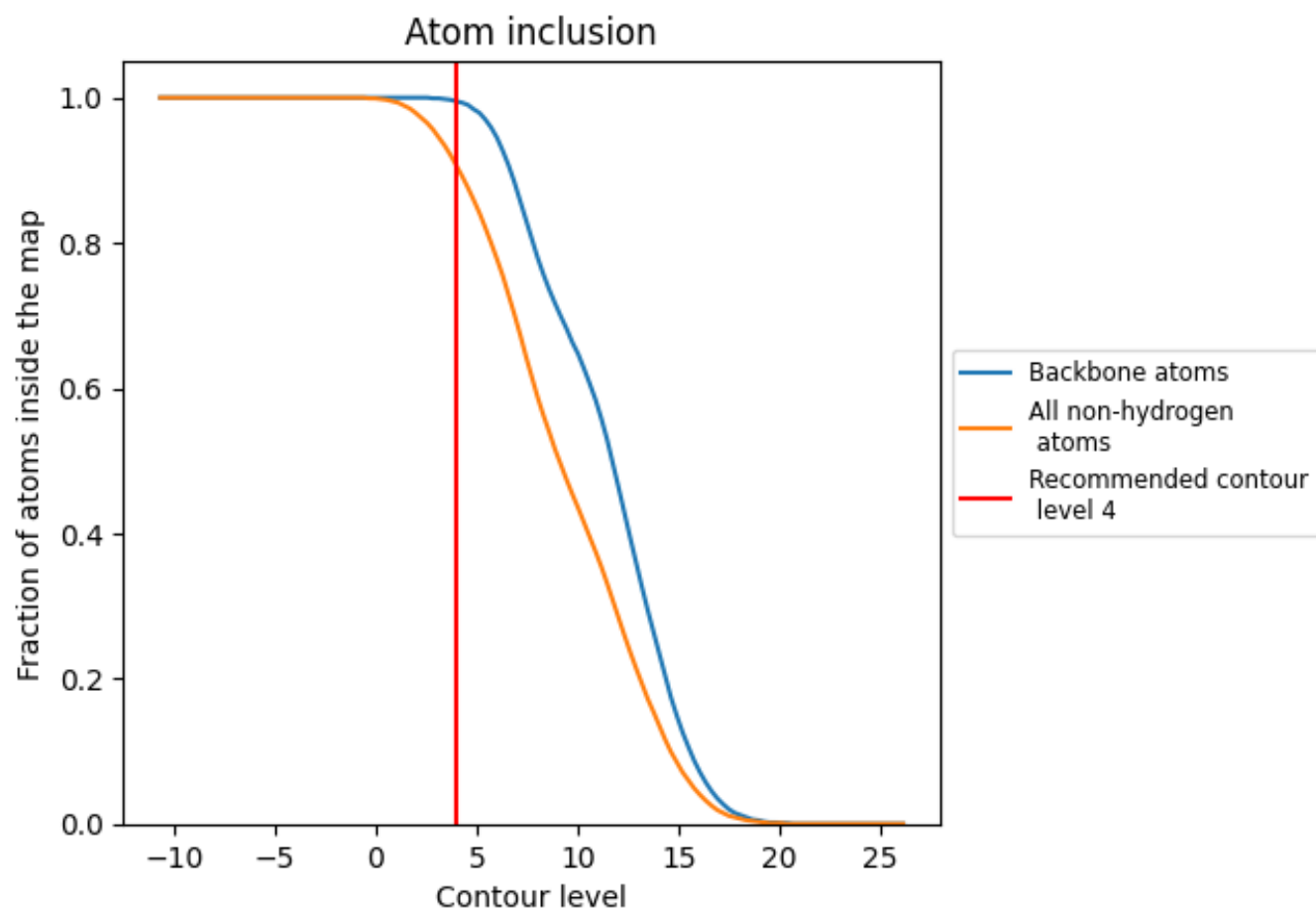
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).

9.4 Atom inclusion ⓘ



At the recommended contour level, 100% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9060	 0.5250
A	 0.9160	 0.5310
B	 0.9080	 0.5290
C	 0.9230	 0.5300
D	 0.8930	 0.5260
E	 0.9130	 0.5370
F	 0.9210	 0.5430
G	 0.9270	 0.5340
H	 0.9300	 0.5470
I	 0.9090	 0.5460
J	 0.9140	 0.5500
K	 0.9390	 0.5490
L	 0.9200	 0.5490
M	 0.9270	 0.5420
N	 0.9270	 0.5540
O	 0.9360	 0.5390
P	 0.9140	 0.5240
Q	 0.9220	 0.5140
R	 0.9060	 0.5210
S	 0.9340	 0.5280
T	 0.9360	 0.5290
U	 0.9310	 0.5330
V	 0.9240	 0.5430
W	 0.9300	 0.5550
X	 0.9180	 0.5500
Y	 0.9300	 0.5410
Z	 0.9330	 0.5530
a	 0.9390	 0.5550
b	 0.9310	 0.5530
c	 0.8330	 0.4640
d	 0.8420	 0.4700
e	 0.8520	 0.4670
f	 0.8420	 0.4710
g	 0.8260	 0.4660
h	 0.8370	 0.4650
i	 0.8470	 0.4680

