



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 05:06 PM UTC

PDB ID : 9GBK / pdb_00009gbk
EMDB ID : EMD-51221
Title : Blm10-20S proteasome complex from pre1-1
Authors : Mark, E.; Ramos, P.C.; Kayser, F.; Hoeckendorff, J.; Dohmen, R.J.; Wendler, P.
Deposited on : 2024-07-31
Resolution : 2.39 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

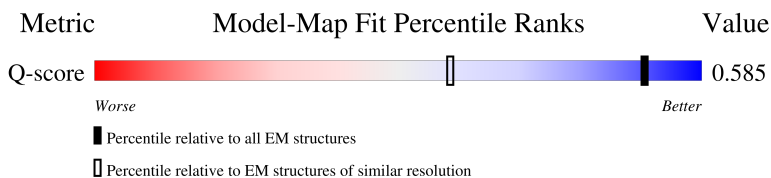
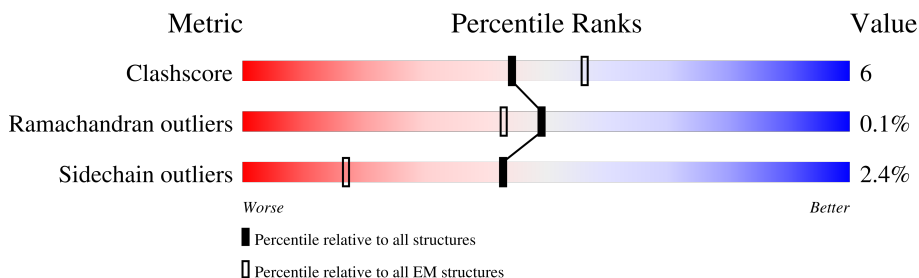
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.39 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	4884 (1.90 - 2.89)

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	1	222	
1	M	222	
2	2	233	
2	N	233	

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Mol	Chain	Length	Quality of chain
3	3	2143	
4	A	252	
4	O	252	
5	B	250	
5	P	250	
6	C	258	
6	Q	258	
7	D	254	
7	R	254	
8	E	260	
8	S	260	
9	F	234	
9	T	234	
10	G	288	
10	U	288	
11	H	196	
11	V	196	
12	I	232	
12	W	232	
13	J	205	
13	X	205	
14	K	212	
14	Y	212	
15	L	212	
15	Z	212	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 64984 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 beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	221	Total	C	N	O	S	0	0
			1747	1110	301	332	4		
1	M	220	Total	C	N	O	S	0	0
			1739	1106	300	329	4		

- Molecule 2 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	229	Total	C	N	O	S	0	0
			1790	1133	306	344	7		
2	N	228	Total	C	N	O	S	0	0
			1786	1131	305	343	7		

- Molecule 3 is a protein called Proteasome activator BLM10.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	1875	Total	C	N	O	S	0	0
			15248	9825	2526	2827	70		

- Molecule 4 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	240	Total	C	N	O	S	0	0
			1903	1212	319	364	8		
4	O	236	Total	C	N	O	S	0	0
			1869	1191	313	357	8		

- Molecule 5 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	233	Total	C	N	O	S	0	0
			1780	1134	294	349	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	242	Total	C	N	O	S	0	0
			1852	1179	306	363	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	228	Total	C	N	O	S	0	0
			1773	1122	296	352	3		
6	Q	133	Total	C	N	O	S	0	0
			1059	674	183	201	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	217	Total	C	N	O	S	0	0
			1716	1070	302	341	3		
7	R	225	Total	C	N	O	S	0	0
			1766	1104	306	352	4		

- Molecule 8 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	220	Total	C	N	O	S	0	0
			1703	1070	286	340	7		
8	S	242	Total	C	N	O	S	0	0
			1861	1162	314	378	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	230	Total	C	N	O	S	1	0
			1777	1117	308	347	5		
9	T	231	Total	C	N	O	S	0	0
			1772	1114	307	347	4		

- Molecule 10 is a protein called Probable proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	217	Total	C	N	O	S	0	0
			1692	1076	296	317	3		
10	U	238	Total	C	N	O	S	0	0
			1861	1185	323	349	4		

- Molecule 11 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	196	Total	C	N	O	S	0	0
			1511	955	250	299	7		
11	V	195	Total	C	N	O	S	0	0
			1503	949	249	298	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	221	Total	C	N	O	S	0	0
			1676	1057	292	320	7		
12	W	215	Total	C	N	O	S	0	0
			1633	1030	285	312	6		

- Molecule 13 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	201	Total	C	N	O	S	0	0
			1559	998	255	298	8		
13	X	203	Total	C	N	O	S	0	0
			1574	1007	257	302	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	188	Total	C	N	O	S	0	0
			1511	961	254	290	6		
14	Y	193	Total	C	N	O	S	0	0
			1554	990	262	296	6		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	142	PHE	SER	engineered mutation	UNP P22141
K	199	ASP	-	expression tag	UNP P22141
K	200	TYR	-	expression tag	UNP P22141
K	201	LYS	-	expression tag	UNP P22141
K	202	ASP	-	expression tag	UNP P22141
K	203	ASP	-	expression tag	UNP P22141
K	204	ASP	-	expression tag	UNP P22141
K	205	ASP	-	expression tag	UNP P22141
K	206	LYS	-	expression tag	UNP P22141

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Chain	Residue	Modelled	Actual	Comment	Reference
K	207	HIS	-	expression tag	UNP P22141
K	208	HIS	-	expression tag	UNP P22141
K	209	HIS	-	expression tag	UNP P22141
K	210	HIS	-	expression tag	UNP P22141
K	211	HIS	-	expression tag	UNP P22141
K	212	HIS	-	expression tag	UNP P22141
Y	142	PHE	SER	engineered mutation	UNP P22141
Y	199	ASP	-	expression tag	UNP P22141
Y	200	TYR	-	expression tag	UNP P22141
Y	201	LYS	-	expression tag	UNP P22141
Y	202	ASP	-	expression tag	UNP P22141
Y	203	ASP	-	expression tag	UNP P22141
Y	204	ASP	-	expression tag	UNP P22141
Y	205	ASP	-	expression tag	UNP P22141
Y	206	LYS	-	expression tag	UNP P22141
Y	207	HIS	-	expression tag	UNP P22141
Y	208	HIS	-	expression tag	UNP P22141
Y	209	HIS	-	expression tag	UNP P22141
Y	210	HIS	-	expression tag	UNP P22141
Y	211	HIS	-	expression tag	UNP P22141
Y	212	HIS	-	expression tag	UNP P22141

- Molecule 15 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	212	Total	C	N	O	S	0	0
			1643	1045	280	311	7		
15	Z	212	Total	C	N	O	S	0	0
			1643	1045	280	311	7		

- Molecule 16 is water.

Mol	Chain	Residues	Atoms		AltConf
16	1	75	Total	O	0
			75	75	
16	2	85	Total	O	0
			85	85	
16	3	685	Total	O	0
			685	685	
16	A	98	Total	O	0
			98	98	
16	B	57	Total	O	0
			57	57	

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Mol	Chain	Residues	Atoms		AltConf
16	C	58	Total 58	O 58	0
16	D	78	Total 78	O 78	0
16	E	80	Total 80	O 80	0
16	F	55	Total 55	O 55	0
16	G	56	Total 56	O 56	0
16	H	49	Total 49	O 49	0
16	I	70	Total 70	O 70	0
16	J	56	Total 56	O 56	0
16	K	46	Total 46	O 46	0
16	L	55	Total 55	O 55	0
16	M	63	Total 63	O 63	0
16	N	74	Total 74	O 74	0
16	O	70	Total 70	O 70	0
16	P	56	Total 56	O 56	0
16	Q	37	Total 37	O 37	0
16	R	79	Total 79	O 79	0
16	S	76	Total 76	O 76	0
16	T	61	Total 61	O 61	0
16	U	82	Total 82	O 82	0
16	V	43	Total 43	O 43	0
16	W	64	Total 64	O 64	0

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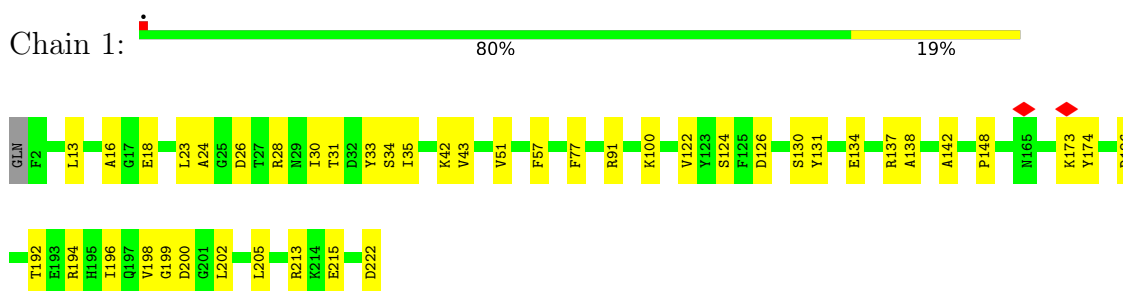
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Mol	Chain	Residues	Atoms		AltConf
16	X	43	Total 43	O 43	0
16	Y	75	Total 75	O 75	0
16	Z	57	Total 57	O 57	0

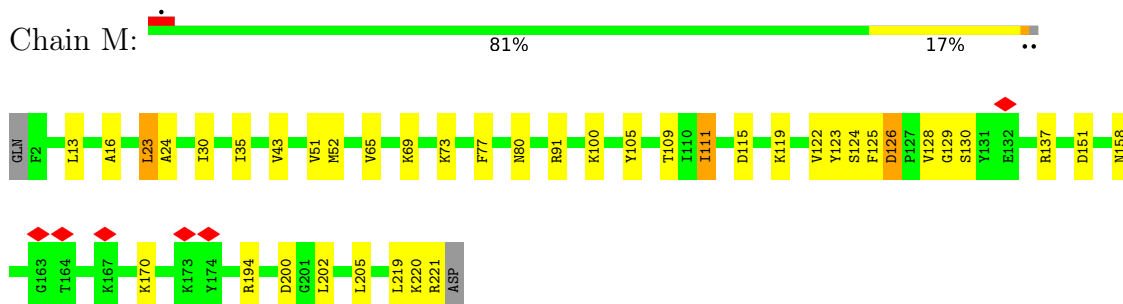
3 Residue-property plots

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.

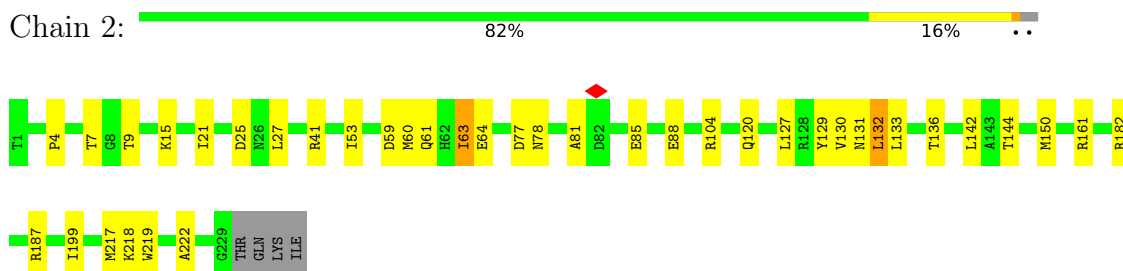
- Molecule 1: Proteasome subunit beta type-6



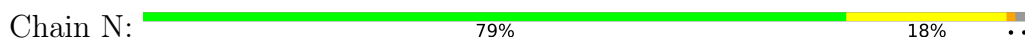
- Molecule 1: Proteasome subunit beta type-6

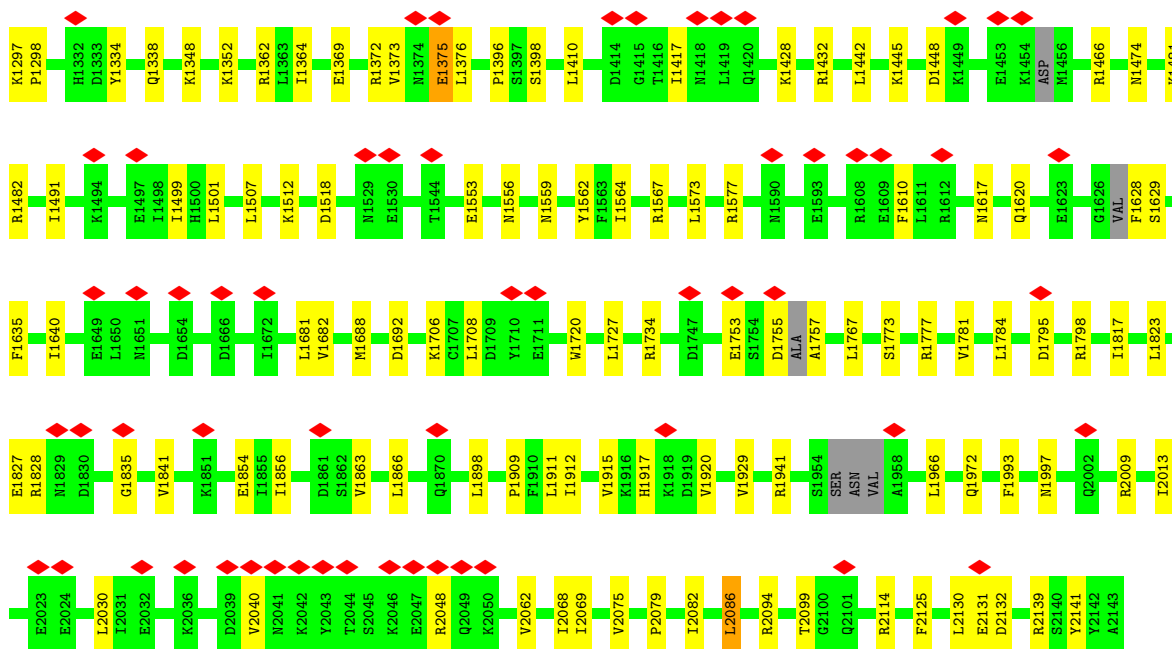


- Molecule 2: Proteasome subunit beta type-7

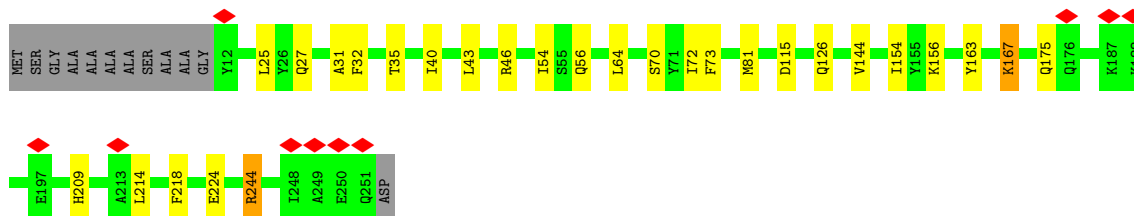
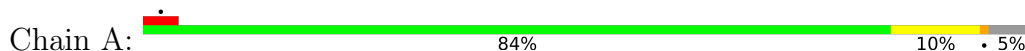


- Molecule 2: Proteasome subunit beta type-7

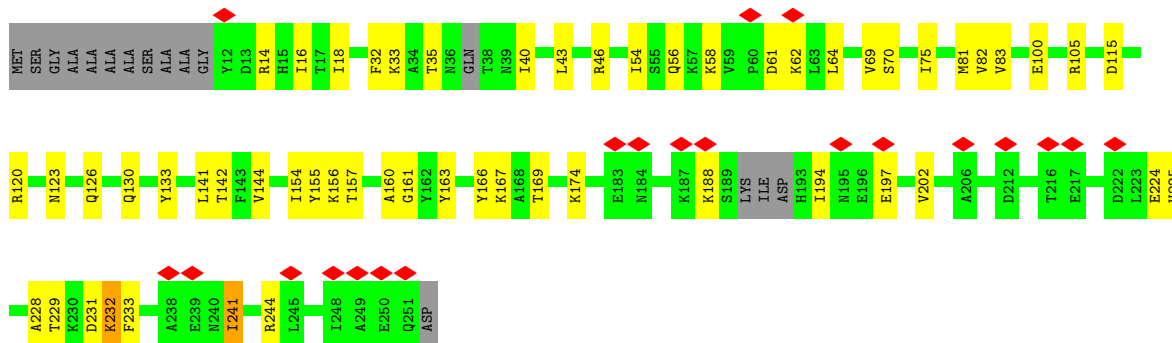




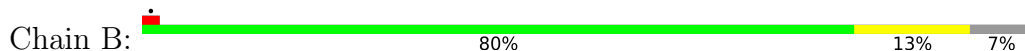
- Molecule 4: Proteasome subunit alpha type-1



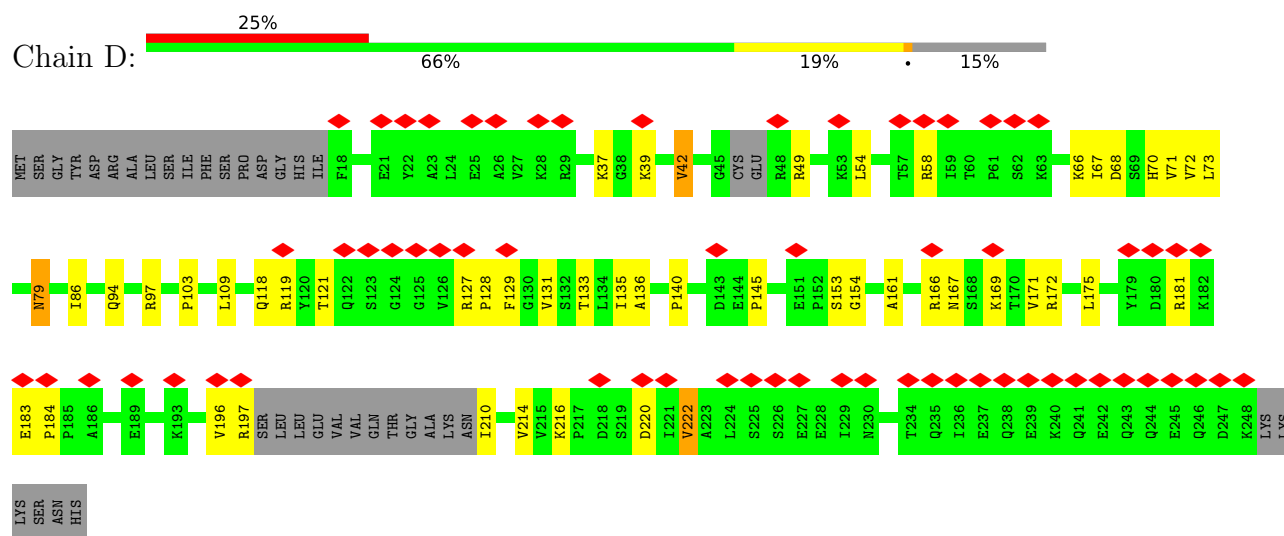
- Molecule 4: Proteasome subunit alpha type-1



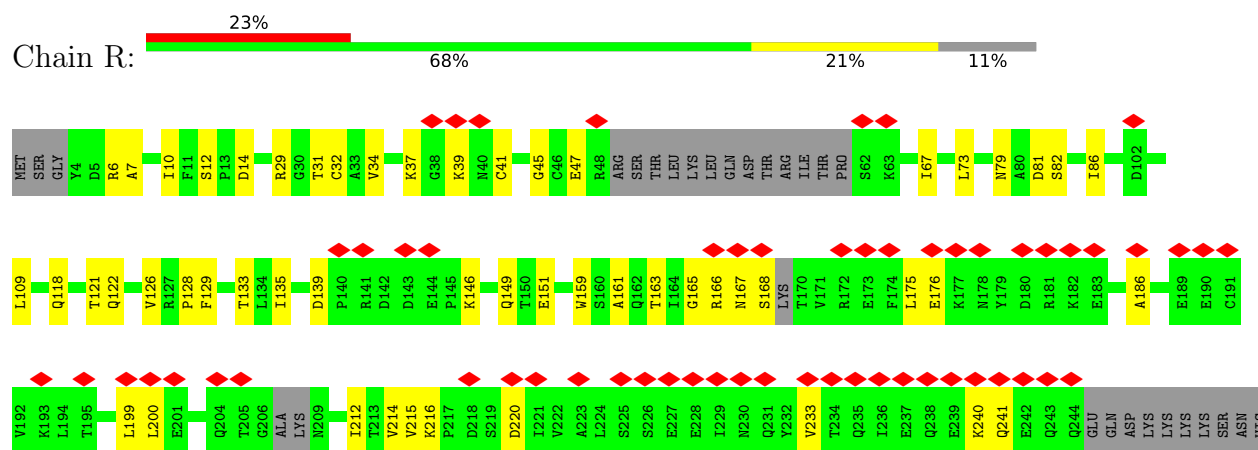
- Molecule 5: Proteasome subunit alpha type-2



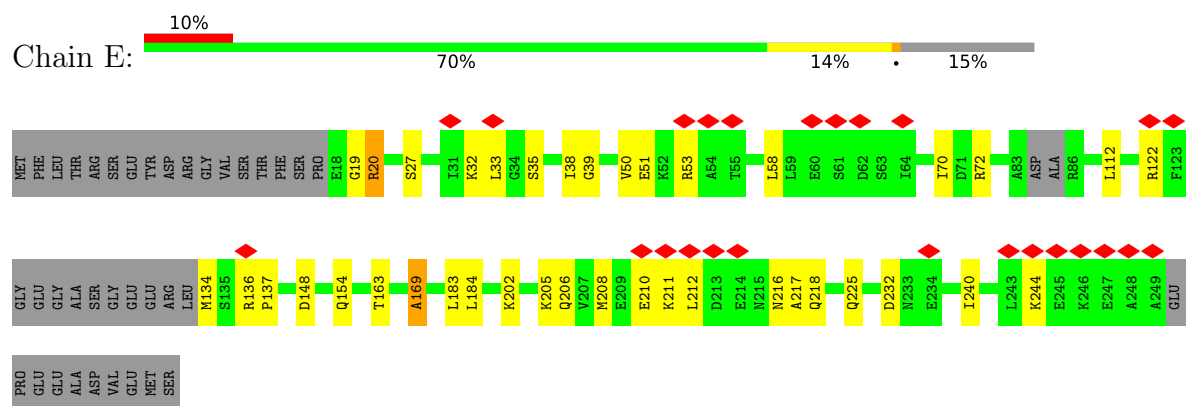
- Molecule 7: Proteasome subunit alpha type-4



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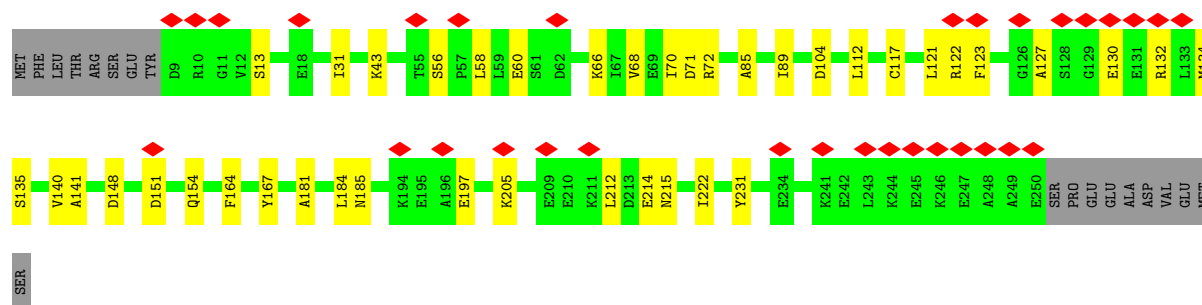


- Molecule 8: Proteasome subunit alpha type-5

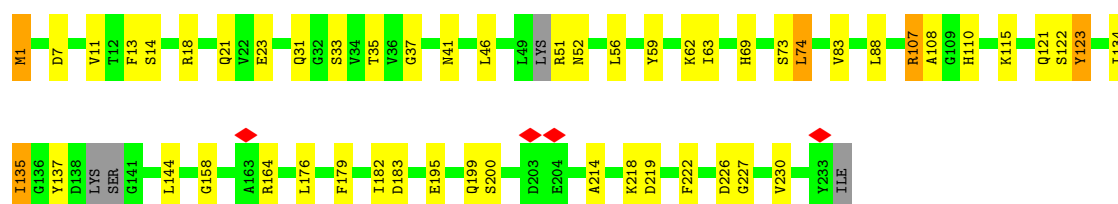
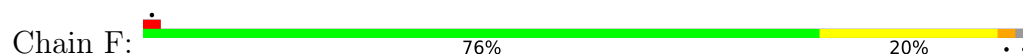


- Molecule 8: Proteasome subunit alpha type-5

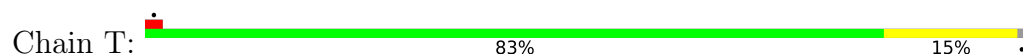




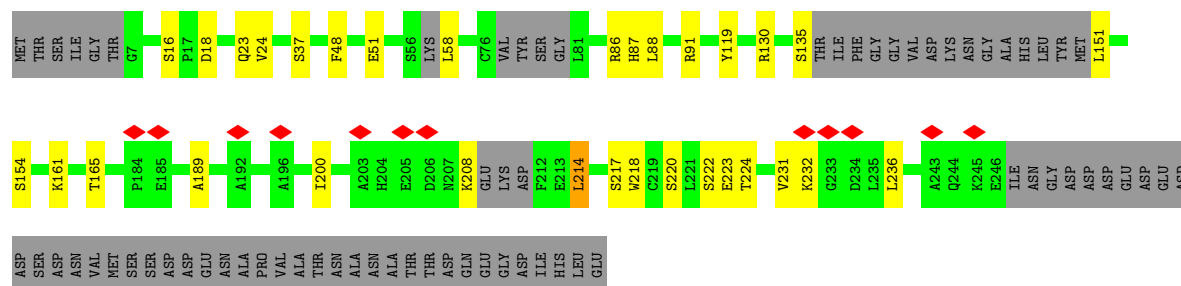
• Molecule 9: Proteasome subunit alpha type-6



• Molecule 9: Proteasome subunit alpha type-6

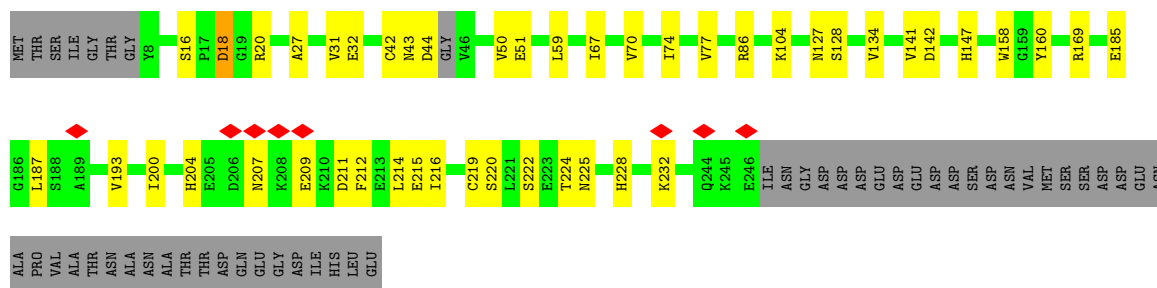


• Molecule 10: Probable proteasome subunit alpha type-7

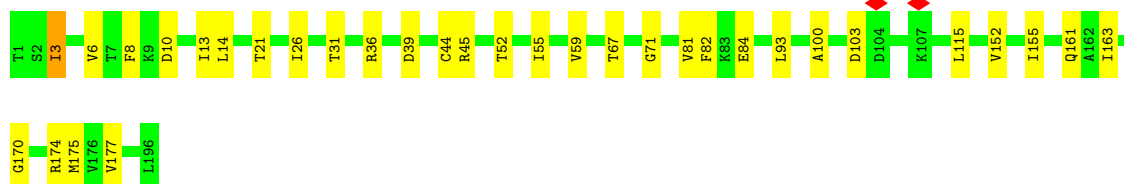
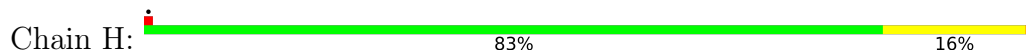


• Molecule 10: Probable proteasome subunit alpha type-7

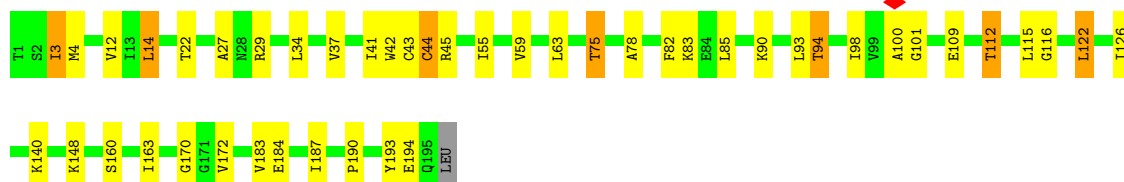
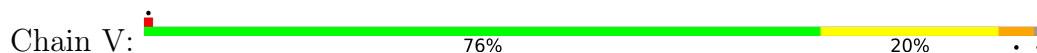




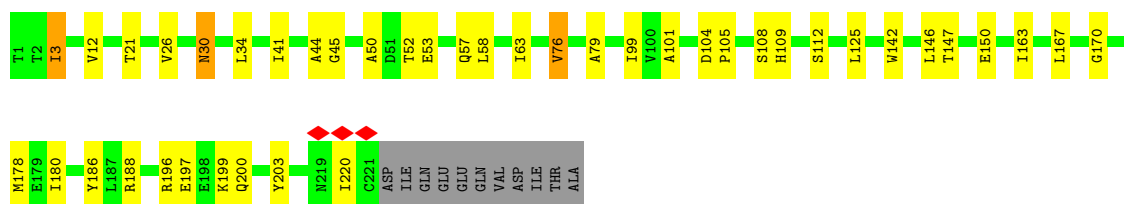
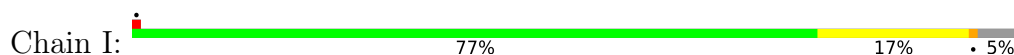
- Molecule 11: Proteasome subunit beta type-1



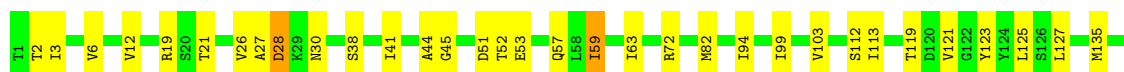
- Molecule 11: Proteasome subunit beta type-1

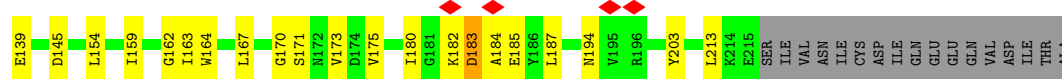


- Molecule 12: Proteasome subunit beta type-2



- Molecule 12: Proteasome subunit beta type-2





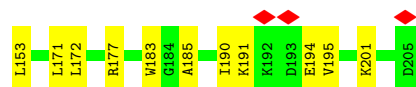
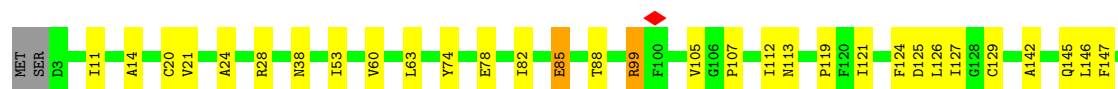
• Molecule 13: Proteasome subunit beta type-3

Chain J: 80% 17% ..



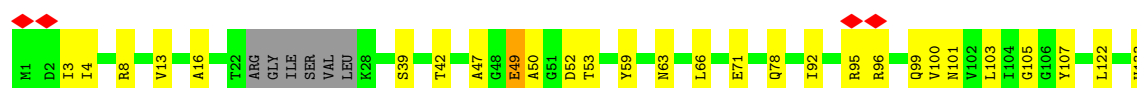
• Molecule 13: Proteasome subunit beta type-3

Chain X: 79% 20% ..



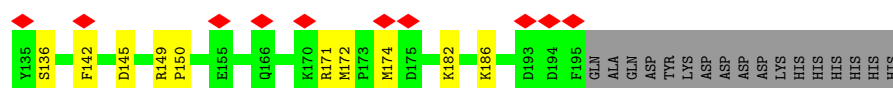
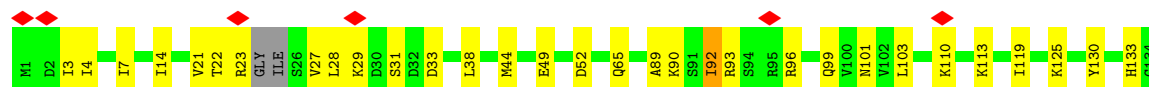
• Molecule 14: Proteasome subunit beta type-4

Chain K: 69% 19% 11%

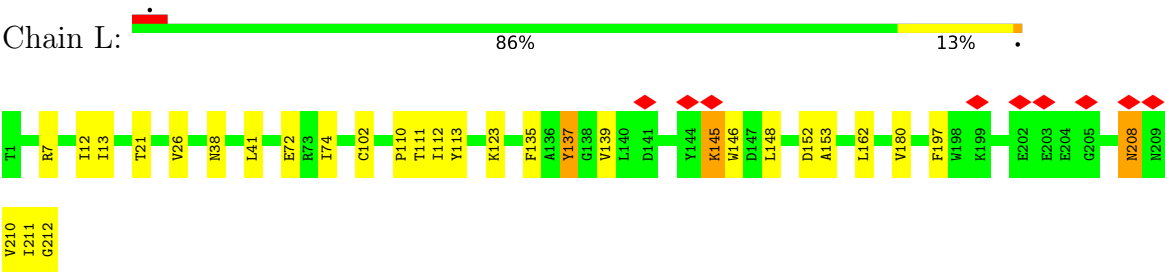


• Molecule 14: Proteasome subunit beta type-4

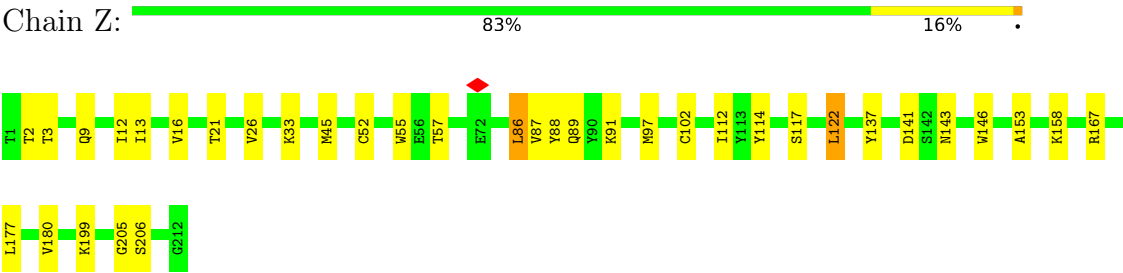
Chain Y: 8% 72% 19% 9%



• Molecule 15: Proteasome subunit beta type-5



● Molecule 15: Proteasome subunit beta type-5



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	129737	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.104	Depositor
Minimum map value	-1.371	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.054	Depositor
Recommended contour level	0.3	Depositor
Map size ($\text{\AA}$)	500.4, 500.4, 500.4	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.834, 0.834, 0.834	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	1	0.08	0/1785	0.26	0/2408
1	M	0.09	0/1777	0.26	0/2397
2	2	0.09	0/1821	0.28	0/2470
2	N	0.09	0/1817	0.27	0/2465
3	3	0.09	0/15586	0.22	0/21106
4	A	0.09	0/1941	0.24	0/2629
4	O	0.10	0/1905	0.24	0/2578
5	B	0.09	0/1813	0.26	0/2456
5	P	0.08	0/1886	0.23	0/2551
6	C	0.08	0/1800	0.22	0/2437
6	Q	0.09	0/1082	0.24	0/1466
7	D	0.09	0/1739	0.25	0/2349
7	R	0.08	0/1791	0.24	0/2422
8	E	0.07	0/1724	0.23	0/2320
8	S	0.07	0/1886	0.23	0/2541
9	F	0.09	0/1803	0.27	0/2436
9	T	0.08	0/1799	0.24	0/2433
10	G	0.09	0/1724	0.24	0/2323
10	U	0.09	0/1900	0.26	0/2564
11	H	0.09	0/1540	0.25	0/2087
11	V	0.10	0/1532	0.30	0/2076
12	I	0.09	0/1707	0.28	0/2315
12	W	0.09	0/1664	0.27	0/2256
13	J	0.09	0/1588	0.27	0/2143
13	X	0.08	0/1604	0.25	0/2166
14	K	0.09	0/1538	0.28	0/2072
14	Y	0.07	0/1582	0.22	0/2131
15	L	0.08	0/1680	0.24	0/2274
15	Z	0.10	0/1680	0.26	0/2274
All	All	0.09	0/63694	0.25	0/86145

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

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	1	1747	0	1700	26	0
1	M	1739	0	1696	23	0
2	2	1790	0	1793	26	0
2	N	1786	0	1790	29	0
3	3	15248	0	15246	162	0
4	A	1903	0	1898	17	0
4	O	1869	0	1860	34	0
5	B	1780	0	1798	19	0
5	P	1852	0	1867	23	0
6	C	1773	0	1777	25	0
6	Q	1059	0	1035	10	0
7	D	1716	0	1726	37	0
7	R	1766	0	1754	35	0
8	E	1703	0	1696	23	0
8	S	1861	0	1836	33	0
9	F	1777	0	1771	31	0
9	T	1772	0	1775	25	0
10	G	1692	0	1684	23	0
10	U	1861	0	1852	28	0
11	H	1511	0	1481	22	0
11	V	1503	0	1470	28	0
12	I	1676	0	1684	25	0
12	W	1633	0	1637	35	0
13	J	1559	0	1555	23	0
13	X	1574	0	1566	30	0
14	K	1511	0	1511	29	0
14	Y	1554	0	1558	24	0
15	L	1643	0	1595	19	0
15	Z	1643	0	1595	24	0
16	1	75	0	0	1	0
16	2	85	0	0	1	0
16	3	685	0	0	12	0
16	A	98	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	B	57	0	0	1	0
16	C	58	0	0	1	0
16	D	78	0	0	6	0
16	E	80	0	0	4	0
16	F	55	0	0	1	0
16	G	56	0	0	2	0
16	H	49	0	0	2	0
16	I	70	0	0	1	0
16	J	56	0	0	0	0
16	K	46	0	0	2	0
16	L	55	0	0	0	0
16	M	63	0	0	2	0
16	N	74	0	0	0	0
16	O	70	0	0	1	0
16	P	56	0	0	1	0
16	Q	37	0	0	0	0
16	R	79	0	0	3	0
16	S	76	0	0	2	0
16	T	61	0	0	2	0
16	U	82	0	0	3	0
16	V	43	0	0	1	0
16	W	64	0	0	1	0
16	X	43	0	0	0	0
16	Y	75	0	0	4	0
16	Z	57	0	0	3	0
All	All	64984	0	62206	802	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 6.

The worst 5 of 802 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)
2:2:15:LYS:HE2	2:2:127:LEU:HB3	1.64	0.79
3:3:1348:LYS:HE2	3:3:1352:LYS:HZ3	1.53	0.74
11:V:14:LEU:HD13	11:V:43:CYS:HA	1.70	0.73
10:G:87:HIS:HE2	10:G:119:TYR:HH	1.37	0.71
1:1:91:ARG:HD2	8:S:104:ASP:HB2	1.71	0.70

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	1	219/222 (99%)	216 (99%)	3 (1%)	0	100	100
1	M	218/222 (98%)	209 (96%)	9 (4%)	0	100	100
2	2	227/233 (97%)	222 (98%)	5 (2%)	0	100	100
2	N	226/233 (97%)	218 (96%)	8 (4%)	0	100	100
3	3	1857/2143 (87%)	1795 (97%)	62 (3%)	0	100	100
4	A	238/252 (94%)	230 (97%)	8 (3%)	0	100	100
4	O	230/252 (91%)	219 (95%)	11 (5%)	0	100	100
5	B	231/250 (92%)	224 (97%)	5 (2%)	2 (1%)	14	22
5	P	238/250 (95%)	235 (99%)	3 (1%)	0	100	100
6	C	226/258 (88%)	218 (96%)	8 (4%)	0	100	100
6	Q	129/258 (50%)	120 (93%)	9 (7%)	0	100	100
7	D	211/254 (83%)	197 (93%)	14 (7%)	0	100	100
7	R	217/254 (85%)	209 (96%)	8 (4%)	0	100	100
8	E	214/260 (82%)	206 (96%)	7 (3%)	1 (0%)	24	37
8	S	240/260 (92%)	236 (98%)	4 (2%)	0	100	100
9	F	225/234 (96%)	213 (95%)	11 (5%)	1 (0%)	30	43
9	T	229/234 (98%)	223 (97%)	6 (3%)	0	100	100
10	G	207/288 (72%)	199 (96%)	8 (4%)	0	100	100
10	U	234/288 (81%)	224 (96%)	9 (4%)	1 (0%)	30	43
11	H	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
11	V	193/196 (98%)	179 (93%)	13 (7%)	1 (0%)	24	37
12	I	219/232 (94%)	214 (98%)	5 (2%)	0	100	100
12	W	213/232 (92%)	207 (97%)	6 (3%)	0	100	100
13	J	199/205 (97%)	190 (96%)	9 (4%)	0	100	100
13	X	201/205 (98%)	189 (94%)	11 (6%)	1 (0%)	24	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	K	184/212 (87%)	172 (94%)	12 (6%)	0	100	100
14	Y	189/212 (89%)	186 (98%)	3 (2%)	0	100	100
15	L	210/212 (99%)	207 (99%)	3 (1%)	0	100	100
15	Z	210/212 (99%)	202 (96%)	8 (4%)	0	100	100
All	All	7828/8759 (89%)	7548 (96%)	273 (4%)	7 (0%)	49	64

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	B	203	GLU
13	X	195	VAL
5	B	34	SER
8	E	169	ALA
9	F	123	TYR

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	1	184/185 (100%)	182 (99%)	2 (1%)	65	82
1	M	183/185 (99%)	175 (96%)	8 (4%)	25	43
2	2	195/199 (98%)	191 (98%)	4 (2%)	47	69
2	N	195/199 (98%)	190 (97%)	5 (3%)	40	63
3	3	1728/1963 (88%)	1697 (98%)	31 (2%)	51	73
4	A	206/210 (98%)	203 (98%)	3 (2%)	57	77
4	O	202/210 (96%)	193 (96%)	9 (4%)	24	42
5	B	193/209 (92%)	191 (99%)	2 (1%)	68	84
5	P	202/209 (97%)	194 (96%)	8 (4%)	28	47
6	C	188/216 (87%)	186 (99%)	2 (1%)	65	82
6	Q	109/216 (50%)	108 (99%)	1 (1%)	70	85
7	D	194/226 (86%)	189 (97%)	5 (3%)	40	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	R	199/226 (88%)	195 (98%)	4 (2%)	48	70
8	E	182/215 (85%)	177 (97%)	5 (3%)	39	62
8	S	198/215 (92%)	196 (99%)	2 (1%)	68	84
9	F	190/193 (98%)	179 (94%)	11 (6%)	18	32
9	T	190/193 (98%)	187 (98%)	3 (2%)	55	76
10	G	180/239 (75%)	176 (98%)	4 (2%)	45	67
10	U	198/239 (83%)	192 (97%)	6 (3%)	36	58
11	H	162/162 (100%)	161 (99%)	1 (1%)	78	89
11	V	161/162 (99%)	152 (94%)	9 (6%)	19	33
12	I	180/190 (95%)	173 (96%)	7 (4%)	28	48
12	W	174/190 (92%)	167 (96%)	7 (4%)	28	47
13	J	169/173 (98%)	163 (96%)	6 (4%)	31	52
13	X	171/173 (99%)	169 (99%)	2 (1%)	63	81
14	K	167/189 (88%)	166 (99%)	1 (1%)	78	89
14	Y	172/189 (91%)	168 (98%)	4 (2%)	44	66
15	L	169/169 (100%)	163 (96%)	6 (4%)	31	52
15	Z	169/169 (100%)	166 (98%)	3 (2%)	51	73
All	All	6810/7513 (91%)	6649 (98%)	161 (2%)	43	65

5 of 161 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	P	43	VAL
11	V	112	THR
5	P	185	LEU
10	U	18	ASP
12	W	182	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
15	L	188	HIS
2	N	62	HIS
15	Z	166	HIS
15	L	191	HIS

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Mol	Chain	Res	Type
1	M	70	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.

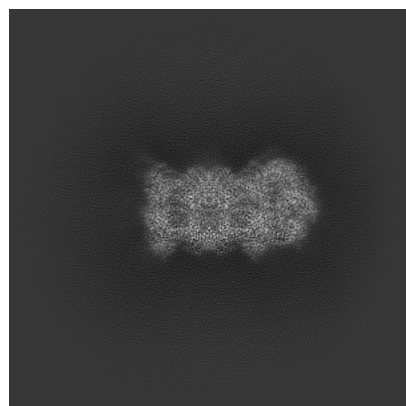
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51221. These allow visual inspection of the internal detail of the map and identification of artifacts.

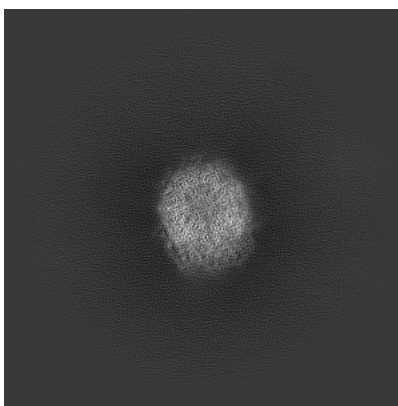
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

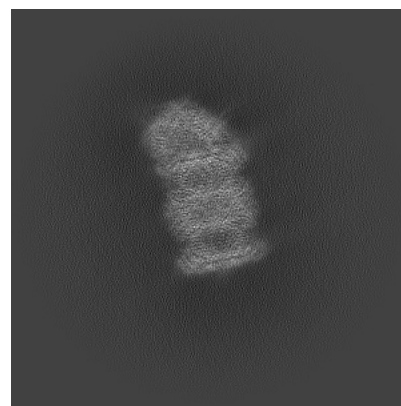
6.1.1 Primary map



X

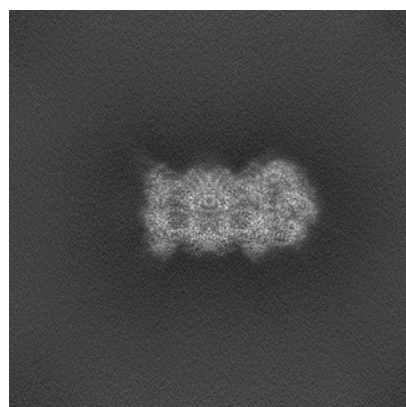


Y

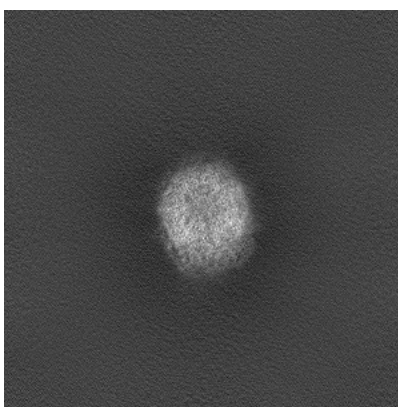


Z

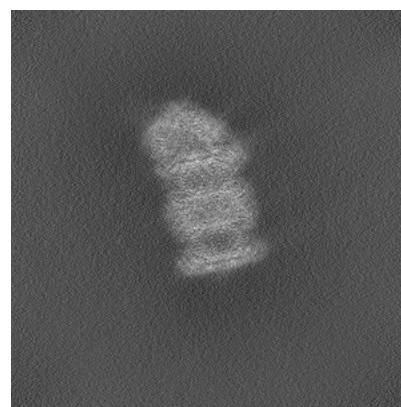
6.1.2 Raw map



X



Y

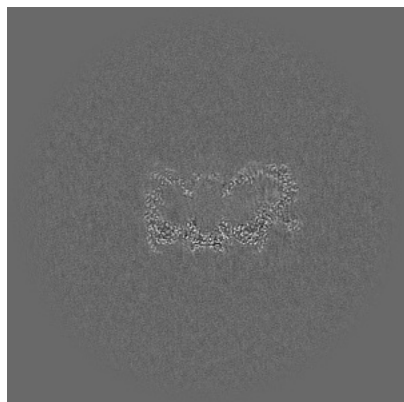


Z

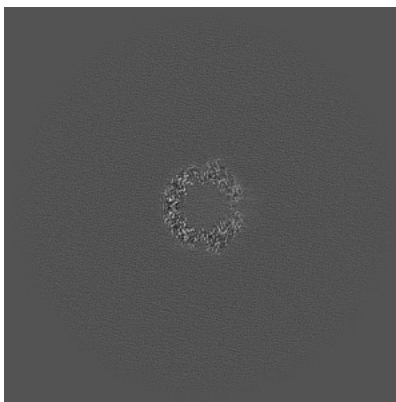
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

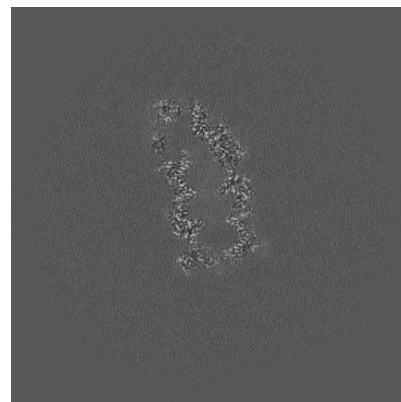
6.2.1 Primary map



X Index: 300

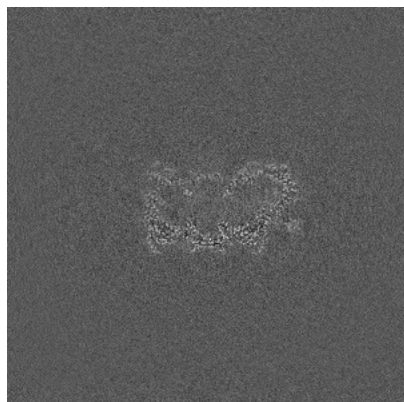


Y Index: 300

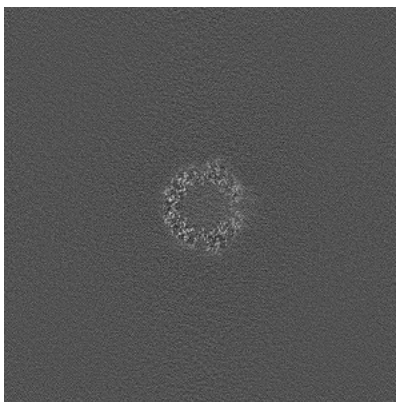


Z Index: 300

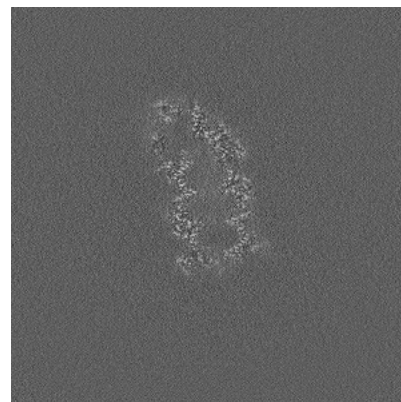
6.2.2 Raw map



X Index: 300



Y Index: 300

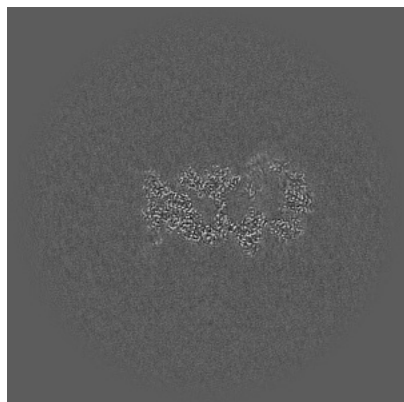


Z Index: 300

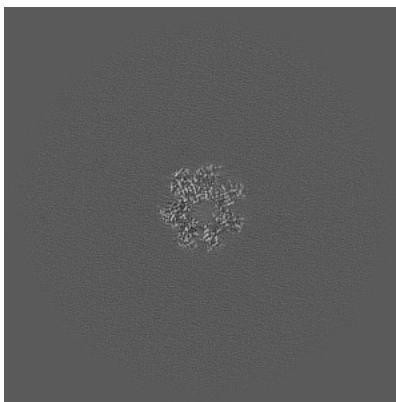
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

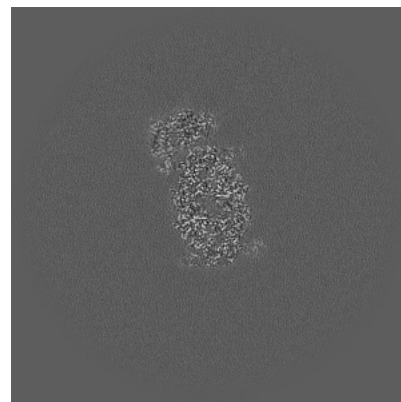
6.3.1 Primary map



X Index: 272

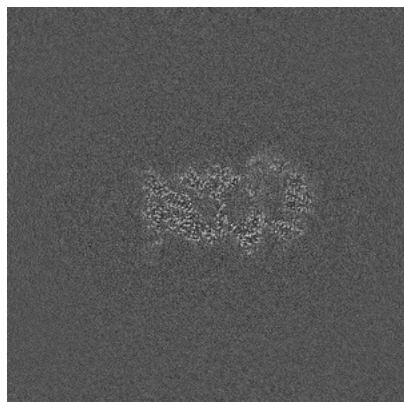


Y Index: 327

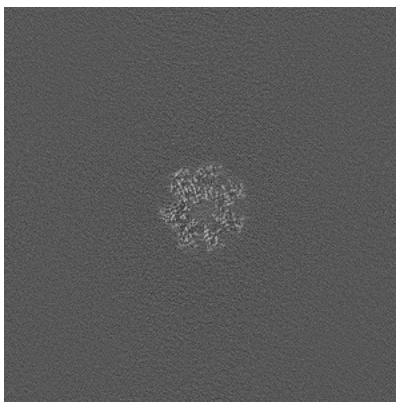


Z Index: 268

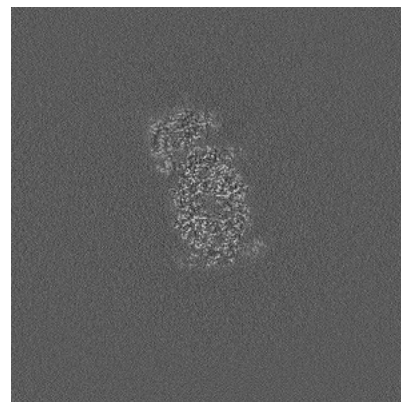
6.3.2 Raw map



X Index: 272



Y Index: 327

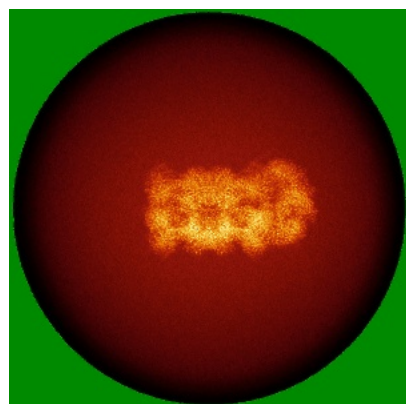


Z Index: 268

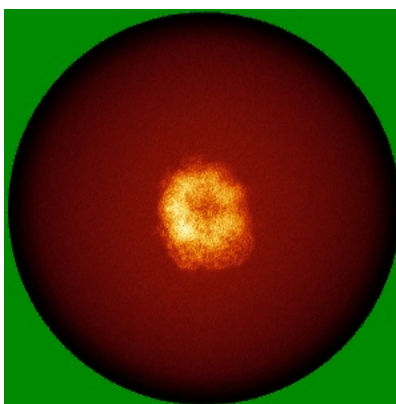
The images above show the largest variance slices of the map in three orthogonal directions.

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

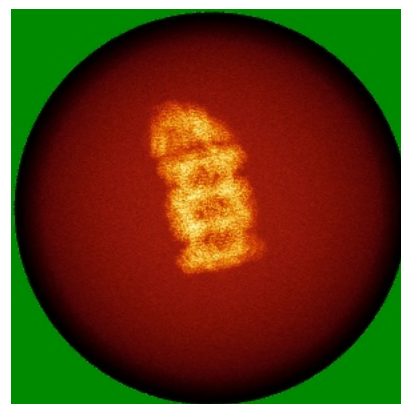
6.4.1 Primary map



X

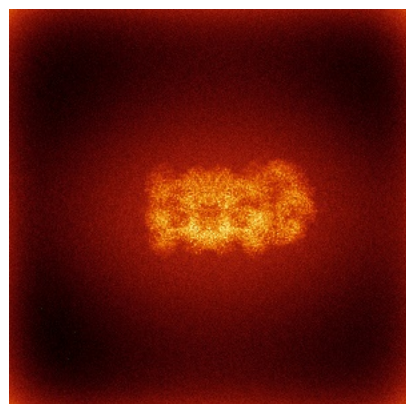


Y

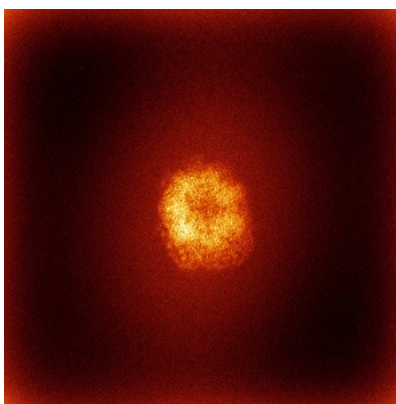


Z

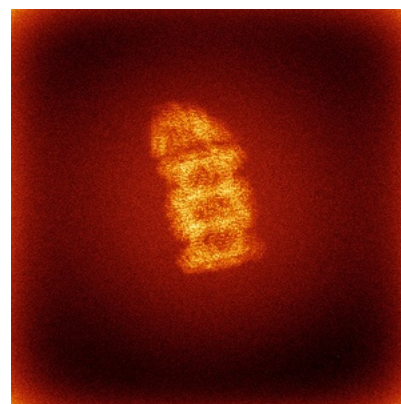
6.4.2 Raw map



X



Y

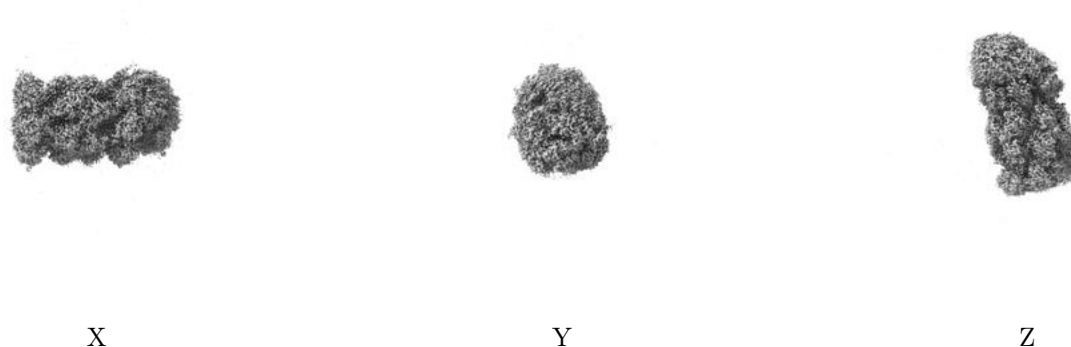


Z

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.

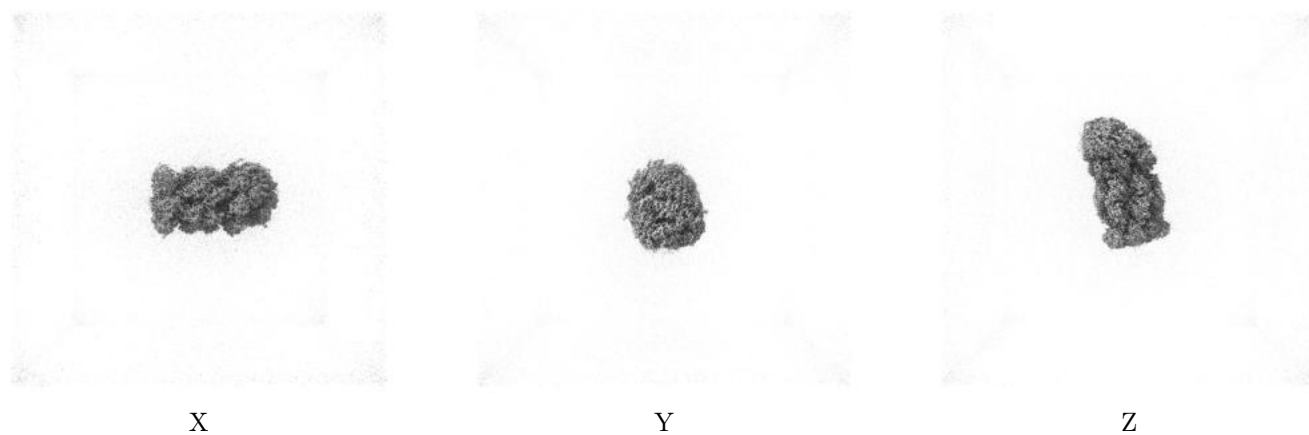
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. 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



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.

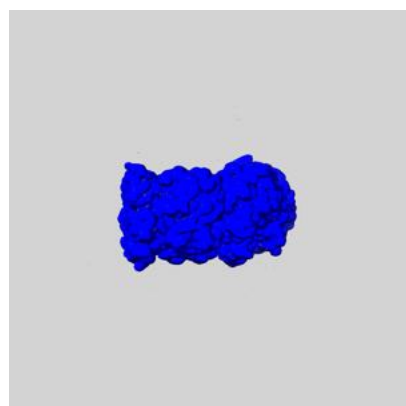
6.6 Mask visualisation [i](#)

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

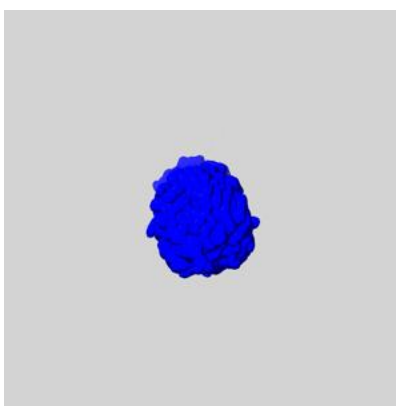
A mask typically either:

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

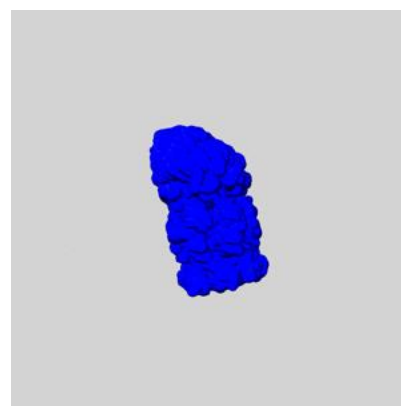
6.6.1 emd_51221_msk_1.map [i](#)



X



Y

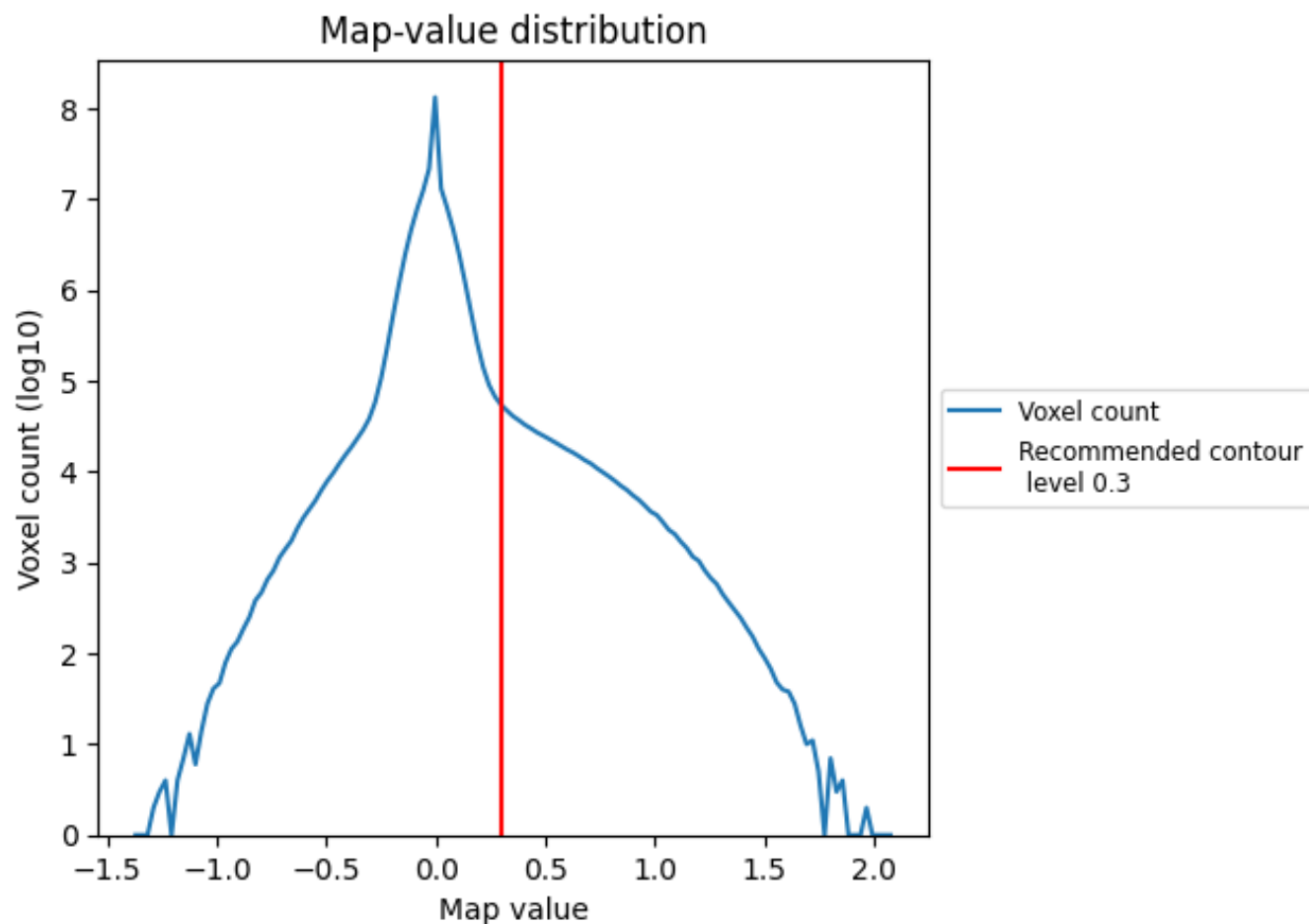


Z

7 Map analysis [i](#)

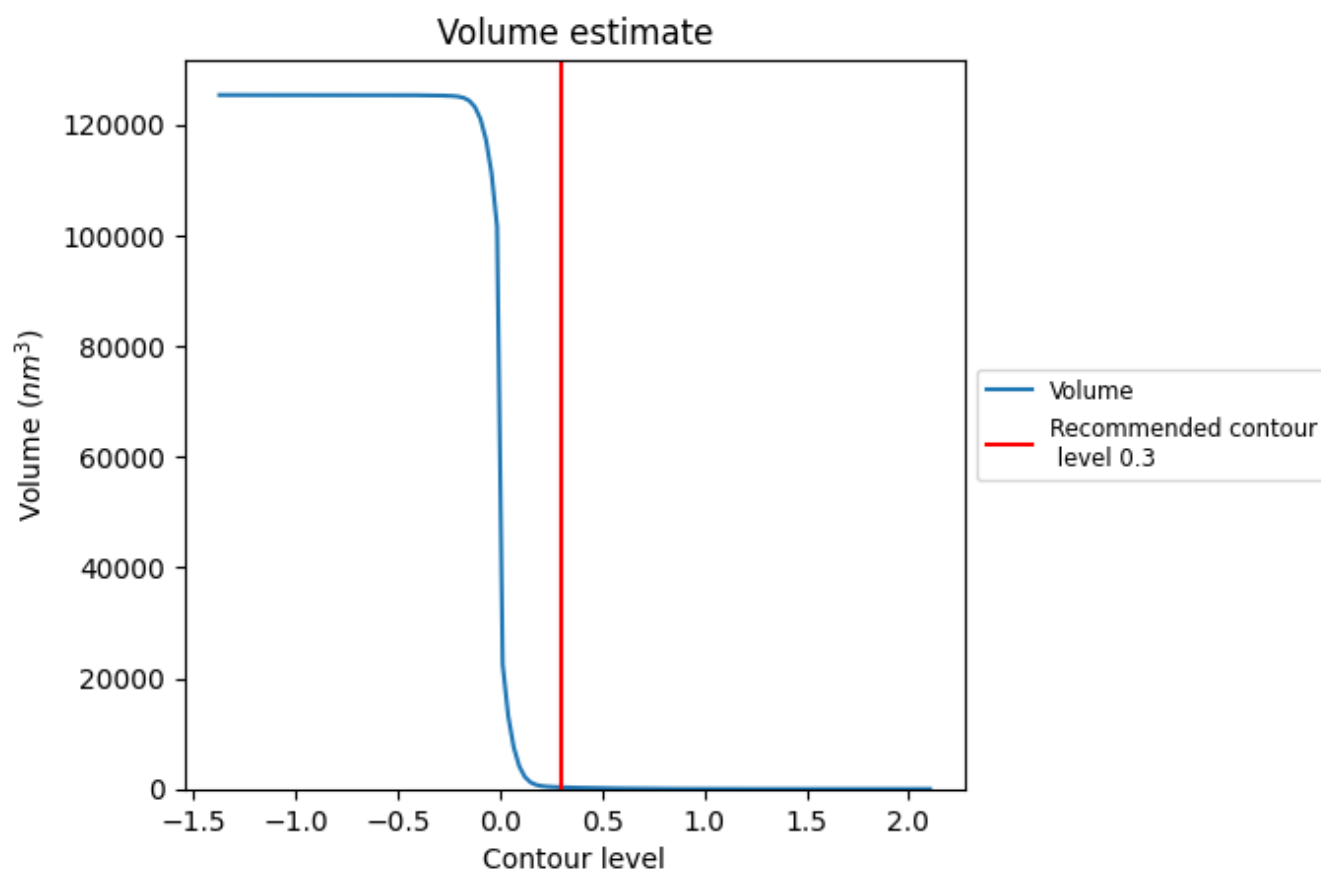
This section contains the results of statistical analysis of the map.

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.

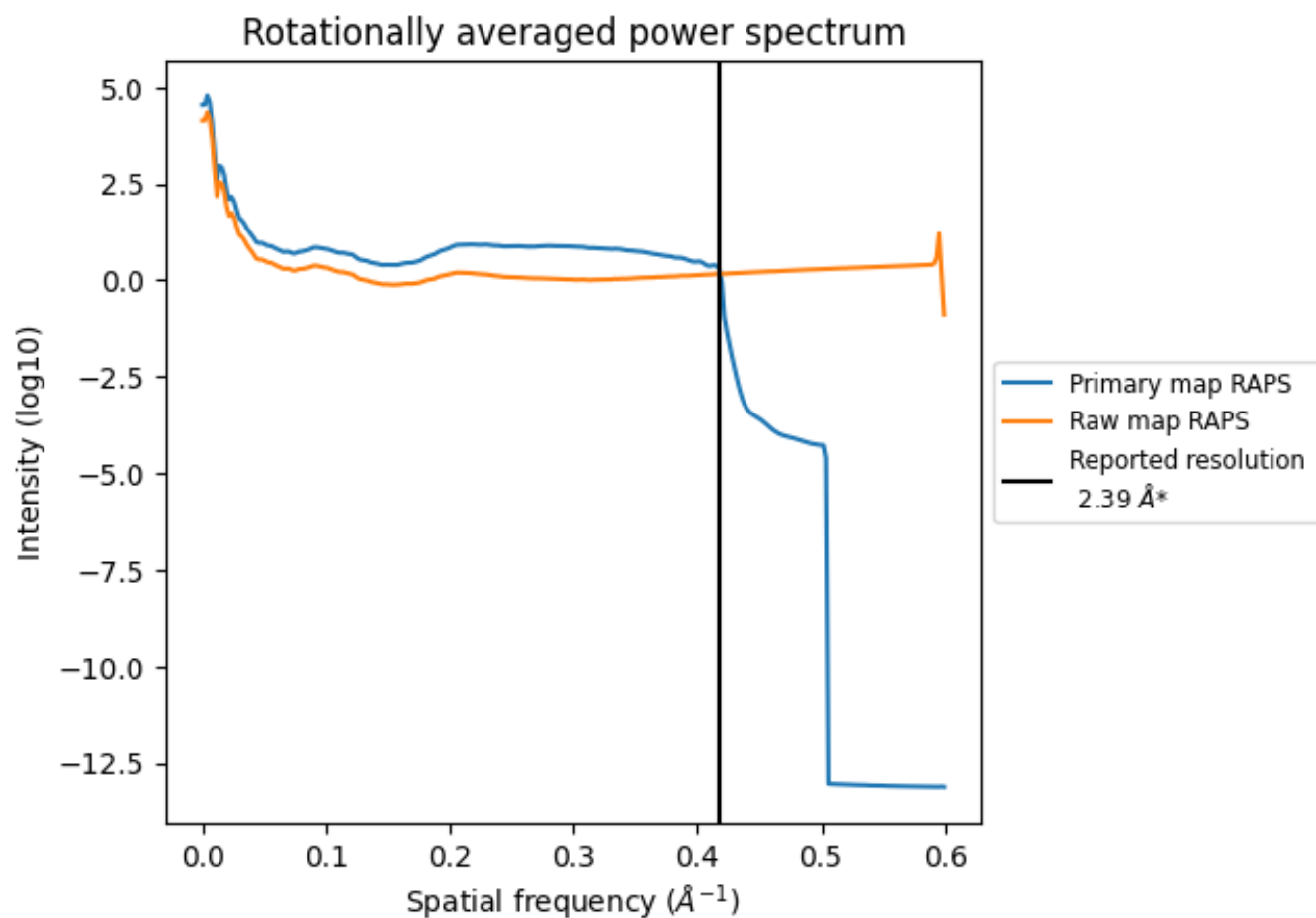
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 302 nm³; this corresponds to an approximate mass of 273 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 ⓘ

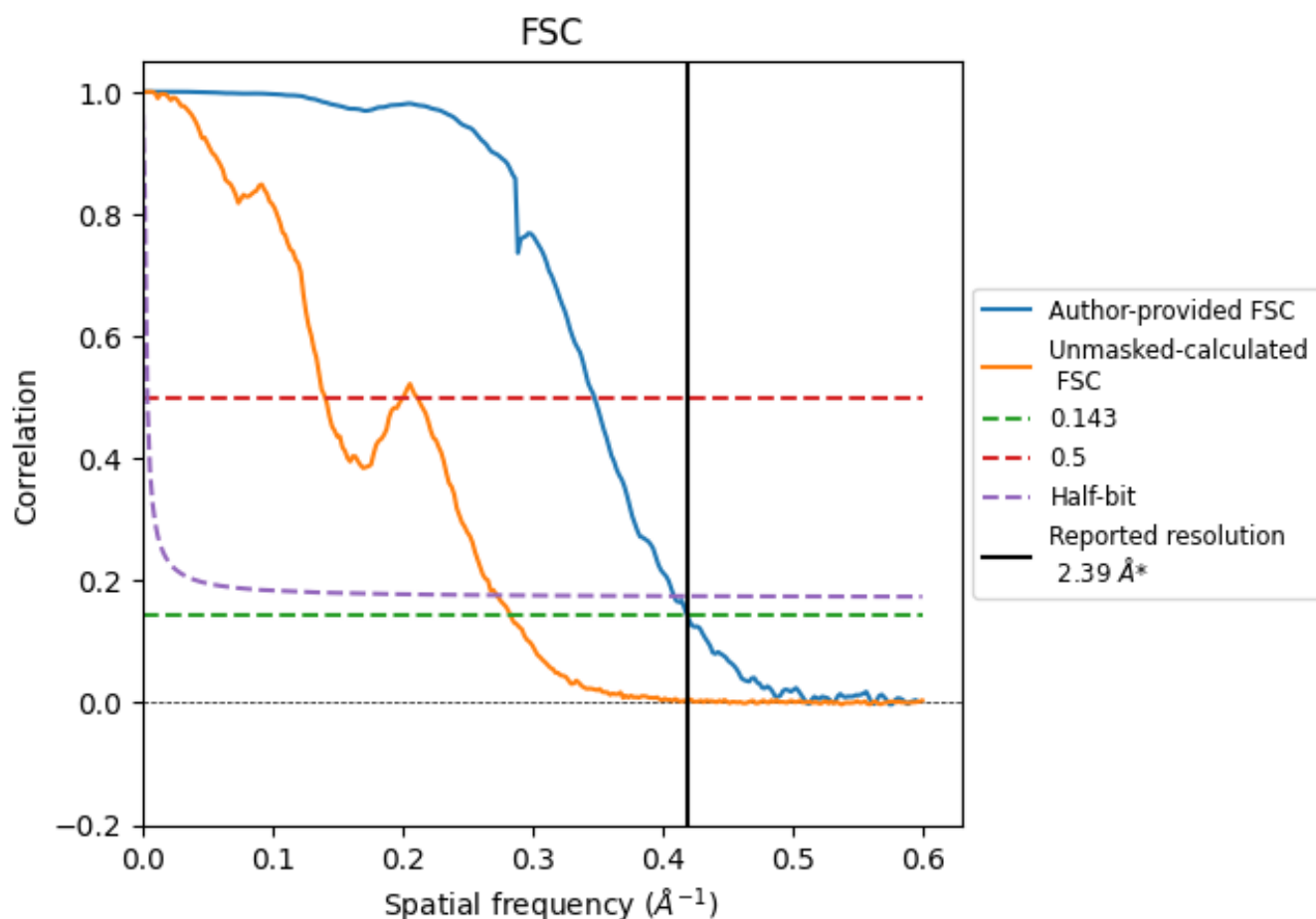


*Reported resolution corresponds to spatial frequency of 0.418 $\text{\AA}^{-1}$

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 0.418 Å⁻¹

8.2 Resolution estimates [i](#)

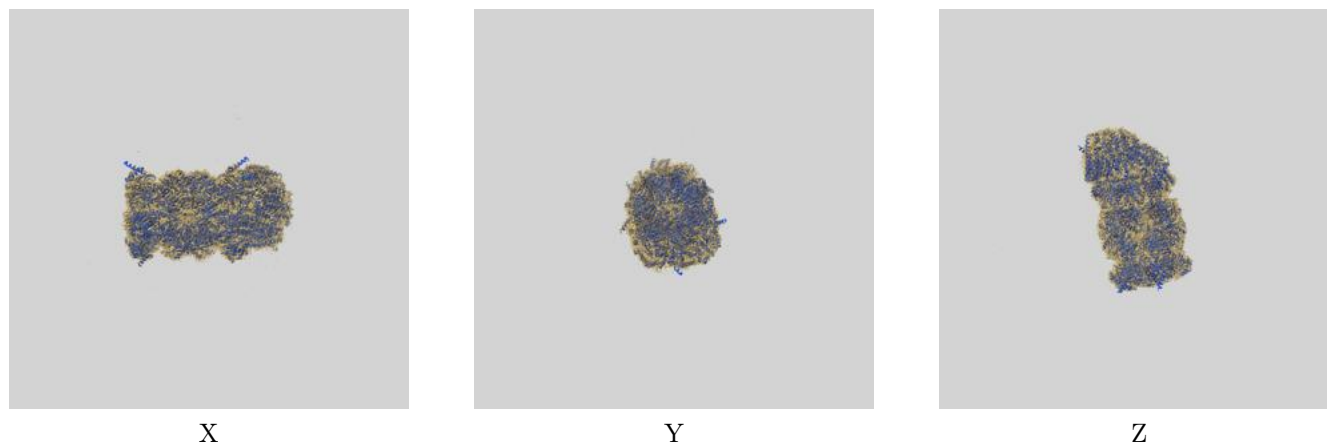
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.39	-	-
Author-provided FSC curve	2.39	2.88	2.45
Unmasked-calculated*	3.53	7.12	3.67

*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 3.53 differs from the reported value 2.39 by more than 10 %

9 Map-model fit [i](#)

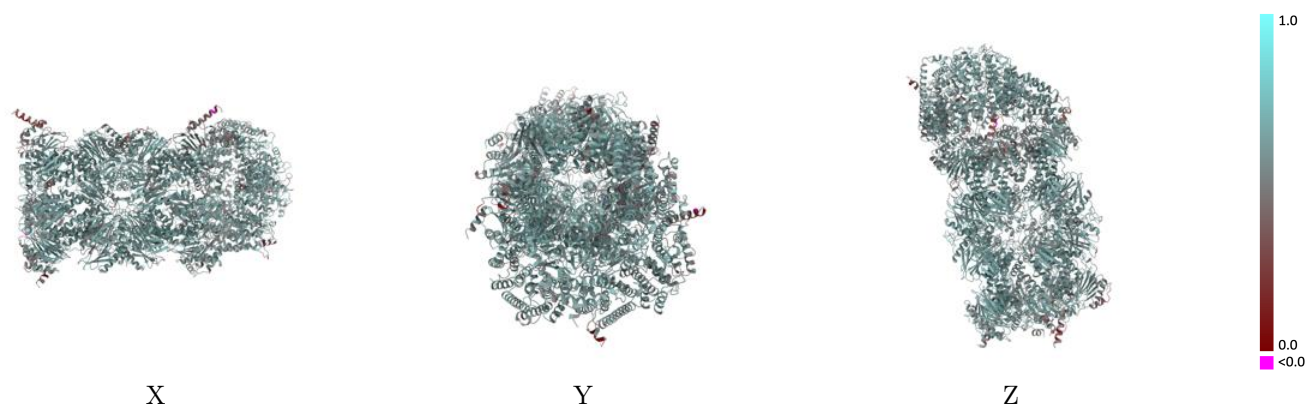
This section contains information regarding the fit between EMDB map EMD-51221 and PDB model 9GBK. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



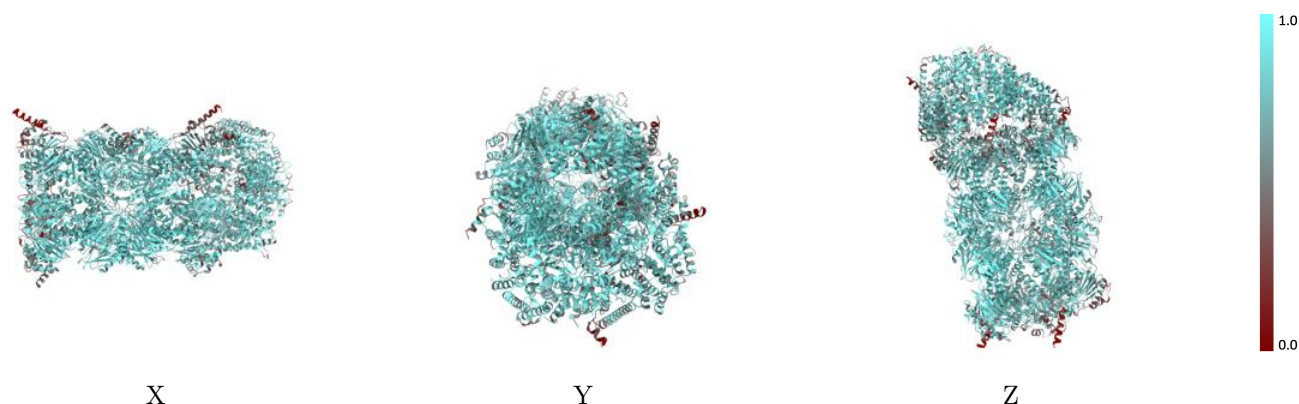
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



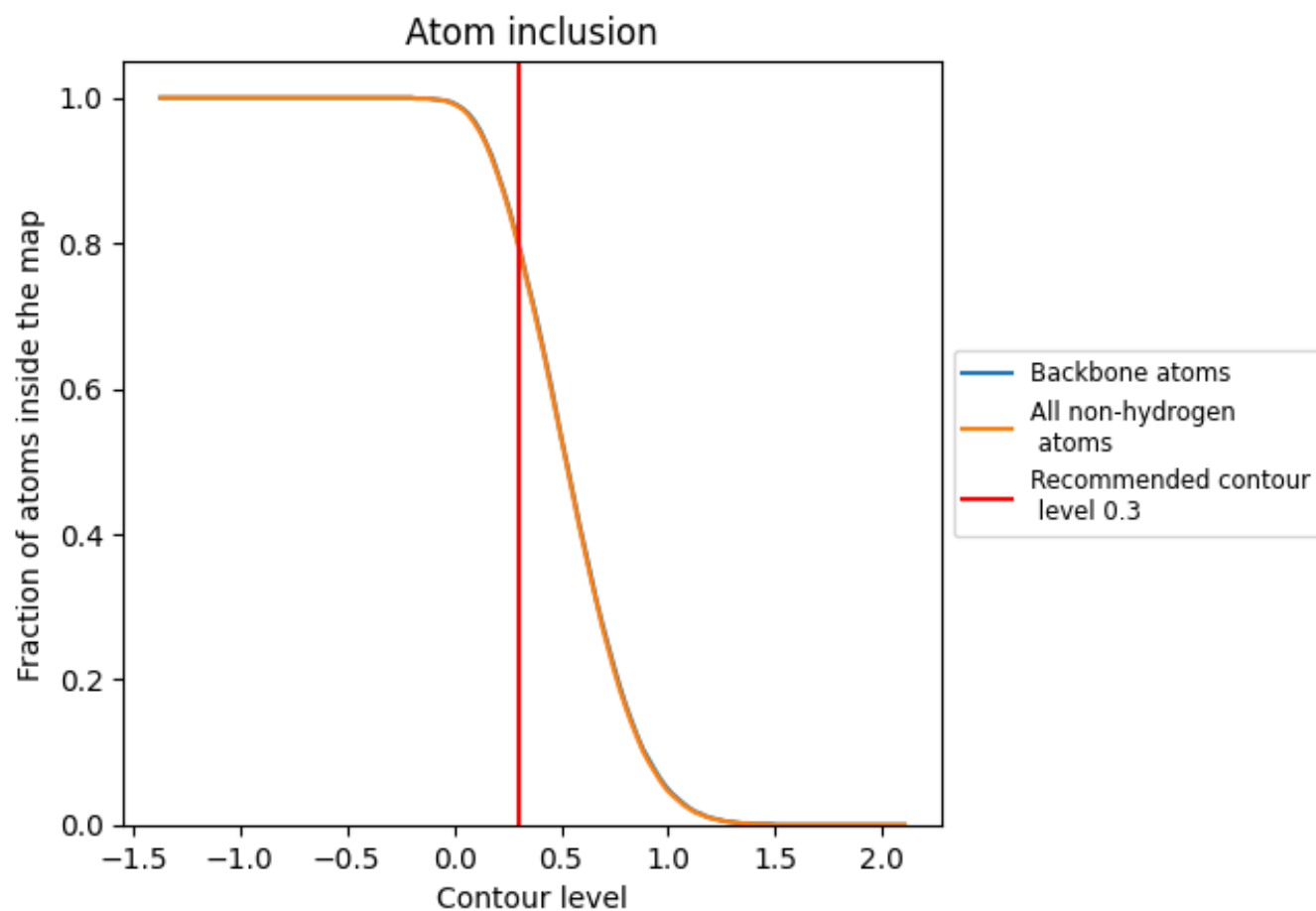
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 80% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7970	 0.5850
1	 0.9010	 0.6330
2	 0.9250	 0.6370
3	 0.7760	 0.5720
A	 0.8440	 0.6020
B	 0.8510	 0.6110
C	 0.7090	 0.5570
D	 0.5600	 0.4820
E	 0.7420	 0.5620
F	 0.8470	 0.5850
G	 0.8140	 0.5760
H	 0.8930	 0.6120
I	 0.8920	 0.6170
J	 0.9100	 0.6400
K	 0.8020	 0.5870
L	 0.8250	 0.5930
M	 0.8520	 0.6020
N	 0.8990	 0.6180
O	 0.7770	 0.5760
P	 0.6970	 0.5590
Q	 0.7380	 0.5660
R	 0.6110	 0.5340
S	 0.7360	 0.5840
T	 0.8410	 0.6080
U	 0.8310	 0.6030
V	 0.8680	 0.5840
W	 0.8450	 0.5850
X	 0.8280	 0.5930
Y	 0.7630	 0.5790
Z	 0.8610	 0.6090

