



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 10:16 AM UTC

PDB ID : 7V66 / pdb_00007v66
EMDB ID : EMD-31736
Title : Structure of Apoferritin
Authors : Zhang, X.; Wu, C.; Shi, H.
Deposited on : 2021-08-19
Resolution : 1.89 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:

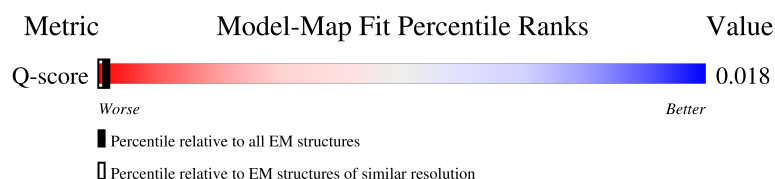
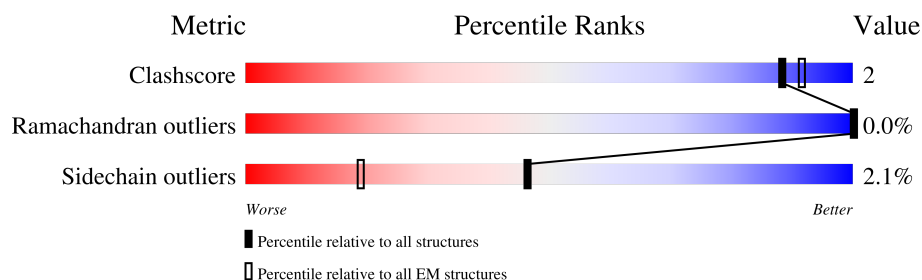
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 1.89 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	1004 (1.39 - 2.38)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	172	94% 94% 6%
1	B	172	94% 92% 8%
1	C	172	94% 92% 8%
1	D	172	94% 92% 8%

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Mol	Chain	Length	Quality of chain
1	E	172	94% 8%
1	F	172	94% 7%
1	G	172	94% 8%
1	H	172	94% 8%
1	I	172	94% 8%
1	J	172	94% 6%
1	K	172	94% 7%
1	L	172	94% 6%
1	M	172	94% 7%
1	N	172	94% 7%
1	O	172	94% 8%
1	P	172	94% 8%
1	Q	172	94% 6%
1	R	172	94% 6%
1	S	172	94% 6% .
1	T	172	94% 9%
1	U	172	94% 96% .
1	V	172	94% 8%
1	W	172	94% 89% 10% ..
1	X	172	94% 93% 7%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 33216 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.

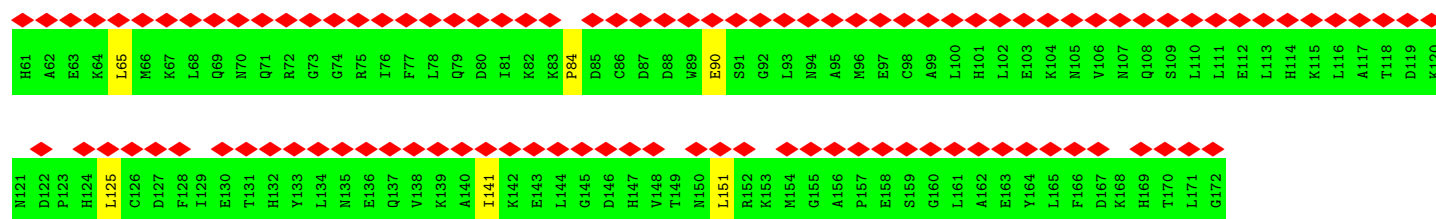
- Molecule 1 is a protein called Ferritin heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	U	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	A	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	B	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	C	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	D	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	E	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	F	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	G	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	H	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	I	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	J	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	K	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	L	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	M	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	N	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	O	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		
1	P	172	Total	C	N	O	S	0	0
			1384	871	242	264	7		

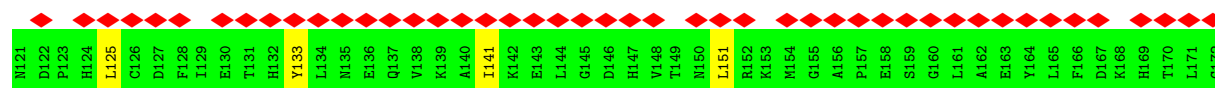
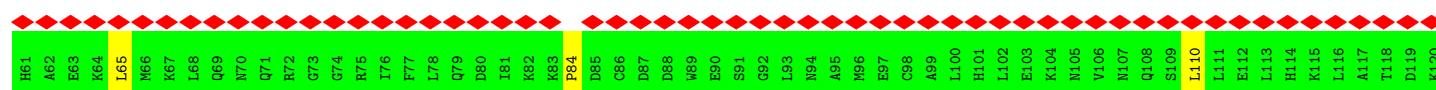
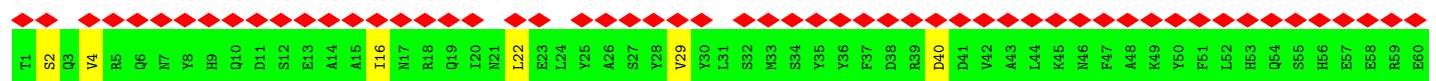
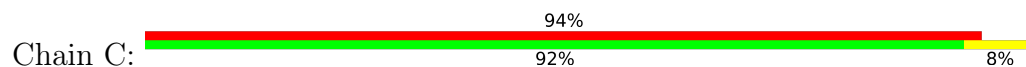
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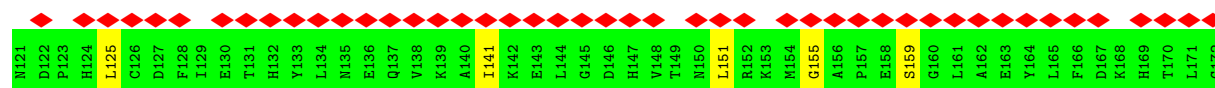
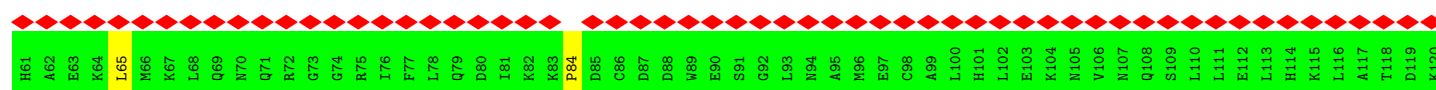
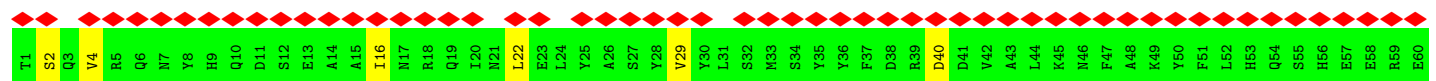
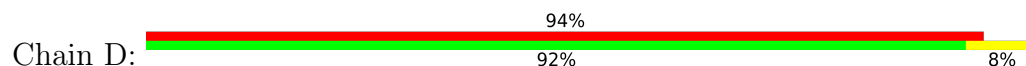
Mol	Chain	Residues	Atoms					AltConf	Trace
1	Q	172	Total 1384	C 871	N 242	O 264	S 7	0	0
1	R	172	Total 1384	C 871	N 242	O 264	S 7	0	0
1	S	172	Total 1384	C 871	N 242	O 264	S 7	0	0
1	T	172	Total 1384	C 871	N 242	O 264	S 7	0	0
1	V	172	Total 1384	C 871	N 242	O 264	S 7	0	0
1	W	172	Total 1384	C 871	N 242	O 264	S 7	0	0
1	X	172	Total 1384	C 871	N 242	O 264	S 7	0	0



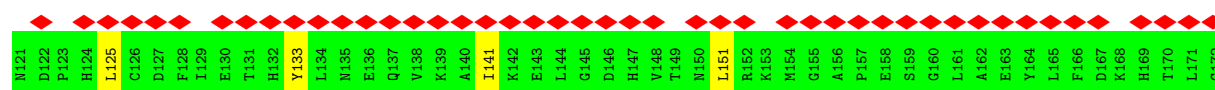
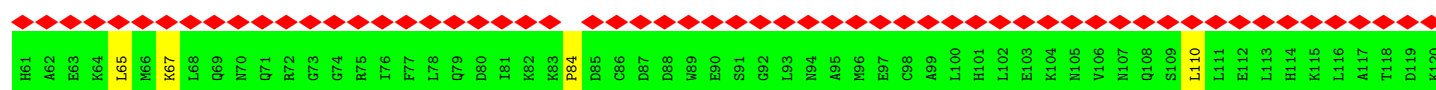
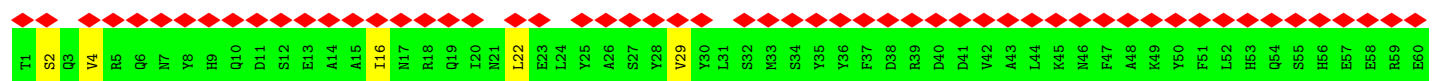
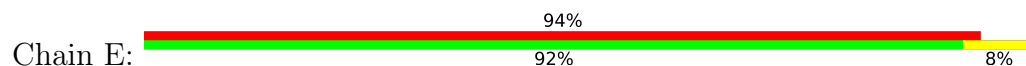
• Molecule 1: Ferritin heavy chain



• Molecule 1: Ferritin heavy chain

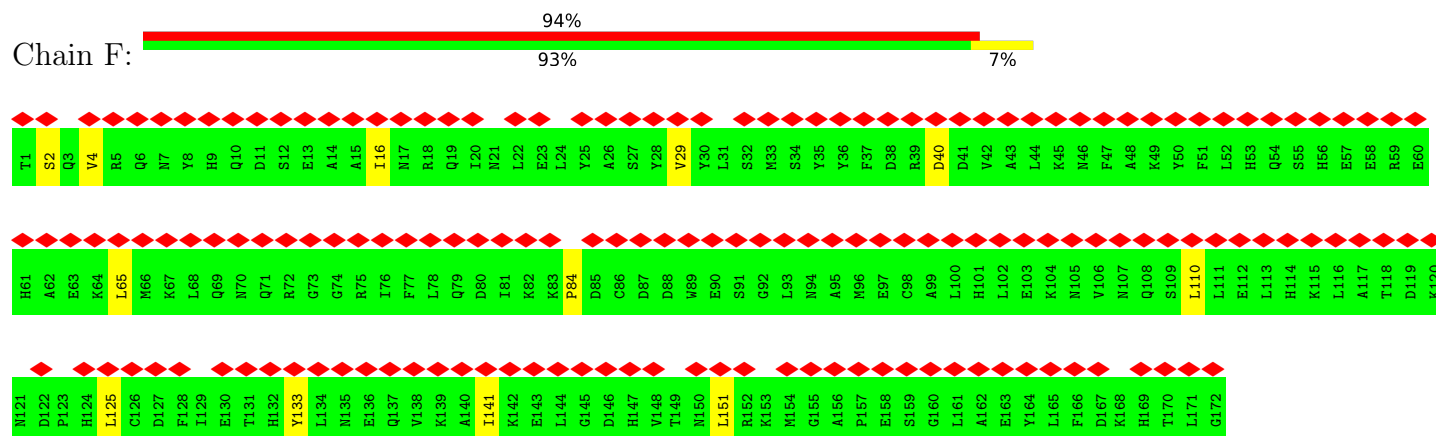


• Molecule 1: Ferritin heavy chain



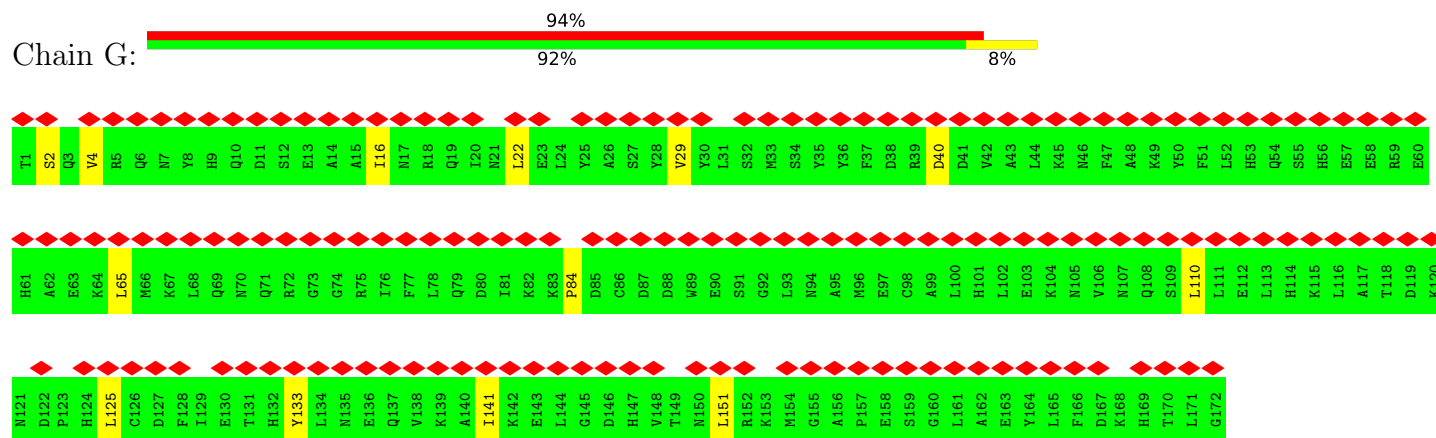
● Molecule 1: Ferritin heavy chain

Chain F:



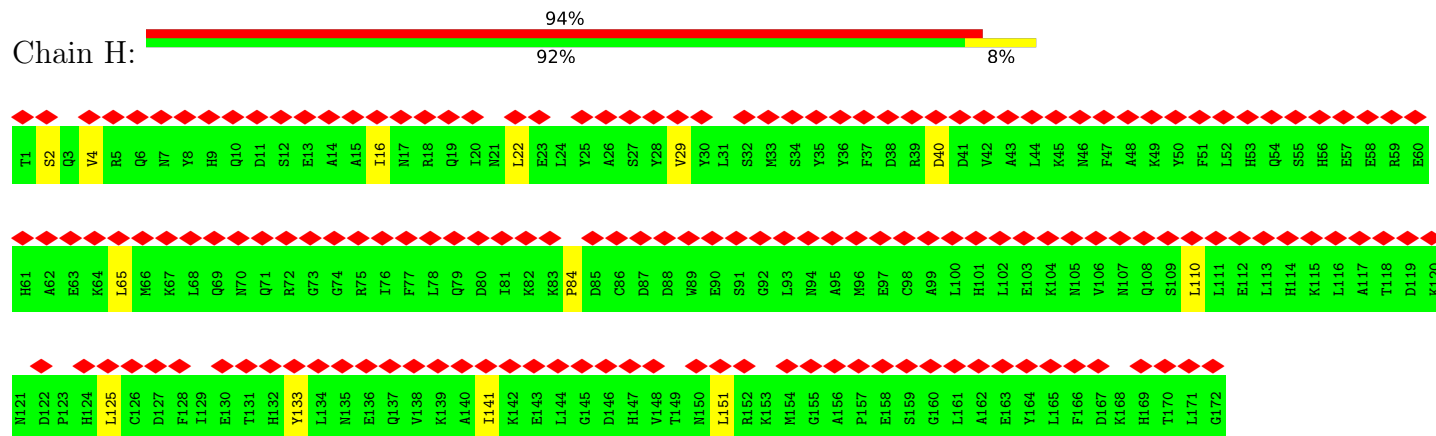
● Molecule 1: Ferritin heavy chain

Chain G:



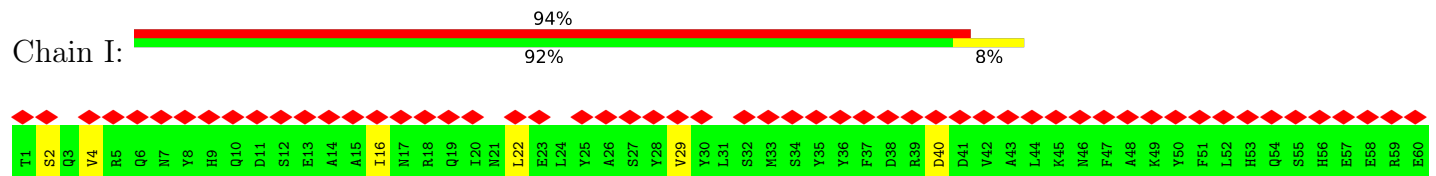
● Molecule 1: Ferritin heavy chain

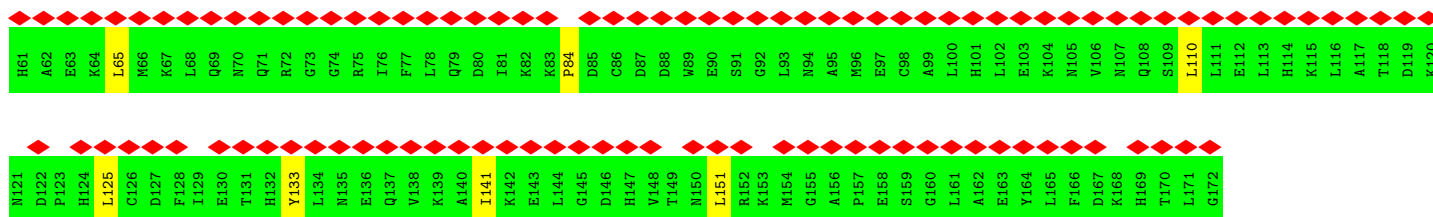
Chain H:



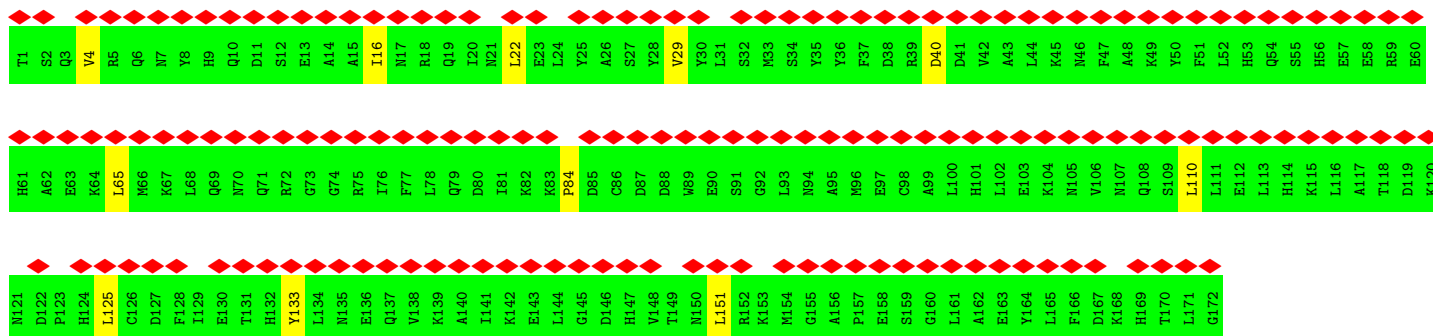
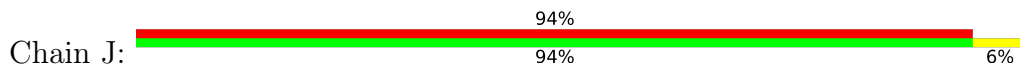
● Molecule 1: Ferritin heavy chain

Chain I:

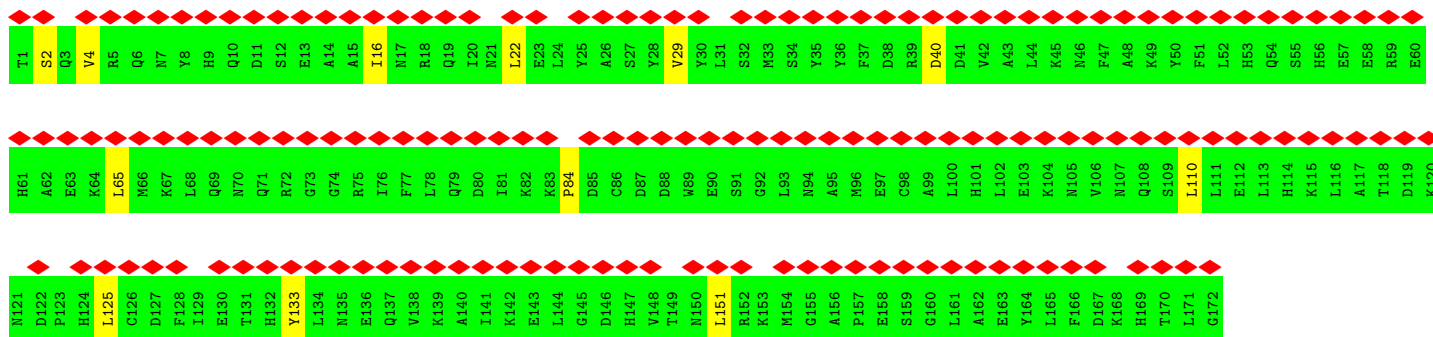




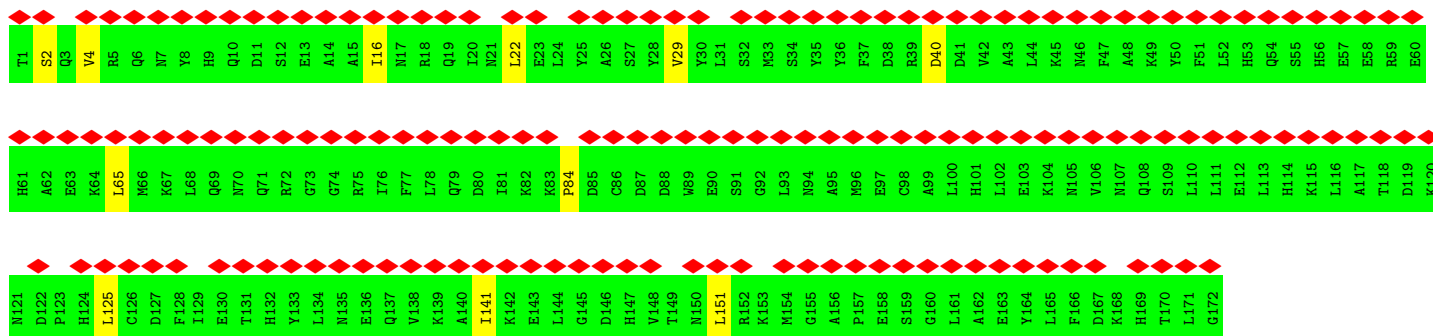
• Molecule 1: Ferritin heavy chain



• Molecule 1: Ferritin heavy chain

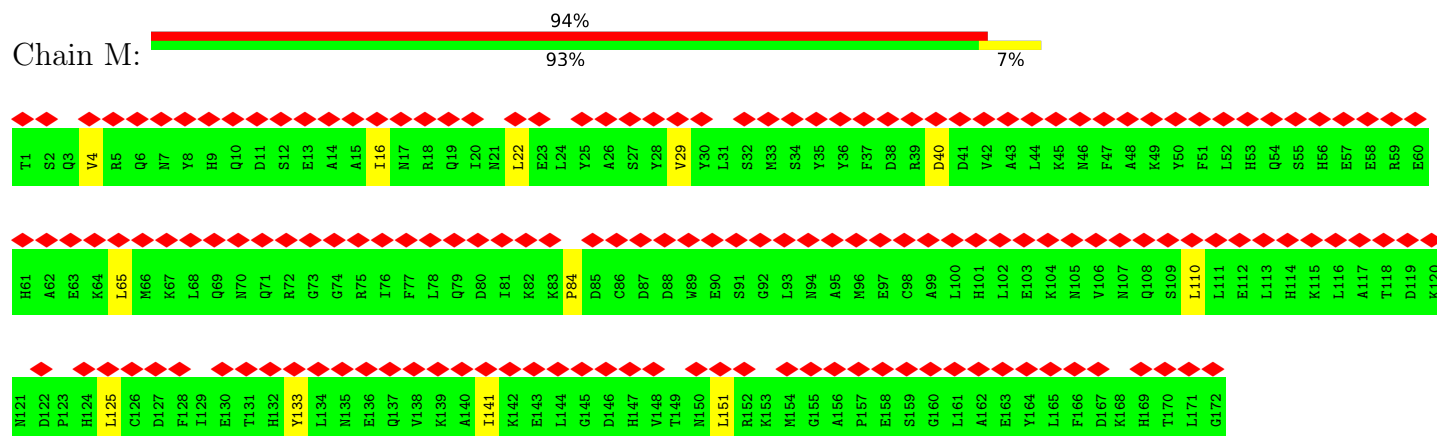


• Molecule 1: Ferritin heavy chain



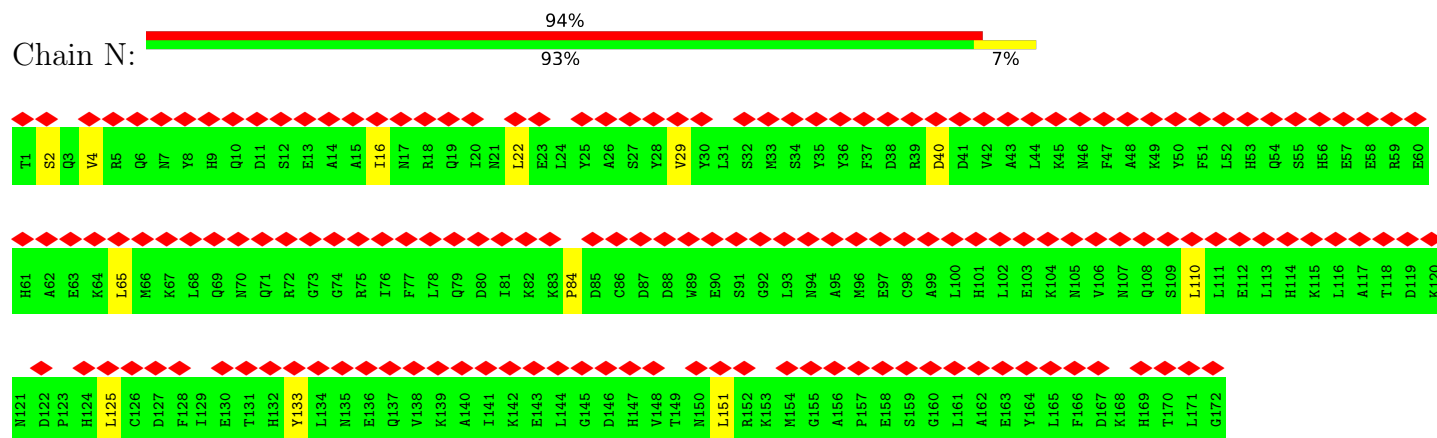
- Molecule 1: Ferritin heavy chain

Chain M:



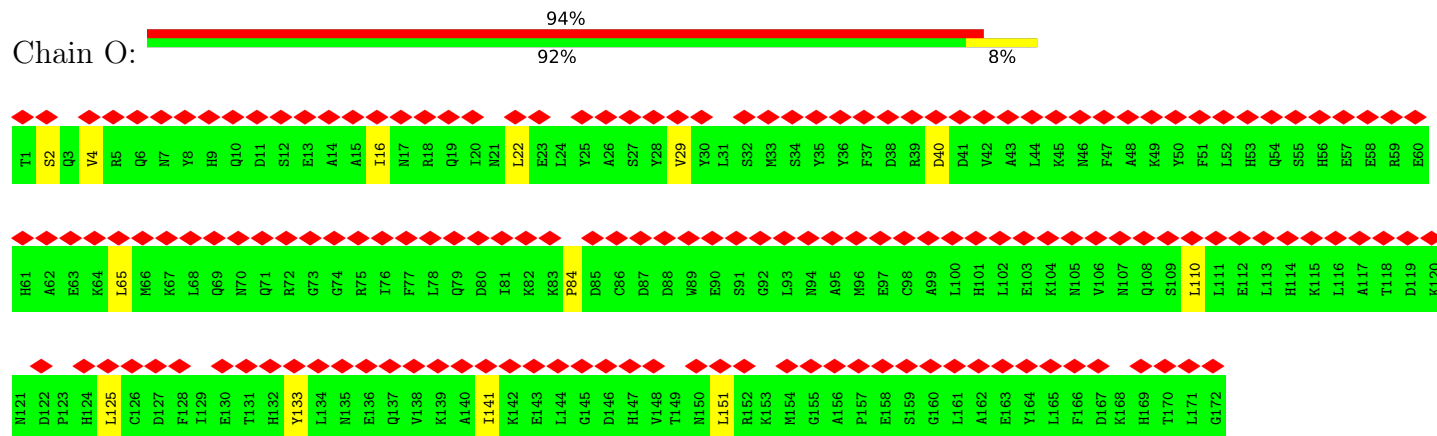
- Molecule 1: Ferritin heavy chain

Chain N:



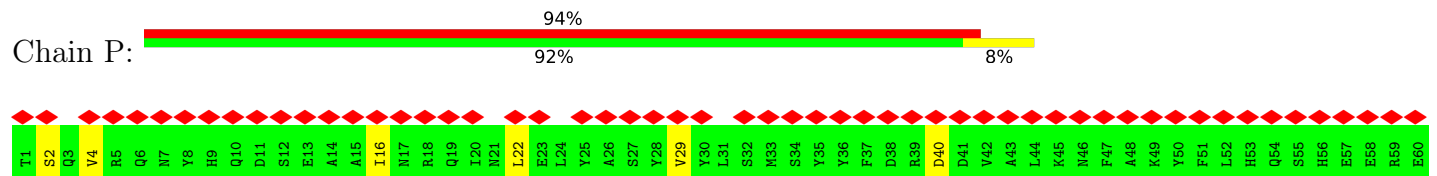
- Molecule 1: Ferritin heavy chain

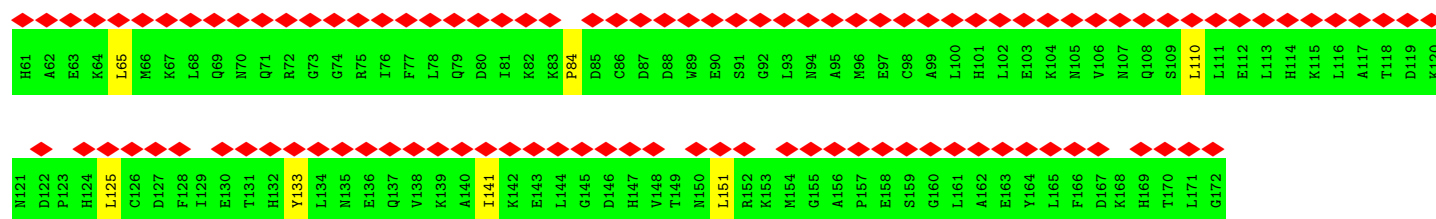
Chain O:



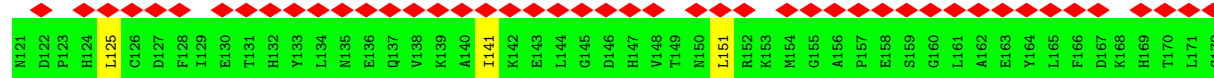
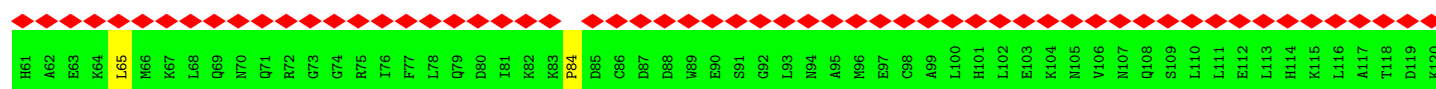
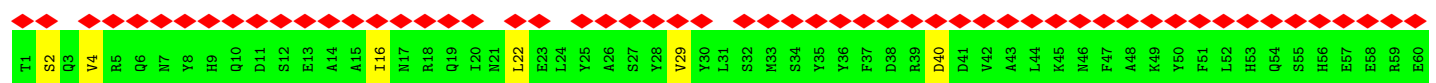
- Molecule 1: Ferritin heavy chain

Chain P:

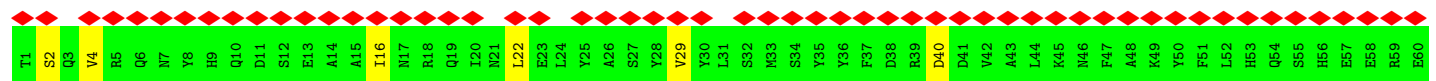




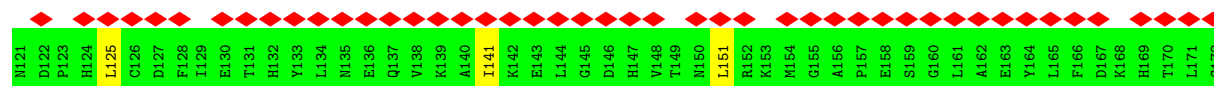
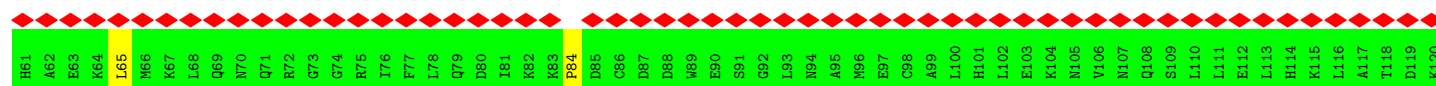
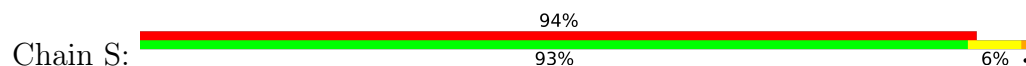
• Molecule 1: Ferritin heavy chain



• Molecule 1: Ferritin heavy chain

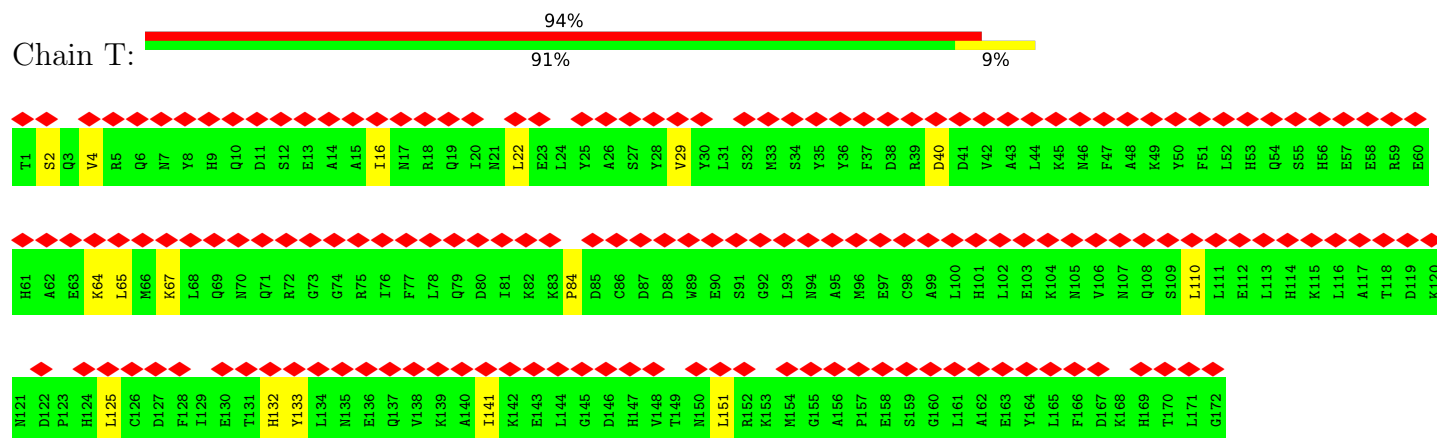


• Molecule 1: Ferritin heavy chain



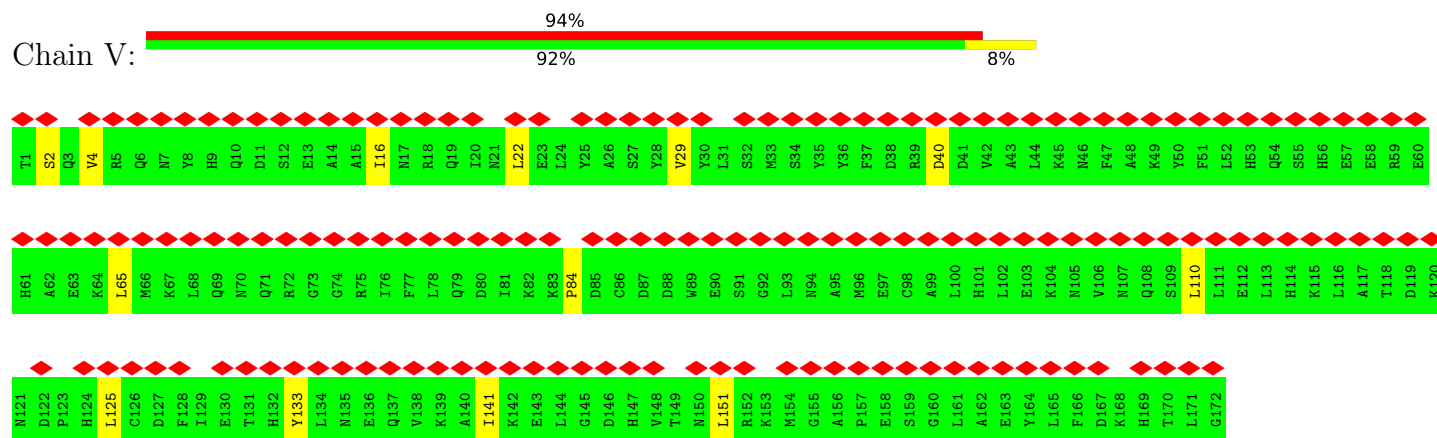
- Molecule 1: Ferritin heavy chain

Chain T:



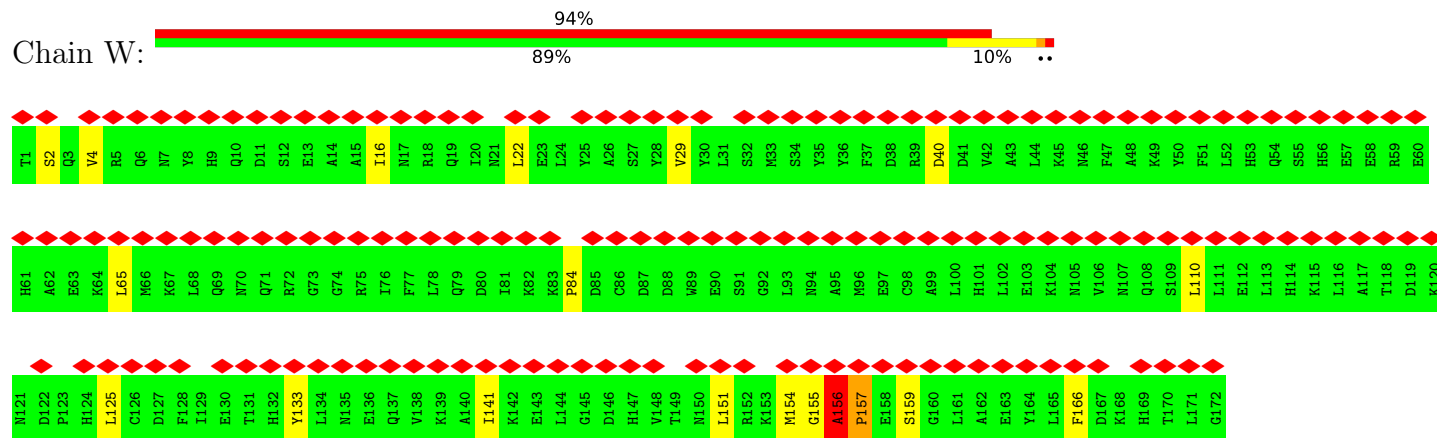
- Molecule 1: Ferritin heavy chain

Chain V:



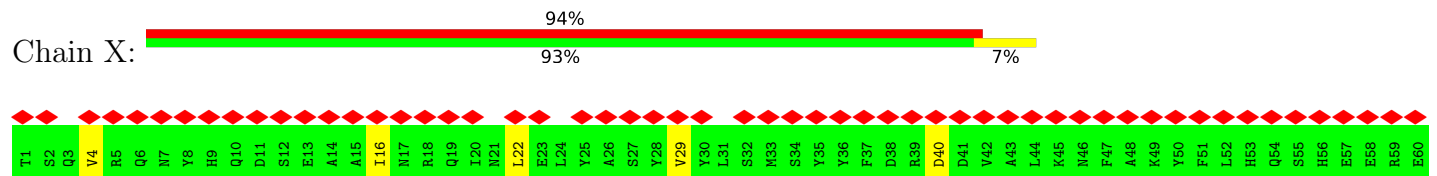
- Molecule 1: Ferritin heavy chain

Chain W:



- Molecule 1: Ferritin heavy chain

Chain X:



H61	A62	E63	K64	L65	M66	K67	L68	Q69	N70	Q71	R72	G73	G74	R75	I76	F77	L78	Q79	D80	I81	K82	K83	P84	D85	C86	D87	D88	W89	E90	S91	G92	L93	N94	A95	M96	E97	C98	A99	L100	H101	L102	E103	K104	N105	V106	N107	Q108	S109	L110	L111	E112	L113	H114	K115	L116	A117	T118	D119	K120
M121	D122	P123	H124	L125	C126	D127	F128	I129	E130	T131	H132	Y133	L134	N135	E136	Q137	V138	K139	A140	I141	K142	E143	L144	G145	D146	H147	V148	T149	N150	L151	R152	K153	M154	G155	A156	P157	E158	S159	G160	L161	A162	E163	Y164	L165	F166	D167	K168	H169	T170	L171	G172								

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	296695	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.095	Depositor
Minimum map value	-0.052	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	206.0, 206.0, 206.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.515, 0.515, 0.515	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.27	0/1413	0.63	0/1908
1	B	0.27	0/1413	0.65	1/1908 (0.1%)
1	C	0.27	0/1413	0.62	0/1908
1	D	0.27	0/1413	0.62	0/1908
1	E	0.27	0/1413	0.63	0/1908
1	F	0.26	0/1413	0.62	0/1908
1	G	0.26	0/1413	0.62	0/1908
1	H	0.26	0/1413	0.62	0/1908
1	I	0.26	0/1413	0.62	0/1908
1	J	0.26	0/1413	0.62	0/1908
1	K	0.26	0/1413	0.62	0/1908
1	L	0.26	0/1413	0.62	0/1908
1	M	0.26	0/1413	0.62	0/1908
1	N	0.26	0/1413	0.62	0/1908
1	O	0.26	0/1413	0.62	0/1908
1	P	0.27	0/1413	0.62	0/1908
1	Q	0.26	0/1413	0.62	0/1908
1	R	0.27	0/1413	0.62	0/1908
1	S	0.27	0/1413	0.64	1/1908 (0.1%)
1	T	0.27	0/1413	0.63	0/1908
1	U	0.27	0/1413	0.63	0/1908
1	V	0.27	0/1413	0.62	0/1908
1	W	0.27	0/1413	0.67	2/1908 (0.1%)
1	X	0.27	0/1413	0.63	0/1908
All	All	0.27	0/33912	0.63	4/45792 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	W	156	ALA	CA-C-N	7.69	129.45	119.84
1	W	156	ALA	C-N-CA	7.69	129.45	119.84
1	B	90	GLU	N-CA-C	6.03	123.65	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	45	LYS	N-CA-C	5.55	117.33	111.28

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	A	1384	0	1310	5	0
1	B	1384	0	1310	7	0
1	C	1384	0	1310	7	0
1	D	1384	0	1310	7	0
1	E	1384	0	1310	6	0
1	F	1384	0	1310	7	0
1	G	1384	0	1310	8	0
1	H	1384	0	1310	8	0
1	I	1384	0	1310	8	0
1	J	1384	0	1310	6	0
1	K	1384	0	1310	6	0
1	L	1384	0	1310	6	0
1	M	1384	0	1310	6	0
1	N	1384	0	1310	6	0
1	O	1384	0	1310	7	0
1	P	1384	0	1310	7	0
1	Q	1384	0	1310	6	0
1	R	1384	0	1310	6	0
1	S	1384	0	1310	6	0
1	T	1384	0	1310	11	0
1	U	1384	0	1310	4	0
1	V	1384	0	1310	7	0
1	W	1384	0	1310	15	0
1	X	1384	0	1310	7	0
All	All	33216	0	31440	124	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 2.

The worst 5 of 124 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)
1:W:156:ALA:HB3	1:W:157:PRO:CD	1.70	1.21
1:W:156:ALA:HB3	1:W:157:PRO:HD2	1.18	1.10
1:W:156:ALA:CB	1:W:157:PRO:CD	2.33	1.00
1:W:156:ALA:CB	1:W:157:PRO:HD2	1.96	0.93
1:D:155:GLY:O	1:D:159:SER:OG	1.93	0.85

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	A	170/172 (99%)	166 (98%)	4 (2%)	0	100	100
1	B	170/172 (99%)	168 (99%)	2 (1%)	0	100	100
1	C	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	D	170/172 (99%)	166 (98%)	4 (2%)	0	100	100
1	E	170/172 (99%)	166 (98%)	4 (2%)	0	100	100
1	F	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	G	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	H	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	I	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	J	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	K	170/172 (99%)	166 (98%)	4 (2%)	0	100	100
1	L	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	M	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	N	170/172 (99%)	167 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	P	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	Q	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	R	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	S	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	T	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	U	170/172 (99%)	165 (97%)	5 (3%)	0	100	100
1	V	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	W	170/172 (99%)	165 (97%)	3 (2%)	2 (1%)	10	4
1	X	170/172 (99%)	166 (98%)	4 (2%)	0	100	100
All	All	4080/4128 (99%)	4000 (98%)	78 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	W	156	ALA
1	W	157	PRO

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	A	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	B	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	C	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	D	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	E	145/153 (95%)	141 (97%)	4 (3%)	38	32
1	F	145/153 (95%)	143 (99%)	2 (1%)	59	59
1	G	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	H	145/153 (95%)	142 (98%)	3 (2%)	47	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	J	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	K	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	L	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	M	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	N	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	O	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	P	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	Q	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	R	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	S	145/153 (95%)	141 (97%)	4 (3%)	38	32
1	T	145/153 (95%)	141 (97%)	4 (3%)	38	32
1	U	145/153 (95%)	144 (99%)	1 (1%)	76	78
1	V	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	W	145/153 (95%)	142 (98%)	3 (2%)	47	44
1	X	145/153 (95%)	142 (98%)	3 (2%)	47	44
All	All	3480/3672 (95%)	3408 (98%)	72 (2%)	46	44

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	S	65	LEU
1	X	151	LEU
1	T	22	LEU
1	V	151	LEU
1	H	151	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	21	ASN
1	F	21	ASN
1	R	135	ASN
1	M	10	GLN
1	P	10	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no 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.

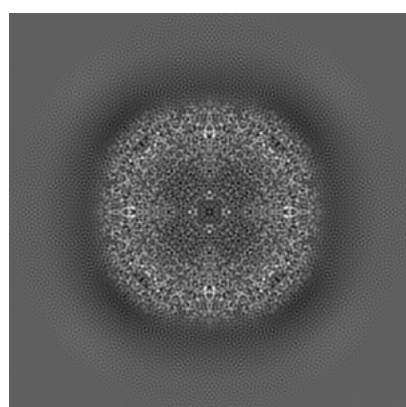
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31736. These allow visual inspection of the internal detail of the map and identification of artifacts.

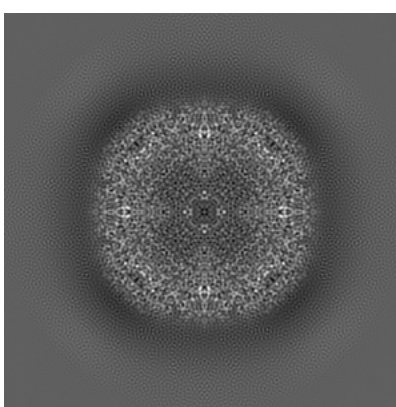
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

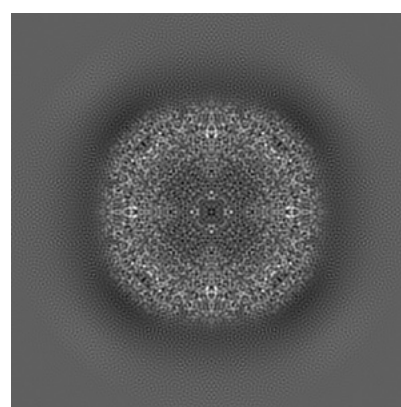
6.1.1 Primary map



X



Y

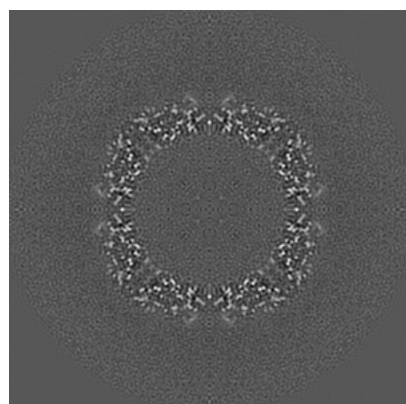


Z

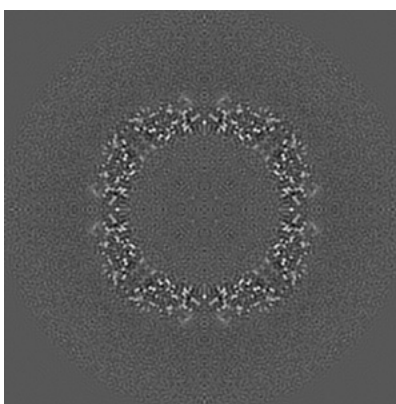
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

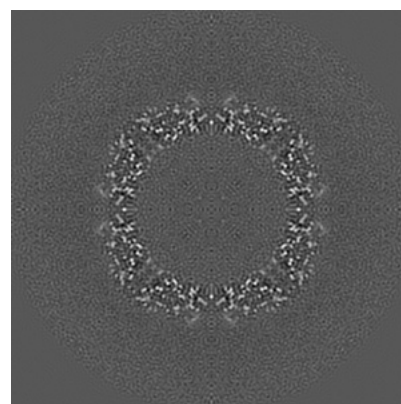
6.2.1 Primary map



X Index: 200



Y Index: 200

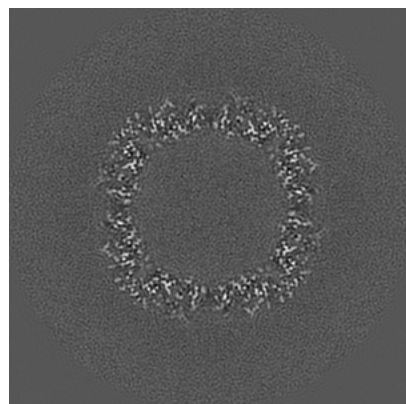


Z Index: 200

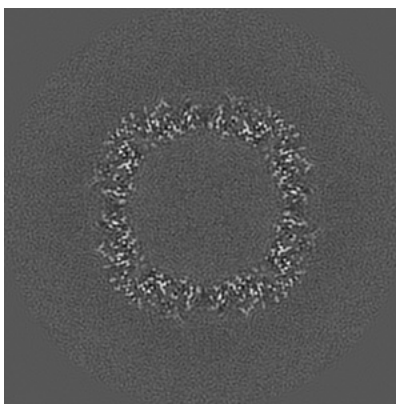
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

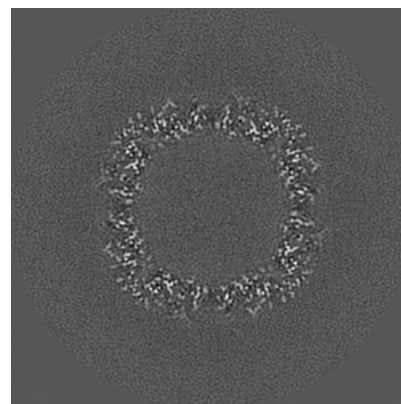
6.3.1 Primary map



X Index: 203



Y Index: 203

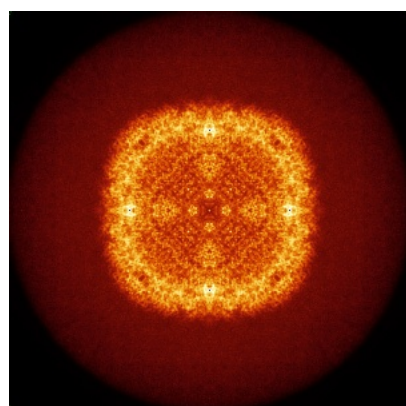


Z Index: 203

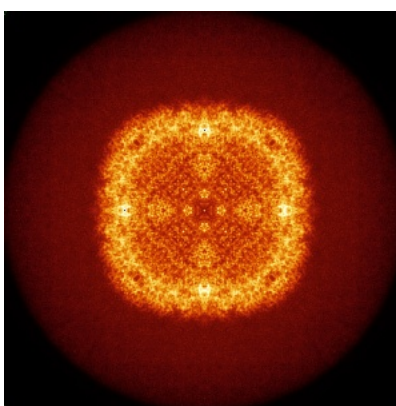
The images above show the largest variance slices of the map in three orthogonal directions.

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

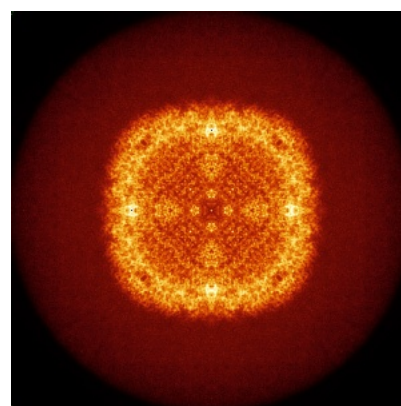
6.4.1 Primary map



X



Y

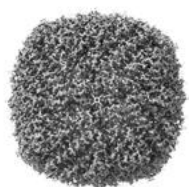


Z

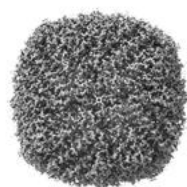
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

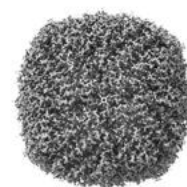
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

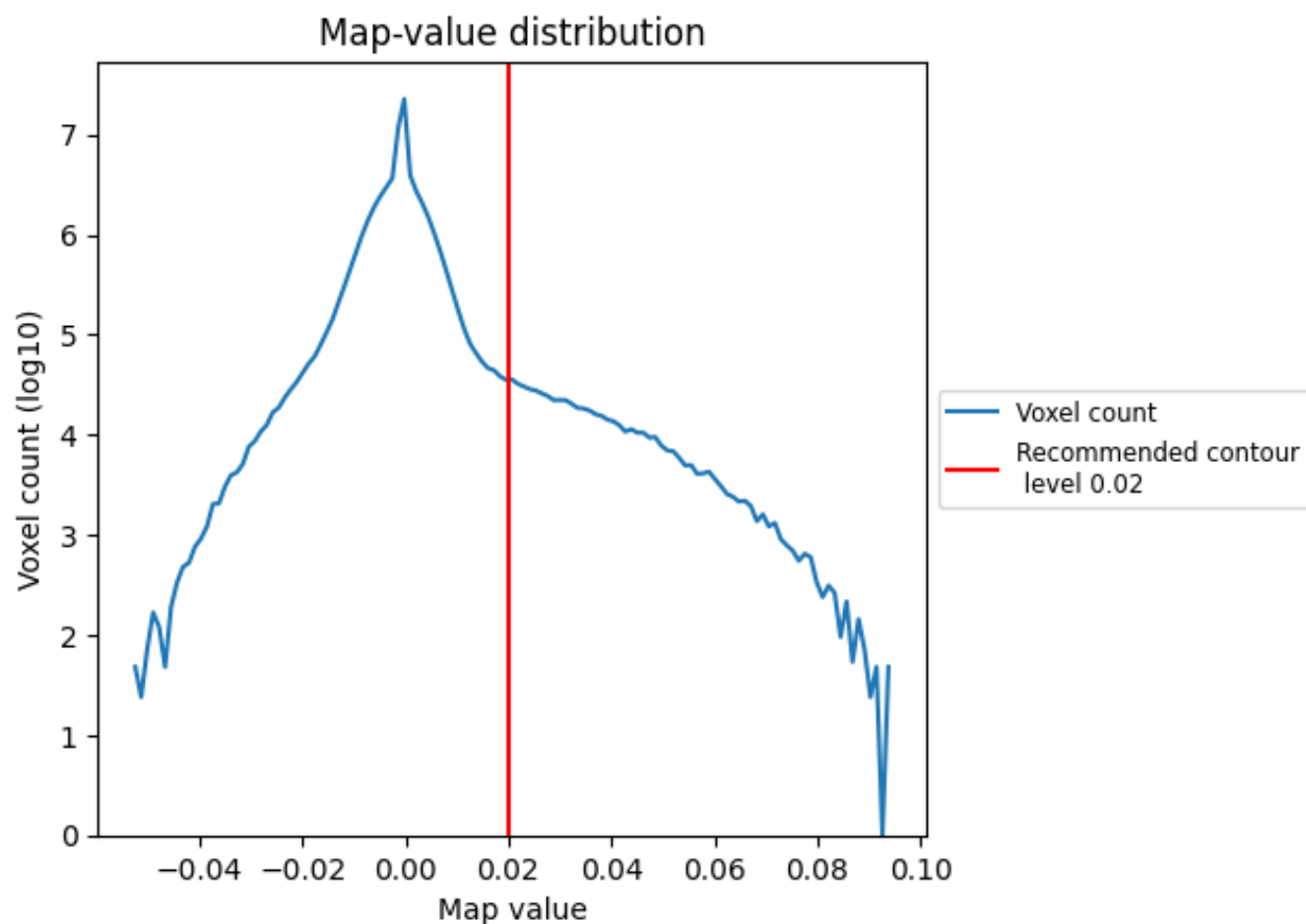
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

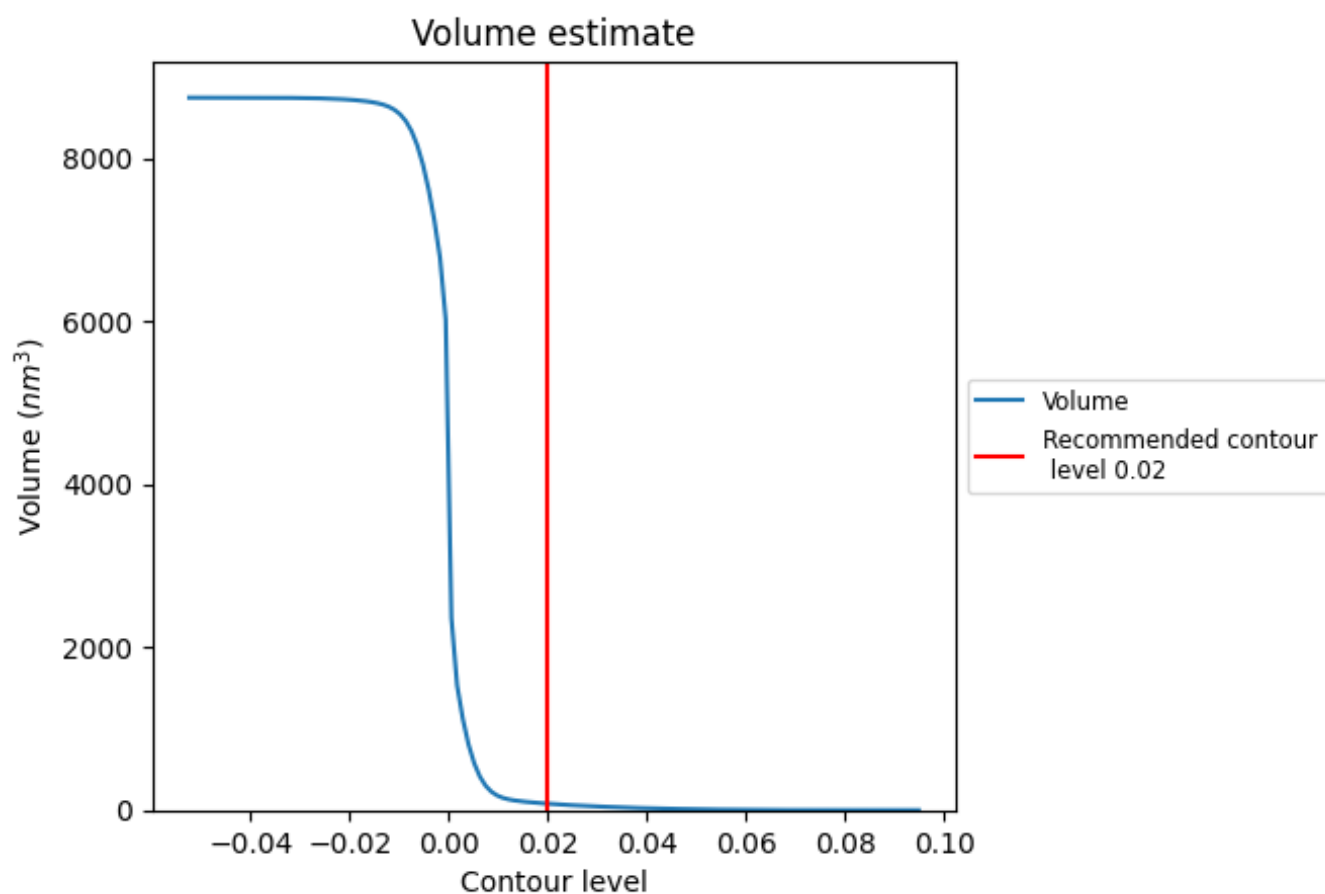
This section contains the results of statistical analysis of the map.

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.

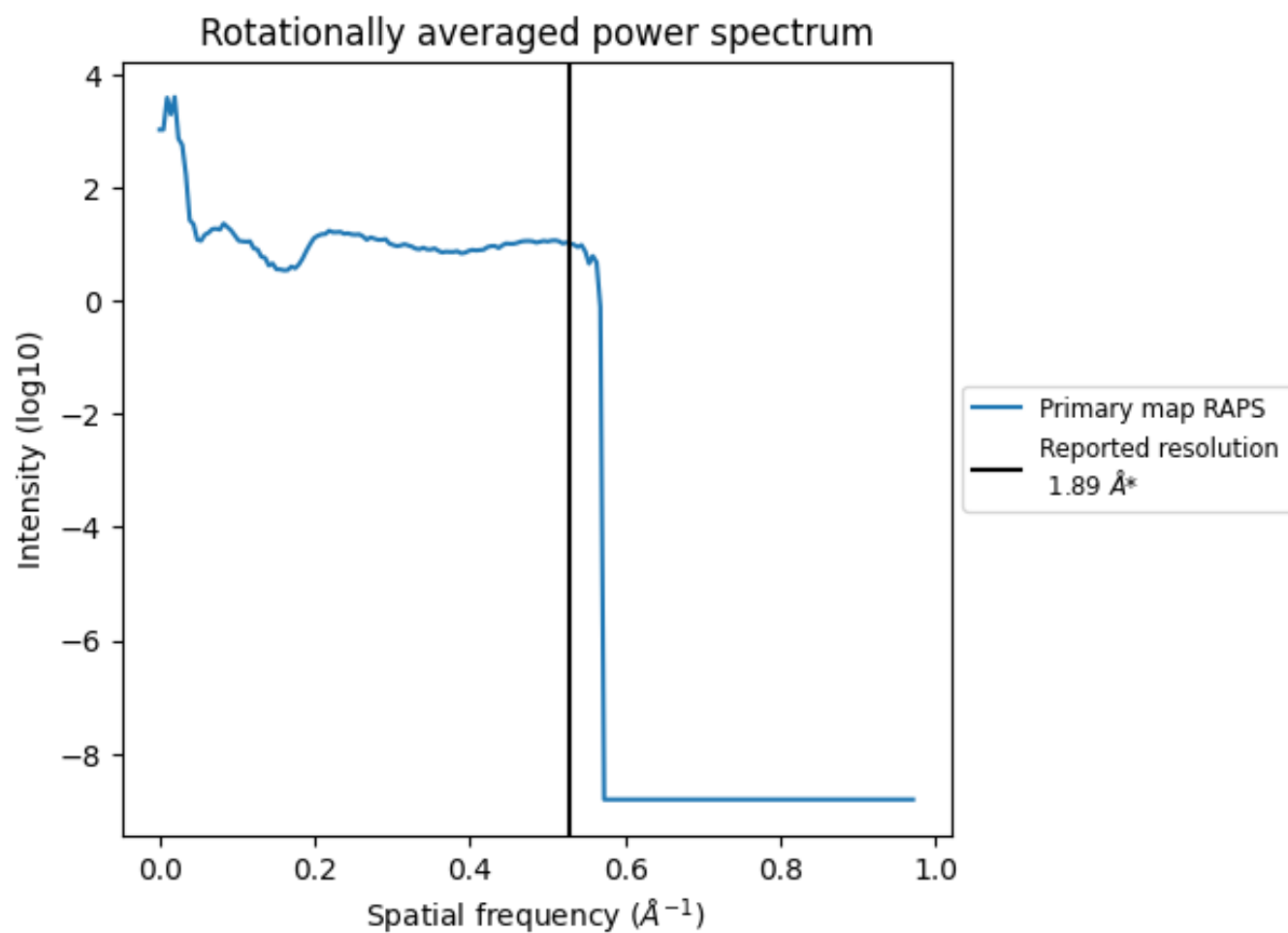
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 79 nm³; this corresponds to an approximate mass of 72 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 0.529 Å⁻¹

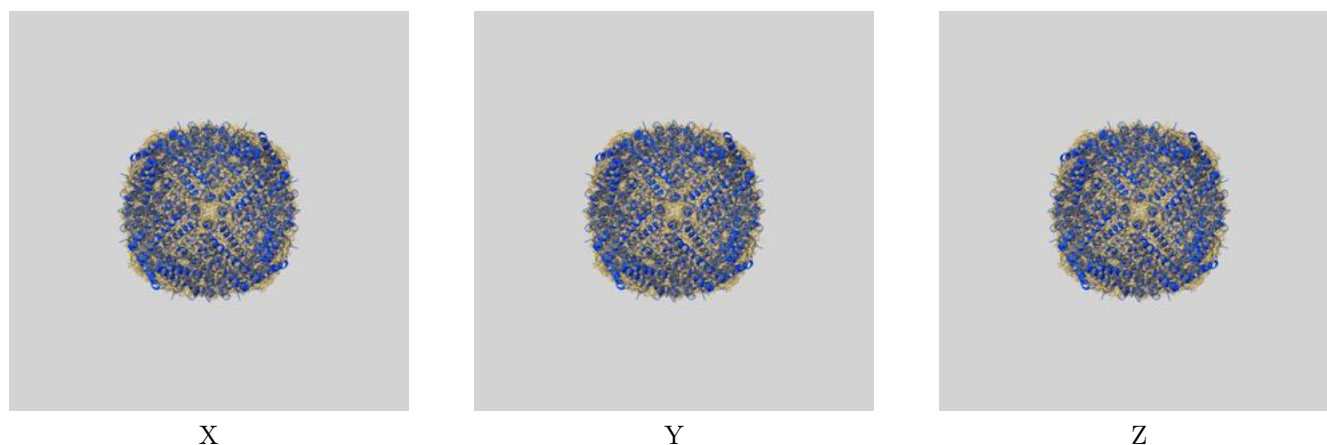
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

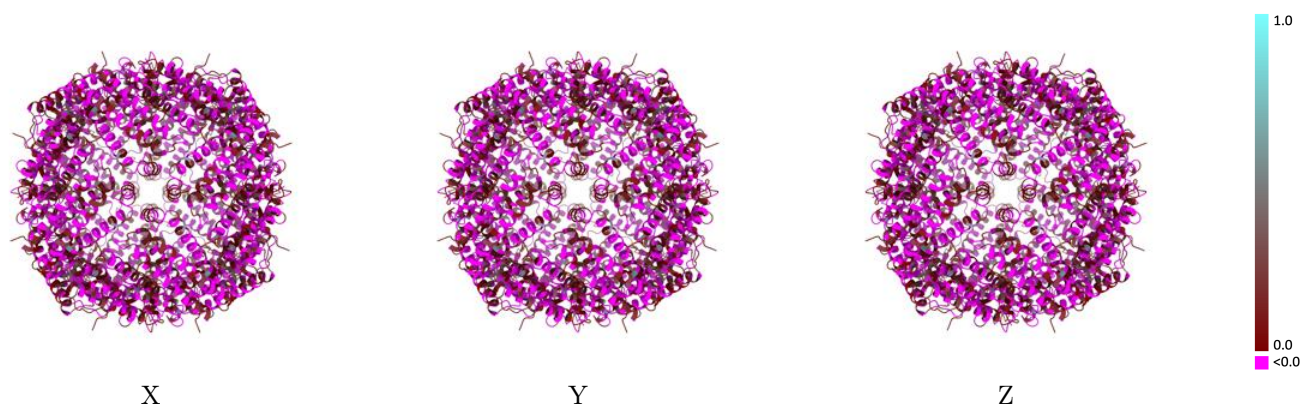
This section contains information regarding the fit between EMDB map EMD-31736 and PDB model 7V66. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



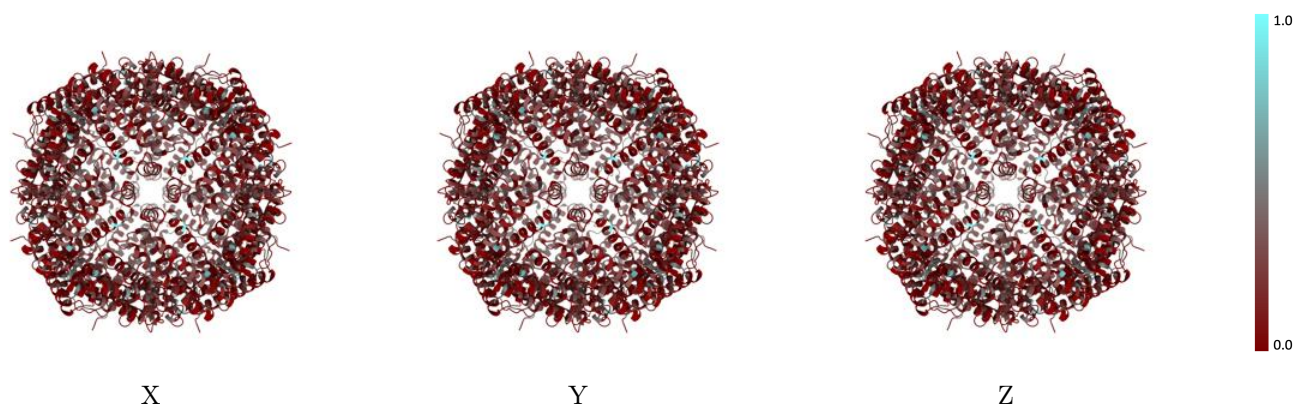
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



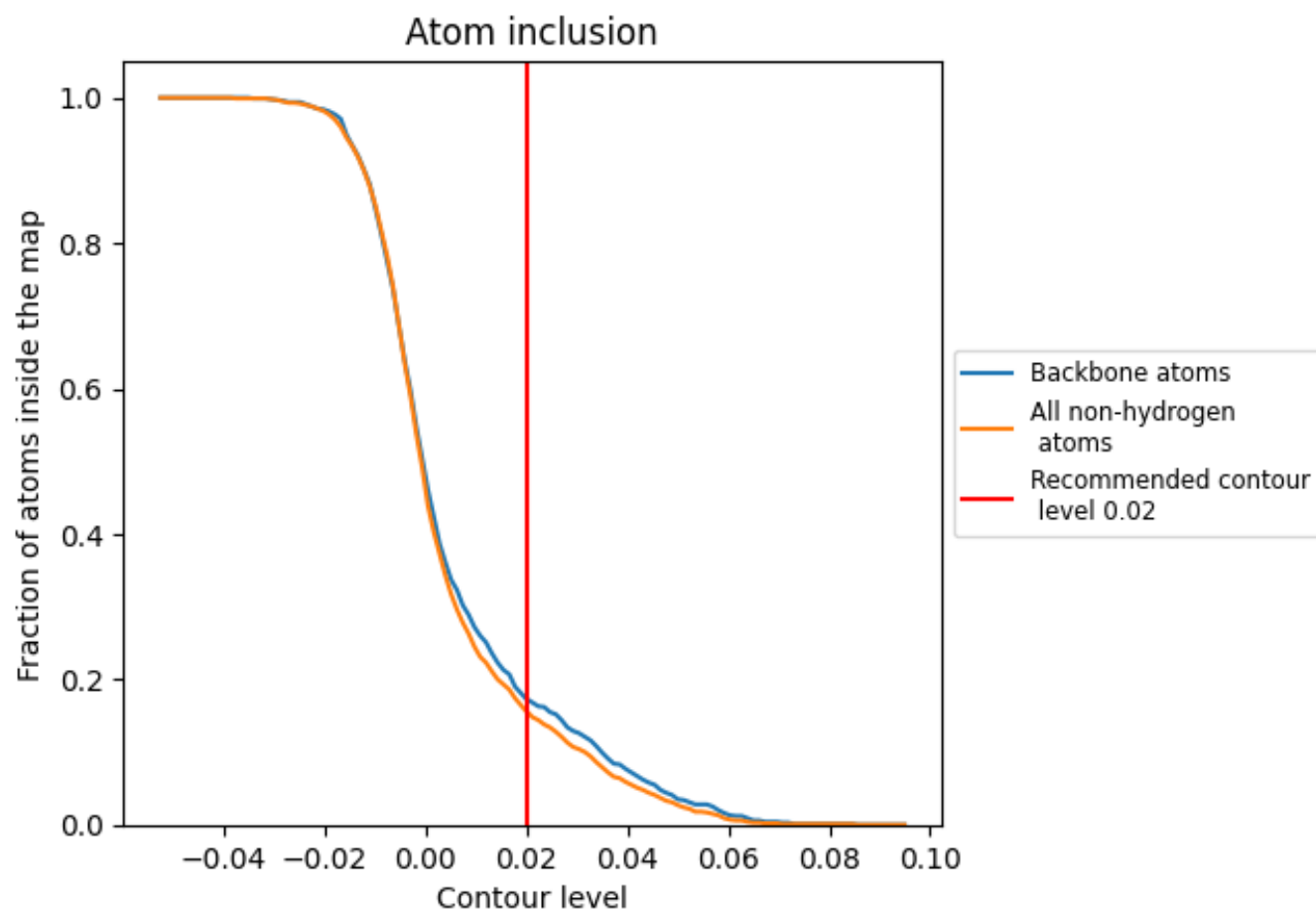
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 17% of all backbone atoms, 16% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.1560	 0.0180
A	 0.1570	 0.0180
B	 0.1560	 0.0180
C	 0.1560	 0.0190
D	 0.1580	 0.0170
E	 0.1550	 0.0180
F	 0.1560	 0.0180
G	 0.1560	 0.0180
H	 0.1560	 0.0180
I	 0.1570	 0.0200
J	 0.1570	 0.0180
K	 0.1580	 0.0190
L	 0.1560	 0.0180
M	 0.1570	 0.0170
N	 0.1570	 0.0180
O	 0.1560	 0.0160
P	 0.1560	 0.0180
Q	 0.1560	 0.0190
R	 0.1560	 0.0200
S	 0.1560	 0.0200
T	 0.1560	 0.0170
U	 0.1560	 0.0200
V	 0.1560	 0.0170
W	 0.1560	 0.0180
X	 0.1560	 0.0160

