



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 11:27 PM UTC

PDB ID : 9KAY / pdb_00009kay
EMDB ID : EMD-62216
Title : Bioengineered protein nanocarrier facilitating siRNA escape from lysosomes
for targeted RNAi therapy in glioblastoma
Authors : Chen, X.; Fan, K.
Deposited on : 2024-10-30
Resolution : 1.73 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

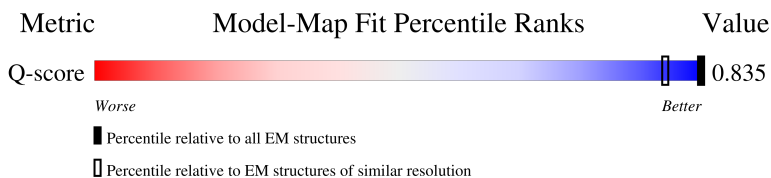
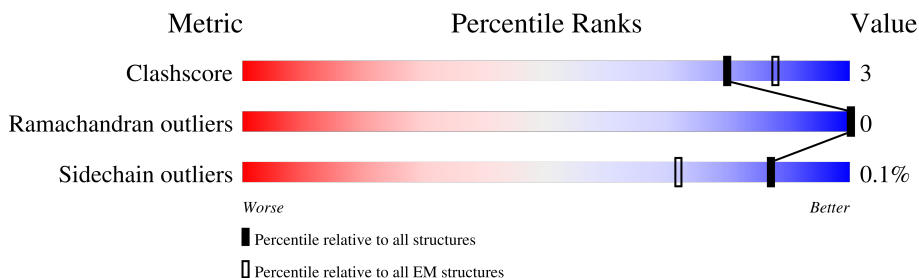
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 1.73 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.



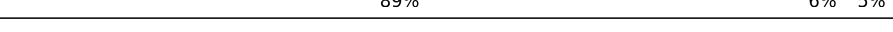
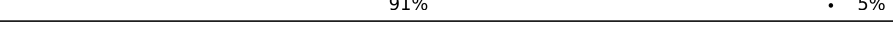
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	627 (1.25 - 2.23)

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	Aa	159	 87% 8% 5%
1	Ab	159	 89% 6% 5%
1	Ac	159	 89% 6% 5%
1	Ad	159	 90% 5% 5%

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Mol	Chain	Length	Quality of chain
1	Ae	159	 88%7%5%
1	Af	159	 89%6%5%
1	Ag	159	 89%6%5%
1	Ah	159	 89%6%5%
1	Ai	159	 90%5%5%
1	Aj	159	 89%6%5%
1	Ak	159	 87%8%5%
1	Al	159	 90%5%5%
1	Am	159	 89%6%5%
1	An	159	 88%6%5%
1	Ao	159	 90%5%5%
1	Ap	159	 90%5%5%
1	Aq	159	 91%5%5%
1	Ar	159	 89%6%5%
1	As	159	 89%6%5%
1	At	159	 89%6%5%
1	Au	159	 91%5%5%
1	Av	159	 89%6%5%
1	Aw	159	 89%6%5%
1	Ax	159	 89%6%5%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 30168 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, N-terminally processed.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Ab	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Ac	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Ad	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Ae	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Af	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Ag	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Ah	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Ai	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Aj	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Ak	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Al	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Am	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	An	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Ao	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Ap	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Aq	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ar	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	As	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	At	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Au	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Av	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Aw	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		
1	Ax	151	Total	C	N	O	S	0	0
			1257	789	229	233	6		

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Aa	61	LYS	GLU	engineered mutation	UNP P02794
Aa	64	ARG	GLU	engineered mutation	UNP P02794
Aa	140	LYS	GLU	engineered mutation	UNP P02794
Aa	147	LYS	GLU	engineered mutation	UNP P02794
Ab	61	LYS	GLU	engineered mutation	UNP P02794
Ab	64	ARG	GLU	engineered mutation	UNP P02794
Ab	140	LYS	GLU	engineered mutation	UNP P02794
Ab	147	LYS	GLU	engineered mutation	UNP P02794
Ac	61	LYS	GLU	engineered mutation	UNP P02794
Ac	64	ARG	GLU	engineered mutation	UNP P02794
Ac	140	LYS	GLU	engineered mutation	UNP P02794
Ac	147	LYS	GLU	engineered mutation	UNP P02794
Ad	61	LYS	GLU	engineered mutation	UNP P02794
Ad	64	ARG	GLU	engineered mutation	UNP P02794
Ad	140	LYS	GLU	engineered mutation	UNP P02794
Ad	147	LYS	GLU	engineered mutation	UNP P02794
Ae	61	LYS	GLU	engineered mutation	UNP P02794
Ae	64	ARG	GLU	engineered mutation	UNP P02794
Ae	140	LYS	GLU	engineered mutation	UNP P02794
Ae	147	LYS	GLU	engineered mutation	UNP P02794
Af	61	LYS	GLU	engineered mutation	UNP P02794
Af	64	ARG	GLU	engineered mutation	UNP P02794
Af	140	LYS	GLU	engineered mutation	UNP P02794
Af	147	LYS	GLU	engineered mutation	UNP P02794
Ag	61	LYS	GLU	engineered mutation	UNP P02794

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Chain	Residue	Modelled	Actual	Comment	Reference
Ag	64	ARG	GLU	engineered mutation	UNP P02794
Ag	140	LYS	GLU	engineered mutation	UNP P02794
Ag	147	LYS	GLU	engineered mutation	UNP P02794
Ah	61	LYS	GLU	engineered mutation	UNP P02794
Ah	64	ARG	GLU	engineered mutation	UNP P02794
Ah	140	LYS	GLU	engineered mutation	UNP P02794
Ah	147	LYS	GLU	engineered mutation	UNP P02794
Ai	61	LYS	GLU	engineered mutation	UNP P02794
Ai	64	ARG	GLU	engineered mutation	UNP P02794
Ai	140	LYS	GLU	engineered mutation	UNP P02794
Ai	147	LYS	GLU	engineered mutation	UNP P02794
Aj	61	LYS	GLU	engineered mutation	UNP P02794
Aj	64	ARG	GLU	engineered mutation	UNP P02794
Aj	140	LYS	GLU	engineered mutation	UNP P02794
Aj	147	LYS	GLU	engineered mutation	UNP P02794
Ak	61	LYS	GLU	engineered mutation	UNP P02794
Ak	64	ARG	GLU	engineered mutation	UNP P02794
Ak	140	LYS	GLU	engineered mutation	UNP P02794
Ak	147	LYS	GLU	engineered mutation	UNP P02794
Al	61	LYS	GLU	engineered mutation	UNP P02794
Al	64	ARG	GLU	engineered mutation	UNP P02794
Al	140	LYS	GLU	engineered mutation	UNP P02794
Al	147	LYS	GLU	engineered mutation	UNP P02794
Am	61	LYS	GLU	engineered mutation	UNP P02794
Am	64	ARG	GLU	engineered mutation	UNP P02794
Am	140	LYS	GLU	engineered mutation	UNP P02794
Am	147	LYS	GLU	engineered mutation	UNP P02794
An	61	LYS	GLU	engineered mutation	UNP P02794
An	64	ARG	GLU	engineered mutation	UNP P02794
An	140	LYS	GLU	engineered mutation	UNP P02794
An	147	LYS	GLU	engineered mutation	UNP P02794
Ao	61	LYS	GLU	engineered mutation	UNP P02794
Ao	64	ARG	GLU	engineered mutation	UNP P02794
Ao	140	LYS	GLU	engineered mutation	UNP P02794
Ao	147	LYS	GLU	engineered mutation	UNP P02794
Ap	61	LYS	GLU	engineered mutation	UNP P02794
Ap	64	ARG	GLU	engineered mutation	UNP P02794
Ap	140	LYS	GLU	engineered mutation	UNP P02794
Ap	147	LYS	GLU	engineered mutation	UNP P02794
Aq	61	LYS	GLU	engineered mutation	UNP P02794
Aq	64	ARG	GLU	engineered mutation	UNP P02794
Aq	140	LYS	GLU	engineered mutation	UNP P02794

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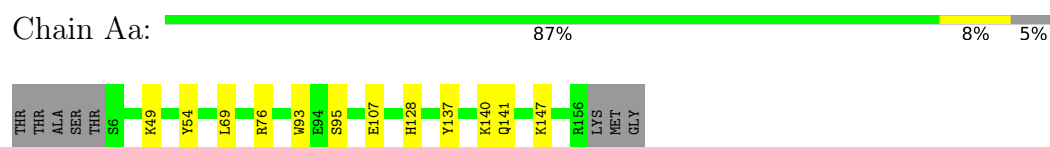
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Chain	Residue	Modelled	Actual	Comment	Reference
Aq	147	LYS	GLU	engineered mutation	UNP P02794
Ar	61	LYS	GLU	engineered mutation	UNP P02794
Ar	64	ARG	GLU	engineered mutation	UNP P02794
Ar	140	LYS	GLU	engineered mutation	UNP P02794
Ar	147	LYS	GLU	engineered mutation	UNP P02794
As	61	LYS	GLU	engineered mutation	UNP P02794
As	64	ARG	GLU	engineered mutation	UNP P02794
As	140	LYS	GLU	engineered mutation	UNP P02794
As	147	LYS	GLU	engineered mutation	UNP P02794
At	61	LYS	GLU	engineered mutation	UNP P02794
At	64	ARG	GLU	engineered mutation	UNP P02794
At	140	LYS	GLU	engineered mutation	UNP P02794
At	147	LYS	GLU	engineered mutation	UNP P02794
Au	61	LYS	GLU	engineered mutation	UNP P02794
Au	64	ARG	GLU	engineered mutation	UNP P02794
Au	140	LYS	GLU	engineered mutation	UNP P02794
Au	147	LYS	GLU	engineered mutation	UNP P02794
Av	61	LYS	GLU	engineered mutation	UNP P02794
Av	64	ARG	GLU	engineered mutation	UNP P02794
Av	140	LYS	GLU	engineered mutation	UNP P02794
Av	147	LYS	GLU	engineered mutation	UNP P02794
Aw	61	LYS	GLU	engineered mutation	UNP P02794
Aw	64	ARG	GLU	engineered mutation	UNP P02794
Aw	140	LYS	GLU	engineered mutation	UNP P02794
Aw	147	LYS	GLU	engineered mutation	UNP P02794
Ax	61	LYS	GLU	engineered mutation	UNP P02794
Ax	64	ARG	GLU	engineered mutation	UNP P02794
Ax	140	LYS	GLU	engineered mutation	UNP P02794
Ax	147	LYS	GLU	engineered mutation	UNP P02794

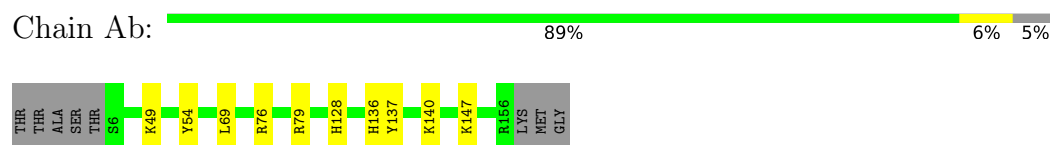
3 Residue-property plots [i](#)

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.

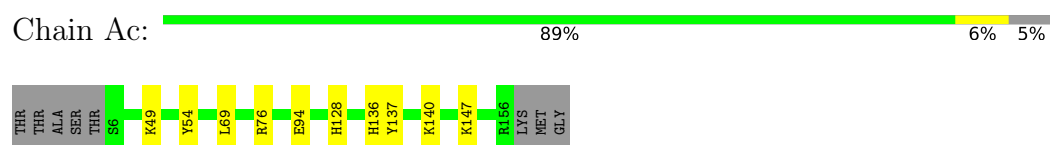
- Molecule 1: Ferritin heavy chain, N-terminally processed



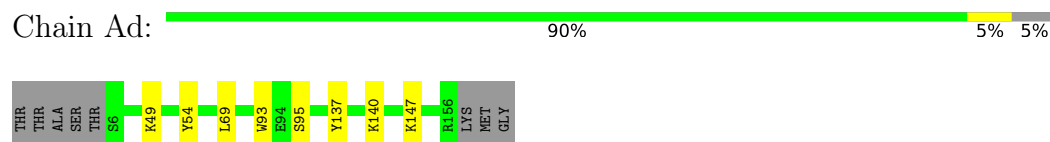
- Molecule 1: Ferritin heavy chain, N-terminally processed



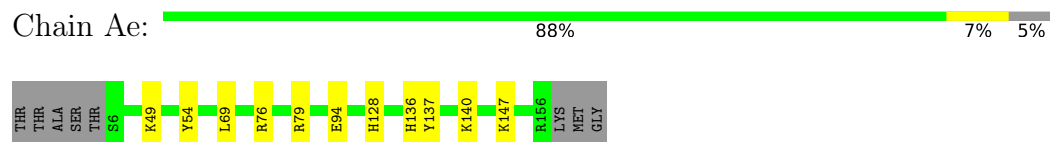
- Molecule 1: Ferritin heavy chain, N-terminally processed



- Molecule 1: Ferritin heavy chain, N-terminally processed



- Molecule 1: Ferritin heavy chain, N-terminally processed



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Af:  89% 6% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Ag:  89% 6% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Ah:  89% 6% 5%



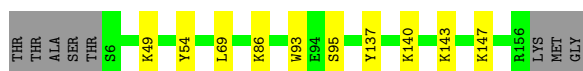
- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Ai:  90% 5% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Aj:  89% 6% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Ak:  87% 8% 5%



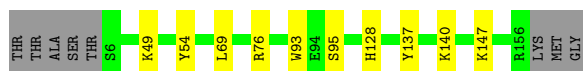
- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Al:  90% 5% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Am:  89% 6% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain An:  88% 6% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Ao:  90% 5% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Ap:  90% 5% 5%



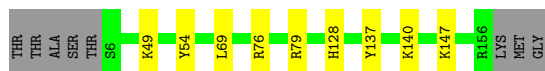
- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Aq:  91% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Ar:  89% 6% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain As:  89% 6% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain At:  89% 6% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Au:  91% 5% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Av:  89% 6% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Aw:  89% 6% 5%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Ax:  89% 6% 5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	966873	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.864	Depositor
Minimum map value	-0.438	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.151	Depositor
Map size (Å)	203.51999, 203.51999, 203.51999	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.53, 0.53, 0.53	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	Aa	0.19	0/1282	0.39	0/1723
1	Ab	0.19	0/1282	0.39	0/1723
1	Ac	0.18	0/1282	0.39	0/1723
1	Ad	0.18	0/1282	0.39	0/1723
1	Ae	0.19	0/1282	0.39	0/1723
1	Af	0.19	0/1282	0.41	0/1723
1	Ag	0.18	0/1282	0.40	0/1723
1	Ah	0.19	0/1282	0.39	0/1723
1	Ai	0.19	0/1282	0.37	0/1723
1	Aj	0.18	0/1282	0.38	0/1723
1	Ak	0.19	0/1282	0.39	0/1723
1	Al	0.18	0/1282	0.40	0/1723
1	Am	0.19	0/1282	0.38	0/1723
1	An	0.19	0/1282	0.40	0/1723
1	Ao	0.19	0/1282	0.42	0/1723
1	Ap	0.18	0/1282	0.38	0/1723
1	Aq	0.19	0/1282	0.39	0/1723
1	Ar	0.19	0/1282	0.39	0/1723
1	As	0.19	0/1282	0.39	0/1723
1	At	0.19	0/1282	0.39	0/1723
1	Au	0.19	0/1282	0.40	0/1723
1	Av	0.18	0/1282	0.41	0/1723
1	Aw	0.19	0/1282	0.41	0/1723
1	Ax	0.27	0/1282	0.46	0/1723
All	All	0.19	0/30768	0.40	0/41352

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	Aa	1257	0	1231	8	0
1	Ab	1257	0	1231	8	0
1	Ac	1257	0	1231	8	0
1	Ad	1257	0	1231	6	0
1	Ae	1257	0	1231	9	0
1	Af	1257	0	1231	7	0
1	Ag	1257	0	1231	7	0
1	Ah	1257	0	1231	6	0
1	Ai	1257	0	1231	6	0
1	Aj	1257	0	1231	6	0
1	Ak	1257	0	1231	9	0
1	Al	1257	0	1231	6	0
1	Am	1257	0	1231	7	0
1	An	1257	0	1231	8	0
1	Ao	1257	0	1231	5	0
1	Ap	1257	0	1231	6	0
1	Aq	1257	0	1231	4	0
1	Ar	1257	0	1231	7	0
1	As	1257	0	1231	6	0
1	At	1257	0	1231	6	0
1	Au	1257	0	1231	4	0
1	Av	1257	0	1231	7	0
1	Aw	1257	0	1231	7	0
1	Ax	1257	0	1231	5	0
All	All	30168	0	29544	158	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 3.

All (158) 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:Ar:54:TYR:OH	1:Ar:147:LYS:NZ	2.31	0.63
1:Ao:54:TYR:OH	1:Ao:147:LYS:NZ	2.37	0.58
1:Av:54:TYR:OH	1:Av:147:LYS:NZ	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Af:54:TYR:OH	1:Af:147:LYS:NZ	2.38	0.57
1:Aw:54:TYR:OH	1:Aw:147:LYS:NZ	2.38	0.56
1:Aq:54:TYR:OH	1:Aq:147:LYS:NZ	2.39	0.56
1:Ax:107:GLU:OE1	1:Ax:141:GLN:NE2	2.39	0.55
1:Al:54:TYR:OH	1:Al:147:LYS:NZ	2.40	0.55
1:Ai:54:TYR:OH	1:Ai:147:LYS:NZ	2.40	0.55
1:Ah:54:TYR:OH	1:Ah:147:LYS:NZ	2.40	0.55
1:Aa:107:GLU:OE1	1:Aa:141:GLN:NE2	2.40	0.54
1:Ak:54:TYR:OH	1:Ak:147:LYS:NZ	2.40	0.54
1:Ab:54:TYR:OH	1:Ab:147:LYS:NZ	2.40	0.54
1:Au:54:TYR:OH	1:Au:147:LYS:NZ	2.41	0.54
1:An:54:TYR:OH	1:An:147:LYS:NZ	2.42	0.53
1:Aj:49:LYS:N	1:Aj:49:LYS:HD2	2.24	0.53
1:Am:54:TYR:OH	1:Am:147:LYS:NZ	2.41	0.53
1:At:54:TYR:OH	1:At:147:LYS:NZ	2.42	0.53
1:Ae:54:TYR:OH	1:Ae:147:LYS:NZ	2.42	0.53
1:Aq:49:LYS:N	1:Aq:49:LYS:HD2	2.24	0.53
1:Aj:54:TYR:OH	1:Aj:147:LYS:NZ	2.41	0.53
1:Av:49:LYS:N	1:Av:49:LYS:HD2	2.24	0.53
1:Ak:49:LYS:HD2	1:Ak:49:LYS:N	2.24	0.52
1:Ai:49:LYS:N	1:Ai:49:LYS:HD2	2.24	0.52
1:Ag:49:LYS:N	1:Ag:49:LYS:HD2	2.24	0.52
1:Af:49:LYS:N	1:Af:49:LYS:HD2	2.25	0.52
1:At:49:LYS:N	1:At:49:LYS:HD2	2.25	0.52
1:Aw:49:LYS:N	1:Aw:49:LYS:HD2	2.24	0.52
1:Ag:54:TYR:OH	1:Ag:147:LYS:NZ	2.43	0.52
1:An:49:LYS:N	1:An:49:LYS:HD2	2.25	0.52
1:Ax:54:TYR:OH	1:Ax:147:LYS:NZ	2.44	0.51
1:Ad:54:TYR:OH	1:Ad:147:LYS:NZ	2.43	0.51
1:Ao:49:LYS:N	1:Ao:49:LYS:HD2	2.25	0.51
1:Am:49:LYS:N	1:Am:49:LYS:HD2	2.26	0.51
1:Ad:49:LYS:HD2	1:Ad:49:LYS:N	2.25	0.51
1:Ac:54:TYR:OH	1:Ac:147:LYS:NZ	2.43	0.51
1:Ar:49:LYS:HD2	1:Ar:49:LYS:N	2.25	0.50
1:As:49:LYS:HD2	1:As:49:LYS:N	2.27	0.50
1:Al:49:LYS:HD2	1:Al:49:LYS:N	2.24	0.50
1:As:54:TYR:OH	1:As:147:LYS:NZ	2.45	0.50
1:Aq:76:ARG:HH11	1:Aq:128:HIS:HD1	1.61	0.49
1:Aw:117:LEU:HD22	1:Aw:133:ILE:HD11	1.95	0.49
1:Ah:112:GLN:O	1:Ah:116:GLU:HG3	2.13	0.48
1:Au:76:ARG:HH11	1:Au:128:HIS:HD1	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ab:76:ARG:HH11	1:Ab:128:HIS:HD1	1.62	0.48
1:Aa:54:TYR:OH	1:Aa:147:LYS:NZ	2.46	0.48
1:An:140:LYS:H	1:An:140:LYS:HE2	1.79	0.47
1:Ap:140:LYS:HE2	1:Ap:140:LYS:H	1.80	0.47
1:Av:117:LEU:HD22	1:Av:133:ILE:HD11	1.96	0.47
1:Ap:76:ARG:HH11	1:Ap:128:HIS:HD1	1.62	0.47
1:Ar:140:LYS:HE2	1:Ar:140:LYS:H	1.79	0.47
1:Av:140:LYS:HE2	1:Av:140:LYS:H	1.80	0.47
1:Ab:140:LYS:HE2	1:Ab:140:LYS:H	1.79	0.47
1:Ai:140:LYS:H	1:Ai:140:LYS:HE2	1.79	0.47
1:Ag:140:LYS:HE2	1:Ag:140:LYS:H	1.80	0.47
1:Ak:76:ARG:HH11	1:Ak:128:HIS:HD1	1.61	0.47
1:Ae:140:LYS:H	1:Ae:140:LYS:HE2	1.80	0.47
1:Aw:140:LYS:H	1:Aw:140:LYS:HE2	1.80	0.47
1:Al:76:ARG:HH11	1:Al:128:HIS:HD1	1.63	0.47
1:Aa:140:LYS:H	1:Aa:140:LYS:HE2	1.80	0.47
1:Ac:140:LYS:HE2	1:Ac:140:LYS:H	1.80	0.47
1:Ac:76:ARG:HH11	1:Ac:128:HIS:HD1	1.63	0.46
1:Al:140:LYS:HE2	1:Al:140:LYS:H	1.79	0.46
1:Ad:140:LYS:H	1:Ad:140:LYS:HE2	1.80	0.46
1:Aa:49:LYS:N	1:Aa:49:LYS:HD2	2.31	0.46
1:Ag:76:ARG:HH11	1:Ag:128:HIS:HD1	1.62	0.46
1:Ap:54:TYR:OH	1:Ap:147:LYS:NZ	2.49	0.46
1:Af:140:LYS:HE2	1:Af:140:LYS:H	1.80	0.46
1:Ak:140:LYS:HE2	1:Ak:140:LYS:H	1.80	0.46
1:Am:140:LYS:HE2	1:Am:140:LYS:H	1.80	0.46
1:An:76:ARG:HH11	1:An:128:HIS:HD1	1.63	0.46
1:Ah:76:ARG:HH11	1:Ah:128:HIS:HD1	1.63	0.46
1:Am:76:ARG:HH11	1:Am:128:HIS:HD1	1.63	0.46
1:Aw:76:ARG:HH11	1:Aw:128:HIS:HD1	1.63	0.46
1:Ab:49:LYS:N	1:Ab:49:LYS:HD2	2.31	0.45
1:Ae:76:ARG:HH11	1:Ae:128:HIS:HD1	1.64	0.45
1:Ao:76:ARG:HH11	1:Ao:128:HIS:HD1	1.63	0.45
1:Ac:49:LYS:HD2	1:Ac:49:LYS:N	2.31	0.45
1:As:76:ARG:HH11	1:As:128:HIS:HD1	1.64	0.45
1:Aa:76:ARG:HH11	1:Aa:128:HIS:HD1	1.65	0.45
1:Ai:69:LEU:HG	1:Ai:137:TYR:OH	2.17	0.45
1:Ae:49:LYS:N	1:Ae:49:LYS:HD2	2.31	0.45
1:Ah:49:LYS:N	1:Ah:49:LYS:HD2	2.31	0.45
1:Aj:140:LYS:HA	1:Aj:143:LYS:HZ3	1.81	0.45
1:An:117:LEU:HD22	1:An:133:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:As:69:LEU:HG	1:As:137:TYR:OH	2.16	0.44
1:Ab:69:LEU:HG	1:Ab:137:TYR:OH	2.17	0.44
1:Ah:69:LEU:HG	1:Ah:137:TYR:OH	2.18	0.44
1:Al:69:LEU:HG	1:Al:137:TYR:OH	2.17	0.44
1:Au:49:LYS:N	1:Au:49:LYS:HD2	2.31	0.44
1:Ad:69:LEU:HG	1:Ad:137:TYR:OH	2.18	0.44
1:Ar:76:ARG:HH11	1:Ar:128:HIS:HD1	1.64	0.44
1:At:69:LEU:HG	1:At:137:TYR:OH	2.17	0.44
1:Af:76:ARG:HH11	1:Af:128:HIS:HD1	1.64	0.44
1:Af:94:GLU:H	1:Af:94:GLU:HG3	1.47	0.44
1:Ax:69:LEU:HG	1:Ax:137:TYR:OH	2.17	0.44
1:Ag:69:LEU:HG	1:Ag:137:TYR:OH	2.17	0.44
1:An:69:LEU:HG	1:An:137:TYR:OH	2.17	0.44
1:Ar:69:LEU:HG	1:Ar:137:TYR:OH	2.18	0.44
1:Aw:69:LEU:HG	1:Aw:137:TYR:OH	2.18	0.44
1:Ak:69:LEU:HG	1:Ak:137:TYR:OH	2.18	0.43
1:Au:69:LEU:HG	1:Au:137:TYR:OH	2.18	0.43
1:Ak:79:ARG:HA	1:Ak:79:ARG:HD3	1.82	0.43
1:Ae:69:LEU:HG	1:Ae:137:TYR:OH	2.18	0.43
1:Am:69:LEU:HG	1:Am:137:TYR:OH	2.18	0.43
1:Av:76:ARG:HH11	1:Av:128:HIS:HD1	1.66	0.43
1:Aa:69:LEU:HG	1:Aa:137:TYR:OH	2.17	0.43
1:Ag:86:LYS:HA	1:Ag:86:LYS:HD2	1.87	0.43
1:Ap:69:LEU:HG	1:Ap:137:TYR:OH	2.17	0.43
1:Ac:69:LEU:HG	1:Ac:137:TYR:OH	2.18	0.43
1:Ae:94:GLU:H	1:Ae:94:GLU:HG3	1.48	0.43
1:Af:69:LEU:HG	1:Af:137:TYR:OH	2.18	0.43
1:Ao:69:LEU:HG	1:Ao:137:TYR:OH	2.18	0.43
1:Aq:69:LEU:HG	1:Aq:137:TYR:OH	2.17	0.43
1:At:93:TRP:O	1:At:95:SER:N	2.52	0.43
1:Am:140:LYS:H	1:Am:140:LYS:CE	2.32	0.43
1:Ab:140:LYS:H	1:Ab:140:LYS:CE	2.32	0.43
1:Ad:140:LYS:H	1:Ad:140:LYS:CE	2.32	0.43
1:Ai:140:LYS:H	1:Ai:140:LYS:CE	2.32	0.43
1:Aj:69:LEU:HG	1:Aj:137:TYR:OH	2.17	0.43
1:Aa:140:LYS:H	1:Aa:140:LYS:CE	2.32	0.43
1:Ai:76:ARG:HH11	1:Ai:128:HIS:HD1	1.67	0.43
1:Ak:140:LYS:H	1:Ak:140:LYS:CE	2.32	0.43
1:Aw:140:LYS:H	1:Aw:140:LYS:CE	2.32	0.43
1:Ax:76:ARG:HH11	1:Ax:128:HIS:HD1	1.65	0.43
1:Ac:94:GLU:H	1:Ac:94:GLU:HG3	1.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ao:94:GLU:H	1:Ao:94:GLU:HG3	1.49	0.42
1:Ac:140:LYS:H	1:Ac:140:LYS:CE	2.32	0.42
1:Af:140:LYS:H	1:Af:140:LYS:CE	2.32	0.42
1:Ap:140:LYS:H	1:Ap:140:LYS:CE	2.32	0.42
1:Av:69:LEU:HG	1:Av:137:TYR:OH	2.18	0.42
1:Aa:93:TRP:O	1:Aa:95:SER:N	2.52	0.42
1:Aj:86:LYS:HA	1:Aj:86:LYS:HD2	1.81	0.42
1:Av:140:LYS:H	1:Av:140:LYS:CE	2.32	0.42
1:Ag:140:LYS:H	1:Ag:140:LYS:CE	2.32	0.42
1:An:140:LYS:H	1:An:140:LYS:CE	2.32	0.42
1:Ar:140:LYS:H	1:Ar:140:LYS:CE	2.32	0.42
1:As:93:TRP:O	1:As:95:SER:N	2.53	0.42
1:Ah:94:GLU:H	1:Ah:94:GLU:HG3	1.54	0.42
1:As:86:LYS:HA	1:As:86:LYS:HD2	1.89	0.42
1:Ak:93:TRP:O	1:Ak:95:SER:N	2.53	0.41
1:At:76:ARG:HH11	1:At:128:HIS:HD1	1.68	0.41
1:Ar:79:ARG:HA	1:Ar:79:ARG:HD3	1.82	0.41
1:At:79:ARG:HA	1:At:79:ARG:HD3	1.82	0.41
1:Ae:140:LYS:H	1:Ae:140:LYS:CE	2.32	0.41
1:Al:140:LYS:H	1:Al:140:LYS:CE	2.32	0.41
1:Ax:79:ARG:HA	1:Ax:79:ARG:HD3	1.86	0.41
1:Ad:93:TRP:O	1:Ad:95:SER:N	2.53	0.41
1:Am:93:TRP:O	1:Am:95:SER:N	2.54	0.41
1:Ak:94:GLU:H	1:Ak:94:GLU:HG3	1.51	0.41
1:Ac:136:HIS:C	1:Ac:140:LYS:HE3	2.46	0.40
1:Ab:136:HIS:C	1:Ab:140:LYS:HE3	2.46	0.40
1:Ae:79:ARG:HA	1:Ae:79:ARG:HD3	1.80	0.40
1:Aj:93:TRP:O	1:Aj:95:SER:N	2.55	0.40
1:Ab:79:ARG:HD3	1:Ab:79:ARG:HA	1.80	0.40
1:Ae:136:HIS:C	1:Ae:140:LYS:HE3	2.47	0.40
1:An:136:HIS:C	1:An:140:LYS:HE3	2.46	0.40
1:Ap:136:HIS:C	1:Ap:140:LYS:HE3	2.47	0.40

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	Aa	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Ab	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Ac	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Ad	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Ae	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Af	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Ag	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Ah	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Ai	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Aj	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Ak	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Al	149/159 (94%)	146 (98%)	3 (2%)	0	100	100
1	Am	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	An	149/159 (94%)	146 (98%)	3 (2%)	0	100	100
1	Ao	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Ap	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Aq	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Ar	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	As	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	At	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Au	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
1	Av	149/159 (94%)	146 (98%)	3 (2%)	0	100	100
1	Aw	149/159 (94%)	146 (98%)	3 (2%)	0	100	100
1	Ax	149/159 (94%)	147 (99%)	2 (1%)	0	100	100
All	All	3576/3816 (94%)	3524 (98%)	52 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	Aa	137/143 (96%)	137 (100%)	0	100	100
1	Ab	137/143 (96%)	137 (100%)	0	100	100
1	Ac	137/143 (96%)	137 (100%)	0	100	100
1	Ad	137/143 (96%)	137 (100%)	0	100	100
1	Ae	137/143 (96%)	137 (100%)	0	100	100
1	Af	137/143 (96%)	137 (100%)	0	100	100
1	Ag	137/143 (96%)	137 (100%)	0	100	100
1	Ah	137/143 (96%)	137 (100%)	0	100	100
1	Ai	137/143 (96%)	137 (100%)	0	100	100
1	Aj	137/143 (96%)	137 (100%)	0	100	100
1	Ak	137/143 (96%)	137 (100%)	0	100	100
1	Al	137/143 (96%)	137 (100%)	0	100	100
1	Am	137/143 (96%)	137 (100%)	0	100	100
1	An	137/143 (96%)	136 (99%)	1 (1%)	76	67
1	Ao	137/143 (96%)	137 (100%)	0	100	100
1	Ap	137/143 (96%)	137 (100%)	0	100	100
1	Aq	137/143 (96%)	137 (100%)	0	100	100
1	Ar	137/143 (96%)	137 (100%)	0	100	100
1	As	137/143 (96%)	137 (100%)	0	100	100
1	At	137/143 (96%)	137 (100%)	0	100	100
1	Au	137/143 (96%)	137 (100%)	0	100	100
1	Av	137/143 (96%)	136 (99%)	1 (1%)	76	67
1	Aw	137/143 (96%)	137 (100%)	0	100	100
1	Ax	137/143 (96%)	136 (99%)	1 (1%)	76	67
All	All	3288/3432 (96%)	3285 (100%)	3 (0%)	87	84

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	An	117	LEU
1	Av	117	LEU
1	Ax	91	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	Aa	139	ASN
1	Aa	154	ASN
1	Ab	112	GLN
1	Ab	154	ASN
1	Ac	139	ASN
1	Ad	154	ASN
1	Ae	112	GLN
1	Ae	154	ASN
1	Af	65	HIS
1	Af	112	GLN
1	Af	154	ASN
1	Ag	139	ASN
1	Ag	154	ASN
1	Ah	58	GLN
1	Ah	154	ASN
1	Ai	112	GLN
1	Ai	154	ASN
1	Aj	154	ASN
1	Ak	25	ASN
1	Ak	65	HIS
1	Ak	154	ASN
1	Am	112	GLN
1	Am	154	ASN
1	An	65	HIS
1	An	154	ASN
1	Ao	65	HIS
1	Ao	154	ASN
1	Ap	112	GLN
1	Ap	154	ASN
1	Aq	154	ASN
1	Ar	58	GLN
1	Ar	65	HIS
1	Ar	136	HIS
1	Ar	154	ASN
1	As	25	ASN
1	As	58	GLN

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Mol	Chain	Res	Type
1	As	154	ASN
1	At	112	GLN
1	At	154	ASN
1	Au	65	HIS
1	Au	112	GLN
1	Au	154	ASN
1	Av	154	ASN
1	Aw	154	ASN
1	Ax	57	HIS
1	Ax	154	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.

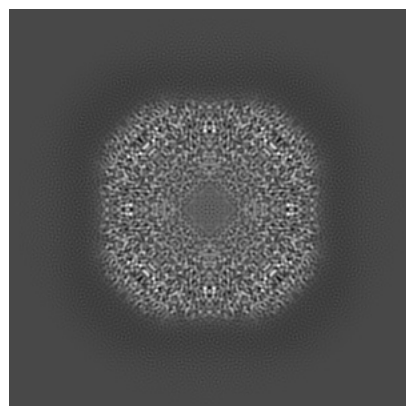
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62216. These allow visual inspection of the internal detail of the map and identification of artifacts.

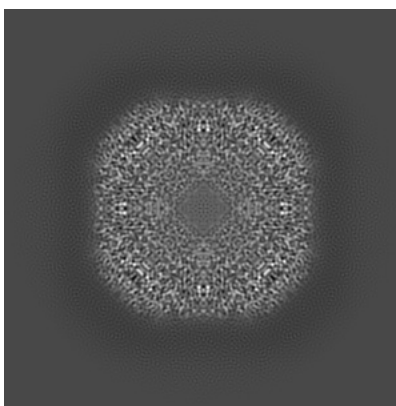
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

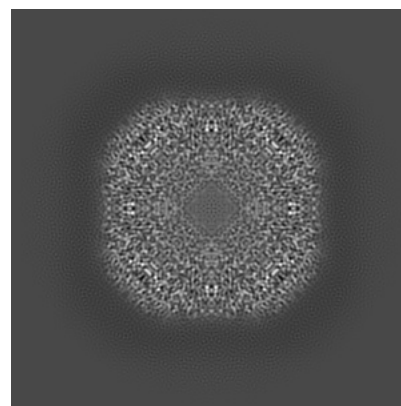
6.1.1 Primary map



X

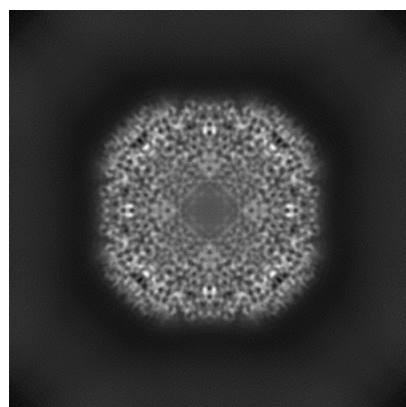


Y

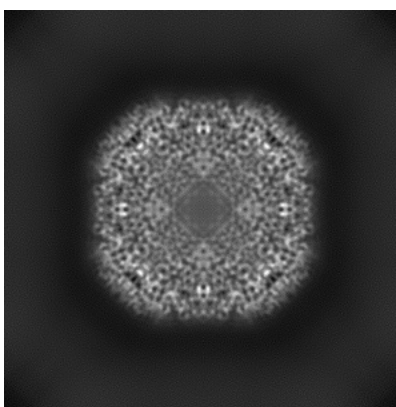


Z

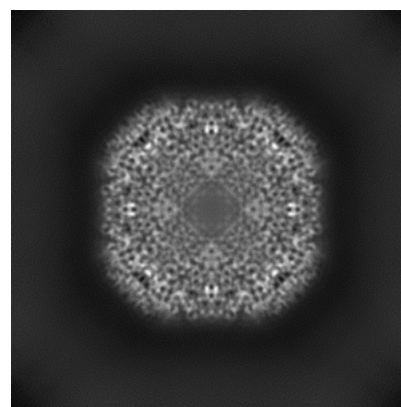
6.1.2 Raw map



X



Y

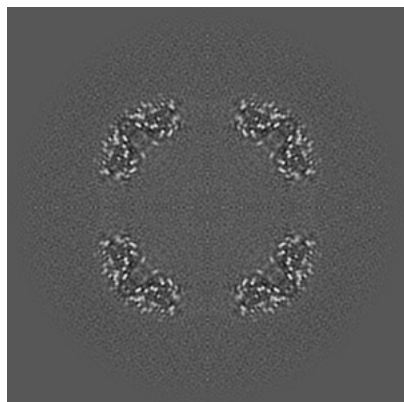


Z

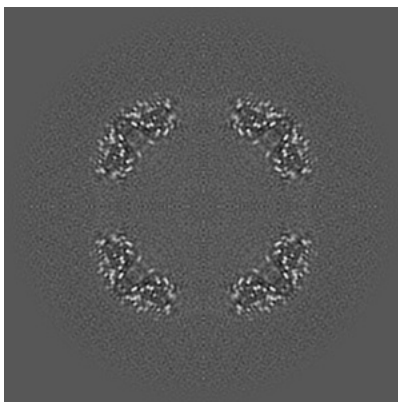
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

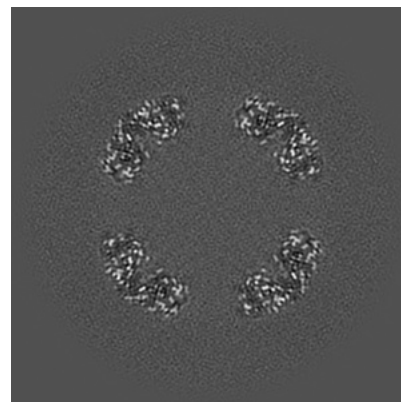
6.2.1 Primary map



X Index: 192

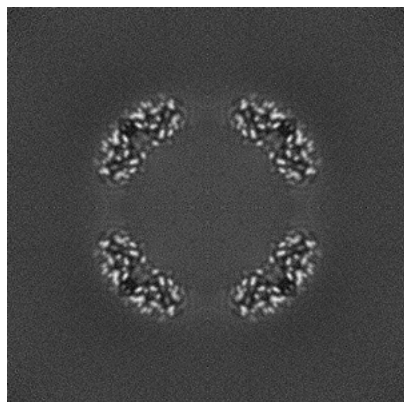


Y Index: 192

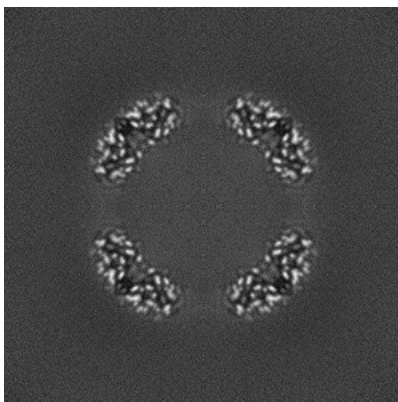


Z Index: 192

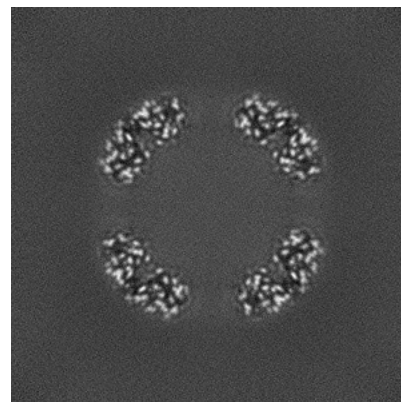
6.2.2 Raw map



X Index: 192



Y Index: 192

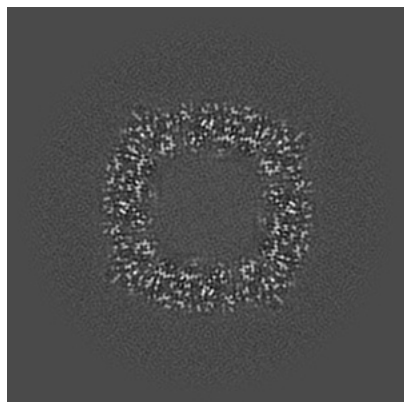


Z Index: 192

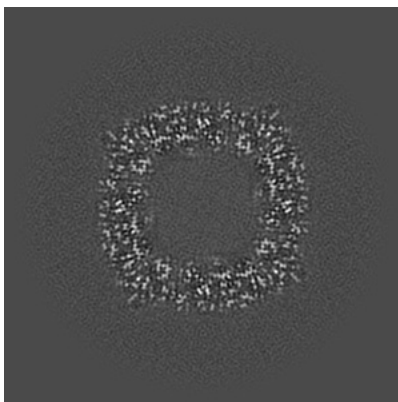
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

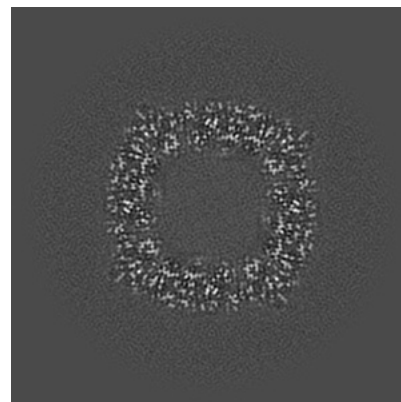
6.3.1 Primary map



X Index: 138

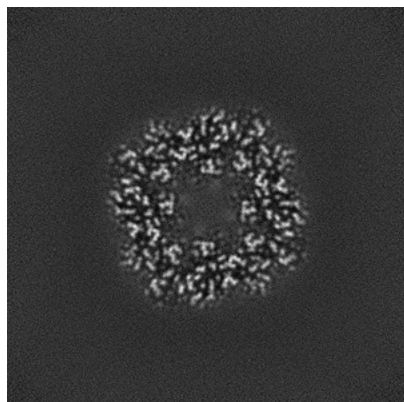


Y Index: 246

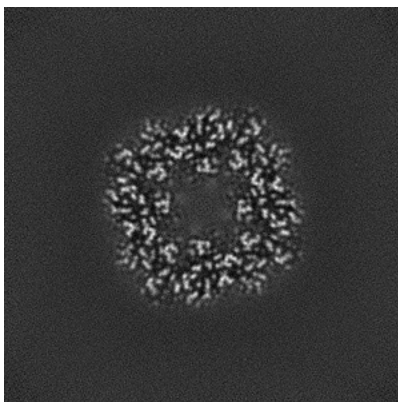


Z Index: 137

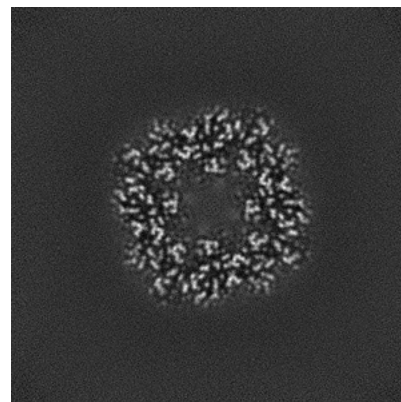
6.3.2 Raw map



X Index: 118



Y Index: 118

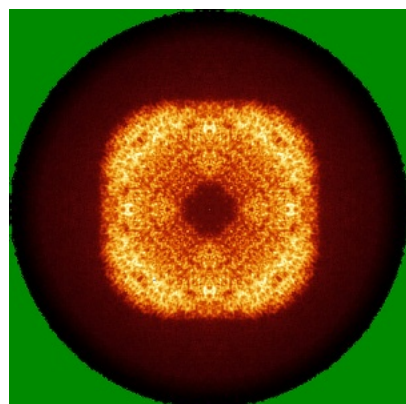


Z Index: 117

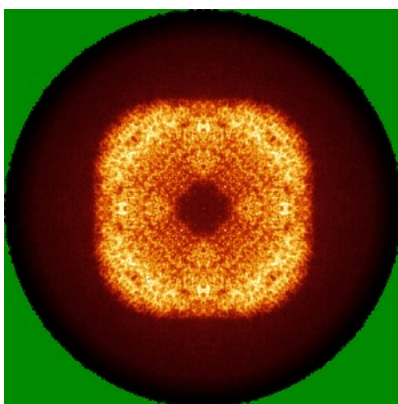
The images above show the largest variance slices of the map in three orthogonal directions.

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

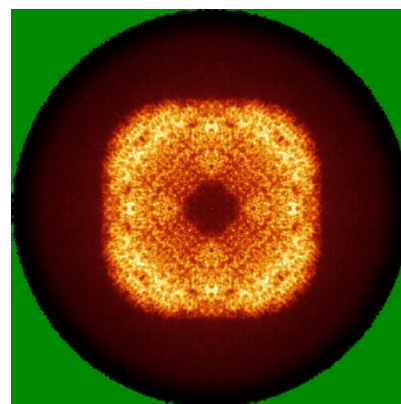
6.4.1 Primary map



X

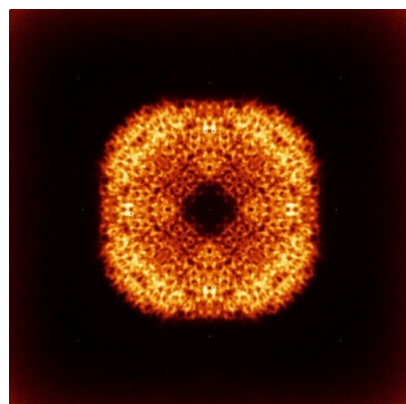


Y

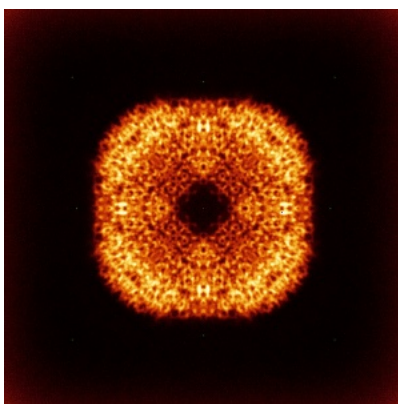


Z

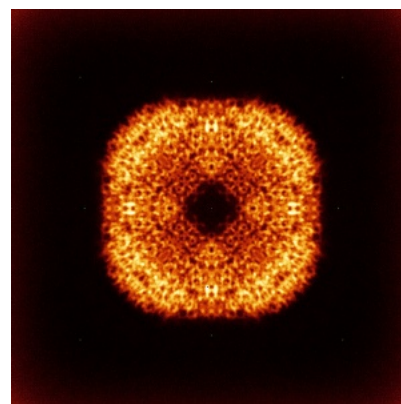
6.4.2 Raw map



X



Y

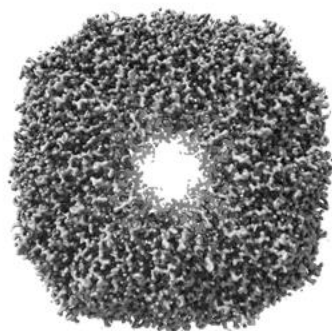


Z

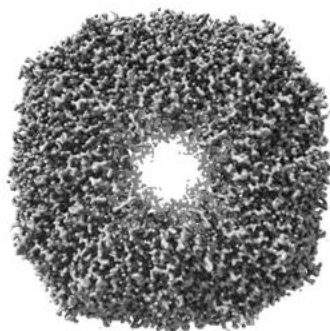
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

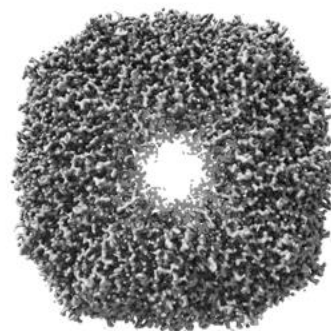
6.5.1 Primary map



X



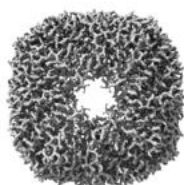
Y



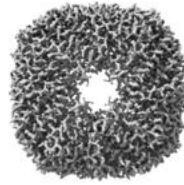
Z

The images above show the 3D surface view of the map at the recommended contour level 0.151. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

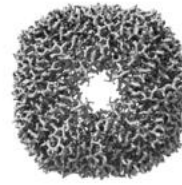
6.5.2 Raw map



X



Y



Z

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

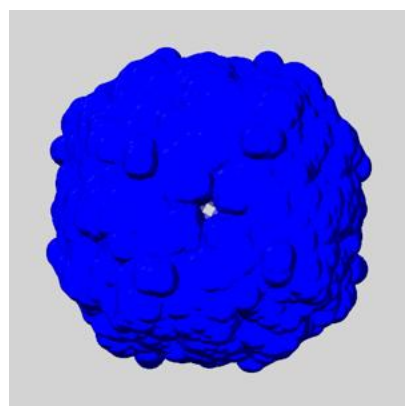
6.6 Mask visualisation [i](#)

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

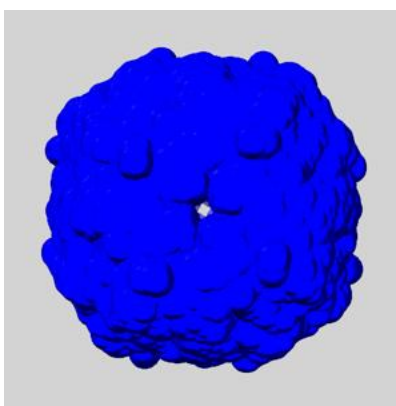
A mask typically either:

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

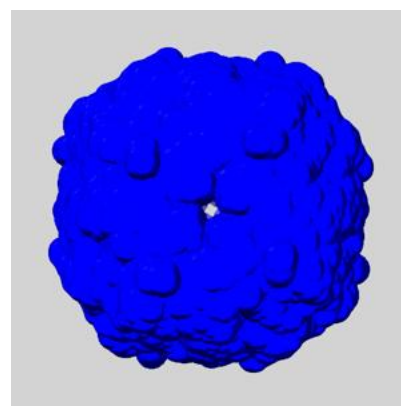
6.6.1 emd_62216_msk_1.map [i](#)



X



Y

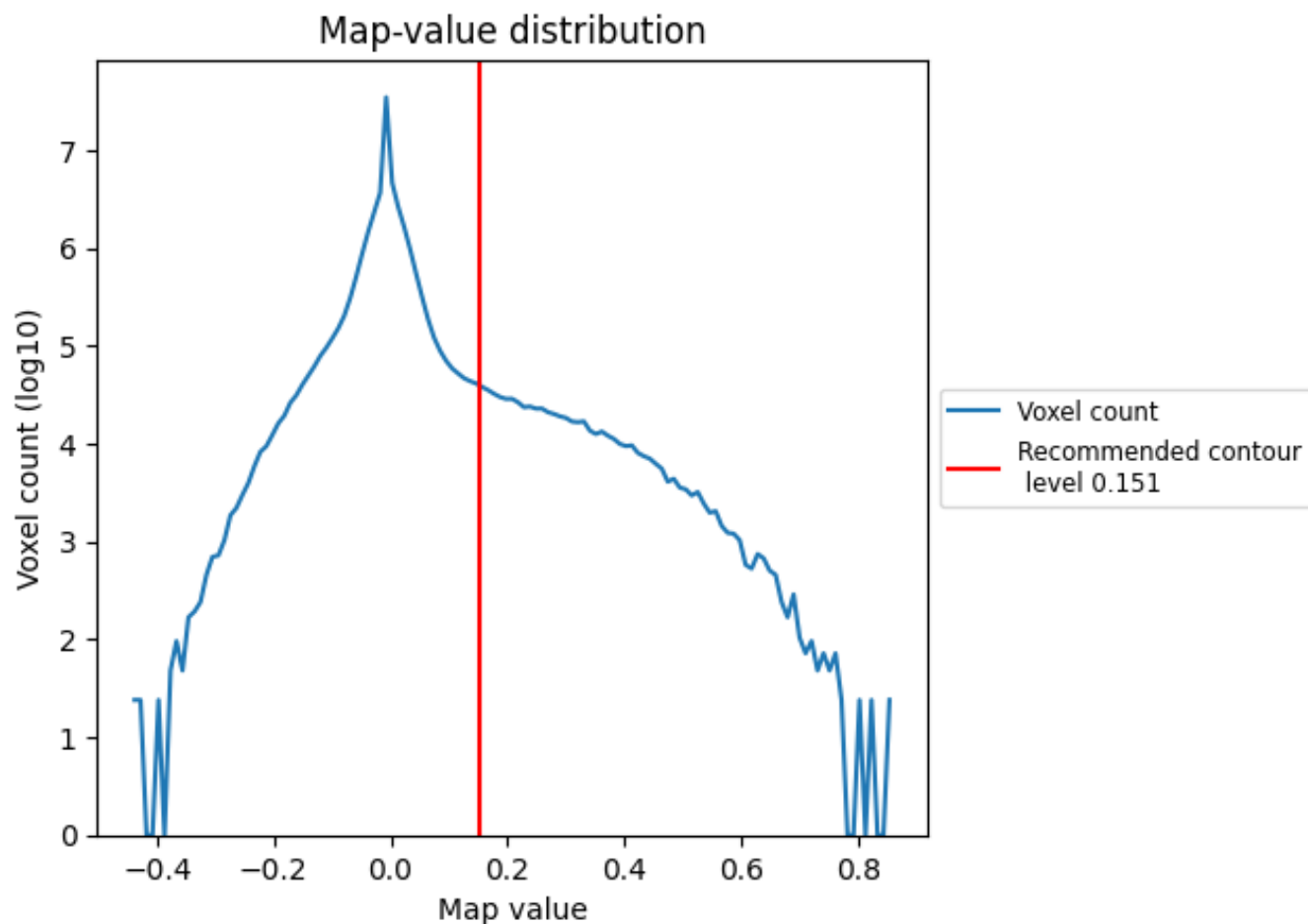


Z

7 Map analysis [i](#)

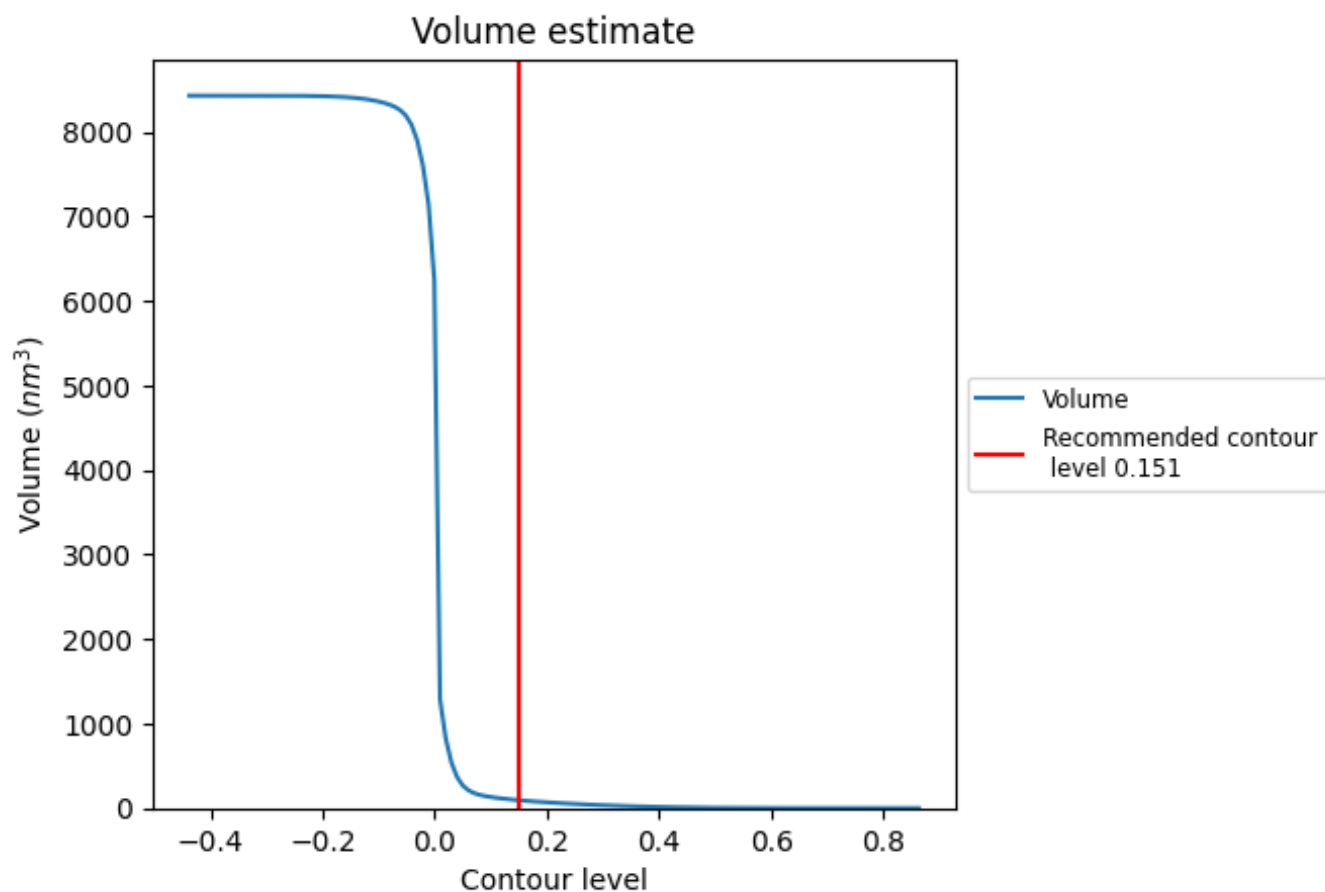
This section contains the results of statistical analysis of the map.

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.

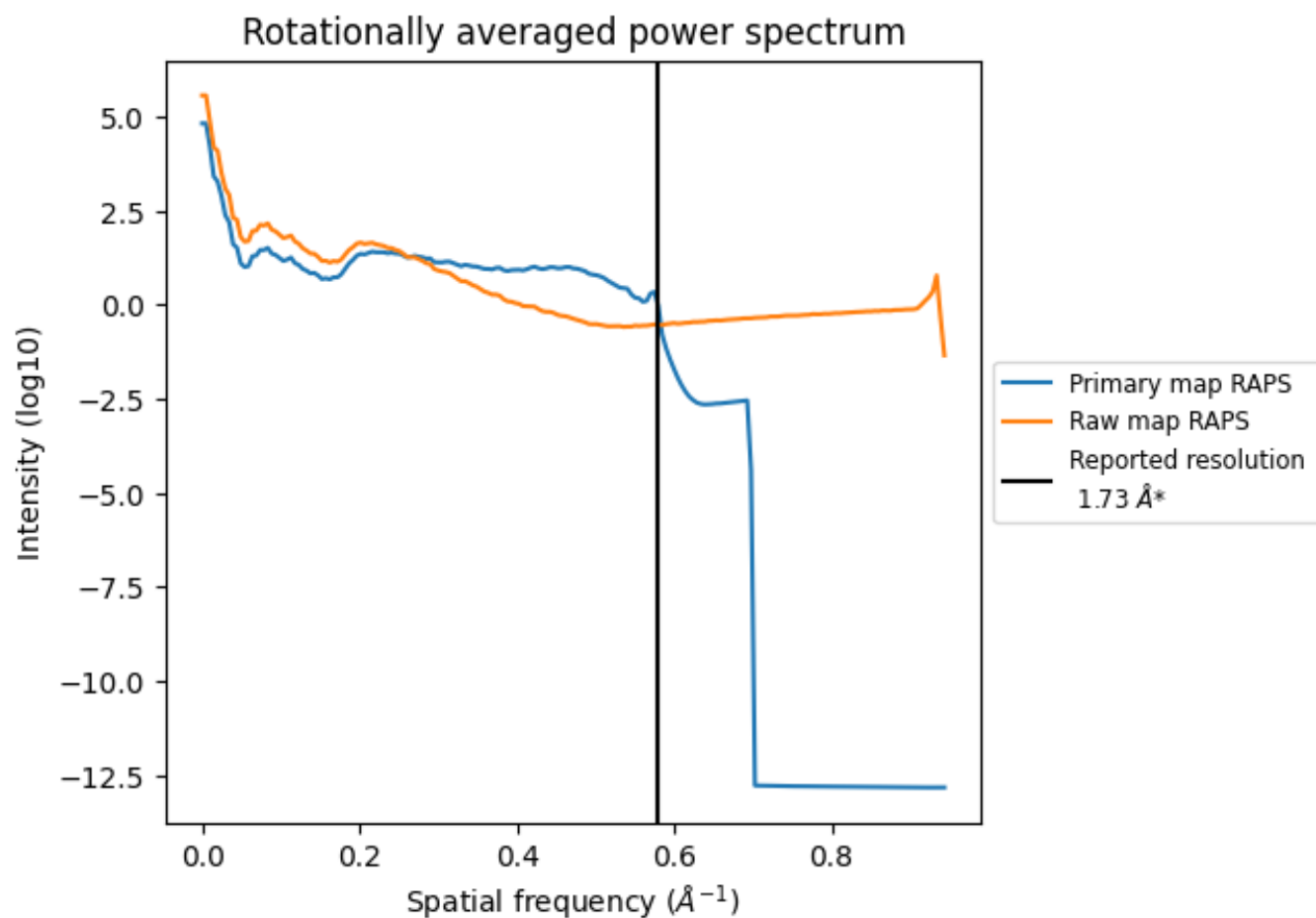
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 93 nm³; this corresponds to an approximate mass of 84 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 ⓘ

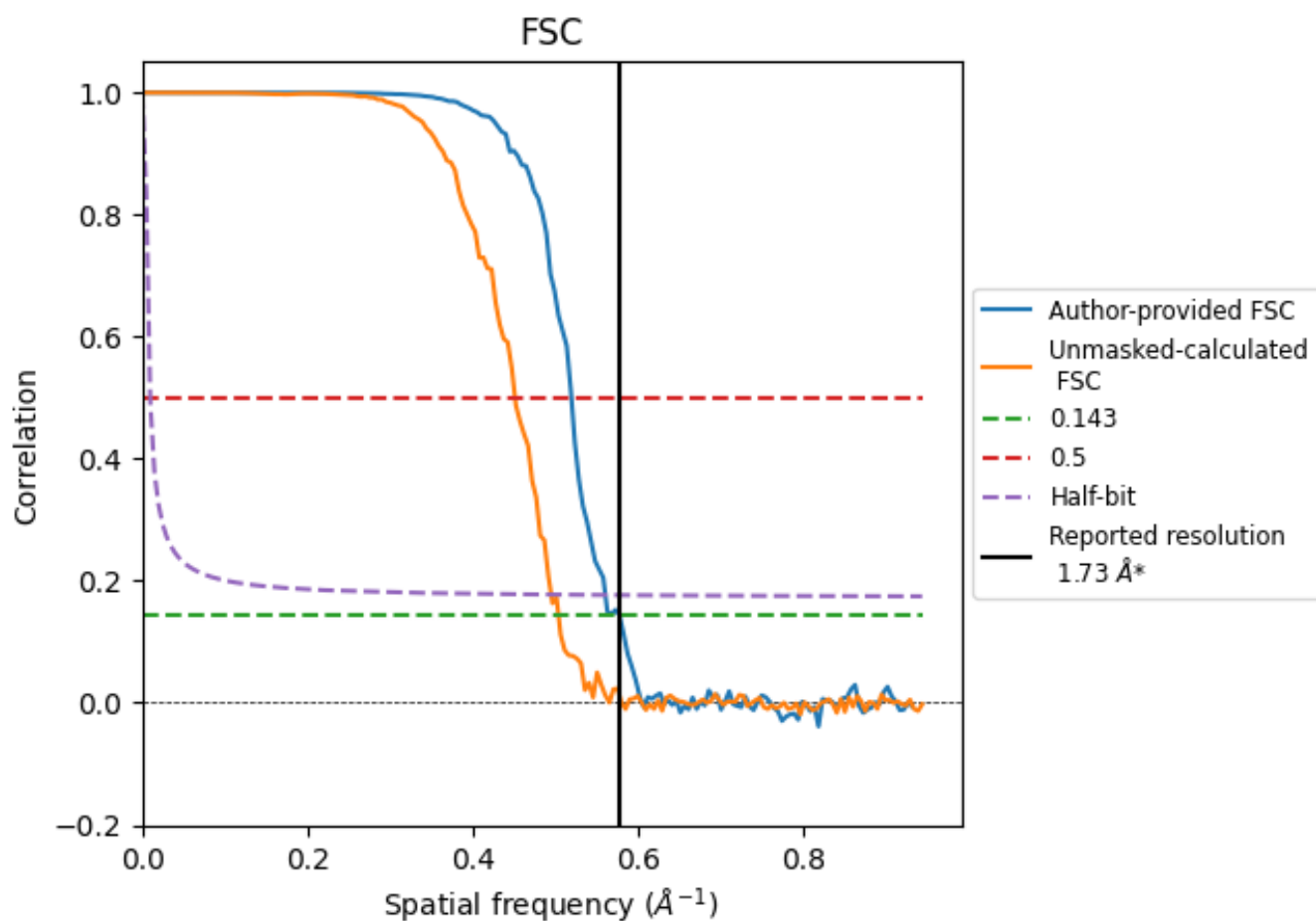


*Reported resolution corresponds to spatial frequency of 0.578 Å⁻¹

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 0.578 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

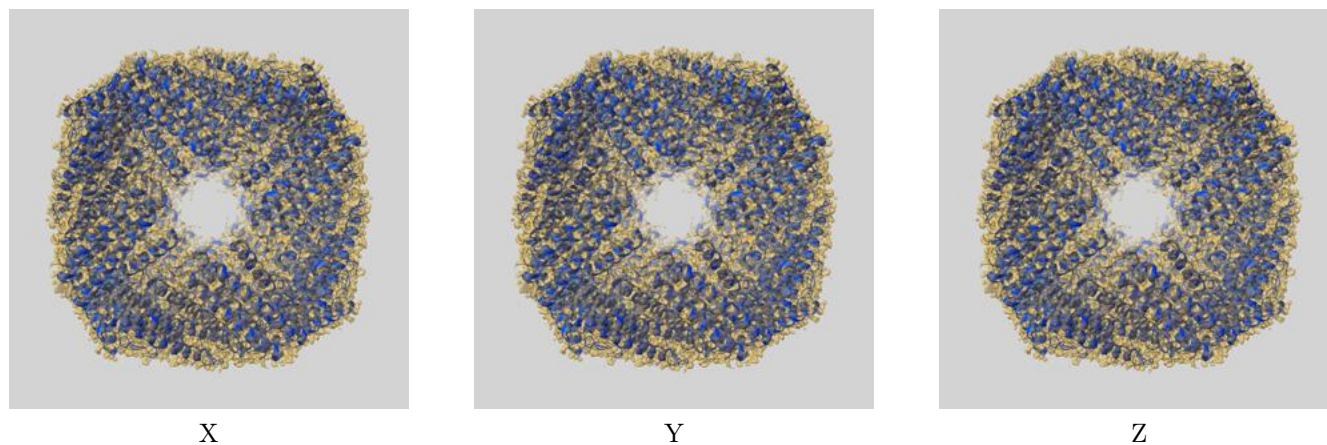
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.73	-	-
Author-provided FSC curve	1.73	1.93	1.79
Unmasked-calculated*	1.99	2.22	2.02

*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 1.99 differs from the reported value 1.73 by more than 10 %

9 Map-model fit [i](#)

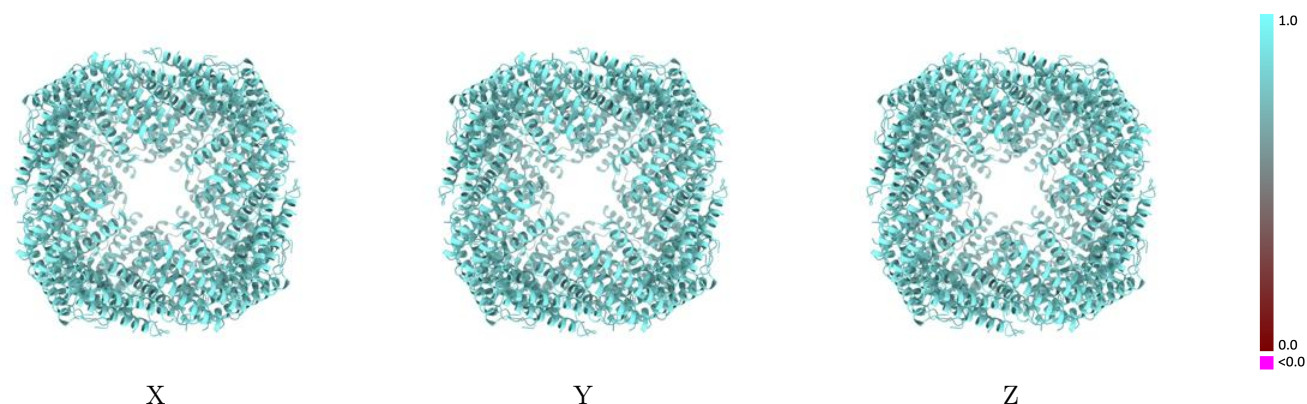
This section contains information regarding the fit between EMDB map EMD-62216 and PDB model 9KAY. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



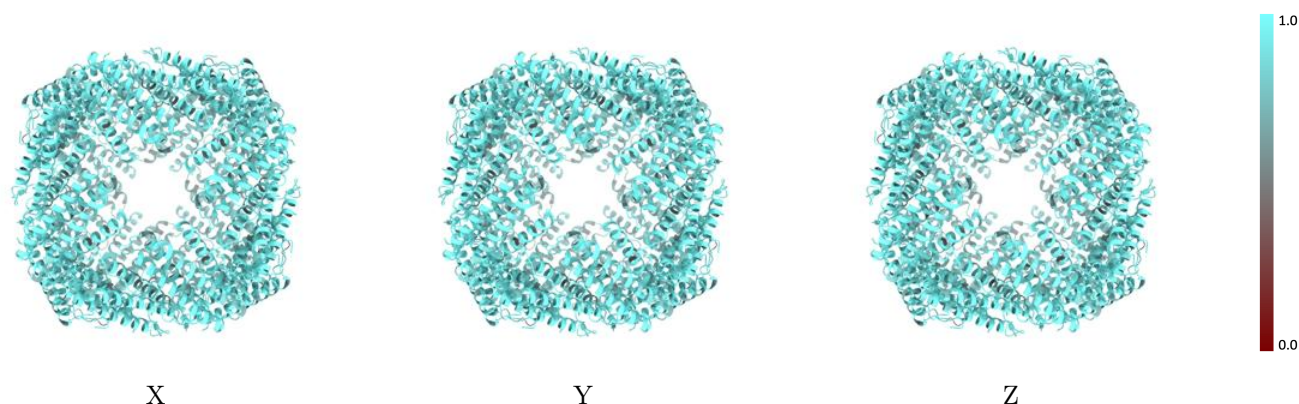
The images above show the 3D surface view of the map at the recommended contour level 0.151 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



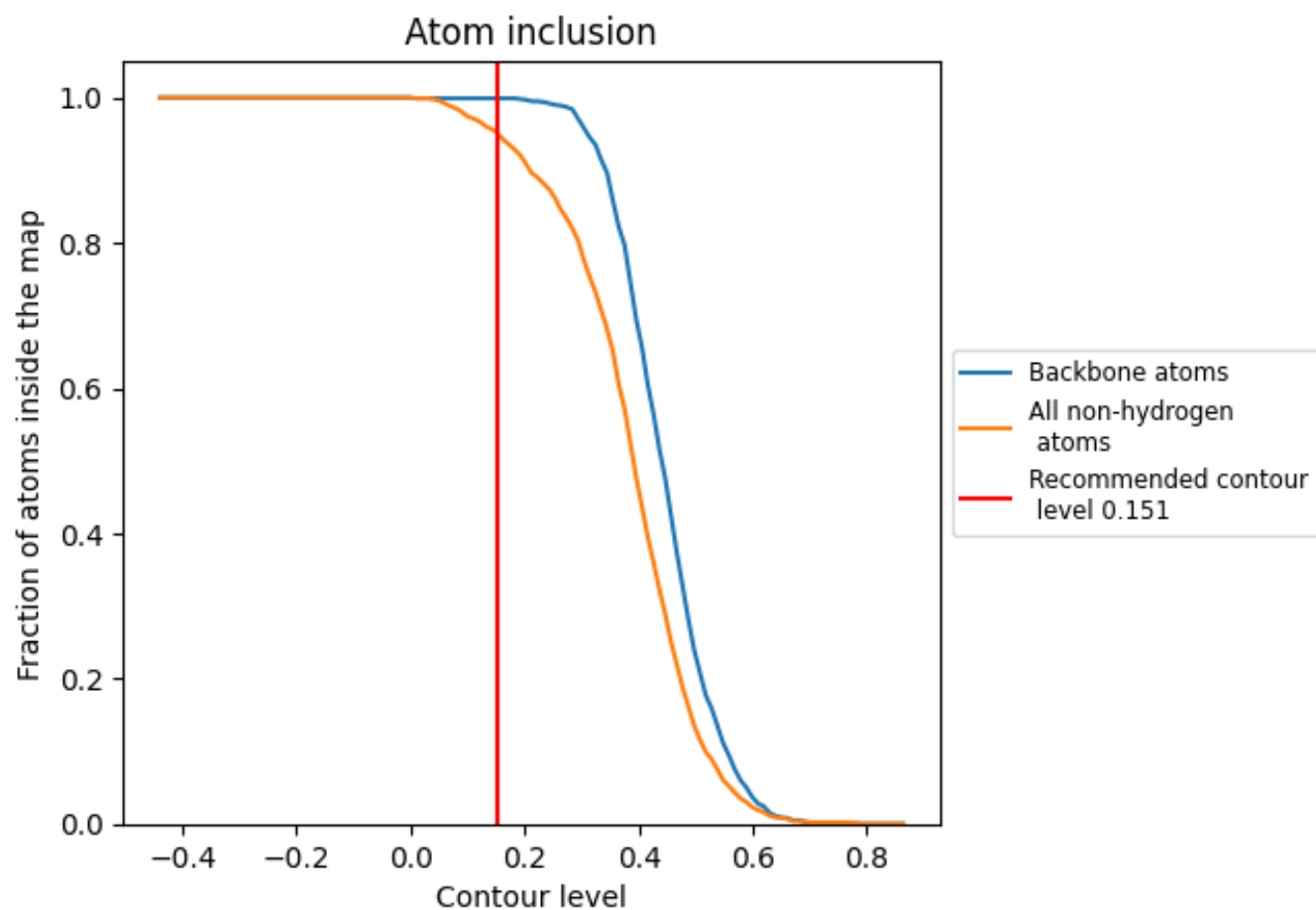
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.151).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 95% 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 (0.151) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9530	 0.8350
Aa	 0.9530	 0.8350
Ab	 0.9550	 0.8360
Ac	 0.9540	 0.8360
Ad	 0.9510	 0.8360
Ae	 0.9550	 0.8340
Af	 0.9520	 0.8370
Ag	 0.9530	 0.8340
Ah	 0.9510	 0.8340
Ai	 0.9510	 0.8370
Aj	 0.9510	 0.8360
Ak	 0.9520	 0.8360
Al	 0.9550	 0.8350
Am	 0.9520	 0.8350
An	 0.9550	 0.8360
Ao	 0.9510	 0.8350
Ap	 0.9510	 0.8360
Aq	 0.9540	 0.8340
Ar	 0.9510	 0.8360
As	 0.9520	 0.8330
At	 0.9510	 0.8350
Au	 0.9540	 0.8360
Av	 0.9530	 0.8350
Aw	 0.9530	 0.8360
Ax	 0.9510	 0.8350

