



wwPDB EM Validation Summary Report ⓘ

Oct 19, 2026 – 08:33 PM JST

PDB ID : 9X10 / pdb_00009x10
EMDB ID : EMD-66451
Title : Cryo-EM structure of the apo form of the KomBC filament
Authors : Li, X.; Liu, M.; Jiang, W.X.; Xing, Q.; Ma, L.X.; Huang, F.T.
Deposited on : 2025-10-01
Resolution : 3.01 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:

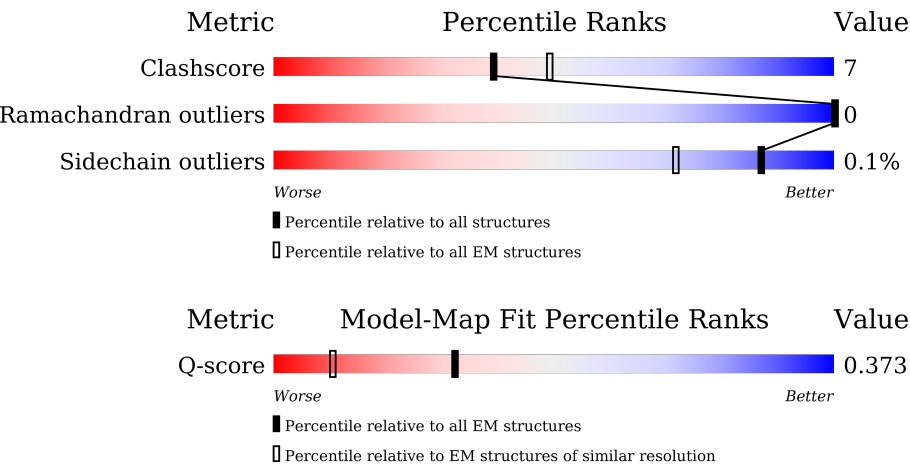
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.2
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.01 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	13882 (2.51 - 3.51)

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	197	<div><div>38%</div><div><div></div><div>78%</div><div>17%</div><div>5%</div></div></div>
1	AB	197	<div><div>40%</div><div><div></div><div>73%</div><div>22%</div><div>5%</div></div></div>
1	AE	197	<div><div>21%</div><div><div></div><div>79%</div><div>16%</div><div>5%</div></div></div>
1	AF	197	<div><div>16%</div><div><div></div><div>82%</div><div>13%</div><div>5%</div></div></div>

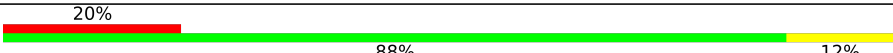
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Mol	Chain	Length	Quality of chain
1	BA	197	
1	BB	197	
1	BE	197	
1	BF	197	
1	BI	197	
1	BJ	197	
1	BM	197	
1	BN	197	
1	CA	197	
1	CB	197	
1	CE	197	
1	CF	197	
1	CI	197	
1	CJ	197	
1	CM	197	
1	CN	197	
1	DI	197	
1	DJ	197	
1	DM	197	
1	DN	197	
2	AC	264	
2	AD	264	
2	AG	264	
2	AH	264	
2	BC	264	

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Mol	Chain	Length	Quality of chain
2	BD	264	 89%11%
2	BG	264	 91%9%
2	BH	264	 92%8%
2	BK	264	 89%11%
2	BL	264	 81%19%
2	BO	264	 89%11%
2	BP	264	 89%11%
2	CC	264	 82%18%
2	CD	264	 91%9%
2	CG	264	 7%90%10%
2	CH	264	 92%8%
2	CK	264	 89%11%
2	CL	264	 80%20%
2	CO	264	 90%10%
2	CP	264	 88%12%
2	DK	264	 90%10%
2	DL	264	 81%19%
2	DO	264	 89%11%
2	DP	264	 20%88%12%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 87720 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 KomB.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	AB	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	AE	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	AF	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	BA	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	BB	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	BE	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	BF	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	BI	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	BJ	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	BM	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	BN	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	CA	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	CB	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	CE	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	CF	187	Total 1489	C 954	N 252	O 277	S 6	0	0
1	CI	187	Total 1489	C 954	N 252	O 277	S 6	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CJ	187	Total	C	N	O	S	0	0
			1489	954	252	277	6		
1	CM	187	Total	C	N	O	S	0	0
			1489	954	252	277	6		
1	CN	187	Total	C	N	O	S	0	0
			1489	954	252	277	6		
1	DI	187	Total	C	N	O	S	0	0
			1489	954	252	277	6		
1	DJ	187	Total	C	N	O	S	0	0
			1489	954	252	277	6		
1	DM	187	Total	C	N	O	S	0	0
			1489	954	252	277	6		
1	DN	187	Total	C	N	O	S	0	0
			1489	954	252	277	6		

- Molecule 2 is a protein called KomC.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AC	264	Total	C	N	O	S	0	0
			2166	1403	348	410	5		
2	AD	264	Total	C	N	O	S	0	0
			2166	1403	348	410	5		
2	AG	264	Total	C	N	O	S	0	0
			2166	1403	348	410	5		
2	AH	264	Total	C	N	O	S	0	0
			2166	1403	348	410	5		
2	BC	264	Total	C	N	O	S	0	0
			2166	1403	348	410	5		
2	BD	264	Total	C	N	O	S	0	0
			2166	1403	348	410	5		
2	BG	264	Total	C	N	O	S	0	0
			2166	1403	348	410	5		
2	BH	264	Total	C	N	O	S	0	0
			2166	1403	348	410	5		
2	BK	264	Total	C	N	O	S	0	0
			2166	1403	348	410	5		
2	BL	264	Total	C	N	O	S	0	0
			2166	1403	348	410	5		
2	BO	264	Total	C	N	O	S	0	0
			2166	1403	348	410	5		
2	BP	264	Total	C	N	O	S	0	0
			2166	1403	348	410	5		

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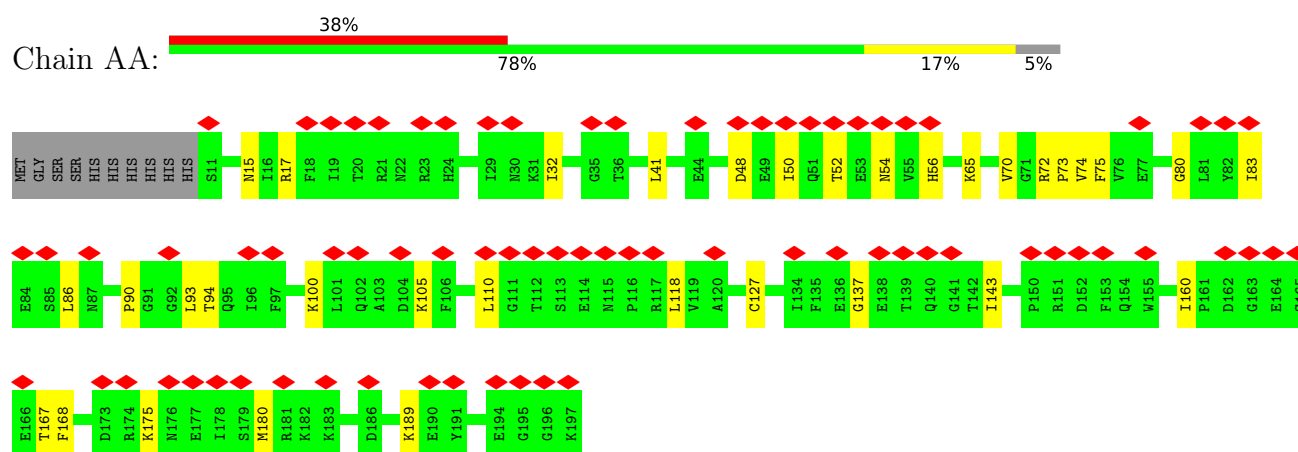
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	CC	264	Total 2166	C 1403	N 348	O 410	S 5	0	0
2	CD	264	Total 2166	C 1403	N 348	O 410	S 5	0	0
2	CG	264	Total 2166	C 1403	N 348	O 410	S 5	0	0
2	CH	264	Total 2166	C 1403	N 348	O 410	S 5	0	0
2	CK	264	Total 2166	C 1403	N 348	O 410	S 5	0	0
2	CL	264	Total 2166	C 1403	N 348	O 410	S 5	0	0
2	CO	264	Total 2166	C 1403	N 348	O 410	S 5	0	0
2	CP	264	Total 2166	C 1403	N 348	O 410	S 5	0	0
2	DK	264	Total 2166	C 1403	N 348	O 410	S 5	0	0
2	DL	264	Total 2166	C 1403	N 348	O 410	S 5	0	0
2	DO	264	Total 2166	C 1403	N 348	O 410	S 5	0	0
2	DP	264	Total 2166	C 1403	N 348	O 410	S 5	0	0

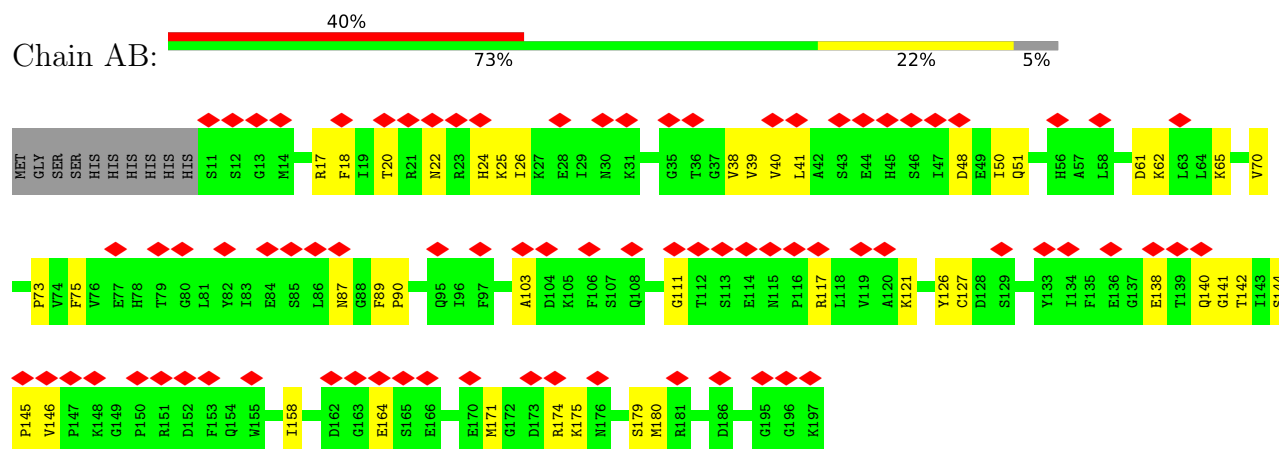
3 Residue-property plots

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.

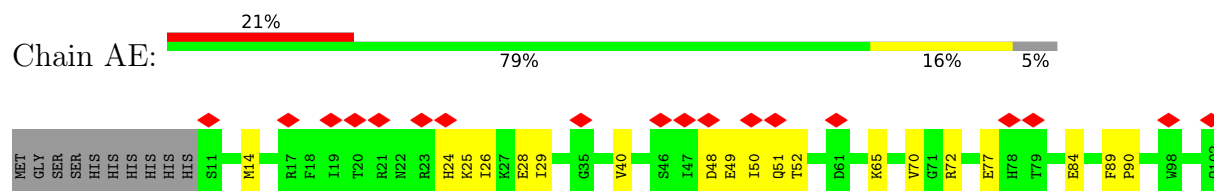
• Molecule 1: KomB



• Molecule 1: KomB

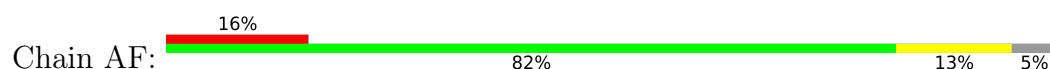
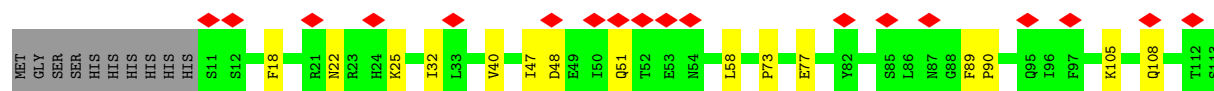
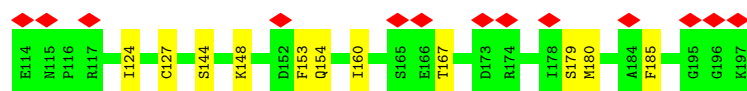


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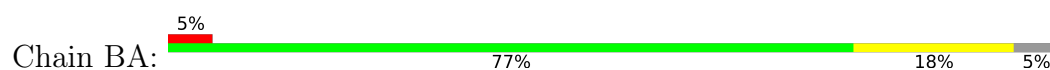
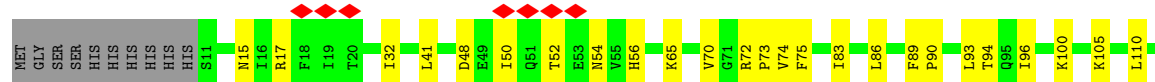




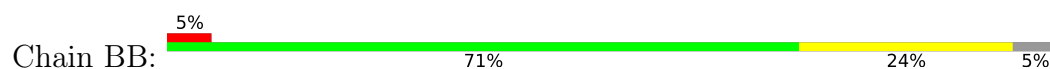
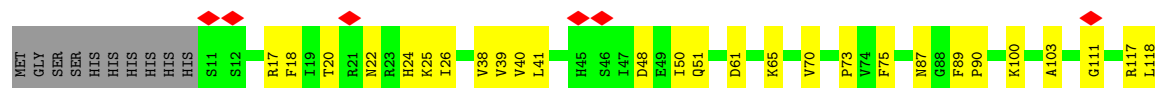
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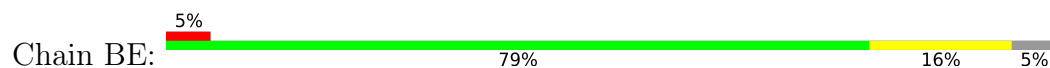
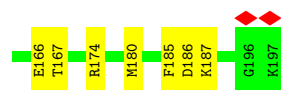
- Molecule 1: KomB



- Molecule 1: KomB

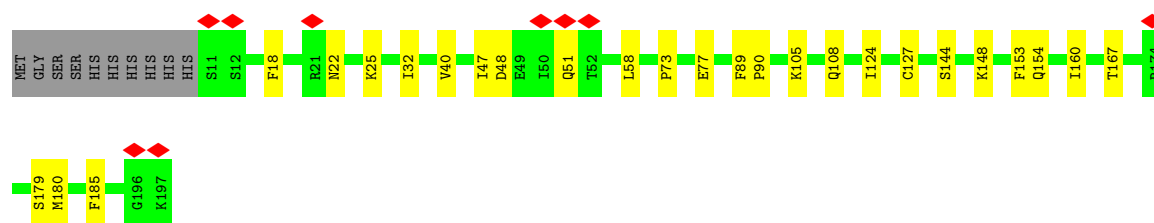


- Molecule 1: KomB



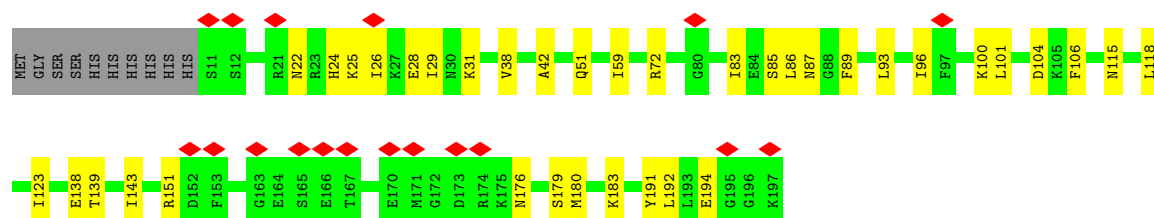
- Molecule 1: KomB

Chain BF: 



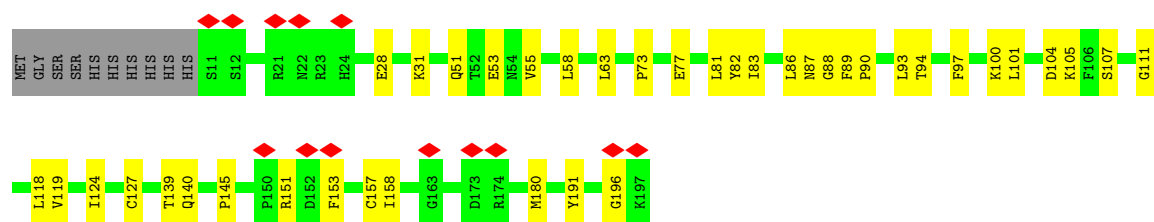
• Molecule 1: KomB

Chain BI: 



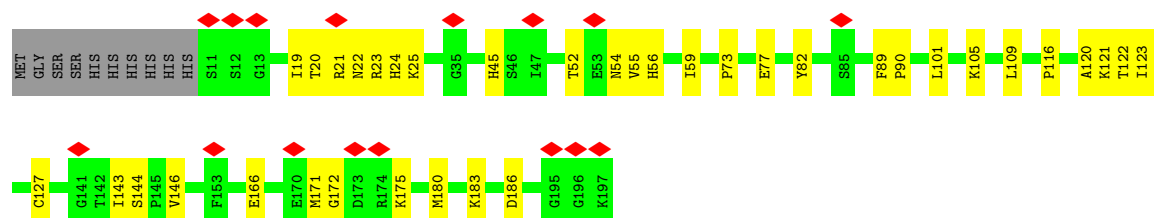
• Molecule 1: KomB

Chain BJ: 



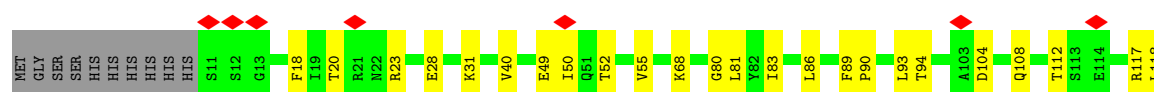
• Molecule 1: KomB

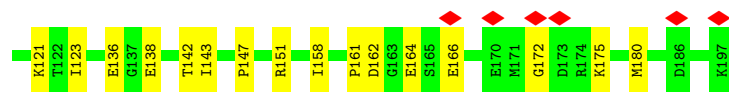
Chain BM: 



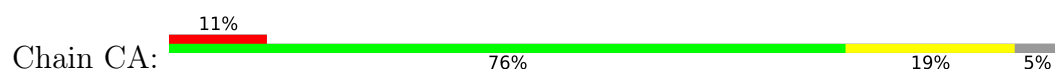
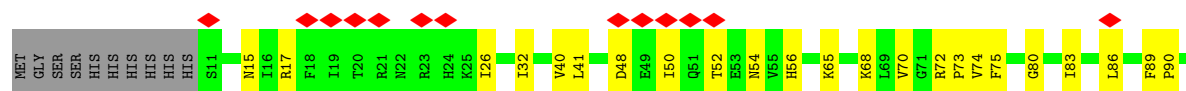
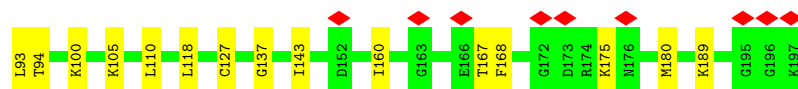
• Molecule 1: KomB

Chain BN: 

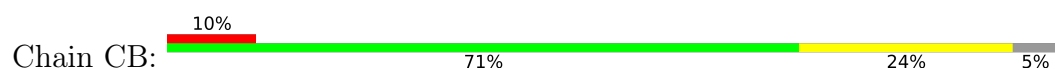
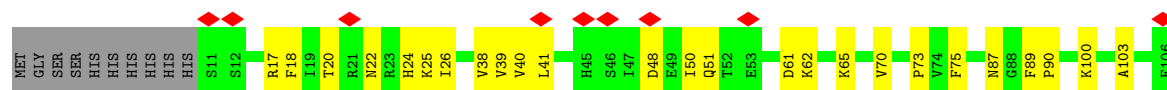
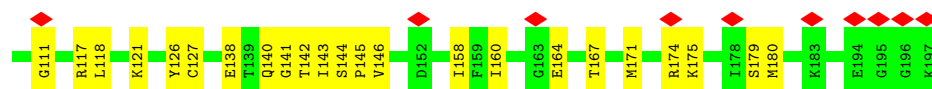




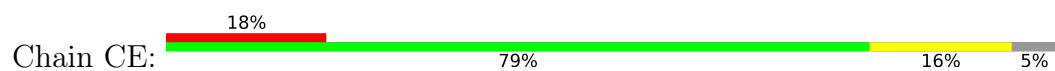
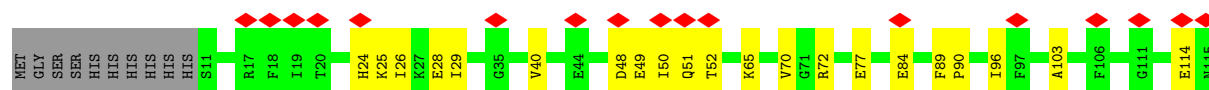
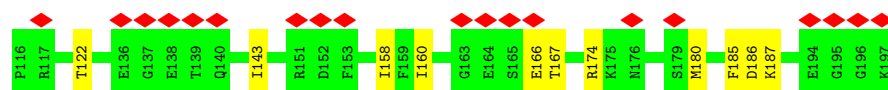
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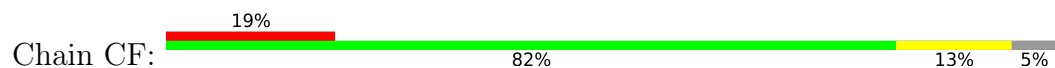
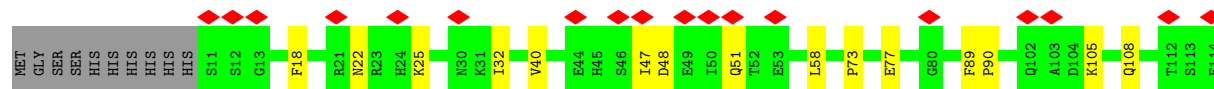
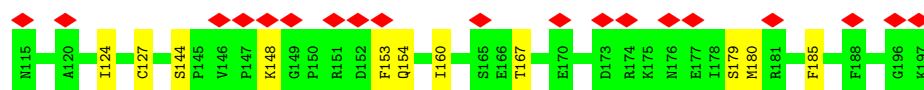
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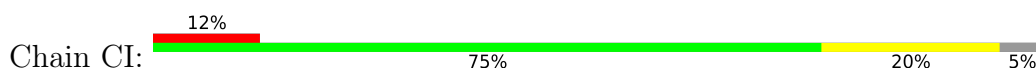
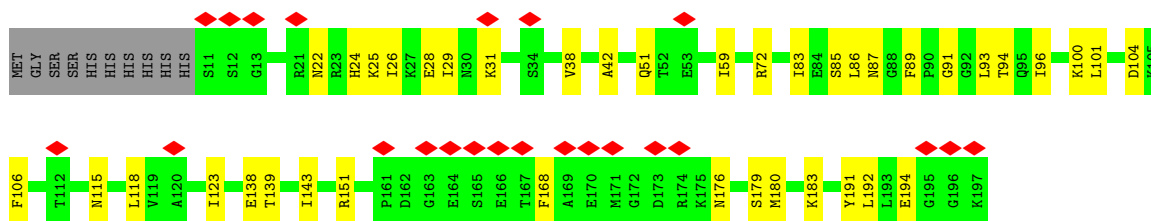
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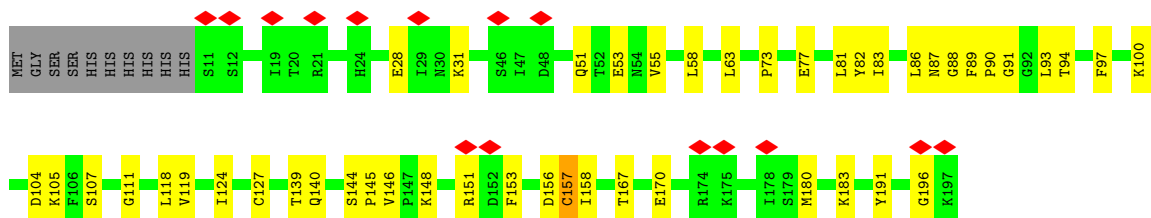
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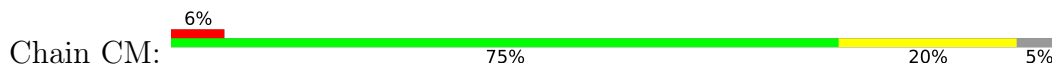
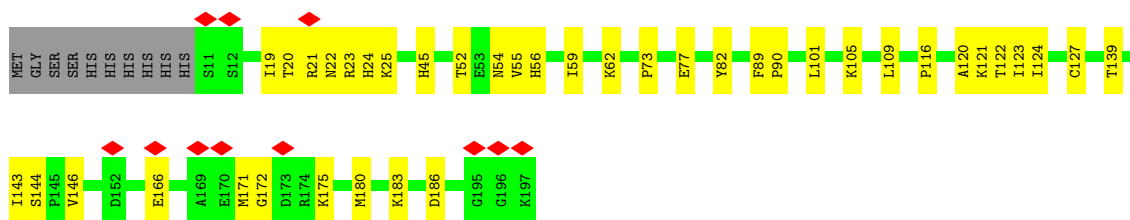
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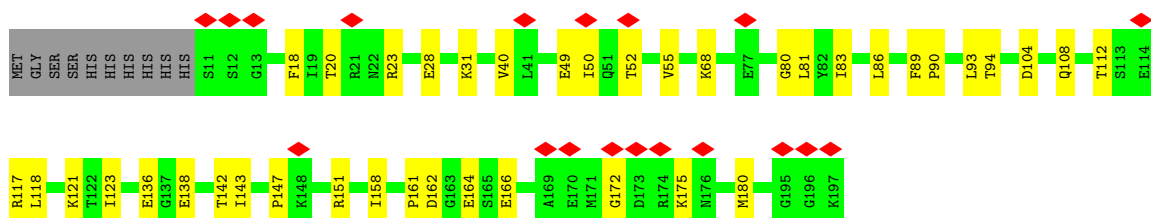
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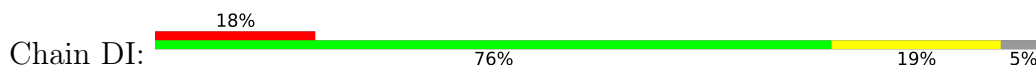
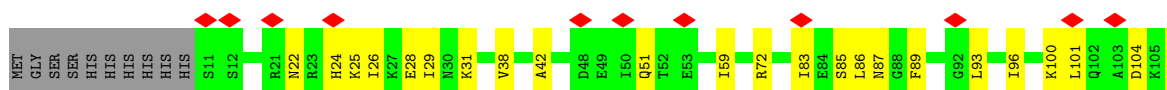
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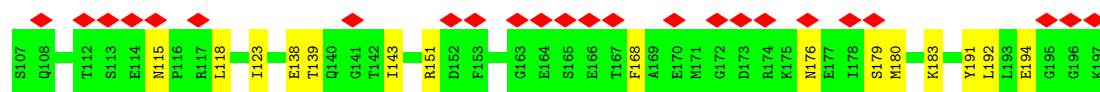


• Molecule 1: KomB

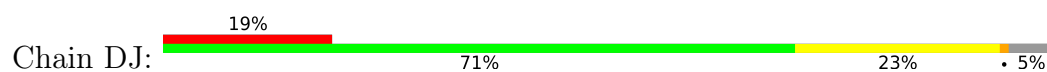
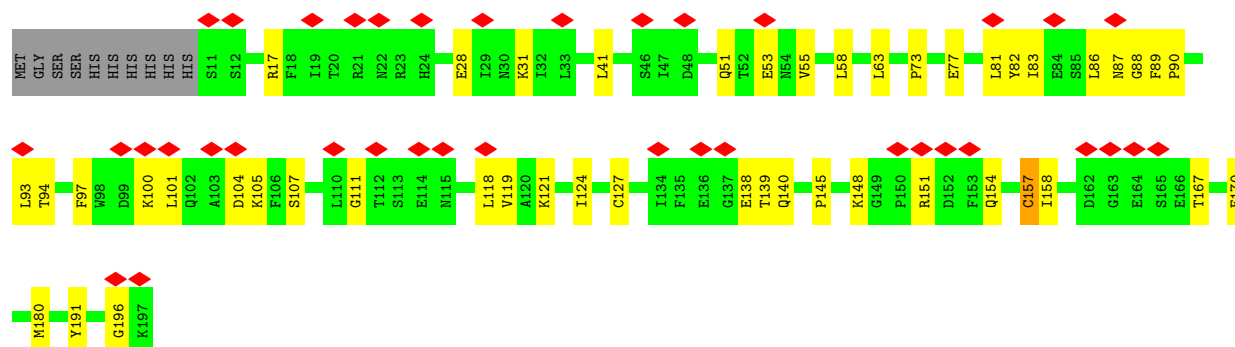


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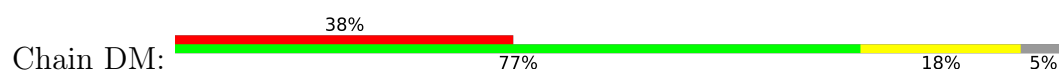
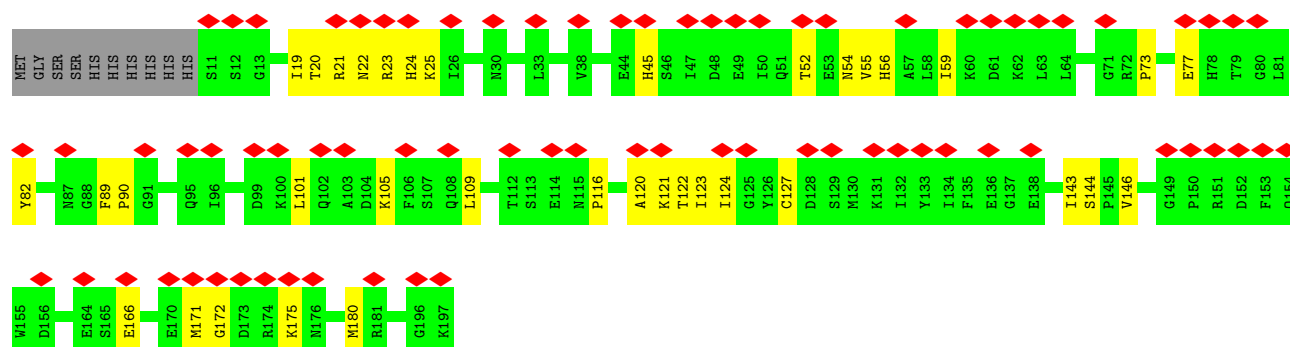




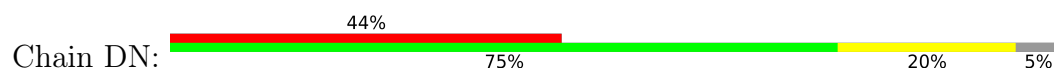
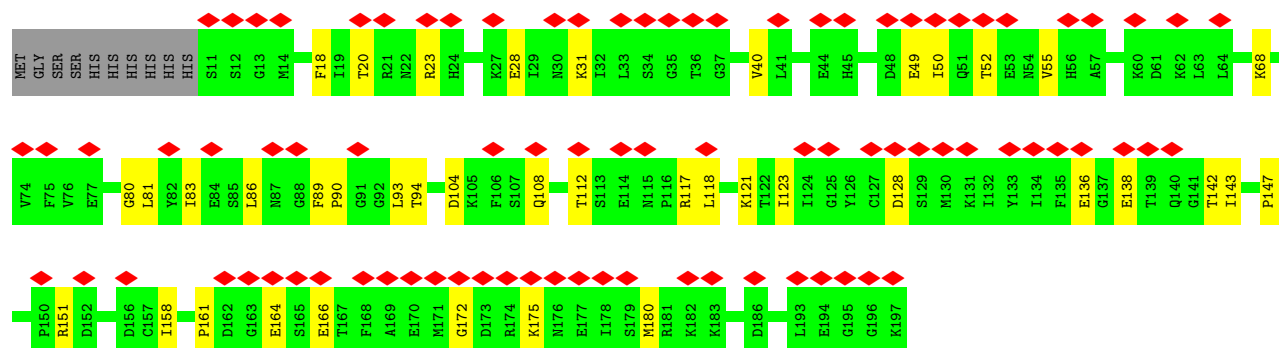
• Molecule 1: KomB



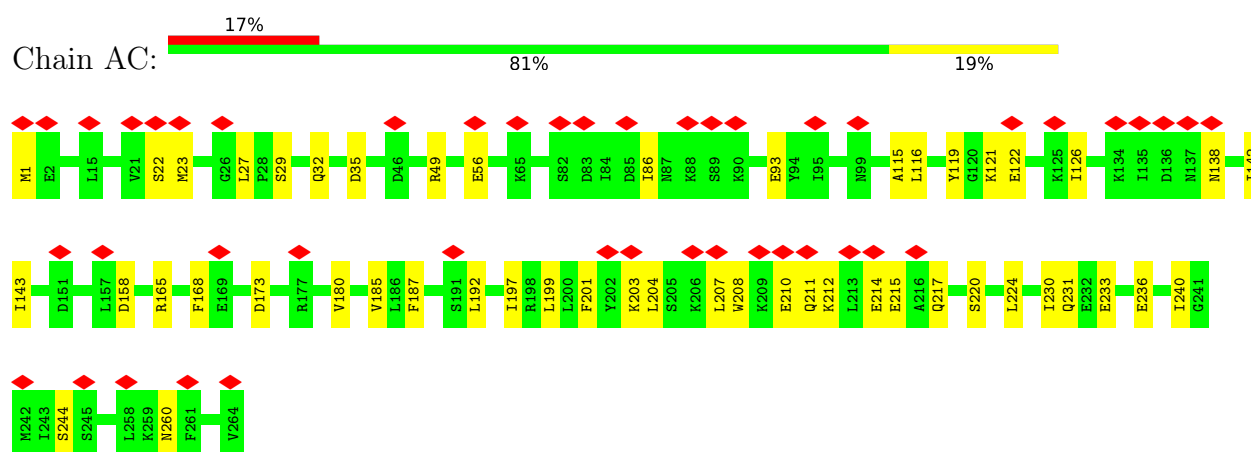
• Molecule 1: KomB



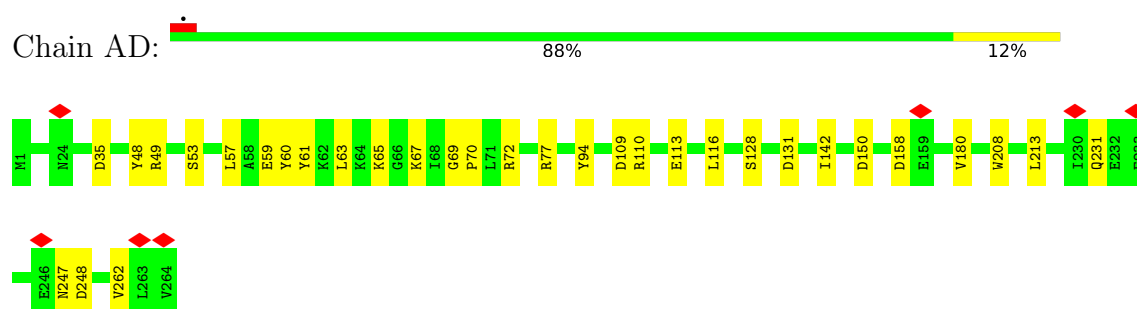
• Molecule 1: KomB



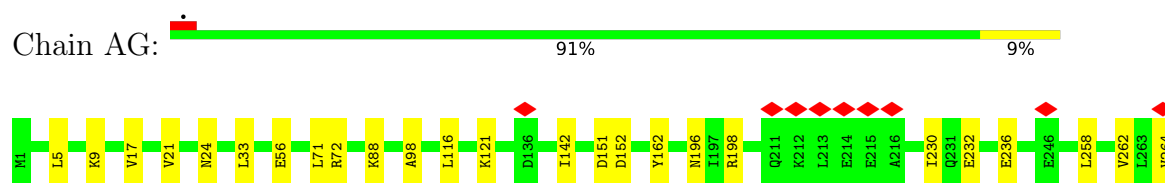
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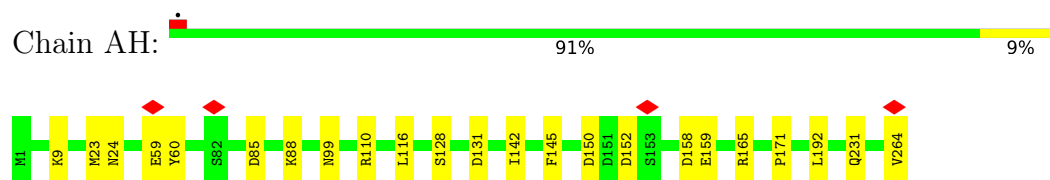
- Molecule 2: KomC



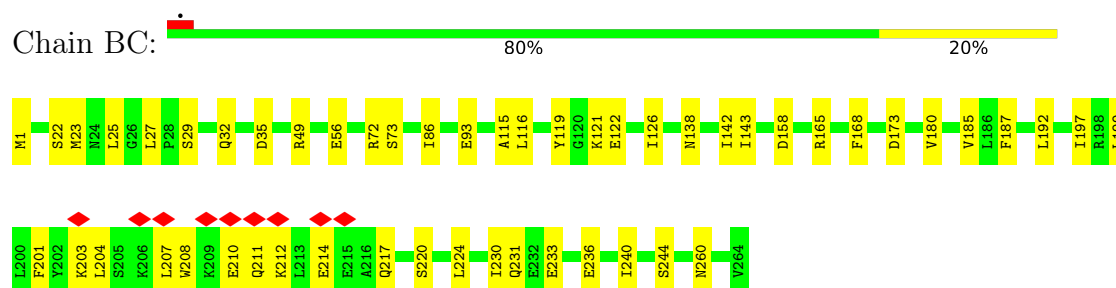
- Molecule 2: KomC



- Molecule 2: KomC



- Molecule 2: KomC



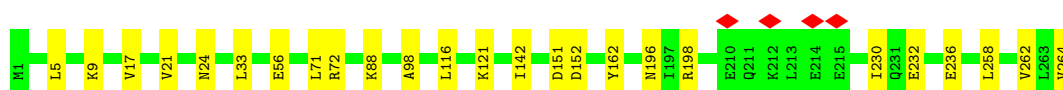
- Molecule 2: KomC

Chain BD:  89% 11%



• Molecule 2: KomC

Chain BG:  91% 9%



• Molecule 2: KomC

Chain BH:  92% 8%



• Molecule 2: KomC

Chain BK:  89% 11%



• Molecule 2: KomC

Chain BL:  81% 19%



• Molecule 2: KomC

Chain BO:  89% 11%

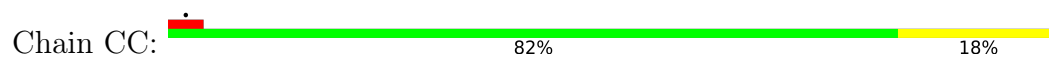


• Molecule 2: KomC

Chain BP:  89% 11%



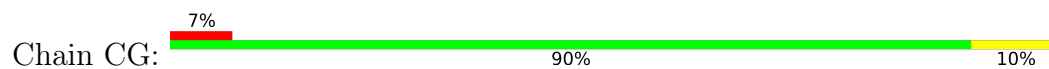
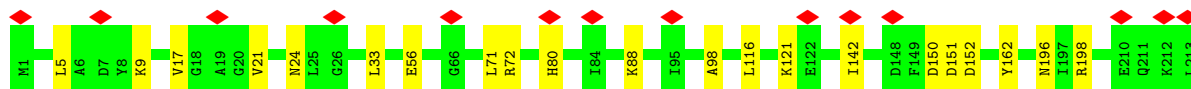
- Molecule 2: KomC



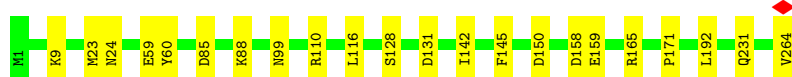
- Molecule 2: KomC



- Molecule 2: KomC



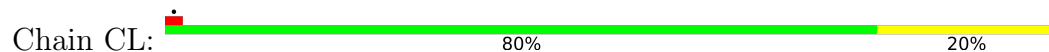
- Molecule 2: KomC

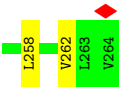


- Molecule 2: KomC

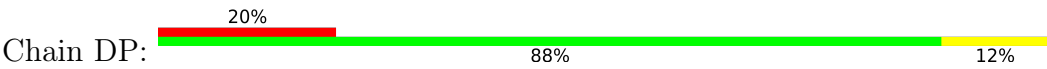
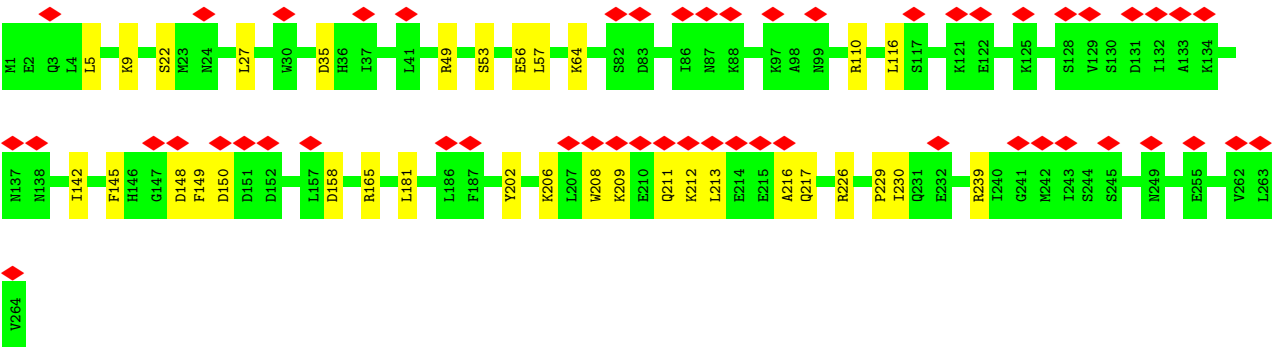


- Molecule 2: KomC





• Molecule 2: KomC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	721973	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.036	Depositor
Minimum map value	-0.607	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	453.59998, 453.59998, 453.59998	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.756, 0.756, 0.756	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.11	0/1519	0.27	0/2039
1	AB	0.10	0/1519	0.28	0/2039
1	AE	0.11	0/1519	0.26	0/2039
1	AF	0.10	0/1519	0.27	0/2039
1	BA	0.10	0/1519	0.27	0/2039
1	BB	0.09	0/1519	0.28	0/2039
1	BE	0.10	0/1519	0.25	0/2039
1	BF	0.09	0/1519	0.27	0/2039
1	BI	0.11	0/1519	0.27	0/2039
1	BJ	0.14	0/1519	0.35	1/2039 (0.0%)
1	BM	0.09	0/1519	0.26	0/2039
1	BN	0.09	0/1519	0.24	0/2039
1	CA	0.11	0/1519	0.27	0/2039
1	CB	0.10	0/1519	0.28	0/2039
1	CE	0.10	0/1519	0.25	0/2039
1	CF	0.10	0/1519	0.27	0/2039
1	CI	0.12	0/1519	0.27	0/2039
1	CJ	0.14	0/1519	0.38	2/2039 (0.1%)
1	CM	0.10	0/1519	0.26	0/2039
1	CN	0.09	0/1519	0.24	0/2039
1	DI	0.12	0/1519	0.27	0/2039
1	DJ	0.14	0/1519	0.35	2/2039 (0.1%)
1	DM	0.10	0/1519	0.26	0/2039
1	DN	0.10	0/1519	0.24	0/2039
2	AC	0.10	0/2218	0.25	0/2997
2	AD	0.10	0/2218	0.25	0/2997
2	AG	0.11	0/2218	0.24	0/2997
2	AH	0.11	0/2218	0.26	0/2997
2	BC	0.09	0/2218	0.25	0/2997
2	BD	0.10	0/2218	0.25	0/2997
2	BG	0.12	0/2218	0.25	0/2997
2	BH	0.10	0/2218	0.26	0/2997
2	BK	0.09	0/2218	0.24	0/2997
2	BL	0.11	0/2218	0.26	0/2997

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	BO	0.10	0/2218	0.25	0/2997
2	BP	0.09	0/2218	0.27	0/2997
2	CC	0.12	0/2218	0.28	0/2997
2	CD	0.12	0/2218	0.25	0/2997
2	CG	0.10	0/2218	0.24	0/2997
2	CH	0.11	0/2218	0.26	0/2997
2	CK	0.09	0/2218	0.24	0/2997
2	CL	0.18	0/2218	0.37	4/2997 (0.1%)
2	CO	0.10	0/2218	0.25	0/2997
2	CP	0.10	0/2218	0.27	0/2997
2	DK	0.10	0/2218	0.24	0/2997
2	DL	0.11	0/2218	0.25	0/2997
2	DO	0.11	0/2218	0.26	0/2997
2	DP	0.10	0/2218	0.27	0/2997
All	All	0.11	0/89688	0.27	9/120864 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	CL	72	ARG	CA-C-N	-8.15	109.85	120.44
2	CL	72	ARG	C-N-CA	-8.15	109.85	120.44
1	CJ	157	CYS	N-CA-C	7.28	119.22	111.28
1	CJ	156	ASP	N-CA-C	6.63	118.51	111.28
1	BJ	157	CYS	N-CA-C	6.55	118.42	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	AA	1489	0	1504	26	0
1	AB	1489	0	1504	33	0
1	AE	1489	0	1504	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AF	1489	0	1504	20	0
1	BA	1489	0	1504	27	0
1	BB	1489	0	1504	35	0
1	BE	1489	0	1504	31	0
1	BF	1489	0	1504	21	0
1	BI	1489	0	1504	37	0
1	BJ	1489	0	1504	46	0
1	BM	1489	0	1504	35	0
1	BN	1489	0	1504	25	0
1	CA	1489	0	1504	28	0
1	CB	1489	0	1504	36	0
1	CE	1489	0	1504	32	0
1	CF	1489	0	1504	20	0
1	CI	1489	0	1504	37	0
1	CJ	1489	0	1504	50	0
1	CM	1489	0	1504	36	0
1	CN	1489	0	1504	25	0
1	DI	1489	0	1504	38	0
1	DJ	1489	0	1504	50	0
1	DM	1489	0	1504	33	0
1	DN	1489	0	1504	25	0
2	AC	2166	0	2150	48	0
2	AD	2166	0	2150	27	0
2	AG	2166	0	2150	17	0
2	AH	2166	0	2150	17	0
2	BC	2166	0	2150	51	0
2	BD	2166	0	2150	28	0
2	BG	2166	0	2150	15	0
2	BH	2166	0	2150	15	0
2	BK	2166	0	2150	22	0
2	BL	2166	0	2150	38	0
2	BO	2166	0	2150	21	0
2	BP	2166	0	2150	25	0
2	CC	2166	0	2150	38	0
2	CD	2166	0	2150	21	0
2	CG	2166	0	2150	25	0
2	CH	2166	0	2150	16	0
2	CK	2166	0	2150	22	0
2	CL	2166	0	2150	45	0
2	CO	2166	0	2150	17	0
2	CP	2166	0	2150	25	0
2	DK	2166	0	2150	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	DL	2166	0	2150	39	0
2	DO	2166	0	2150	28	0
2	DP	2166	0	2150	22	0
All	All	87720	0	87696	1268	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 7.

The worst 5 of 1268 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:CG:72:ARG:NH2	2:DO:150:ASP:HA	1.42	1.35
2:BC:187:PHE:CZ	2:BC:201:PHE:HZ	1.55	1.24
2:CC:187:PHE:CZ	2:CC:201:PHE:HZ	1.55	1.24
2:AC:187:PHE:CZ	2:AC:201:PHE:HZ	1.55	1.22
2:BC:187:PHE:CE2	2:BC:201:PHE:HZ	1.58	1.20

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	AA	185/197 (94%)	177 (96%)	8 (4%)	0	100	100
1	AB	185/197 (94%)	175 (95%)	10 (5%)	0	100	100
1	AE	185/197 (94%)	177 (96%)	8 (4%)	0	100	100
1	AF	185/197 (94%)	181 (98%)	4 (2%)	0	100	100
1	BA	185/197 (94%)	177 (96%)	8 (4%)	0	100	100
1	BB	185/197 (94%)	175 (95%)	10 (5%)	0	100	100
1	BE	185/197 (94%)	176 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BF	185/197 (94%)	181 (98%)	4 (2%)	0	100	100
1	BI	185/197 (94%)	178 (96%)	7 (4%)	0	100	100
1	BJ	185/197 (94%)	179 (97%)	6 (3%)	0	100	100
1	BM	185/197 (94%)	180 (97%)	5 (3%)	0	100	100
1	BN	185/197 (94%)	181 (98%)	4 (2%)	0	100	100
1	CA	185/197 (94%)	177 (96%)	8 (4%)	0	100	100
1	CB	185/197 (94%)	175 (95%)	10 (5%)	0	100	100
1	CE	185/197 (94%)	176 (95%)	9 (5%)	0	100	100
1	CF	185/197 (94%)	181 (98%)	4 (2%)	0	100	100
1	CI	185/197 (94%)	178 (96%)	7 (4%)	0	100	100
1	CJ	185/197 (94%)	180 (97%)	5 (3%)	0	100	100
1	CM	185/197 (94%)	180 (97%)	5 (3%)	0	100	100
1	CN	185/197 (94%)	181 (98%)	4 (2%)	0	100	100
1	DI	185/197 (94%)	178 (96%)	7 (4%)	0	100	100
1	DJ	185/197 (94%)	180 (97%)	5 (3%)	0	100	100
1	DM	185/197 (94%)	179 (97%)	6 (3%)	0	100	100
1	DN	185/197 (94%)	180 (97%)	5 (3%)	0	100	100
2	AC	262/264 (99%)	259 (99%)	3 (1%)	0	100	100
2	AD	262/264 (99%)	261 (100%)	1 (0%)	0	100	100
2	AG	262/264 (99%)	260 (99%)	2 (1%)	0	100	100
2	AH	262/264 (99%)	258 (98%)	4 (2%)	0	100	100
2	BC	262/264 (99%)	259 (99%)	3 (1%)	0	100	100
2	BD	262/264 (99%)	261 (100%)	1 (0%)	0	100	100
2	BG	262/264 (99%)	260 (99%)	2 (1%)	0	100	100
2	BH	262/264 (99%)	258 (98%)	4 (2%)	0	100	100
2	BK	262/264 (99%)	260 (99%)	2 (1%)	0	100	100
2	BL	262/264 (99%)	256 (98%)	6 (2%)	0	100	100
2	BO	262/264 (99%)	259 (99%)	3 (1%)	0	100	100
2	BP	262/264 (99%)	255 (97%)	7 (3%)	0	100	100
2	CC	262/264 (99%)	258 (98%)	4 (2%)	0	100	100
2	CD	262/264 (99%)	261 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	CG	262/264 (99%)	260 (99%)	2 (1%)	0	100	100
2	CH	262/264 (99%)	258 (98%)	4 (2%)	0	100	100
2	CK	262/264 (99%)	260 (99%)	2 (1%)	0	100	100
2	CL	262/264 (99%)	256 (98%)	6 (2%)	0	100	100
2	CO	262/264 (99%)	260 (99%)	2 (1%)	0	100	100
2	CP	262/264 (99%)	255 (97%)	7 (3%)	0	100	100
2	DK	262/264 (99%)	260 (99%)	2 (1%)	0	100	100
2	DL	262/264 (99%)	256 (98%)	6 (2%)	0	100	100
2	DO	262/264 (99%)	259 (99%)	3 (1%)	0	100	100
2	DP	262/264 (99%)	255 (97%)	7 (3%)	0	100	100
All	All	10728/11064 (97%)	10486 (98%)	242 (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	163/172 (95%)	163 (100%)	0	100	100
1	AB	163/172 (95%)	163 (100%)	0	100	100
1	AE	163/172 (95%)	163 (100%)	0	100	100
1	AF	163/172 (95%)	163 (100%)	0	100	100
1	BA	163/172 (95%)	163 (100%)	0	100	100
1	BB	163/172 (95%)	163 (100%)	0	100	100
1	BE	163/172 (95%)	163 (100%)	0	100	100
1	BF	163/172 (95%)	163 (100%)	0	100	100
1	BI	163/172 (95%)	163 (100%)	0	100	100
1	BJ	163/172 (95%)	162 (99%)	1 (1%)	78	87
1	BM	163/172 (95%)	163 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BN	163/172 (95%)	162 (99%)	1 (1%)	78	87
1	CA	163/172 (95%)	163 (100%)	0	100	100
1	CB	163/172 (95%)	163 (100%)	0	100	100
1	CE	163/172 (95%)	163 (100%)	0	100	100
1	CF	163/172 (95%)	163 (100%)	0	100	100
1	CI	163/172 (95%)	162 (99%)	1 (1%)	78	87
1	CJ	163/172 (95%)	162 (99%)	1 (1%)	78	87
1	CM	163/172 (95%)	163 (100%)	0	100	100
1	CN	163/172 (95%)	162 (99%)	1 (1%)	78	87
1	DI	163/172 (95%)	162 (99%)	1 (1%)	78	87
1	DJ	163/172 (95%)	163 (100%)	0	100	100
1	DM	163/172 (95%)	163 (100%)	0	100	100
1	DN	163/172 (95%)	162 (99%)	1 (1%)	78	87
2	AC	240/240 (100%)	240 (100%)	0	100	100
2	AD	240/240 (100%)	240 (100%)	0	100	100
2	AG	240/240 (100%)	240 (100%)	0	100	100
2	AH	240/240 (100%)	240 (100%)	0	100	100
2	BC	240/240 (100%)	240 (100%)	0	100	100
2	BD	240/240 (100%)	240 (100%)	0	100	100
2	BG	240/240 (100%)	240 (100%)	0	100	100
2	BH	240/240 (100%)	240 (100%)	0	100	100
2	BK	240/240 (100%)	240 (100%)	0	100	100
2	BL	240/240 (100%)	240 (100%)	0	100	100
2	BO	240/240 (100%)	240 (100%)	0	100	100
2	BP	240/240 (100%)	240 (100%)	0	100	100
2	CC	240/240 (100%)	240 (100%)	0	100	100
2	CD	240/240 (100%)	240 (100%)	0	100	100
2	CG	240/240 (100%)	240 (100%)	0	100	100
2	CH	240/240 (100%)	240 (100%)	0	100	100
2	CK	240/240 (100%)	240 (100%)	0	100	100
2	CL	240/240 (100%)	240 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	CO	240/240 (100%)	240 (100%)	0	100	100
2	CP	240/240 (100%)	240 (100%)	0	100	100
2	DK	240/240 (100%)	240 (100%)	0	100	100
2	DL	240/240 (100%)	240 (100%)	0	100	100
2	DO	240/240 (100%)	240 (100%)	0	100	100
2	DP	240/240 (100%)	240 (100%)	0	100	100
All	All	9672/9888 (98%)	9665 (100%)	7 (0%)	87	92

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	CJ	153	PHE
1	CN	180	MET
1	DN	180	MET
1	DI	168	PHE
1	CI	168	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 105 such sidechains are listed below:

Mol	Chain	Res	Type
2	CC	107	ASN
1	CJ	95	GLN
1	DM	51	GLN
2	CC	260	ASN
1	CF	154	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

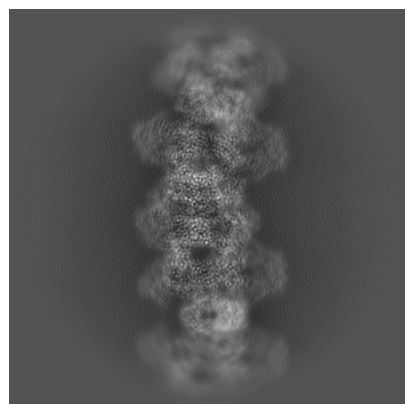
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66451. These allow visual inspection of the internal detail of the map and identification of artifacts.

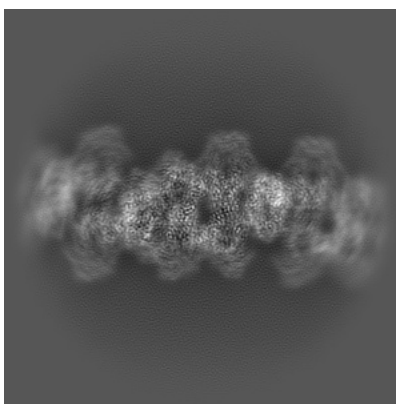
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

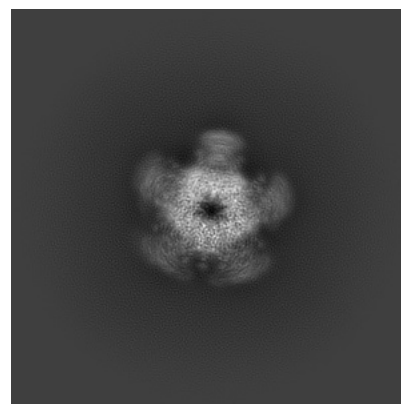
6.1.1 Primary map



X

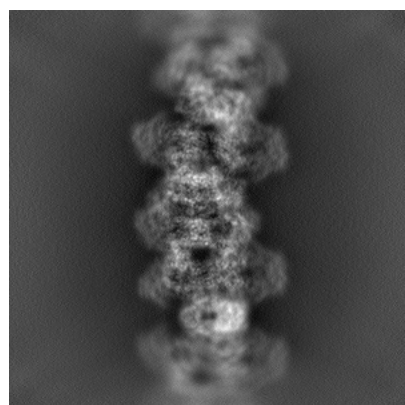


Y

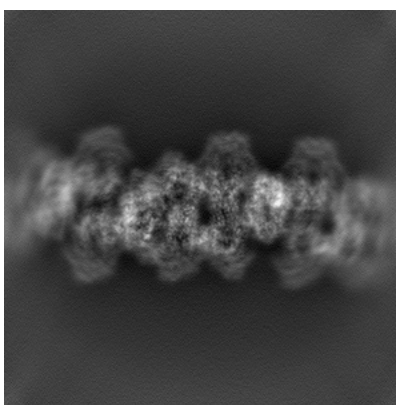


Z

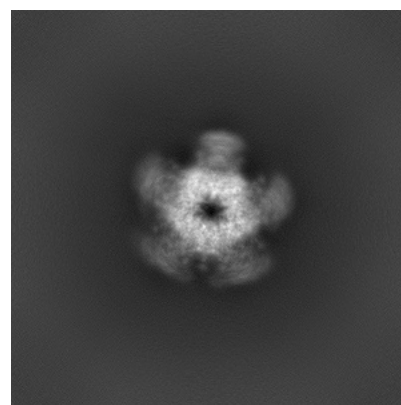
6.1.2 Raw map



X



Y

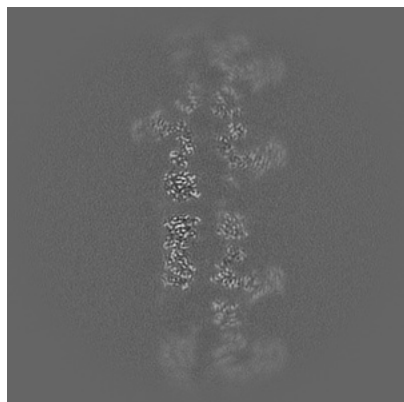


Z

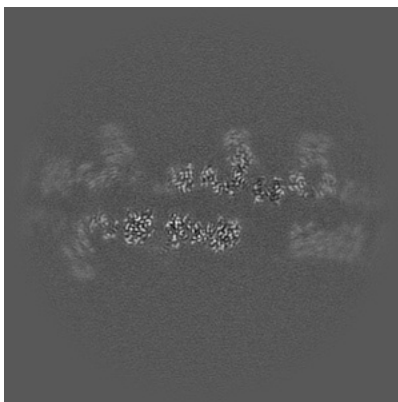
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

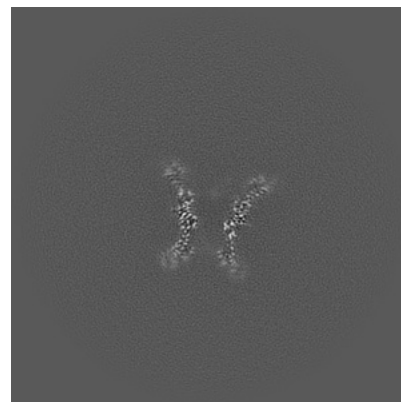
6.2.1 Primary map



X Index: 300

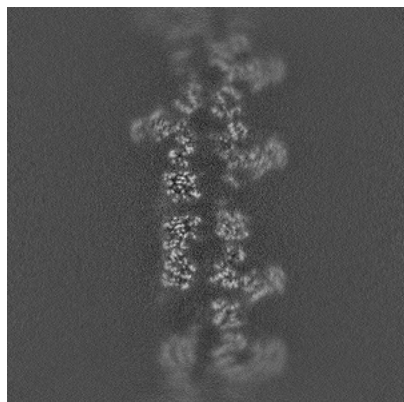


Y Index: 300

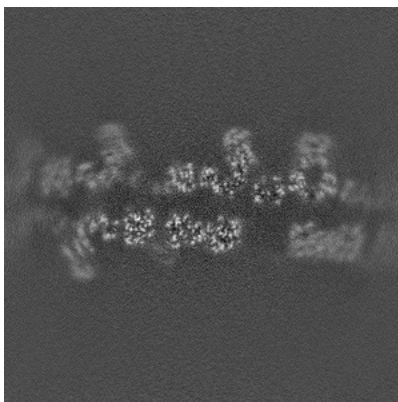


Z Index: 300

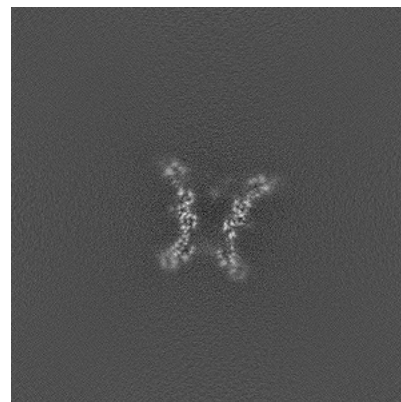
6.2.2 Raw map



X Index: 300



Y Index: 300

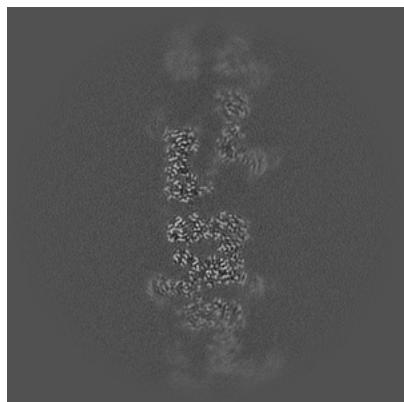


Z Index: 300

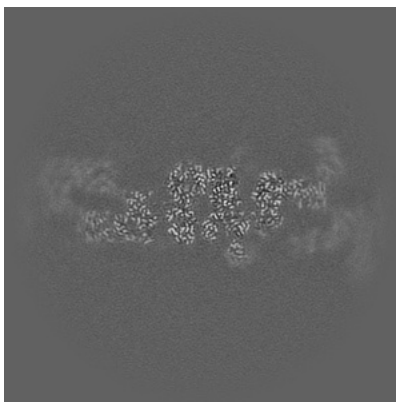
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

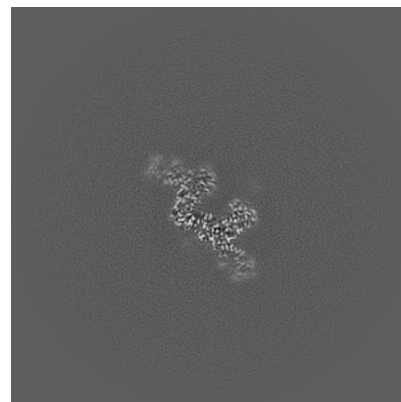
6.3.1 Primary map



X Index: 282

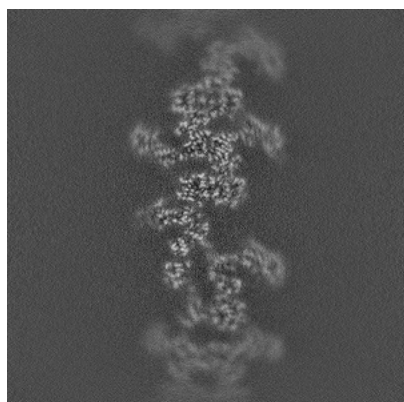


Y Index: 275

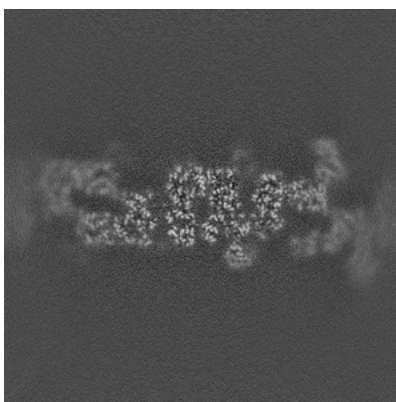


Z Index: 282

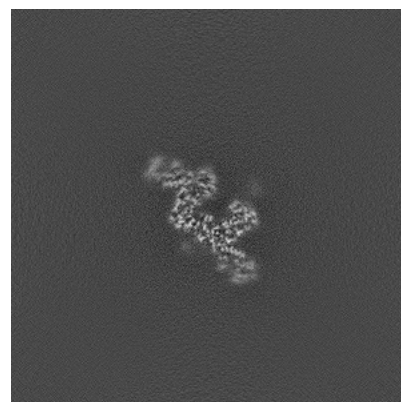
6.3.2 Raw map



X Index: 325



Y Index: 275

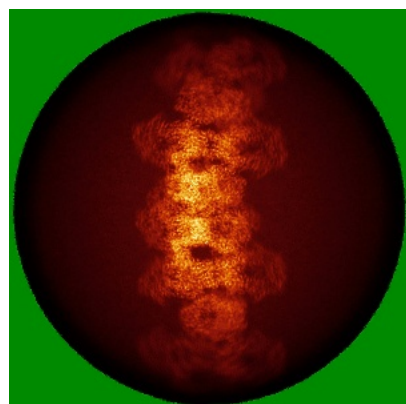


Z Index: 282

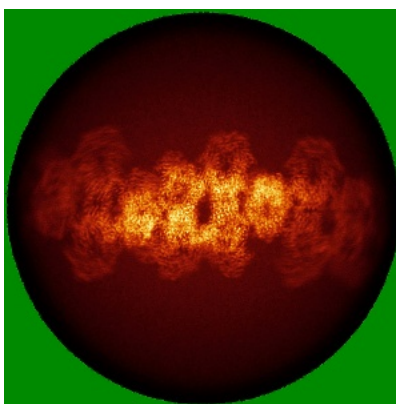
The images above show the largest variance slices of the map in three orthogonal directions.

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

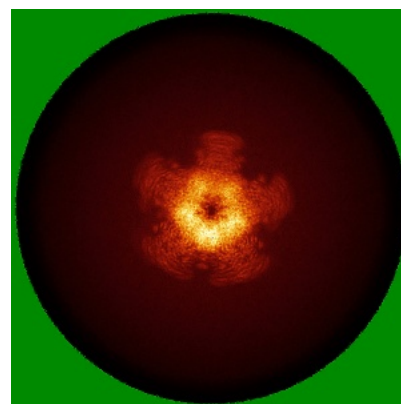
6.4.1 Primary map



X

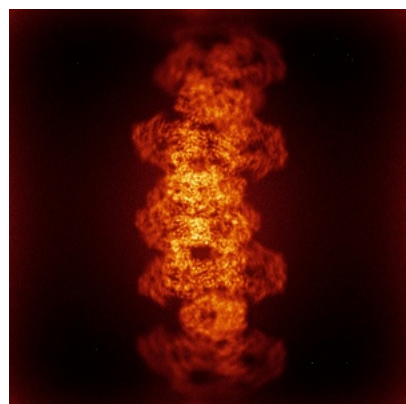


Y

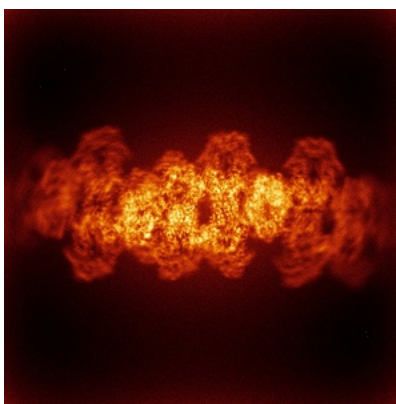


Z

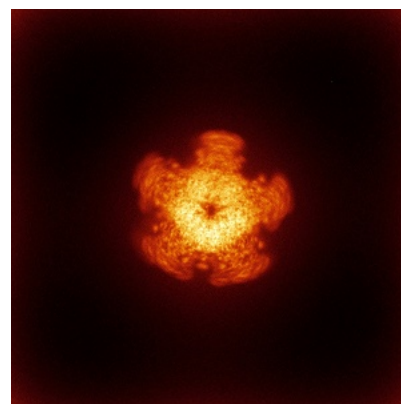
6.4.2 Raw map



X



Y



Z

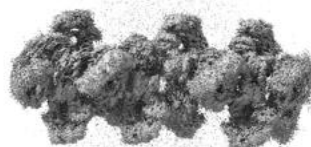
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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 0.07. 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.

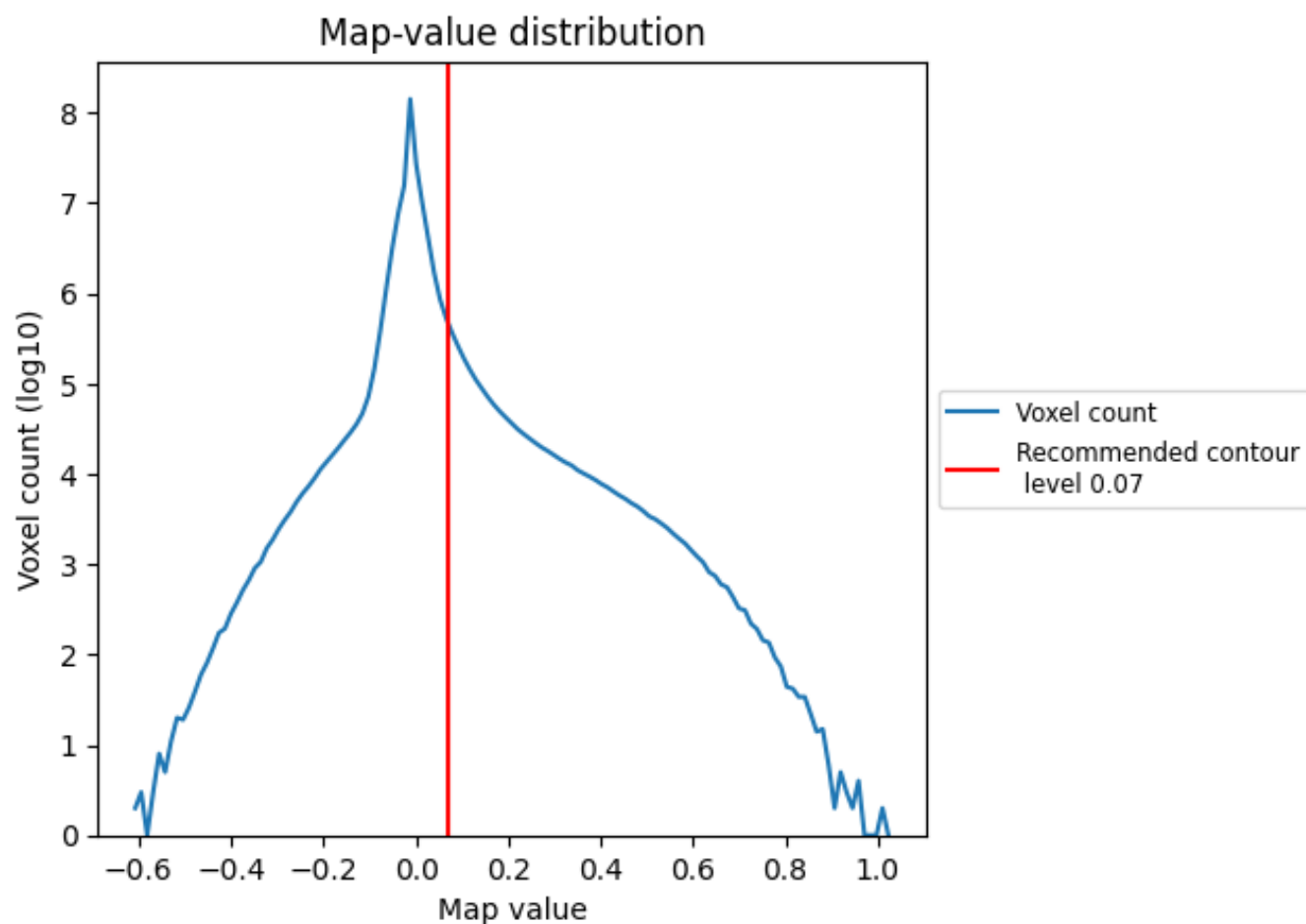
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

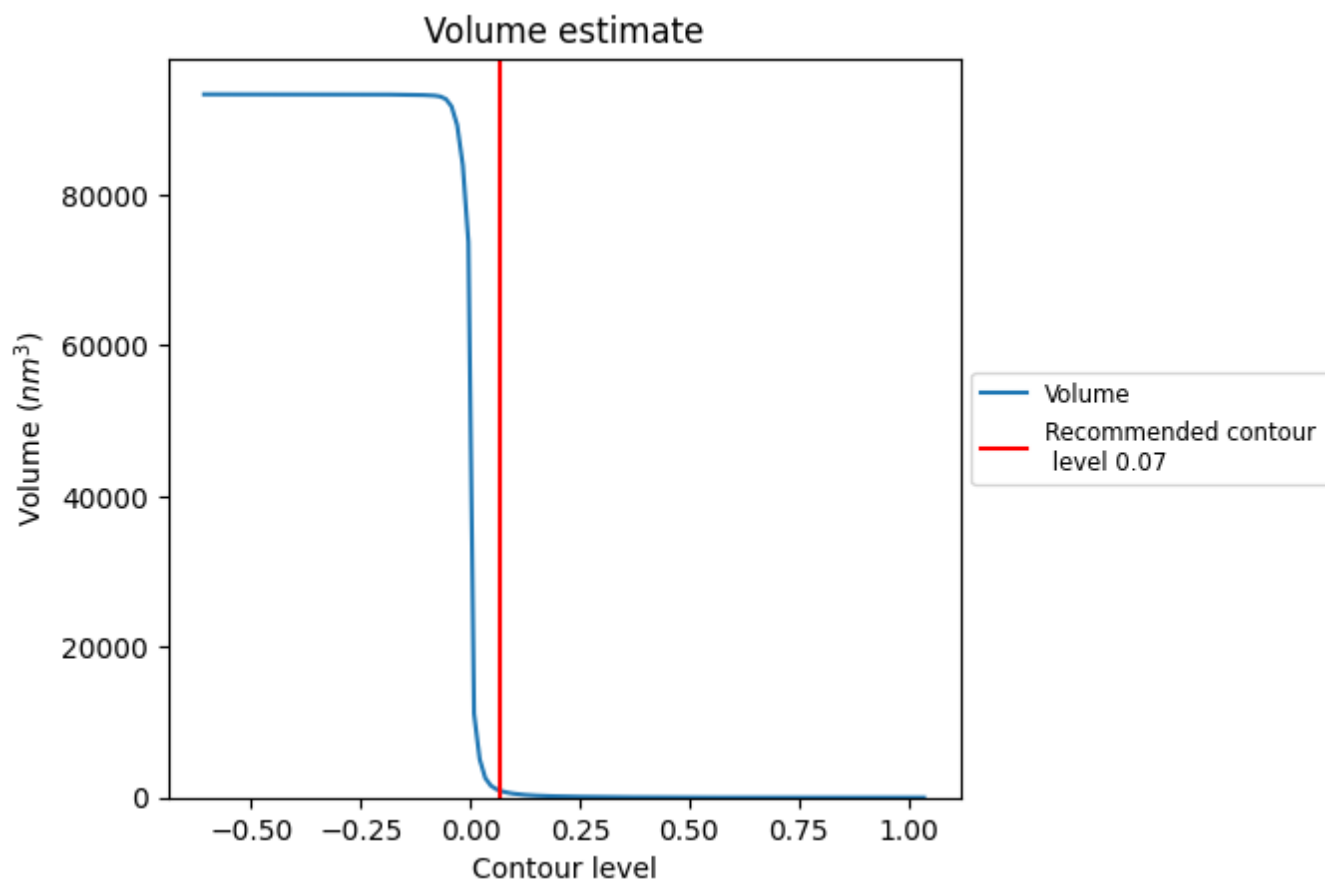
This section contains the results of statistical analysis of the map.

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.

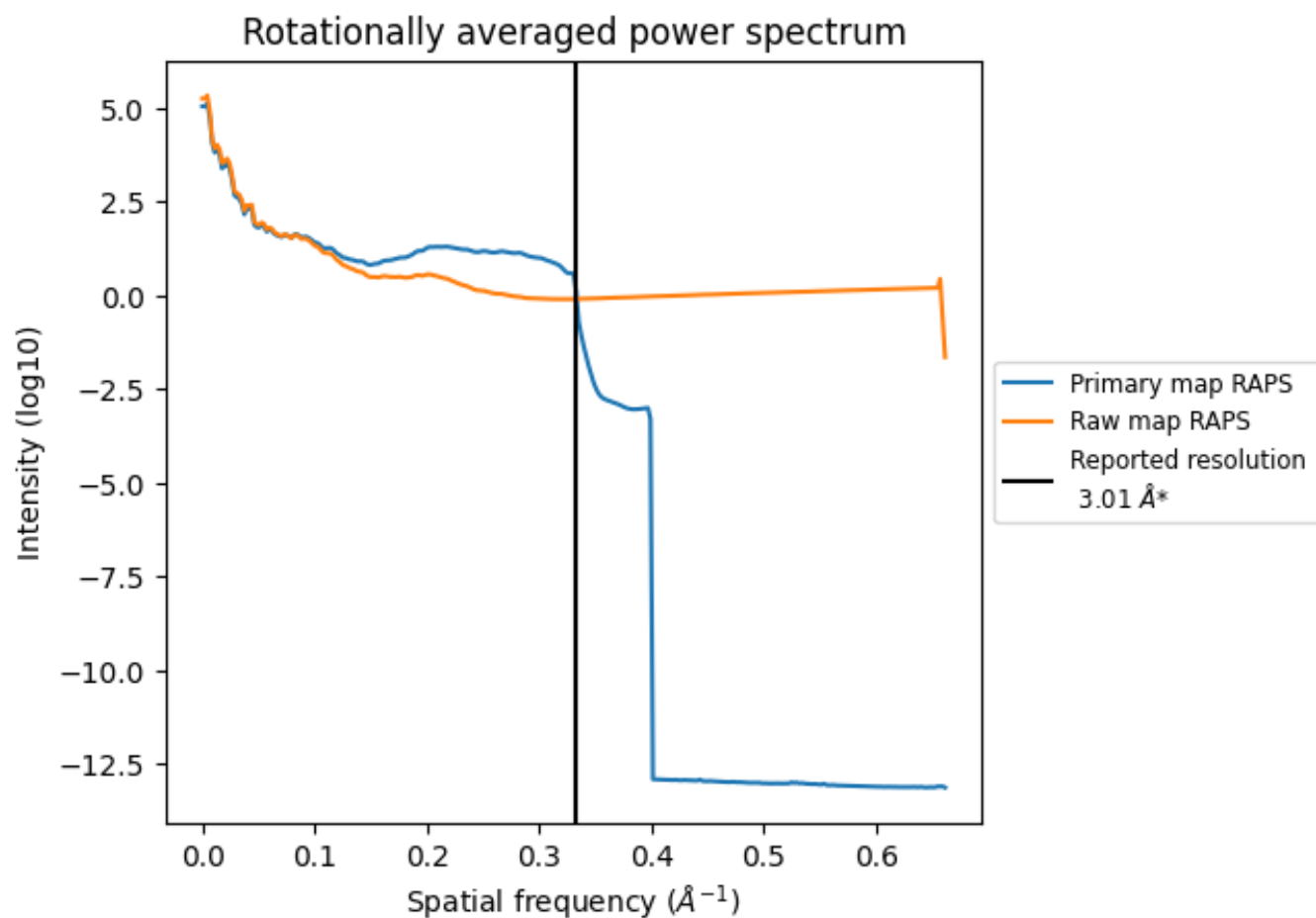
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 893 nm³; this corresponds to an approximate mass of 806 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 ⓘ

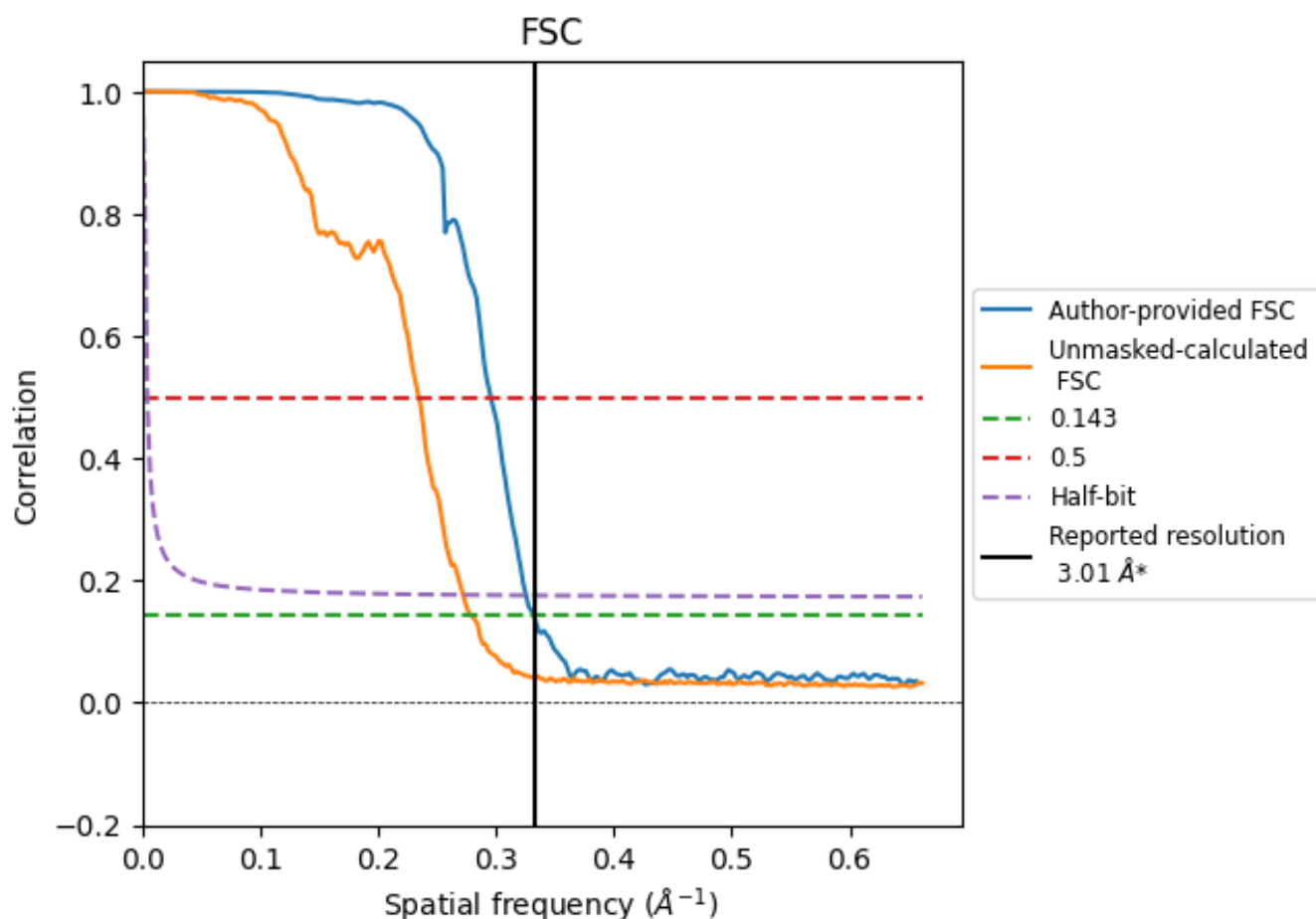


*Reported resolution corresponds to spatial frequency of 0.332 $\text{\AA}^{-1}$

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 $0.332 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

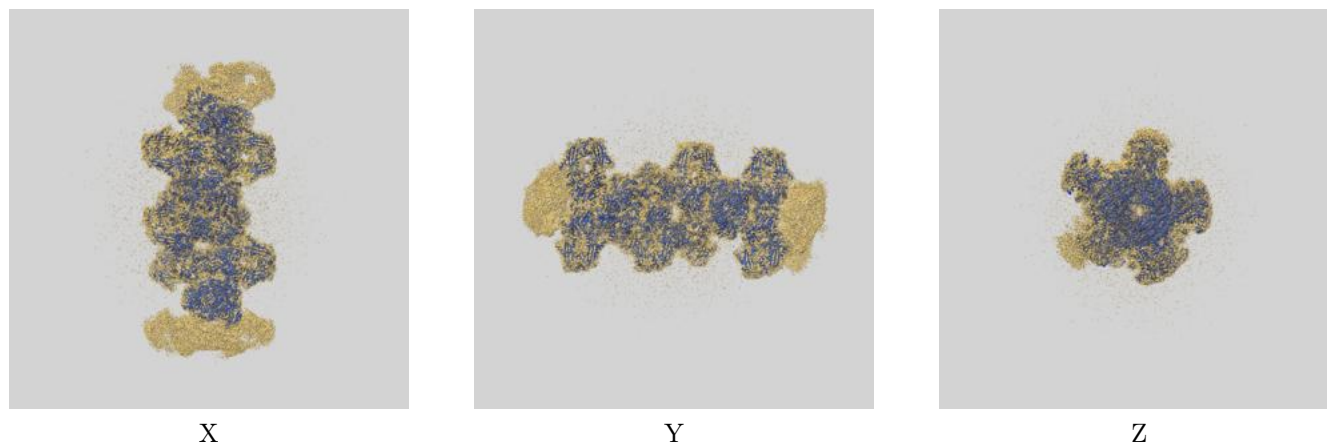
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.01	-	-
Author-provided FSC curve	3.01	3.38	3.07
Unmasked-calculated*	3.59	4.26	3.68

*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 3.59 differs from the reported value 3.01 by more than 10 %

9 Map-model fit [i](#)

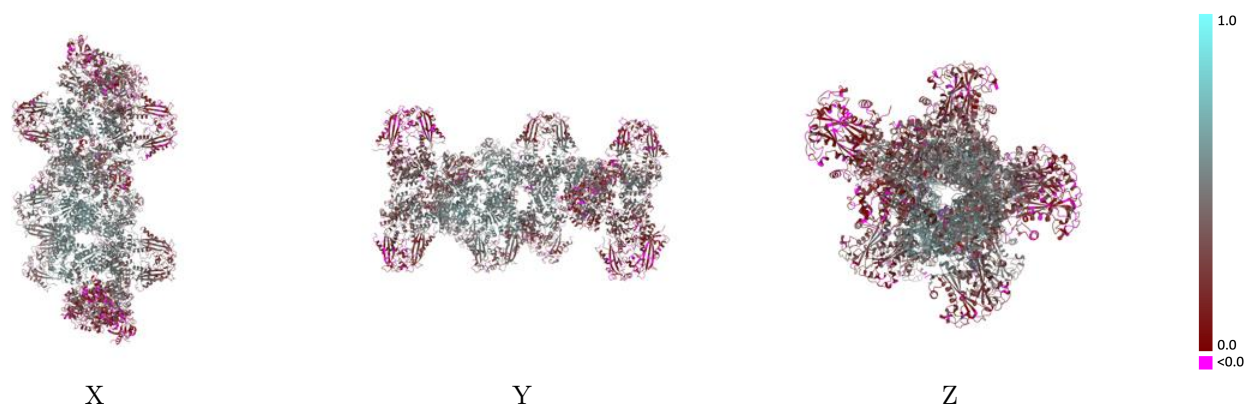
This section contains information regarding the fit between EMDB map EMD-66451 and PDB model 9X10. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



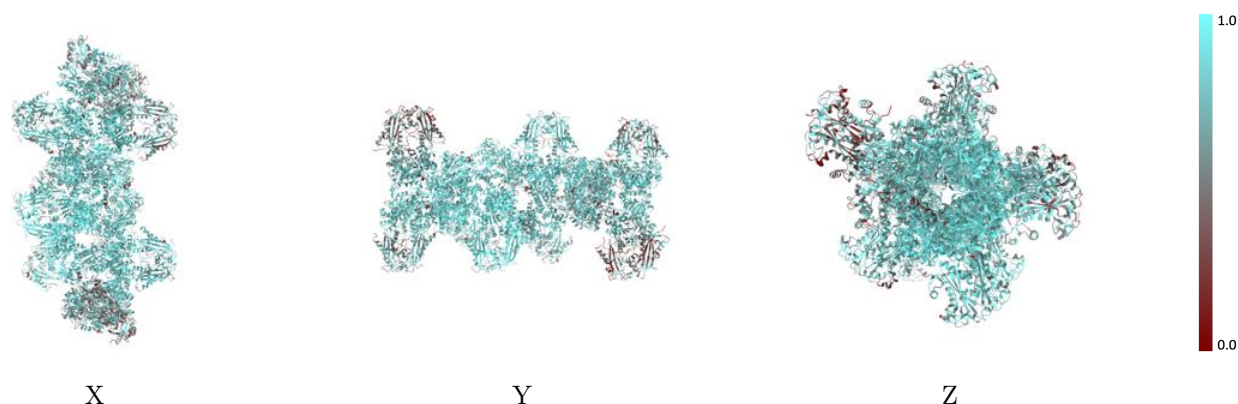
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



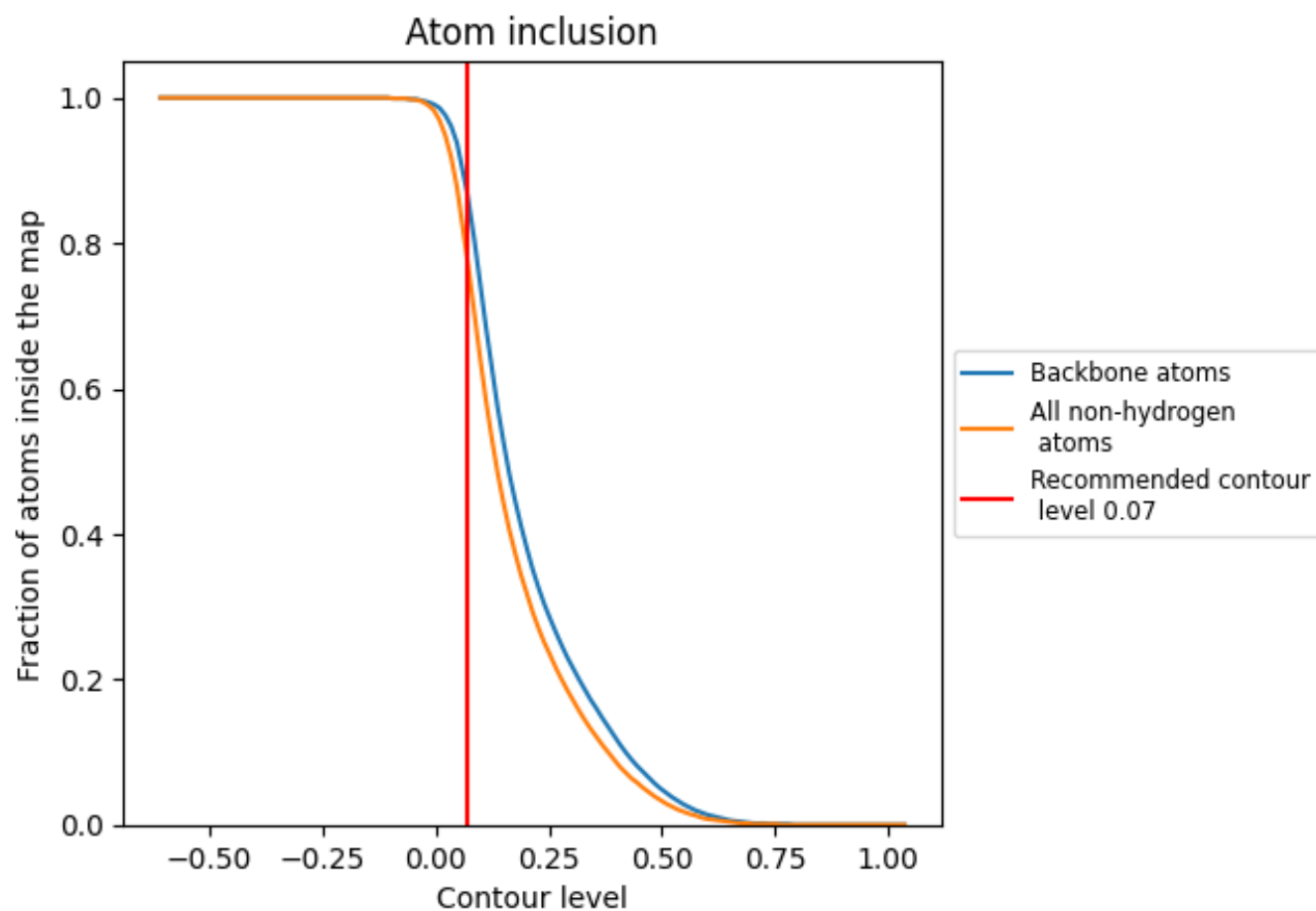
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 78% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7800	 0.3730
AA	 0.4490	 0.1190
AB	 0.4640	 0.0930
AC	 0.6180	 0.2210
AD	 0.7850	 0.3670
AE	 0.5830	 0.1450
AF	 0.6370	 0.2190
AG	 0.8210	 0.4050
AH	 0.8110	 0.3850
BA	 0.8230	 0.3990
BB	 0.8310	 0.4280
BC	 0.8990	 0.5090
BD	 0.9530	 0.5830
BE	 0.8320	 0.4350
BF	 0.8380	 0.4430
BG	 0.9410	 0.5570
BH	 0.9580	 0.5900
BI	 0.7470	 0.3330
BJ	 0.7680	 0.3340
BK	 0.9390	 0.5510
BL	 0.8580	 0.4520
BM	 0.8070	 0.3880
BN	 0.7930	 0.3610
BO	 0.9490	 0.5700
BP	 0.9210	 0.5500
CA	 0.7190	 0.2630
CB	 0.7220	 0.2710
CC	 0.8680	 0.4970
CD	 0.9100	 0.5170
CE	 0.6240	 0.1870
CF	 0.6240	 0.1790
CG	 0.7160	 0.2640
CH	 0.8990	 0.4890
CI	 0.7020	 0.2440
CJ	 0.7220	 0.2770



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Chain	Atom inclusion	Q-score
CK	 0.9260	 0.5260
CL	 0.8120	 0.3760
CM	 0.7650	 0.3230
CN	 0.7170	 0.2680
CO	 0.9040	 0.5210
CP	 0.8510	 0.4600
DI	 0.6250	 0.2230
DJ	 0.6180	 0.1700
DK	 0.8360	 0.4270
DL	 0.8080	 0.3900
DM	 0.4740	 0.1150
DN	 0.4330	 0.1260
DO	 0.7830	 0.3630
DP	 0.5920	 0.1870