



wwPDB EM Validation Summary Report ⓘ

Nov 6, 2022 – 01:03 PM EST

PDB ID : 6MZV
EMDB ID : EMD-9308
Title : Cryo-EM structure of the HO BMC shell: BMC-TD focused structure, widened inner ring
Authors : Greber, B.J.; Sutter, M.; Kerfeld, C.A.
Deposited on : 2018-11-05
Resolution : 3.40 Å(reported)
Based on initial model : 5V74

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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

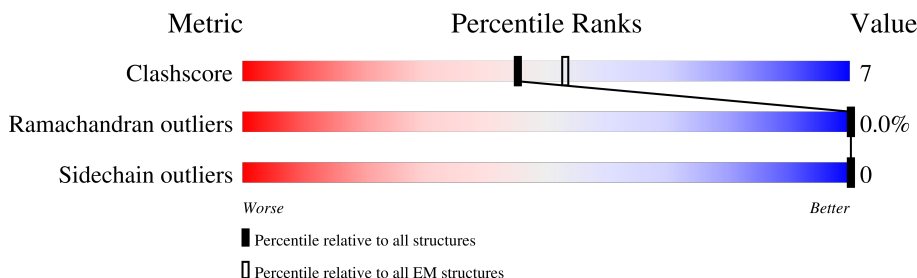
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.





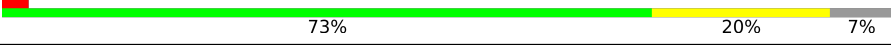

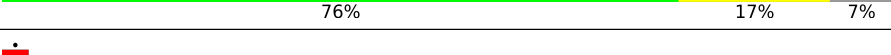
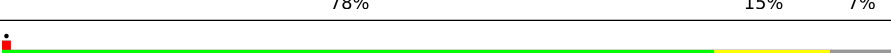
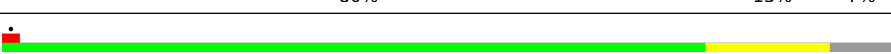
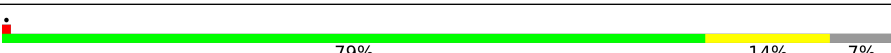


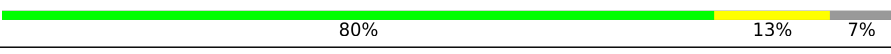




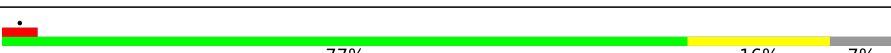


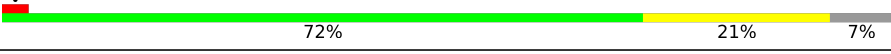


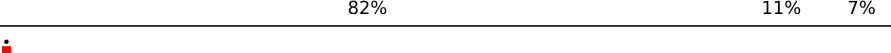



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	212	78% 17% 5%
1	B	212	80% 15% 5%
1	C	212	82% 13% 5%
1	D	212	81% 15% 5%
1	E	212	76% 18% 5%
1	F	212	80% 15% 5%
2	GA	99	79% 14% 7%
2	GB	99	79% 14% 7%



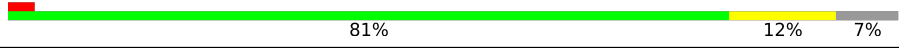



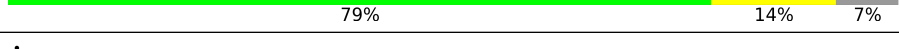
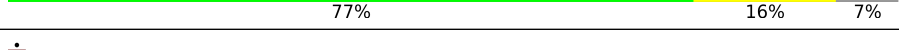
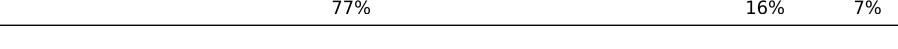
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Mol	Chain	Length	Quality of chain
2	GC	99	
2	GD	99	
2	GE	99	
2	GF	99	
2	HA	99	
2	HB	99	
2	HC	99	
2	HD	99	
2	HE	99	
2	HF	99	
2	IA	99	
2	IB	99	
2	IC	99	
2	ID	99	
2	IE	99	
2	IF	99	
2	JA	99	
2	JB	99	
2	JC	99	
2	JD	99	
2	JE	99	
2	JF	99	
2	KA	99	
2	KB	99	
2	KC	99	

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Mol	Chain	Length	Quality of chain
2	KD	99	 73%20%7%
2	KE	99	 77%16%7%
2	KF	99	 81%12%7%
2	LA	99	 73%20%7%
2	LB	99	 5%74%19%7%
2	LC	99	 80%13%7%
2	LD	99	 79%14%7%
2	LE	99	 77%16%7%
2	LF	99	 77%16%7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 32833 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 Microcompartments protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	202	Total	C	N	O	S	0	0
			1525	971	265	286	3		
1	B	202	Total	C	N	O	S	0	0
			1525	971	265	286	3		
1	C	202	Total	C	N	O	S	0	0
			1525	971	265	286	3		
1	D	202	Total	C	N	O	S	0	0
			1525	971	265	286	3		
1	E	202	Total	C	N	O	S	0	0
			1525	971	265	286	3		
1	F	201	Total	C	N	O	S	0	0
			1520	968	264	285	3		

- Molecule 2 is a protein called Microcompartments protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	GA	92	Total	C	N	O	S	0	0
			658	413	120	122	3		
2	GB	92	Total	C	N	O	S	0	0
			658	413	120	122	3		
2	GC	92	Total	C	N	O	S	0	0
			658	413	120	122	3		
2	GD	92	Total	C	N	O	S	0	0
			658	413	120	122	3		
2	GE	92	Total	C	N	O	S	0	0
			658	413	120	122	3		
2	GF	92	Total	C	N	O	S	0	0
			658	413	120	122	3		
2	HA	92	Total	C	N	O	S	0	0
			658	413	120	122	3		
2	HB	92	Total	C	N	O	S	0	0
			658	413	120	122	3		
2	HC	92	Total	C	N	O	S	0	0
			658	413	120	122	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	HD	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	HE	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	HF	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	IA	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	IB	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	IC	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	ID	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	IE	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	IF	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	JA	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	JB	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	JC	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	JD	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	JE	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	JF	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	KA	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	KB	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	KC	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	KD	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	KE	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	KF	92	Total 658	C 413	N 120	O 122	S 3	0	0

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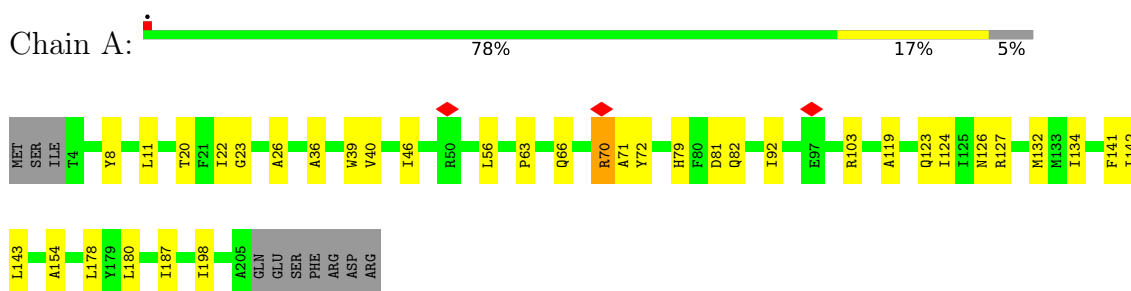
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Mol	Chain	Residues	Atoms					AltConf	Trace
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2	LB	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	LC	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	LD	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	LE	92	Total 658	C 413	N 120	O 122	S 3	0	0
2	LF	92	Total 658	C 413	N 120	O 122	S 3	0	0

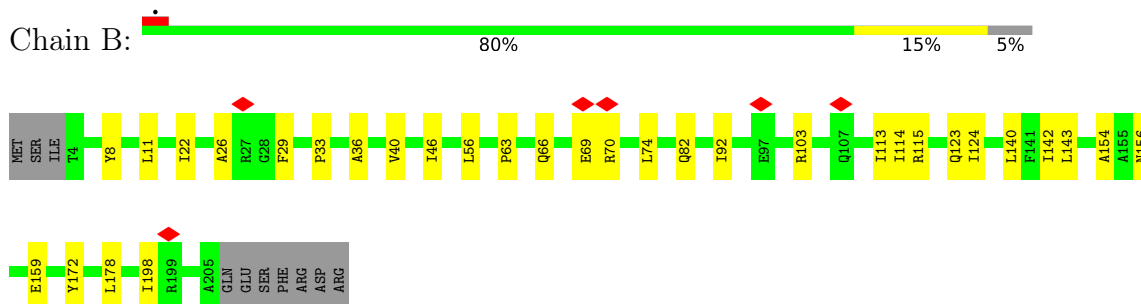
3 Residue-property plots

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.

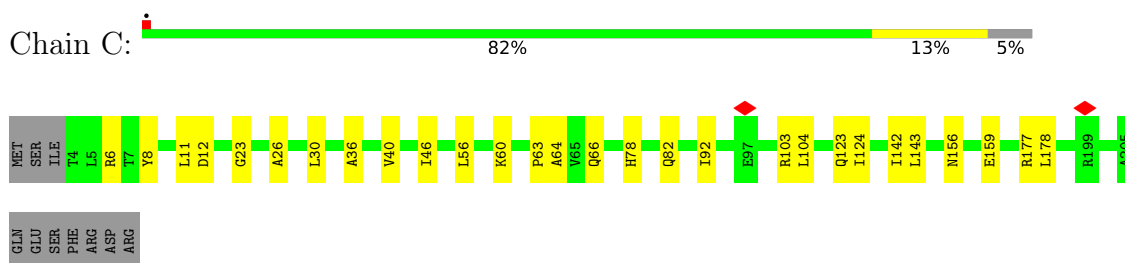
- Molecule 1: Microcompartments protein



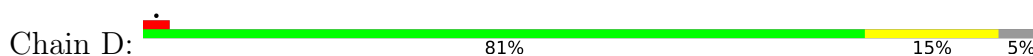
- Molecule 1: Microcompartments protein

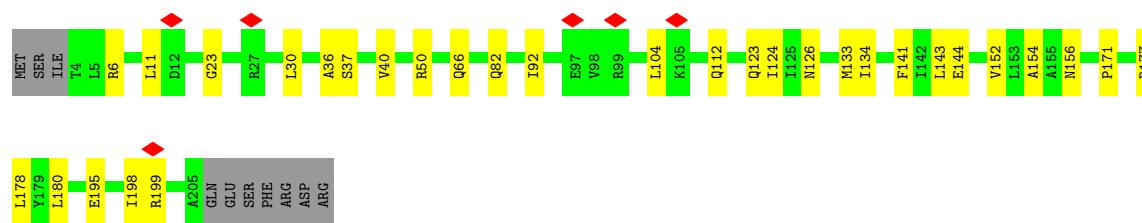


- Molecule 1: Microcompartments protein



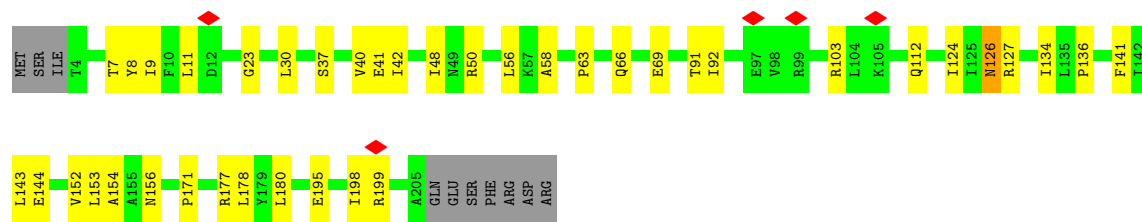
- Molecule 1: Microcompartments protein





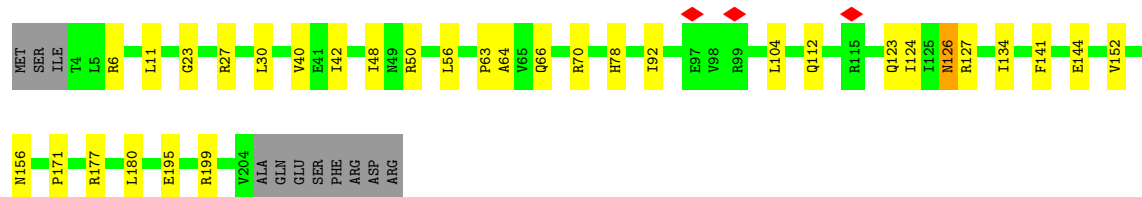
- Molecule 1: Microcompartments protein

Chain E: 76% 18% 5%



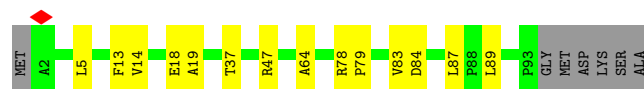
- Molecule 1: Microcompartments protein

Chain F: 80% 15% 5%



- Molecule 2: Microcompartments protein

Chain GA: 79% 14% 7%



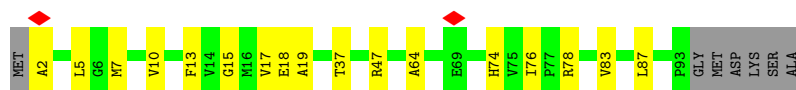
- Molecule 2: Microcompartments protein

Chain GB: 79% 14% 7%

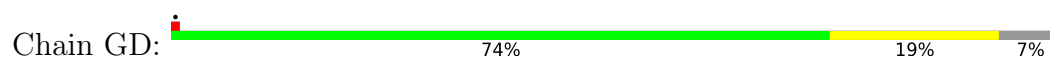


- Molecule 2: Microcompartments protein

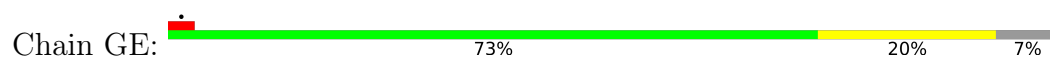
Chain GC: 76% 17% 7%



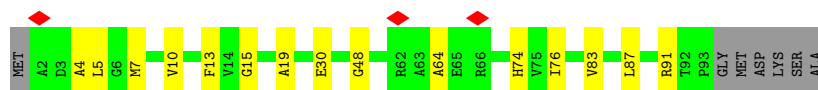
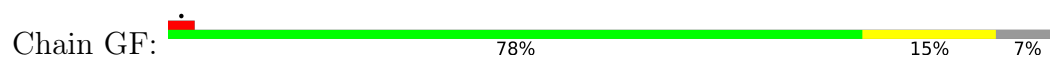
- Molecule 2: Microcompartments protein



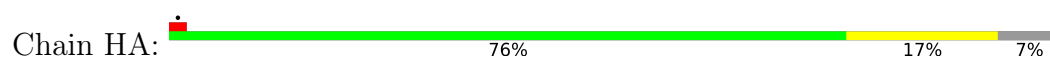
- Molecule 2: Microcompartments protein



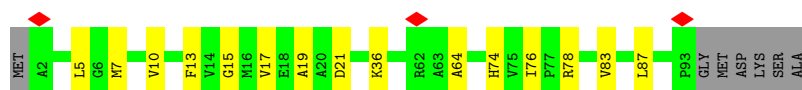
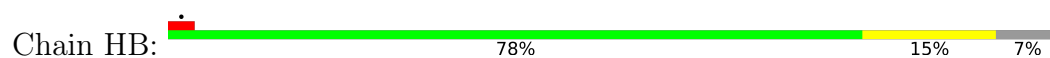
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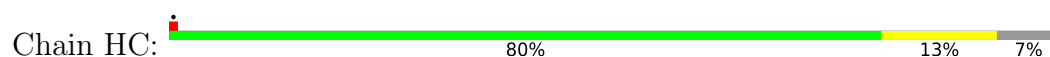
- Molecule 2: Microcompartments protein




- Molecule 2: Microcompartments protein



- Molecule 2: Microcompartments protein




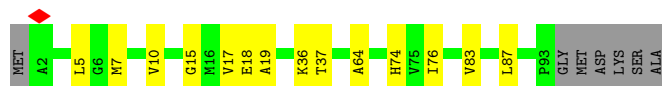
- Molecule 2: Microcompartments protein

Chain HD:  79% 14% 7%




- Molecule 2: Microcompartments protein

Chain HE:  79% 14% 7%




- Molecule 2: Microcompartments protein

Chain HF:  73% 20% 7%



- Molecule 2: Microcompartments protein

Chain IA:  84% 9% 7%




- Molecule 2: Microcompartments protein

Chain IB:  80% 13% 7%




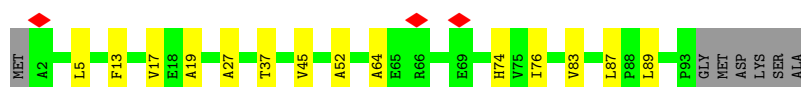
- Molecule 2: Microcompartments protein

Chain IC:  76% 17% 7%

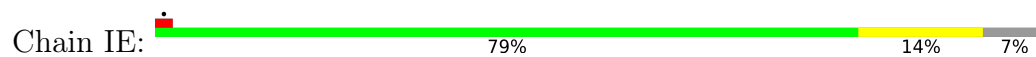


- Molecule 2: Microcompartments protein

Chain ID:  79% 14% 7%



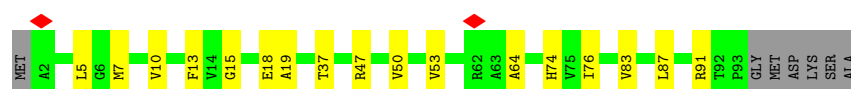
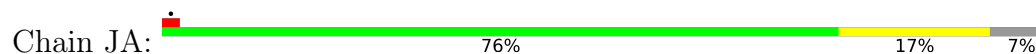
- Molecule 2: Microcompartments protein



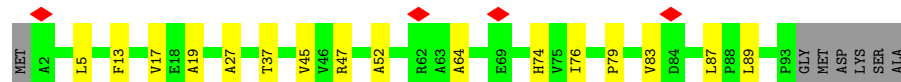
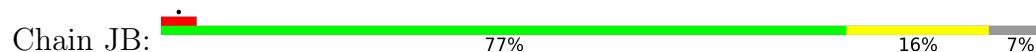
- Molecule 2: Microcompartments protein



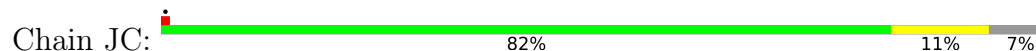
- Molecule 2: Microcompartments protein



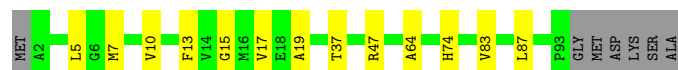
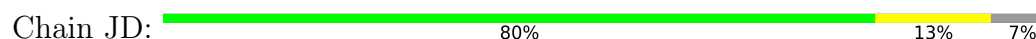
- Molecule 2: Microcompartments protein



- Molecule 2: Microcompartments protein




- Molecule 2: Microcompartments protein



- Molecule 2: Microcompartments protein




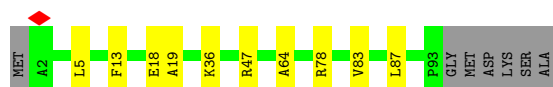
- Molecule 2: Microcompartments protein

Chain JF:  73% 20% 7%




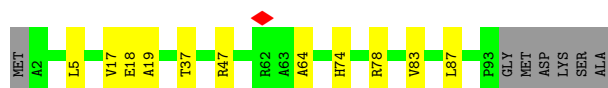
- Molecule 2: Microcompartments protein

Chain KA:  83% 10% 7%




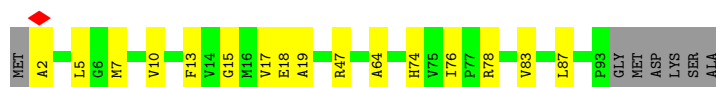
- Molecule 2: Microcompartments protein

Chain KB:  82% 11% 7%




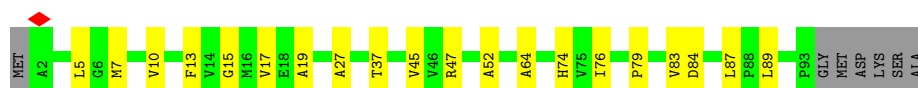
- Molecule 2: Microcompartments protein

Chain KC:  77% 16% 7%




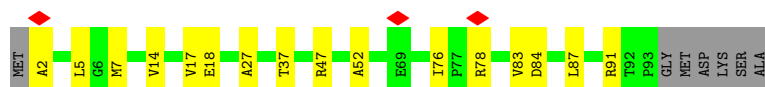
- Molecule 2: Microcompartments protein

Chain KD:  73% 20% 7%




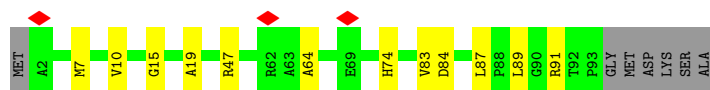
- Molecule 2: Microcompartments protein

Chain KE:  77% 16% 7%

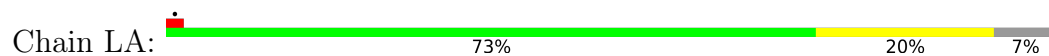


- Molecule 2: Microcompartments protein

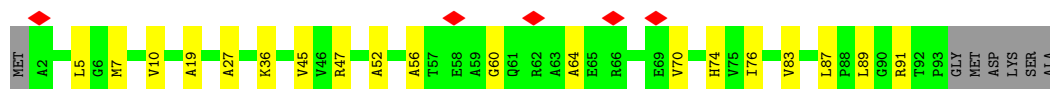
Chain KF:  81% 12% 7%



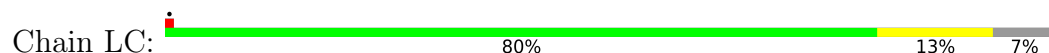
- Molecule 2: Microcompartments protein



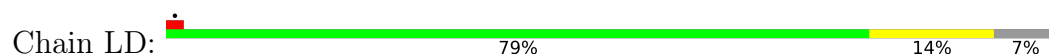
- Molecule 2: Microcompartments protein



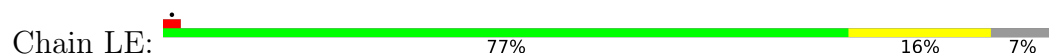
- Molecule 2: Microcompartments protein



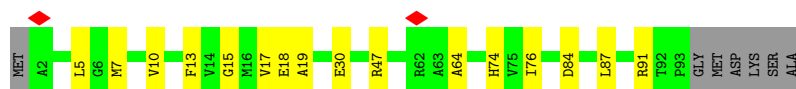
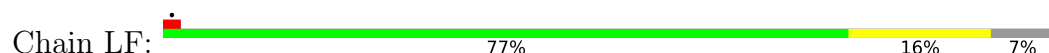
- Molecule 2: Microcompartments protein



- Molecule 2: Microcompartments protein



- Molecule 2: Microcompartments protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	149628	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Initial CTF fitting using CTFFIND4, CTF correction applied within RELION.	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	48543	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.148	Depositor
Minimum map value	-0.086	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.03	Depositor
Map size (\AA)	527.36, 527.36, 527.36	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.03, 1.03, 1.03	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	A	0.34	0/1551	0.52	0/2111
1	B	0.34	0/1551	0.52	0/2111
1	C	0.34	0/1551	0.51	0/2111
1	D	0.32	0/1551	0.50	0/2111
1	E	0.32	0/1551	0.50	0/2111
1	F	0.32	0/1546	0.49	0/2104
2	GA	0.36	0/666	0.52	0/904
2	GB	0.36	0/666	0.52	0/904
2	GC	0.35	0/666	0.51	0/904
2	GD	0.34	0/666	0.50	0/904
2	GE	0.33	0/666	0.51	0/904
2	GF	0.35	0/666	0.51	0/904
2	HA	0.37	0/666	0.52	0/904
2	HB	0.33	0/666	0.51	0/904
2	HC	0.34	0/666	0.52	0/904
2	HD	0.35	0/666	0.51	0/904
2	HE	0.36	0/666	0.52	0/904
2	HF	0.38	0/666	0.53	0/904
2	IA	0.36	0/666	0.52	0/904
2	IB	0.39	0/666	0.53	0/904
2	IC	0.35	0/666	0.52	0/904
2	ID	0.37	0/666	0.51	0/904
2	IE	0.34	0/666	0.52	0/904
2	IF	0.35	0/666	0.53	0/904
2	JA	0.38	0/666	0.52	0/904
2	JB	0.34	0/666	0.52	0/904
2	JC	0.35	0/666	0.50	0/904
2	JD	0.35	0/666	0.51	0/904
2	JE	0.36	0/666	0.52	0/904
2	JF	0.36	0/666	0.52	0/904
2	KA	0.36	0/666	0.51	0/904
2	KB	0.38	0/666	0.53	0/904
2	KC	0.35	0/666	0.53	0/904
2	KD	0.35	0/666	0.51	0/904

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	KE	0.34	0/666	0.51	0/904
2	KF	0.36	0/666	0.53	0/904
2	LA	0.37	0/666	0.54	0/904
2	LB	0.34	0/666	0.51	0/904
2	LC	0.35	0/666	0.51	0/904
2	LD	0.35	0/666	0.50	0/904
2	LE	0.37	0/666	0.53	0/904
2	LF	0.38	0/666	0.52	0/904
All	All	0.35	0/33277	0.51	0/45203

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	E	0	1
1	F	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	70	ARG	Peptide
1	E	126	ASN	Peptide
1	F	126	ASN	Peptide

5.2 Too-close contacts [i](#)

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	1525	0	1549	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1525	0	1549	21	0
1	C	1525	0	1549	21	0
1	D	1525	0	1549	21	0
1	E	1525	0	1549	26	0
1	F	1520	0	1544	23	0
2	GA	658	0	678	11	0
2	GB	658	0	678	11	0
2	GC	658	0	678	15	0
2	GD	658	0	678	17	0
2	GE	658	0	678	16	0
2	GF	658	0	678	10	0
2	HA	658	0	678	13	0
2	HB	658	0	678	13	0
2	HC	658	0	678	10	0
2	HD	658	0	678	11	0
2	HE	658	0	678	13	0
2	HF	658	0	678	16	0
2	IA	658	0	678	8	0
2	IB	658	0	678	10	0
2	IC	658	0	678	12	0
2	ID	658	0	678	12	0
2	IE	658	0	678	12	0
2	IF	658	0	678	17	0
2	JA	658	0	678	13	0
2	JB	658	0	678	11	0
2	JC	658	0	678	11	0
2	JD	658	0	678	10	0
2	JE	658	0	678	17	0
2	JF	658	0	678	19	0
2	KA	658	0	678	7	0
2	KB	658	0	678	9	0
2	KC	658	0	678	13	0
2	KD	658	0	678	16	0
2	KE	658	0	678	15	0
2	KF	658	0	678	10	0
2	LA	658	0	678	15	0
2	LB	658	0	678	11	0
2	LC	658	0	678	9	0
2	LD	658	0	678	12	0
2	LE	658	0	678	12	0
2	LF	658	0	678	14	0
All	All	32833	0	33697	446	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 446 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:A:22:ILE:O	1:A:26:ALA:HB2	1.94	0.67
2:HF:5:LEU:HD23	2:HF:76:ILE:HD12	1.80	0.63
1:A:124:ILE:HG21	1:C:66:GLN:HB3	1.80	0.63
1:B:11:LEU:HD22	1:B:156:ASN:HD22	1.65	0.62
2:HE:5:LEU:HD23	2:HE:76:ILE:HD12	1.82	0.62

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	200/212 (94%)	188 (94%)	11 (6%)	1 (0%)	29	61
1	B	200/212 (94%)	190 (95%)	10 (5%)	0	100	100
1	C	200/212 (94%)	188 (94%)	12 (6%)	0	100	100
1	D	200/212 (94%)	194 (97%)	6 (3%)	0	100	100
1	E	200/212 (94%)	192 (96%)	8 (4%)	0	100	100
1	F	199/212 (94%)	189 (95%)	10 (5%)	0	100	100
2	GA	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	GB	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	GC	90/99 (91%)	87 (97%)	3 (3%)	0	100	100
2	GD	90/99 (91%)	87 (97%)	3 (3%)	0	100	100
2	GE	90/99 (91%)	86 (96%)	4 (4%)	0	100	100
2	GF	90/99 (91%)	87 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	HA	90/99 (91%)	89 (99%)	1 (1%)	0	100	100
2	HB	90/99 (91%)	85 (94%)	5 (6%)	0	100	100
2	HC	90/99 (91%)	87 (97%)	3 (3%)	0	100	100
2	HD	90/99 (91%)	86 (96%)	4 (4%)	0	100	100
2	HE	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	HF	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	IA	90/99 (91%)	89 (99%)	1 (1%)	0	100	100
2	IB	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	IC	90/99 (91%)	85 (94%)	5 (6%)	0	100	100
2	ID	90/99 (91%)	87 (97%)	3 (3%)	0	100	100
2	IE	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	IF	90/99 (91%)	87 (97%)	3 (3%)	0	100	100
2	JA	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	JB	90/99 (91%)	86 (96%)	4 (4%)	0	100	100
2	JC	90/99 (91%)	89 (99%)	1 (1%)	0	100	100
2	JD	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	JE	90/99 (91%)	87 (97%)	3 (3%)	0	100	100
2	JF	90/99 (91%)	87 (97%)	3 (3%)	0	100	100
2	KA	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	KB	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	KC	90/99 (91%)	89 (99%)	1 (1%)	0	100	100
2	KD	90/99 (91%)	87 (97%)	3 (3%)	0	100	100
2	KE	90/99 (91%)	86 (96%)	4 (4%)	0	100	100
2	KF	90/99 (91%)	87 (97%)	3 (3%)	0	100	100
2	LA	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	LB	90/99 (91%)	86 (96%)	4 (4%)	0	100	100
2	LC	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	LD	90/99 (91%)	87 (97%)	3 (3%)	0	100	100
2	LE	90/99 (91%)	88 (98%)	2 (2%)	0	100	100
2	LF	90/99 (91%)	89 (99%)	1 (1%)	0	100	100
All	All	4439/4836 (92%)	4287 (97%)	151 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	71	ALA

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	154/164 (94%)	154 (100%)	0	100	100
1	B	154/164 (94%)	154 (100%)	0	100	100
1	C	154/164 (94%)	154 (100%)	0	100	100
1	D	154/164 (94%)	154 (100%)	0	100	100
1	E	154/164 (94%)	154 (100%)	0	100	100
1	F	154/164 (94%)	154 (100%)	0	100	100
2	GA	63/68 (93%)	63 (100%)	0	100	100
2	GB	63/68 (93%)	63 (100%)	0	100	100
2	GC	63/68 (93%)	63 (100%)	0	100	100
2	GD	63/68 (93%)	63 (100%)	0	100	100
2	GE	63/68 (93%)	63 (100%)	0	100	100
2	GF	63/68 (93%)	63 (100%)	0	100	100
2	HA	63/68 (93%)	63 (100%)	0	100	100
2	HB	63/68 (93%)	63 (100%)	0	100	100
2	HC	63/68 (93%)	63 (100%)	0	100	100
2	HD	63/68 (93%)	63 (100%)	0	100	100
2	HE	63/68 (93%)	63 (100%)	0	100	100
2	HF	63/68 (93%)	63 (100%)	0	100	100
2	IA	63/68 (93%)	63 (100%)	0	100	100
2	IB	63/68 (93%)	63 (100%)	0	100	100
2	IC	63/68 (93%)	63 (100%)	0	100	100
2	ID	63/68 (93%)	63 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	IE	63/68 (93%)	63 (100%)	0	100	100
2	IF	63/68 (93%)	63 (100%)	0	100	100
2	JA	63/68 (93%)	63 (100%)	0	100	100
2	JB	63/68 (93%)	63 (100%)	0	100	100
2	JC	63/68 (93%)	63 (100%)	0	100	100
2	JD	63/68 (93%)	63 (100%)	0	100	100
2	JE	63/68 (93%)	63 (100%)	0	100	100
2	JF	63/68 (93%)	63 (100%)	0	100	100
2	KA	63/68 (93%)	63 (100%)	0	100	100
2	KB	63/68 (93%)	63 (100%)	0	100	100
2	KC	63/68 (93%)	63 (100%)	0	100	100
2	KD	63/68 (93%)	63 (100%)	0	100	100
2	KE	63/68 (93%)	63 (100%)	0	100	100
2	KF	63/68 (93%)	63 (100%)	0	100	100
2	LA	63/68 (93%)	63 (100%)	0	100	100
2	LB	63/68 (93%)	63 (100%)	0	100	100
2	LC	63/68 (93%)	63 (100%)	0	100	100
2	LD	63/68 (93%)	63 (100%)	0	100	100
2	LE	63/68 (93%)	63 (100%)	0	100	100
2	LF	63/68 (93%)	63 (100%)	0	100	100
All	All	3192/3432 (93%)	3192 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	79	HIS
2	JF	82	ASN
1	D	156	ASN
2	KB	82	ASN
1	F	123	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 monosaccharides 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.

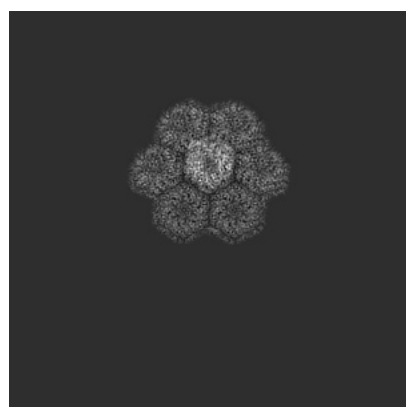
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9308. These allow visual inspection of the internal detail of the map and identification of artifacts.

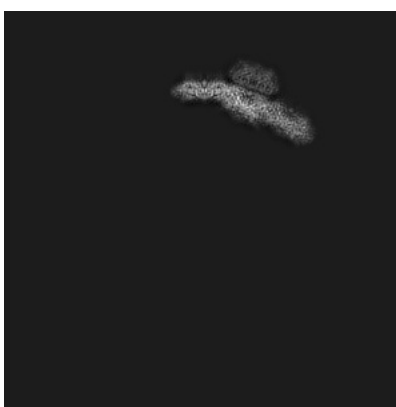
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

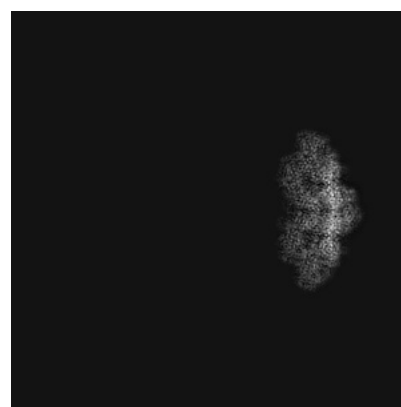
6.1.1 Primary map



X



Y

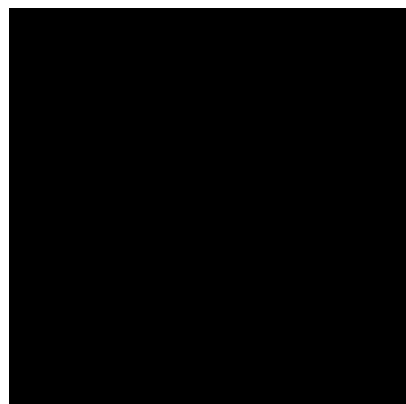


Z

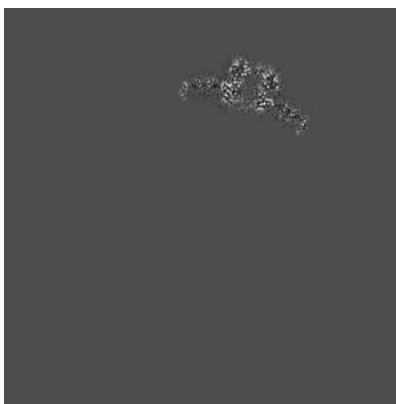
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 256



Y Index: 256

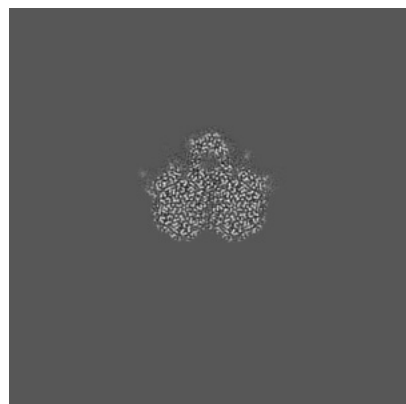


Z Index: 256

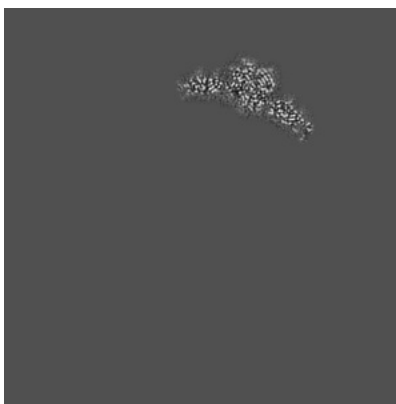
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 410



Y Index: 242

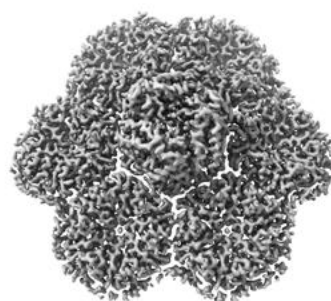


Z Index: 297

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

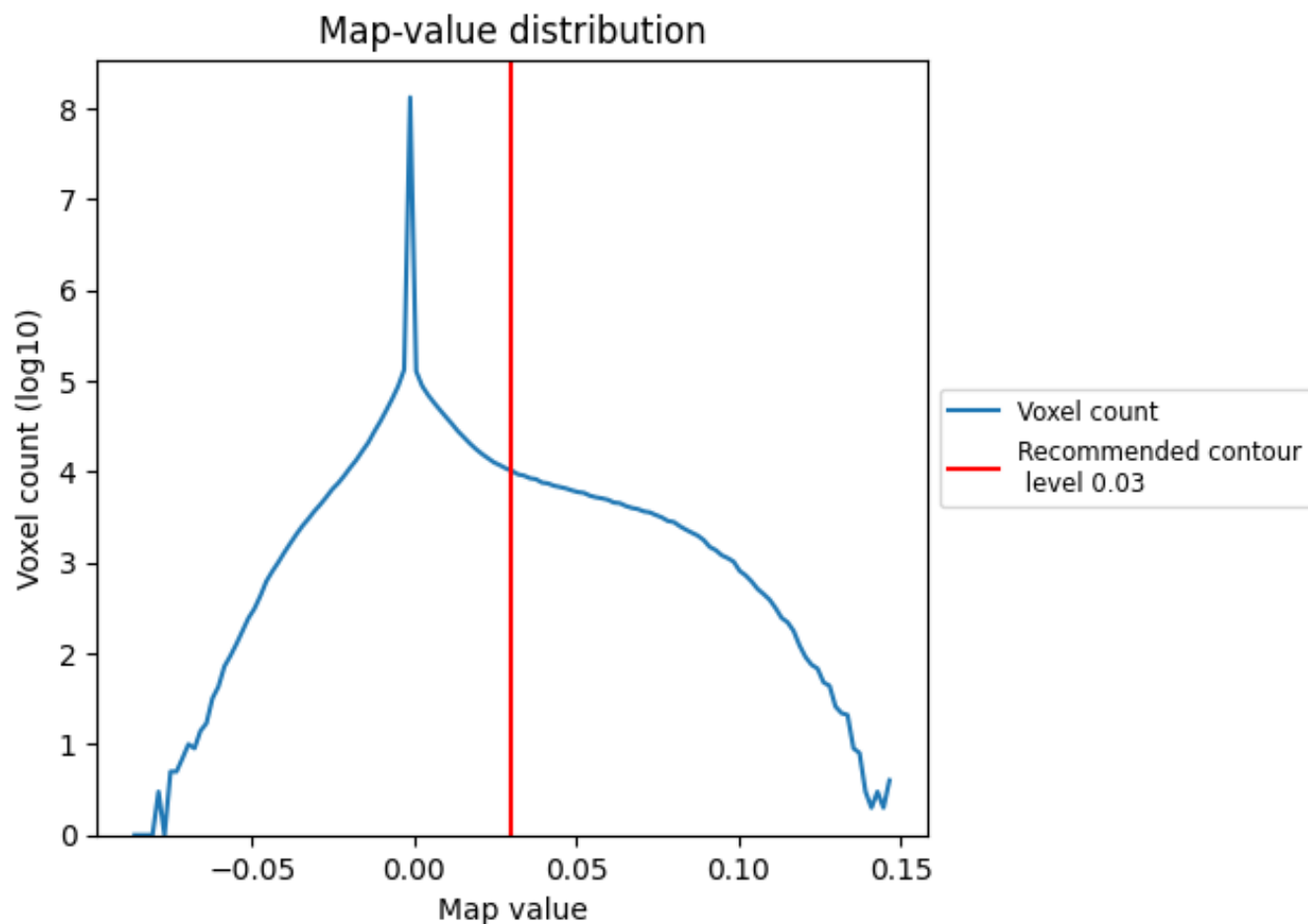
6.5 Mask visualisation

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

7 Map analysis [i](#)

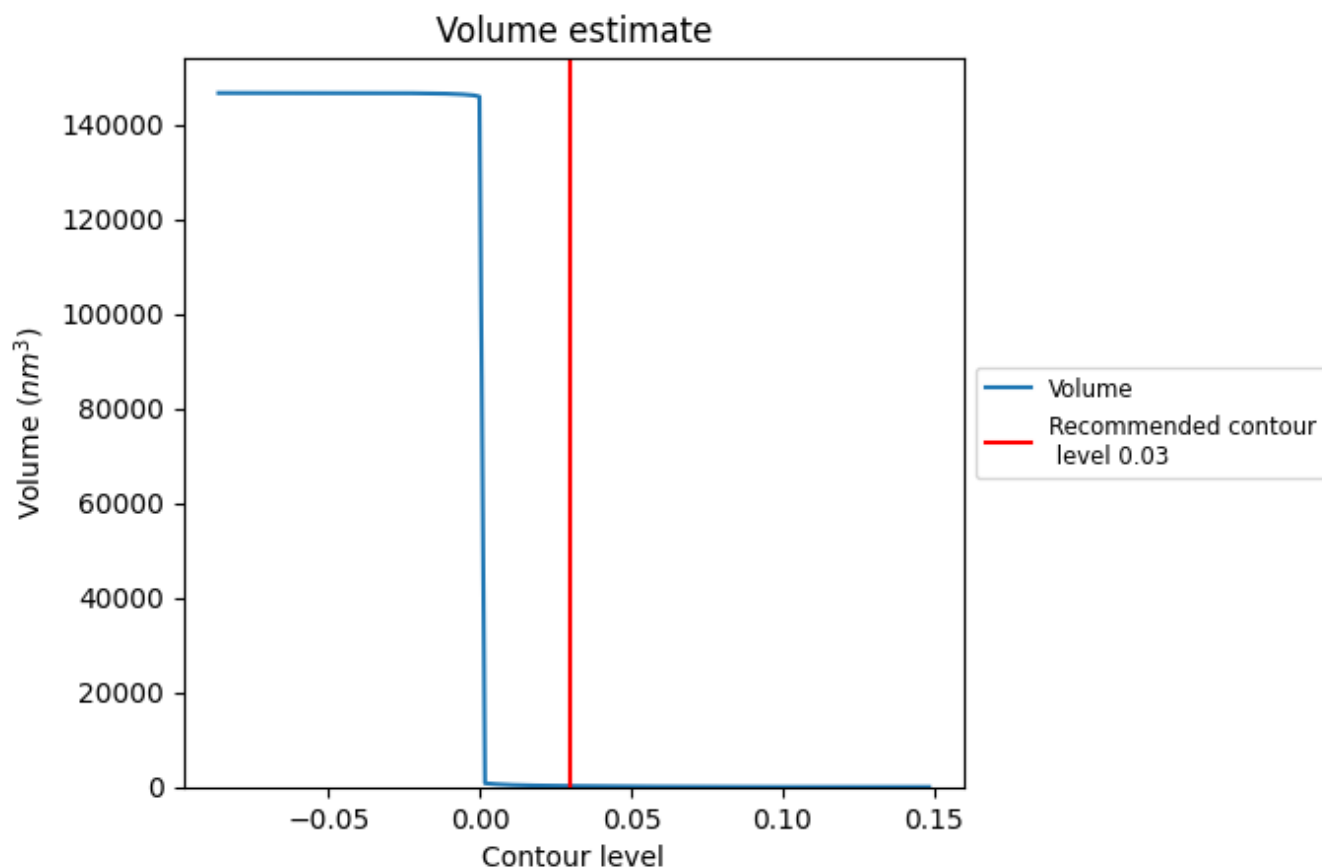
This section contains the results of statistical analysis of the map.

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.

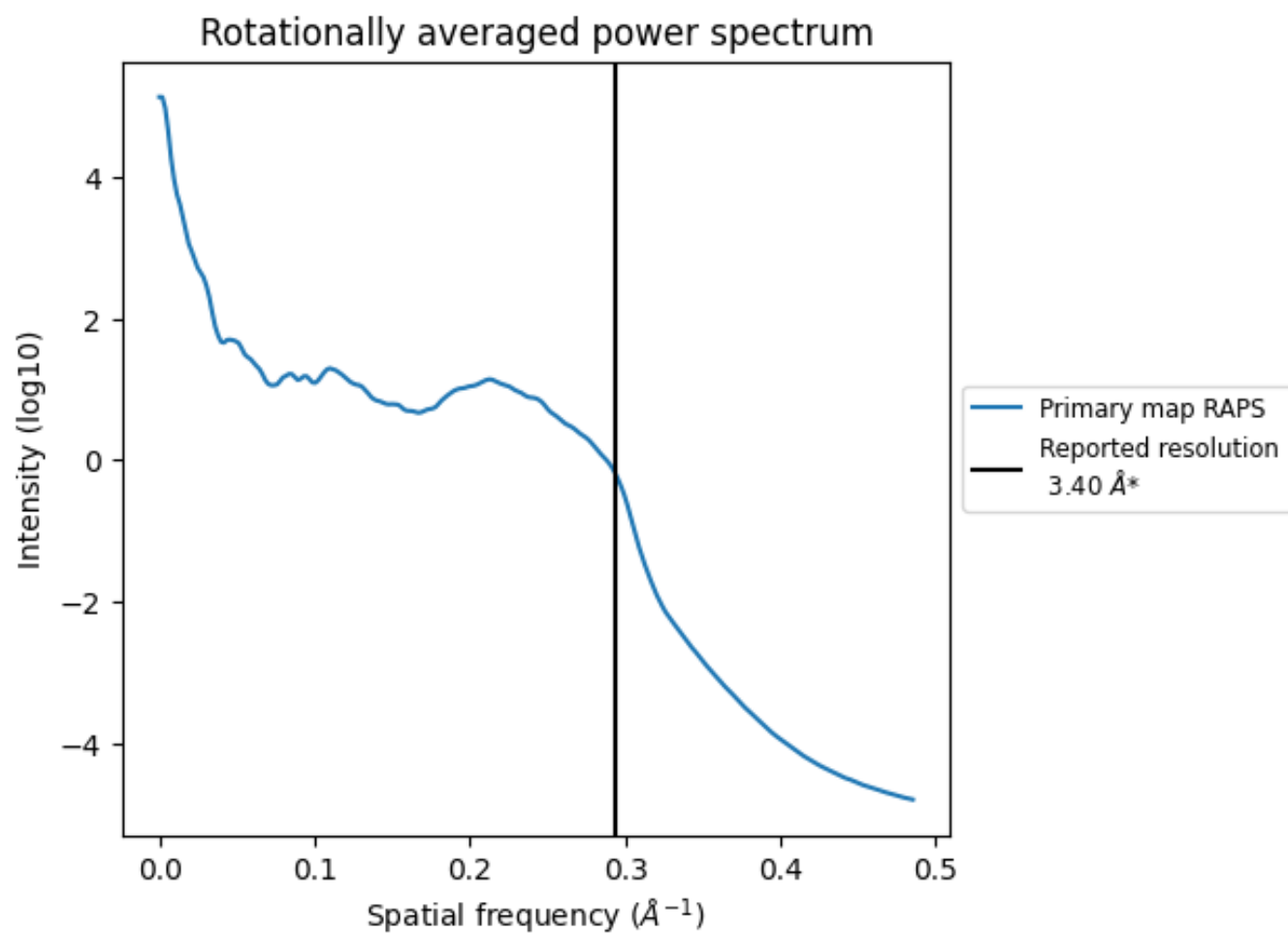
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 200 nm³; this corresponds to an approximate mass of 181 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 0.294 Å⁻¹

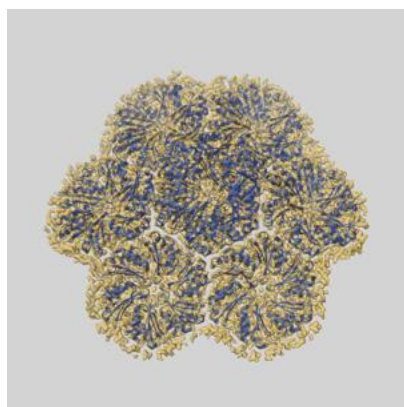
8 Fourier-Shell correlation

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

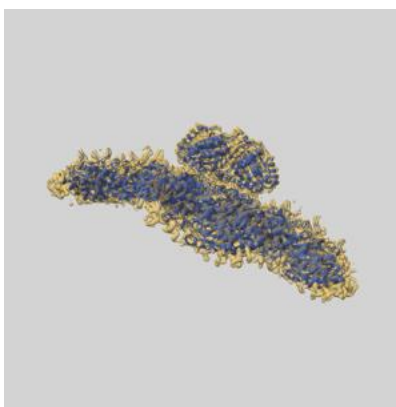
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9308 and PDB model 6MZV. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

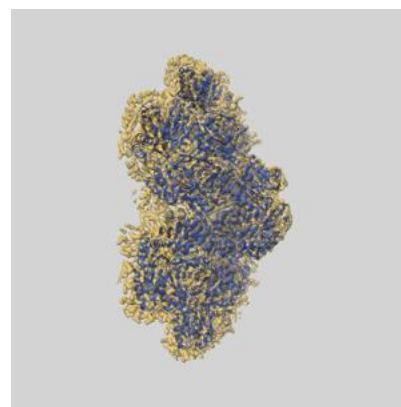
9.1 Map-model overlay [i](#)



X



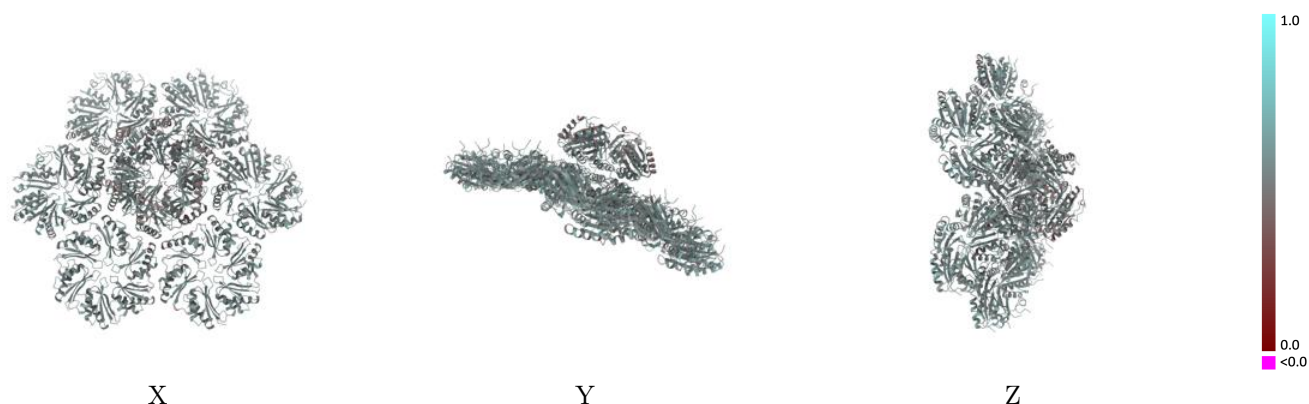
Y



Z

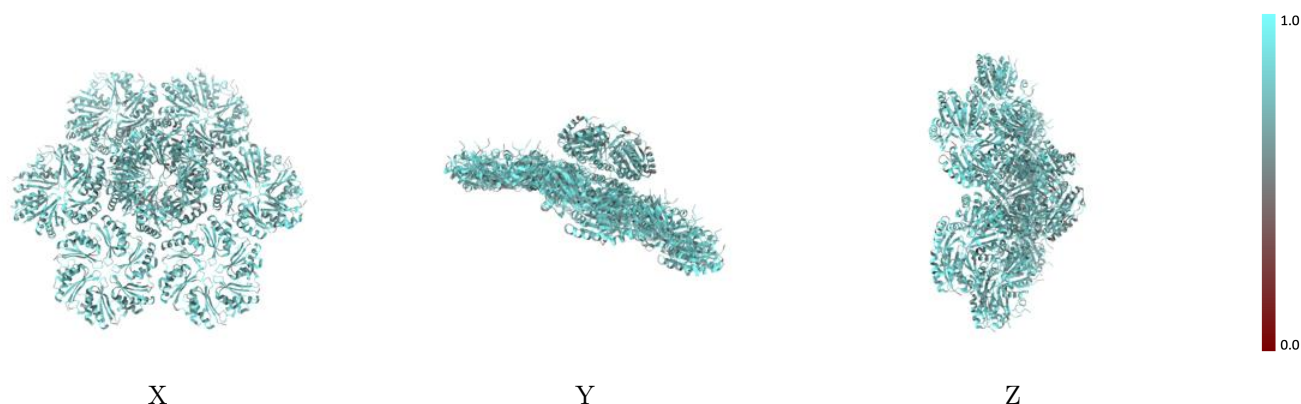
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



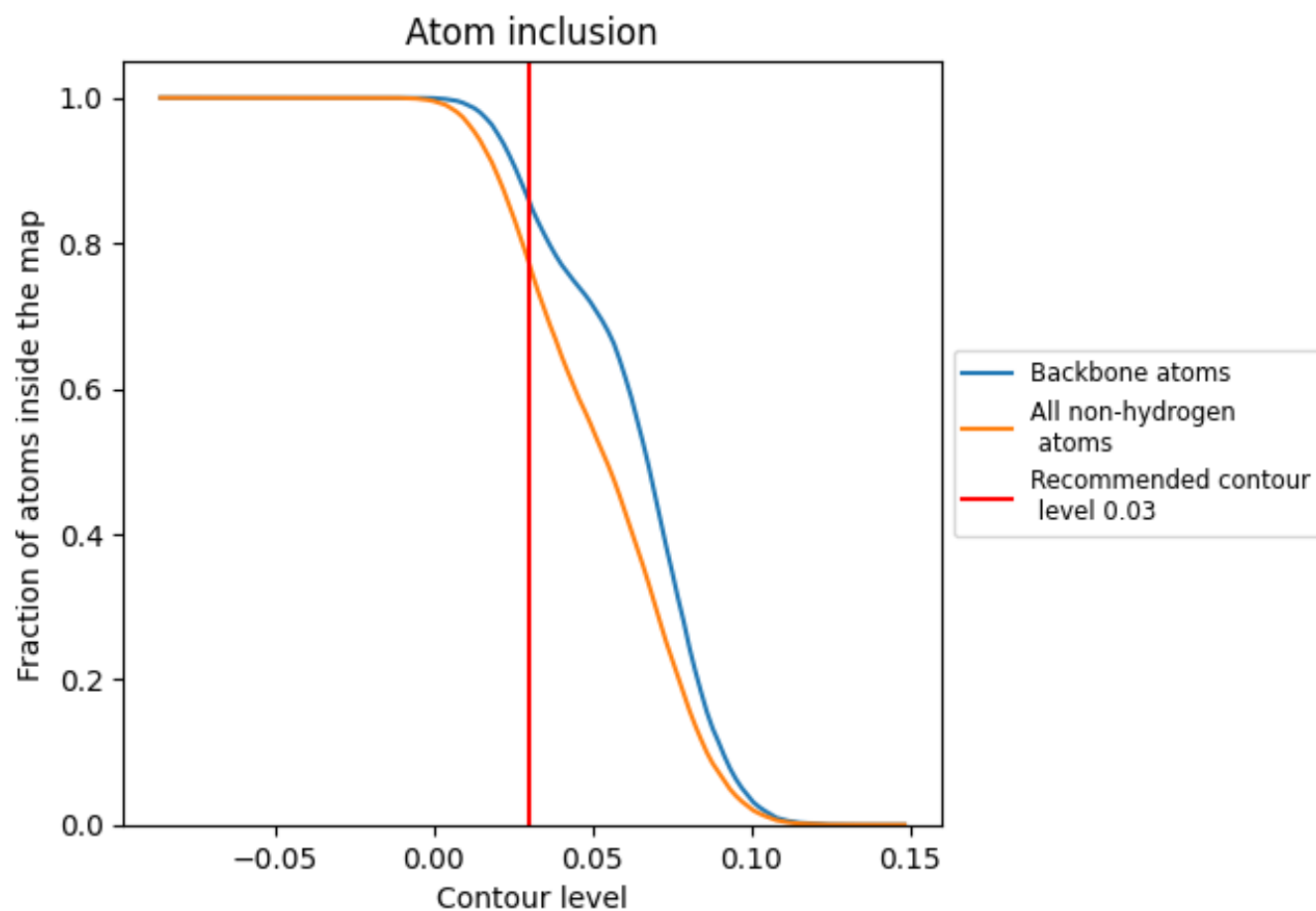
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 77% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7724	 0.5240
A	 0.7563	 0.5140
B	 0.7470	 0.5110
C	 0.7617	 0.5150
D	 0.7430	 0.5040
E	 0.7430	 0.5040
F	 0.7461	 0.5040
GA	 0.8121	 0.5350
GB	 0.7904	 0.5350
GC	 0.7686	 0.5370
GD	 0.7764	 0.5300
GE	 0.7780	 0.5240
GF	 0.7717	 0.5180
HA	 0.7888	 0.5270
HB	 0.7407	 0.5200
HC	 0.7655	 0.5330
HD	 0.7795	 0.5330
HE	 0.7811	 0.5330
HF	 0.7997	 0.5330
IA	 0.7966	 0.5380
IB	 0.8043	 0.5410
IC	 0.7857	 0.5340
ID	 0.7547	 0.5300
IE	 0.7702	 0.5230
IF	 0.7811	 0.5180
JA	 0.7919	 0.5300
JB	 0.7593	 0.5250
JC	 0.7702	 0.5330
JD	 0.7997	 0.5330
JE	 0.7826	 0.5300
JF	 0.7981	 0.5270
KA	 0.8043	 0.5370
KB	 0.7966	 0.5340
KC	 0.7857	 0.5340
KD	 0.7811	 0.5280



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Chain	Atom inclusion	Q-score
KE	 0.7748	 0.5260
KF	 0.7811	 0.5280
LA	 0.7904	 0.5260
LB	 0.7547	 0.5210
LC	 0.7593	 0.5220
LD	 0.7811	 0.5360
LE	 0.7904	 0.5350
LF	 0.7811	 0.5280