



## wwPDB EM Validation Summary Report ⓘ

Nov 27, 2022 – 08:16 PM EST

PDB ID : 7KVC  
EMDB ID : EMD-23046  
Title : Cryo-EM structure of Mal de Rio Cuarto virus P9-1 viroplasm protein (decamer)  
Authors : Llauger, G.; Melero, R.; Monti, D.; Sycz, G.; Huck-Iriart, C.; Cerutti, M.L.; Klinke, S.; Arranz, R.; Carazo, J.M.; Goldbaum, F.A.; del Vas, M.; Otero, L.H.  
Deposited on : 2020-11-27  
Resolution : 4.70 Å(reported)  
Based on initial model : 6UCT

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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

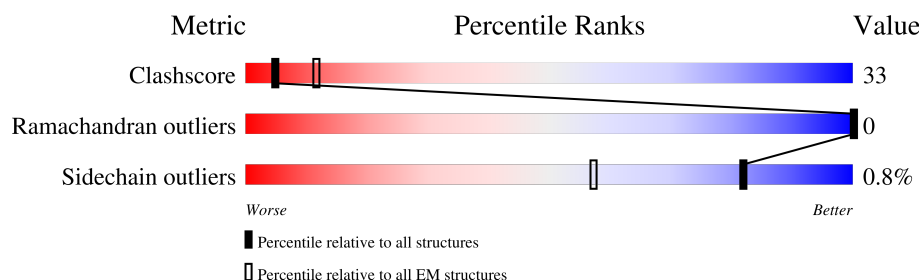
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.70 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  $\geq 3$ , 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	388	
1	B	388	
1	C	388	
1	D	388	
1	E	388	
1	F	388	
1	G	388	
1	H	388	

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Mol	Chain	Length	Quality of chain
1	I	388	<div><div></div><div>9%</div><div>28%</div><div>40%</div><div>31%</div></div>
1	J	388	<div><div></div><div>8%</div><div>28%</div><div>40%</div><div>31%</div></div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 21920 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 p9-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	266	Total	C	N	O	S	0	0
			2192	1412	359	417	4		
1	B	266	Total	C	N	O	S	0	0
			2192	1412	359	417	4		
1	C	266	Total	C	N	O	S	0	0
			2192	1412	359	417	4		
1	D	266	Total	C	N	O	S	0	0
			2192	1412	359	417	4		
1	E	266	Total	C	N	O	S	0	0
			2192	1412	359	417	4		
1	F	266	Total	C	N	O	S	0	0
			2192	1412	359	417	4		
1	G	266	Total	C	N	O	S	0	0
			2192	1412	359	417	4		
1	H	266	Total	C	N	O	S	0	0
			2192	1412	359	417	4		
1	I	266	Total	C	N	O	S	0	0
			2192	1412	359	417	4		
1	J	266	Total	C	N	O	S	0	0
			2192	1412	359	417	4		

There are 520 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-50	MET	-	expression tag	UNP D9U542
A	-49	ARG	-	expression tag	UNP D9U542
A	-48	GLY	-	expression tag	UNP D9U542
A	-47	SER	-	expression tag	UNP D9U542
A	-46	HIS	-	expression tag	UNP D9U542
A	-45	HIS	-	expression tag	UNP D9U542
A	-44	HIS	-	expression tag	UNP D9U542
A	-43	HIS	-	expression tag	UNP D9U542
A	-42	HIS	-	expression tag	UNP D9U542
A	-41	HIS	-	expression tag	UNP D9U542

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-40	GLY	-	expression tag	UNP D9U542
A	-39	MET	-	expression tag	UNP D9U542
A	-38	ALA	-	expression tag	UNP D9U542
A	-37	SER	-	expression tag	UNP D9U542
A	-36	MET	-	expression tag	UNP D9U542
A	-35	THR	-	expression tag	UNP D9U542
A	-34	GLY	-	expression tag	UNP D9U542
A	-33	GLY	-	expression tag	UNP D9U542
A	-32	GLN	-	expression tag	UNP D9U542
A	-31	GLN	-	expression tag	UNP D9U542
A	-30	MET	-	expression tag	UNP D9U542
A	-29	GLY	-	expression tag	UNP D9U542
A	-28	ARG	-	expression tag	UNP D9U542
A	-27	ASP	-	expression tag	UNP D9U542
A	-26	LEU	-	expression tag	UNP D9U542
A	-25	TYR	-	expression tag	UNP D9U542
A	-24	ASP	-	expression tag	UNP D9U542
A	-23	ASP	-	expression tag	UNP D9U542
A	-22	ASP	-	expression tag	UNP D9U542
A	-21	ASP	-	expression tag	UNP D9U542
A	-20	LYS	-	expression tag	UNP D9U542
A	-19	ASP	-	expression tag	UNP D9U542
A	-18	ARG	-	expression tag	UNP D9U542
A	-17	TRP	-	expression tag	UNP D9U542
A	-16	GLY	-	expression tag	UNP D9U542
A	-15	SER	-	expression tag	UNP D9U542
A	-14	GLU	-	expression tag	UNP D9U542
A	-13	LEU	-	expression tag	UNP D9U542
A	-12	GLU	-	expression tag	UNP D9U542
A	-11	ILE	-	expression tag	UNP D9U542
A	-10	CYS	-	expression tag	UNP D9U542
A	-9	SER	-	expression tag	UNP D9U542
A	-8	TRP	-	expression tag	UNP D9U542
A	-7	TYR	-	expression tag	UNP D9U542
A	-6	HIS	-	expression tag	UNP D9U542
A	-5	GLY	-	expression tag	UNP D9U542
A	-4	GLY	-	expression tag	UNP D9U542
A	-3	ARG	-	expression tag	UNP D9U542
A	-2	GLY	-	expression tag	UNP D9U542
A	-1	ASN	-	expression tag	UNP D9U542
A	0	SER	-	expression tag	UNP D9U542
A	1	ILE	-	expression tag	UNP D9U542

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-50	MET	-	expression tag	UNP D9U542
B	-49	ARG	-	expression tag	UNP D9U542
B	-48	GLY	-	expression tag	UNP D9U542
B	-47	SER	-	expression tag	UNP D9U542
B	-46	HIS	-	expression tag	UNP D9U542
B	-45	HIS	-	expression tag	UNP D9U542
B	-44	HIS	-	expression tag	UNP D9U542
B	-43	HIS	-	expression tag	UNP D9U542
B	-42	HIS	-	expression tag	UNP D9U542
B	-41	HIS	-	expression tag	UNP D9U542
B	-40	GLY	-	expression tag	UNP D9U542
B	-39	MET	-	expression tag	UNP D9U542
B	-38	ALA	-	expression tag	UNP D9U542
B	-37	SER	-	expression tag	UNP D9U542
B	-36	MET	-	expression tag	UNP D9U542
B	-35	THR	-	expression tag	UNP D9U542
B	-34	GLY	-	expression tag	UNP D9U542
B	-33	GLY	-	expression tag	UNP D9U542
B	-32	GLN	-	expression tag	UNP D9U542
B	-31	GLN	-	expression tag	UNP D9U542
B	-30	MET	-	expression tag	UNP D9U542
B	-29	GLY	-	expression tag	UNP D9U542
B	-28	ARG	-	expression tag	UNP D9U542
B	-27	ASP	-	expression tag	UNP D9U542
B	-26	LEU	-	expression tag	UNP D9U542
B	-25	TYR	-	expression tag	UNP D9U542
B	-24	ASP	-	expression tag	UNP D9U542
B	-23	ASP	-	expression tag	UNP D9U542
B	-22	ASP	-	expression tag	UNP D9U542
B	-21	ASP	-	expression tag	UNP D9U542
B	-20	LYS	-	expression tag	UNP D9U542
B	-19	ASP	-	expression tag	UNP D9U542
B	-18	ARG	-	expression tag	UNP D9U542
B	-17	TRP	-	expression tag	UNP D9U542
B	-16	GLY	-	expression tag	UNP D9U542
B	-15	SER	-	expression tag	UNP D9U542
B	-14	GLU	-	expression tag	UNP D9U542
B	-13	LEU	-	expression tag	UNP D9U542
B	-12	GLU	-	expression tag	UNP D9U542
B	-11	ILE	-	expression tag	UNP D9U542
B	-10	CYS	-	expression tag	UNP D9U542
B	-9	SER	-	expression tag	UNP D9U542

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	TRP	-	expression tag	UNP D9U542
B	-7	TYR	-	expression tag	UNP D9U542
B	-6	HIS	-	expression tag	UNP D9U542
B	-5	GLY	-	expression tag	UNP D9U542
B	-4	GLY	-	expression tag	UNP D9U542
B	-3	ARG	-	expression tag	UNP D9U542
B	-2	GLY	-	expression tag	UNP D9U542
B	-1	ASN	-	expression tag	UNP D9U542
B	0	SER	-	expression tag	UNP D9U542
B	1	ILE	-	expression tag	UNP D9U542
C	-50	MET	-	expression tag	UNP D9U542
C	-49	ARG	-	expression tag	UNP D9U542
C	-48	GLY	-	expression tag	UNP D9U542
C	-47	SER	-	expression tag	UNP D9U542
C	-46	HIS	-	expression tag	UNP D9U542
C	-45	HIS	-	expression tag	UNP D9U542
C	-44	HIS	-	expression tag	UNP D9U542
C	-43	HIS	-	expression tag	UNP D9U542
C	-42	HIS	-	expression tag	UNP D9U542
C	-41	HIS	-	expression tag	UNP D9U542
C	-40	GLY	-	expression tag	UNP D9U542
C	-39	MET	-	expression tag	UNP D9U542
C	-38	ALA	-	expression tag	UNP D9U542
C	-37	SER	-	expression tag	UNP D9U542
C	-36	MET	-	expression tag	UNP D9U542
C	-35	THR	-	expression tag	UNP D9U542
C	-34	GLY	-	expression tag	UNP D9U542
C	-33	GLY	-	expression tag	UNP D9U542
C	-32	GLN	-	expression tag	UNP D9U542
C	-31	GLN	-	expression tag	UNP D9U542
C	-30	MET	-	expression tag	UNP D9U542
C	-29	GLY	-	expression tag	UNP D9U542
C	-28	ARG	-	expression tag	UNP D9U542
C	-27	ASP	-	expression tag	UNP D9U542
C	-26	LEU	-	expression tag	UNP D9U542
C	-25	TYR	-	expression tag	UNP D9U542
C	-24	ASP	-	expression tag	UNP D9U542
C	-23	ASP	-	expression tag	UNP D9U542
C	-22	ASP	-	expression tag	UNP D9U542
C	-21	ASP	-	expression tag	UNP D9U542
C	-20	LYS	-	expression tag	UNP D9U542
C	-19	ASP	-	expression tag	UNP D9U542

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-18	ARG	-	expression tag	UNP D9U542
C	-17	TRP	-	expression tag	UNP D9U542
C	-16	GLY	-	expression tag	UNP D9U542
C	-15	SER	-	expression tag	UNP D9U542
C	-14	GLU	-	expression tag	UNP D9U542
C	-13	LEU	-	expression tag	UNP D9U542
C	-12	GLU	-	expression tag	UNP D9U542
C	-11	ILE	-	expression tag	UNP D9U542
C	-10	CYS	-	expression tag	UNP D9U542
C	-9	SER	-	expression tag	UNP D9U542
C	-8	TRP	-	expression tag	UNP D9U542
C	-7	TYR	-	expression tag	UNP D9U542
C	-6	HIS	-	expression tag	UNP D9U542
C	-5	GLY	-	expression tag	UNP D9U542
C	-4	GLY	-	expression tag	UNP D9U542
C	-3	ARG	-	expression tag	UNP D9U542
C	-2	GLY	-	expression tag	UNP D9U542
C	-1	ASN	-	expression tag	UNP D9U542
C	0	SER	-	expression tag	UNP D9U542
C	1	ILE	-	expression tag	UNP D9U542
D	-50	MET	-	expression tag	UNP D9U542
D	-49	ARG	-	expression tag	UNP D9U542
D	-48	GLY	-	expression tag	UNP D9U542
D	-47	SER	-	expression tag	UNP D9U542
D	-46	HIS	-	expression tag	UNP D9U542
D	-45	HIS	-	expression tag	UNP D9U542
D	-44	HIS	-	expression tag	UNP D9U542
D	-43	HIS	-	expression tag	UNP D9U542
D	-42	HIS	-	expression tag	UNP D9U542
D	-41	HIS	-	expression tag	UNP D9U542
D	-40	GLY	-	expression tag	UNP D9U542
D	-39	MET	-	expression tag	UNP D9U542
D	-38	ALA	-	expression tag	UNP D9U542
D	-37	SER	-	expression tag	UNP D9U542
D	-36	MET	-	expression tag	UNP D9U542
D	-35	THR	-	expression tag	UNP D9U542
D	-34	GLY	-	expression tag	UNP D9U542
D	-33	GLY	-	expression tag	UNP D9U542
D	-32	GLN	-	expression tag	UNP D9U542
D	-31	GLN	-	expression tag	UNP D9U542
D	-30	MET	-	expression tag	UNP D9U542
D	-29	GLY	-	expression tag	UNP D9U542

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-28	ARG	-	expression tag	UNP D9U542
D	-27	ASP	-	expression tag	UNP D9U542
D	-26	LEU	-	expression tag	UNP D9U542
D	-25	TYR	-	expression tag	UNP D9U542
D	-24	ASP	-	expression tag	UNP D9U542
D	-23	ASP	-	expression tag	UNP D9U542
D	-22	ASP	-	expression tag	UNP D9U542
D	-21	ASP	-	expression tag	UNP D9U542
D	-20	LYS	-	expression tag	UNP D9U542
D	-19	ASP	-	expression tag	UNP D9U542
D	-18	ARG	-	expression tag	UNP D9U542
D	-17	TRP	-	expression tag	UNP D9U542
D	-16	GLY	-	expression tag	UNP D9U542
D	-15	SER	-	expression tag	UNP D9U542
D	-14	GLU	-	expression tag	UNP D9U542
D	-13	LEU	-	expression tag	UNP D9U542
D	-12	GLU	-	expression tag	UNP D9U542
D	-11	ILE	-	expression tag	UNP D9U542
D	-10	CYS	-	expression tag	UNP D9U542
D	-9	SER	-	expression tag	UNP D9U542
D	-8	TRP	-	expression tag	UNP D9U542
D	-7	TYR	-	expression tag	UNP D9U542
D	-6	HIS	-	expression tag	UNP D9U542
D	-5	GLY	-	expression tag	UNP D9U542
D	-4	GLY	-	expression tag	UNP D9U542
D	-3	ARG	-	expression tag	UNP D9U542
D	-2	GLY	-	expression tag	UNP D9U542
D	-1	ASN	-	expression tag	UNP D9U542
D	0	SER	-	expression tag	UNP D9U542
D	1	ILE	-	expression tag	UNP D9U542
E	-50	MET	-	expression tag	UNP D9U542
E	-49	ARG	-	expression tag	UNP D9U542
E	-48	GLY	-	expression tag	UNP D9U542
E	-47	SER	-	expression tag	UNP D9U542
E	-46	HIS	-	expression tag	UNP D9U542
E	-45	HIS	-	expression tag	UNP D9U542
E	-44	HIS	-	expression tag	UNP D9U542
E	-43	HIS	-	expression tag	UNP D9U542
E	-42	HIS	-	expression tag	UNP D9U542
E	-41	HIS	-	expression tag	UNP D9U542
E	-40	GLY	-	expression tag	UNP D9U542
E	-39	MET	-	expression tag	UNP D9U542

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-38	ALA	-	expression tag	UNP D9U542
E	-37	SER	-	expression tag	UNP D9U542
E	-36	MET	-	expression tag	UNP D9U542
E	-35	THR	-	expression tag	UNP D9U542
E	-34	GLY	-	expression tag	UNP D9U542
E	-33	GLY	-	expression tag	UNP D9U542
E	-32	GLN	-	expression tag	UNP D9U542
E	-31	GLN	-	expression tag	UNP D9U542
E	-30	MET	-	expression tag	UNP D9U542
E	-29	GLY	-	expression tag	UNP D9U542
E	-28	ARG	-	expression tag	UNP D9U542
E	-27	ASP	-	expression tag	UNP D9U542
E	-26	LEU	-	expression tag	UNP D9U542
E	-25	TYR	-	expression tag	UNP D9U542
E	-24	ASP	-	expression tag	UNP D9U542
E	-23	ASP	-	expression tag	UNP D9U542
E	-22	ASP	-	expression tag	UNP D9U542
E	-21	ASP	-	expression tag	UNP D9U542
E	-20	LYS	-	expression tag	UNP D9U542
E	-19	ASP	-	expression tag	UNP D9U542
E	-18	ARG	-	expression tag	UNP D9U542
E	-17	TRP	-	expression tag	UNP D9U542
E	-16	GLY	-	expression tag	UNP D9U542
E	-15	SER	-	expression tag	UNP D9U542
E	-14	GLU	-	expression tag	UNP D9U542
E	-13	LEU	-	expression tag	UNP D9U542
E	-12	GLU	-	expression tag	UNP D9U542
E	-11	ILE	-	expression tag	UNP D9U542
E	-10	CYS	-	expression tag	UNP D9U542
E	-9	SER	-	expression tag	UNP D9U542
E	-8	TRP	-	expression tag	UNP D9U542
E	-7	TYR	-	expression tag	UNP D9U542
E	-6	HIS	-	expression tag	UNP D9U542
E	-5	GLY	-	expression tag	UNP D9U542
E	-4	GLY	-	expression tag	UNP D9U542
E	-3	ARG	-	expression tag	UNP D9U542
E	-2	GLY	-	expression tag	UNP D9U542
E	-1	ASN	-	expression tag	UNP D9U542
E	0	SER	-	expression tag	UNP D9U542
E	1	ILE	-	expression tag	UNP D9U542
F	-50	MET	-	expression tag	UNP D9U542
F	-49	ARG	-	expression tag	UNP D9U542

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-48	GLY	-	expression tag	UNP D9U542
F	-47	SER	-	expression tag	UNP D9U542
F	-46	HIS	-	expression tag	UNP D9U542
F	-45	HIS	-	expression tag	UNP D9U542
F	-44	HIS	-	expression tag	UNP D9U542
F	-43	HIS	-	expression tag	UNP D9U542
F	-42	HIS	-	expression tag	UNP D9U542
F	-41	HIS	-	expression tag	UNP D9U542
F	-40	GLY	-	expression tag	UNP D9U542
F	-39	MET	-	expression tag	UNP D9U542
F	-38	ALA	-	expression tag	UNP D9U542
F	-37	SER	-	expression tag	UNP D9U542
F	-36	MET	-	expression tag	UNP D9U542
F	-35	THR	-	expression tag	UNP D9U542
F	-34	GLY	-	expression tag	UNP D9U542
F	-33	GLY	-	expression tag	UNP D9U542
F	-32	GLN	-	expression tag	UNP D9U542
F	-31	GLN	-	expression tag	UNP D9U542
F	-30	MET	-	expression tag	UNP D9U542
F	-29	GLY	-	expression tag	UNP D9U542
F	-28	ARG	-	expression tag	UNP D9U542
F	-27	ASP	-	expression tag	UNP D9U542
F	-26	LEU	-	expression tag	UNP D9U542
F	-25	TYR	-	expression tag	UNP D9U542
F	-24	ASP	-	expression tag	UNP D9U542
F	-23	ASP	-	expression tag	UNP D9U542
F	-22	ASP	-	expression tag	UNP D9U542
F	-21	ASP	-	expression tag	UNP D9U542
F	-20	LYS	-	expression tag	UNP D9U542
F	-19	ASP	-	expression tag	UNP D9U542
F	-18	ARG	-	expression tag	UNP D9U542
F	-17	TRP	-	expression tag	UNP D9U542
F	-16	GLY	-	expression tag	UNP D9U542
F	-15	SER	-	expression tag	UNP D9U542
F	-14	GLU	-	expression tag	UNP D9U542
F	-13	LEU	-	expression tag	UNP D9U542
F	-12	GLU	-	expression tag	UNP D9U542
F	-11	ILE	-	expression tag	UNP D9U542
F	-10	CYS	-	expression tag	UNP D9U542
F	-9	SER	-	expression tag	UNP D9U542
F	-8	TRP	-	expression tag	UNP D9U542
F	-7	TYR	-	expression tag	UNP D9U542

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-6	HIS	-	expression tag	UNP D9U542
F	-5	GLY	-	expression tag	UNP D9U542
F	-4	GLY	-	expression tag	UNP D9U542
F	-3	ARG	-	expression tag	UNP D9U542
F	-2	GLY	-	expression tag	UNP D9U542
F	-1	ASN	-	expression tag	UNP D9U542
F	0	SER	-	expression tag	UNP D9U542
F	1	ILE	-	expression tag	UNP D9U542
G	-50	MET	-	expression tag	UNP D9U542
G	-49	ARG	-	expression tag	UNP D9U542
G	-48	GLY	-	expression tag	UNP D9U542
G	-47	SER	-	expression tag	UNP D9U542
G	-46	HIS	-	expression tag	UNP D9U542
G	-45	HIS	-	expression tag	UNP D9U542
G	-44	HIS	-	expression tag	UNP D9U542
G	-43	HIS	-	expression tag	UNP D9U542
G	-42	HIS	-	expression tag	UNP D9U542
G	-41	HIS	-	expression tag	UNP D9U542
G	-40	GLY	-	expression tag	UNP D9U542
G	-39	MET	-	expression tag	UNP D9U542
G	-38	ALA	-	expression tag	UNP D9U542
G	-37	SER	-	expression tag	UNP D9U542
G	-36	MET	-	expression tag	UNP D9U542
G	-35	THR	-	expression tag	UNP D9U542
G	-34	GLY	-	expression tag	UNP D9U542
G	-33	GLY	-	expression tag	UNP D9U542
G	-32	GLN	-	expression tag	UNP D9U542
G	-31	GLN	-	expression tag	UNP D9U542
G	-30	MET	-	expression tag	UNP D9U542
G	-29	GLY	-	expression tag	UNP D9U542
G	-28	ARG	-	expression tag	UNP D9U542
G	-27	ASP	-	expression tag	UNP D9U542
G	-26	LEU	-	expression tag	UNP D9U542
G	-25	TYR	-	expression tag	UNP D9U542
G	-24	ASP	-	expression tag	UNP D9U542
G	-23	ASP	-	expression tag	UNP D9U542
G	-22	ASP	-	expression tag	UNP D9U542
G	-21	ASP	-	expression tag	UNP D9U542
G	-20	LYS	-	expression tag	UNP D9U542
G	-19	ASP	-	expression tag	UNP D9U542
G	-18	ARG	-	expression tag	UNP D9U542
G	-17	TRP	-	expression tag	UNP D9U542

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-16	GLY	-	expression tag	UNP D9U542
G	-15	SER	-	expression tag	UNP D9U542
G	-14	GLU	-	expression tag	UNP D9U542
G	-13	LEU	-	expression tag	UNP D9U542
G	-12	GLU	-	expression tag	UNP D9U542
G	-11	ILE	-	expression tag	UNP D9U542
G	-10	CYS	-	expression tag	UNP D9U542
G	-9	SER	-	expression tag	UNP D9U542
G	-8	TRP	-	expression tag	UNP D9U542
G	-7	TYR	-	expression tag	UNP D9U542
G	-6	HIS	-	expression tag	UNP D9U542
G	-5	GLY	-	expression tag	UNP D9U542
G	-4	GLY	-	expression tag	UNP D9U542
G	-3	ARG	-	expression tag	UNP D9U542
G	-2	GLY	-	expression tag	UNP D9U542
G	-1	ASN	-	expression tag	UNP D9U542
G	0	SER	-	expression tag	UNP D9U542
G	1	ILE	-	expression tag	UNP D9U542
H	-50	MET	-	expression tag	UNP D9U542
H	-49	ARG	-	expression tag	UNP D9U542
H	-48	GLY	-	expression tag	UNP D9U542
H	-47	SER	-	expression tag	UNP D9U542
H	-46	HIS	-	expression tag	UNP D9U542
H	-45	HIS	-	expression tag	UNP D9U542
H	-44	HIS	-	expression tag	UNP D9U542
H	-43	HIS	-	expression tag	UNP D9U542
H	-42	HIS	-	expression tag	UNP D9U542
H	-41	HIS	-	expression tag	UNP D9U542
H	-40	GLY	-	expression tag	UNP D9U542
H	-39	MET	-	expression tag	UNP D9U542
H	-38	ALA	-	expression tag	UNP D9U542
H	-37	SER	-	expression tag	UNP D9U542
H	-36	MET	-	expression tag	UNP D9U542
H	-35	THR	-	expression tag	UNP D9U542
H	-34	GLY	-	expression tag	UNP D9U542
H	-33	GLY	-	expression tag	UNP D9U542
H	-32	GLN	-	expression tag	UNP D9U542
H	-31	GLN	-	expression tag	UNP D9U542
H	-30	MET	-	expression tag	UNP D9U542
H	-29	GLY	-	expression tag	UNP D9U542
H	-28	ARG	-	expression tag	UNP D9U542
H	-27	ASP	-	expression tag	UNP D9U542

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-26	LEU	-	expression tag	UNP D9U542
H	-25	TYR	-	expression tag	UNP D9U542
H	-24	ASP	-	expression tag	UNP D9U542
H	-23	ASP	-	expression tag	UNP D9U542
H	-22	ASP	-	expression tag	UNP D9U542
H	-21	ASP	-	expression tag	UNP D9U542
H	-20	LYS	-	expression tag	UNP D9U542
H	-19	ASP	-	expression tag	UNP D9U542
H	-18	ARG	-	expression tag	UNP D9U542
H	-17	TRP	-	expression tag	UNP D9U542
H	-16	GLY	-	expression tag	UNP D9U542
H	-15	SER	-	expression tag	UNP D9U542
H	-14	GLU	-	expression tag	UNP D9U542
H	-13	LEU	-	expression tag	UNP D9U542
H	-12	GLU	-	expression tag	UNP D9U542
H	-11	ILE	-	expression tag	UNP D9U542
H	-10	CYS	-	expression tag	UNP D9U542
H	-9	SER	-	expression tag	UNP D9U542
H	-8	TRP	-	expression tag	UNP D9U542
H	-7	TYR	-	expression tag	UNP D9U542
H	-6	HIS	-	expression tag	UNP D9U542
H	-5	GLY	-	expression tag	UNP D9U542
H	-4	GLY	-	expression tag	UNP D9U542
H	-3	ARG	-	expression tag	UNP D9U542
H	-2	GLY	-	expression tag	UNP D9U542
H	-1	ASN	-	expression tag	UNP D9U542
H	0	SER	-	expression tag	UNP D9U542
H	1	ILE	-	expression tag	UNP D9U542
I	-50	MET	-	expression tag	UNP D9U542
I	-49	ARG	-	expression tag	UNP D9U542
I	-48	GLY	-	expression tag	UNP D9U542
I	-47	SER	-	expression tag	UNP D9U542
I	-46	HIS	-	expression tag	UNP D9U542
I	-45	HIS	-	expression tag	UNP D9U542
I	-44	HIS	-	expression tag	UNP D9U542
I	-43	HIS	-	expression tag	UNP D9U542
I	-42	HIS	-	expression tag	UNP D9U542
I	-41	HIS	-	expression tag	UNP D9U542
I	-40	GLY	-	expression tag	UNP D9U542
I	-39	MET	-	expression tag	UNP D9U542
I	-38	ALA	-	expression tag	UNP D9U542
I	-37	SER	-	expression tag	UNP D9U542

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-36	MET	-	expression tag	UNP D9U542
I	-35	THR	-	expression tag	UNP D9U542
I	-34	GLY	-	expression tag	UNP D9U542
I	-33	GLY	-	expression tag	UNP D9U542
I	-32	GLN	-	expression tag	UNP D9U542
I	-31	GLN	-	expression tag	UNP D9U542
I	-30	MET	-	expression tag	UNP D9U542
I	-29	GLY	-	expression tag	UNP D9U542
I	-28	ARG	-	expression tag	UNP D9U542
I	-27	ASP	-	expression tag	UNP D9U542
I	-26	LEU	-	expression tag	UNP D9U542
I	-25	TYR	-	expression tag	UNP D9U542
I	-24	ASP	-	expression tag	UNP D9U542
I	-23	ASP	-	expression tag	UNP D9U542
I	-22	ASP	-	expression tag	UNP D9U542
I	-21	ASP	-	expression tag	UNP D9U542
I	-20	LYS	-	expression tag	UNP D9U542
I	-19	ASP	-	expression tag	UNP D9U542
I	-18	ARG	-	expression tag	UNP D9U542
I	-17	TRP	-	expression tag	UNP D9U542
I	-16	GLY	-	expression tag	UNP D9U542
I	-15	SER	-	expression tag	UNP D9U542
I	-14	GLU	-	expression tag	UNP D9U542
I	-13	LEU	-	expression tag	UNP D9U542
I	-12	GLU	-	expression tag	UNP D9U542
I	-11	ILE	-	expression tag	UNP D9U542
I	-10	CYS	-	expression tag	UNP D9U542
I	-9	SER	-	expression tag	UNP D9U542
I	-8	TRP	-	expression tag	UNP D9U542
I	-7	TYR	-	expression tag	UNP D9U542
I	-6	HIS	-	expression tag	UNP D9U542
I	-5	GLY	-	expression tag	UNP D9U542
I	-4	GLY	-	expression tag	UNP D9U542
I	-3	ARG	-	expression tag	UNP D9U542
I	-2	GLY	-	expression tag	UNP D9U542
I	-1	ASN	-	expression tag	UNP D9U542
I	0	SER	-	expression tag	UNP D9U542
I	1	ILE	-	expression tag	UNP D9U542
J	-50	MET	-	expression tag	UNP D9U542
J	-49	ARG	-	expression tag	UNP D9U542
J	-48	GLY	-	expression tag	UNP D9U542
J	-47	SER	-	expression tag	UNP D9U542

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-46	HIS	-	expression tag	UNP D9U542
J	-45	HIS	-	expression tag	UNP D9U542
J	-44	HIS	-	expression tag	UNP D9U542
J	-43	HIS	-	expression tag	UNP D9U542
J	-42	HIS	-	expression tag	UNP D9U542
J	-41	HIS	-	expression tag	UNP D9U542
J	-40	GLY	-	expression tag	UNP D9U542
J	-39	MET	-	expression tag	UNP D9U542
J	-38	ALA	-	expression tag	UNP D9U542
J	-37	SER	-	expression tag	UNP D9U542
J	-36	MET	-	expression tag	UNP D9U542
J	-35	THR	-	expression tag	UNP D9U542
J	-34	GLY	-	expression tag	UNP D9U542
J	-33	GLY	-	expression tag	UNP D9U542
J	-32	GLN	-	expression tag	UNP D9U542
J	-31	GLN	-	expression tag	UNP D9U542
J	-30	MET	-	expression tag	UNP D9U542
J	-29	GLY	-	expression tag	UNP D9U542
J	-28	ARG	-	expression tag	UNP D9U542
J	-27	ASP	-	expression tag	UNP D9U542
J	-26	LEU	-	expression tag	UNP D9U542
J	-25	TYR	-	expression tag	UNP D9U542
J	-24	ASP	-	expression tag	UNP D9U542
J	-23	ASP	-	expression tag	UNP D9U542
J	-22	ASP	-	expression tag	UNP D9U542
J	-21	ASP	-	expression tag	UNP D9U542
J	-20	LYS	-	expression tag	UNP D9U542
J	-19	ASP	-	expression tag	UNP D9U542
J	-18	ARG	-	expression tag	UNP D9U542
J	-17	TRP	-	expression tag	UNP D9U542
J	-16	GLY	-	expression tag	UNP D9U542
J	-15	SER	-	expression tag	UNP D9U542
J	-14	GLU	-	expression tag	UNP D9U542
J	-13	LEU	-	expression tag	UNP D9U542
J	-12	GLU	-	expression tag	UNP D9U542
J	-11	ILE	-	expression tag	UNP D9U542
J	-10	CYS	-	expression tag	UNP D9U542
J	-9	SER	-	expression tag	UNP D9U542
J	-8	TRP	-	expression tag	UNP D9U542
J	-7	TYR	-	expression tag	UNP D9U542
J	-6	HIS	-	expression tag	UNP D9U542
J	-5	GLY	-	expression tag	UNP D9U542

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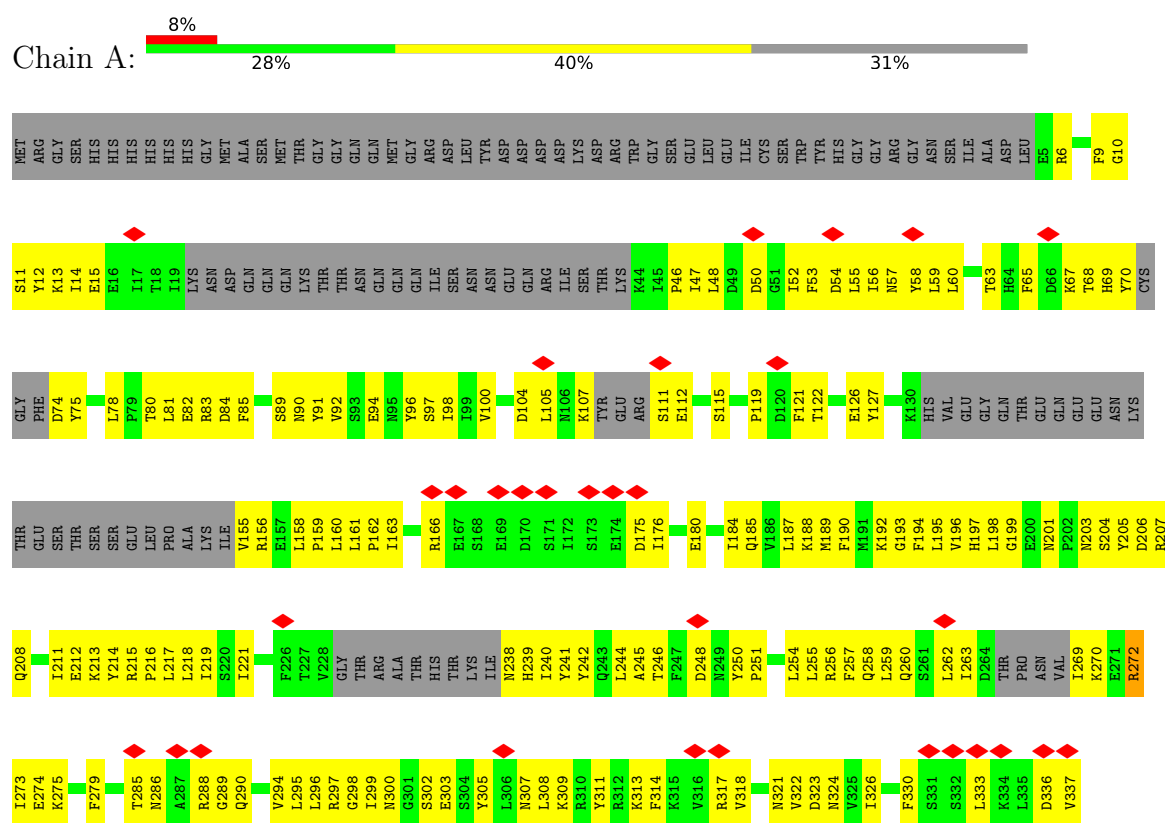
*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
J	-4	GLY	-	expression tag	UNP D9U542
J	-3	ARG	-	expression tag	UNP D9U542
J	-2	GLY	-	expression tag	UNP D9U542
J	-1	ASN	-	expression tag	UNP D9U542
J	0	SER	-	expression tag	UNP D9U542
J	1	ILE	-	expression tag	UNP D9U542

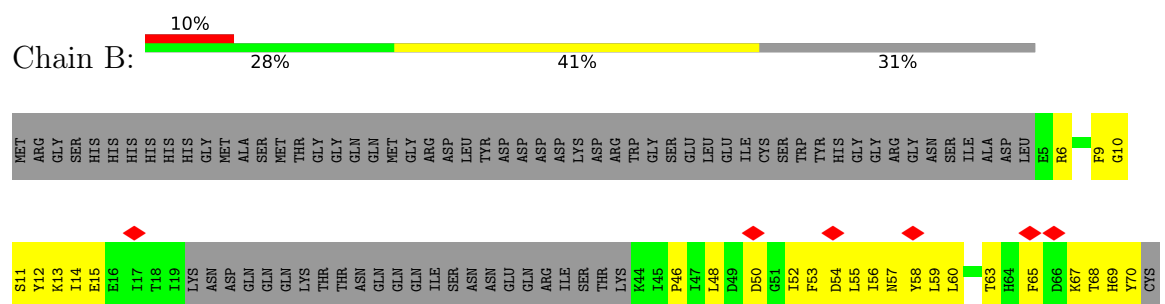
### 3 Residue-property plots

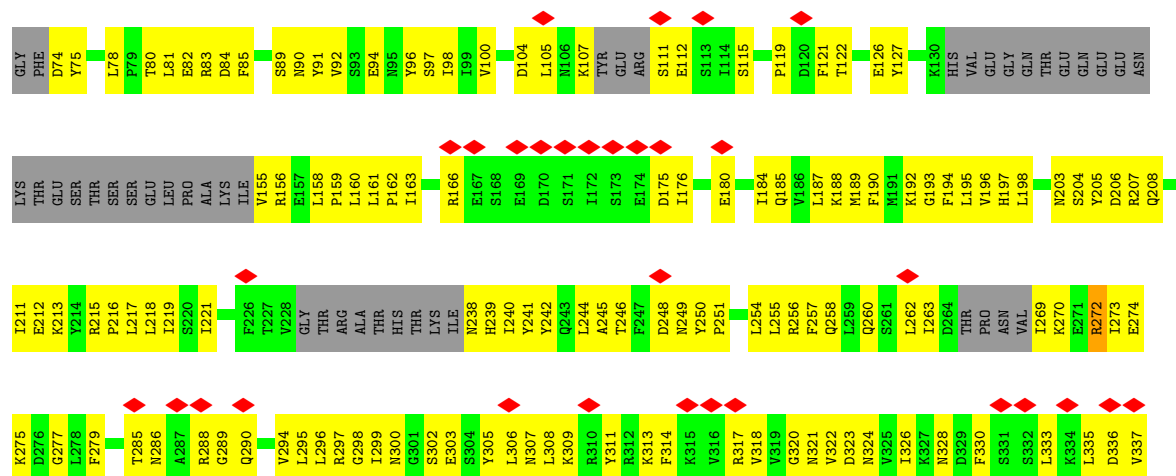
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: p9-1

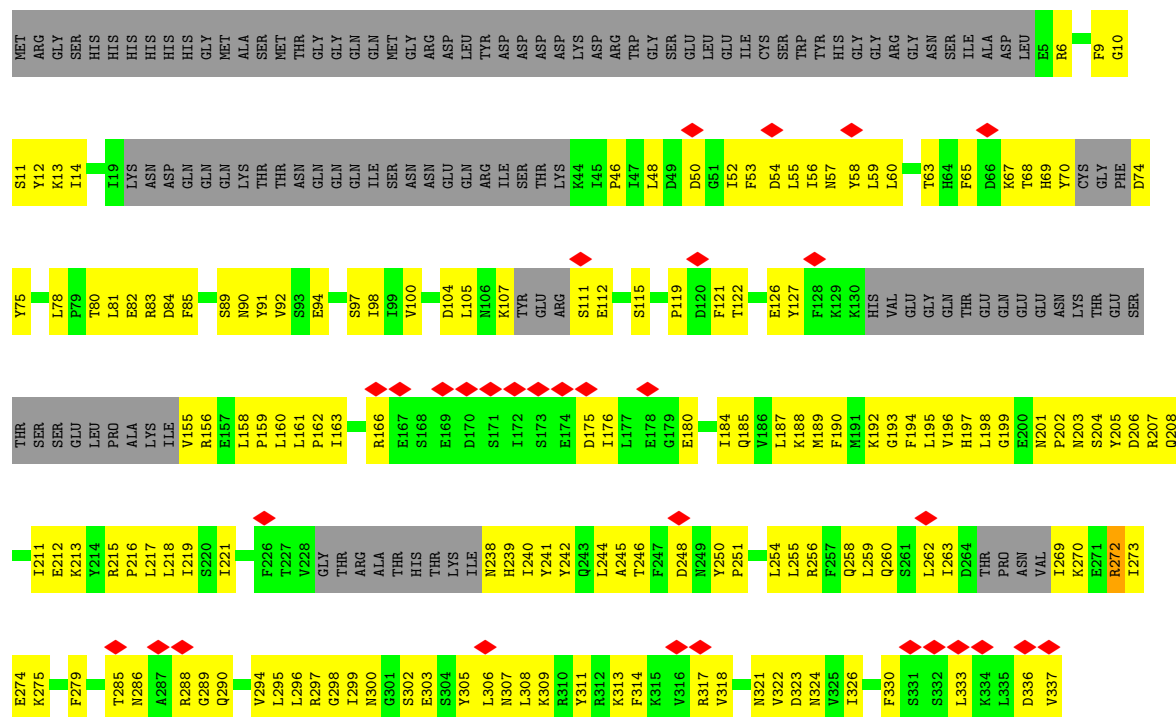


#### • Molecule 1: p9-1

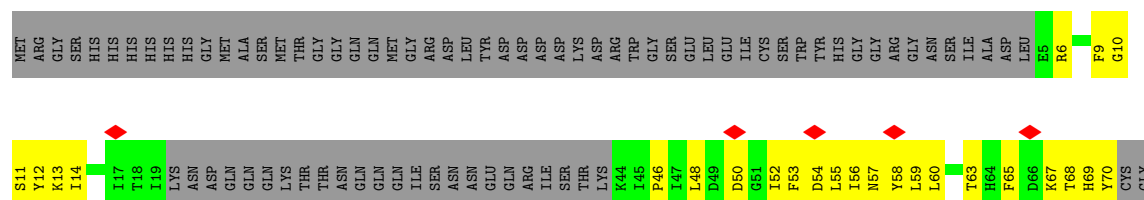


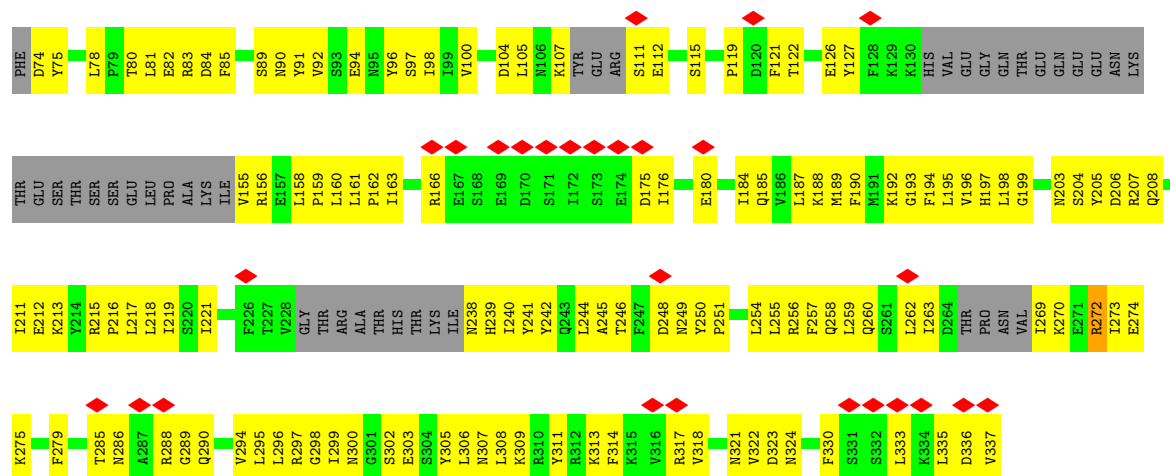


• Molecule 1: p9-1

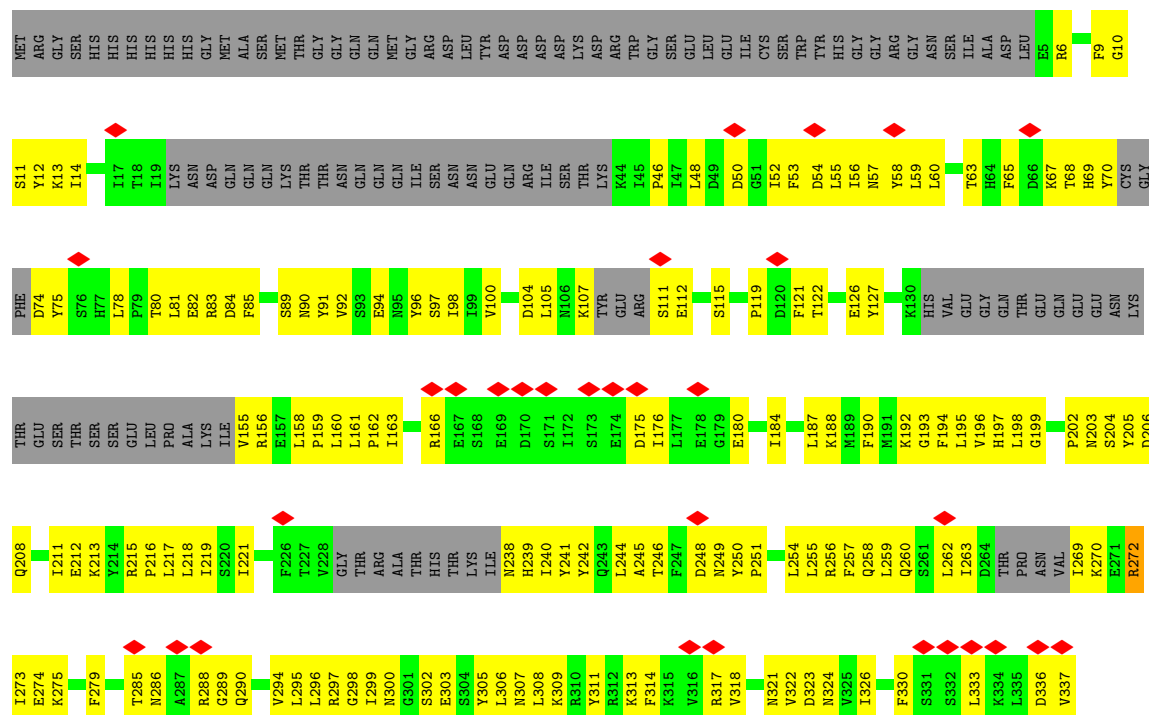


• Molecule 1: p9-1

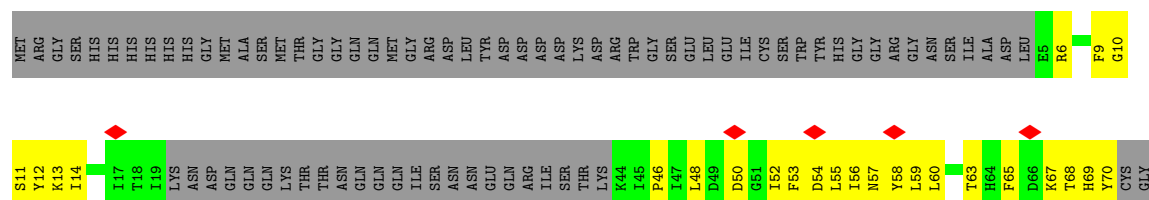


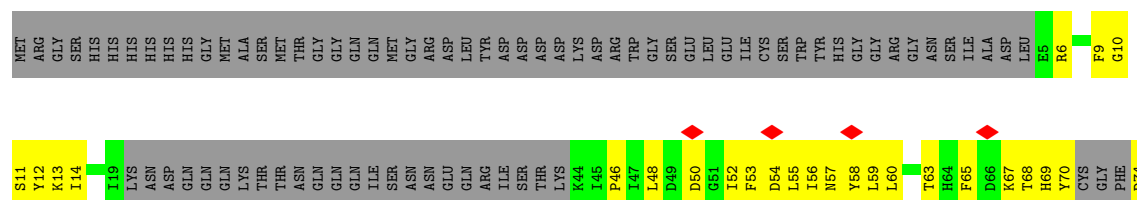


• Molecule 1: p9-1



• Molecule 1: p9-1







PHE	D74	Y75	L78	F79	T80	L81	E82	R83	D84	F85	S89	N90	Y91	V92	S93	E94	N95	Y96	S97	I98	I99	V100	D104	L105	N106	K107	TYR	GLU	ARG	S111	E112	S115	P119	D120	F121	T122	E126	Y127	F128	K129	K130	HIS	VAL	GLU	GLY	GLN	THR	GLU	GLU	ASN	LYS						
THR	GLU	SER	THR	SER	GLU	LEU	PRO	ALA	ALA	LYS	I155	R156	E157	L158	P159	L160	L161	P162	I163	R166	E167	S168	E169	D170	S171	I172	S173	E174	D175	I176	E180	I184	K185	V186	L187	K188	M189	F190	M191	K192	G193	F194	L195	V196	H197	L198	G199	E200	N201	P202	N203	S204	Y205	D206	R207		
Q208	I211	E212	K213	Y214	R215	P216	L217	L218	I219	S220	I221	F226	T227	V228	GLY	THR	ARG	ALA	ALA	THR	HIS	THR	LYS	ILE	N238	H239	I240	Y241	Y242	Q243	L244	A245	T246	F247	D248	N249	Y250	P251	L254	L255	R256	F257	Q258	L259	Q260	S261	L262	I263	D264	THR	PRO	ASN	VAL	I269	K270	E271	R272
I273	E274	K275	F279	T285	N286	A287	R288	G289	Q290	V294	L295	L296	R297	G298	I299	N300	G301	S302	E303	S304	Y305	L306	N307	L308	K309	R310	Y311	R312	K313	F314	K315	V316	R317	V318	V319	G320	N321	V322	D323	N324	V325	I326	K327	N328	D329	F330	S331	S332	L333	K334	L335	D336	V337				

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D5	Depositor
Number of particles used	99682	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)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30.0	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3800	Depositor
Magnification	120000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.143	Depositor
Minimum map value	-0.068	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	204.0, 204.0, 204.0	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.34	0/2229	0.52	0/3000
1	B	0.33	0/2229	0.52	0/3000
1	C	0.34	0/2229	0.52	0/3000
1	D	0.34	0/2229	0.52	0/3000
1	E	0.33	0/2229	0.52	0/3000
1	F	0.34	0/2229	0.52	0/3000
1	G	0.34	0/2229	0.52	0/3000
1	H	0.33	0/2229	0.52	0/3000
1	I	0.34	0/2229	0.53	0/3000
1	J	0.34	0/2229	0.52	0/3000
All	All	0.34	0/22290	0.52	0/30000

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 [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	2192	0	2191	152	0
1	B	2192	0	2191	160	0
1	C	2192	0	2191	154	0
1	D	2192	0	2191	157	0
1	E	2192	0	2191	151	0
1	F	2192	0	2191	155	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	2192	0	2191	164	0
1	H	2192	0	2191	147	0
1	I	2192	0	2191	157	0
1	J	2192	0	2191	150	0
All	All	21920	0	21910	1449	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 33.

The worst 5 of 1449 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:G:269:ILE:HG21	1:I:326:ILE:HD11	1.45	0.96
1:H:259:LEU:HD13	1:I:333:LEU:HD22	1.48	0.93
1:B:335:LEU:HD21	1:C:241:TYR:OH	1.80	0.81
1:B:269:ILE:HG21	1:J:326:ILE:HD11	1.62	0.79
1:B:330:PHE:CD2	1:C:196:VAL:HA	2.20	0.76

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	A	252/388 (65%)	225 (89%)	27 (11%)	0	100	100
1	B	252/388 (65%)	225 (89%)	27 (11%)	0	100	100
1	C	252/388 (65%)	225 (89%)	27 (11%)	0	100	100
1	D	252/388 (65%)	225 (89%)	27 (11%)	0	100	100
1	E	252/388 (65%)	225 (89%)	27 (11%)	0	100	100
1	F	252/388 (65%)	225 (89%)	27 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	252/388 (65%)	225 (89%)	27 (11%)	0	100	100
1	H	252/388 (65%)	225 (89%)	27 (11%)	0	100	100
1	I	252/388 (65%)	225 (89%)	27 (11%)	0	100	100
1	J	252/388 (65%)	225 (89%)	27 (11%)	0	100	100
All	All	2520/3880 (65%)	2250 (89%)	270 (11%)	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	A	249/355 (70%)	247 (99%)	2 (1%)	81	89
1	B	249/355 (70%)	247 (99%)	2 (1%)	81	89
1	C	249/355 (70%)	247 (99%)	2 (1%)	81	89
1	D	249/355 (70%)	247 (99%)	2 (1%)	81	89
1	E	249/355 (70%)	247 (99%)	2 (1%)	81	89
1	F	249/355 (70%)	247 (99%)	2 (1%)	81	89
1	G	249/355 (70%)	247 (99%)	2 (1%)	81	89
1	H	249/355 (70%)	247 (99%)	2 (1%)	81	89
1	I	249/355 (70%)	247 (99%)	2 (1%)	81	89
1	J	249/355 (70%)	247 (99%)	2 (1%)	81	89
All	All	2490/3550 (70%)	2470 (99%)	20 (1%)	82	89

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	272	ARG
1	I	275	LYS
1	J	275	LYS
1	J	272	ARG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	D	272	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	258	GLN
1	I	258	GLN
1	J	258	GLN
1	D	258	GLN
1	E	258	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.

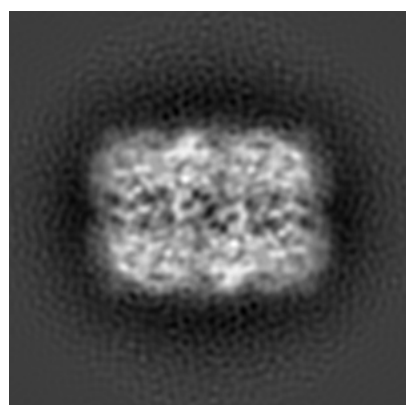
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23046. These allow visual inspection of the internal detail of the map and identification of artifacts.

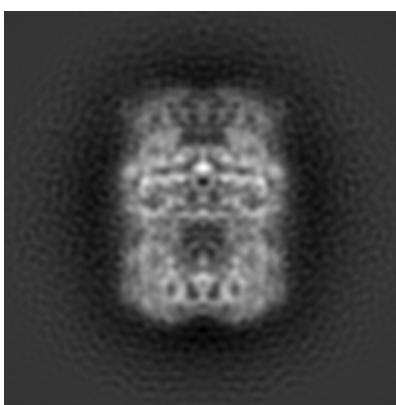
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

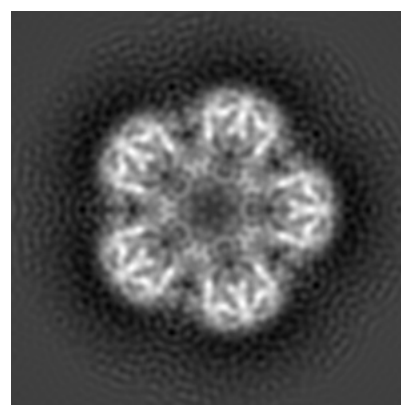
#### 6.1.1 Primary map



X



Y

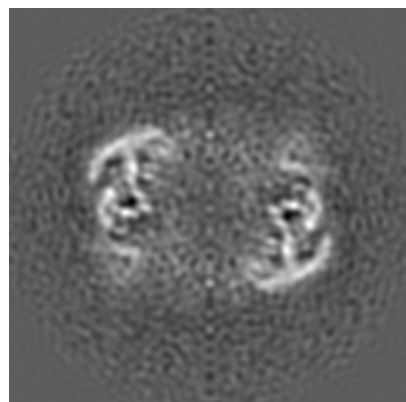


Z

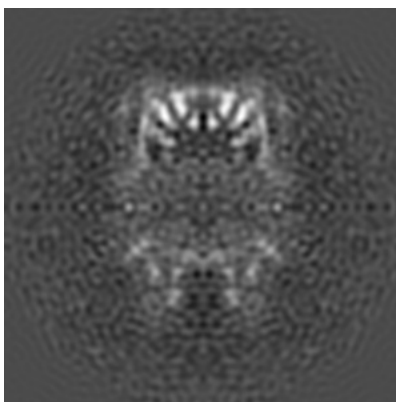
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

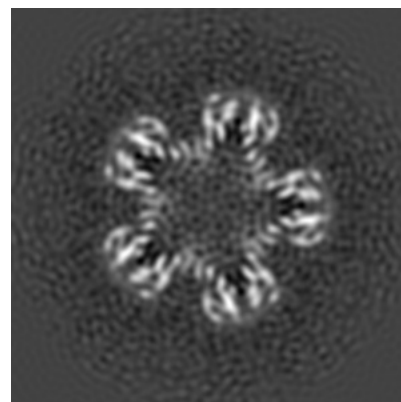
#### 6.2.1 Primary map



X Index: 120



Y Index: 120

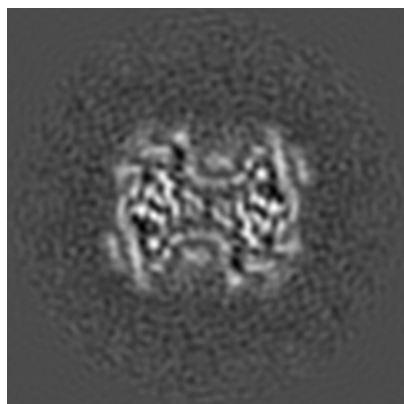


Z Index: 120

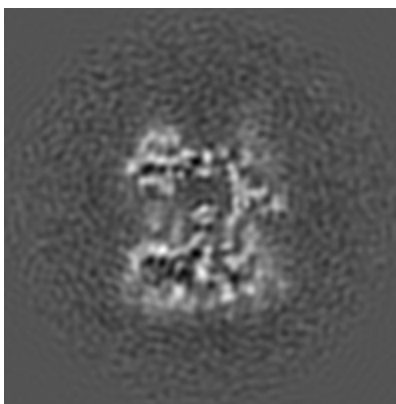
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

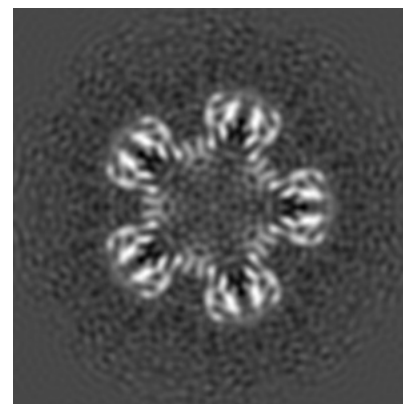
### 6.3.1 Primary map



X Index: 79



Y Index: 82

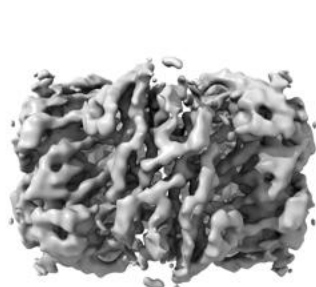


Z Index: 119

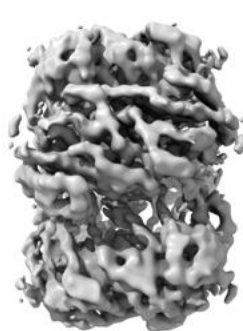
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

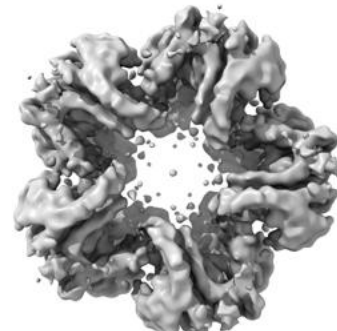
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

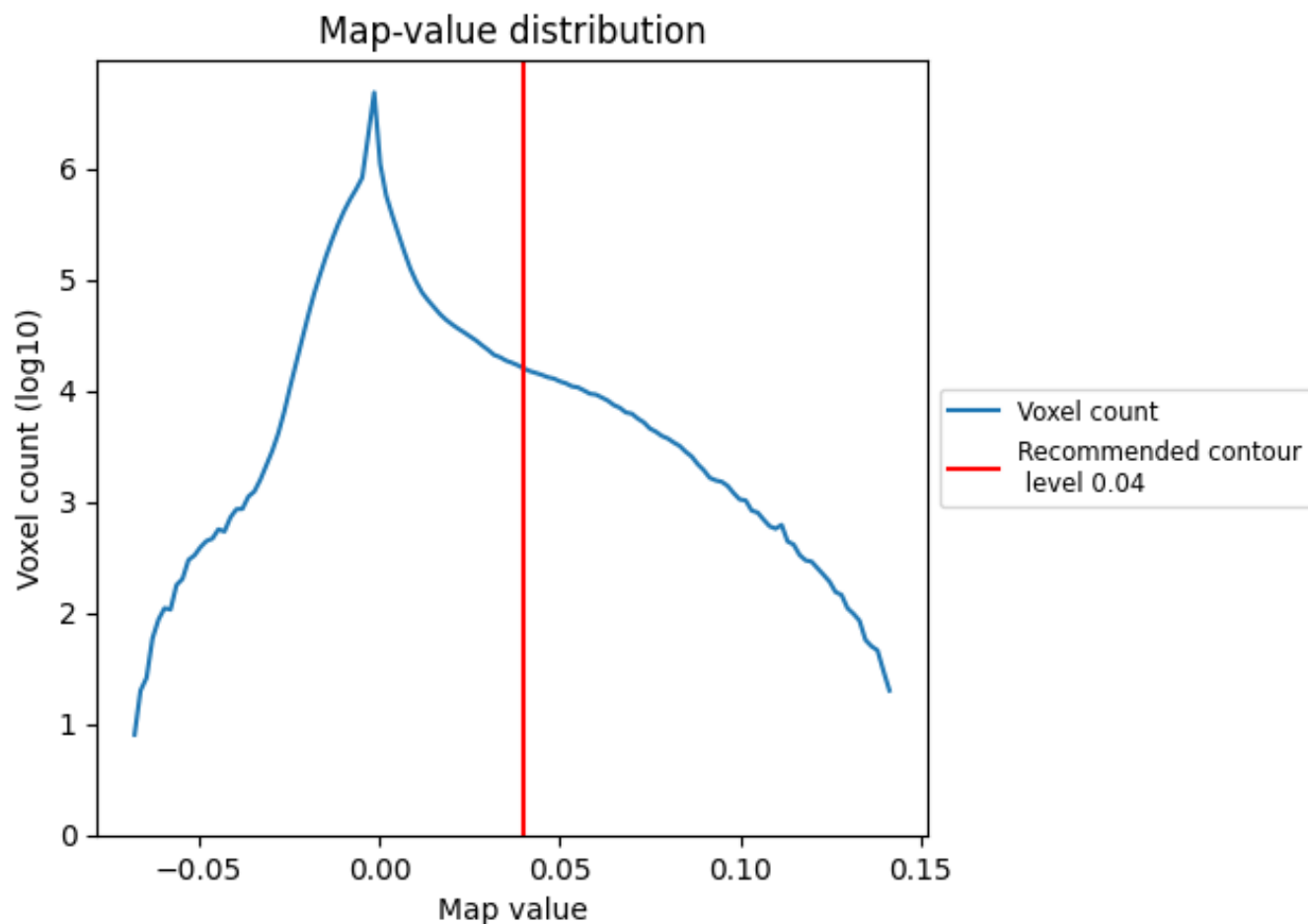
## 6.5 Mask visualisation

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.

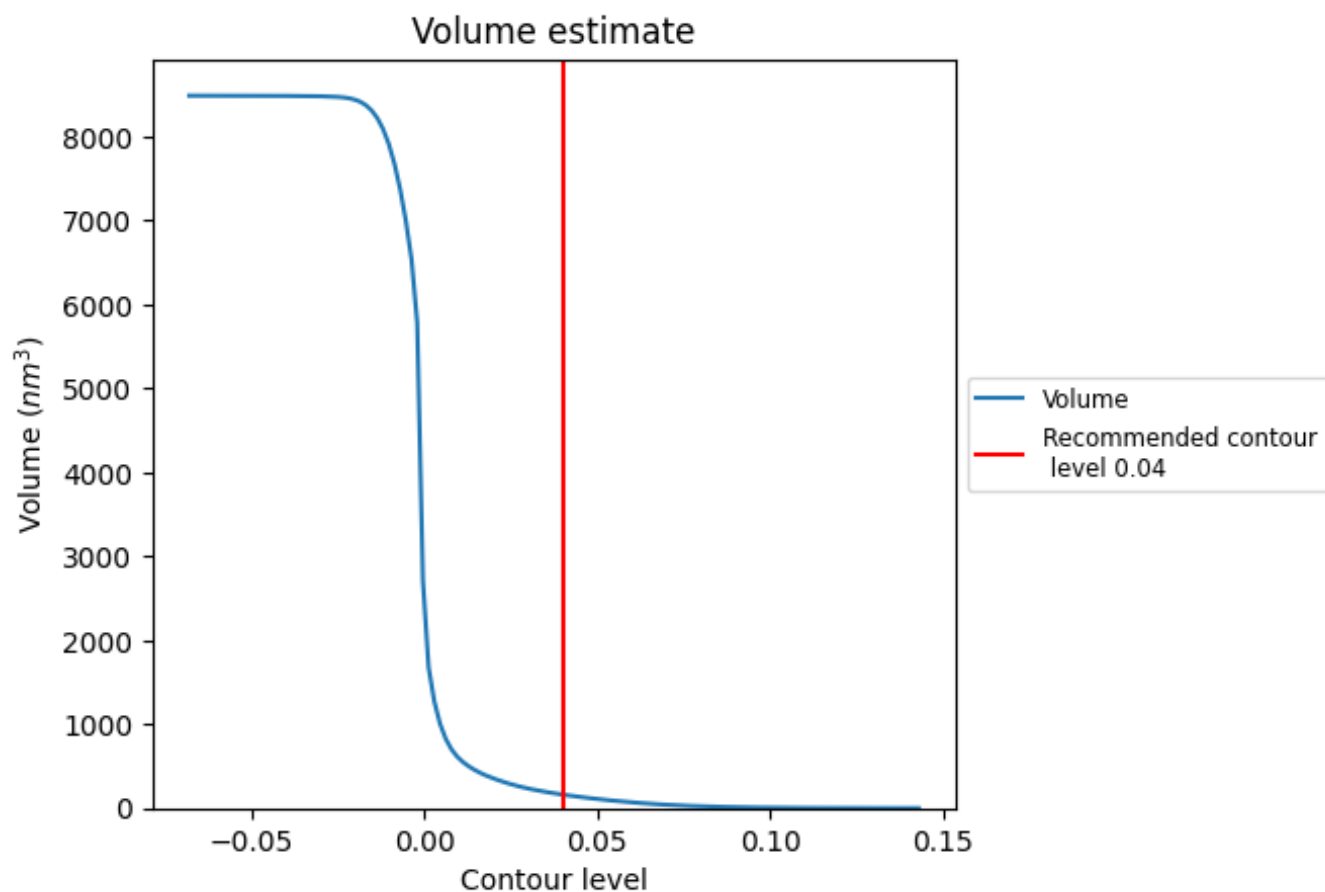
### 7.1 Map-value distribution [i](#)



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.



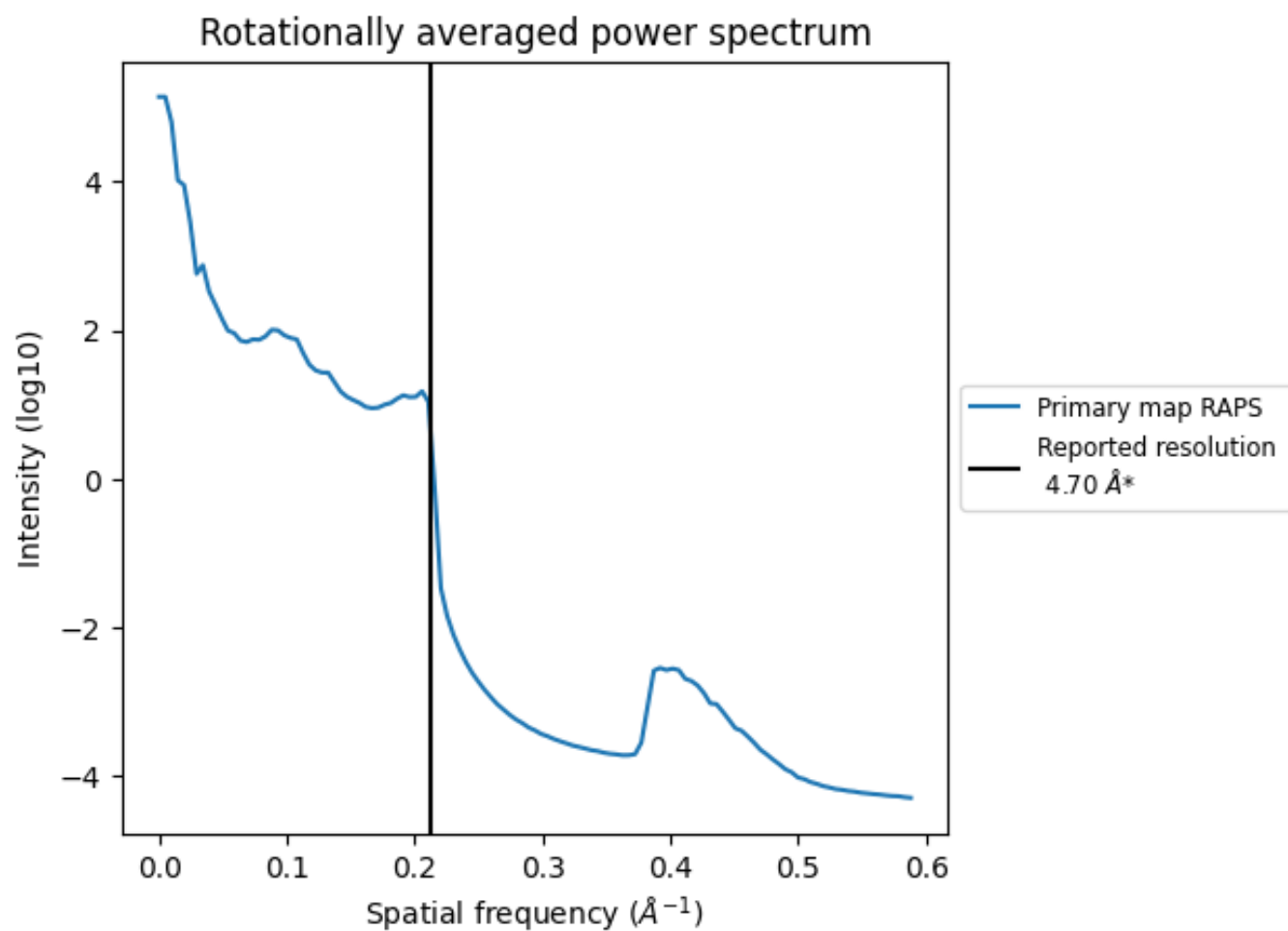
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 162 nm<sup>3</sup>; this corresponds to an approximate mass of 146 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 0.213 Å<sup>-1</sup>

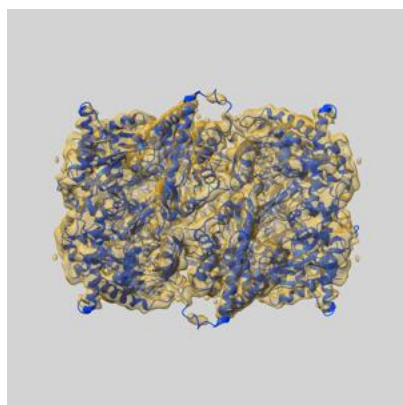
## 8 Fourier-Shell correlation

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

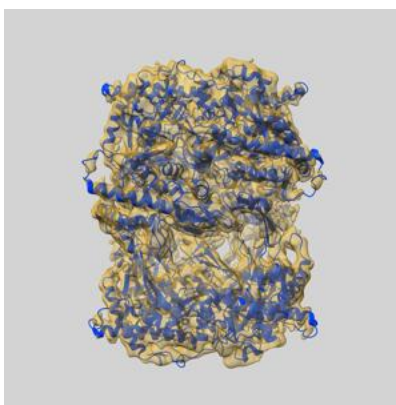
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23046 and PDB model 7KVC. Per-residue inclusion information can be found in section [3](#) on page [18](#).

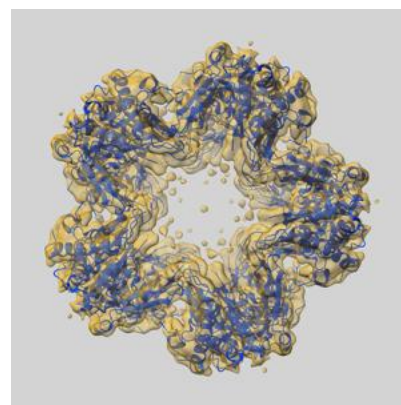
### 9.1 Map-model overlay [i](#)



X



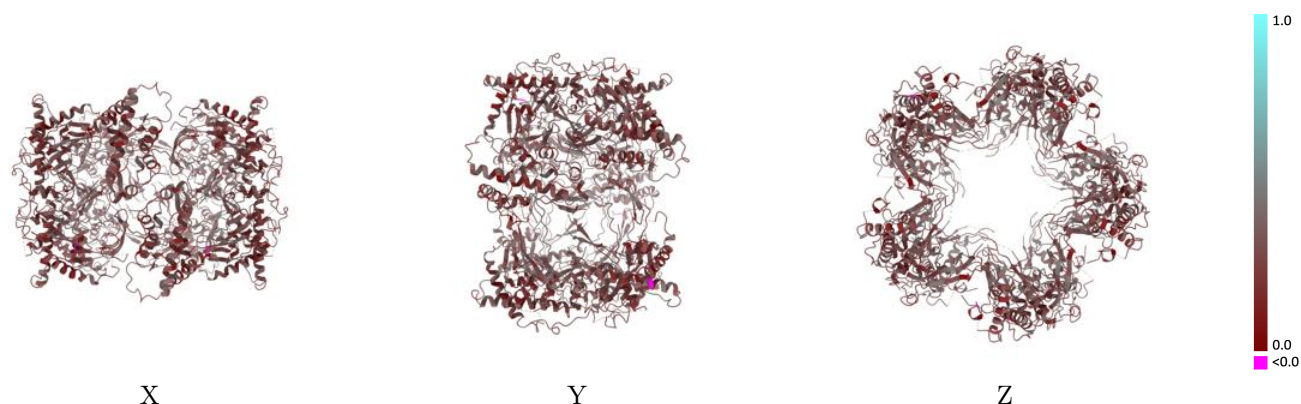
Y



Z

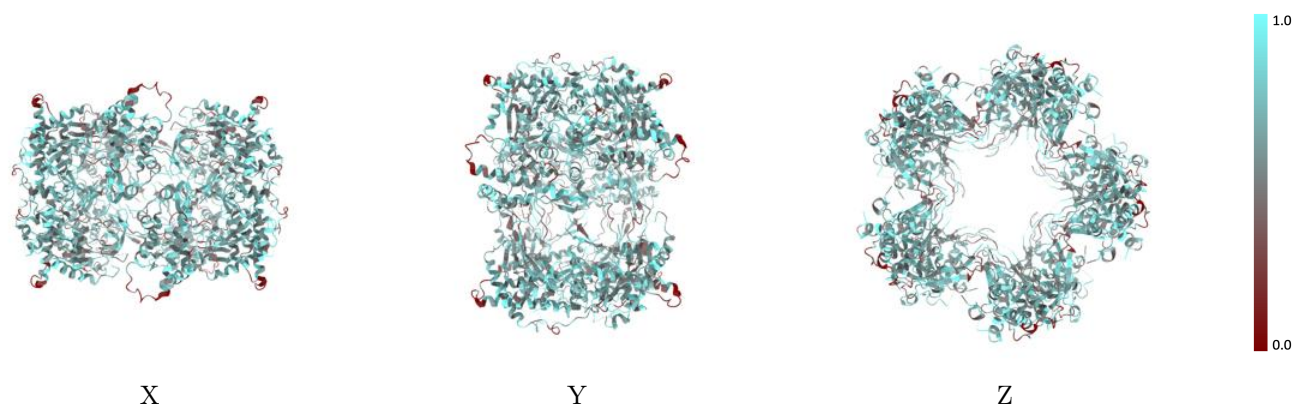
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



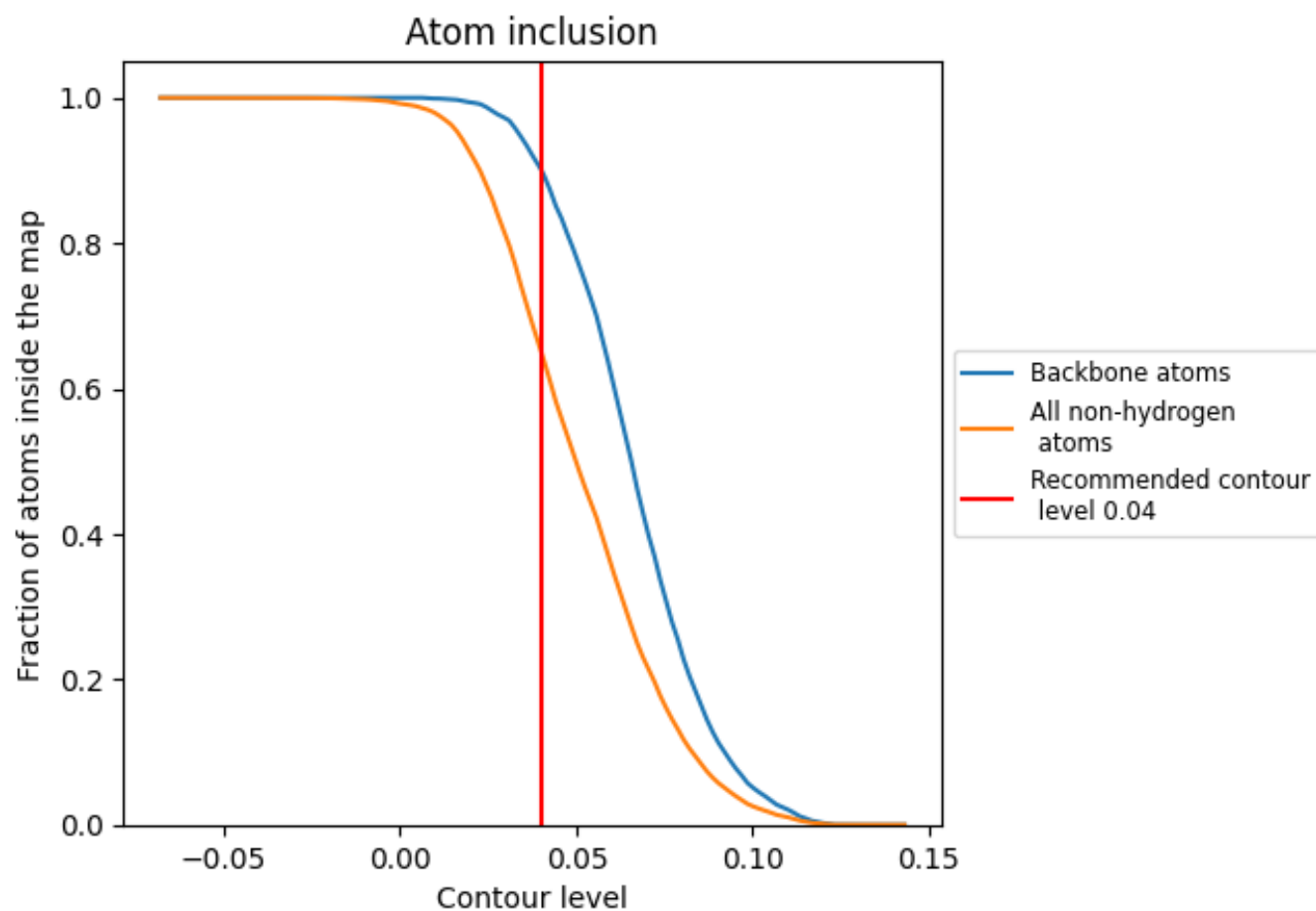
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 65% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6514	<div></div> 0.3050
A	<div></div> 0.6494	<div></div> 0.3070
B	<div></div> 0.6508	<div></div> 0.3040
C	<div></div> 0.6518	<div></div> 0.3060
D	<div></div> 0.6513	<div></div> 0.3060
E	<div></div> 0.6541	<div></div> 0.3050
F	<div></div> 0.6527	<div></div> 0.3060
G	<div></div> 0.6536	<div></div> 0.3070
H	<div></div> 0.6504	<div></div> 0.3050
I	<div></div> 0.6453	<div></div> 0.3000
J	<div></div> 0.6546	<div></div> 0.3060

1.0

0.0

<0.0