



wwPDB EM Validation Summary Report ⓘ

May 17, 2026 – 02:38 PM JST

PDB ID : 9VUM / pdb_00009vum
EMDB ID : EMD-65368
Title : Cryo-EM structure of the Nipah virus RNA-dependent RNA polymerase complex bound to allosteric inhibitor ERDRP-0519
Authors : Du, T.; Wang, J.; Wu, S.; Ru, H.
Deposited on : 2025-07-13
Resolution : 2.84 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

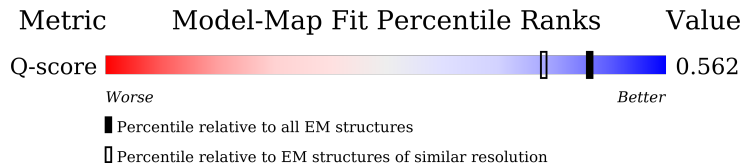
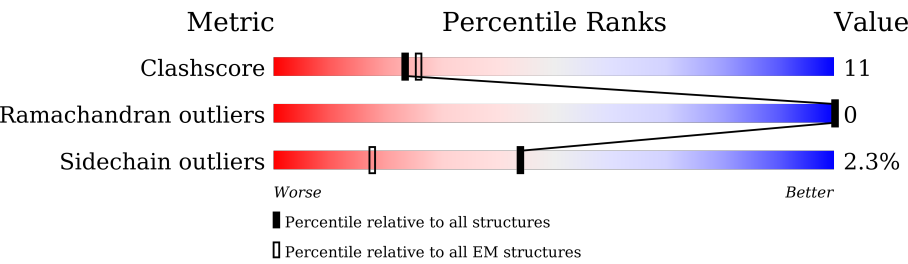
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.84 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	11884 (2.34 - 3.34)

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	L	1904	<div><div>50%17%33%</div><div>6%</div><div>15%7%</div><div>78%</div></div>
2	A	638	<div><div>5%</div><div>92%</div></div>
2	B	638	<div><div>8%</div><div>89%</div></div>

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Mol	Chain	Length	Quality of chain
2	D	638	<div><div></div><div>6%</div><div>92%</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12867 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 Maltose/maltodextrin-binding periplasmic protein,RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L	1281	Total	C	N	O	S	0	0
			10317	6572	1764	1915	66		

There are 75 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-428	MET	-	initiating methionine	UNP P0AEX9
L	-427	GLY	-	expression tag	UNP P0AEX9
L	-426	SER	-	expression tag	UNP P0AEX9
L	-425	GLY	-	expression tag	UNP P0AEX9
L	-424	TRP	-	expression tag	UNP P0AEX9
L	-423	SER	-	expression tag	UNP P0AEX9
L	-422	HIS	-	expression tag	UNP P0AEX9
L	-421	PRO	-	expression tag	UNP P0AEX9
L	-420	GLN	-	expression tag	UNP P0AEX9
L	-419	PHE	-	expression tag	UNP P0AEX9
L	-418	GLU	-	expression tag	UNP P0AEX9
L	-417	LYS	-	expression tag	UNP P0AEX9
L	-416	GLY	-	expression tag	UNP P0AEX9
L	-415	GLY	-	expression tag	UNP P0AEX9
L	-414	GLY	-	expression tag	UNP P0AEX9
L	-413	SER	-	expression tag	UNP P0AEX9
L	-412	GLY	-	expression tag	UNP P0AEX9
L	-411	GLY	-	expression tag	UNP P0AEX9
L	-410	GLY	-	expression tag	UNP P0AEX9
L	-409	SER	-	expression tag	UNP P0AEX9
L	-408	GLY	-	expression tag	UNP P0AEX9
L	-407	GLY	-	expression tag	UNP P0AEX9
L	-406	SER	-	expression tag	UNP P0AEX9
L	-405	ALA	-	expression tag	UNP P0AEX9
L	-404	TRP	-	expression tag	UNP P0AEX9
L	-403	SER	-	expression tag	UNP P0AEX9
L	-402	HIS	-	expression tag	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-401	PRO	-	expression tag	UNP P0AEX9
L	-400	GLN	-	expression tag	UNP P0AEX9
L	-399	PHE	-	expression tag	UNP P0AEX9
L	-398	GLU	-	expression tag	UNP P0AEX9
L	-397	LYS	-	expression tag	UNP P0AEX9
L	-396	GLY	-	expression tag	UNP P0AEX9
L	-395	SER	-	expression tag	UNP P0AEX9
L	-394	ALA	-	expression tag	UNP P0AEX9
L	-393	SER	-	expression tag	UNP P0AEX9
L	-392	HIS	-	expression tag	UNP P0AEX9
L	-391	HIS	-	expression tag	UNP P0AEX9
L	-390	HIS	-	expression tag	UNP P0AEX9
L	-389	HIS	-	expression tag	UNP P0AEX9
L	-388	HIS	-	expression tag	UNP P0AEX9
L	-387	HIS	-	expression tag	UNP P0AEX9
L	-386	GLY	-	expression tag	UNP P0AEX9
L	-385	THR	-	expression tag	UNP P0AEX9
L	-384	LYS	-	expression tag	UNP P0AEX9
L	-383	THR	-	expression tag	UNP P0AEX9
L	-18	GLY	-	linker	UNP P0AEX9
L	-17	THR	-	linker	UNP P0AEX9
L	-16	ASP	-	linker	UNP P0AEX9
L	-15	TYR	-	linker	UNP P0AEX9
L	-14	ASP	-	linker	UNP P0AEX9
L	-13	ILE	-	linker	UNP P0AEX9
L	-12	PRO	-	linker	UNP P0AEX9
L	-11	THR	-	linker	UNP P0AEX9
L	-10	THR	-	linker	UNP P0AEX9
L	-9	LEU	-	linker	UNP P0AEX9
L	-8	GLU	-	linker	UNP P0AEX9
L	-7	VAL	-	linker	UNP P0AEX9
L	-6	LEU	-	linker	UNP P0AEX9
L	-5	PHE	-	linker	UNP P0AEX9
L	-4	GLN	-	linker	UNP P0AEX9
L	-3	GLY	-	linker	UNP P0AEX9
L	-2	PRO	-	linker	UNP P0AEX9
L	-1	GLY	-	linker	UNP P0AEX9
L	0	SER	-	linker	UNP P0AEX9
L	1466	SER	-	expression tag	UNP Q997F0
L	1467	ARG	-	expression tag	UNP Q997F0
L	1468	ASP	-	expression tag	UNP Q997F0
L	1469	TYR	-	expression tag	UNP Q997F0

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Chain	Residue	Modelled	Actual	Comment	Reference
L	1470	LYS	-	expression tag	UNP Q997F0
L	1471	ASP	-	expression tag	UNP Q997F0
L	1472	ASP	-	expression tag	UNP Q997F0
L	1473	ASP	-	expression tag	UNP Q997F0
L	1474	ASP	-	expression tag	UNP Q997F0
L	1475	LYS	-	expression tag	UNP Q997F0

- Molecule 2 is a protein called Maltose/maltodextrin-binding periplasmic protein, Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	143	Total	C	N	O	S	0	0
			1138	712	193	229	4		
2	B	50	Total	C	N	O	S	0	0
			396	250	68	74	4		
2	C	71	Total	C	N	O	S	0	0
			556	350	100	102	4		
2	D	54	Total	C	N	O	S	0	0
			421	266	73	78	4		

There are 136 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	MET	-	initiating methionine	UNP P0AEX9
A	73	GLY	-	expression tag	UNP P0AEX9
A	74	SER	-	expression tag	UNP P0AEX9
A	75	SER	-	expression tag	UNP P0AEX9
A	76	HIS	-	expression tag	UNP P0AEX9
A	77	HIS	-	expression tag	UNP P0AEX9
A	78	HIS	-	expression tag	UNP P0AEX9
A	79	HIS	-	expression tag	UNP P0AEX9
A	80	HIS	-	expression tag	UNP P0AEX9
A	81	HIS	-	expression tag	UNP P0AEX9
A	82	GLY	-	expression tag	UNP P0AEX9
A	83	THR	-	expression tag	UNP P0AEX9
A	84	LYS	-	expression tag	UNP P0AEX9
A	85	THR	-	expression tag	UNP P0AEX9
A	450	GLY	-	linker	UNP P0AEX9
A	451	THR	-	linker	UNP P0AEX9
A	452	ASP	-	linker	UNP P0AEX9
A	453	TYR	-	linker	UNP P0AEX9
A	454	ASP	-	linker	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	455	ILE	-	linker	UNP P0AEX9
A	456	PRO	-	linker	UNP P0AEX9
A	457	THR	-	linker	UNP P0AEX9
A	458	THR	-	linker	UNP P0AEX9
A	459	LEU	-	linker	UNP P0AEX9
A	460	GLU	-	linker	UNP P0AEX9
A	461	VAL	-	linker	UNP P0AEX9
A	462	LEU	-	linker	UNP P0AEX9
A	463	PHE	-	linker	UNP P0AEX9
A	464	GLN	-	linker	UNP P0AEX9
A	465	GLY	-	linker	UNP P0AEX9
A	466	PRO	-	linker	UNP P0AEX9
A	467	LEU	-	linker	UNP P0AEX9
A	468	GLY	-	linker	UNP P0AEX9
A	469	SER	-	linker	UNP P0AEX9
B	72	MET	-	initiating methionine	UNP P0AEX9
B	73	GLY	-	expression tag	UNP P0AEX9
B	74	SER	-	expression tag	UNP P0AEX9
B	75	SER	-	expression tag	UNP P0AEX9
B	76	HIS	-	expression tag	UNP P0AEX9
B	77	HIS	-	expression tag	UNP P0AEX9
B	78	HIS	-	expression tag	UNP P0AEX9
B	79	HIS	-	expression tag	UNP P0AEX9
B	80	HIS	-	expression tag	UNP P0AEX9
B	81	HIS	-	expression tag	UNP P0AEX9
B	82	GLY	-	expression tag	UNP P0AEX9
B	83	THR	-	expression tag	UNP P0AEX9
B	84	LYS	-	expression tag	UNP P0AEX9
B	85	THR	-	expression tag	UNP P0AEX9
B	450	GLY	-	linker	UNP P0AEX9
B	451	THR	-	linker	UNP P0AEX9
B	452	ASP	-	linker	UNP P0AEX9
B	453	TYR	-	linker	UNP P0AEX9
B	454	ASP	-	linker	UNP P0AEX9
B	455	ILE	-	linker	UNP P0AEX9
B	456	PRO	-	linker	UNP P0AEX9
B	457	THR	-	linker	UNP P0AEX9
B	458	THR	-	linker	UNP P0AEX9
B	459	LEU	-	linker	UNP P0AEX9
B	460	GLU	-	linker	UNP P0AEX9
B	461	VAL	-	linker	UNP P0AEX9
B	462	LEU	-	linker	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	463	PHE	-	linker	UNP P0AEX9
B	464	GLN	-	linker	UNP P0AEX9
B	465	GLY	-	linker	UNP P0AEX9
B	466	PRO	-	linker	UNP P0AEX9
B	467	LEU	-	linker	UNP P0AEX9
B	468	GLY	-	linker	UNP P0AEX9
B	469	SER	-	linker	UNP P0AEX9
C	72	MET	-	initiating methionine	UNP P0AEX9
C	73	GLY	-	expression tag	UNP P0AEX9
C	74	SER	-	expression tag	UNP P0AEX9
C	75	SER	-	expression tag	UNP P0AEX9
C	76	HIS	-	expression tag	UNP P0AEX9
C	77	HIS	-	expression tag	UNP P0AEX9
C	78	HIS	-	expression tag	UNP P0AEX9
C	79	HIS	-	expression tag	UNP P0AEX9
C	80	HIS	-	expression tag	UNP P0AEX9
C	81	HIS	-	expression tag	UNP P0AEX9
C	82	GLY	-	expression tag	UNP P0AEX9
C	83	THR	-	expression tag	UNP P0AEX9
C	84	LYS	-	expression tag	UNP P0AEX9
C	85	THR	-	expression tag	UNP P0AEX9
C	450	GLY	-	linker	UNP P0AEX9
C	451	THR	-	linker	UNP P0AEX9
C	452	ASP	-	linker	UNP P0AEX9
C	453	TYR	-	linker	UNP P0AEX9
C	454	ASP	-	linker	UNP P0AEX9
C	455	ILE	-	linker	UNP P0AEX9
C	456	PRO	-	linker	UNP P0AEX9
C	457	THR	-	linker	UNP P0AEX9
C	458	THR	-	linker	UNP P0AEX9
C	459	LEU	-	linker	UNP P0AEX9
C	460	GLU	-	linker	UNP P0AEX9
C	461	VAL	-	linker	UNP P0AEX9
C	462	LEU	-	linker	UNP P0AEX9
C	463	PHE	-	linker	UNP P0AEX9
C	464	GLN	-	linker	UNP P0AEX9
C	465	GLY	-	linker	UNP P0AEX9
C	466	PRO	-	linker	UNP P0AEX9
C	467	LEU	-	linker	UNP P0AEX9
C	468	GLY	-	linker	UNP P0AEX9
C	469	SER	-	linker	UNP P0AEX9
D	72	MET	-	initiating methionine	UNP P0AEX9

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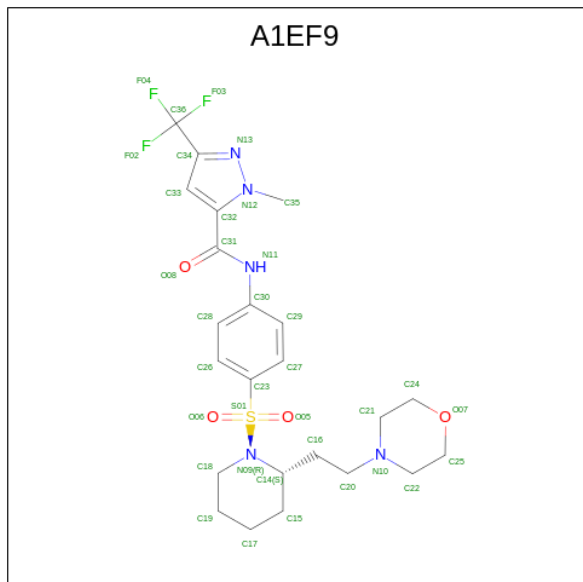
Chain	Residue	Modelled	Actual	Comment	Reference
D	73	GLY	-	expression tag	UNP P0AEX9
D	74	SER	-	expression tag	UNP P0AEX9
D	75	SER	-	expression tag	UNP P0AEX9
D	76	HIS	-	expression tag	UNP P0AEX9
D	77	HIS	-	expression tag	UNP P0AEX9
D	78	HIS	-	expression tag	UNP P0AEX9
D	79	HIS	-	expression tag	UNP P0AEX9
D	80	HIS	-	expression tag	UNP P0AEX9
D	81	HIS	-	expression tag	UNP P0AEX9
D	82	GLY	-	expression tag	UNP P0AEX9
D	83	THR	-	expression tag	UNP P0AEX9
D	84	LYS	-	expression tag	UNP P0AEX9
D	85	THR	-	expression tag	UNP P0AEX9
D	450	GLY	-	linker	UNP P0AEX9
D	451	THR	-	linker	UNP P0AEX9
D	452	ASP	-	linker	UNP P0AEX9
D	453	TYR	-	linker	UNP P0AEX9
D	454	ASP	-	linker	UNP P0AEX9
D	455	ILE	-	linker	UNP P0AEX9
D	456	PRO	-	linker	UNP P0AEX9
D	457	THR	-	linker	UNP P0AEX9
D	458	THR	-	linker	UNP P0AEX9
D	459	LEU	-	linker	UNP P0AEX9
D	460	GLU	-	linker	UNP P0AEX9
D	461	VAL	-	linker	UNP P0AEX9
D	462	LEU	-	linker	UNP P0AEX9
D	463	PHE	-	linker	UNP P0AEX9
D	464	GLN	-	linker	UNP P0AEX9
D	465	GLY	-	linker	UNP P0AEX9
D	466	PRO	-	linker	UNP P0AEX9
D	467	LEU	-	linker	UNP P0AEX9
D	468	GLY	-	linker	UNP P0AEX9
D	469	SER	-	linker	UNP P0AEX9

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
3	L	2	Total Zn 2 2	0

- Molecule 4 is 2-methyl- {N}-[4-[(2 {S})-2-(2-morpholin-4-ylethyl)piperidin-1-yl]sul

fonylphenyl]-5-(trifluoromethyl)pyrazole-3-carboxamide (CCD ID: A1EF9) (formula: $C_{23}H_{30}F_3N_5O_4S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
			Total	C	F	N	O	S	
4	L	1	36	23	3	5	4	1	0

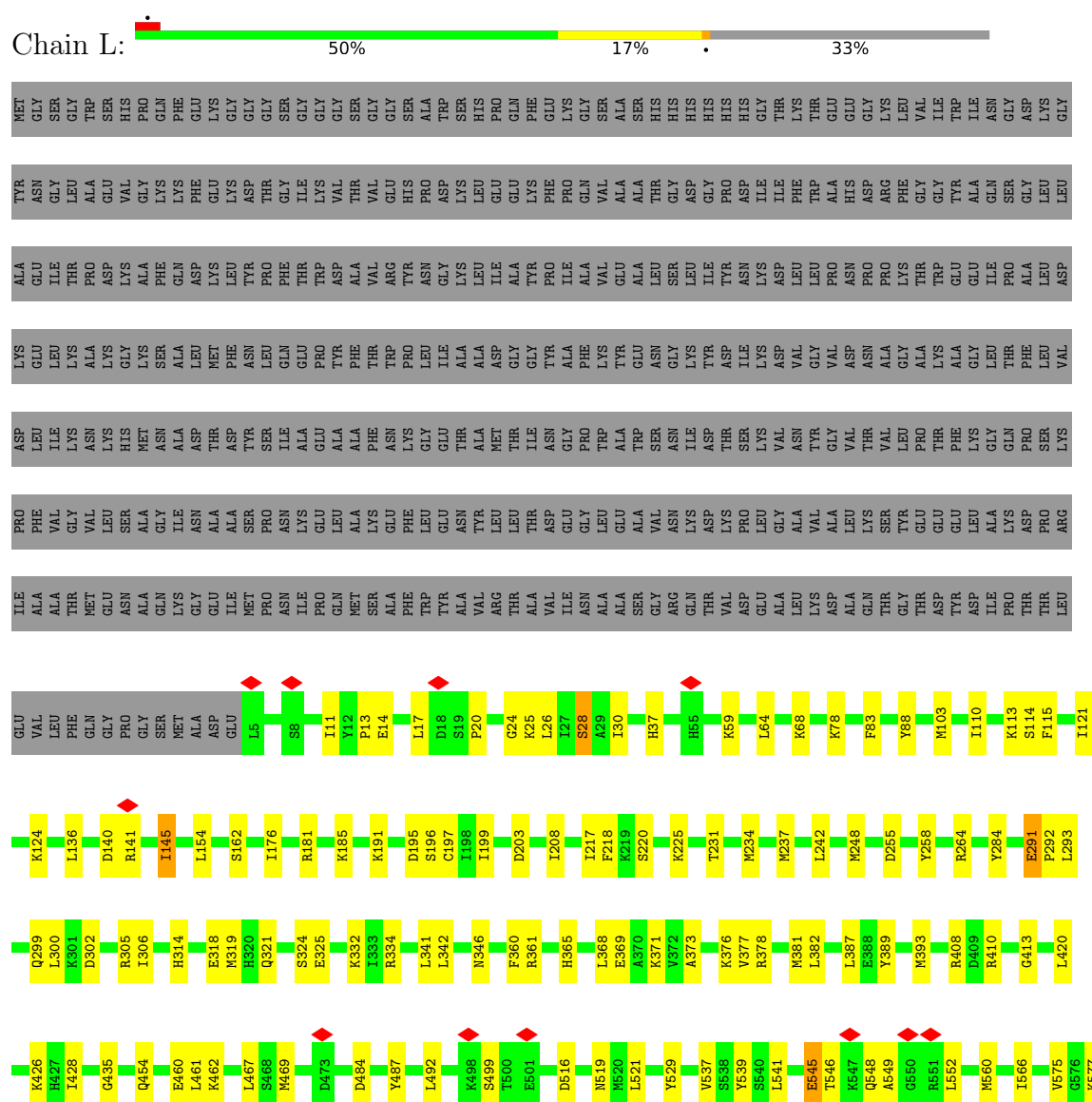
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		AltConf
5	L	1	Total	O	0
			1	1	

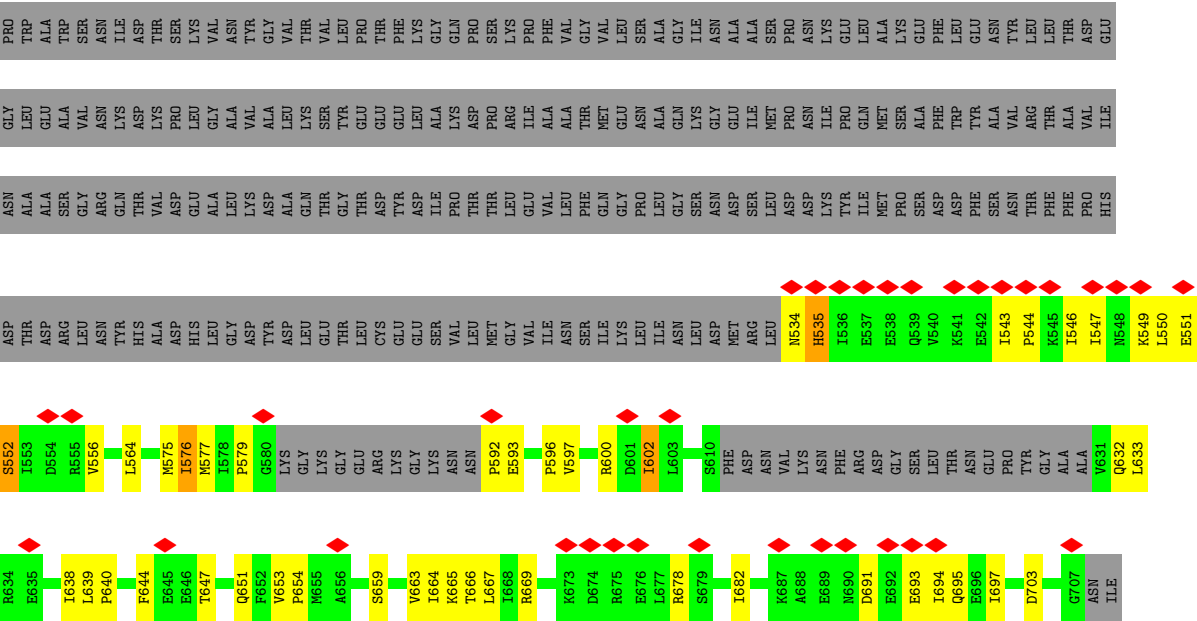
3 Residue-property plots

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: Maltose/maltodextrin-binding periplasmic protein,RNA-directed RNA polymerase L

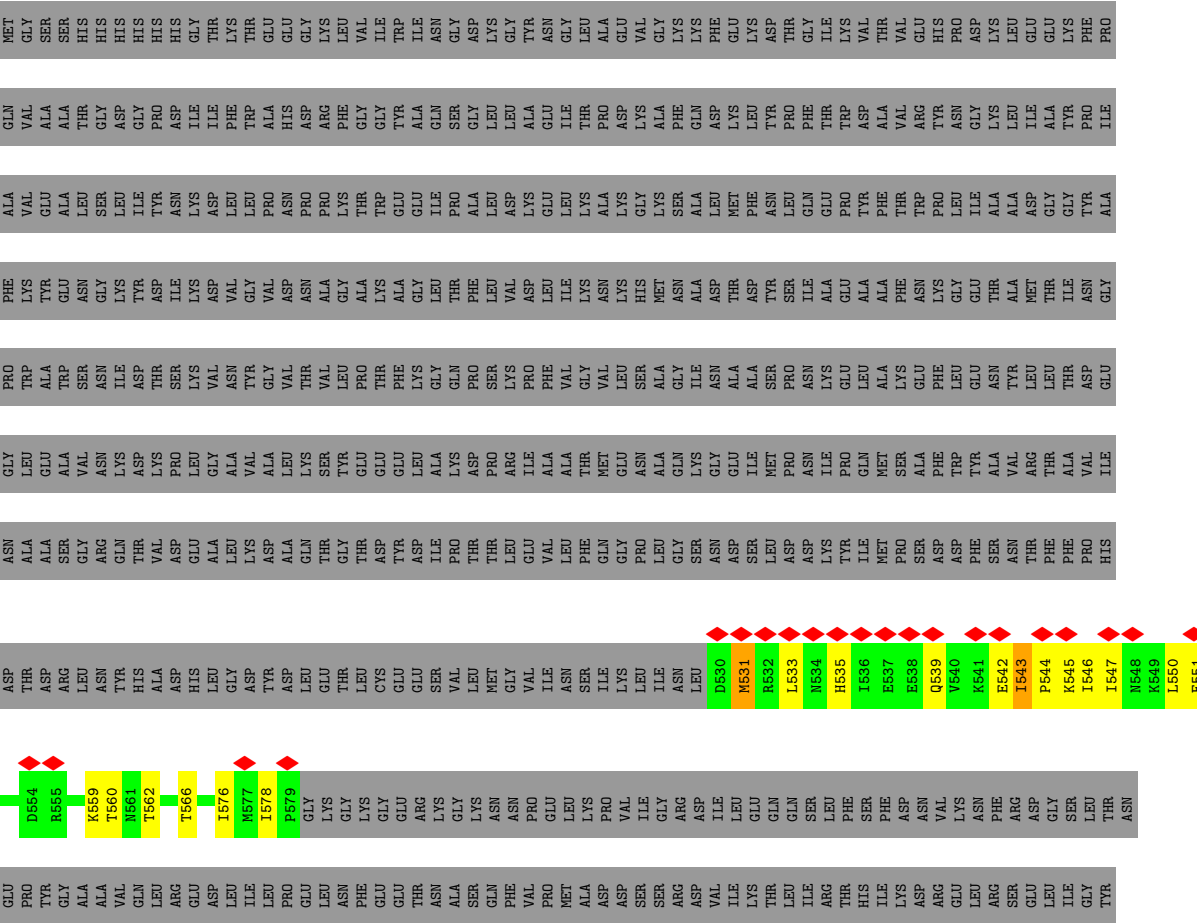


[illegible]



● Molecule 2: Maltose/maltodextrin-binding periplasmic protein,Phosphoprotein

Chain B: 5% 92%



ASN	ALA	R555	ASP	ASN	GLY	PRO
ASP	VAL		THR	ALA	LEU	TRP
GLU	GLN	T560	ASP	ALA	GLU	ALA
GLU	LEU	N661	ARG	SER	ALA	TRP
ILE	ARG		LEU	GLY	VAL	SER
GLN	GLU	S573	ASN	ARG	ASN	ASN
ASP	ASP		TYR	GLN	ASP	ILE
LEU	LEU	M577	HIS	THR	LYS	THR
ILE	ILE	I578	ALA	VAL	ASP	LYS
ASN	LEU	P579	ASP	ASP	PRO	SER
THR	PRO	G680	HIS	GLU	LEU	LYS
VAL	GLU	K581	LEU	ALA	GLY	VAL
ASN	LEU	G582	GLY	ALA	ALA	VAL
ASP	ASN	LYS	ASP	LYS	ALA	ASN
ILE	PHE	GLY	TYR	ASP	VAL	TYR
ILE	GLU	GLU	LEU	ALA	LEU	GLY
ASP	GLU	ARG	LEU	GLN	LYS	THR
GLY	THR	LYS	GLU	THR	SER	VAL
ASN	ASN	GLY	THR	GLY	TYR	VAL
ILE	ALA	LYS	LEU	THR	GLU	PRO
	SER	ASN	CYS	ASP	GLU	THR
	GLN	ASN	GLU	TYR	LEU	PHE
	PHE	PRO	GLU	ASP	LEU	LYS
	VAL	GLU	SER	ILE	ALA	GLY
	PRO	LEU	VAL	VAL	LYS	GLN
	MET	LEU	VAL	LEU	ASP	PRO
	ALA	PRO	GLY	GLU	ARG	LYS
	ASP	VAL	ILE	VAL	ILE	PHE
	SER	GLY	ILE	VAL	ALA	VAL
	SER	ARG	ASN	LEU	ALA	GLY
	ARG	ASP	SER	PHE	THR	VAL
	ASP	ILE	LYS	GLN	MET	VAL
	VAL	ILE	ILE	GLY	GLU	LEU
	ILE	GLU	ILE	PRO	ASN	SER
	LYS	GLN	ILE	LEU	ALA	ALA
	THR	GLN	ASN	GLY	GLN	GLY
	LEU	SER	L529	SER	LYS	ILE
	ILE	LEU	D530	ASN	GLY	ASN
	ARG	PHE	M531	SER	GLU	ALA
	THR	SER	R532	LEU	MET	SER
	HIS	PHE	L533	ASP	PRO	PRO
	ILE	ASP	L533	ASP	ASN	ASN
	LYS	VAL	N534	LYS	ILE	LYS
	ARG	ARG	H535	TYR	PRO	GLU
	GLU	GLU	I536	ASN	GLN	LEU
	LEU	PHE	E537	ILE	MET	ALA
	ARG	ARG	E538	PRO	SER	LYS
	SER	ASP	Q539	SER	ALA	GLU
	GLU	GLY	V540	ASP	PHE	PHE
	LEU	SER	K541	THR	TYR	LEU
	ILE	THR	E542	PHE	TRP	GLU
	GLY	LEU	I543	SER	ALA	ASN
	TYR	THR	P544	ASN	VAL	TYR
	LEU	GLU	I543	THR	ARG	LEU
	ASN	ASN	P544	ASN	THR	LEU
	LYS	PRO		PHE	THR	THR
	TYR	TYR	I547	PHE	ALA	ASP
	GLY	GLY	I548	PRO	VAL	GLU
	ALA	THR		HIS	THR	THR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	158764	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	4.856	Depositor
Minimum map value	-2.887	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.084	Depositor
Recommended contour level	0.48	Depositor
Map size (Å)	334.8, 334.8, 334.8	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.92999995, 0.92999995, 0.92999995	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, A1EF9

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	L	0.18	0/10530	0.35	4/14238 (0.0%)
2	A	0.17	0/1148	0.43	0/1547
2	B	0.20	0/399	0.55	0/536
2	C	0.23	0/561	0.47	0/750
2	D	0.18	0/424	0.43	0/568
All	All	0.18	0/13062	0.37	4/17639 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	784	THR	CA-C-N	5.97	125.88	119.85
1	L	784	THR	C-N-CA	5.97	125.88	119.85
1	L	790	PHE	N-CA-C	5.31	117.57	110.35
1	L	548	GLN	N-CA-C	-5.24	108.14	114.75

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	L	10317	0	10341	214	0
2	A	1138	0	1157	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	396	0	424	17	0
2	C	556	0	602	21	0
2	D	421	0	454	18	0
3	L	2	0	0	0	0
4	L	36	0	0	0	0
5	L	1	0	0	0	0
All	All	12867	0	12978	283	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 11.

The worst 5 of 283 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:L:371:LYS:HE2	1:L:788:ASP:OD1	1.66	0.94
1:L:1004:LEU:HB2	1:L:1022:ASP:OD2	1.67	0.94
1:L:1020:LEU:HD13	1:L:1195:LEU:HB3	1.61	0.81
2:B:546:ILE:HD11	2:C:547:ILE:HD11	1.66	0.78
1:L:1004:LEU:HB2	1:L:1022:ASP:CG	2.12	0.73

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	L	1271/1904 (67%)	1248 (98%)	23 (2%)	0	100	100
2	A	137/638 (22%)	130 (95%)	7 (5%)	0	100	100
2	B	48/638 (8%)	48 (100%)	0	0	100	100
2	C	69/638 (11%)	63 (91%)	6 (9%)	0	100	100
2	D	52/638 (8%)	51 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1577/4456 (35%)	1540 (98%)	37 (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	L	1151/1668 (69%)	1127 (98%)	24 (2%)	47	70
2	A	132/539 (24%)	128 (97%)	4 (3%)	36	60
2	B	47/539 (9%)	45 (96%)	2 (4%)	26	50
2	C	64/539 (12%)	63 (98%)	1 (2%)	55	76
2	D	49/539 (9%)	47 (96%)	2 (4%)	27	52
All	All	1443/3824 (38%)	1410 (98%)	33 (2%)	44	68

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	531	MET
2	B	543	ILE
2	D	547	ILE
1	L	839	THR
1	L	830	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	76	ASN
1	L	131	ASN
1	L	149	HIS
1	L	1256	GLN
2	B	535	HIS

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 ⓘ

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	A1EF9	L	1503	-	39,39,39	2.80	15 (38%)	54,57,57	2.64	19 (35%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A1EF9	L	1503	-	-	5/31/50/50	0/4/4/4

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	1503	A1EF9	C20-N10	-7.54	1.30	1.47
4	L	1503	A1EF9	S01-N09	6.87	1.73	1.63
4	L	1503	A1EF9	C31-N11	6.10	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	1503	A1EF9	C23-S01	5.88	1.84	1.76
4	L	1503	A1EF9	C30-N11	3.58	1.48	1.41

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	1503	A1EF9	O06-S01-O05	-10.87	101.91	119.52
4	L	1503	A1EF9	C36-C34-N13	6.83	127.91	119.23
4	L	1503	A1EF9	C32-C33-C34	4.25	107.89	103.64
4	L	1503	A1EF9	C18-N09-C14	-4.15	110.78	116.10
4	L	1503	A1EF9	C33-C34-N13	-4.01	107.09	111.92

There are no chirality outliers.

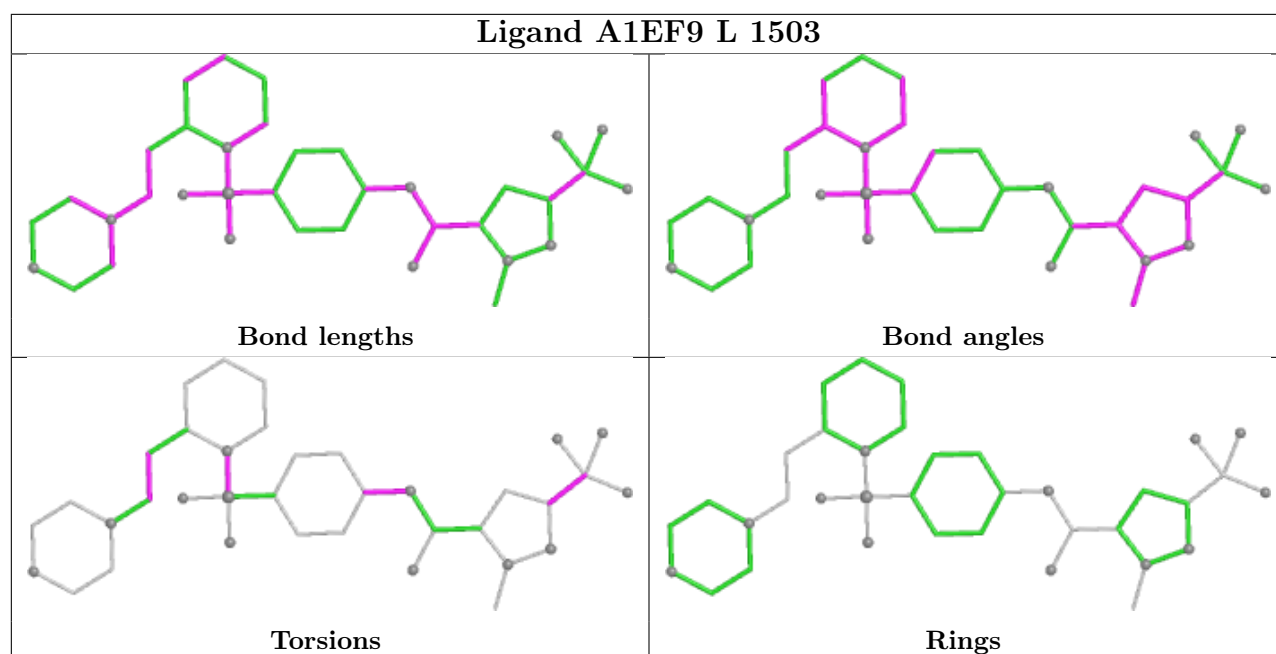
All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	L	1503	A1EF9	C28-C30-N11-C31
4	L	1503	A1EF9	C29-C30-N11-C31
4	L	1503	A1EF9	C14-C16-C20-N10
4	L	1503	A1EF9	C14-N09-S01-O06
4	L	1503	A1EF9	N13-C34-C36-F03

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

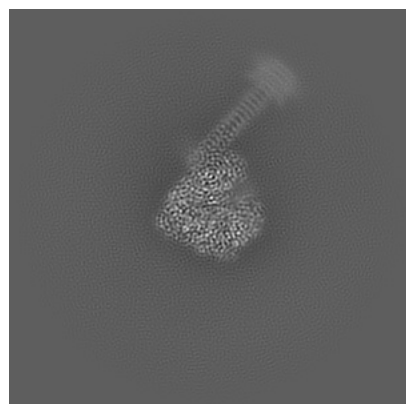
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65368. These allow visual inspection of the internal detail of the map and identification of artifacts.

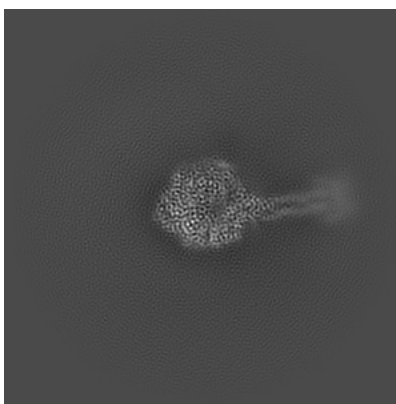
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

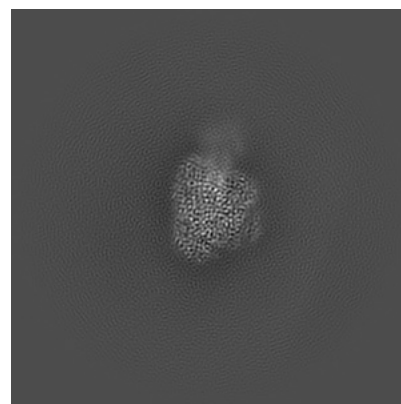
6.1.1 Primary map



X

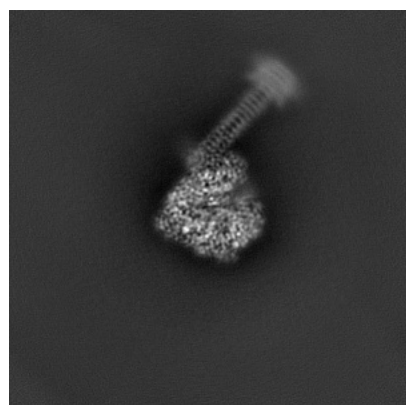


Y

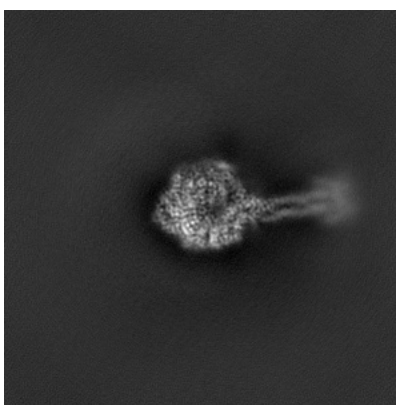


Z

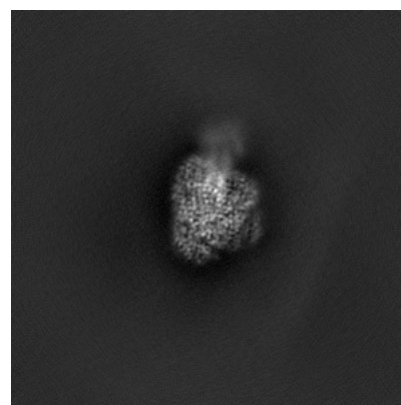
6.1.2 Raw map



X



Y

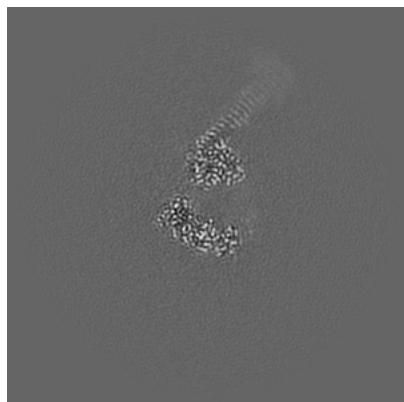


Z

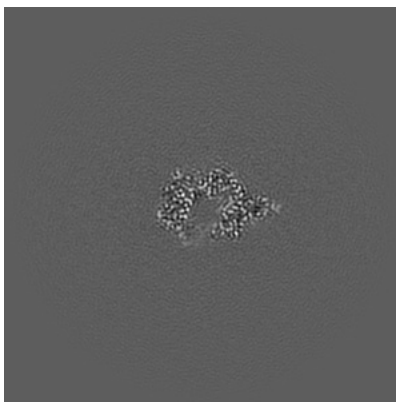
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

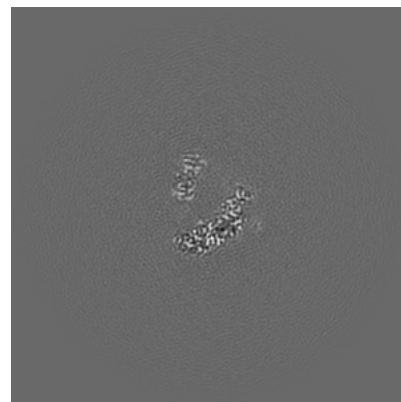
6.2.1 Primary map



X Index: 180

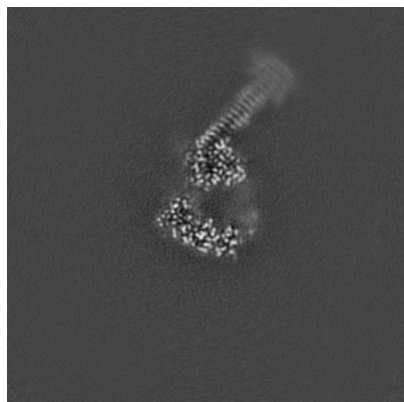


Y Index: 180

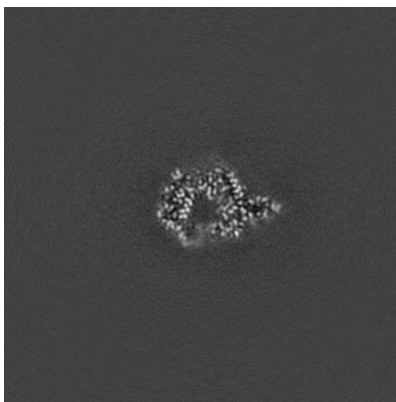


Z Index: 180

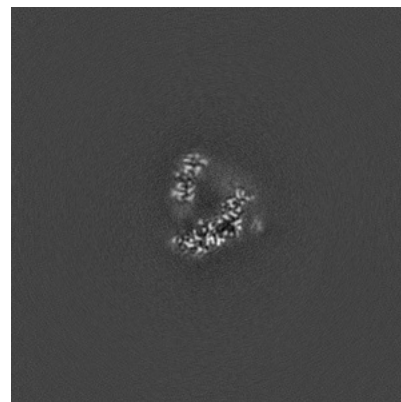
6.2.2 Raw map



X Index: 180



Y Index: 180

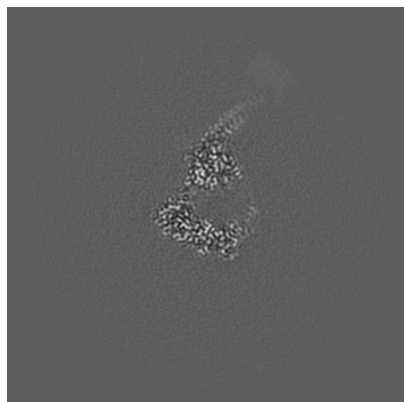


Z Index: 180

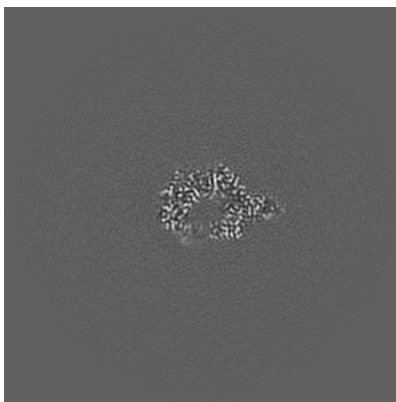
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

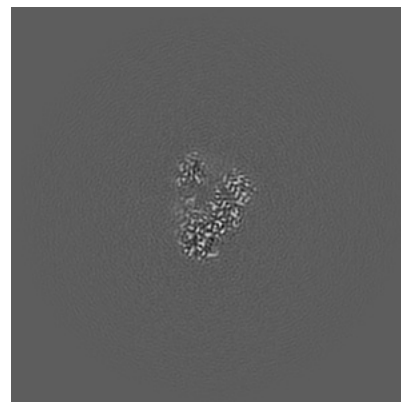
6.3.1 Primary map



X Index: 176

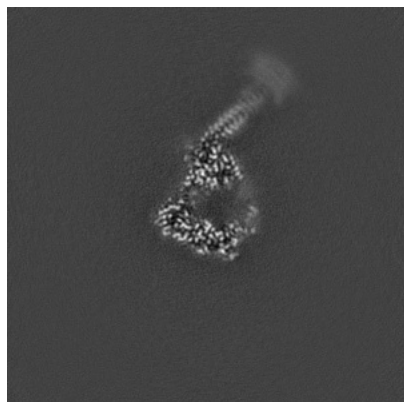


Y Index: 182

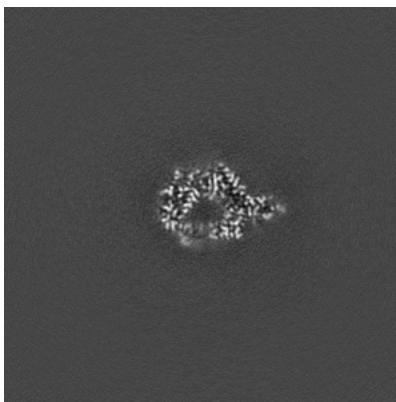


Z Index: 168

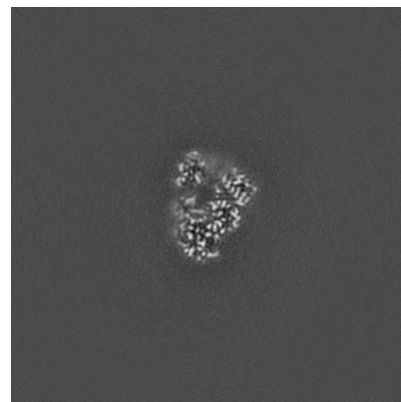
6.3.2 Raw map



X Index: 176



Y Index: 182

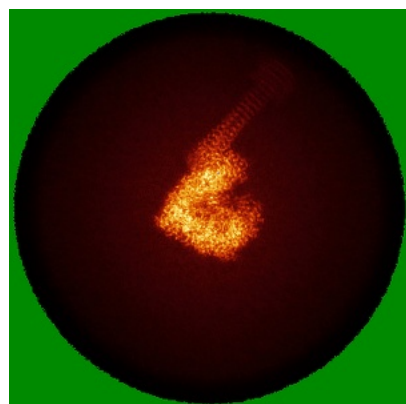


Z Index: 168

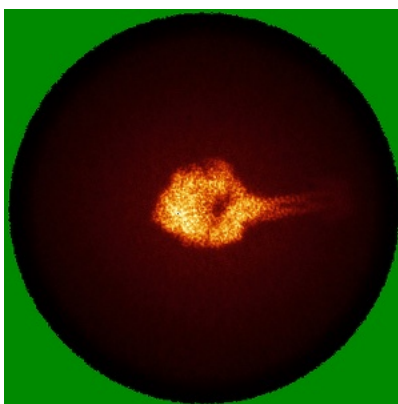
The images above show the largest variance slices of the map in three orthogonal directions.

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

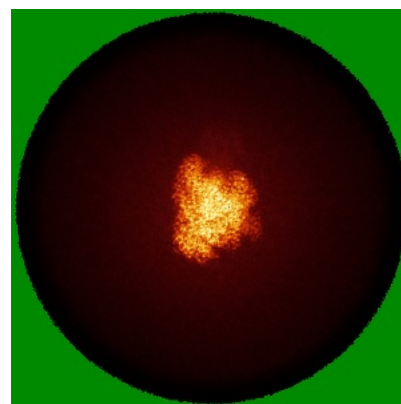
6.4.1 Primary map



X

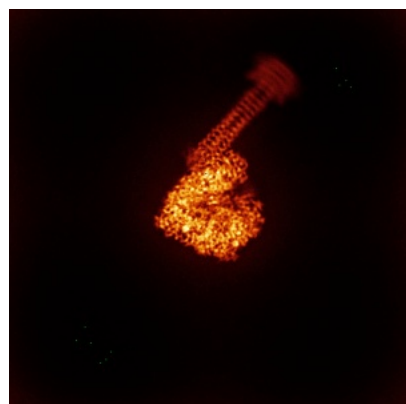


Y

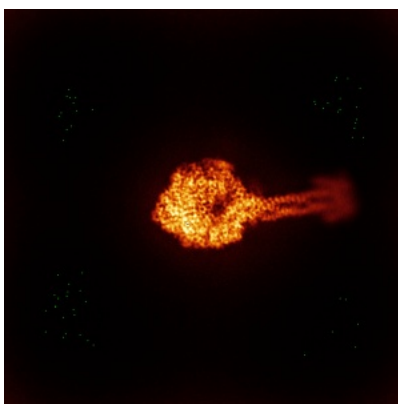


Z

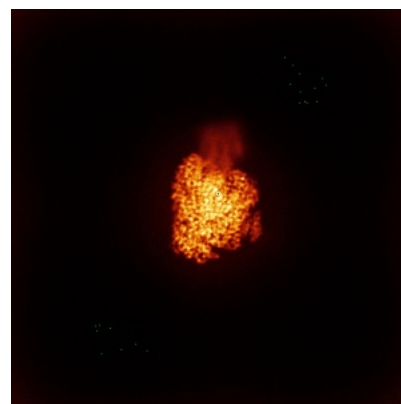
6.4.2 Raw map



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.

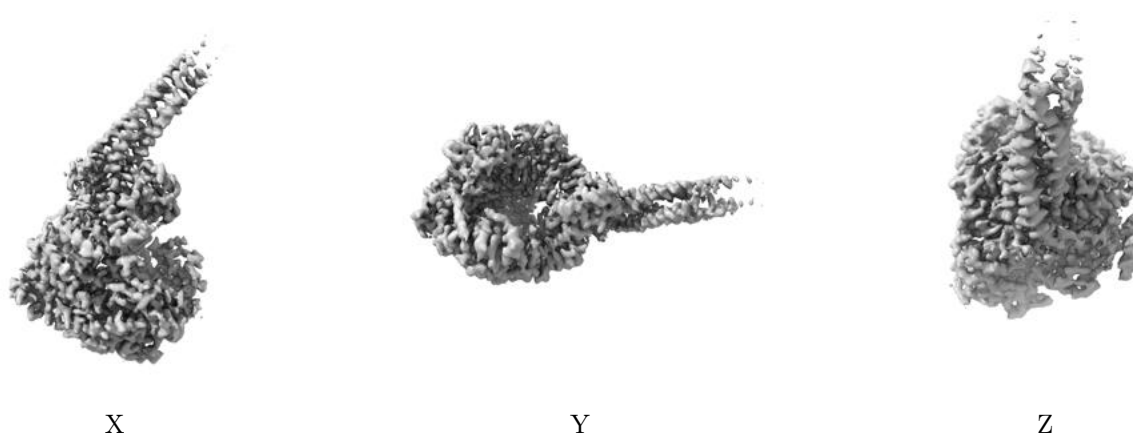
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.48. 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



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

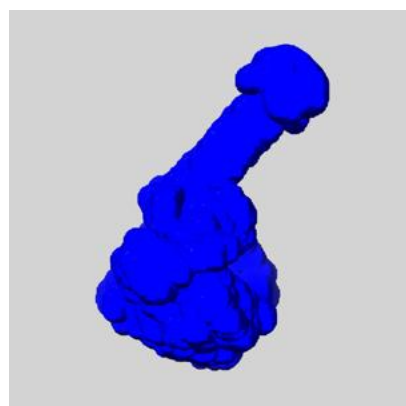
6.6 Mask visualisation [i](#)

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

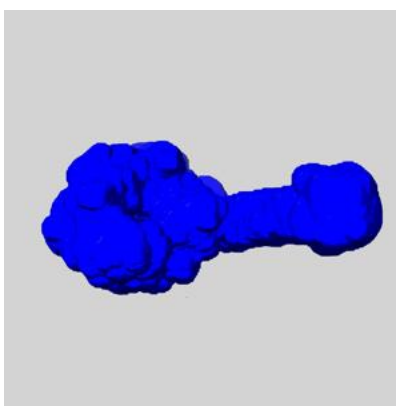
A mask typically either:

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

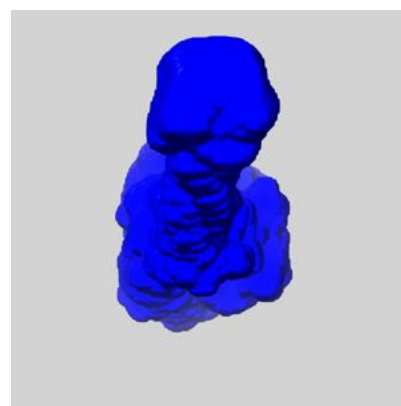
6.6.1 emd_65368_msk_1.map [i](#)



X



Y

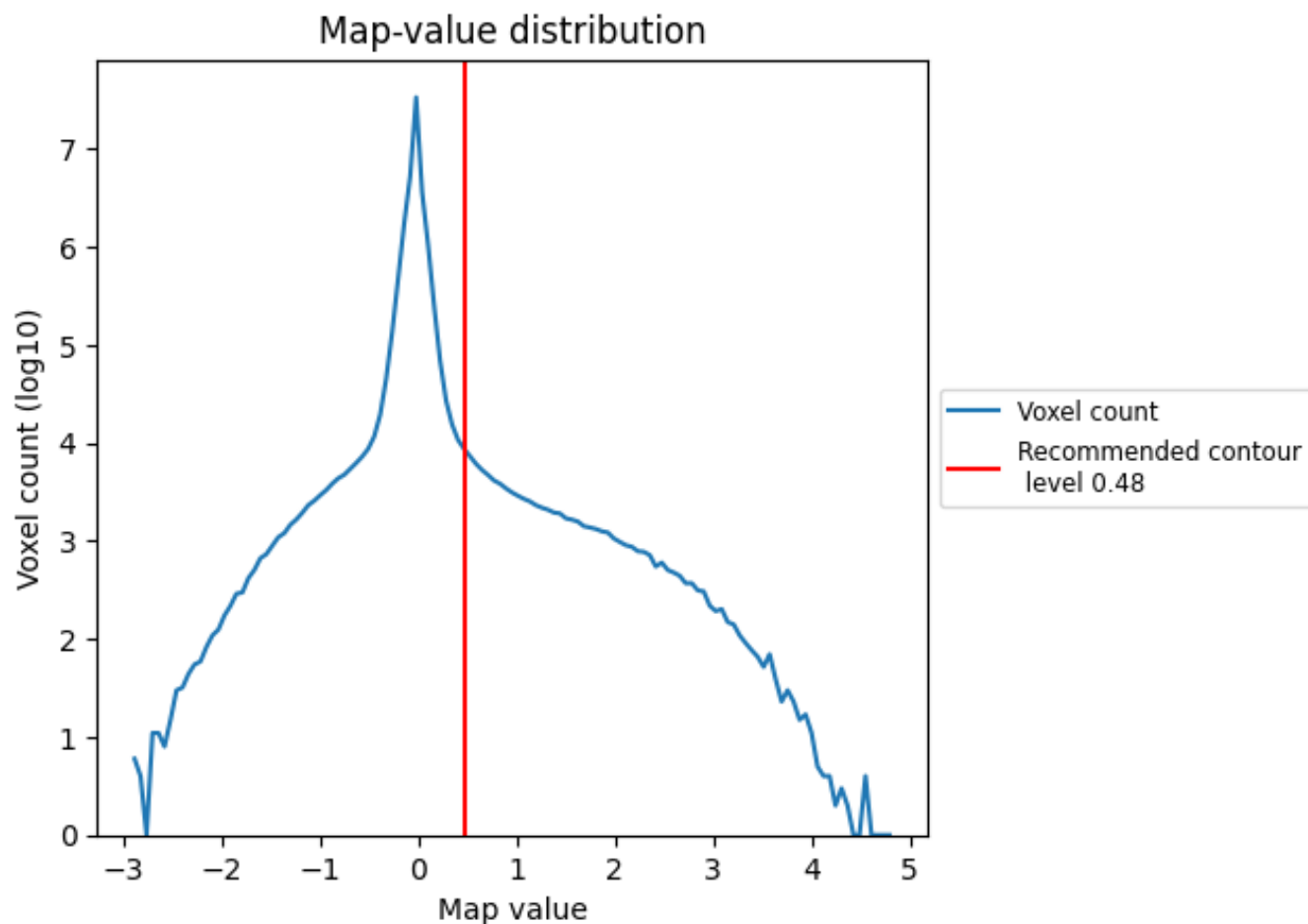


Z

7 Map analysis [i](#)

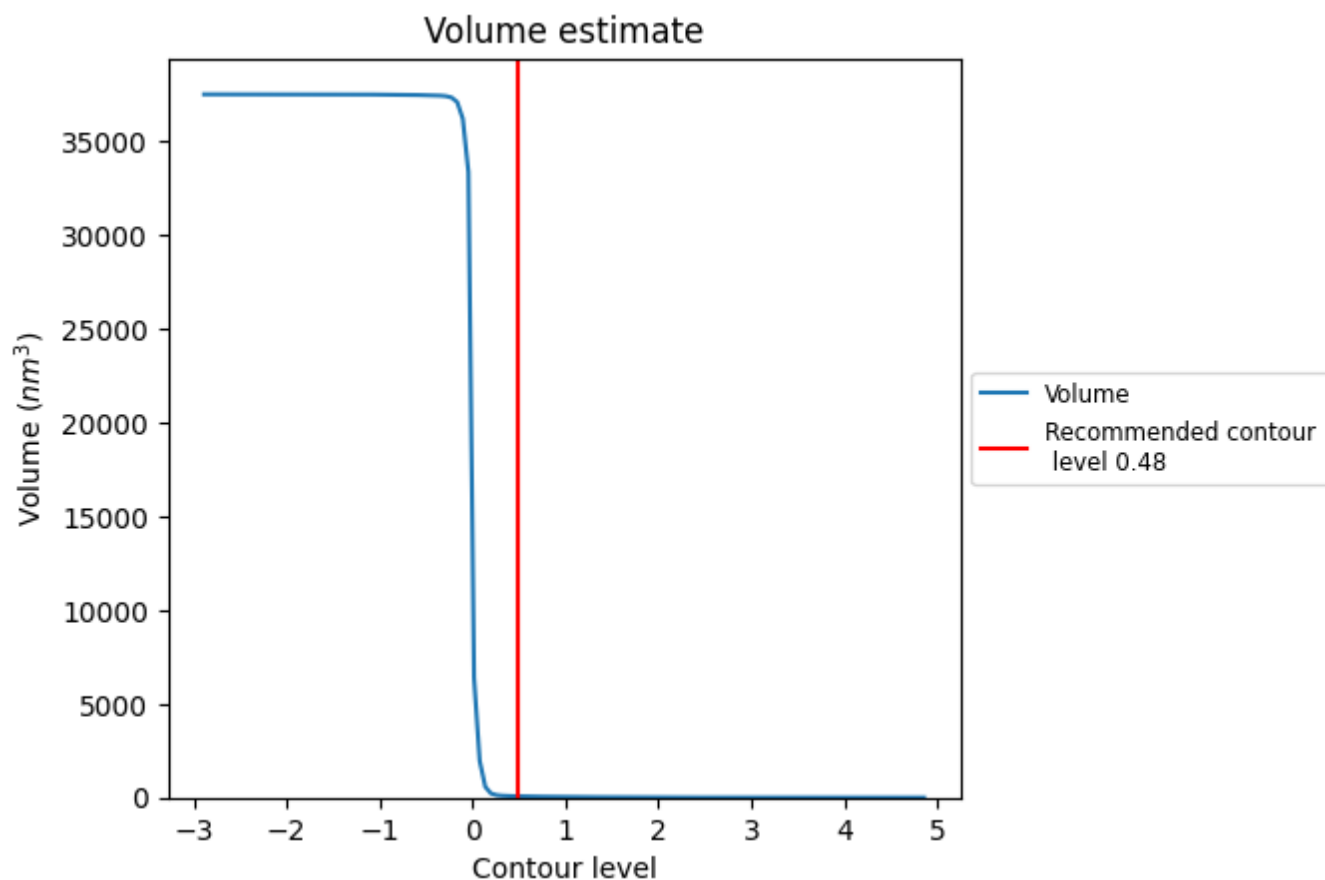
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

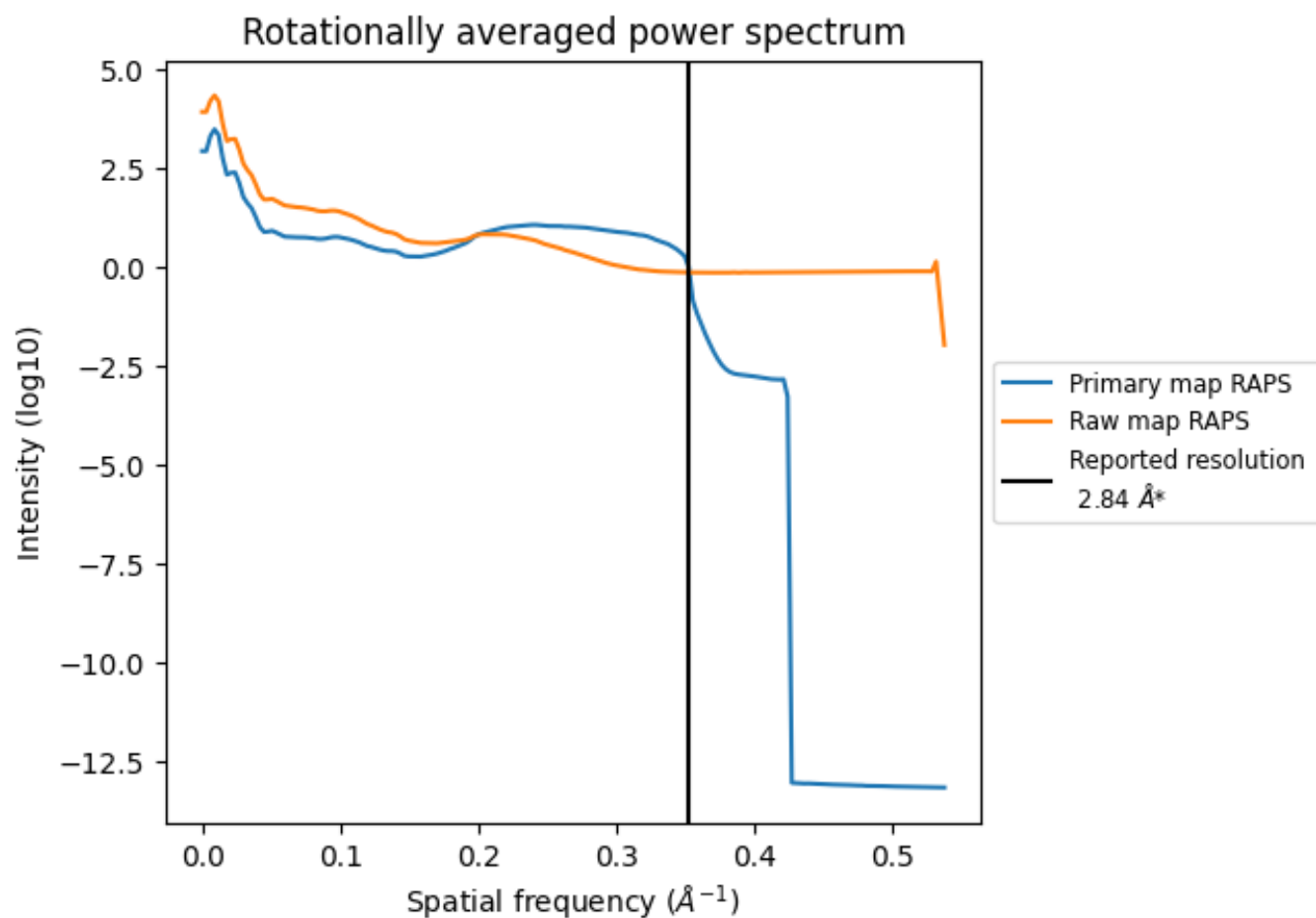
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 70 nm^3 ; this corresponds to an approximate mass of 63 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 ⓘ

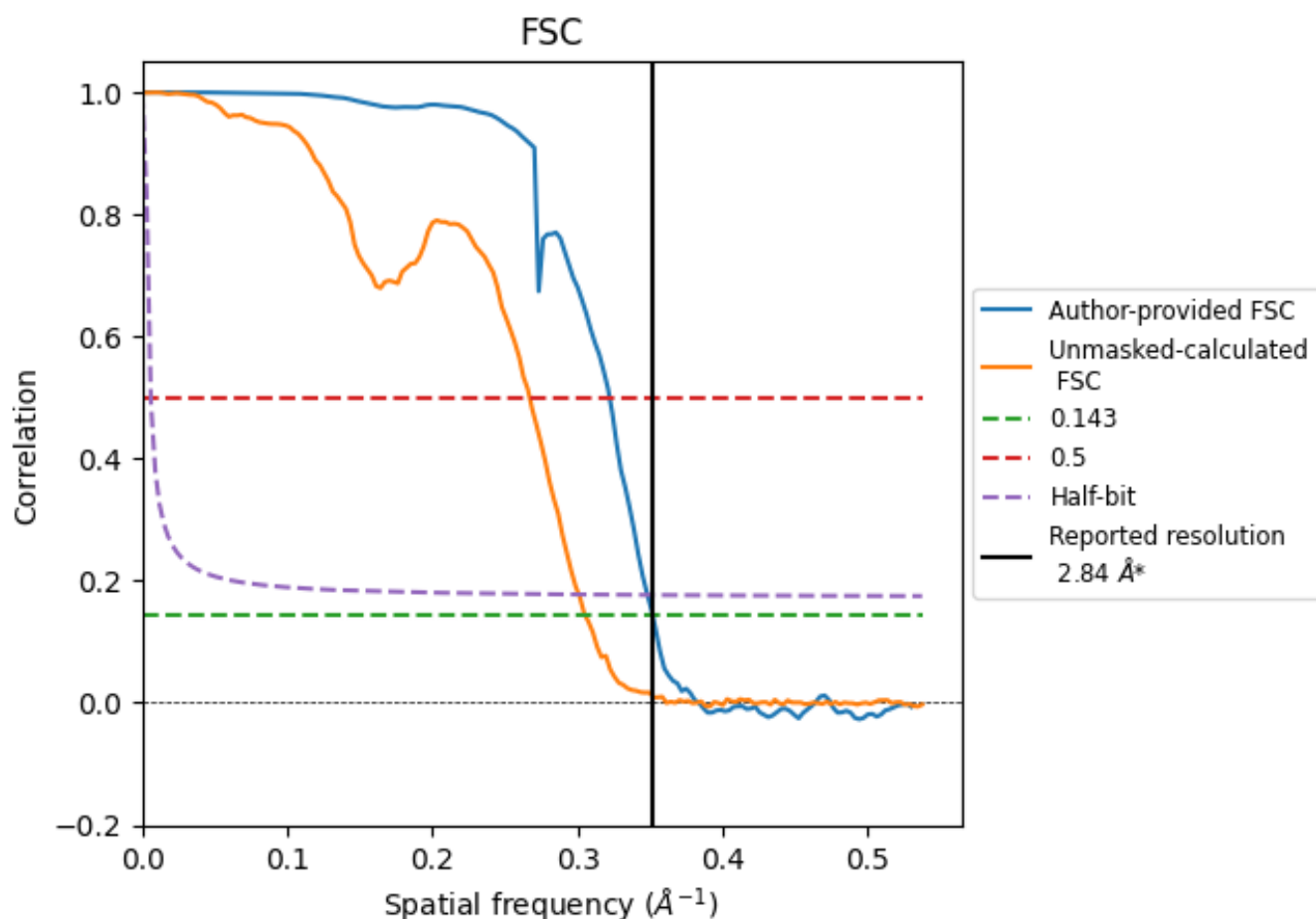


*Reported resolution corresponds to spatial frequency of 0.352 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.352 \AA^{-1}

8.2 Resolution estimates [i](#)

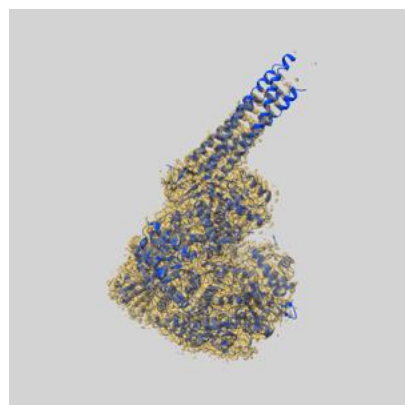
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.84	-	-
Author-provided FSC curve	2.84	3.10	2.87
Unmasked-calculated*	3.28	3.74	3.32

*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 3.28 differs from the reported value 2.84 by more than 10 %

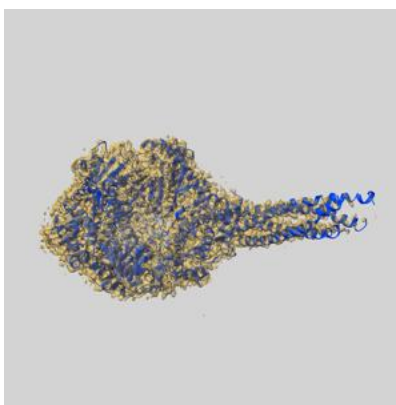
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65368 and PDB model 9VUM. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

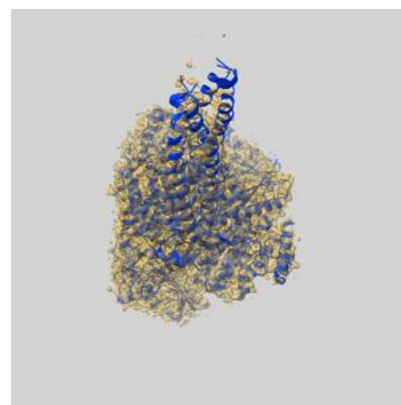
9.1 Map-model overlay [i](#)



X



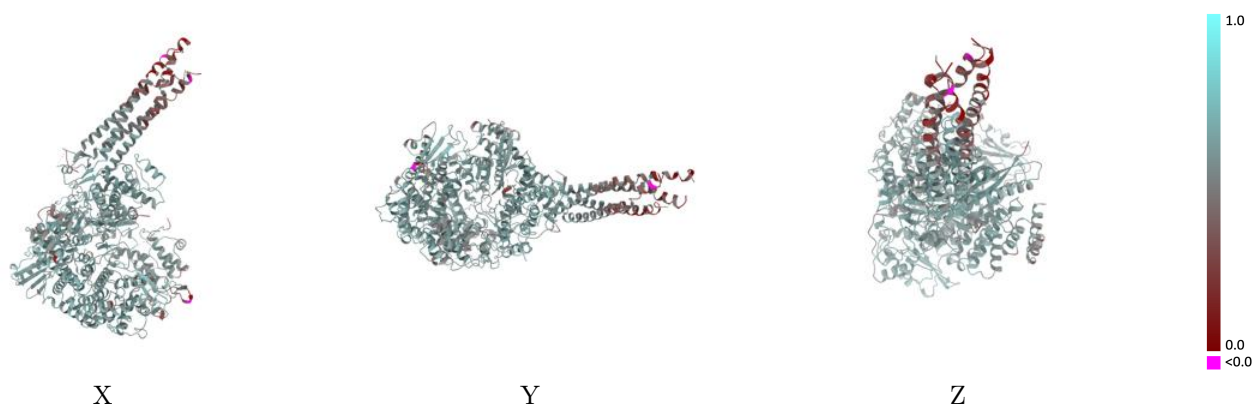
Y



Z

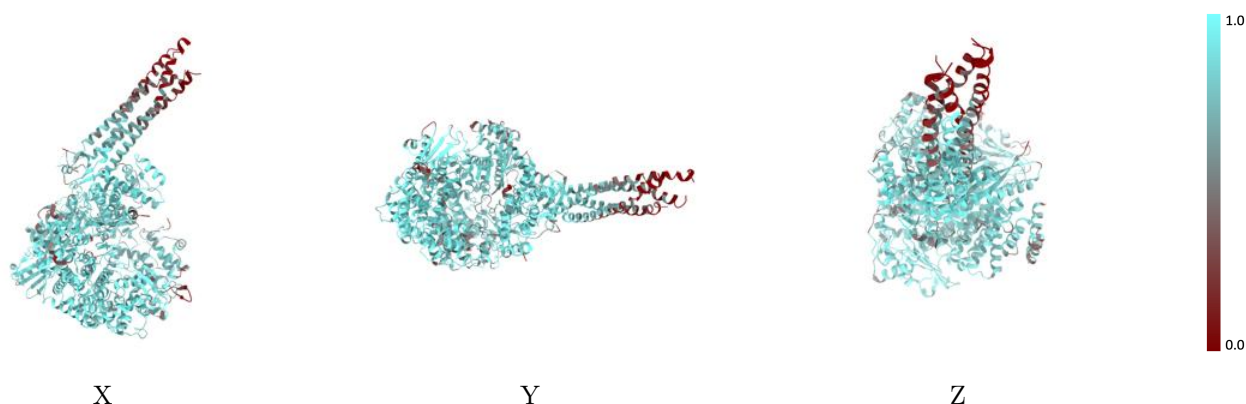
The images above show the 3D surface view of the map at the recommended contour level 0.48 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



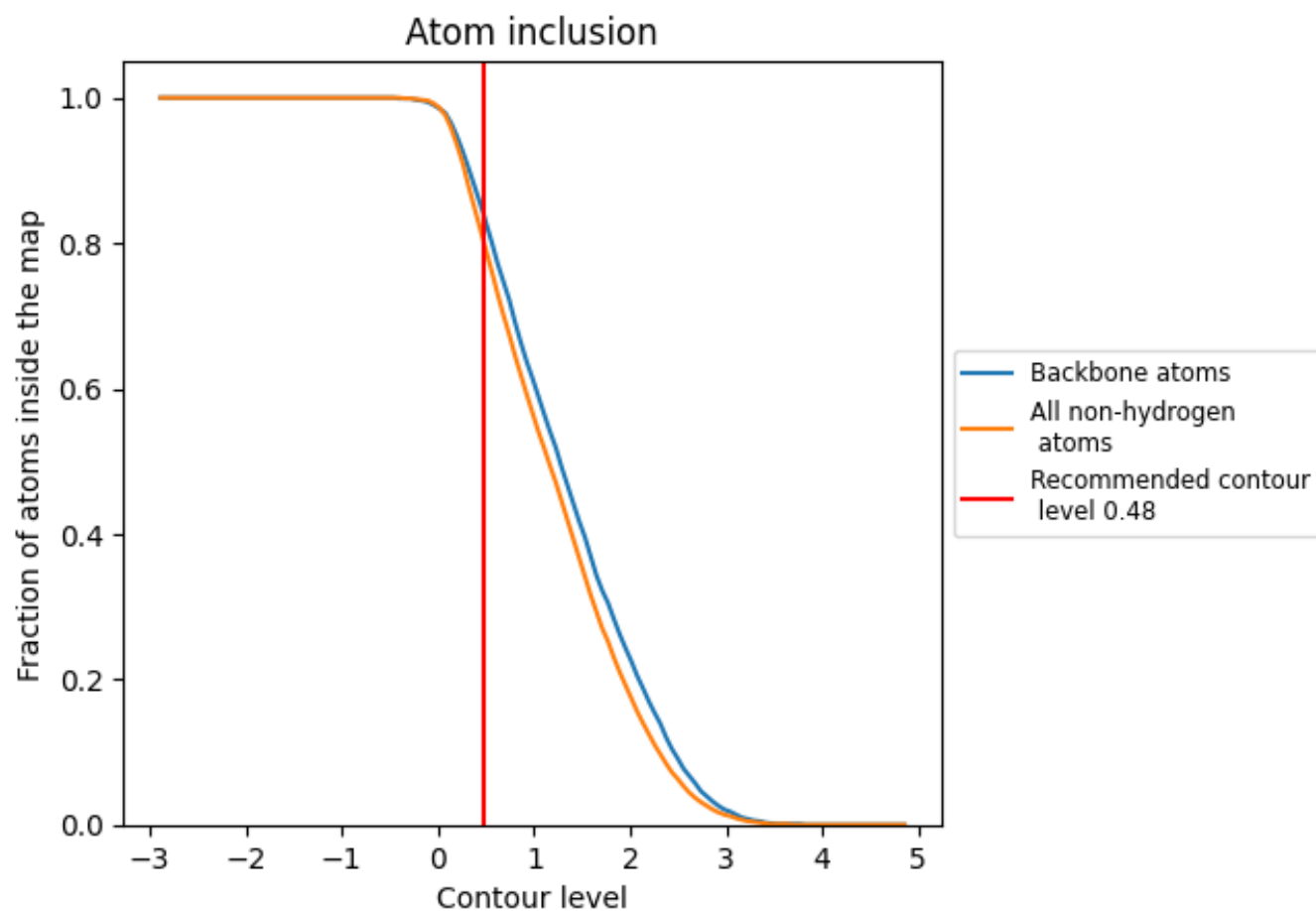
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.48).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 80% 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 (0.48) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8010	<div></div> 0.5620
A	<div></div> 0.6270	<div></div> 0.4930
B	<div></div> 0.4590	<div></div> 0.4100
C	<div></div> 0.5130	<div></div> 0.4500
D	<div></div> 0.5400	<div></div> 0.4340
L	<div></div> 0.8610	<div></div> 0.5860

