



## Full wwPDB EM Validation Report ⓘ

Nov 3, 2024 – 05:01 PM EST

PDB ID : 8G5A  
EMDB ID : EMD-29737  
Title : X-31 hemagglutinin in complex with FL-1061 Fab  
Authors : Windsor, I.W.; Thornlow, D.; Schmidt, A.G.  
Deposited on : 2023-02-12  
Resolution : 3.30 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](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.dev113  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

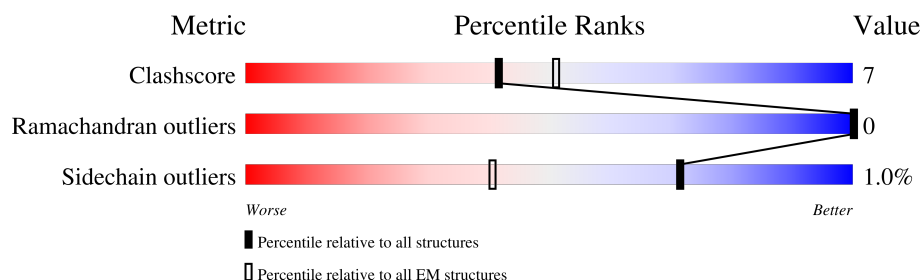
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.30 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	637	
1	B	637	
1	C	637	
2	H	246	
2	I	246	
2	J	246	
3	L	216	
3	M	216	

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Mol	Chain	Length	Quality of chain
3	N	216	<div><div></div><div>23%</div><div></div><div>85%</div><div></div><div>12%</div><div>..</div></div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 21666 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	493	Total	C	N	O	S	0	0
			3880	2420	683	758	19		
1	B	493	Total	C	N	O	S	0	0
			3880	2420	683	758	19		
1	C	493	Total	C	N	O	S	0	0
			3880	2420	683	758	19		

There are 390 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	initiating methionine	UNP A4JZ28
A	-20	LYS	-	expression tag	UNP A4JZ28
A	-19	ARG	-	expression tag	UNP A4JZ28
A	-18	GLY	-	expression tag	UNP A4JZ28
A	-17	LEU	-	expression tag	UNP A4JZ28
A	-16	CYS	-	expression tag	UNP A4JZ28
A	-15	CYS	-	expression tag	UNP A4JZ28
A	-14	VAL	-	expression tag	UNP A4JZ28
A	-13	LEU	-	expression tag	UNP A4JZ28
A	-12	LEU	-	expression tag	UNP A4JZ28
A	-11	LEU	-	expression tag	UNP A4JZ28
A	-10	CYS	-	expression tag	UNP A4JZ28
A	-9	GLY	-	expression tag	UNP A4JZ28
A	-8	ALA	-	expression tag	UNP A4JZ28
A	-7	VAL	-	expression tag	UNP A4JZ28
A	-6	PHE	-	expression tag	UNP A4JZ28
A	-5	VAL	-	expression tag	UNP A4JZ28
A	-4	SER	-	expression tag	UNP A4JZ28
A	-3	PRO	-	expression tag	UNP A4JZ28
A	-2	SER	-	expression tag	UNP A4JZ28
A	-1	ALA	-	expression tag	UNP A4JZ28
A	0	SER	-	expression tag	UNP A4JZ28
A	31	ASP	ASN	conflict	UNP A4JZ28
A	182	ILE	VAL	conflict	UNP A4JZ28

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Chain	Residue	Modelled	Actual	Comment	Reference
A	188	ASP	ASN	conflict	UNP A4JZ28
A	512	ALA	-	expression tag	UNP A4JZ28
A	513	GLY	-	expression tag	UNP A4JZ28
A	514	SER	-	expression tag	UNP A4JZ28
A	515	SER	-	expression tag	UNP A4JZ28
A	516	LEU	-	expression tag	UNP A4JZ28
A	517	GLU	-	expression tag	UNP A4JZ28
A	518	VAL	-	expression tag	UNP A4JZ28
A	519	LEU	-	expression tag	UNP A4JZ28
A	520	PHE	-	expression tag	UNP A4JZ28
A	521	GLN	-	expression tag	UNP A4JZ28
A	522	GLY	-	expression tag	UNP A4JZ28
A	523	PRO	-	expression tag	UNP A4JZ28
A	524	GLY	-	expression tag	UNP A4JZ28
A	525	SER	-	expression tag	UNP A4JZ28
A	526	GLY	-	expression tag	UNP A4JZ28
A	527	SER	-	expression tag	UNP A4JZ28
A	528	SER	-	expression tag	UNP A4JZ28
A	529	LEU	-	expression tag	UNP A4JZ28
A	530	GLY	-	expression tag	UNP A4JZ28
A	531	GLY	-	expression tag	UNP A4JZ28
A	532	SER	-	expression tag	UNP A4JZ28
A	533	GLY	-	expression tag	UNP A4JZ28
A	534	TYR	-	expression tag	UNP A4JZ28
A	535	ILE	-	expression tag	UNP A4JZ28
A	536	PRO	-	expression tag	UNP A4JZ28
A	537	GLU	-	expression tag	UNP A4JZ28
A	538	ALA	-	expression tag	UNP A4JZ28
A	539	PRO	-	expression tag	UNP A4JZ28
A	540	ARG	-	expression tag	UNP A4JZ28
A	541	ASP	-	expression tag	UNP A4JZ28
A	542	GLY	-	expression tag	UNP A4JZ28
A	543	GLN	-	expression tag	UNP A4JZ28
A	544	ALA	-	expression tag	UNP A4JZ28
A	545	TYR	-	expression tag	UNP A4JZ28
A	546	VAL	-	expression tag	UNP A4JZ28
A	547	ARG	-	expression tag	UNP A4JZ28
A	548	LYS	-	expression tag	UNP A4JZ28
A	549	ASP	-	expression tag	UNP A4JZ28
A	550	GLY	-	expression tag	UNP A4JZ28
A	551	GLU	-	expression tag	UNP A4JZ28
A	552	TRP	-	expression tag	UNP A4JZ28

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Chain	Residue	Modelled	Actual	Comment	Reference
A	553	VAL	-	expression tag	UNP A4JZ28
A	554	LEU	-	expression tag	UNP A4JZ28
A	555	LEU	-	expression tag	UNP A4JZ28
A	556	SER	-	expression tag	UNP A4JZ28
A	557	THR	-	expression tag	UNP A4JZ28
A	558	PHE	-	expression tag	UNP A4JZ28
A	559	LEU	-	expression tag	UNP A4JZ28
A	560	GLY	-	expression tag	UNP A4JZ28
A	561	SER	-	expression tag	UNP A4JZ28
A	562	GLY	-	expression tag	UNP A4JZ28
A	563	SER	-	expression tag	UNP A4JZ28
A	564	SER	-	expression tag	UNP A4JZ28
A	565	HIS	-	expression tag	UNP A4JZ28
A	566	HIS	-	expression tag	UNP A4JZ28
A	567	HIS	-	expression tag	UNP A4JZ28
A	568	HIS	-	expression tag	UNP A4JZ28
A	569	HIS	-	expression tag	UNP A4JZ28
A	570	HIS	-	expression tag	UNP A4JZ28
A	571	HIS	-	expression tag	UNP A4JZ28
A	572	HIS	-	expression tag	UNP A4JZ28
A	573	GLY	-	expression tag	UNP A4JZ28
A	574	GLY	-	expression tag	UNP A4JZ28
A	575	SER	-	expression tag	UNP A4JZ28
A	576	GLY	-	expression tag	UNP A4JZ28
A	577	SER	-	expression tag	UNP A4JZ28
A	578	SER	-	expression tag	UNP A4JZ28
A	579	MET	-	expression tag	UNP A4JZ28
A	580	ASP	-	expression tag	UNP A4JZ28
A	581	GLU	-	expression tag	UNP A4JZ28
A	582	LYS	-	expression tag	UNP A4JZ28
A	583	THR	-	expression tag	UNP A4JZ28
A	584	THR	-	expression tag	UNP A4JZ28
A	585	GLY	-	expression tag	UNP A4JZ28
A	586	TRP	-	expression tag	UNP A4JZ28
A	587	ARG	-	expression tag	UNP A4JZ28
A	588	GLY	-	expression tag	UNP A4JZ28
A	589	GLY	-	expression tag	UNP A4JZ28
A	590	HIS	-	expression tag	UNP A4JZ28
A	591	VAL	-	expression tag	UNP A4JZ28
A	592	VAL	-	expression tag	UNP A4JZ28
A	593	GLU	-	expression tag	UNP A4JZ28
A	594	GLY	-	expression tag	UNP A4JZ28

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Chain	Residue	Modelled	Actual	Comment	Reference
A	595	LEU	-	expression tag	UNP A4JZ28
A	596	ALA	-	expression tag	UNP A4JZ28
A	597	GLY	-	expression tag	UNP A4JZ28
A	598	GLU	-	expression tag	UNP A4JZ28
A	599	LEU	-	expression tag	UNP A4JZ28
A	600	GLU	-	expression tag	UNP A4JZ28
A	601	GLN	-	expression tag	UNP A4JZ28
A	602	LEU	-	expression tag	UNP A4JZ28
A	603	ARG	-	expression tag	UNP A4JZ28
A	604	ALA	-	expression tag	UNP A4JZ28
A	605	ARG	-	expression tag	UNP A4JZ28
A	606	LEU	-	expression tag	UNP A4JZ28
A	607	GLU	-	expression tag	UNP A4JZ28
A	608	HIS	-	expression tag	UNP A4JZ28
A	609	HIS	-	expression tag	UNP A4JZ28
A	610	PRO	-	expression tag	UNP A4JZ28
A	611	GLN	-	expression tag	UNP A4JZ28
A	612	GLY	-	expression tag	UNP A4JZ28
A	613	GLN	-	expression tag	UNP A4JZ28
A	614	ARG	-	expression tag	UNP A4JZ28
A	615	GLU	-	expression tag	UNP A4JZ28
A	616	PRO	-	expression tag	UNP A4JZ28
B	-21	MET	-	initiating methionine	UNP A4JZ28
B	-20	LYS	-	expression tag	UNP A4JZ28
B	-19	ARG	-	expression tag	UNP A4JZ28
B	-18	GLY	-	expression tag	UNP A4JZ28
B	-17	LEU	-	expression tag	UNP A4JZ28
B	-16	CYS	-	expression tag	UNP A4JZ28
B	-15	CYS	-	expression tag	UNP A4JZ28
B	-14	VAL	-	expression tag	UNP A4JZ28
B	-13	LEU	-	expression tag	UNP A4JZ28
B	-12	LEU	-	expression tag	UNP A4JZ28
B	-11	LEU	-	expression tag	UNP A4JZ28
B	-10	CYS	-	expression tag	UNP A4JZ28
B	-9	GLY	-	expression tag	UNP A4JZ28
B	-8	ALA	-	expression tag	UNP A4JZ28
B	-7	VAL	-	expression tag	UNP A4JZ28
B	-6	PHE	-	expression tag	UNP A4JZ28
B	-5	VAL	-	expression tag	UNP A4JZ28
B	-4	SER	-	expression tag	UNP A4JZ28
B	-3	PRO	-	expression tag	UNP A4JZ28
B	-2	SER	-	expression tag	UNP A4JZ28

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	ALA	-	expression tag	UNP A4JZ28
B	0	SER	-	expression tag	UNP A4JZ28
B	31	ASP	ASN	conflict	UNP A4JZ28
B	182	ILE	VAL	conflict	UNP A4JZ28
B	188	ASP	ASN	conflict	UNP A4JZ28
B	512	ALA	-	expression tag	UNP A4JZ28
B	513	GLY	-	expression tag	UNP A4JZ28
B	514	SER	-	expression tag	UNP A4JZ28
B	515	SER	-	expression tag	UNP A4JZ28
B	516	LEU	-	expression tag	UNP A4JZ28
B	517	GLU	-	expression tag	UNP A4JZ28
B	518	VAL	-	expression tag	UNP A4JZ28
B	519	LEU	-	expression tag	UNP A4JZ28
B	520	PHE	-	expression tag	UNP A4JZ28
B	521	GLN	-	expression tag	UNP A4JZ28
B	522	GLY	-	expression tag	UNP A4JZ28
B	523	PRO	-	expression tag	UNP A4JZ28
B	524	GLY	-	expression tag	UNP A4JZ28
B	525	SER	-	expression tag	UNP A4JZ28
B	526	GLY	-	expression tag	UNP A4JZ28
B	527	SER	-	expression tag	UNP A4JZ28
B	528	SER	-	expression tag	UNP A4JZ28
B	529	LEU	-	expression tag	UNP A4JZ28
B	530	GLY	-	expression tag	UNP A4JZ28
B	531	GLY	-	expression tag	UNP A4JZ28
B	532	SER	-	expression tag	UNP A4JZ28
B	533	GLY	-	expression tag	UNP A4JZ28
B	534	TYR	-	expression tag	UNP A4JZ28
B	535	ILE	-	expression tag	UNP A4JZ28
B	536	PRO	-	expression tag	UNP A4JZ28
B	537	GLU	-	expression tag	UNP A4JZ28
B	538	ALA	-	expression tag	UNP A4JZ28
B	539	PRO	-	expression tag	UNP A4JZ28
B	540	ARG	-	expression tag	UNP A4JZ28
B	541	ASP	-	expression tag	UNP A4JZ28
B	542	GLY	-	expression tag	UNP A4JZ28
B	543	GLN	-	expression tag	UNP A4JZ28
B	544	ALA	-	expression tag	UNP A4JZ28
B	545	TYR	-	expression tag	UNP A4JZ28
B	546	VAL	-	expression tag	UNP A4JZ28
B	547	ARG	-	expression tag	UNP A4JZ28
B	548	LYS	-	expression tag	UNP A4JZ28

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Chain	Residue	Modelled	Actual	Comment	Reference
B	549	ASP	-	expression tag	UNP A4JZ28
B	550	GLY	-	expression tag	UNP A4JZ28
B	551	GLU	-	expression tag	UNP A4JZ28
B	552	TRP	-	expression tag	UNP A4JZ28
B	553	VAL	-	expression tag	UNP A4JZ28
B	554	LEU	-	expression tag	UNP A4JZ28
B	555	LEU	-	expression tag	UNP A4JZ28
B	556	SER	-	expression tag	UNP A4JZ28
B	557	THR	-	expression tag	UNP A4JZ28
B	558	PHE	-	expression tag	UNP A4JZ28
B	559	LEU	-	expression tag	UNP A4JZ28
B	560	GLY	-	expression tag	UNP A4JZ28
B	561	SER	-	expression tag	UNP A4JZ28
B	562	GLY	-	expression tag	UNP A4JZ28
B	563	SER	-	expression tag	UNP A4JZ28
B	564	SER	-	expression tag	UNP A4JZ28
B	565	HIS	-	expression tag	UNP A4JZ28
B	566	HIS	-	expression tag	UNP A4JZ28
B	567	HIS	-	expression tag	UNP A4JZ28
B	568	HIS	-	expression tag	UNP A4JZ28
B	569	HIS	-	expression tag	UNP A4JZ28
B	570	HIS	-	expression tag	UNP A4JZ28
B	571	HIS	-	expression tag	UNP A4JZ28
B	572	HIS	-	expression tag	UNP A4JZ28
B	573	GLY	-	expression tag	UNP A4JZ28
B	574	GLY	-	expression tag	UNP A4JZ28
B	575	SER	-	expression tag	UNP A4JZ28
B	576	GLY	-	expression tag	UNP A4JZ28
B	577	SER	-	expression tag	UNP A4JZ28
B	578	SER	-	expression tag	UNP A4JZ28
B	579	MET	-	expression tag	UNP A4JZ28
B	580	ASP	-	expression tag	UNP A4JZ28
B	581	GLU	-	expression tag	UNP A4JZ28
B	582	LYS	-	expression tag	UNP A4JZ28
B	583	THR	-	expression tag	UNP A4JZ28
B	584	THR	-	expression tag	UNP A4JZ28
B	585	GLY	-	expression tag	UNP A4JZ28
B	586	TRP	-	expression tag	UNP A4JZ28
B	587	ARG	-	expression tag	UNP A4JZ28
B	588	GLY	-	expression tag	UNP A4JZ28
B	589	GLY	-	expression tag	UNP A4JZ28
B	590	HIS	-	expression tag	UNP A4JZ28

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Chain	Residue	Modelled	Actual	Comment	Reference
B	591	VAL	-	expression tag	UNP A4JZ28
B	592	VAL	-	expression tag	UNP A4JZ28
B	593	GLU	-	expression tag	UNP A4JZ28
B	594	GLY	-	expression tag	UNP A4JZ28
B	595	LEU	-	expression tag	UNP A4JZ28
B	596	ALA	-	expression tag	UNP A4JZ28
B	597	GLY	-	expression tag	UNP A4JZ28
B	598	GLU	-	expression tag	UNP A4JZ28
B	599	LEU	-	expression tag	UNP A4JZ28
B	600	GLU	-	expression tag	UNP A4JZ28
B	601	GLN	-	expression tag	UNP A4JZ28
B	602	LEU	-	expression tag	UNP A4JZ28
B	603	ARG	-	expression tag	UNP A4JZ28
B	604	ALA	-	expression tag	UNP A4JZ28
B	605	ARG	-	expression tag	UNP A4JZ28
B	606	LEU	-	expression tag	UNP A4JZ28
B	607	GLU	-	expression tag	UNP A4JZ28
B	608	HIS	-	expression tag	UNP A4JZ28
B	609	HIS	-	expression tag	UNP A4JZ28
B	610	PRO	-	expression tag	UNP A4JZ28
B	611	GLN	-	expression tag	UNP A4JZ28
B	612	GLY	-	expression tag	UNP A4JZ28
B	613	GLN	-	expression tag	UNP A4JZ28
B	614	ARG	-	expression tag	UNP A4JZ28
B	615	GLU	-	expression tag	UNP A4JZ28
B	616	PRO	-	expression tag	UNP A4JZ28
C	-21	MET	-	initiating methionine	UNP A4JZ28
C	-20	LYS	-	expression tag	UNP A4JZ28
C	-19	ARG	-	expression tag	UNP A4JZ28
C	-18	GLY	-	expression tag	UNP A4JZ28
C	-17	LEU	-	expression tag	UNP A4JZ28
C	-16	CYS	-	expression tag	UNP A4JZ28
C	-15	CYS	-	expression tag	UNP A4JZ28
C	-14	VAL	-	expression tag	UNP A4JZ28
C	-13	LEU	-	expression tag	UNP A4JZ28
C	-12	LEU	-	expression tag	UNP A4JZ28
C	-11	LEU	-	expression tag	UNP A4JZ28
C	-10	CYS	-	expression tag	UNP A4JZ28
C	-9	GLY	-	expression tag	UNP A4JZ28
C	-8	ALA	-	expression tag	UNP A4JZ28
C	-7	VAL	-	expression tag	UNP A4JZ28
C	-6	PHE	-	expression tag	UNP A4JZ28

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	VAL	-	expression tag	UNP A4JZ28
C	-4	SER	-	expression tag	UNP A4JZ28
C	-3	PRO	-	expression tag	UNP A4JZ28
C	-2	SER	-	expression tag	UNP A4JZ28
C	-1	ALA	-	expression tag	UNP A4JZ28
C	0	SER	-	expression tag	UNP A4JZ28
C	31	ASP	ASN	conflict	UNP A4JZ28
C	182	ILE	VAL	conflict	UNP A4JZ28
C	188	ASP	ASN	conflict	UNP A4JZ28
C	512	ALA	-	expression tag	UNP A4JZ28
C	513	GLY	-	expression tag	UNP A4JZ28
C	514	SER	-	expression tag	UNP A4JZ28
C	515	SER	-	expression tag	UNP A4JZ28
C	516	LEU	-	expression tag	UNP A4JZ28
C	517	GLU	-	expression tag	UNP A4JZ28
C	518	VAL	-	expression tag	UNP A4JZ28
C	519	LEU	-	expression tag	UNP A4JZ28
C	520	PHE	-	expression tag	UNP A4JZ28
C	521	GLN	-	expression tag	UNP A4JZ28
C	522	GLY	-	expression tag	UNP A4JZ28
C	523	PRO	-	expression tag	UNP A4JZ28
C	524	GLY	-	expression tag	UNP A4JZ28
C	525	SER	-	expression tag	UNP A4JZ28
C	526	GLY	-	expression tag	UNP A4JZ28
C	527	SER	-	expression tag	UNP A4JZ28
C	528	SER	-	expression tag	UNP A4JZ28
C	529	LEU	-	expression tag	UNP A4JZ28
C	530	GLY	-	expression tag	UNP A4JZ28
C	531	GLY	-	expression tag	UNP A4JZ28
C	532	SER	-	expression tag	UNP A4JZ28
C	533	GLY	-	expression tag	UNP A4JZ28
C	534	TYR	-	expression tag	UNP A4JZ28
C	535	ILE	-	expression tag	UNP A4JZ28
C	536	PRO	-	expression tag	UNP A4JZ28
C	537	GLU	-	expression tag	UNP A4JZ28
C	538	ALA	-	expression tag	UNP A4JZ28
C	539	PRO	-	expression tag	UNP A4JZ28
C	540	ARG	-	expression tag	UNP A4JZ28
C	541	ASP	-	expression tag	UNP A4JZ28
C	542	GLY	-	expression tag	UNP A4JZ28
C	543	GLN	-	expression tag	UNP A4JZ28
C	544	ALA	-	expression tag	UNP A4JZ28

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Chain	Residue	Modelled	Actual	Comment	Reference
C	545	TYR	-	expression tag	UNP A4JZ28
C	546	VAL	-	expression tag	UNP A4JZ28
C	547	ARG	-	expression tag	UNP A4JZ28
C	548	LYS	-	expression tag	UNP A4JZ28
C	549	ASP	-	expression tag	UNP A4JZ28
C	550	GLY	-	expression tag	UNP A4JZ28
C	551	GLU	-	expression tag	UNP A4JZ28
C	552	TRP	-	expression tag	UNP A4JZ28
C	553	VAL	-	expression tag	UNP A4JZ28
C	554	LEU	-	expression tag	UNP A4JZ28
C	555	LEU	-	expression tag	UNP A4JZ28
C	556	SER	-	expression tag	UNP A4JZ28
C	557	THR	-	expression tag	UNP A4JZ28
C	558	PHE	-	expression tag	UNP A4JZ28
C	559	LEU	-	expression tag	UNP A4JZ28
C	560	GLY	-	expression tag	UNP A4JZ28
C	561	SER	-	expression tag	UNP A4JZ28
C	562	GLY	-	expression tag	UNP A4JZ28
C	563	SER	-	expression tag	UNP A4JZ28
C	564	SER	-	expression tag	UNP A4JZ28
C	565	HIS	-	expression tag	UNP A4JZ28
C	566	HIS	-	expression tag	UNP A4JZ28
C	567	HIS	-	expression tag	UNP A4JZ28
C	568	HIS	-	expression tag	UNP A4JZ28
C	569	HIS	-	expression tag	UNP A4JZ28
C	570	HIS	-	expression tag	UNP A4JZ28
C	571	HIS	-	expression tag	UNP A4JZ28
C	572	HIS	-	expression tag	UNP A4JZ28
C	573	GLY	-	expression tag	UNP A4JZ28
C	574	GLY	-	expression tag	UNP A4JZ28
C	575	SER	-	expression tag	UNP A4JZ28
C	576	GLY	-	expression tag	UNP A4JZ28
C	577	SER	-	expression tag	UNP A4JZ28
C	578	SER	-	expression tag	UNP A4JZ28
C	579	MET	-	expression tag	UNP A4JZ28
C	580	ASP	-	expression tag	UNP A4JZ28
C	581	GLU	-	expression tag	UNP A4JZ28
C	582	LYS	-	expression tag	UNP A4JZ28
C	583	THR	-	expression tag	UNP A4JZ28
C	584	THR	-	expression tag	UNP A4JZ28
C	585	GLY	-	expression tag	UNP A4JZ28
C	586	TRP	-	expression tag	UNP A4JZ28

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Chain	Residue	Modelled	Actual	Comment	Reference
C	587	ARG	-	expression tag	UNP A4JZ28
C	588	GLY	-	expression tag	UNP A4JZ28
C	589	GLY	-	expression tag	UNP A4JZ28
C	590	HIS	-	expression tag	UNP A4JZ28
C	591	VAL	-	expression tag	UNP A4JZ28
C	592	VAL	-	expression tag	UNP A4JZ28
C	593	GLU	-	expression tag	UNP A4JZ28
C	594	GLY	-	expression tag	UNP A4JZ28
C	595	LEU	-	expression tag	UNP A4JZ28
C	596	ALA	-	expression tag	UNP A4JZ28
C	597	GLY	-	expression tag	UNP A4JZ28
C	598	GLU	-	expression tag	UNP A4JZ28
C	599	LEU	-	expression tag	UNP A4JZ28
C	600	GLU	-	expression tag	UNP A4JZ28
C	601	GLN	-	expression tag	UNP A4JZ28
C	602	LEU	-	expression tag	UNP A4JZ28
C	603	ARG	-	expression tag	UNP A4JZ28
C	604	ALA	-	expression tag	UNP A4JZ28
C	605	ARG	-	expression tag	UNP A4JZ28
C	606	LEU	-	expression tag	UNP A4JZ28
C	607	GLU	-	expression tag	UNP A4JZ28
C	608	HIS	-	expression tag	UNP A4JZ28
C	609	HIS	-	expression tag	UNP A4JZ28
C	610	PRO	-	expression tag	UNP A4JZ28
C	611	GLN	-	expression tag	UNP A4JZ28
C	612	GLY	-	expression tag	UNP A4JZ28
C	613	GLN	-	expression tag	UNP A4JZ28
C	614	ARG	-	expression tag	UNP A4JZ28
C	615	GLU	-	expression tag	UNP A4JZ28
C	616	PRO	-	expression tag	UNP A4JZ28

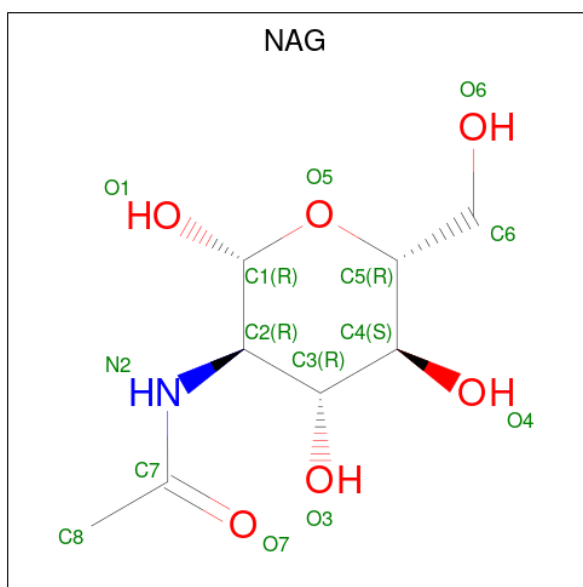
- Molecule 2 is a protein called FL-1086 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	221	Total	C	N	O	S	0	0
			1639	1035	271	326	7		
2	I	221	Total	C	N	O	S	0	0
			1639	1035	271	326	7		
2	J	221	Total	C	N	O	S	0	0
			1639	1035	271	326	7		

- Molecule 3 is a protein called FL-1086 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	213	Total	C	N	O	S	0	0
			1647	1035	271	335	6		
3	M	213	Total	C	N	O	S	0	0
			1647	1035	271	335	6		
3	N	213	Total	C	N	O	S	0	0
			1647	1035	271	335	6		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	

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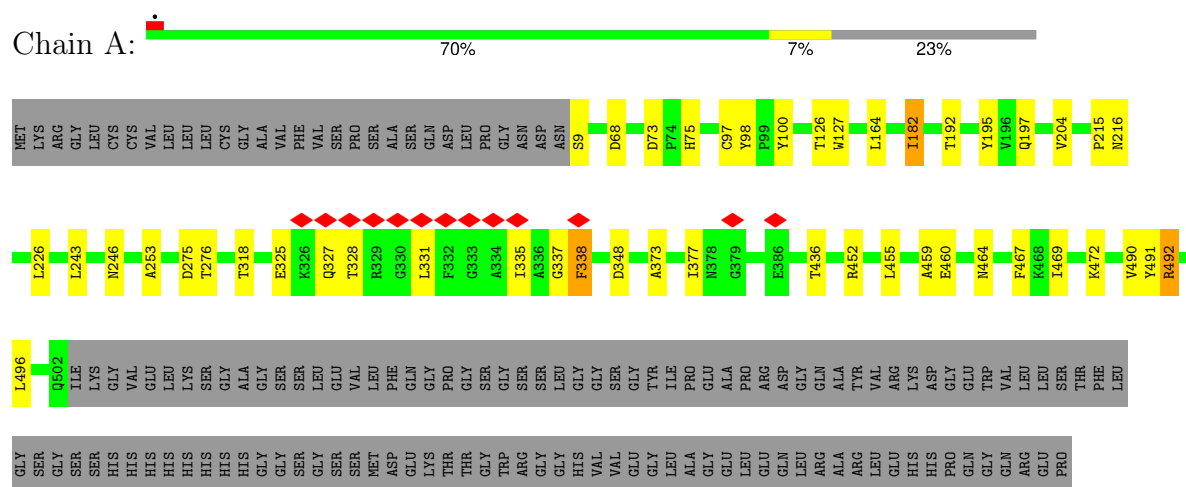
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Mol	Chain	Residues	Atoms				AltConf
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	

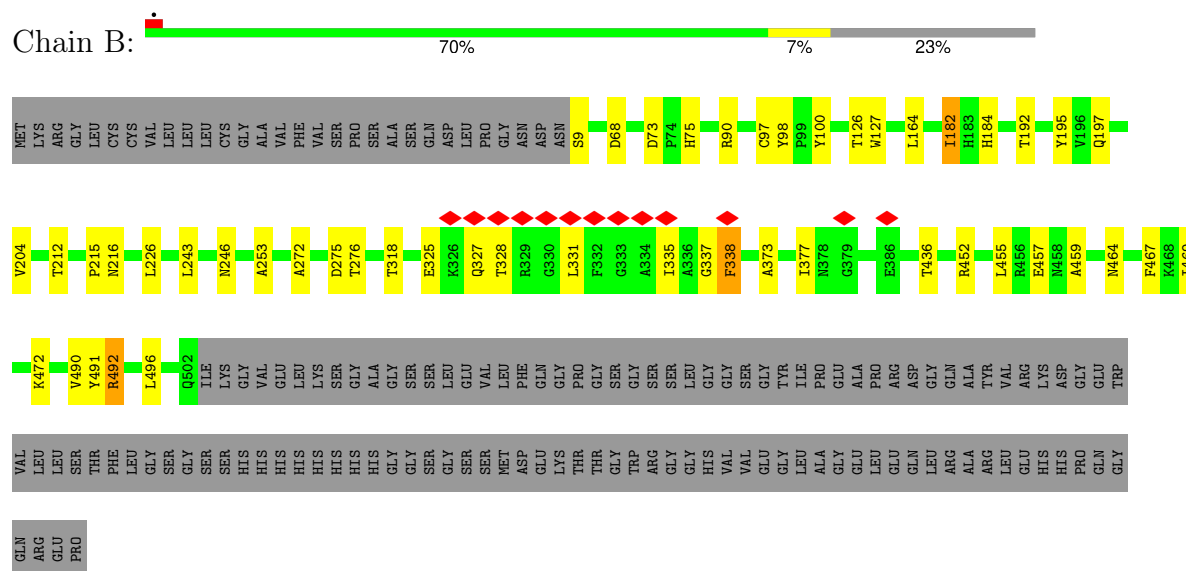
### 3 Residue-property plots

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: Hemagglutinin



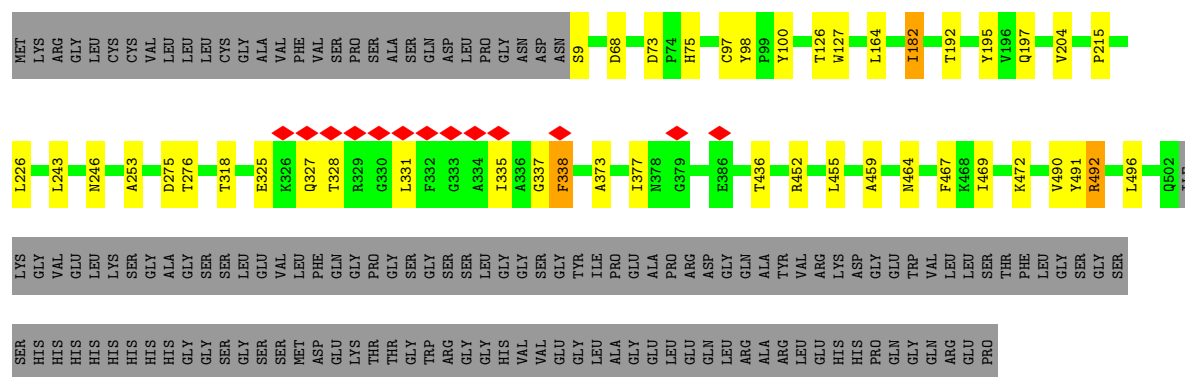
#### • Molecule 1: Hemagglutinin




#### • Molecule 1: Hemagglutinin

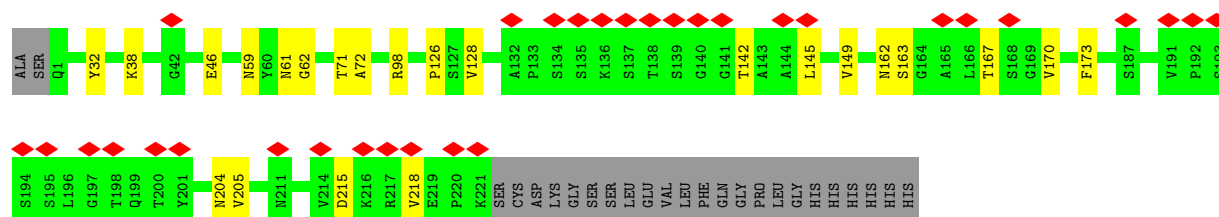


Chain C: 




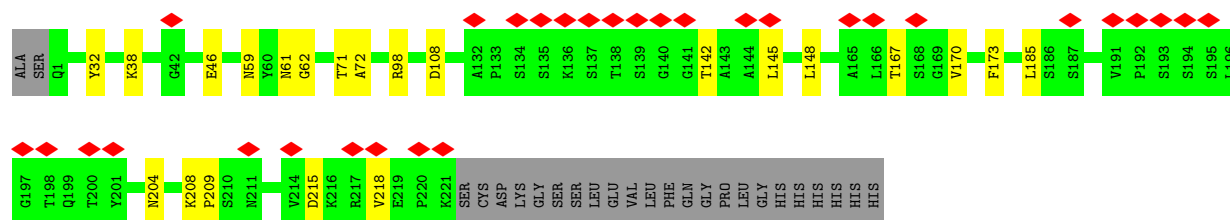
• Molecule 2: FL-1086 Fab heavy chain

Chain H: 




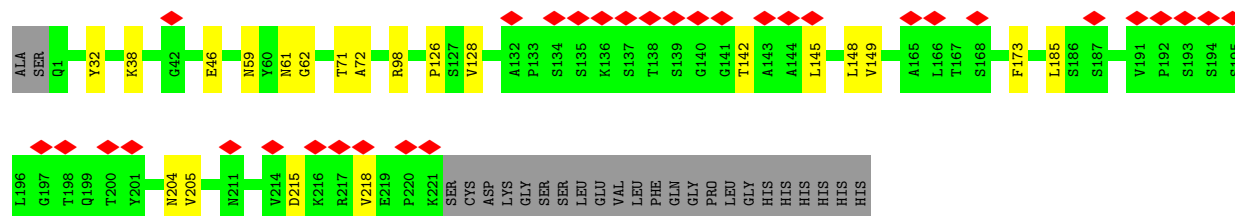
• Molecule 2: FL-1086 Fab heavy chain

Chain I: 




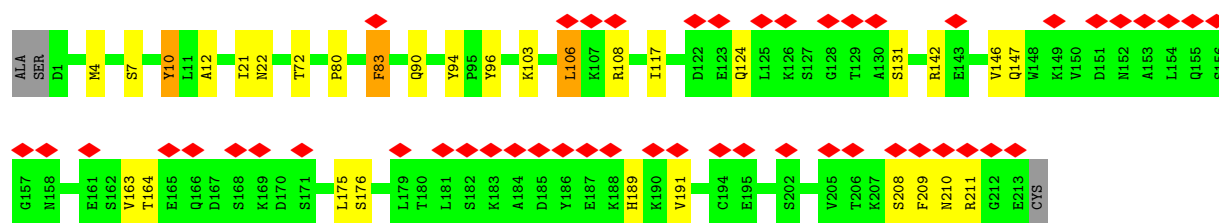
• Molecule 2: FL-1086 Fab heavy chain

Chain J: 




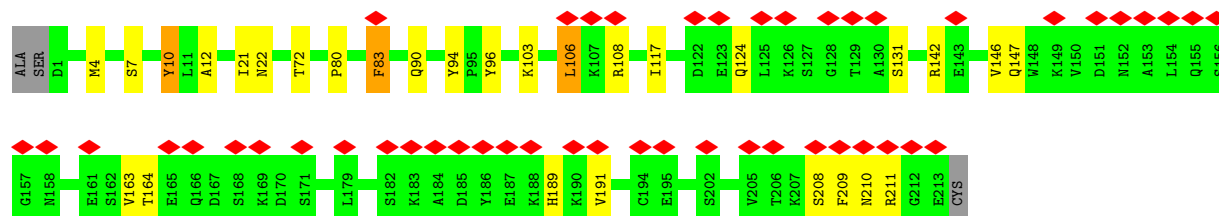
• Molecule 3: FL-1086 light chain

Chain L:  23% 84% 13% ..




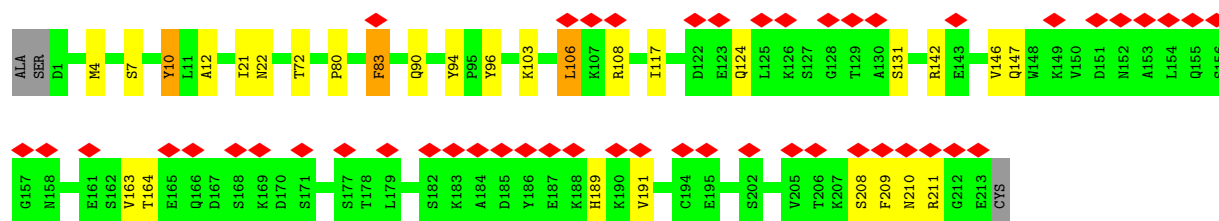
• Molecule 3: FL-1086 light chain

Chain M:  22% 85% 12% ..



• Molecule 3: FL-1086 light chain

Chain N:  23% 85% 12% ..



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	85028	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.2	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.089	Depositor
Minimum map value	-0.047	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	297.0, 297.0, 297.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	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: NAG

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	0.33	0/3961	0.52	0/5371
1	B	0.33	0/3961	0.52	0/5371
1	C	0.33	0/3961	0.52	0/5371
2	H	0.32	0/1680	0.49	0/2288
2	I	0.32	0/1680	0.49	0/2288
2	J	0.32	0/1680	0.49	0/2288
3	L	0.29	0/1684	0.50	0/2283
3	M	0.29	0/1684	0.50	0/2283
3	N	0.29	0/1684	0.50	0/2283
All	All	0.32	0/21975	0.51	0/29826

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	3880	0	3747	51	0
1	B	3880	0	3747	53	0
1	C	3880	0	3747	47	0
2	H	1639	0	1596	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	1639	0	1596	12	0
2	J	1639	0	1596	11	0
3	L	1647	0	1596	35	0
3	M	1647	0	1596	34	0
3	N	1647	0	1596	34	0
4	A	56	0	52	0	0
4	B	56	0	52	0	0
4	C	56	0	52	0	0
All	All	21666	0	20973	281	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.

All (281) 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:C:337:GLY:O	1:C:338:PHE:HD1	1.16	1.28
1:B:337:GLY:O	1:B:338:PHE:HD1	1.16	1.27
1:A:337:GLY:O	1:A:338:PHE:HD1	1.16	1.22
1:A:182:ILE:CD1	1:A:215:PRO:HG3	1.79	1.12
1:A:337:GLY:C	1:A:338:PHE:CD1	2.23	1.12
1:C:337:GLY:C	1:C:338:PHE:CD1	2.23	1.12
1:B:182:ILE:CD1	1:B:215:PRO:HG3	1.79	1.11
1:B:337:GLY:C	1:B:338:PHE:CD1	2.23	1.11
1:C:182:ILE:CD1	1:C:215:PRO:HG3	1.79	1.10
1:B:337:GLY:O	1:B:338:PHE:CD1	2.04	1.09
1:C:337:GLY:O	1:C:338:PHE:CD1	2.04	1.09
1:A:337:GLY:O	1:A:338:PHE:CD1	2.04	1.09
1:C:182:ILE:HD11	1:C:215:PRO:HG3	1.34	1.08
1:B:182:ILE:HD11	1:B:215:PRO:HG3	1.34	1.06
1:A:182:ILE:HD11	1:A:215:PRO:HG3	1.34	1.03
1:B:338:PHE:HB3	1:B:464:ASN:O	1.74	0.87
1:A:338:PHE:HB3	1:A:464:ASN:O	1.74	0.86
1:C:338:PHE:HB3	1:C:464:ASN:O	1.74	0.86
1:C:331:LEU:HD13	1:C:335:ILE:HG23	1.63	0.81
1:B:331:LEU:HD13	1:B:335:ILE:HG23	1.63	0.81
1:A:331:LEU:HD13	1:A:335:ILE:HG23	1.63	0.80
3:M:80:PRO:O	3:M:83:PHE:CD1	2.39	0.76
3:L:80:PRO:O	3:L:83:PHE:CD1	2.39	0.74
3:N:80:PRO:O	3:N:83:PHE:CD1	2.39	0.74
3:N:83:PHE:HD2	3:N:106:LEU:HD12	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:83:PHE:HD2	3:L:106:LEU:HD12	1.53	0.73
3:M:83:PHE:HD2	3:M:106:LEU:HD12	1.54	0.72
1:C:331:LEU:HD13	1:C:335:ILE:CG2	2.21	0.71
1:B:331:LEU:HD13	1:B:335:ILE:CG2	2.21	0.71
3:M:10:TYR:HD2	3:M:142:ARG:HH21	1.40	0.70
1:A:331:LEU:HD13	1:A:335:ILE:CG2	2.21	0.70
1:C:182:ILE:CD1	1:C:215:PRO:CG	2.66	0.70
1:C:182:ILE:HD13	1:C:215:PRO:HG3	1.74	0.69
1:A:182:ILE:HD11	1:A:215:PRO:CG	2.19	0.69
1:A:182:ILE:HD13	1:A:215:PRO:HG3	1.74	0.69
3:L:10:TYR:HD2	3:L:142:ARG:HH21	1.40	0.69
1:C:182:ILE:HD11	1:C:215:PRO:CG	2.19	0.69
3:M:106:LEU:C	3:M:106:LEU:HD22	2.14	0.69
3:N:106:LEU:C	3:N:106:LEU:HD22	2.13	0.69
1:B:182:ILE:HD11	1:B:215:PRO:CG	2.19	0.68
1:A:182:ILE:CD1	1:A:215:PRO:CG	2.66	0.68
3:L:106:LEU:C	3:L:106:LEU:HD22	2.13	0.68
1:C:338:PHE:CB	1:C:464:ASN:O	2.42	0.67
3:N:10:TYR:HD2	3:N:142:ARG:HH21	1.40	0.67
3:N:80:PRO:O	3:N:83:PHE:CE1	2.48	0.67
3:L:80:PRO:O	3:L:83:PHE:CE1	2.48	0.67
1:B:338:PHE:CB	1:B:464:ASN:O	2.42	0.67
1:A:338:PHE:CB	1:A:464:ASN:O	2.42	0.66
3:L:12:ALA:HB1	3:L:108:ARG:HG3	1.78	0.66
3:M:80:PRO:O	3:M:83:PHE:CE1	2.48	0.66
1:B:331:LEU:CD1	1:B:335:ILE:HG23	2.26	0.65
1:B:182:ILE:HD13	1:B:215:PRO:HG3	1.74	0.65
3:M:12:ALA:HB1	3:M:108:ARG:HG3	1.79	0.64
3:N:12:ALA:HB1	3:N:108:ARG:HG3	1.78	0.64
1:C:331:LEU:CD1	1:C:335:ILE:HG23	2.27	0.64
3:N:106:LEU:HD13	3:N:106:LEU:H	1.63	0.64
1:C:73:ASP:OD2	1:C:75:HIS:ND1	2.31	0.63
1:A:331:LEU:CD1	1:A:335:ILE:HG23	2.27	0.63
3:M:106:LEU:HD13	3:M:106:LEU:H	1.63	0.63
1:A:73:ASP:OD2	1:A:75:HIS:ND1	2.31	0.63
1:B:275:ASP:OD1	1:B:276:THR:N	2.32	0.63
3:L:106:LEU:HD13	3:L:106:LEU:H	1.63	0.63
3:N:142:ARG:O	3:N:142:ARG:HG2	1.99	0.63
1:A:275:ASP:OD1	1:A:276:THR:N	2.32	0.62
1:B:182:ILE:CD1	1:B:215:PRO:CG	2.66	0.62
3:L:142:ARG:O	3:L:142:ARG:HG2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:ASP:OD2	1:B:75:HIS:ND1	2.31	0.62
3:M:142:ARG:O	3:M:142:ARG:HG2	1.99	0.62
1:C:275:ASP:OD1	1:C:276:THR:N	2.32	0.61
1:C:337:GLY:N	1:C:338:PHE:CE1	2.69	0.61
1:B:337:GLY:N	1:B:338:PHE:CE1	2.69	0.61
1:A:337:GLY:N	1:A:338:PHE:CE1	2.69	0.61
1:B:455:LEU:HD13	1:B:459:ALA:CB	2.32	0.60
1:A:455:LEU:HD13	1:A:459:ALA:CB	2.32	0.59
1:A:68:ASP:OD1	1:A:100:TYR:OH	2.20	0.59
1:C:68:ASP:OD1	1:C:100:TYR:OH	2.20	0.59
3:M:124:GLN:OE1	3:M:131:SER:OG	2.20	0.59
1:C:455:LEU:HD13	1:C:459:ALA:CB	2.31	0.59
2:H:145:LEU:HD21	2:H:218:VAL:HB	1.85	0.59
2:I:145:LEU:HD21	2:I:218:VAL:HB	1.85	0.58
2:J:145:LEU:HD21	2:J:218:VAL:HB	1.84	0.58
1:C:492:ARG:O	1:C:496:LEU:HD23	2.05	0.57
1:B:492:ARG:O	1:B:496:LEU:HD23	2.05	0.57
3:L:10:TYR:HD2	3:L:142:ARG:NH2	2.02	0.57
3:M:10:TYR:HD2	3:M:142:ARG:NH2	2.02	0.57
1:B:338:PHE:CD1	1:B:338:PHE:N	2.73	0.57
3:N:124:GLN:OE1	3:N:131:SER:OG	2.20	0.56
1:C:338:PHE:CD1	1:C:338:PHE:N	2.73	0.56
3:N:106:LEU:HD13	3:N:106:LEU:N	2.21	0.56
3:N:10:TYR:HD2	3:N:142:ARG:NH2	2.02	0.56
1:A:338:PHE:CD1	1:A:338:PHE:N	2.73	0.55
1:A:492:ARG:O	1:A:496:LEU:HD23	2.05	0.55
3:L:106:LEU:HD13	3:L:106:LEU:N	2.21	0.55
1:B:68:ASP:OD1	1:B:100:TYR:OH	2.20	0.55
1:A:455:LEU:HB3	1:A:459:ALA:HB3	1.88	0.55
3:M:106:LEU:HD13	3:M:106:LEU:N	2.21	0.55
1:B:455:LEU:HB3	1:B:459:ALA:HB3	1.88	0.54
1:A:318:THR:O	1:A:318:THR:HG22	2.08	0.54
1:A:452:ARG:HB2	1:A:467:PHE:CZ	2.43	0.54
1:C:318:THR:O	1:C:318:THR:HG22	2.08	0.54
1:B:318:THR:HG22	1:B:318:THR:O	2.08	0.54
1:B:184:HIS:HD1	1:B:216:ASN:H	1.56	0.53
3:L:22:ASN:OD1	3:L:72:THR:HG22	2.09	0.53
1:C:452:ARG:HB2	1:C:467:PHE:CZ	2.43	0.53
1:C:455:LEU:HB3	1:C:459:ALA:HB3	1.88	0.53
1:B:452:ARG:HB2	1:B:467:PHE:CZ	2.43	0.53
1:A:455:LEU:HD13	1:A:459:ALA:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:455:LEU:HD13	1:B:469:ILE:CD1	2.39	0.53
2:I:61:ASN:OD1	2:I:62:GLY:N	2.42	0.53
3:L:124:GLN:OE1	3:L:131:SER:OG	2.20	0.53
3:N:22:ASN:OD1	3:N:72:THR:HG22	2.09	0.53
1:C:455:LEU:HD13	1:C:469:ILE:CD1	2.39	0.53
2:J:61:ASN:OD1	2:J:62:GLY:N	2.42	0.53
2:H:61:ASN:OD1	2:H:62:GLY:N	2.42	0.52
1:C:455:LEU:HD13	1:C:459:ALA:HB2	1.91	0.52
3:M:22:ASN:OD1	3:M:72:THR:HG22	2.09	0.52
1:A:455:LEU:HD13	1:A:469:ILE:CD1	2.39	0.52
1:B:455:LEU:HD13	1:B:459:ALA:HB2	1.91	0.52
3:L:10:TYR:CD2	3:L:142:ARG:NH2	2.77	0.52
3:L:106:LEU:N	3:L:106:LEU:CD1	2.73	0.52
2:I:38:LYS:O	2:I:46:GLU:N	2.41	0.52
3:L:189:HIS:O	3:L:211:ARG:NH1	2.44	0.51
2:H:38:LYS:O	2:H:46:GLU:N	2.41	0.51
3:M:189:HIS:O	3:M:211:ARG:NH1	2.44	0.51
3:N:106:LEU:N	3:N:106:LEU:CD1	2.73	0.51
3:N:189:HIS:O	3:N:211:ARG:NH1	2.44	0.51
1:B:459:ALA:HB2	1:B:469:ILE:HD13	1.93	0.51
1:C:327:GLN:O	1:C:328:THR:OG1	2.27	0.51
3:M:106:LEU:N	3:M:106:LEU:CD1	2.73	0.51
1:C:9:SER:N	1:C:472:LYS:HZ1	2.09	0.51
1:A:459:ALA:HB2	1:A:469:ILE:HD13	1.93	0.50
1:B:9:SER:N	1:B:472:LYS:HZ1	2.08	0.50
1:A:9:SER:N	1:A:472:LYS:HZ1	2.09	0.50
3:L:83:PHE:HD2	3:L:106:LEU:CD1	2.24	0.50
1:C:459:ALA:HB2	1:C:469:ILE:HD13	1.93	0.50
3:M:10:TYR:CD2	3:M:142:ARG:NH2	2.77	0.50
3:N:10:TYR:C	3:N:10:TYR:HD1	2.15	0.50
3:L:10:TYR:C	3:L:10:TYR:HD1	2.15	0.49
1:B:97:CYS:SG	1:B:98:TYR:N	2.84	0.49
1:C:97:CYS:SG	1:C:98:TYR:N	2.84	0.49
2:J:38:LYS:O	2:J:46:GLU:N	2.41	0.49
3:N:10:TYR:C	3:N:10:TYR:CD1	2.86	0.49
3:M:10:TYR:HD1	3:M:10:TYR:C	2.15	0.49
3:M:10:TYR:C	3:M:10:TYR:CD1	2.86	0.49
3:L:10:TYR:C	3:L:10:TYR:CD1	2.86	0.48
3:M:83:PHE:HD2	3:M:106:LEU:CD1	2.24	0.48
1:C:455:LEU:CD1	1:C:469:ILE:HD11	2.44	0.47
2:H:204:ASN:OD1	2:H:215:ASP:OD1	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:204:ASN:OD1	2:I:215:ASP:OD1	2.32	0.47
1:A:455:LEU:CD1	1:A:469:ILE:HD11	2.43	0.47
1:B:455:LEU:CD1	1:B:469:ILE:HD11	2.43	0.47
2:I:59:ASN:HB3	3:M:94:TYR:OH	2.15	0.47
1:A:97:CYS:SG	1:A:98:TYR:N	2.84	0.47
1:C:98:TYR:CE1	1:C:226:LEU:HD13	2.50	0.47
2:J:204:ASN:OD1	2:J:215:ASP:OD1	2.33	0.47
1:A:98:TYR:CE1	1:A:226:LEU:HD13	2.50	0.47
2:J:59:ASN:HB3	3:N:94:TYR:OH	2.15	0.47
3:N:83:PHE:CD1	3:N:83:PHE:N	2.83	0.47
3:N:83:PHE:HD2	3:N:106:LEU:CD1	2.24	0.47
2:H:59:ASN:HB3	3:L:94:TYR:OH	2.15	0.47
1:B:98:TYR:CE1	1:B:226:LEU:HD13	2.50	0.46
3:L:83:PHE:CD1	3:L:83:PHE:N	2.83	0.46
3:M:83:PHE:CD1	3:M:83:PHE:N	2.83	0.46
1:C:197:GLN:OE1	1:C:197:GLN:N	2.47	0.46
1:A:455:LEU:HD13	1:A:469:ILE:HD11	1.98	0.46
1:A:73:ASP:OD1	1:A:97:CYS:HB2	2.16	0.46
1:C:204:VAL:CG1	1:C:243:LEU:HD11	2.46	0.46
3:N:10:TYR:CD2	3:N:142:ARG:NH2	2.77	0.46
1:C:492:ARG:HG3	1:C:496:LEU:HD23	1.98	0.45
1:B:73:ASP:OD1	1:B:97:CYS:HB2	2.16	0.45
1:A:492:ARG:HG3	1:A:496:LEU:HD23	1.98	0.45
1:B:197:GLN:OE1	1:B:197:GLN:N	2.47	0.45
1:A:127:TRP:CZ2	1:A:253:ALA:HB1	2.52	0.45
1:B:204:VAL:CG1	1:B:243:LEU:HD11	2.46	0.45
1:A:204:VAL:CG1	1:A:243:LEU:HD11	2.46	0.45
1:A:373:ALA:O	1:A:377:ILE:HG12	2.17	0.45
3:L:117:ILE:HD12	3:L:209:PHE:HD2	1.82	0.45
1:B:373:ALA:O	1:B:377:ILE:HG12	2.17	0.45
1:B:455:LEU:HD13	1:B:469:ILE:HD11	1.98	0.45
1:C:455:LEU:HD13	1:C:469:ILE:HD11	1.98	0.45
3:M:146:VAL:HG12	3:M:147:GLN:N	2.32	0.45
3:L:146:VAL:HG12	3:L:147:GLN:N	2.32	0.45
3:M:94:TYR:O	3:M:96:TYR:N	2.50	0.45
3:N:94:TYR:O	3:N:96:TYR:N	2.50	0.45
1:B:492:ARG:HG3	1:B:496:LEU:HD23	1.98	0.45
3:L:94:TYR:O	3:L:96:TYR:N	2.50	0.45
1:A:197:GLN:OE1	1:A:197:GLN:N	2.47	0.44
1:B:127:TRP:CZ2	1:B:253:ALA:HB1	2.52	0.44
1:C:73:ASP:OD1	1:C:97:CYS:HB2	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:373:ALA:O	1:C:377:ILE:HG12	2.17	0.44
3:M:117:ILE:HD12	3:M:209:PHE:HD2	1.82	0.44
3:M:83:PHE:CD1	3:M:83:PHE:O	2.71	0.44
1:B:327:GLN:O	1:B:328:THR:OG1	2.27	0.44
3:L:83:PHE:N	3:L:83:PHE:HD1	2.16	0.44
3:N:83:PHE:CD1	3:N:83:PHE:O	2.70	0.44
3:N:117:ILE:HD12	3:N:209:PHE:HD2	1.82	0.44
3:N:146:VAL:HG12	3:N:147:GLN:N	2.32	0.44
1:C:328:THR:HB	1:C:331:LEU:O	2.18	0.44
1:B:328:THR:HB	1:B:331:LEU:O	2.18	0.44
2:J:173:PHE:CD2	3:N:164:THR:HG23	2.53	0.44
3:M:106:LEU:HD22	3:M:106:LEU:O	2.18	0.44
2:J:71:THR:HG22	2:J:72:ALA:N	2.33	0.44
3:N:106:LEU:C	3:N:106:LEU:CD2	2.86	0.44
1:C:490:VAL:HG23	1:C:491:TYR:CE1	2.53	0.43
2:I:71:THR:HG22	2:I:72:ALA:N	2.33	0.43
2:I:108:ASP:OD1	2:I:108:ASP:N	2.51	0.43
2:I:173:PHE:CD2	3:M:164:THR:HG23	2.53	0.43
1:A:490:VAL:HG23	1:A:491:TYR:CE1	2.53	0.43
3:L:83:PHE:CD1	3:L:83:PHE:O	2.71	0.43
3:M:83:PHE:N	3:M:83:PHE:HD1	2.16	0.43
1:B:126:THR:HG23	1:B:126:THR:O	2.19	0.43
1:B:490:VAL:HG23	1:B:491:TYR:CE1	2.54	0.43
1:C:127:TRP:CZ2	1:C:253:ALA:HB1	2.52	0.43
2:H:173:PHE:CD2	3:L:164:THR:HG23	2.53	0.43
1:C:126:THR:HG23	1:C:126:THR:O	2.19	0.43
3:N:83:PHE:N	3:N:83:PHE:HD1	2.16	0.43
2:H:71:THR:HG22	2:H:72:ALA:N	2.33	0.43
3:N:83:PHE:O	3:N:83:PHE:CG	2.72	0.43
1:A:126:THR:HG23	1:A:126:THR:O	2.19	0.43
1:A:328:THR:HB	1:A:331:LEU:O	2.18	0.43
3:L:106:LEU:HD22	3:L:106:LEU:O	2.18	0.43
3:M:191:VAL:HG22	3:M:210:ASN:OD1	2.19	0.43
3:M:83:PHE:O	3:M:83:PHE:CG	2.72	0.43
1:A:9:SER:CA	1:A:472:LYS:HZ1	2.32	0.42
1:B:331:LEU:CD1	1:B:335:ILE:CG2	2.92	0.42
1:C:164:LEU:O	1:C:246:ASN:HA	2.19	0.42
3:N:106:LEU:HD22	3:N:106:LEU:O	2.18	0.42
3:L:83:PHE:O	3:L:83:PHE:CG	2.72	0.42
3:M:117:ILE:HD11	3:M:208:SER:C	2.40	0.42
3:N:191:VAL:HG22	3:N:210:ASN:OD1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:LEU:O	1:B:246:ASN:HA	2.19	0.42
1:C:377:ILE:CD1	1:C:436:THR:HG23	2.50	0.42
2:I:32:TYR:CD2	2:I:98:ARG:HD3	2.55	0.42
2:J:32:TYR:CD2	2:J:98:ARG:HD3	2.54	0.42
3:L:163:VAL:HG12	3:L:164:THR:N	2.34	0.42
3:M:4:MET:HE1	3:M:90:GLN:HB3	2.01	0.42
1:B:192:THR:HA	1:B:195:TYR:O	2.20	0.42
3:L:191:VAL:HG22	3:L:210:ASN:OD1	2.19	0.42
3:M:163:VAL:HG12	3:M:164:THR:N	2.35	0.42
3:N:163:VAL:HG12	3:N:164:THR:N	2.34	0.42
2:H:32:TYR:CD2	2:H:98:ARG:HD3	2.54	0.42
3:N:117:ILE:HD11	3:N:208:SER:C	2.40	0.42
3:N:4:MET:CE	3:N:90:GLN:HB3	2.50	0.42
1:B:377:ILE:CD1	1:B:436:THR:HG23	2.50	0.42
1:C:192:THR:HA	1:C:195:TYR:O	2.20	0.42
3:L:4:MET:CE	3:L:90:GLN:HB3	2.50	0.42
3:L:7:SER:O	3:L:21:ILE:HD12	2.20	0.42
3:M:4:MET:CE	3:M:90:GLN:HB3	2.50	0.42
1:A:164:LEU:O	1:A:246:ASN:HA	2.19	0.41
1:C:9:SER:CA	1:C:472:LYS:HZ1	2.32	0.41
3:L:106:LEU:C	3:L:106:LEU:CD2	2.86	0.41
3:L:117:ILE:HD11	3:L:208:SER:C	2.40	0.41
3:M:7:SER:O	3:M:21:ILE:HD12	2.20	0.41
1:A:327:GLN:O	1:A:328:THR:OG1	2.27	0.41
1:B:9:SER:CA	1:B:472:LYS:HZ1	2.32	0.41
1:B:325:GLU:HG2	1:B:325:GLU:O	2.21	0.41
3:N:7:SER:O	3:N:21:ILE:HD12	2.20	0.41
1:A:325:GLU:O	1:A:325:GLU:HG2	2.21	0.41
1:B:90:ARG:NH1	1:B:272:ALA:O	2.47	0.41
3:L:175:LEU:HD23	3:L:176:SER:N	2.36	0.41
1:A:377:ILE:CD1	1:A:436:THR:HG23	2.50	0.41
1:C:325:GLU:O	1:C:325:GLU:HG2	2.21	0.41
1:A:192:THR:HA	1:A:195:TYR:O	2.20	0.41
2:H:128:VAL:HG21	2:H:205:VAL:HG11	2.03	0.41
2:H:162:ASN:O	2:H:163:SER:OG	2.35	0.41
1:A:460:GLU:OE2	1:B:457:GLU:HG2	2.21	0.41
2:J:126:PRO:HB2	2:J:149:VAL:HG13	2.03	0.41
2:J:128:VAL:HG21	2:J:205:VAL:HG11	2.03	0.41
1:B:452:ARG:HB2	1:B:467:PHE:HZ	1.85	0.41
1:A:348:ASP:OD1	1:A:348:ASP:N	2.53	0.40
1:A:459:ALA:HB2	1:A:469:ILE:CD1	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:459:ALA:HB2	1:C:469:ILE:CD1	2.51	0.40
2:I:148:LEU:HD12	2:I:185:LEU:O	2.22	0.40
1:B:459:ALA:HB2	1:B:469:ILE:CD1	2.51	0.40
2:H:126:PRO:HB2	2:H:149:VAL:HG13	2.03	0.40
2:H:167:THR:O	2:H:170:VAL:HG12	2.22	0.40
1:A:216:ASN:HB3	1:B:212:THR:HG21	2.03	0.40
1:A:452:ARG:HB2	1:A:467:PHE:HZ	1.85	0.40
2:I:167:THR:O	2:I:170:VAL:HG12	2.22	0.40
2:I:208:LYS:N	2:I:209:PRO:HD2	2.37	0.40
2:J:148:LEU:HD12	2:J:185:LEU:O	2.22	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	491/637 (77%)	472 (96%)	19 (4%)	0	100	100
1	B	491/637 (77%)	472 (96%)	19 (4%)	0	100	100
1	C	491/637 (77%)	472 (96%)	19 (4%)	0	100	100
2	H	219/246 (89%)	216 (99%)	3 (1%)	0	100	100
2	I	219/246 (89%)	216 (99%)	3 (1%)	0	100	100
2	J	219/246 (89%)	216 (99%)	3 (1%)	0	100	100
3	L	211/216 (98%)	200 (95%)	11 (5%)	0	100	100
3	M	211/216 (98%)	200 (95%)	11 (5%)	0	100	100
3	N	211/216 (98%)	200 (95%)	11 (5%)	0	100	100
All	All	2763/3297 (84%)	2664 (96%)	99 (4%)	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	430/542 (79%)	427 (99%)	3 (1%)	81	88
1	B	430/542 (79%)	427 (99%)	3 (1%)	81	88
1	C	430/542 (79%)	427 (99%)	3 (1%)	81	88
2	H	180/201 (90%)	179 (99%)	1 (1%)	84	90
2	I	180/201 (90%)	179 (99%)	1 (1%)	84	90
2	J	180/201 (90%)	179 (99%)	1 (1%)	84	90
3	L	187/189 (99%)	183 (98%)	4 (2%)	48	70
3	M	187/189 (99%)	183 (98%)	4 (2%)	48	70
3	N	187/189 (99%)	183 (98%)	4 (2%)	48	70
All	All	2391/2796 (86%)	2367 (99%)	24 (1%)	71	84

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	182	ILE
1	A	338	PHE
1	A	492	ARG
1	B	182	ILE
1	B	338	PHE
1	B	492	ARG
1	C	182	ILE
1	C	338	PHE
1	C	492	ARG
2	H	142	THR
2	I	142	THR
2	J	142	THR
3	L	10	TYR
3	L	83	PHE
3	L	103	LYS
3	L	106	LEU
3	M	10	TYR
3	M	83	PHE

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Mol	Chain	Res	Type
3	M	103	LYS
3	M	106	LEU
3	N	10	TYR
3	N	83	PHE
3	N	103	LYS
3	N	106	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	341	ASN
1	B	341	ASN
1	B	435	HIS
1	C	341	ASN
1	C	435	HIS
3	L	147	GLN
3	L	152	ASN
3	M	147	GLN
3	M	152	ASN
3	N	147	GLN
3	N	152	ASN

### 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 ⓘ

12 ligands are modelled in this entry.

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	NAG	C	701	1	14,14,15	0.17	0	17,19,21	0.44	0
4	NAG	B	704	1	14,14,15	0.17	0	17,19,21	0.42	0
4	NAG	A	704	1	14,14,15	0.17	0	17,19,21	0.42	0
4	NAG	C	704	1	14,14,15	0.18	0	17,19,21	0.43	0
4	NAG	B	701	1	14,14,15	0.17	0	17,19,21	0.44	0
4	NAG	C	703	1	14,14,15	0.24	0	17,19,21	0.42	0
4	NAG	C	702	1	14,14,15	0.35	0	17,19,21	1.99	4 (23%)
4	NAG	A	702	1	14,14,15	0.35	0	17,19,21	1.99	4 (23%)
4	NAG	A	701	1	14,14,15	0.16	0	17,19,21	0.44	0
4	NAG	A	703	1	14,14,15	0.24	0	17,19,21	0.43	0
4	NAG	B	703	1	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	B	702	1	14,14,15	0.35	0	17,19,21	2.00	4 (23%)

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	NAG	C	701	1	-	0/6/23/26	0/1/1/1
4	NAG	B	704	1	-	0/6/23/26	0/1/1/1
4	NAG	A	704	1	-	0/6/23/26	0/1/1/1
4	NAG	C	704	1	-	0/6/23/26	0/1/1/1
4	NAG	B	701	1	-	0/6/23/26	0/1/1/1
4	NAG	C	703	1	-	0/6/23/26	0/1/1/1
4	NAG	C	702	1	-	1/6/23/26	0/1/1/1
4	NAG	A	702	1	-	1/6/23/26	0/1/1/1
4	NAG	A	701	1	-	0/6/23/26	0/1/1/1
4	NAG	A	703	1	-	0/6/23/26	0/1/1/1
4	NAG	B	703	1	-	0/6/23/26	0/1/1/1
4	NAG	B	702	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
4	C	702	NAG	O4-C4-C5	4.63	120.73	109.32
4	A	702	NAG	O4-C4-C5	4.62	120.70	109.32
4	B	702	NAG	O4-C4-C5	4.62	120.69	109.32
4	B	702	NAG	C1-C2-N2	4.49	117.50	110.43
4	A	702	NAG	C1-C2-N2	4.47	117.47	110.43
4	C	702	NAG	C1-C2-N2	4.46	117.46	110.43
4	A	702	NAG	O4-C4-C3	3.76	119.23	110.38
4	B	702	NAG	O4-C4-C3	3.75	119.23	110.38
4	C	702	NAG	O4-C4-C3	3.74	119.20	110.38
4	B	702	NAG	C3-C4-C5	3.13	115.91	110.23
4	A	702	NAG	C3-C4-C5	3.11	115.88	110.23
4	C	702	NAG	C3-C4-C5	3.11	115.87	110.23

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	702	NAG	O5-C5-C6-O6
4	B	702	NAG	O5-C5-C6-O6
4	C	702	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

## 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.



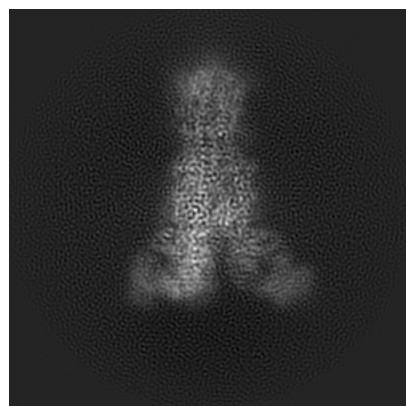
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29737. These allow visual inspection of the internal detail of the map and identification of artifacts.

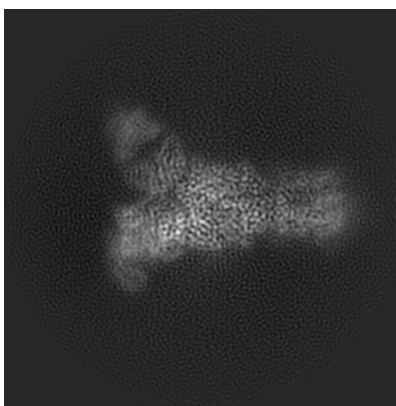
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

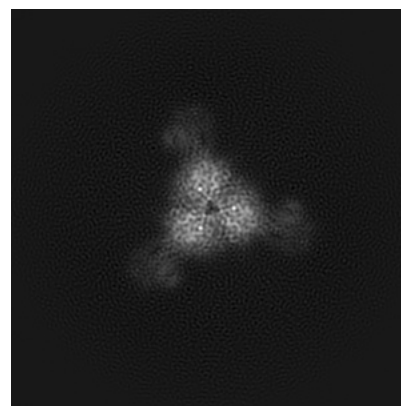
#### 6.1.1 Primary map



X

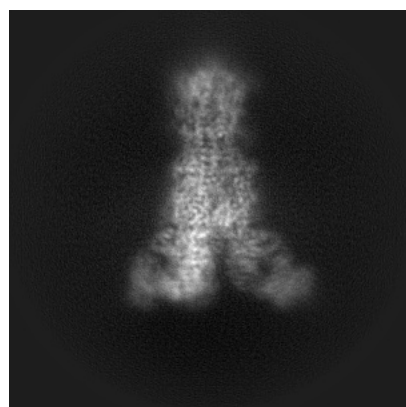


Y

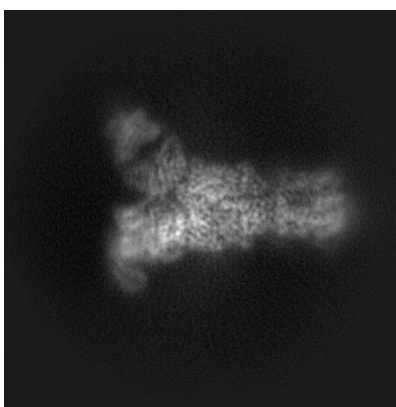


Z

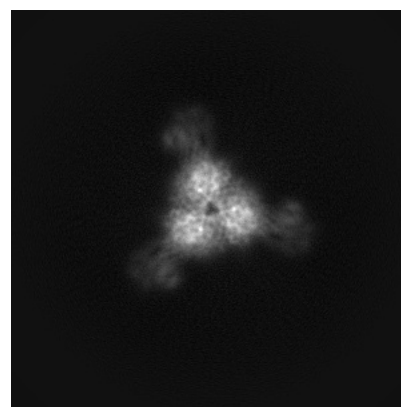
#### 6.1.2 Raw map



X



Y

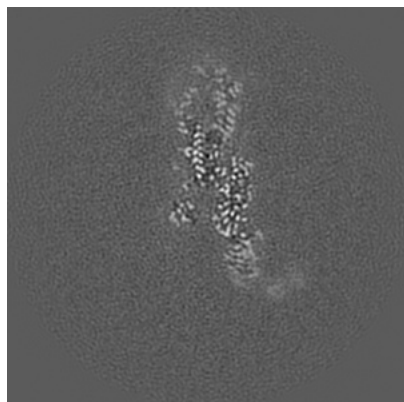


Z

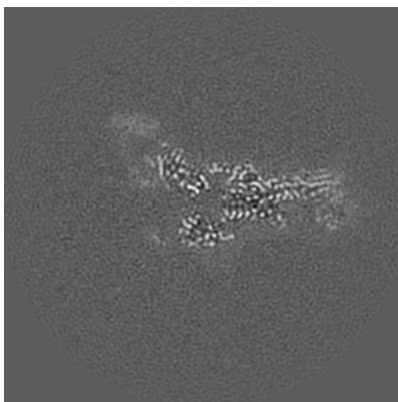
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

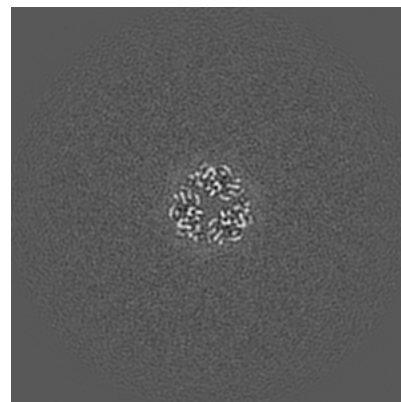
### 6.2.1 Primary map



X Index: 180

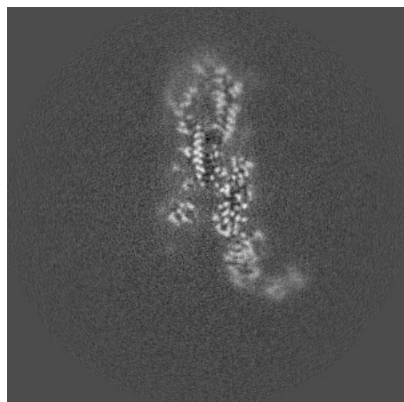


Y Index: 180

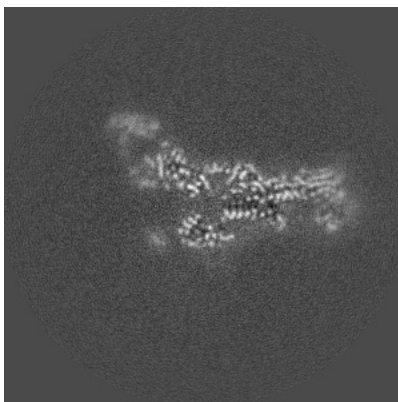


Z Index: 180

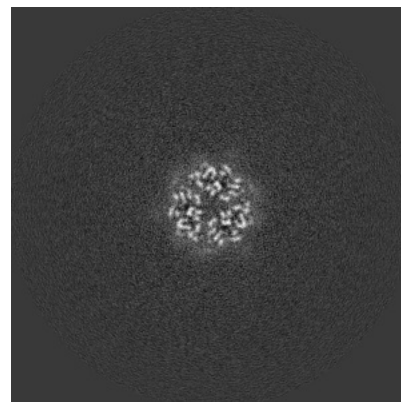
### 6.2.2 Raw map



X Index: 180



Y Index: 180

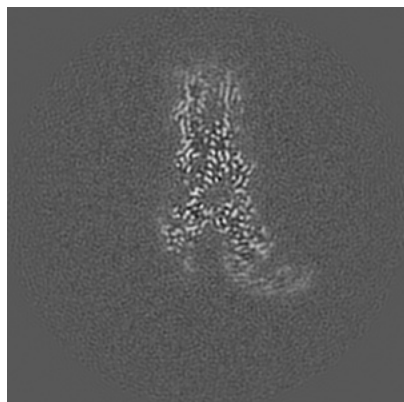


Z Index: 180

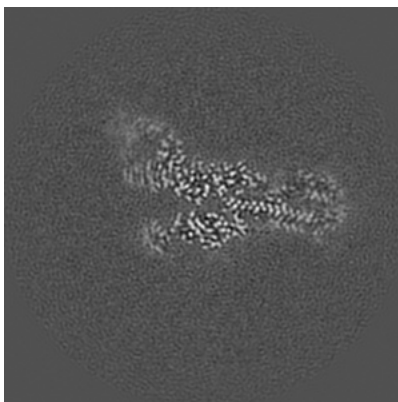
The images above show central slices of the map in three orthogonal directions.

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

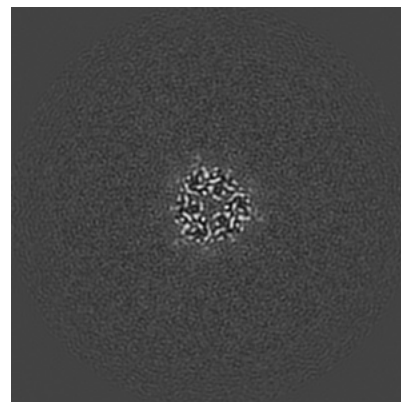
### 6.3.1 Primary map



X Index: 170

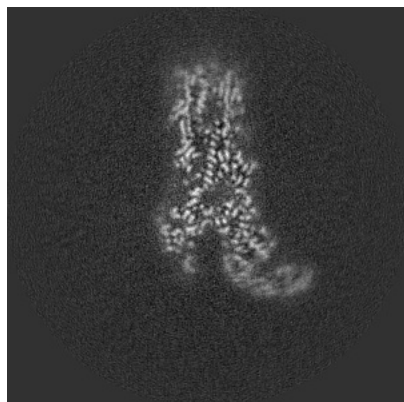


Y Index: 172

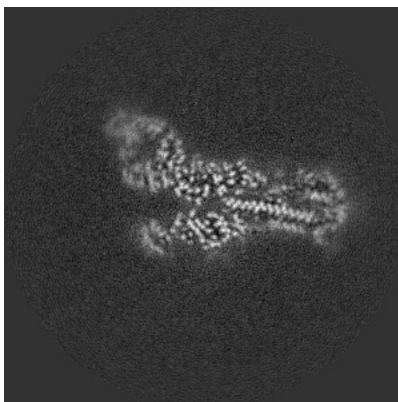


Z Index: 174

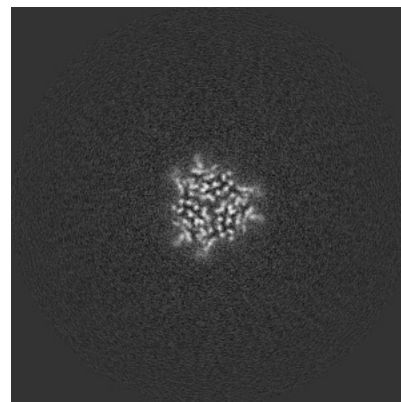
### 6.3.2 Raw map



X Index: 170



Y Index: 172

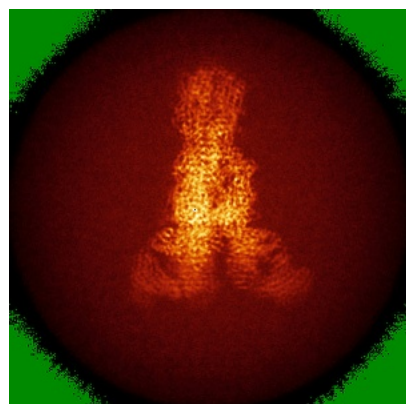


Z Index: 170

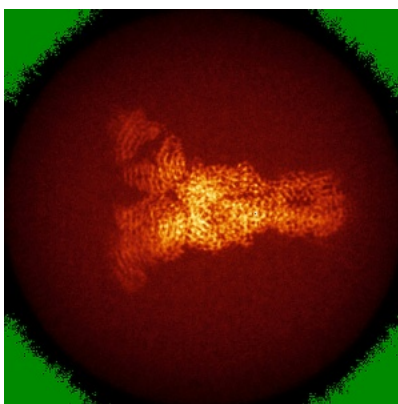
The images above show the largest variance slices of the map in three orthogonal directions.

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

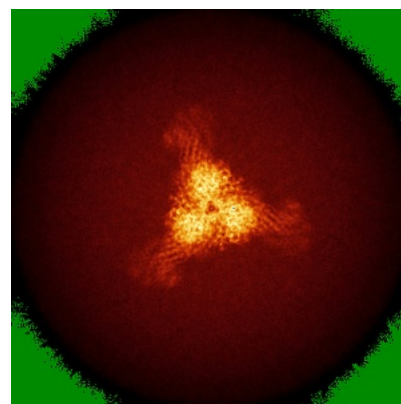
### 6.4.1 Primary map



X

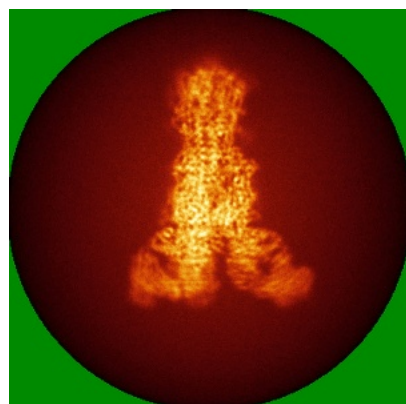


Y

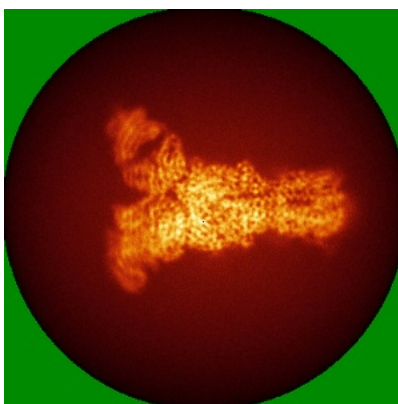


Z

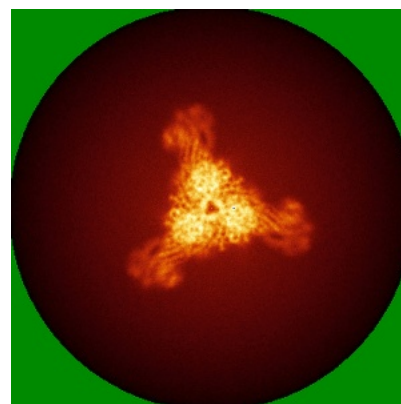
### 6.4.2 Raw map



X



Y



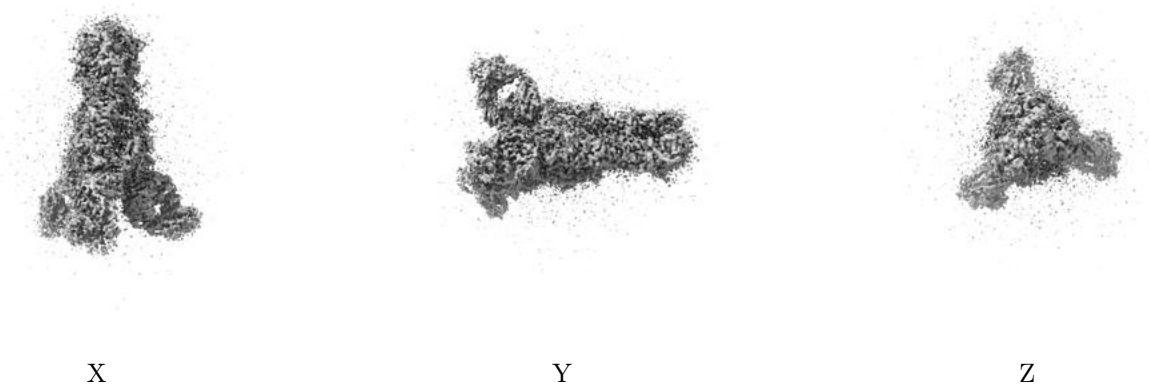
Z

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.



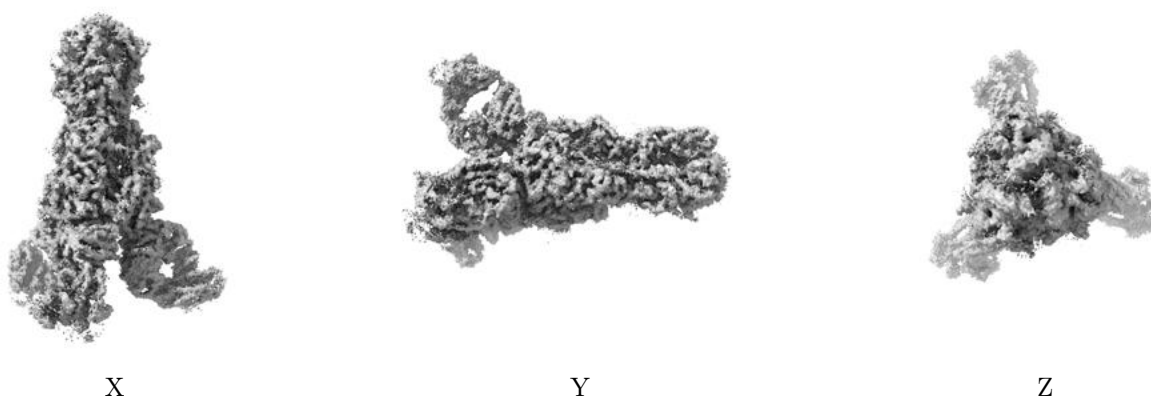
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.012. 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.

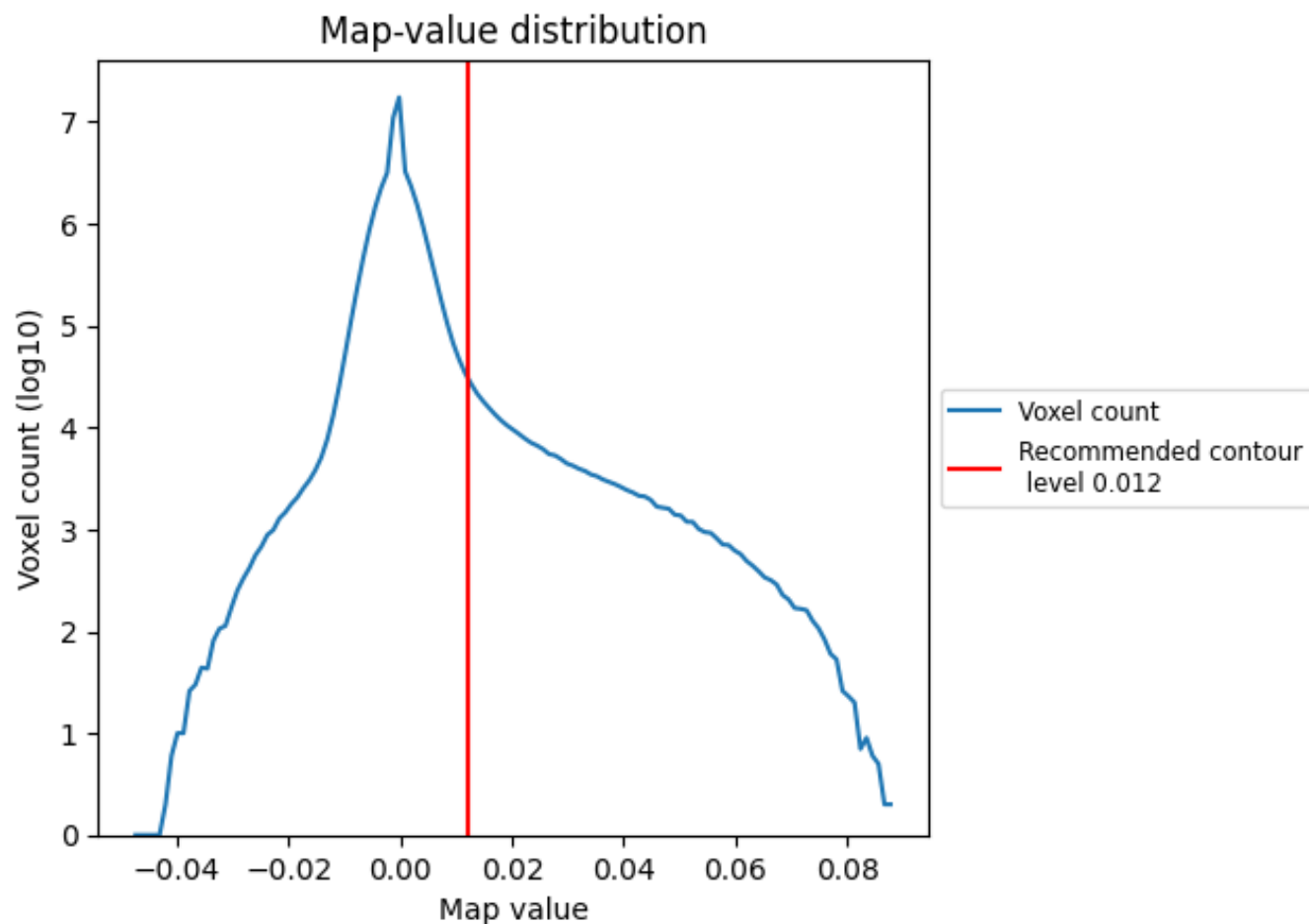
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

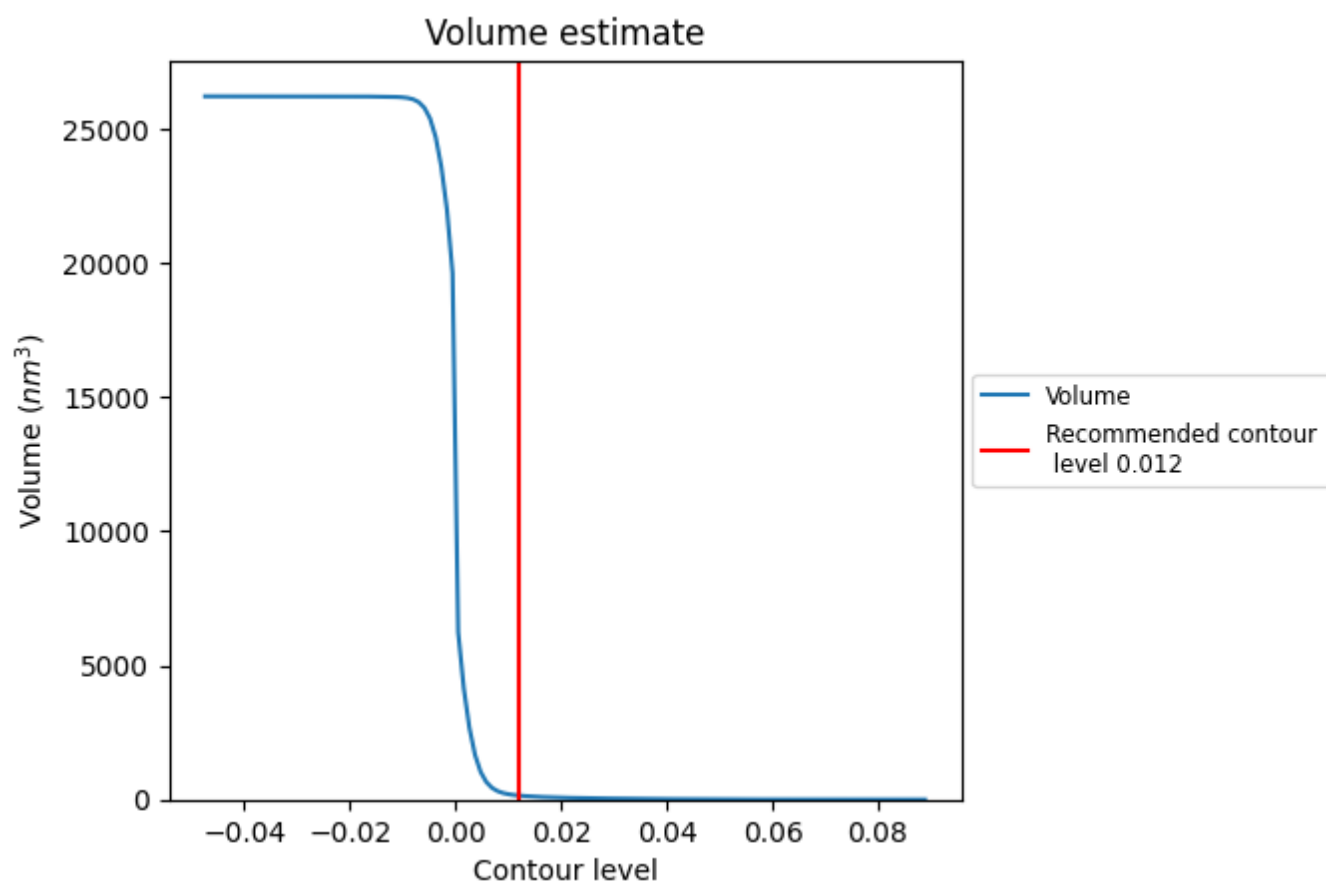
This section contains the results of statistical analysis of the map.

### 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.

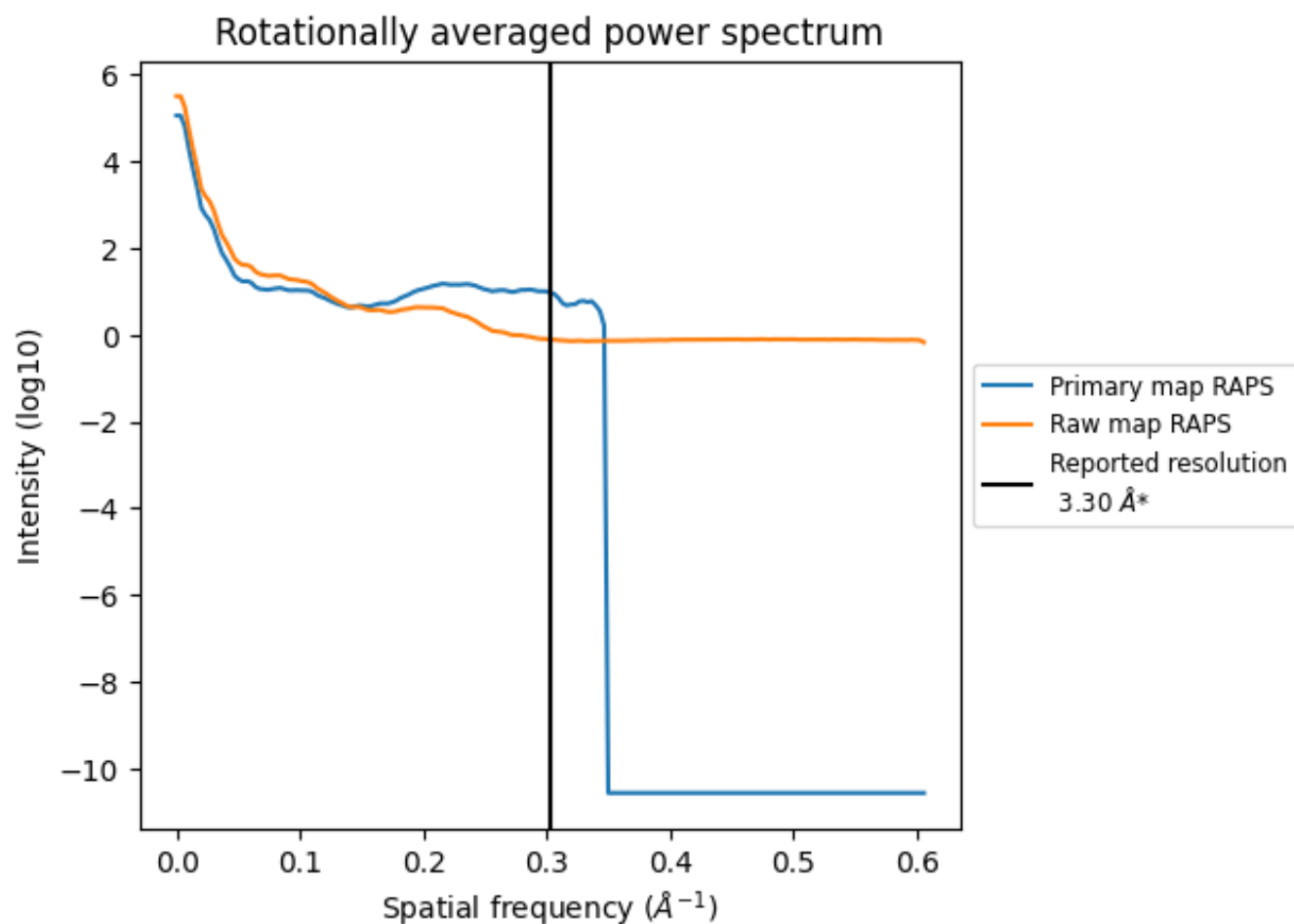
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 150  $\text{nm}^3$ ; this corresponds to an approximate mass of 136 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 ⓘ



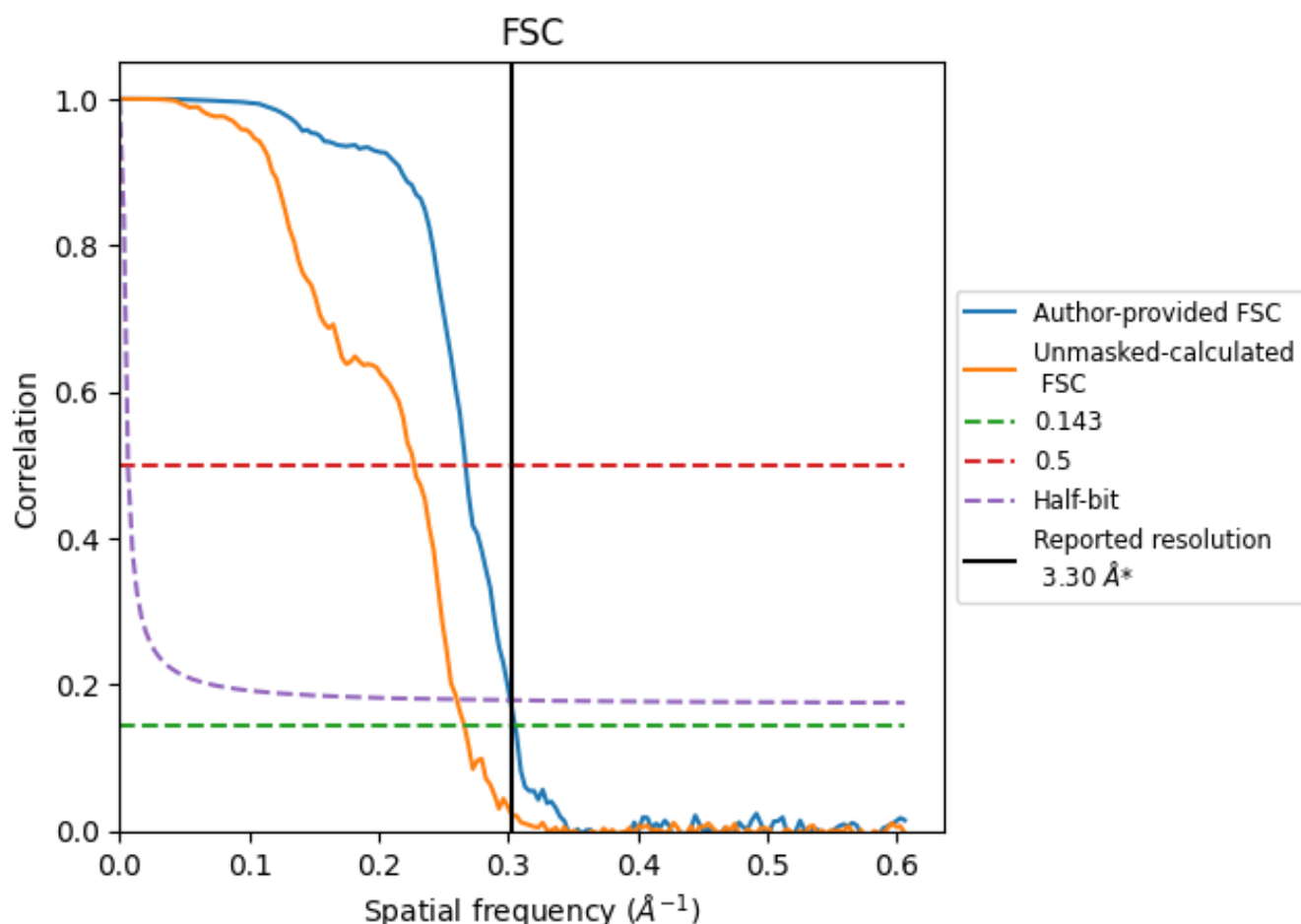
\*Reported resolution corresponds to spatial frequency of 0.303  $\text{\AA}^{-1}$



## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

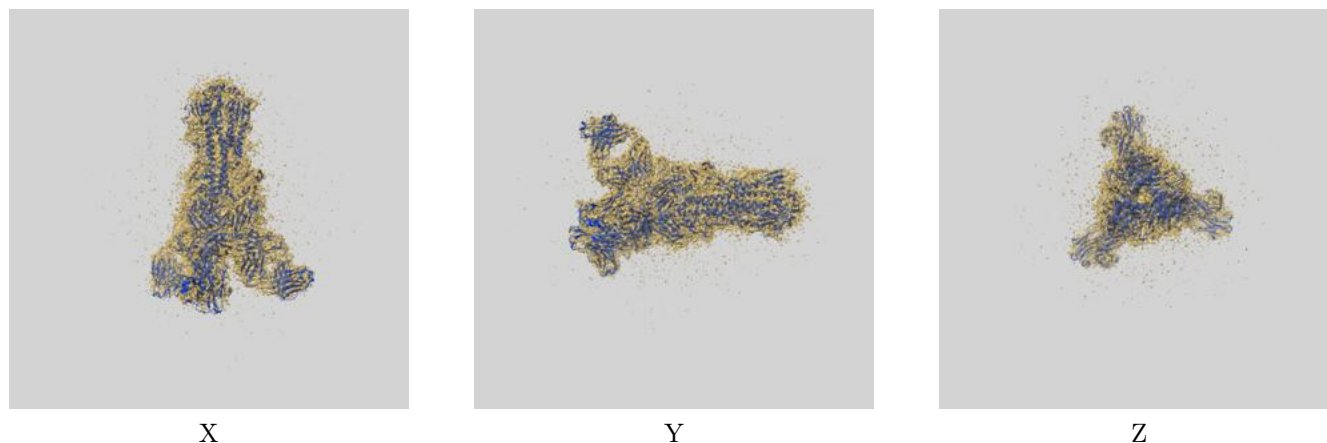
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.28	3.74	3.32
Unmasked-calculated*	3.76	4.40	3.84

\*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 3.76 differs from the reported value 3.3 by more than 10 %

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

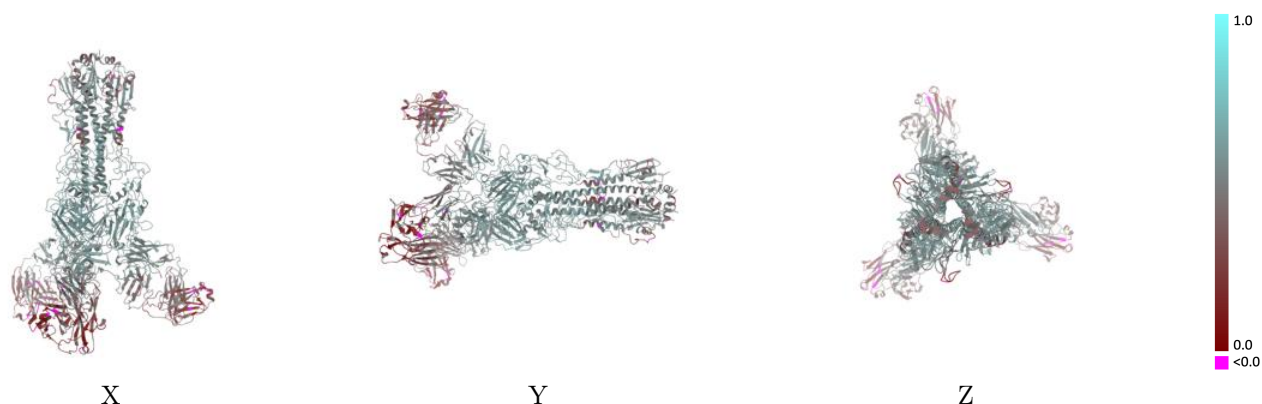
This section contains information regarding the fit between EMDB map EMD-29737 and PDB model 8G5A. Per-residue inclusion information can be found in section 3 on page 16.

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



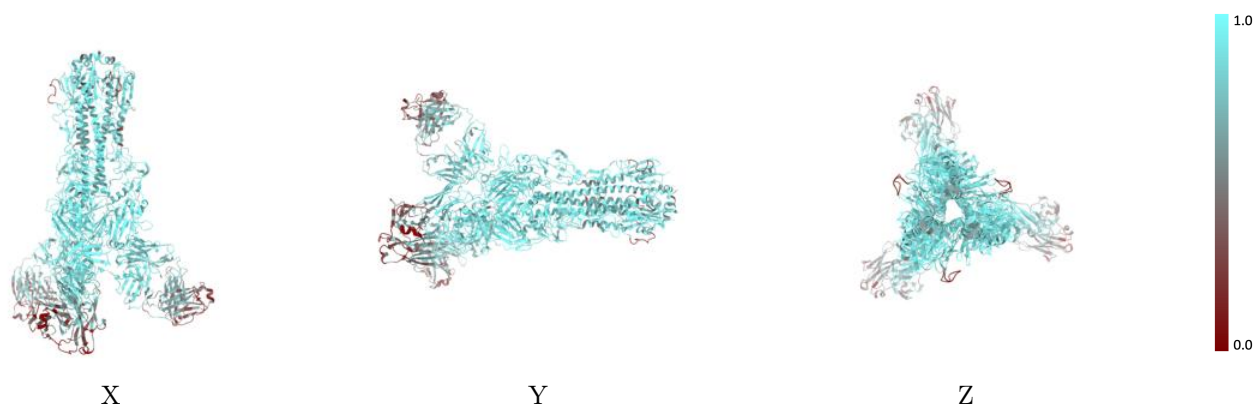
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



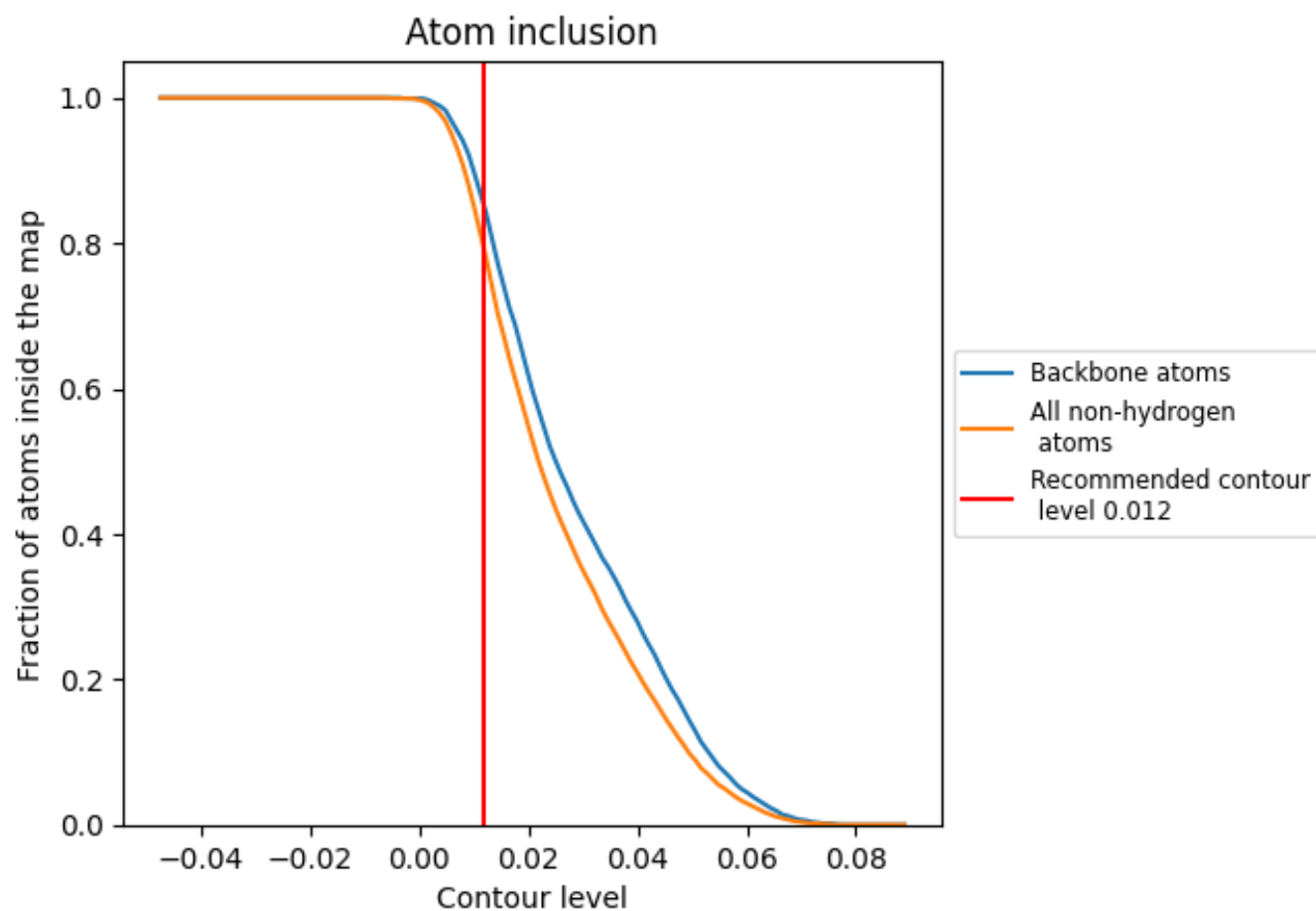
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.012).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 79% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7880	<div></div> 0.4770
A	<div></div> 0.8800	<div></div> 0.5400
B	<div></div> 0.8800	<div></div> 0.5390
C	<div></div> 0.8830	<div></div> 0.5390
H	<div></div> 0.7230	<div></div> 0.4420
I	<div></div> 0.7250	<div></div> 0.4420
J	<div></div> 0.7200	<div></div> 0.4430
L	<div></div> 0.6320	<div></div> 0.3640
M	<div></div> 0.6300	<div></div> 0.3660
N	<div></div> 0.6300	<div></div> 0.3640

1.0

0.0

<0.0