



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 01:21 AM UTC

PDB ID : 8IK0 / pdb_00008ik0
EMDB ID : EMD-35503
Title : Cryo-EM structure of Stimulator of interferon genes
Authors : Lu, D.F.; Shang, G.J.
Deposited on : 2023-02-28
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

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:

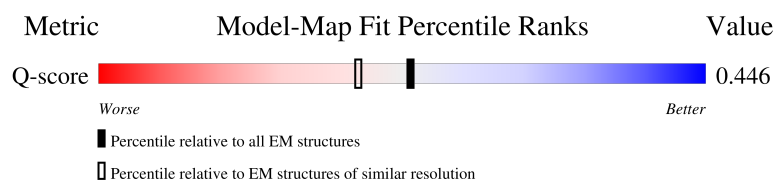
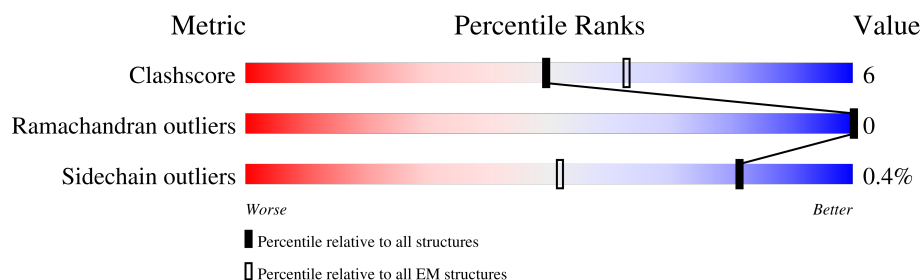
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	490	6% 58% 8% 35%
1	B	490	7% 57% 9% 35%
1	C	490	8% 56% 9% 35%
1	D	490	6% 56% 9% 35%

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Mol	Chain	Length	Quality of chain
1	E	490	
1	F	490	
1	G	490	
1	H	490	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 19536 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 Stimulator of interferon genes protein, Immune protein Tsi3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	319	Total	C	N	O	S	0	0
			2435	1563	428	425	19		
1	B	320	Total	C	N	O	S	0	0
			2449	1571	431	429	18		
1	C	319	Total	C	N	O	S	0	0
			2435	1563	428	425	19		
1	F	320	Total	C	N	O	S	0	0
			2449	1571	431	429	18		
1	D	319	Total	C	N	O	S	0	0
			2435	1563	428	425	19		
1	G	320	Total	C	N	O	S	0	0
			2449	1571	431	429	18		
1	E	319	Total	C	N	O	S	0	0
			2435	1563	428	425	19		
1	H	320	Total	C	N	O	S	0	0
			2449	1571	431	429	18		

There are 224 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	THR	ILE	conflict	UNP E1C7U0
A	52	ARG	SER	conflict	UNP E1C7U0
A	100	HIS	TYR	conflict	UNP E1C7U0
A	187	ILE	LEU	conflict	UNP E1C7U0
A	343	ARG	-	linker	UNP E1C7U0
A	344	GLU	-	linker	UNP E1C7U0
A	345	GLU	-	linker	UNP E1C7U0
A	346	TYR	-	linker	UNP E1C7U0
A	347	MET	-	linker	UNP E1C7U0
A	348	VAL	-	linker	UNP E1C7U0
A	349	LEU	-	linker	UNP E1C7U0
A	350	GLU	-	linker	UNP E1C7U0
A	351	VAL	-	linker	UNP E1C7U0
A	352	LEU	-	linker	UNP E1C7U0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	353	PHE	-	linker	UNP E1C7U0
A	354	GLN	-	linker	UNP E1C7U0
A	355	GLY	-	linker	UNP E1C7U0
A	356	PRO	-	linker	UNP E1C7U0
A	481	SER	-	expression tag	UNP Q9HYC4
A	482	SER	-	expression tag	UNP Q9HYC4
A	483	HIS	-	expression tag	UNP Q9HYC4
A	484	HIS	-	expression tag	UNP Q9HYC4
A	485	HIS	-	expression tag	UNP Q9HYC4
A	486	HIS	-	expression tag	UNP Q9HYC4
A	487	HIS	-	expression tag	UNP Q9HYC4
A	488	HIS	-	expression tag	UNP Q9HYC4
A	489	HIS	-	expression tag	UNP Q9HYC4
A	490	HIS	-	expression tag	UNP Q9HYC4
B	50	THR	ILE	conflict	UNP E1C7U0
B	52	ARG	SER	conflict	UNP E1C7U0
B	100	HIS	TYR	conflict	UNP E1C7U0
B	187	ILE	LEU	conflict	UNP E1C7U0
B	343	ARG	-	linker	UNP E1C7U0
B	344	GLU	-	linker	UNP E1C7U0
B	345	GLU	-	linker	UNP E1C7U0
B	346	TYR	-	linker	UNP E1C7U0
B	347	MET	-	linker	UNP E1C7U0
B	348	VAL	-	linker	UNP E1C7U0
B	349	LEU	-	linker	UNP E1C7U0
B	350	GLU	-	linker	UNP E1C7U0
B	351	VAL	-	linker	UNP E1C7U0
B	352	LEU	-	linker	UNP E1C7U0
B	353	PHE	-	linker	UNP E1C7U0
B	354	GLN	-	linker	UNP E1C7U0
B	355	GLY	-	linker	UNP E1C7U0
B	356	PRO	-	linker	UNP E1C7U0
B	481	SER	-	expression tag	UNP Q9HYC4
B	482	SER	-	expression tag	UNP Q9HYC4
B	483	HIS	-	expression tag	UNP Q9HYC4
B	484	HIS	-	expression tag	UNP Q9HYC4
B	485	HIS	-	expression tag	UNP Q9HYC4
B	486	HIS	-	expression tag	UNP Q9HYC4
B	487	HIS	-	expression tag	UNP Q9HYC4
B	488	HIS	-	expression tag	UNP Q9HYC4
B	489	HIS	-	expression tag	UNP Q9HYC4
B	490	HIS	-	expression tag	UNP Q9HYC4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	50	THR	ILE	conflict	UNP E1C7U0
C	52	ARG	SER	conflict	UNP E1C7U0
C	100	HIS	TYR	conflict	UNP E1C7U0
C	187	ILE	LEU	conflict	UNP E1C7U0
C	343	ARG	-	linker	UNP E1C7U0
C	344	GLU	-	linker	UNP E1C7U0
C	345	GLU	-	linker	UNP E1C7U0
C	346	TYR	-	linker	UNP E1C7U0
C	347	MET	-	linker	UNP E1C7U0
C	348	VAL	-	linker	UNP E1C7U0
C	349	LEU	-	linker	UNP E1C7U0
C	350	GLU	-	linker	UNP E1C7U0
C	351	VAL	-	linker	UNP E1C7U0
C	352	LEU	-	linker	UNP E1C7U0
C	353	PHE	-	linker	UNP E1C7U0
C	354	GLN	-	linker	UNP E1C7U0
C	355	GLY	-	linker	UNP E1C7U0
C	356	PRO	-	linker	UNP E1C7U0
C	481	SER	-	expression tag	UNP Q9HYC4
C	482	SER	-	expression tag	UNP Q9HYC4
C	483	HIS	-	expression tag	UNP Q9HYC4
C	484	HIS	-	expression tag	UNP Q9HYC4
C	485	HIS	-	expression tag	UNP Q9HYC4
C	486	HIS	-	expression tag	UNP Q9HYC4
C	487	HIS	-	expression tag	UNP Q9HYC4
C	488	HIS	-	expression tag	UNP Q9HYC4
C	489	HIS	-	expression tag	UNP Q9HYC4
C	490	HIS	-	expression tag	UNP Q9HYC4
F	50	THR	ILE	conflict	UNP E1C7U0
F	52	ARG	SER	conflict	UNP E1C7U0
F	100	HIS	TYR	conflict	UNP E1C7U0
F	187	ILE	LEU	conflict	UNP E1C7U0
F	343	ARG	-	linker	UNP E1C7U0
F	344	GLU	-	linker	UNP E1C7U0
F	345	GLU	-	linker	UNP E1C7U0
F	346	TYR	-	linker	UNP E1C7U0
F	347	MET	-	linker	UNP E1C7U0
F	348	VAL	-	linker	UNP E1C7U0
F	349	LEU	-	linker	UNP E1C7U0
F	350	GLU	-	linker	UNP E1C7U0
F	351	VAL	-	linker	UNP E1C7U0
F	352	LEU	-	linker	UNP E1C7U0

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Chain	Residue	Modelled	Actual	Comment	Reference
F	353	PHE	-	linker	UNP E1C7U0
F	354	GLN	-	linker	UNP E1C7U0
F	355	GLY	-	linker	UNP E1C7U0
F	356	PRO	-	linker	UNP E1C7U0
F	481	SER	-	expression tag	UNP Q9HYC4
F	482	SER	-	expression tag	UNP Q9HYC4
F	483	HIS	-	expression tag	UNP Q9HYC4
F	484	HIS	-	expression tag	UNP Q9HYC4
F	485	HIS	-	expression tag	UNP Q9HYC4
F	486	HIS	-	expression tag	UNP Q9HYC4
F	487	HIS	-	expression tag	UNP Q9HYC4
F	488	HIS	-	expression tag	UNP Q9HYC4
F	489	HIS	-	expression tag	UNP Q9HYC4
F	490	HIS	-	expression tag	UNP Q9HYC4
D	50	THR	ILE	conflict	UNP E1C7U0
D	52	ARG	SER	conflict	UNP E1C7U0
D	100	HIS	TYR	conflict	UNP E1C7U0
D	187	ILE	LEU	conflict	UNP E1C7U0
D	343	ARG	-	linker	UNP E1C7U0
D	344	GLU	-	linker	UNP E1C7U0
D	345	GLU	-	linker	UNP E1C7U0
D	346	TYR	-	linker	UNP E1C7U0
D	347	MET	-	linker	UNP E1C7U0
D	348	VAL	-	linker	UNP E1C7U0
D	349	LEU	-	linker	UNP E1C7U0
D	350	GLU	-	linker	UNP E1C7U0
D	351	VAL	-	linker	UNP E1C7U0
D	352	LEU	-	linker	UNP E1C7U0
D	353	PHE	-	linker	UNP E1C7U0
D	354	GLN	-	linker	UNP E1C7U0
D	355	GLY	-	linker	UNP E1C7U0
D	356	PRO	-	linker	UNP E1C7U0
D	481	SER	-	expression tag	UNP Q9HYC4
D	482	SER	-	expression tag	UNP Q9HYC4
D	483	HIS	-	expression tag	UNP Q9HYC4
D	484	HIS	-	expression tag	UNP Q9HYC4
D	485	HIS	-	expression tag	UNP Q9HYC4
D	486	HIS	-	expression tag	UNP Q9HYC4
D	487	HIS	-	expression tag	UNP Q9HYC4
D	488	HIS	-	expression tag	UNP Q9HYC4
D	489	HIS	-	expression tag	UNP Q9HYC4
D	490	HIS	-	expression tag	UNP Q9HYC4

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Chain	Residue	Modelled	Actual	Comment	Reference
G	50	THR	ILE	conflict	UNP E1C7U0
G	52	ARG	SER	conflict	UNP E1C7U0
G	100	HIS	TYR	conflict	UNP E1C7U0
G	187	ILE	LEU	conflict	UNP E1C7U0
G	343	ARG	-	linker	UNP E1C7U0
G	344	GLU	-	linker	UNP E1C7U0
G	345	GLU	-	linker	UNP E1C7U0
G	346	TYR	-	linker	UNP E1C7U0
G	347	MET	-	linker	UNP E1C7U0
G	348	VAL	-	linker	UNP E1C7U0
G	349	LEU	-	linker	UNP E1C7U0
G	350	GLU	-	linker	UNP E1C7U0
G	351	VAL	-	linker	UNP E1C7U0
G	352	LEU	-	linker	UNP E1C7U0
G	353	PHE	-	linker	UNP E1C7U0
G	354	GLN	-	linker	UNP E1C7U0
G	355	GLY	-	linker	UNP E1C7U0
G	356	PRO	-	linker	UNP E1C7U0
G	481	SER	-	expression tag	UNP Q9HYC4
G	482	SER	-	expression tag	UNP Q9HYC4
G	483	HIS	-	expression tag	UNP Q9HYC4
G	484	HIS	-	expression tag	UNP Q9HYC4
G	485	HIS	-	expression tag	UNP Q9HYC4
G	486	HIS	-	expression tag	UNP Q9HYC4
G	487	HIS	-	expression tag	UNP Q9HYC4
G	488	HIS	-	expression tag	UNP Q9HYC4
G	489	HIS	-	expression tag	UNP Q9HYC4
G	490	HIS	-	expression tag	UNP Q9HYC4
E	50	THR	ILE	conflict	UNP E1C7U0
E	52	ARG	SER	conflict	UNP E1C7U0
E	100	HIS	TYR	conflict	UNP E1C7U0
E	187	ILE	LEU	conflict	UNP E1C7U0
E	343	ARG	-	linker	UNP E1C7U0
E	344	GLU	-	linker	UNP E1C7U0
E	345	GLU	-	linker	UNP E1C7U0
E	346	TYR	-	linker	UNP E1C7U0
E	347	MET	-	linker	UNP E1C7U0
E	348	VAL	-	linker	UNP E1C7U0
E	349	LEU	-	linker	UNP E1C7U0
E	350	GLU	-	linker	UNP E1C7U0
E	351	VAL	-	linker	UNP E1C7U0
E	352	LEU	-	linker	UNP E1C7U0

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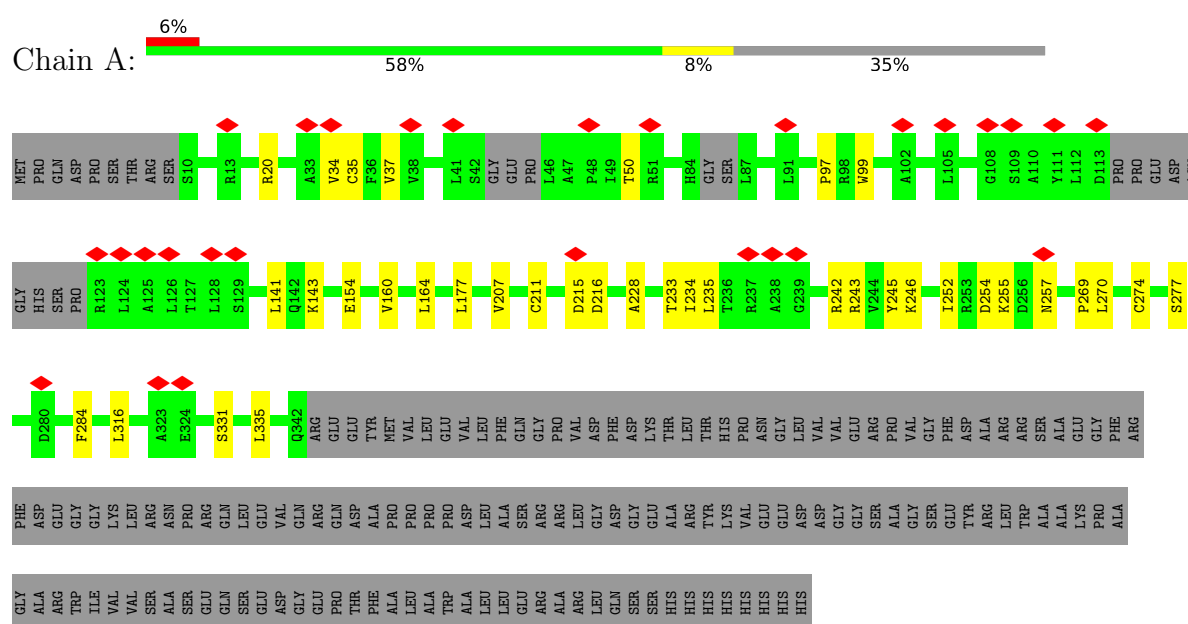
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Chain	Residue	Modelled	Actual	Comment	Reference
E	353	PHE	-	linker	UNP E1C7U0
E	354	GLN	-	linker	UNP E1C7U0
E	355	GLY	-	linker	UNP E1C7U0
E	356	PRO	-	linker	UNP E1C7U0
E	481	SER	-	expression tag	UNP Q9HYC4
E	482	SER	-	expression tag	UNP Q9HYC4
E	483	HIS	-	expression tag	UNP Q9HYC4
E	484	HIS	-	expression tag	UNP Q9HYC4
E	485	HIS	-	expression tag	UNP Q9HYC4
E	486	HIS	-	expression tag	UNP Q9HYC4
E	487	HIS	-	expression tag	UNP Q9HYC4
E	488	HIS	-	expression tag	UNP Q9HYC4
E	489	HIS	-	expression tag	UNP Q9HYC4
E	490	HIS	-	expression tag	UNP Q9HYC4
H	50	THR	ILE	conflict	UNP E1C7U0
H	52	ARG	SER	conflict	UNP E1C7U0
H	100	HIS	TYR	conflict	UNP E1C7U0
H	187	ILE	LEU	conflict	UNP E1C7U0
H	343	ARG	-	linker	UNP E1C7U0
H	344	GLU	-	linker	UNP E1C7U0
H	345	GLU	-	linker	UNP E1C7U0
H	346	TYR	-	linker	UNP E1C7U0
H	347	MET	-	linker	UNP E1C7U0
H	348	VAL	-	linker	UNP E1C7U0
H	349	LEU	-	linker	UNP E1C7U0
H	350	GLU	-	linker	UNP E1C7U0
H	351	VAL	-	linker	UNP E1C7U0
H	352	LEU	-	linker	UNP E1C7U0
H	353	PHE	-	linker	UNP E1C7U0
H	354	GLN	-	linker	UNP E1C7U0
H	355	GLY	-	linker	UNP E1C7U0
H	356	PRO	-	linker	UNP E1C7U0
H	481	SER	-	expression tag	UNP Q9HYC4
H	482	SER	-	expression tag	UNP Q9HYC4
H	483	HIS	-	expression tag	UNP Q9HYC4
H	484	HIS	-	expression tag	UNP Q9HYC4
H	485	HIS	-	expression tag	UNP Q9HYC4
H	486	HIS	-	expression tag	UNP Q9HYC4
H	487	HIS	-	expression tag	UNP Q9HYC4
H	488	HIS	-	expression tag	UNP Q9HYC4
H	489	HIS	-	expression tag	UNP Q9HYC4
H	490	HIS	-	expression tag	UNP Q9HYC4

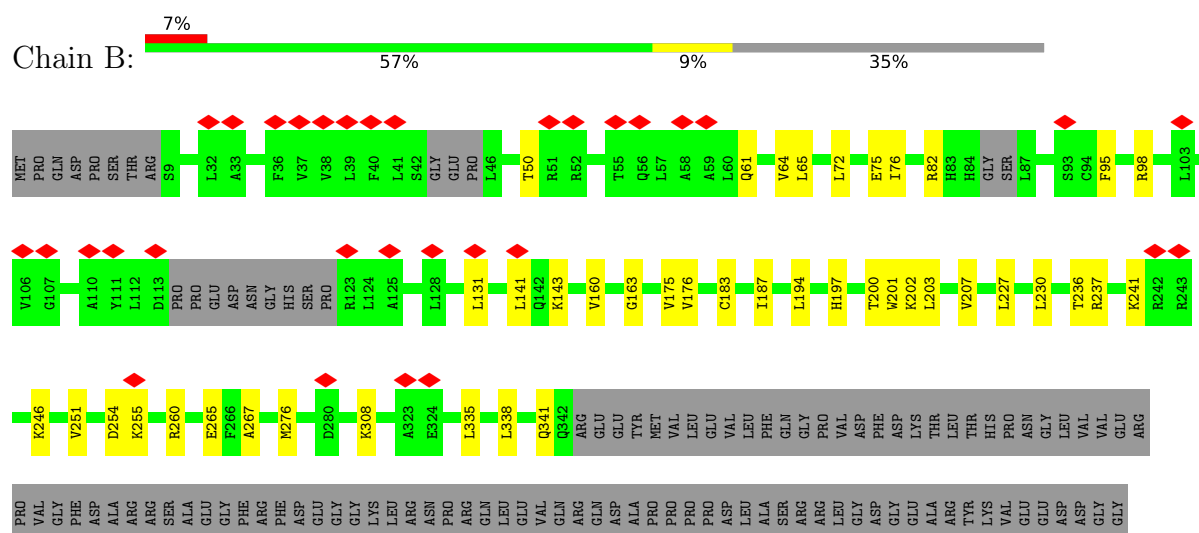
3 Residue-property plots

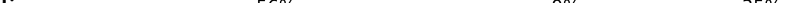
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Stimulator of interferon genes protein, Immune protein Tsi3



- Molecule 1: Stimulator of interferon genes protein, Immune protein Tsi3



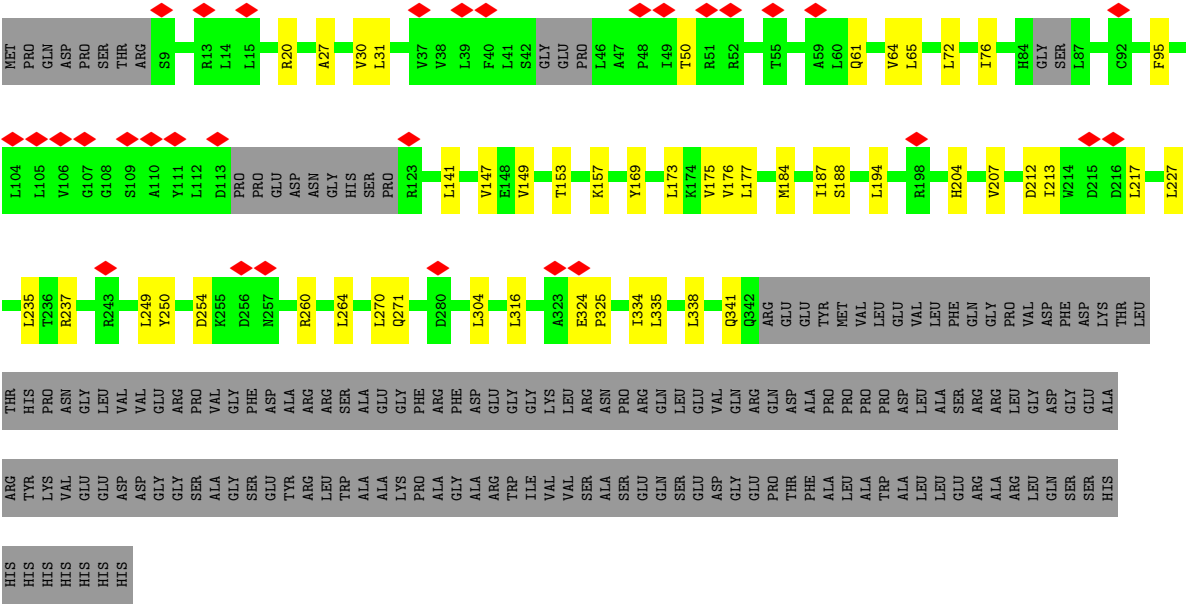
Chain D: 



PRO VAL GLY PHE ASP ALA ARG ARG SER SER ALA GLU ALA LYS PRO PHE ARG ARG PHE ASP ALA ASP ARG GLU TRP GLY GLY LYS LEU VAL ARG ASN PRO ARG ARG GLN LEU GLU VAL GLN GLY VAL ASP VAL GLY GLN ARG GLN ASP PRO PHE ALA PRO PRO PRO ASP ALA LEU LEU ALA SER ARG ARG ARG LEU GLY ASP GLY GLY ALA ARG TYR LYS VAL HIS HIS HIS HIS HIS HIS

SER ALA GLY SER PHE ASP TYR ARG LEU TRP ALA ALA LYS PRO ALA GLY PHE ASP ARG TRP ILE VAL VAL SER ALA ALA SER GLN GLN SER LEU ASP VAL GLY GLN ARG GLN ASP THR PHE ALA LEU TRP ALA ASP LEU LEU ALA SER ARG ARG ALA ARG LEU GLY ASP GLY SER SER HIS HIS HIS HIS HIS HIS

- Molecule 1: Stimulator of interferon genes protein,Immune protein Tsi3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1057869	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.324	Depositor
Minimum map value	-2.987	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.109	Depositor
Recommended contour level	0.339	Depositor
Map size ($\text{\AA}$)	280.32, 280.32, 280.32	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.095, 1.095, 1.095	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.10	0/2484	0.28	0/3375
1	B	0.10	0/2499	0.28	0/3394
1	C	0.10	0/2484	0.28	0/3375
1	D	0.10	0/2484	0.27	0/3375
1	E	0.10	0/2484	0.28	0/3375
1	F	0.11	0/2499	0.27	0/3394
1	G	0.10	0/2499	0.28	0/3394
1	H	0.11	0/2499	0.28	0/3394
All	All	0.10	0/19932	0.28	0/27076

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	2435	0	2426	28	0
1	B	2449	0	2431	28	0
1	C	2435	0	2426	30	0
1	D	2435	0	2426	34	0
1	E	2435	0	2426	31	0
1	F	2449	0	2431	34	0
1	G	2449	0	2431	31	0
1	H	2449	0	2431	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	19536	0	19428	220	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 6.

All (220) 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:E:254:ASP:OD1	1:E:255:LYS:N	2.16	0.79
1:C:254:ASP:OD1	1:C:255:LYS:N	2.16	0.77
1:C:232:GLU:OE2	1:C:246:LYS:NZ	2.21	0.70
1:C:233:THR:HB	1:C:245:TYR:HB2	1.74	0.70
1:E:232:GLU:OE2	1:E:246:LYS:NZ	2.20	0.69
1:E:233:THR:HB	1:E:245:TYR:HB2	1.74	0.69
1:D:277:SER:HA	1:D:284:PHE:HB3	1.75	0.68
1:A:277:SER:HA	1:A:284:PHE:HB3	1.75	0.68
1:A:160:VAL:HG13	1:B:163:GLY:HA2	1.77	0.66
1:H:207:VAL:HG23	1:H:270:LEU:HD11	1.81	0.62
1:F:207:VAL:HG23	1:F:270:LEU:HD11	1.82	0.62
1:D:233:THR:HB	1:D:245:TYR:HB2	1.82	0.61
1:F:20:ARG:HH21	1:F:147:VAL:HG13	1.65	0.61
1:A:233:THR:HB	1:A:245:TYR:HB2	1.84	0.60
1:C:277:SER:HA	1:C:284:PHE:HB3	1.83	0.60
1:E:277:SER:HA	1:E:284:PHE:HB3	1.83	0.59
1:H:204:HIS:NE2	1:H:341:GLN:OE1	2.34	0.59
1:E:186:GLU:HG3	1:E:187:ILE:HD12	1.84	0.58
1:A:164:LEU:HB3	1:A:269:PRO:HB3	1.85	0.58
1:D:164:LEU:HB3	1:D:269:PRO:HB3	1.85	0.58
1:C:186:GLU:HG3	1:C:187:ILE:HD12	1.84	0.58
1:A:228:ALA:HB2	1:G:230:LEU:HD13	1.85	0.57
1:G:197:HIS:O	1:G:201:TRP:NE1	2.38	0.57
1:A:207:VAL:HG23	1:A:270:LEU:HD11	1.87	0.56
1:D:207:VAL:HG23	1:D:270:LEU:HD11	1.87	0.56
1:F:175:VAL:HG23	1:F:176:VAL:HG13	1.88	0.56
1:B:183:CYS:O	1:B:187:ILE:HG12	2.06	0.55
1:F:204:HIS:NE2	1:F:341:GLN:OE1	2.35	0.55
1:H:227:LEU:HD23	1:H:249:LEU:HD23	1.89	0.55
1:H:175:VAL:HG23	1:H:176:VAL:HG13	1.88	0.55
1:D:160:VAL:HG13	1:G:163:GLY:HA2	1.88	0.55
1:E:272:THR:O	1:E:276:MET:HG2	2.07	0.55
1:C:272:THR:O	1:C:276:MET:HG2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:229:ASP:OD1	1:F:246:LYS:NZ	2.38	0.54
1:G:183:CYS:O	1:G:187:ILE:HG12	2.07	0.54
1:A:20:ARG:NH2	1:B:75:GLU:OE2	2.40	0.53
1:F:169:TYR:HA	1:F:173:LEU:HB2	1.90	0.53
1:G:254:ASP:OD2	1:G:260:ARG:NH1	2.36	0.53
1:H:169:TYR:HA	1:H:173:LEU:HB2	1.91	0.53
1:F:227:LEU:HB2	1:F:251:VAL:HG13	1.90	0.53
1:B:197:HIS:O	1:B:201:TRP:NE1	2.41	0.53
1:F:65:LEU:HA	1:F:95:PHE:HE1	1.75	0.52
1:B:200:THR:HG22	1:B:200:THR:O	2.10	0.52
1:F:72:LEU:O	1:F:76:ILE:HG12	2.10	0.52
1:H:65:LEU:HA	1:H:95:PHE:HE1	1.75	0.52
1:B:65:LEU:HA	1:B:95:PHE:HE1	1.76	0.51
1:C:246:LYS:HG3	1:F:235:LEU:HD11	1.91	0.51
1:F:227:LEU:HD23	1:F:249:LEU:HD23	1.92	0.51
1:A:255:LYS:O	1:A:257:ASN:N	2.42	0.51
1:B:160:VAL:HG11	1:B:276:MET:HE1	1.93	0.51
1:H:72:LEU:O	1:H:76:ILE:HG12	2.10	0.51
1:E:246:LYS:HG3	1:H:235:LEU:HD11	1.92	0.51
1:D:20:ARG:NH2	1:G:75:GLU:OE2	2.40	0.50
1:A:254:ASP:OD1	1:A:335:LEU:HD11	2.11	0.50
1:H:254:ASP:OD2	1:H:260:ARG:NH1	2.41	0.50
1:G:65:LEU:HA	1:G:95:PHE:HE1	1.76	0.50
1:H:20:ARG:HH22	1:H:147:VAL:HG13	1.77	0.50
1:A:97:PRO:HD2	1:B:143:LYS:HE2	1.93	0.50
1:D:159:ASN:HD21	1:G:153:THR:HG23	1.76	0.50
1:G:200:THR:HG22	1:G:200:THR:O	2.12	0.50
1:B:175:VAL:HG13	1:B:176:VAL:HG13	1.93	0.50
1:D:97:PRO:HD2	1:G:143:LYS:HE2	1.94	0.50
1:D:255:LYS:O	1:D:257:ASN:N	2.43	0.50
1:E:197:HIS:O	1:E:201:TRP:NE1	2.44	0.49
1:B:227:LEU:HB2	1:B:251:VAL:HG23	1.95	0.49
1:B:72:LEU:O	1:B:76:ILE:HG12	2.13	0.48
1:H:334:ILE:O	1:H:338:LEU:HD23	2.13	0.48
1:A:99:TRP:H	1:A:99:TRP:CD1	2.31	0.48
1:G:175:VAL:HG13	1:G:176:VAL:HG13	1.95	0.48
1:B:203:LEU:HD11	1:B:265:GLU:HG3	1.95	0.48
1:D:235:LEU:HB2	1:D:243:ARG:HB2	1.96	0.48
1:F:176:VAL:HG23	1:F:177:LEU:HD12	1.95	0.48
1:G:72:LEU:O	1:G:76:ILE:HG12	2.14	0.48
1:C:141:LEU:HD23	1:C:141:LEU:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:176:VAL:HG23	1:H:177:LEU:HD12	1.95	0.47
1:D:141:LEU:H	1:D:141:LEU:HD23	1.79	0.47
1:E:141:LEU:HD23	1:E:141:LEU:H	1.79	0.47
1:H:188:SER:HB2	1:H:194:LEU:HD11	1.96	0.47
1:B:202:LYS:HD2	1:B:341:GLN:OE1	2.13	0.47
1:H:217:LEU:HD21	1:H:264:LEU:HD22	1.95	0.47
1:D:99:TRP:H	1:D:99:TRP:CD1	2.31	0.47
1:A:141:LEU:HD23	1:A:141:LEU:H	1.80	0.47
1:B:308:LYS:HE3	1:F:212:ASP:HB3	1.96	0.47
1:C:197:HIS:O	1:C:201:TRP:NE1	2.47	0.47
1:G:230:LEU:HB2	1:G:246:LYS:HE3	1.97	0.47
1:B:254:ASP:OD2	1:B:260:ARG:NH1	2.35	0.47
1:F:254:ASP:HA	1:F:335:LEU:HD11	1.97	0.47
1:G:254:ASP:OD1	1:G:255:LYS:N	2.42	0.47
1:E:181:LYS:O	1:E:185:GLU:HG2	2.14	0.47
1:C:181:LYS:O	1:C:185:GLU:HG2	2.14	0.47
1:F:61:GLN:O	1:F:64:VAL:HG22	2.15	0.47
1:F:188:SER:HB2	1:F:194:LEU:HD11	1.97	0.47
1:G:141:LEU:HD23	1:G:141:LEU:H	1.80	0.47
1:G:207:VAL:HG12	1:G:267:ALA:HB2	1.97	0.47
1:E:336:TRP:O	1:E:340:GLN:HG2	2.15	0.47
1:A:154:GLU:OE1	1:B:82:ARG:NH2	2.48	0.47
1:H:254:ASP:HA	1:H:335:LEU:HD11	1.97	0.47
1:A:331:SER:O	1:A:335:LEU:HD23	2.15	0.47
1:E:331:SER:O	1:E:335:LEU:HD23	2.15	0.46
1:A:143:LYS:HZ1	1:B:98:ARG:H	1.62	0.46
1:F:336:TRP:NE1	1:F:340:GLN:HE21	2.13	0.46
1:D:254:ASP:OD1	1:D:255:LYS:N	2.44	0.46
1:G:236:THR:HG22	1:G:241:LYS:HA	1.98	0.46
1:B:141:LEU:HD23	1:B:141:LEU:H	1.80	0.46
1:C:336:TRP:O	1:C:340:GLN:HG2	2.15	0.46
1:D:143:LYS:HZ1	1:G:98:ARG:H	1.63	0.46
1:H:61:GLN:O	1:H:64:VAL:HG22	2.15	0.46
1:B:230:LEU:HD13	1:D:228:ALA:HB2	1.98	0.46
1:F:262:CYS:SG	1:F:338:LEU:HD11	2.56	0.46
1:A:215:ASP:OD1	1:A:216:ASP:N	2.47	0.46
1:B:194:LEU:HD23	1:B:194:LEU:H	1.81	0.46
1:H:264:LEU:HD21	1:H:334:ILE:HD13	1.98	0.46
1:B:207:VAL:HG12	1:B:267:ALA:HB2	1.97	0.46
1:C:255:LYS:O	1:C:257:ASN:N	2.43	0.46
1:F:230:LEU:H	1:F:246:LYS:HE3	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:246:LYS:HE2	1:H:235:LEU:HD11	1.97	0.46
1:C:331:SER:O	1:C:335:LEU:HD23	2.15	0.46
1:G:203:LEU:HD11	1:G:265:GLU:HG3	1.98	0.46
1:C:79:LEU:O	1:C:84:HIS:N	2.49	0.46
1:C:246:LYS:HE2	1:F:235:LEU:HD11	1.96	0.46
1:A:252:ILE:HD12	1:A:335:LEU:HD22	1.97	0.45
1:H:141:LEU:HD23	1:H:141:LEU:H	1.81	0.45
1:B:61:GLN:O	1:B:64:VAL:HG22	2.17	0.45
1:G:61:GLN:O	1:G:64:VAL:HG22	2.17	0.45
1:G:194:LEU:HD23	1:G:194:LEU:H	1.82	0.45
1:E:246:LYS:HB2	1:H:237:ARG:HA	1.99	0.45
1:A:246:LYS:HB2	1:B:237:ARG:HA	1.98	0.45
1:E:191:ASN:HD22	1:E:191:ASN:N	2.15	0.45
1:H:217:LEU:HD23	1:H:250:TYR:CE2	2.52	0.45
1:C:191:ASN:N	1:C:191:ASN:HD22	2.14	0.45
1:G:227:LEU:HB2	1:G:251:VAL:HG23	1.99	0.45
1:E:79:LEU:O	1:E:84:HIS:N	2.50	0.45
1:H:184:MET:HA	1:H:187:ILE:HB	1.99	0.45
1:A:235:LEU:HB2	1:A:243:ARG:HB2	1.99	0.44
1:D:246:LYS:HB2	1:G:237:ARG:HA	1.99	0.44
1:C:246:LYS:HB2	1:F:237:ARG:HA	2.00	0.44
1:D:234:ILE:HG23	1:D:242:ARG:HD3	1.99	0.44
1:A:234:ILE:HG23	1:A:242:ARG:HD3	2.00	0.43
1:F:254:ASP:OD2	1:F:260:ARG:NH1	2.42	0.43
1:B:236:THR:HG22	1:B:241:LYS:HA	1.99	0.43
1:G:308:LYS:HE3	1:H:212:ASP:HB3	2.00	0.43
1:H:173:LEU:HD13	1:H:304:LEU:HD21	2.00	0.43
1:C:288:GLN:H	1:C:288:GLN:HG3	1.70	0.43
1:D:177:LEU:HD23	1:D:177:LEU:HA	1.87	0.43
1:E:173:LEU:O	1:E:177:LEU:HB2	2.18	0.43
1:F:179:ARG:HE	1:F:179:ARG:HB2	1.67	0.43
1:F:231:PRO:HG3	1:E:231:PRO:HD3	2.01	0.43
1:E:255:LYS:O	1:E:257:ASN:N	2.43	0.43
1:D:253:ARG:HH11	1:D:253:ARG:HG3	1.83	0.43
1:D:35:CYS:HB3	1:G:131:LEU:HD21	2.00	0.43
1:D:254:ASP:CG	1:D:255:LYS:H	2.26	0.43
1:E:215:ASP:OD1	1:E:215:ASP:N	2.51	0.43
1:A:242:ARG:NH1	1:D:232:GLU:HB2	2.34	0.42
1:C:173:LEU:O	1:C:177:LEU:HB2	2.18	0.42
1:D:207:VAL:O	1:D:207:VAL:HG13	2.19	0.42
1:C:172:TYR:O	1:C:176:VAL:HG22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:159:ASN:HD21	1:H:153:THR:HB	1.84	0.42
1:A:211:CYS:HB3	1:A:274:CYS:HB2	2.01	0.42
1:E:60:LEU:HD23	1:E:60:LEU:H	1.84	0.42
1:E:186:GLU:O	1:E:189:ARG:HG2	2.20	0.42
1:D:316:LEU:HD23	1:D:316:LEU:H	1.85	0.42
1:E:172:TYR:O	1:E:176:VAL:HG22	2.19	0.42
1:A:177:LEU:HD23	1:A:177:LEU:HA	1.87	0.42
1:F:149:VAL:O	1:F:153:THR:HG23	2.20	0.42
1:F:173:LEU:HD13	1:F:304:LEU:HD21	2.00	0.42
1:H:324:GLU:HA	1:H:325:PRO:HD3	1.94	0.42
1:B:335:LEU:HD23	1:B:338:LEU:HD12	2.02	0.42
1:F:207:VAL:O	1:F:207:VAL:HG13	2.19	0.42
1:D:280:ASP:OD1	1:D:280:ASP:N	2.51	0.42
1:G:246:LYS:HE2	1:G:246:LYS:HB2	1.86	0.42
1:D:215:ASP:OD1	1:D:216:ASP:N	2.53	0.42
1:C:215:ASP:OD1	1:C:215:ASP:N	2.51	0.42
1:G:336:TRP:O	1:G:340:GLN:HG2	2.20	0.42
1:H:207:VAL:O	1:H:207:VAL:HG13	2.19	0.42
1:A:207:VAL:HG13	1:A:207:VAL:O	2.19	0.42
1:A:316:LEU:H	1:A:316:LEU:HD23	1.84	0.42
1:C:207:VAL:HA	1:C:270:LEU:HD11	2.02	0.42
1:D:252:ILE:HD12	1:D:335:LEU:HD22	2.02	0.42
1:C:60:LEU:H	1:C:60:LEU:HD23	1.84	0.41
1:C:186:GLU:O	1:C:189:ARG:HG2	2.20	0.41
1:E:252:ILE:HD11	1:E:264:LEU:HD11	2.02	0.41
1:H:27:ALA:O	1:H:31:LEU:HD23	2.20	0.41
1:F:27:ALA:HA	1:F:30:VAL:HG22	2.03	0.41
1:H:27:ALA:HA	1:H:30:VAL:HG22	2.03	0.41
1:B:254:ASP:OD1	1:B:255:LYS:N	2.42	0.41
1:D:159:ASN:ND2	1:G:153:THR:HG23	2.36	0.41
1:A:35:CYS:HB3	1:B:131:LEU:HD21	2.01	0.41
1:F:216:ASP:HB3	1:F:219:LYS:HE2	2.02	0.41
1:H:149:VAL:O	1:H:153:THR:HG23	2.20	0.41
1:E:280:ASP:OD1	1:E:280:ASP:N	2.53	0.41
1:E:330:LEU:O	1:E:334:ILE:HG13	2.20	0.41
1:C:237:ARG:HG2	1:C:241:LYS:HD3	2.01	0.41
1:F:27:ALA:O	1:F:31:LEU:HD23	2.21	0.41
1:C:280:ASP:N	1:C:280:ASP:OD1	2.53	0.41
1:C:330:LEU:O	1:C:334:ILE:HG13	2.20	0.41
1:A:34:VAL:HA	1:A:37:VAL:HG22	2.03	0.41
1:C:159:ASN:HD21	1:F:153:THR:HB	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:324:GLU:HA	1:F:325:PRO:HD3	1.95	0.41
1:D:211:CYS:HB3	1:D:274:CYS:HB2	2.02	0.41
1:D:246:LYS:HG3	1:G:235:LEU:HD11	2.03	0.41
1:G:255:LYS:O	1:G:257:ASN:N	2.50	0.41
1:E:175:VAL:HG13	1:E:176:VAL:HG13	2.03	0.41
1:E:237:ARG:HG2	1:E:241:LYS:HD3	2.01	0.41
1:H:213:ILE:HG13	1:H:271:GLN:HG3	2.03	0.41
1:B:230:LEU:HB2	1:B:246:LYS:HE3	2.02	0.41
1:C:29:CYS:O	1:C:32:LEU:HB2	2.21	0.41
1:H:157:LYS:HE3	1:H:157:LYS:HB3	1.74	0.41
1:H:335:LEU:HD23	1:H:335:LEU:HA	1.92	0.41
1:A:160:VAL:HG12	1:A:164:LEU:HG	2.02	0.40
1:C:175:VAL:HG13	1:C:176:VAL:HG13	2.03	0.40
1:D:331:SER:O	1:D:335:LEU:HD23	2.22	0.40
1:D:34:VAL:HA	1:D:37:VAL:HG22	2.03	0.40
1:F:255:LYS:O	1:F:257:ASN:N	2.50	0.40
1:D:150:SER:O	1:D:154:GLU:HG3	2.21	0.40
1:G:21:ALA:HB3	1:G:23:ARG:HE	1.86	0.40
1:E:75:GLU:OE2	1:H:20:ARG:NH1	2.54	0.40
1:H:316:LEU:H	1:H:316:LEU:HD23	1.87	0.40
1:D:186:GLU:HG3	1:D:187:ILE:HD12	2.03	0.40
1:F:316:LEU:HD23	1:F:316:LEU:H	1.87	0.40
1:E:207:VAL:HA	1:E:270:LEU:HD11	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	311/490 (64%)	300 (96%)	11 (4%)	0	100	100
1	B	312/490 (64%)	303 (97%)	9 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	311/490 (64%)	302 (97%)	9 (3%)	0	100	100
1	D	311/490 (64%)	300 (96%)	11 (4%)	0	100	100
1	E	311/490 (64%)	303 (97%)	8 (3%)	0	100	100
1	F	312/490 (64%)	303 (97%)	9 (3%)	0	100	100
1	G	312/490 (64%)	302 (97%)	10 (3%)	0	100	100
1	H	312/490 (64%)	304 (97%)	8 (3%)	0	100	100
All	All	2492/3920 (64%)	2417 (97%)	75 (3%)	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	252/417 (60%)	251 (100%)	1 (0%)	84	84
1	B	253/417 (61%)	252 (100%)	1 (0%)	84	84
1	C	252/417 (60%)	251 (100%)	1 (0%)	84	84
1	D	252/417 (60%)	251 (100%)	1 (0%)	84	84
1	E	252/417 (60%)	251 (100%)	1 (0%)	84	84
1	F	253/417 (61%)	252 (100%)	1 (0%)	84	84
1	G	253/417 (61%)	252 (100%)	1 (0%)	84	84
1	H	253/417 (61%)	252 (100%)	1 (0%)	84	84
All	All	2020/3336 (61%)	2012 (100%)	8 (0%)	81	84

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	THR
1	B	50	THR
1	C	191	ASN
1	F	50	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	50	THR
1	G	50	THR
1	E	191	ASN
1	H	50	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	HIS
1	A	84	HIS
1	A	191	ASN
1	A	340	GLN
1	C	83	HIS
1	C	84	HIS
1	C	191	ASN
1	C	197	HIS
1	C	340	GLN
1	F	84	HIS
1	F	278	GLN
1	F	340	GLN
1	D	83	HIS
1	D	84	HIS
1	D	159	ASN
1	D	191	ASN
1	D	340	GLN
1	G	341	GLN
1	E	83	HIS
1	E	84	HIS
1	E	191	ASN
1	E	197	HIS
1	E	340	GLN
1	H	84	HIS
1	H	162	HIS
1	H	278	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

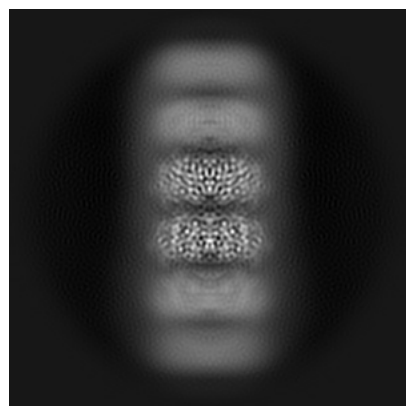
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35503. These allow visual inspection of the internal detail of the map and identification of artifacts.

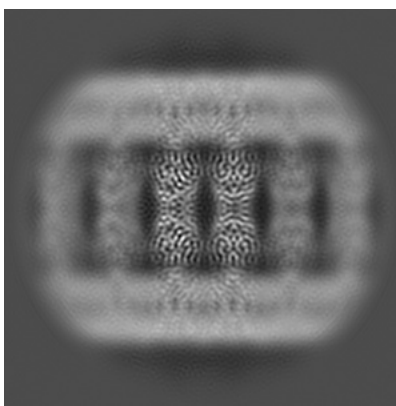
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

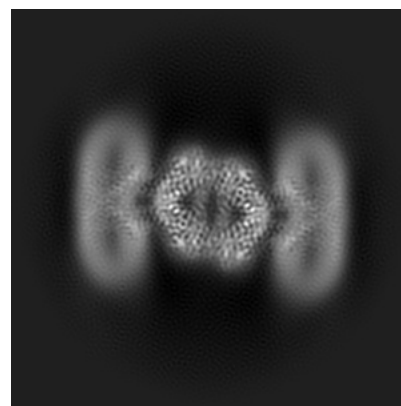
6.1.1 Primary map



X

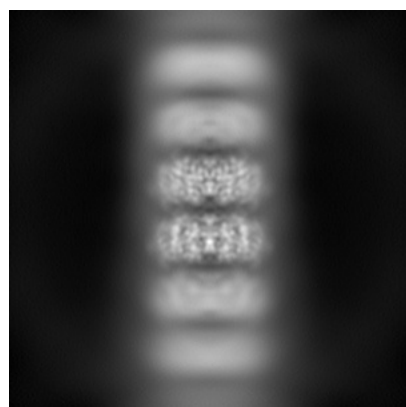


Y

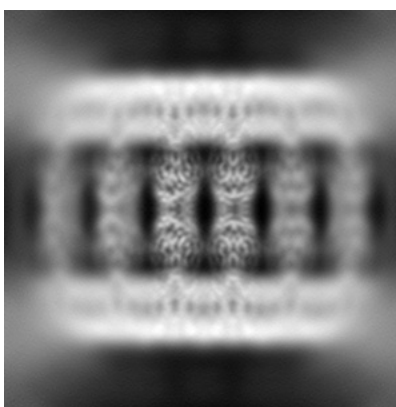


Z

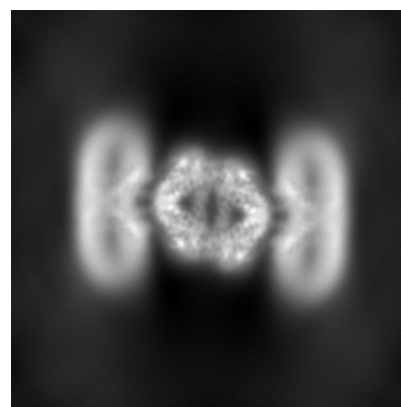
6.1.2 Raw map



X



Y

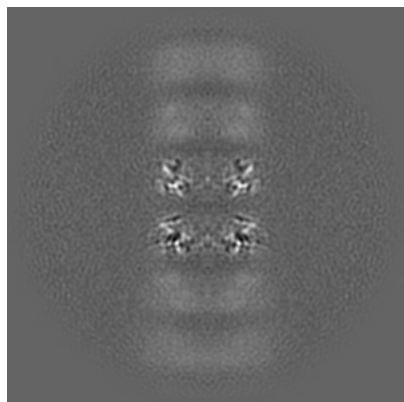


Z

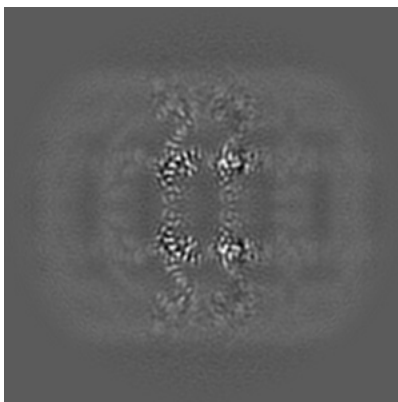
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

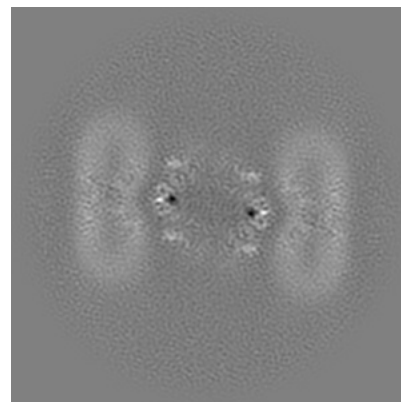
6.2.1 Primary map



X Index: 128

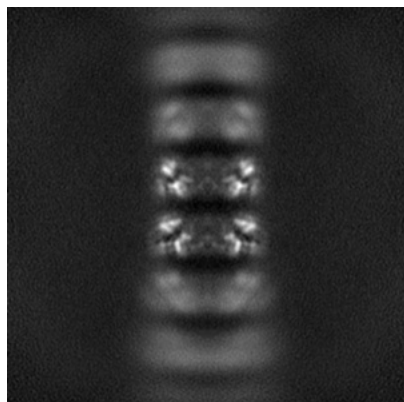


Y Index: 128

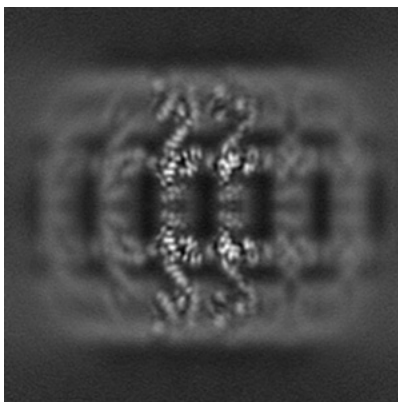


Z Index: 128

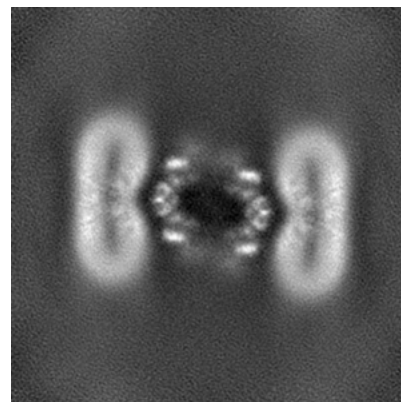
6.2.2 Raw map



X Index: 128



Y Index: 128

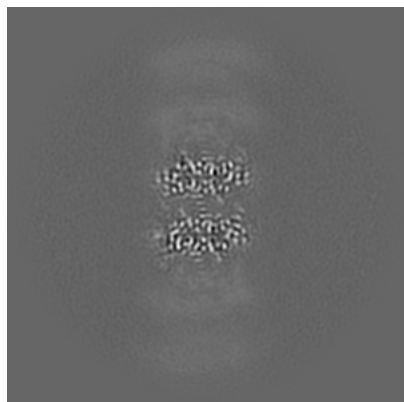


Z Index: 128

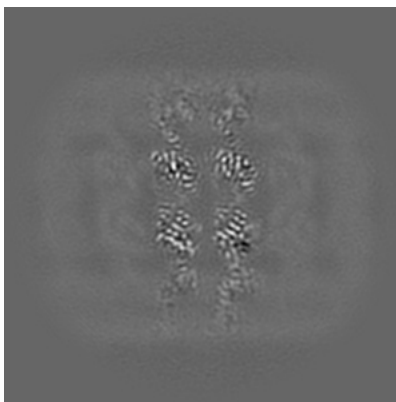
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

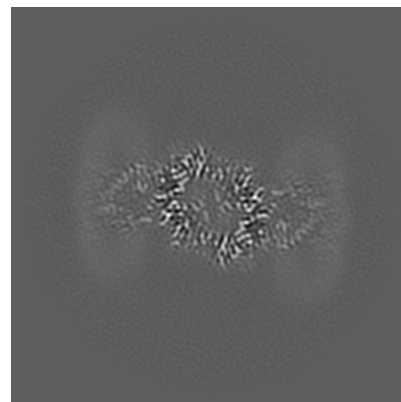
6.3.1 Primary map



X Index: 151

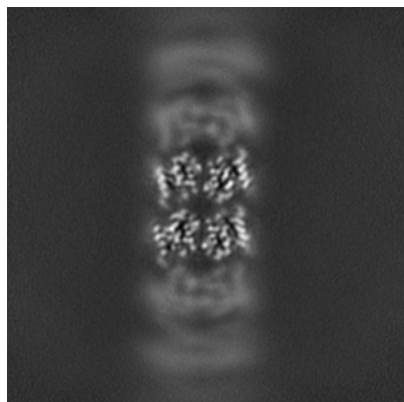


Y Index: 115

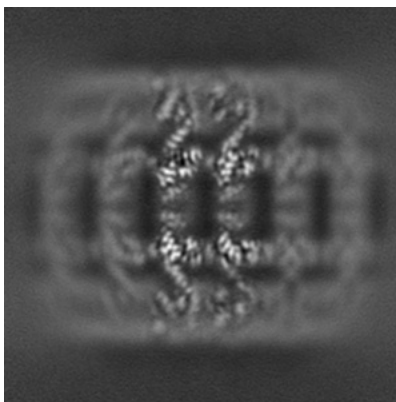


Z Index: 106

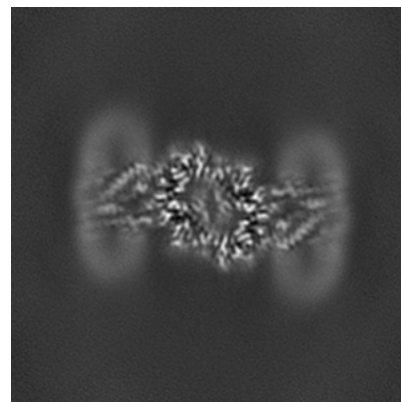
6.3.2 Raw map



X Index: 148



Y Index: 129

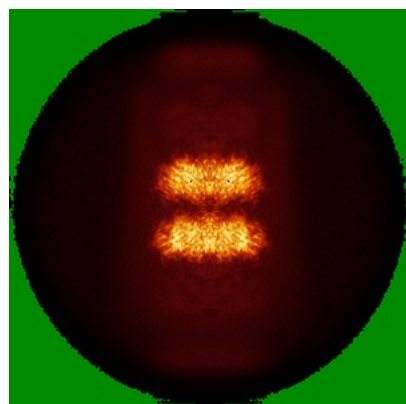


Z Index: 106

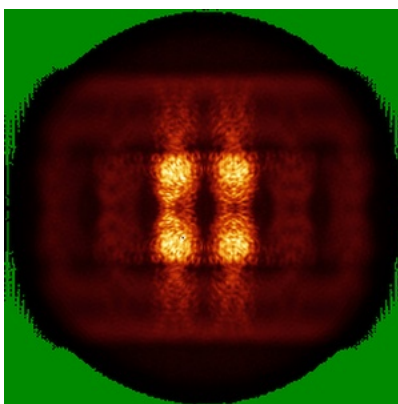
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

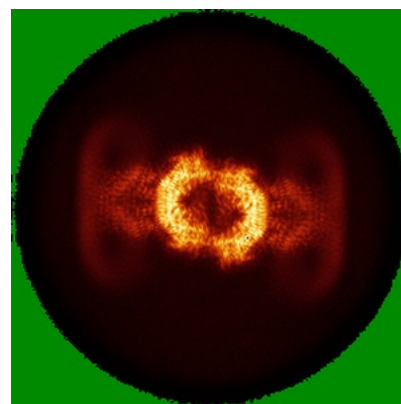
6.4.1 Primary map



X

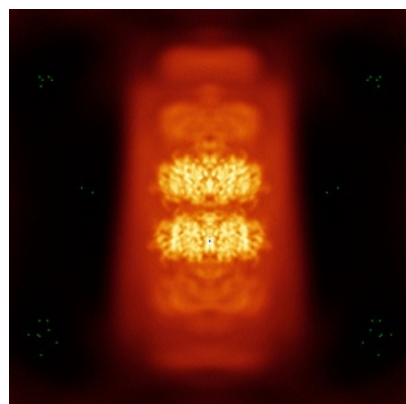


Y

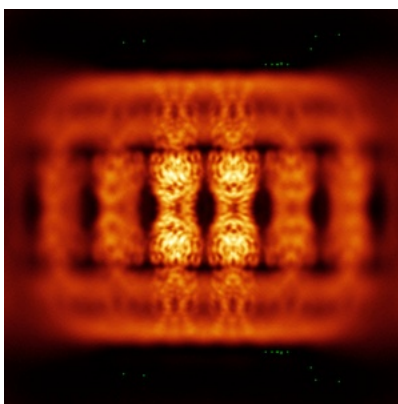


Z

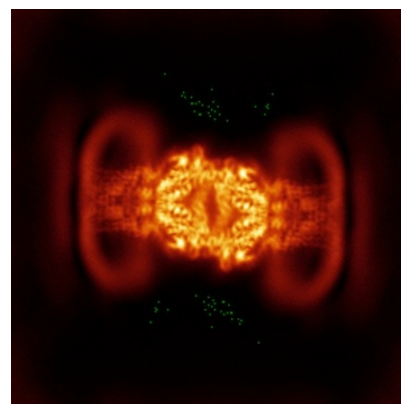
6.4.2 Raw map



X



Y

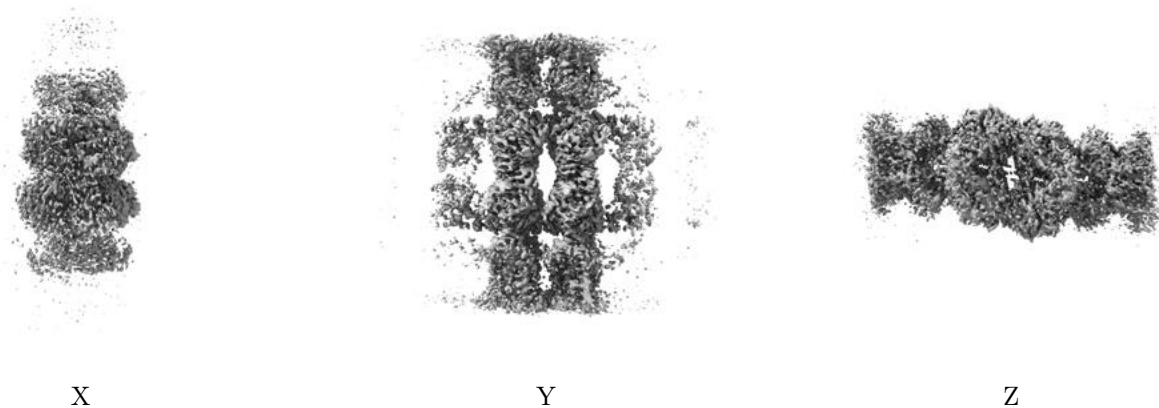


Z

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.

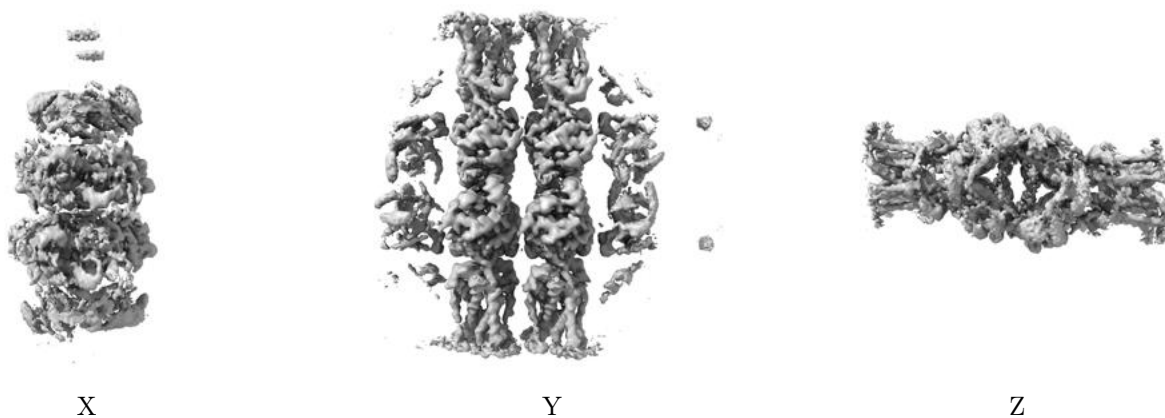
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.339. 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.

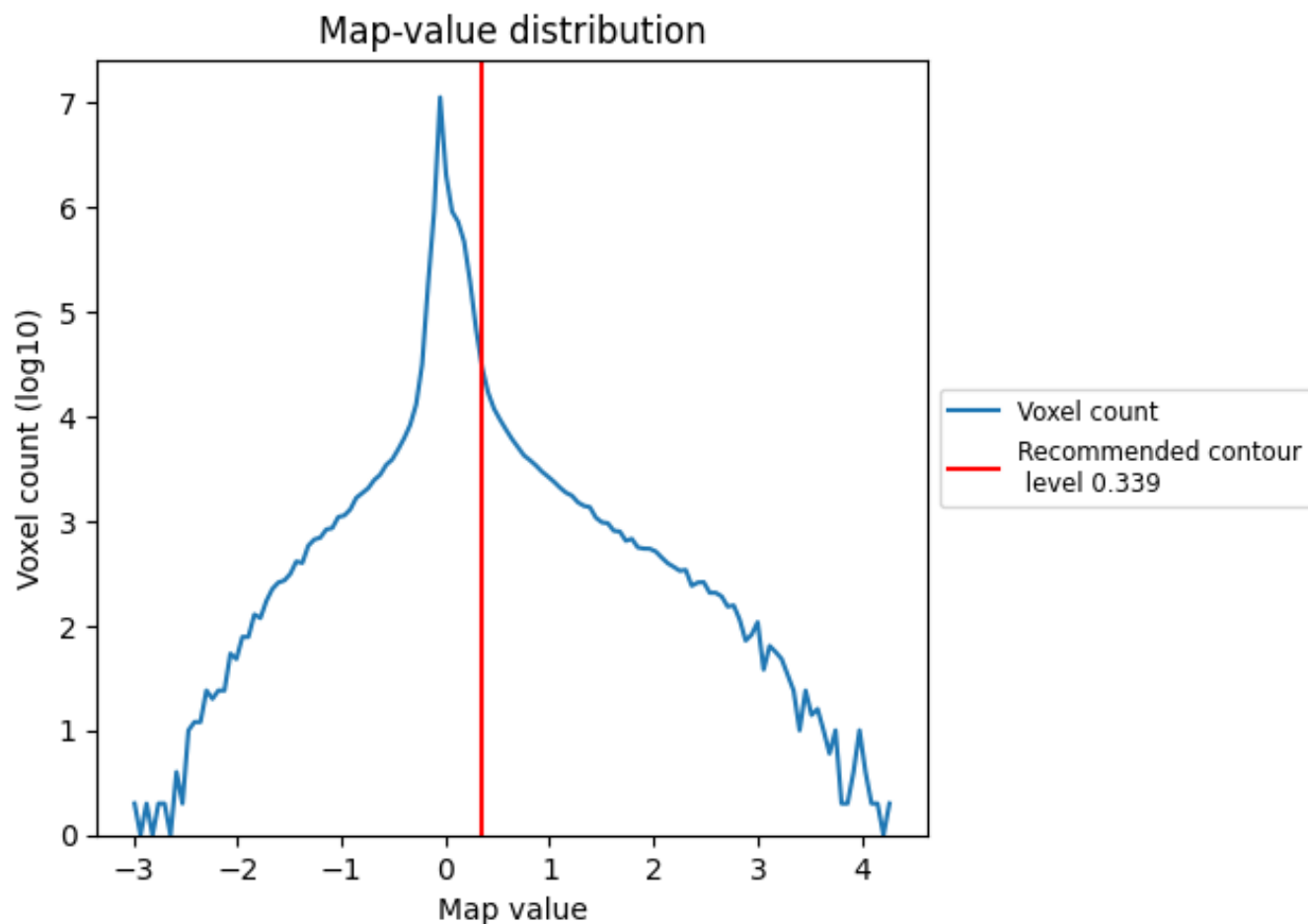
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

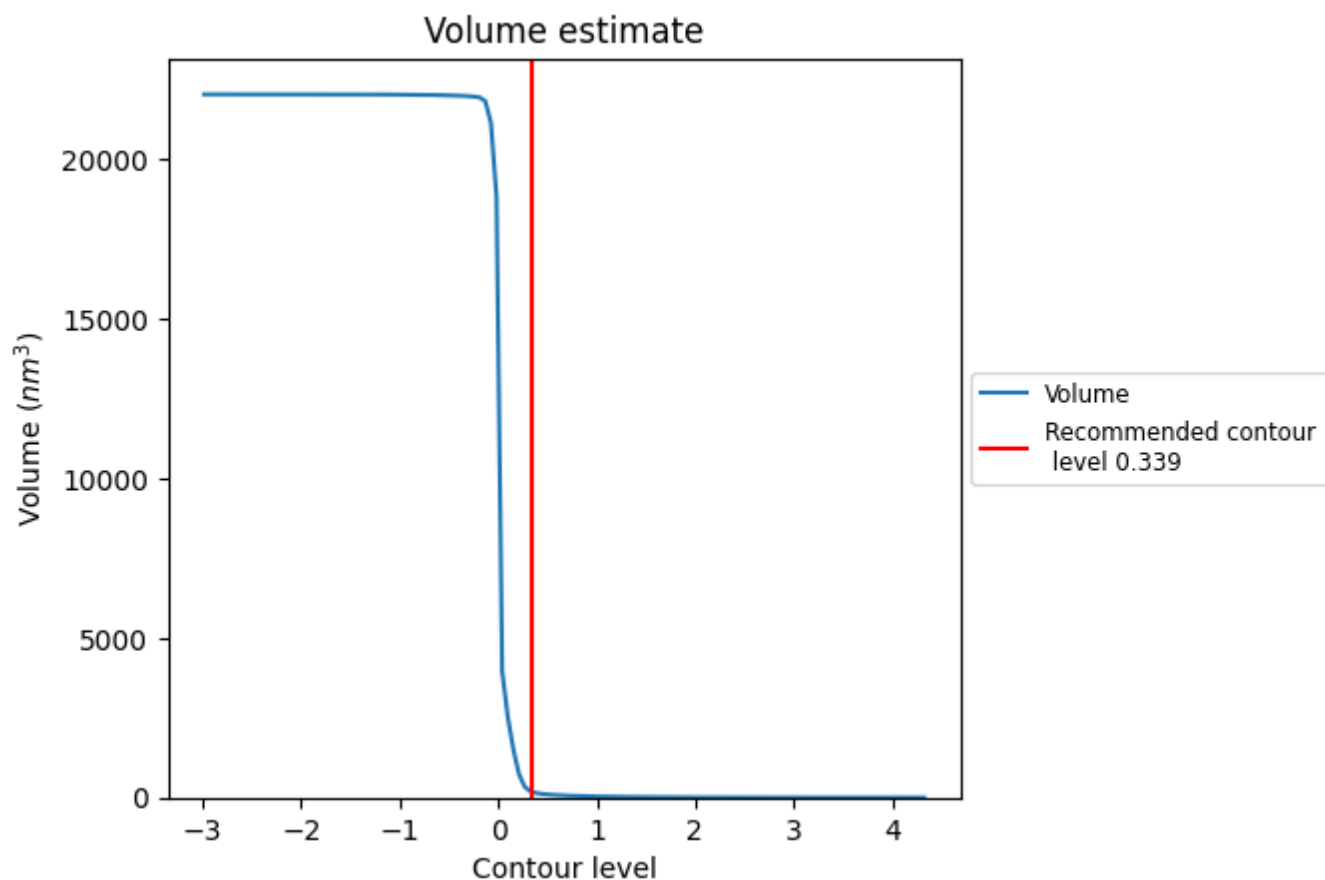
This section contains the results of statistical analysis of the map.

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.

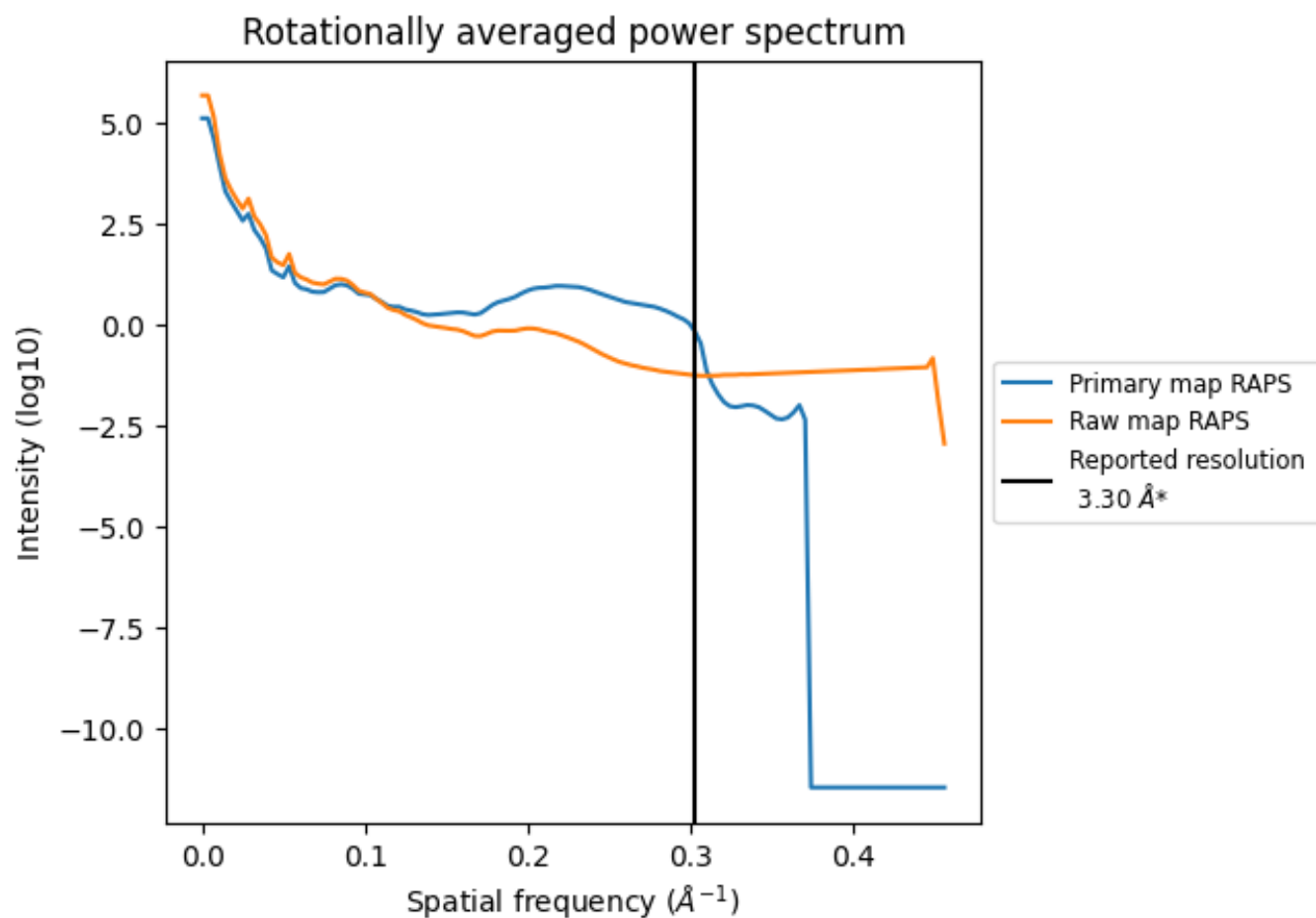
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 186 nm³; this corresponds to an approximate mass of 168 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 ⓘ

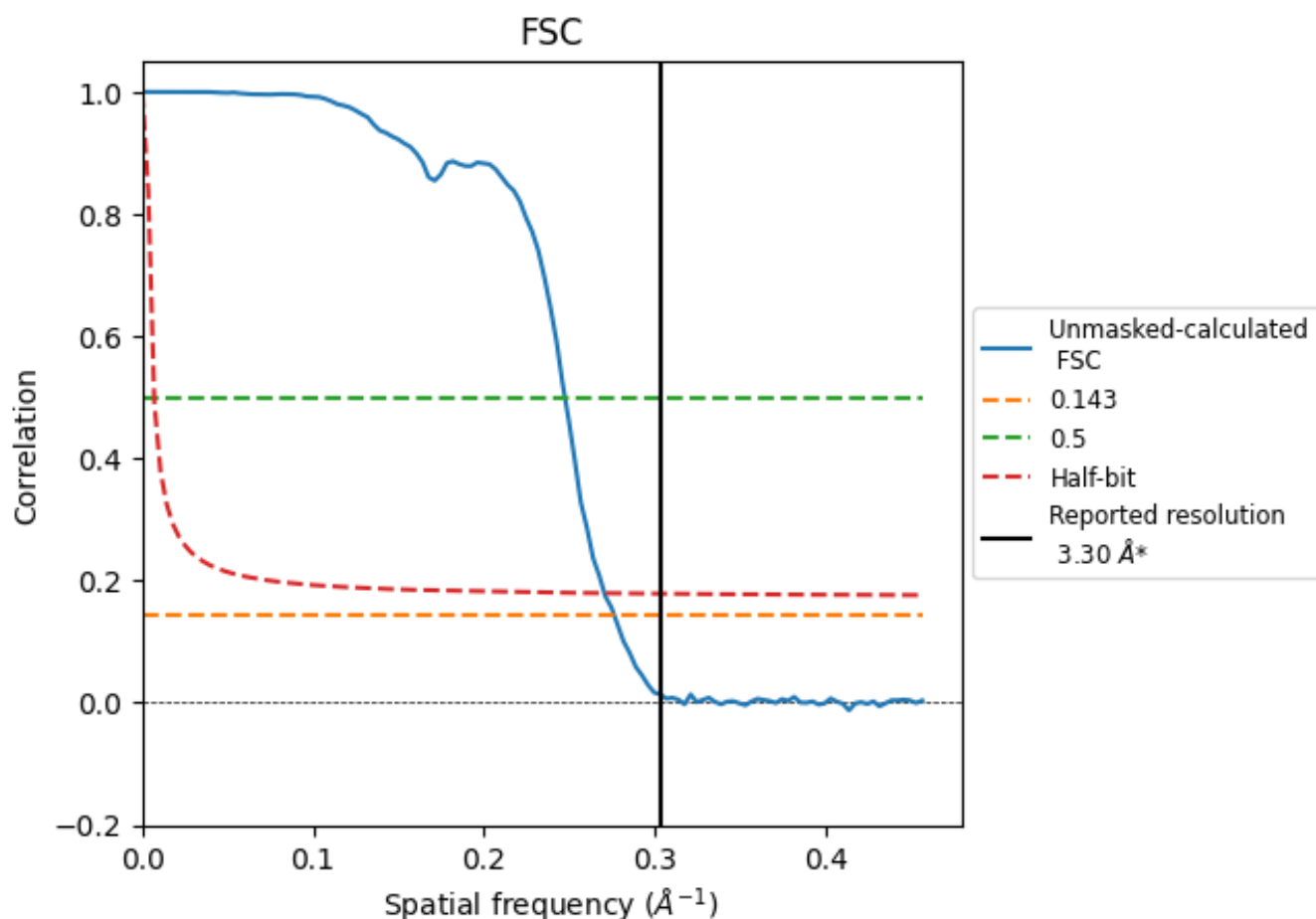


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

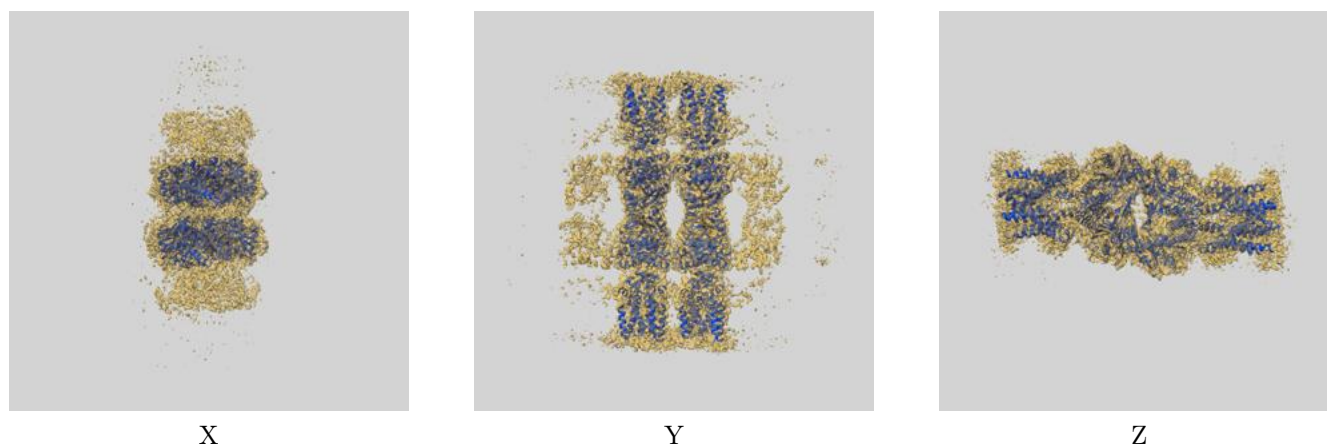
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.62	4.04	3.70

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

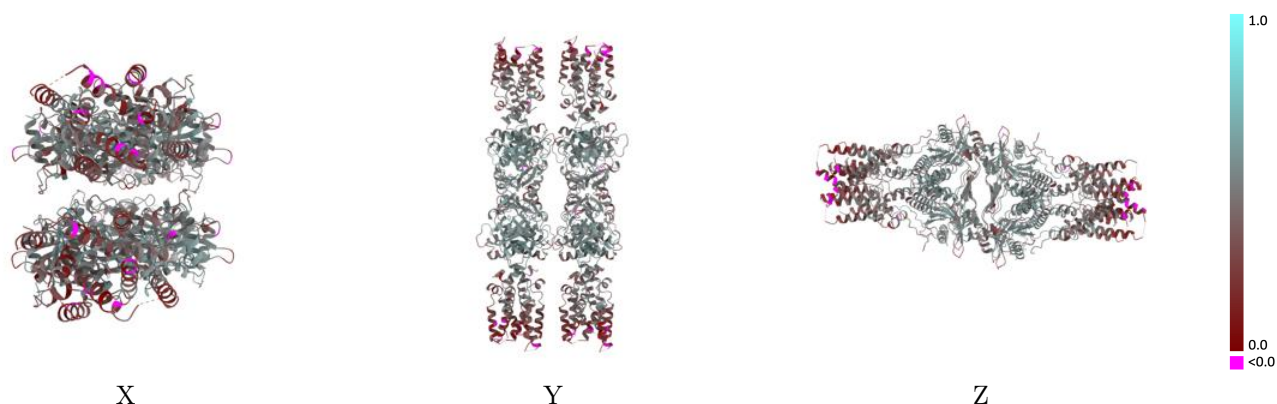
This section contains information regarding the fit between EMDB map EMD-35503 and PDB model 8IK0. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



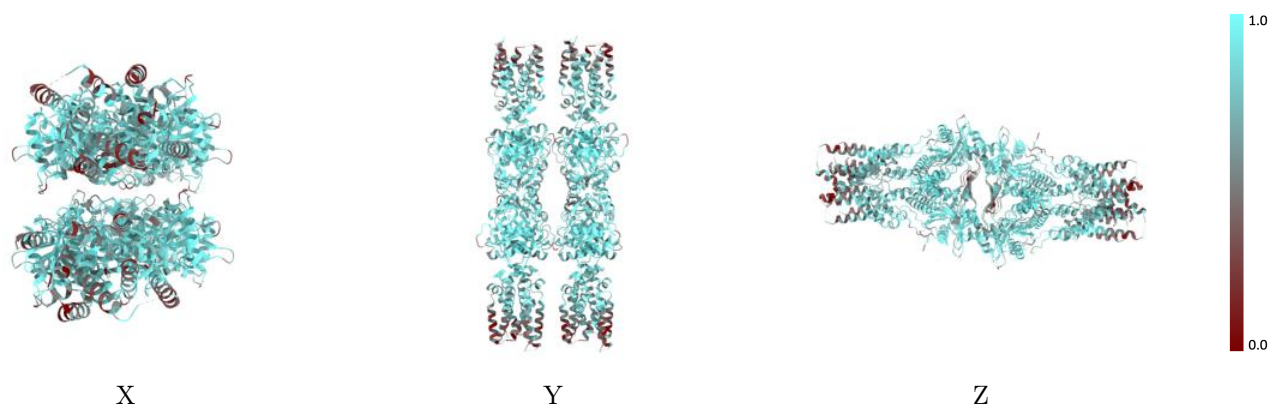
The images above show the 3D surface view of the map at the recommended contour level 0.339 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



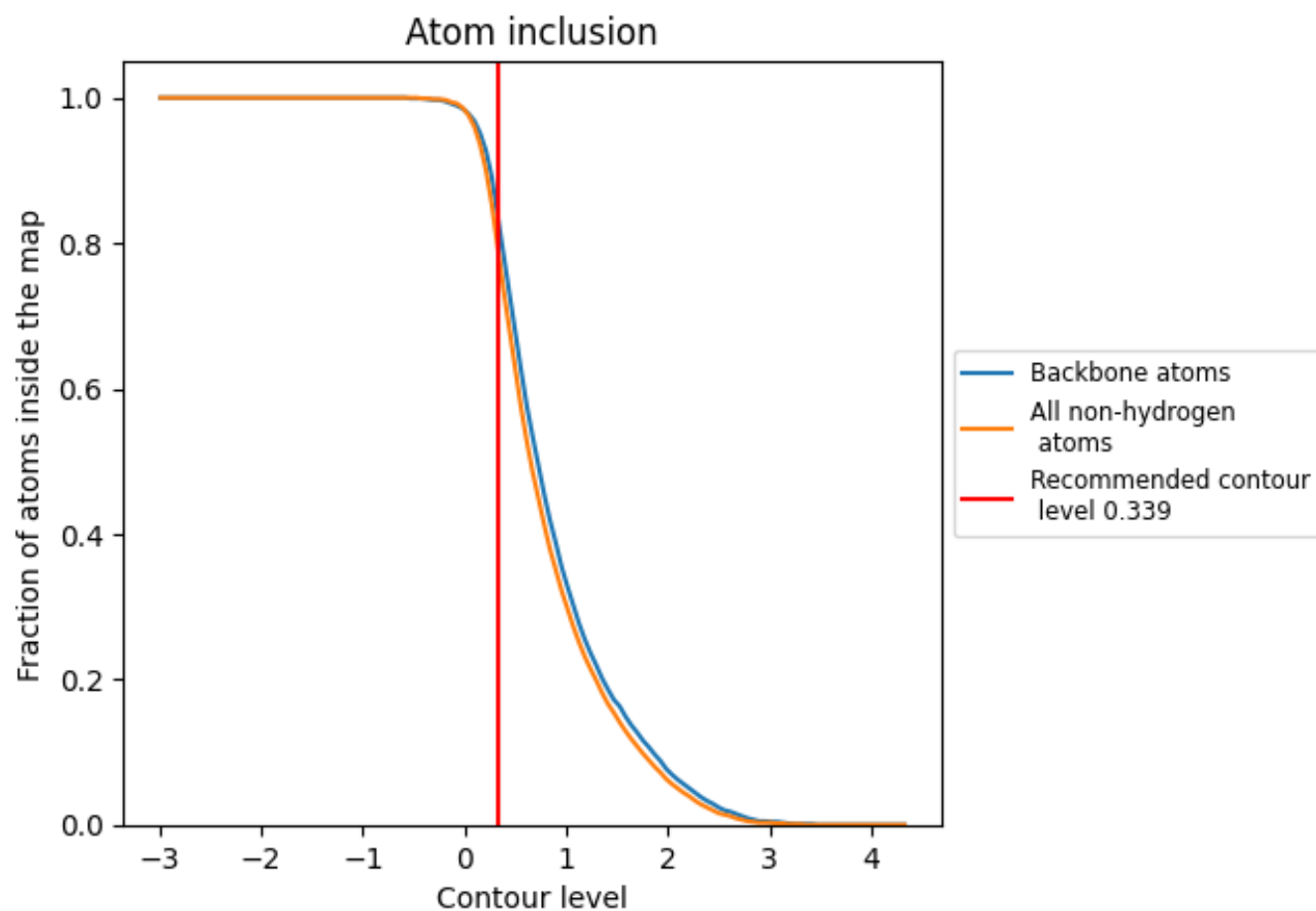
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.339).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.339) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7810	0.4460
A	0.8030	0.4590
B	0.7750	0.4430
C	0.7640	0.4410
D	0.8070	0.4610
E	0.7650	0.4430
F	0.7780	0.4370
G	0.7760	0.4440
H	0.7790	0.4380

1.0

0.0

<0.0