



# wwPDB EM Validation Summary Report ⓘ

May 8, 2023 – 04:24 PM JST

PDB ID : 8IK0  
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 wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

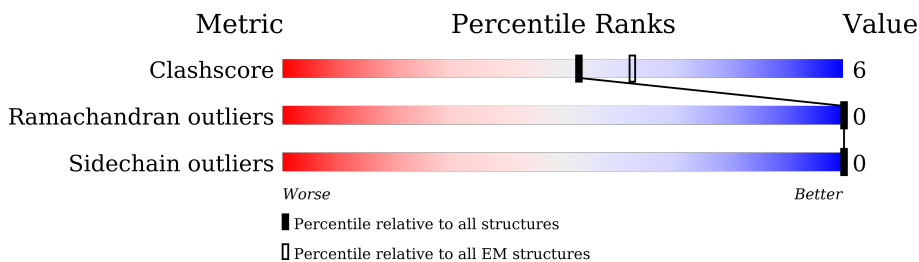
EMDB validation analysis : 0.0.1.dev50  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.32.2

# 1 Overall quality at a glance

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

The reported resolution of this entry is 3.30 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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

Mol	Chain	Length	Quality of chain
1	A	490	
1	B	490	
1	C	490	
1	D	490	
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
			Total	C	N	O	S		
1	A	319	2435	1563	428	425	19	0	0
1	B	320	2449	1571	431	429	18	0	0
1	C	319	2435	1563	428	425	19	0	0
1	F	320	2449	1571	431	429	18	0	0
1	D	319	2435	1563	428	425	19	0	0
1	G	320	2449	1571	431	429	18	0	0
1	E	319	2435	1563	428	425	19	0	0
1	H	320	2449	1571	431	429	18	0	0

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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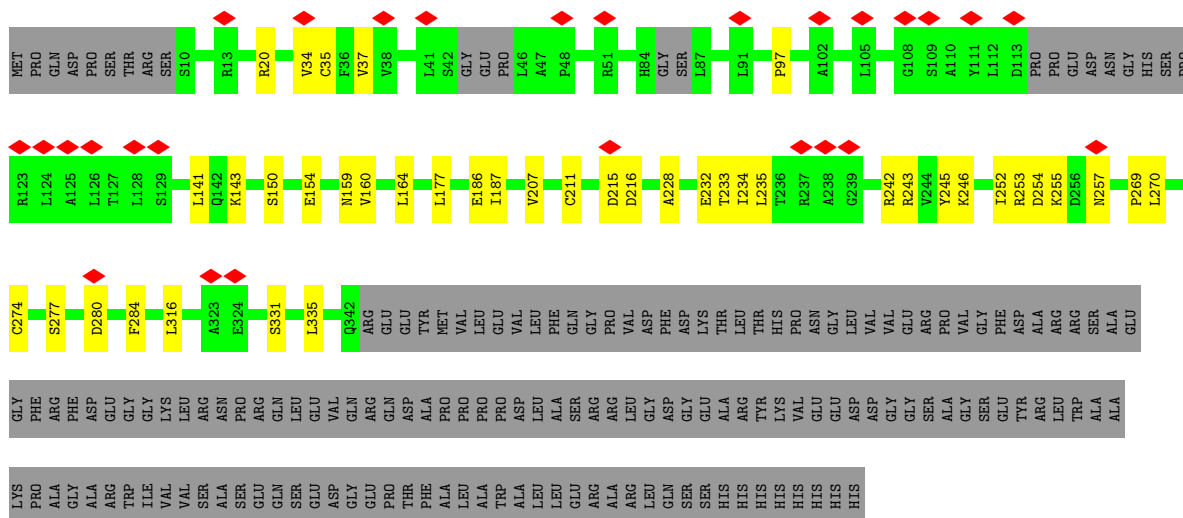
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Chain	Residue	Modelled	Actual	Comment	Reference
E	353	PHE	-	linker	UNP E1C7U0
E	354	GLN	-	linker	UNP E1C7U0
E	355	GLY	-	linker	UNP E1C7U0
E	356	PRO	-	linker	UNP E1C7U0
E	481	SER	-	expression tag	UNP Q9HYC4
E	482	SER	-	expression tag	UNP Q9HYC4
E	483	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

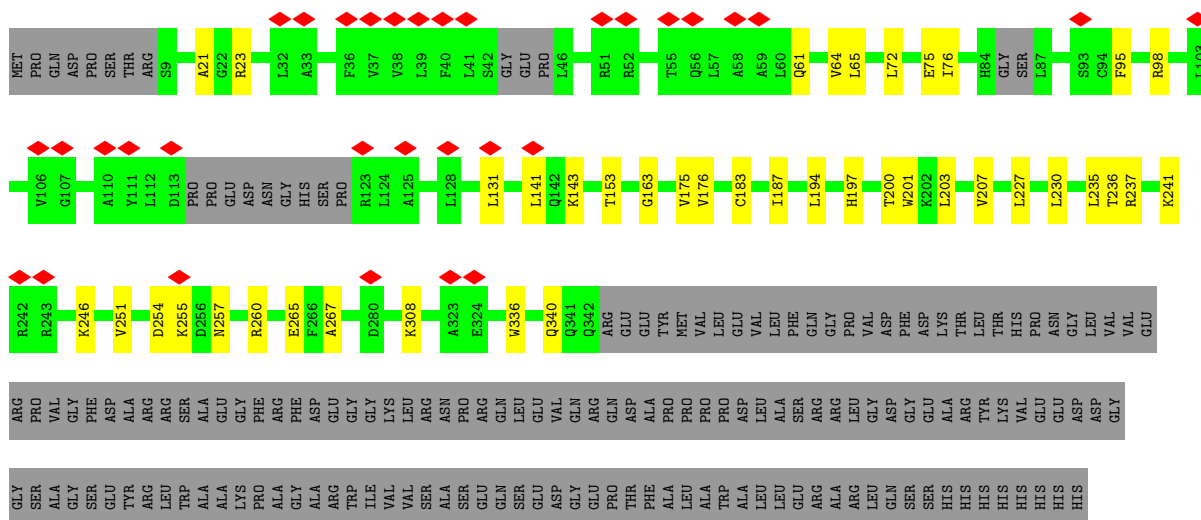




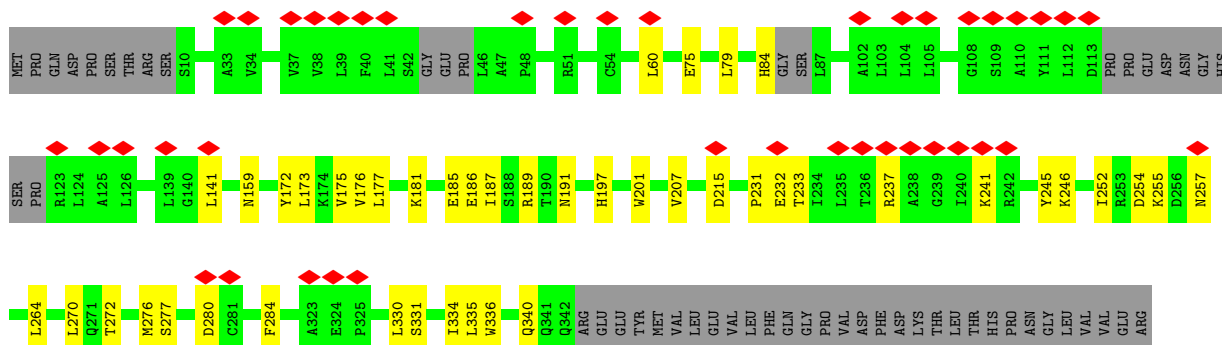




● Molecule 1: Stimulator of interferon genes protein, Immune protein Tsi3



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



PRO VAL  
GLY PHE  
ASP  
ALA  
ARG  
SER  
SER  
ALA  
GLU  
GLY  
PHE  
ARG  
PHE  
ASP  
GLY  
TRP  
GLY  
ILE  
VAL  
VAL  
SER  
ALA  
ASN  
ARG  
GLN  
LEU  
GLU  
VAL  
GLY  
GLN  
ARG  
GLN  
ASP  
PHE  
ALA  
PRO  
PRO  
PRO  
PRO  
ASP  
LEU  
ALA  
SER  
ARG  
ARG  
LEU  
GLY  
GLY  
GLY  
ALA

SER  
ALA  
GLY  
SER  
GLY  
TYR  
ARG  
LEU  
TRP  
ALA  
ALA  
ALA  
LYS  
PRO  
PHE  
ALA  
GLY  
ALA  
ARG  
TRP  
ILE  
VAL  
VAL  
SER  
ALA  
ALA  
SER  
GLY  
GLN  
SER  
SER  
ASP  
VAL  
GLY  
GLN  
GLY  
GLY  
PRO  
THR  
PHE  
ALA  
ALA  
LEU  
LEU  
TRP  
ALA  
ALA  
SER  
GLY  
SER  
HIS  
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● Molecule 1: Stimulator of interferon genes protein, Immune protein Tsi3



MET PRO GLN ASP PRO SER THR ARG S9 R13 L14 L15 R20 A27 Y30 L31 V37 V38 L39 F40 L41 S42 I46 A47 P48 I49 T50 R51 R52 T55 A59 L60 Q61 V64 L65 L72 I76 H84 SER L87 C92 F95

L104 L105 V106 G107 S108 A110 Y111 L112 D113 PRO PRO ASP ASN GLY HIS SER PRO R123 L141 V147 F148 V149 T153 K157 Y169 L173 K174 V175 V176 L177 M184 I187 S188 L194 R198 H204 V207 D212 I213 W214 D215 D216 L217 L227

L236 T237 R237 R243 L249 Y250 D254 K256 D257 R260 L264 L270 Q271 D280 L304 L316 A323 E324 P325 I334 L336 L338 Q341 Q342 ARG GLU TYR MET VAL LEU VAL LEU PHE GLN ARG ALA PRO PRO PRO PRO ASP LEU LEU PHE GLN ARG ALA ARG LEU VAL ASP VAL ASP ASP LYS THR LEU

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

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

HIS  
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## 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	0.23	0/2484	0.50	0/3375
1	B	0.24	0/2499	0.49	0/3394
1	C	0.23	0/2484	0.50	0/3375
1	D	0.23	0/2484	0.50	0/3375
1	E	0.23	0/2484	0.51	0/3375
1	F	0.24	0/2499	0.50	0/3394
1	G	0.24	0/2499	0.49	0/3394
1	H	0.24	0/2499	0.50	0/3394
All	All	0.24	0/19932	0.50	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	27	0
1	C	2435	0	2426	30	0
1	D	2435	0	2426	32	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

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	19536	0	19428	217	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.

The worst 5 of 217 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

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
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 [i](#)

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%)	252 (100%)	0	100	100
1	B	253/417 (61%)	253 (100%)	0	100	100
1	C	252/417 (60%)	252 (100%)	0	100	100
1	D	252/417 (60%)	252 (100%)	0	100	100
1	E	252/417 (60%)	252 (100%)	0	100	100
1	F	253/417 (61%)	253 (100%)	0	100	100
1	G	253/417 (61%)	253 (100%)	0	100	100
1	H	253/417 (61%)	253 (100%)	0	100	100
All	All	2020/3336 (61%)	2020 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	191	ASN
1	H	278	GLN
1	H	341	GLN
1	C	191	ASN
1	A	191	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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



## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

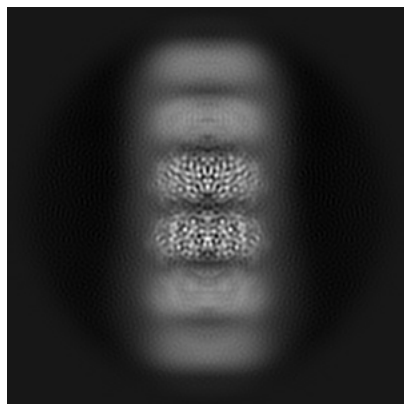
## 6 Map visualisation [i](#)

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

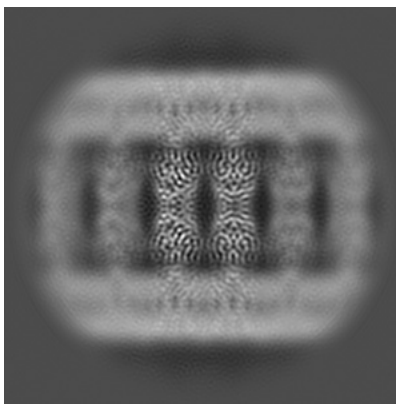
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

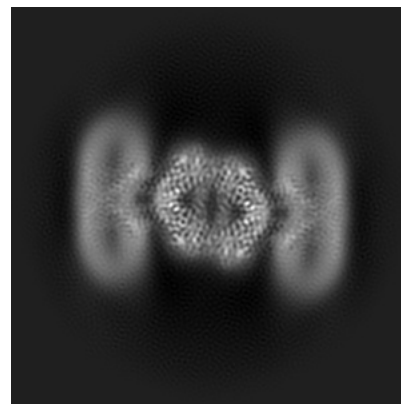
#### 6.1.1 Primary map



X

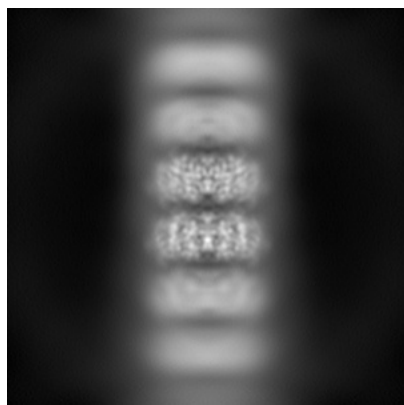


Y

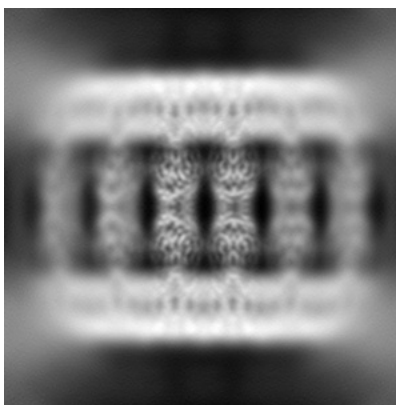


Z

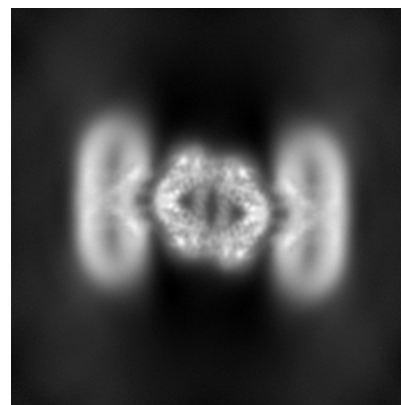
#### 6.1.2 Raw map



X



Y

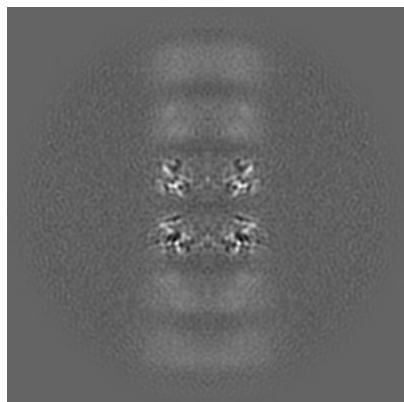


Z

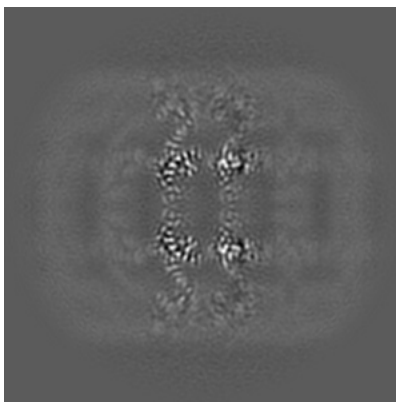
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

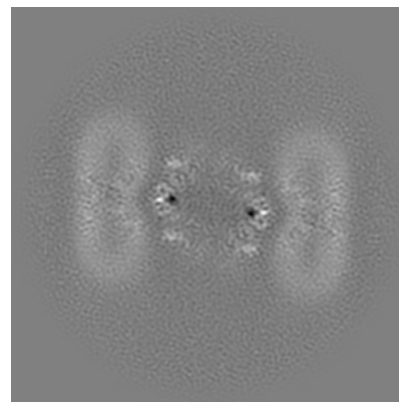
### 6.2.1 Primary map



X Index: 128

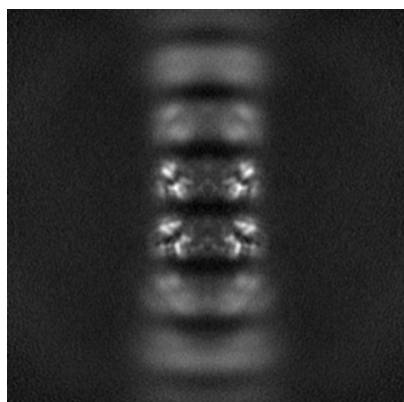


Y Index: 128

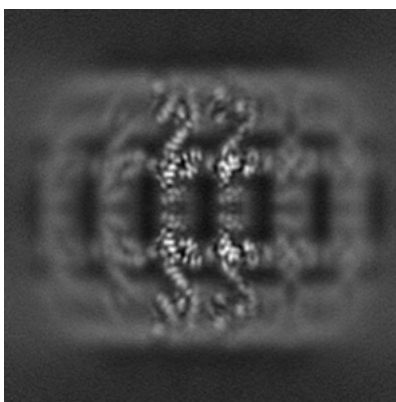


Z Index: 128

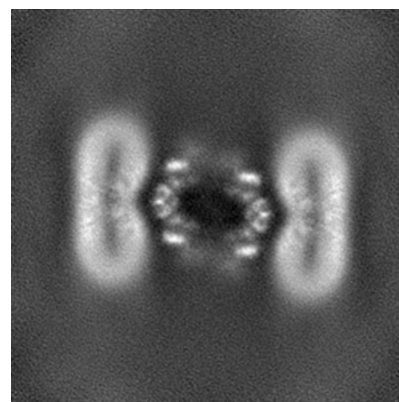
### 6.2.2 Raw map



X Index: 128



Y Index: 128

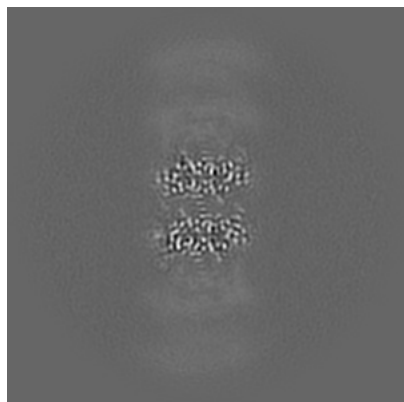


Z Index: 128

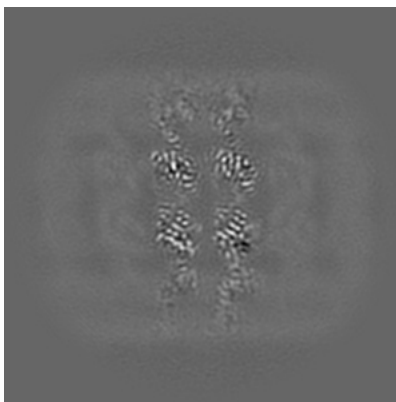
The images above show central slices of the map in three orthogonal directions.

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

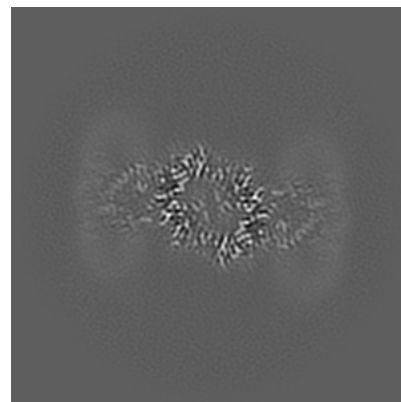
### 6.3.1 Primary map



X Index: 151

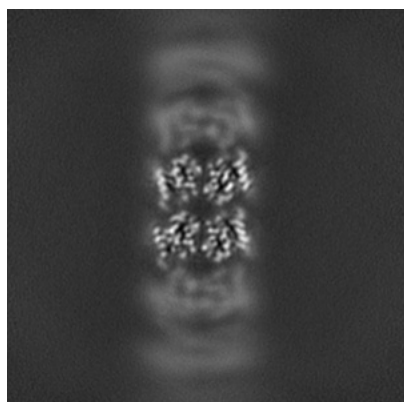


Y Index: 115

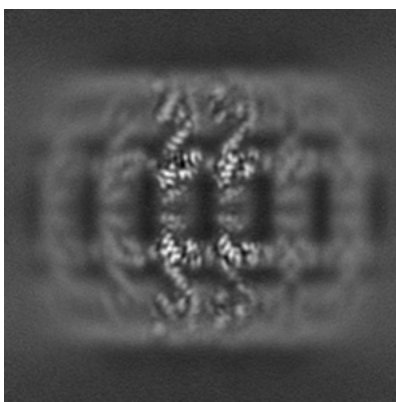


Z Index: 106

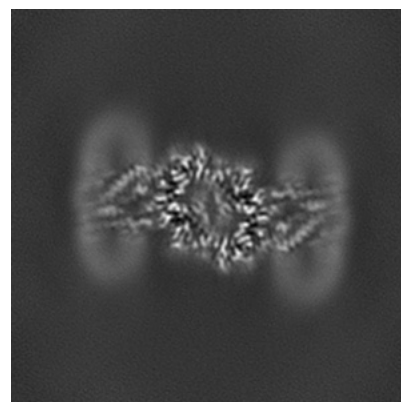
### 6.3.2 Raw map



X Index: 148



Y Index: 129

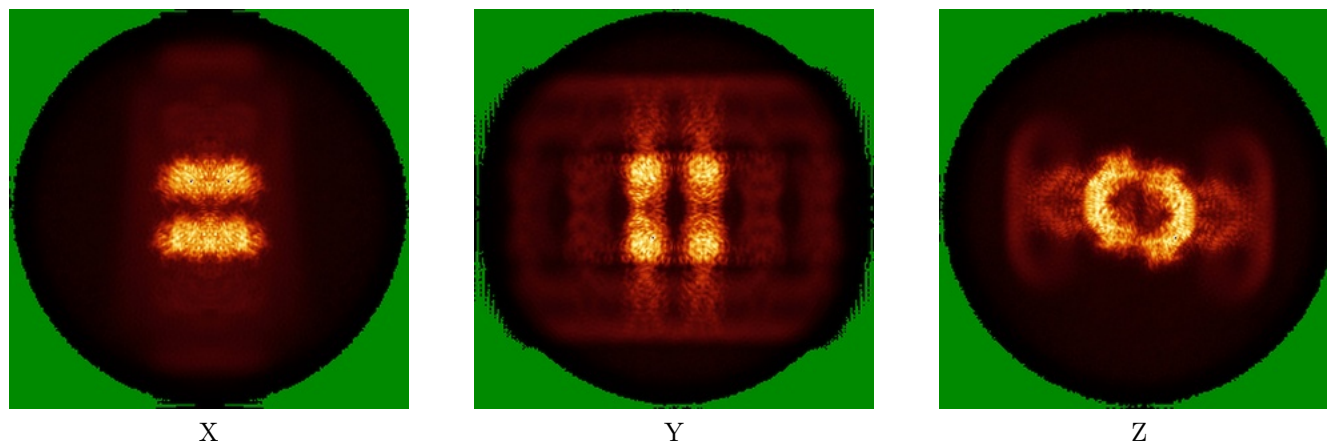


Z Index: 106

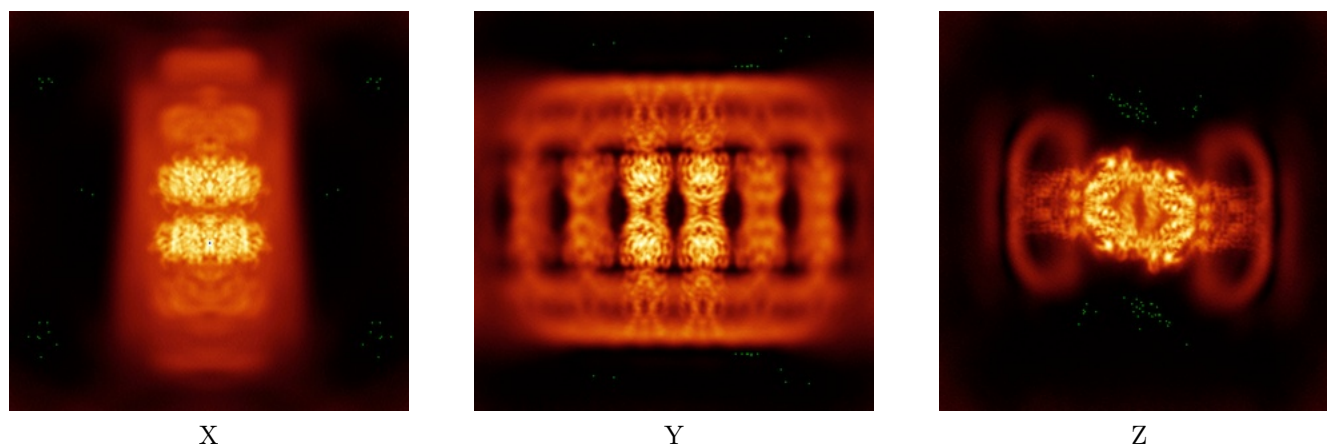
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



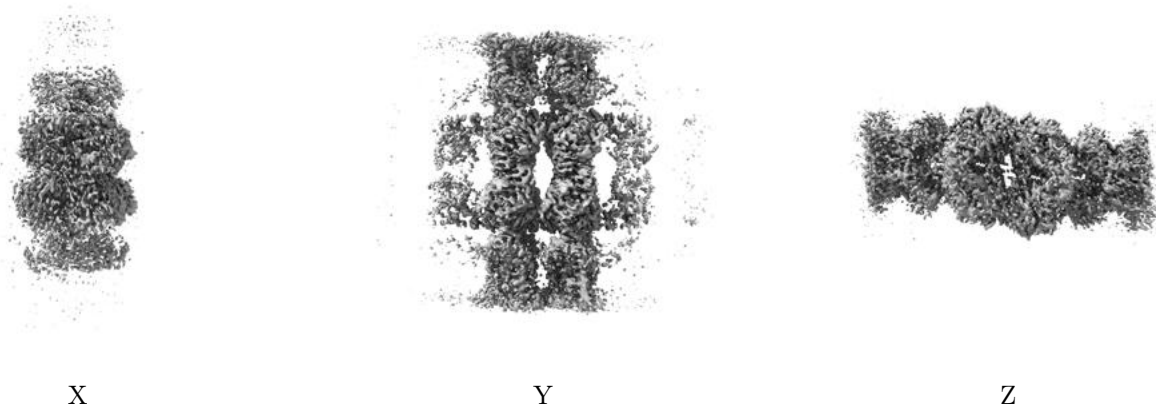
### 6.4.2 Raw map



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.

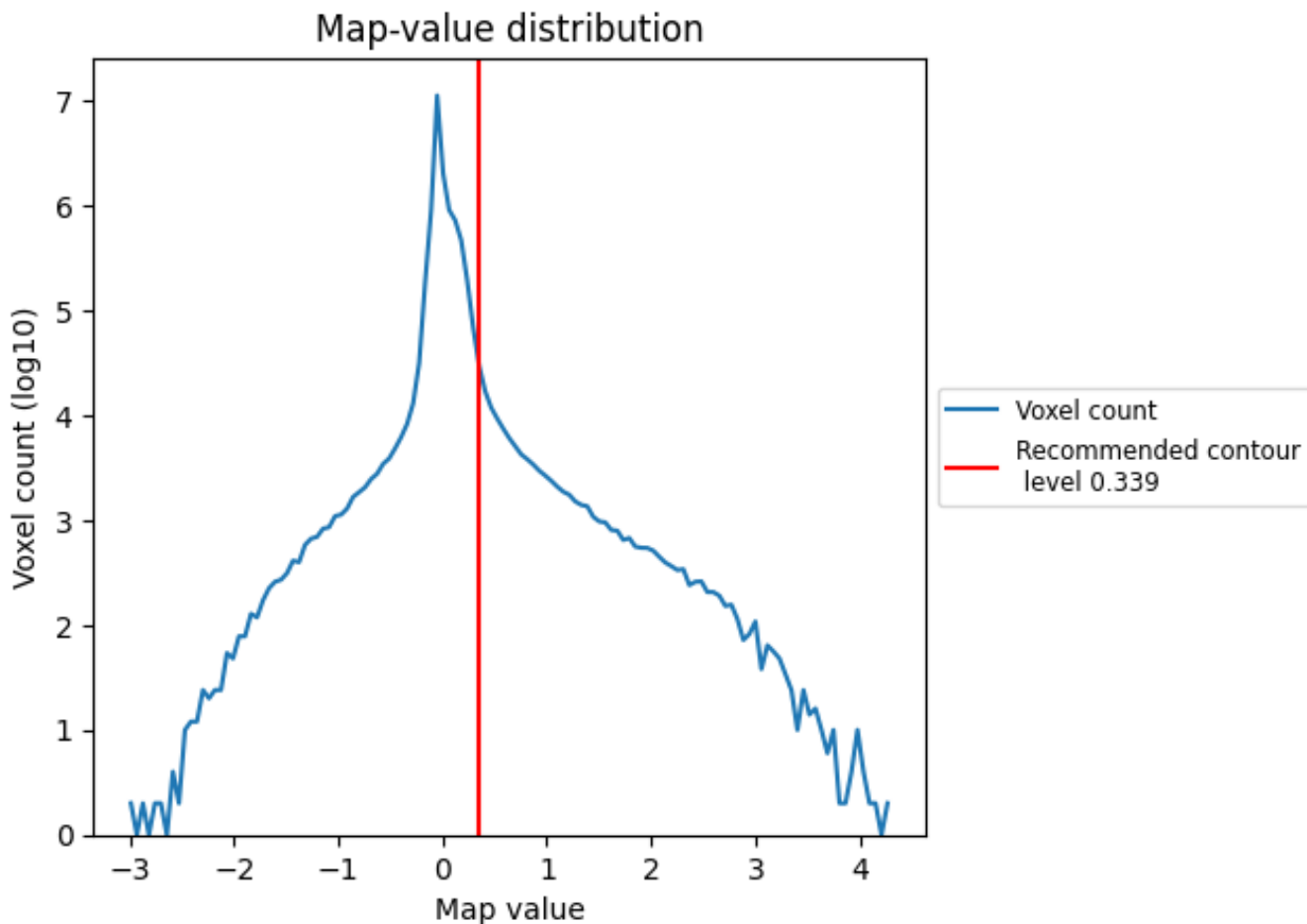
## 6.6 Mask visualisation [i](#)

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.

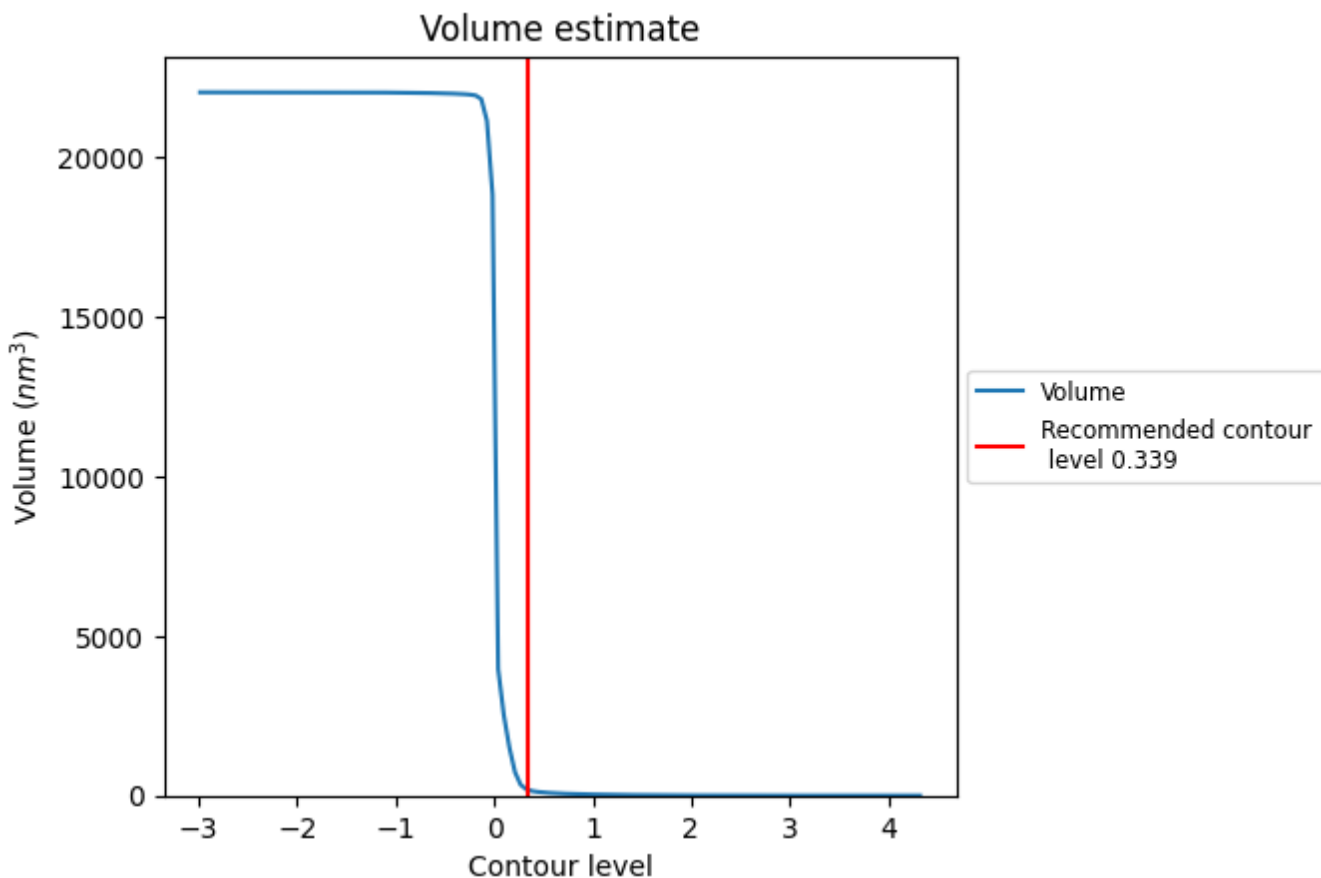
### 7.1 Map-value distribution [i](#)



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](#)

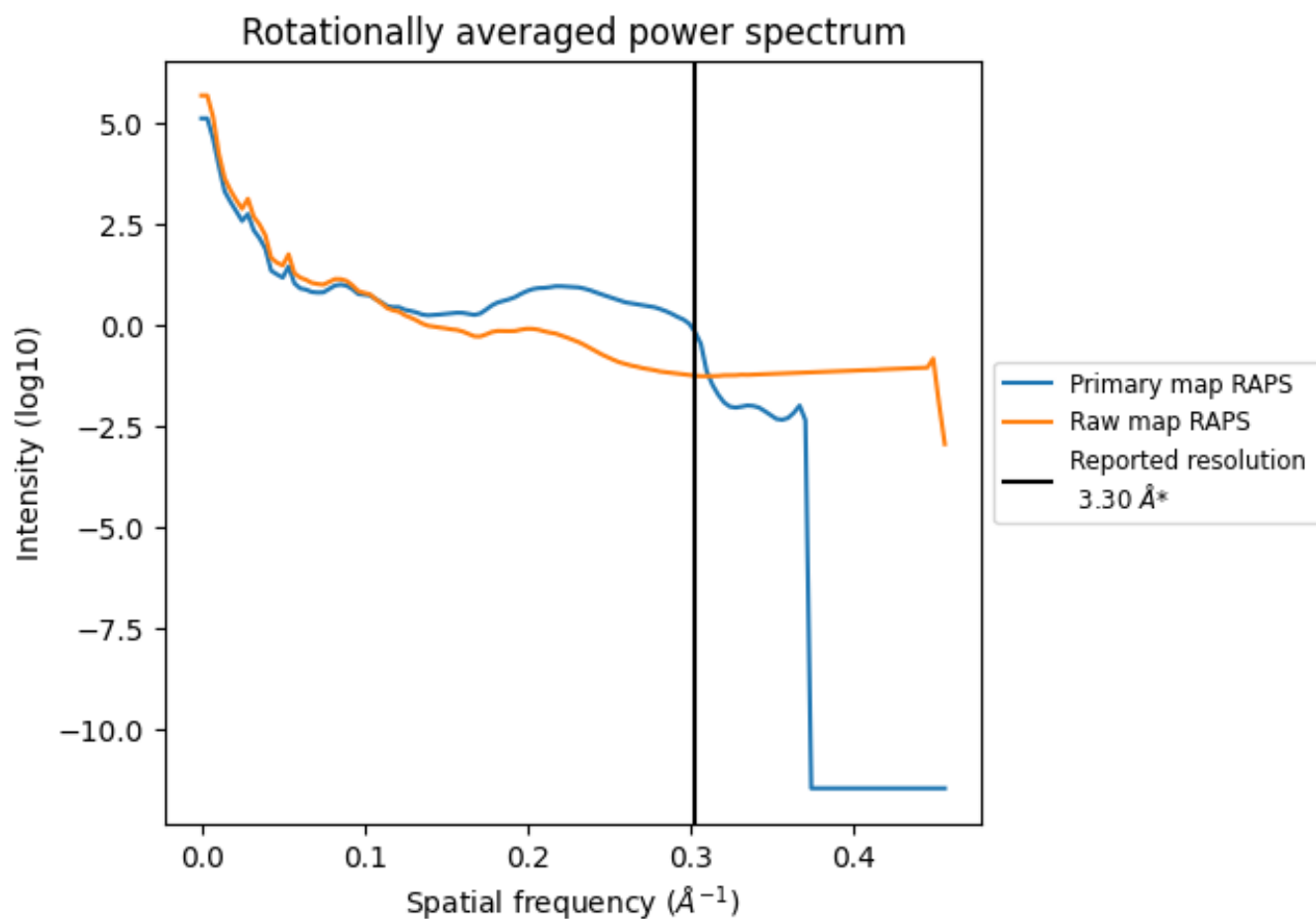


The volume at the recommended contour level is 186 nm<sup>3</sup>; this corresponds to an approximate mass of 168 kDa.

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 [i](#)

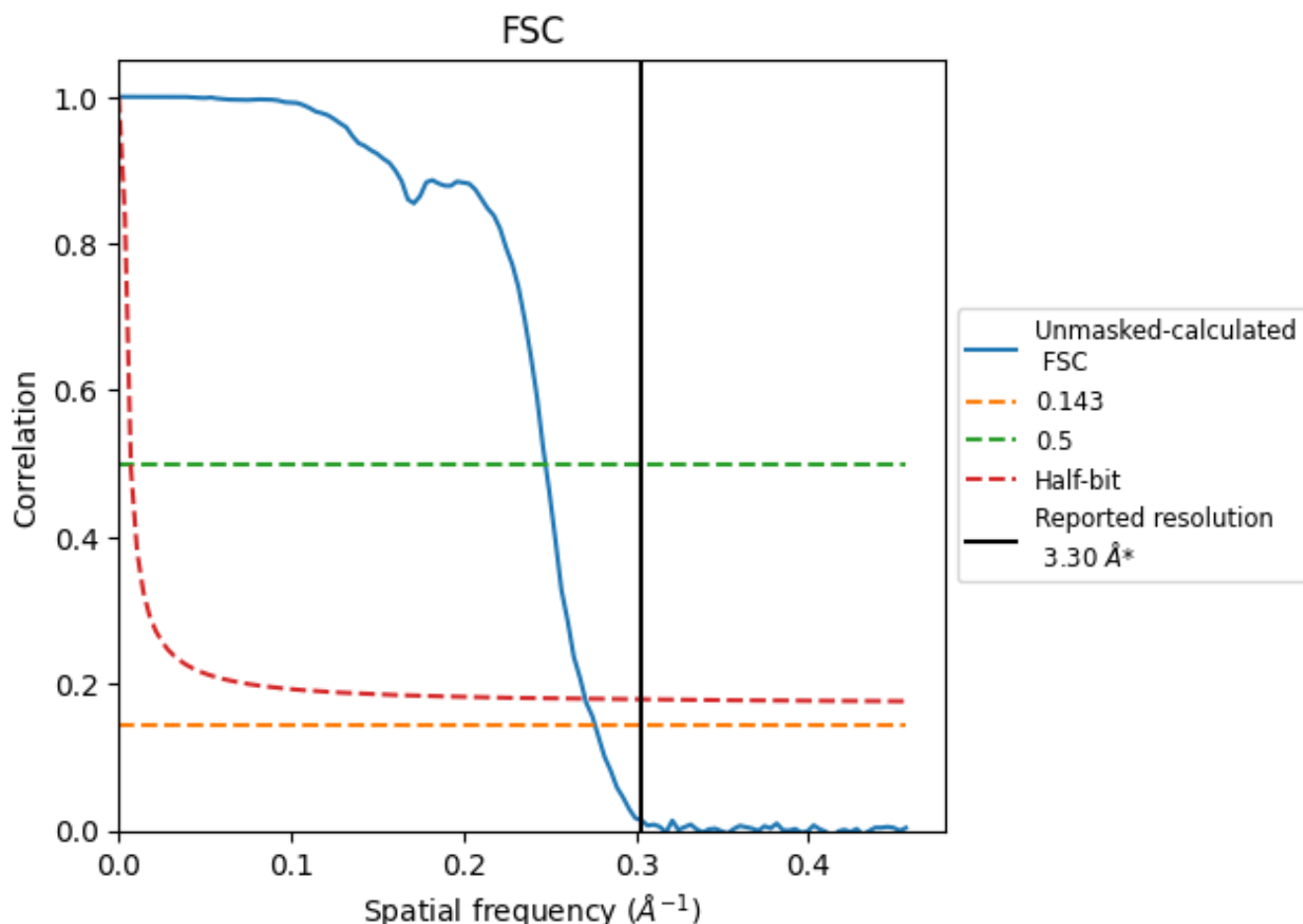


\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>

## 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](#)

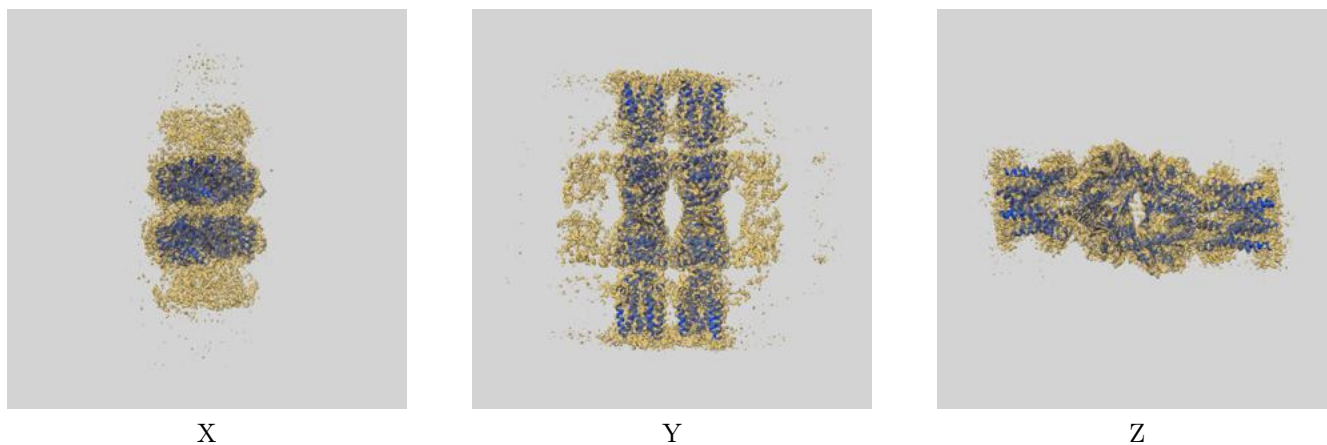
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.62	4.04	3.70

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

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

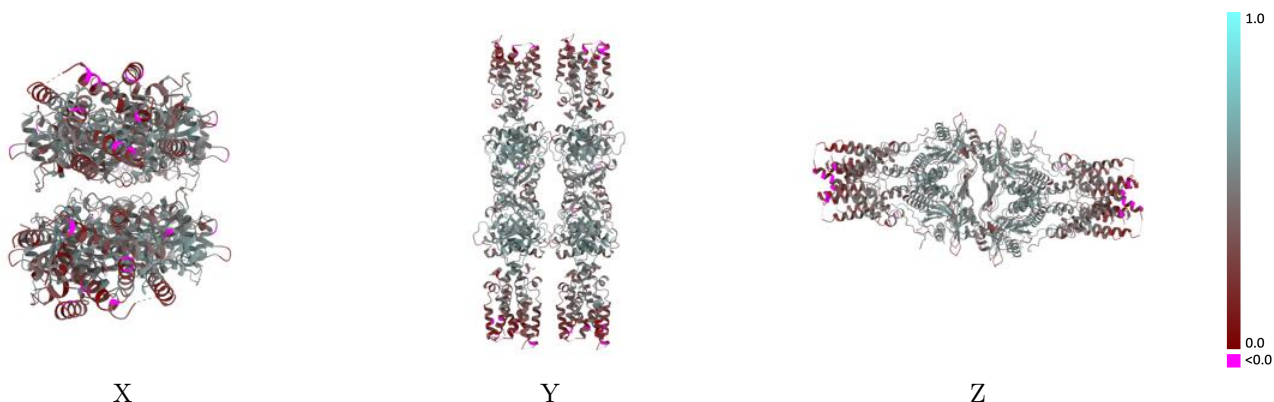
This section contains information regarding the fit between EMDB map EMD-35503 and PDB model 8IK0. Per-residue inclusion information can be found in section 3 on page 9.

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



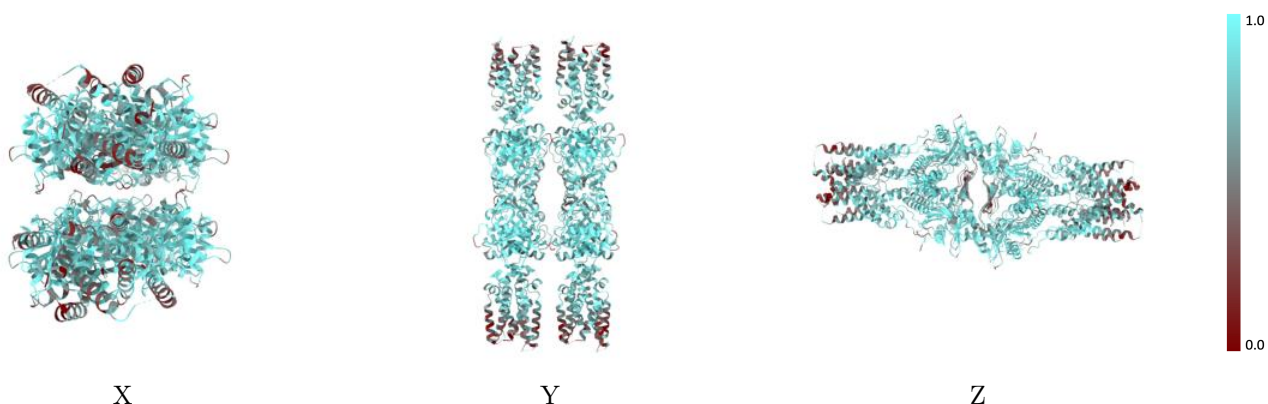
The images above show the 3D surface view of the map at the recommended contour level 0.339 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



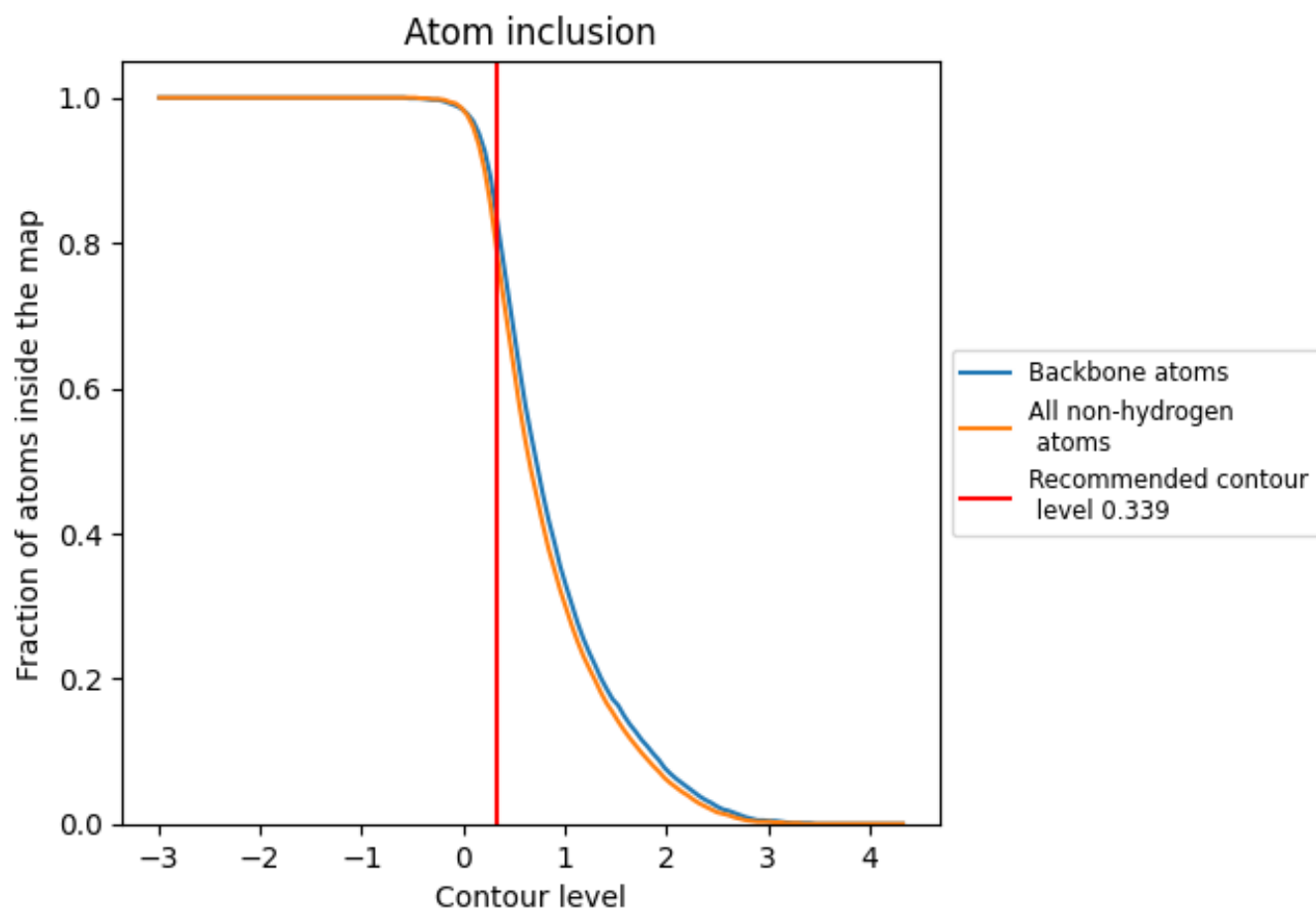
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



















## 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

