



## Full wwPDB EM Validation Report ⓘ

Jul 28, 2025 – 02:30 PM EDT

PDB ID : 9PFG / pdb\_00009pfg  
EMDB ID : EMD-71601  
Title : Min22bin20S complex (NSF-alphaSNAP-2:2 syntaxin-1a H3:SNAP-25 SN1),  
4:2:2 alphaSNAP-syntaxin-1a H3-SNAP-25 SN1 subcomplex local refinement,  
non-hydrolyzing, class 28  
Authors : White, K.I.; Brunger, A.T.  
Deposited on : 2025-07-04  
Resolution : 3.58 Å (reported)  
Based on initial models : 1JTH, 6MDM

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.dev126  
MolProbity : 4-5-2 with Phenix2.0rc1  
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) : 2.45.1

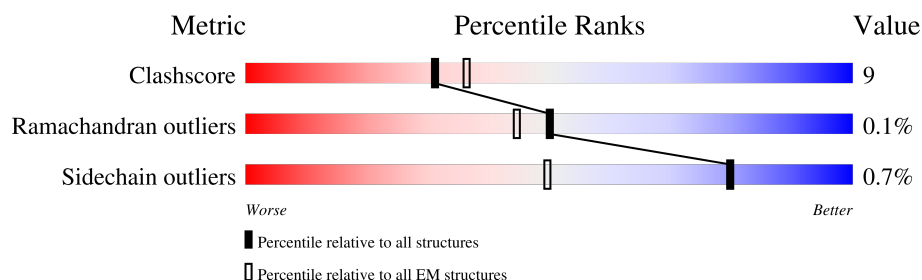
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.58 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	84	
1	C	84	
2	B	78	
2	D	78	
3	E	296	
3	F	296	
3	G	296	
3	H	296	

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Mol	Chain	Length	Quality of chain
4	J	747	<div><div><div></div><div></div><div></div></div><div>17%7%75%</div></div>
4	K	747	<div><div><div></div><div></div><div></div></div><div>5%18%7%75%</div></div>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 27563 atoms, of which 13655 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 Synaptosomal-associated protein 25.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	65	Total	C	H	N	O	S	2	0
			1041	316	513	93	115	4		
1	C	64	Total	C	H	N	O	S	2	0
			1027	310	508	91	114	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP P60881
C	0	SER	-	expression tag	UNP P60881

- Molecule 2 is a protein called Syntaxin-1A.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	68	Total	C	H	N	O	S	0	0
			1100	345	544	94	112	5		
2	D	68	Total	C	H	N	O	S	0	0
			1062	345	506	94	112	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	190	MET	-	initiating methionine	UNP P32851
D	190	MET	-	initiating methionine	UNP P32851

- Molecule 3 is a protein called Alpha-soluble NSF attachment protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	H	284	Total	C	H	N	O	S	2	0
			4450	1410	2205	377	440	18		
3	E	280	Total	C	H	N	O	S	0	0
			4372	1387	2170	368	429	18		

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Mol	Chain	Residues	Atoms						AltConf	Trace
3	F	280	Total	C	H	N	O	S	0	0
			4370	1387	2168	368	429	18		
3	G	281	Total	C	H	N	O	S	0	0
			4377	1389	2171	369	430	18		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	0	GLY	-	expression tag	UNP P54921
E	0	GLY	-	expression tag	UNP P54921
F	0	GLY	-	expression tag	UNP P54921
G	0	GLY	-	expression tag	UNP P54921

- Molecule 4 is a protein called Vesicle-fusing ATPase.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	J	185	Total	C	H	N	O	S	0	0
			2870	909	1435	244	275	7		
4	K	185	Total	C	H	N	O	S	0	0
			2870	909	1435	244	275	7		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	-2	GLY	-	expression tag	UNP P18708
J	-1	ALA	-	expression tag	UNP P18708
J	0	HIS	-	expression tag	UNP P18708
K	-2	GLY	-	expression tag	UNP P18708
K	-1	ALA	-	expression tag	UNP P18708
K	0	HIS	-	expression tag	UNP P18708

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		AltConf
5	B	3	Total	O	0
			3	3	
5	C	5	Total	O	0
			5	5	
5	D	2	Total	O	0
			2	2	
5	H	4	Total	O	0
			4	4	

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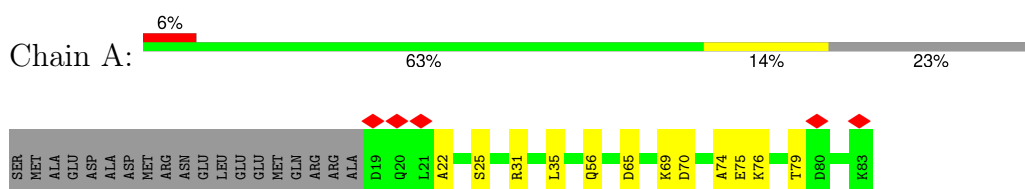
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Mol	Chain	Residues	Atoms		AltConf
5	E	4	Total 4	O 4	0
5	F	4	Total 4	O 4	0
5	G	2	Total 2	O 2	0

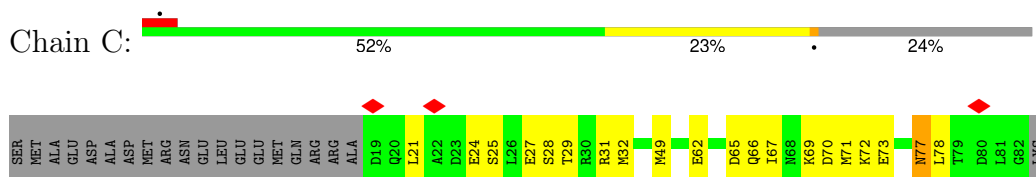
### 3 Residue-property plots [i](#)

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.

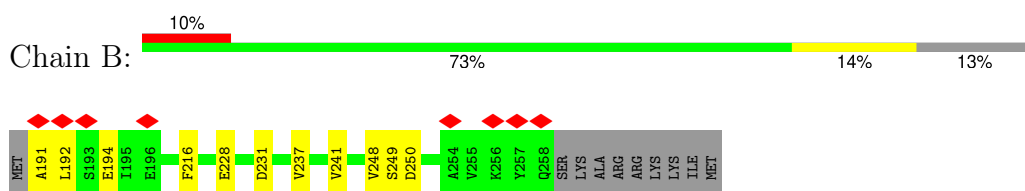
- Molecule 1: Synaptosomal-associated protein 25



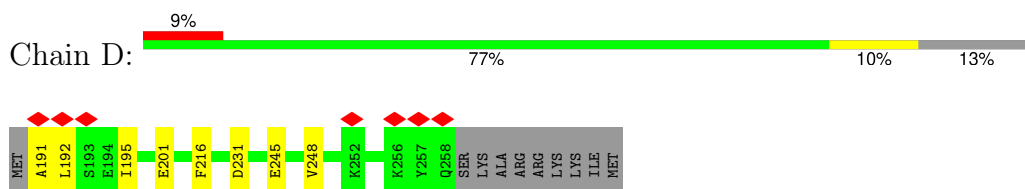
- Molecule 1: Synaptosomal-associated protein 25



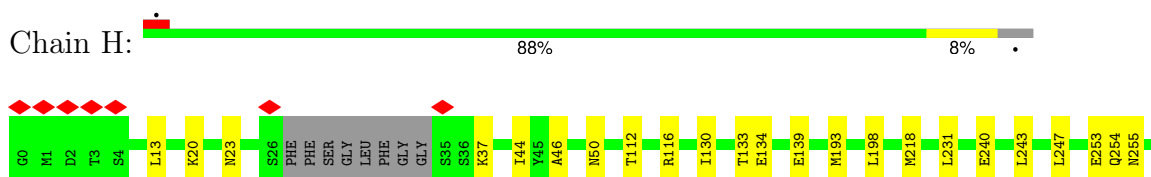
- Molecule 2: Syntaxin-1A

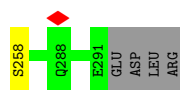


- Molecule 2: Syntaxin-1A

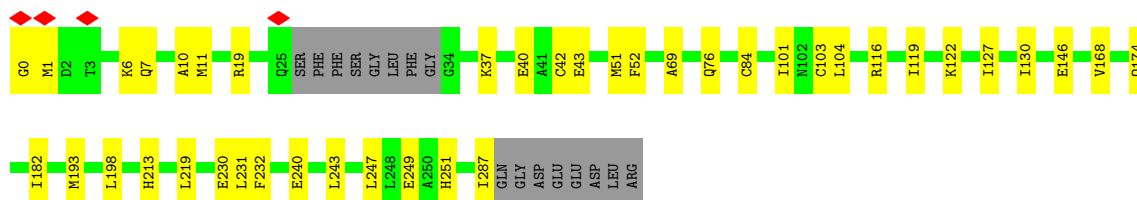
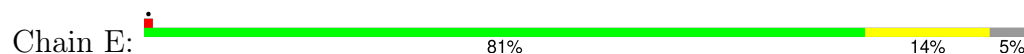


- Molecule 3: Alpha-soluble NSF attachment protein

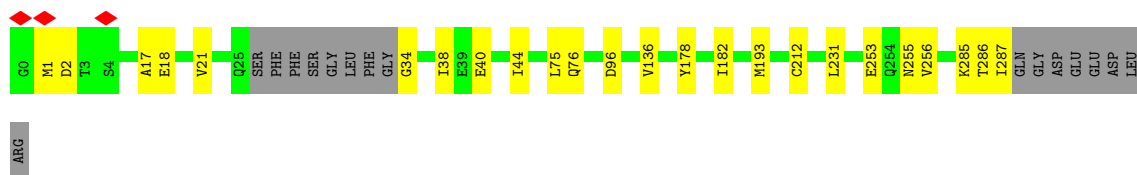
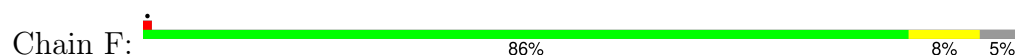




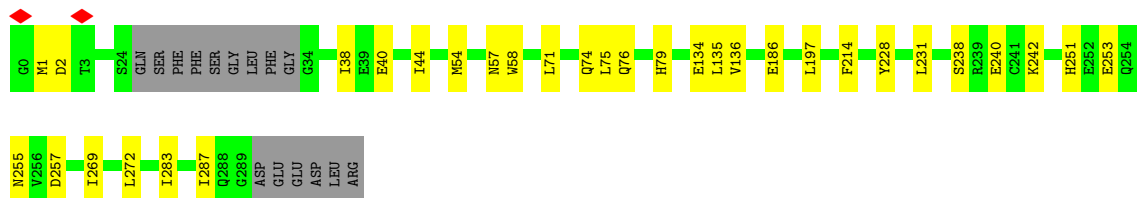
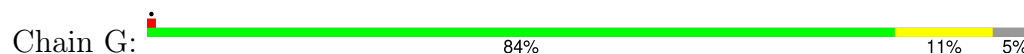
- Molecule 3: Alpha-soluble NSF attachment protein



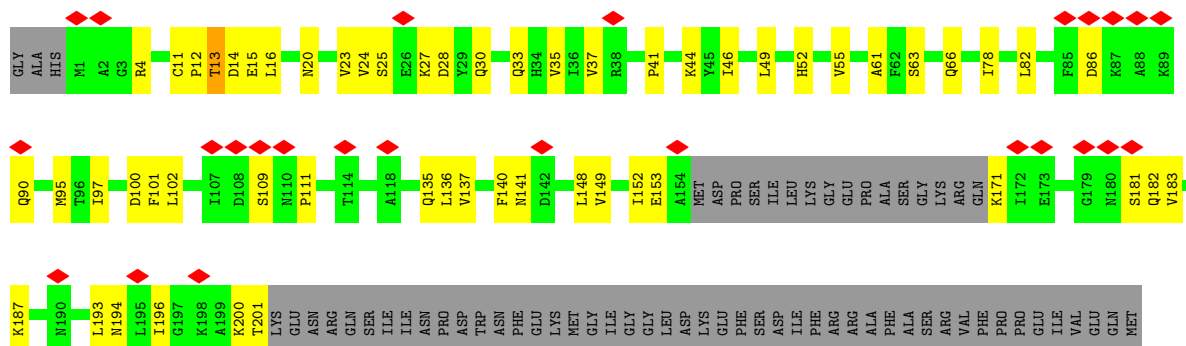
- Molecule 3: Alpha-soluble NSF attachment protein



- Molecule 3: Alpha-soluble NSF attachment protein



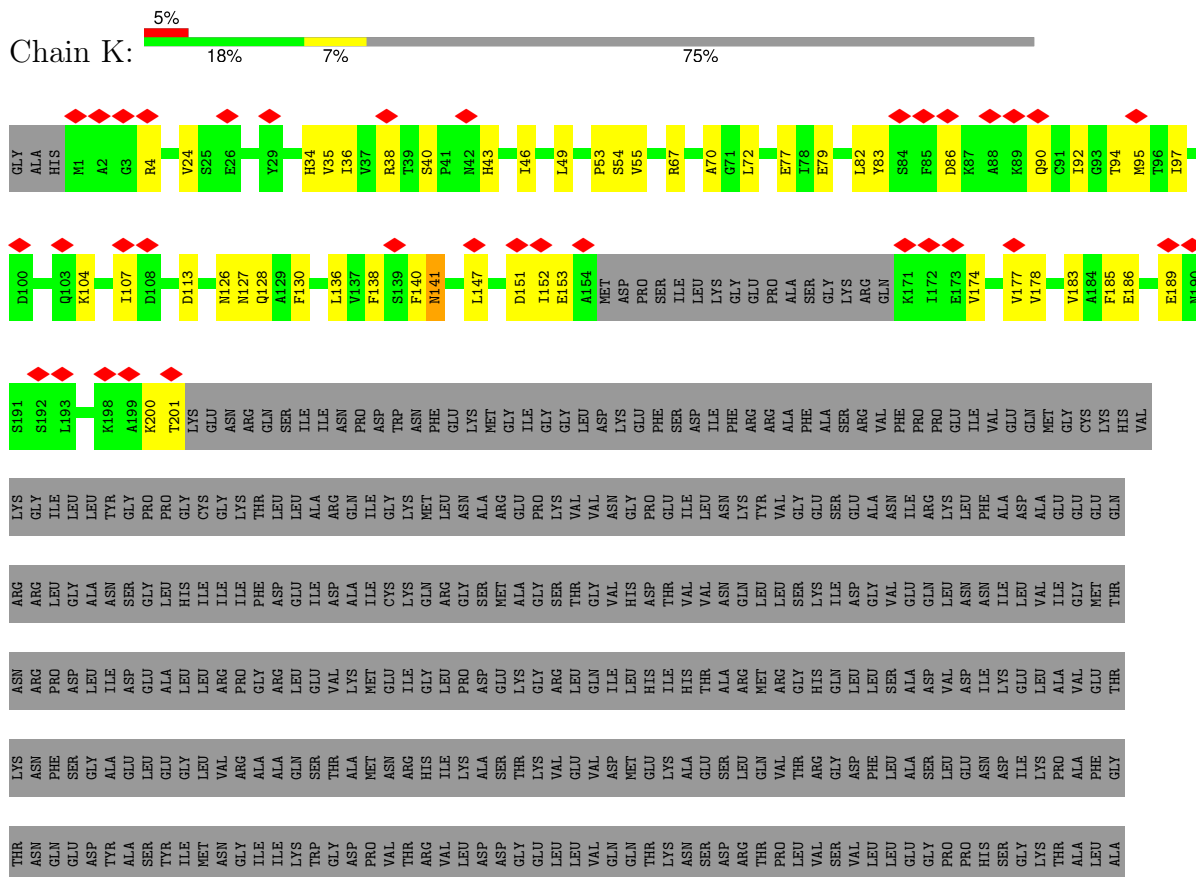
- Molecule 4: Vesicle-fusing ATPase





[illegible]

- Molecule 4: Vesicle-fusing ATPase



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

ARG
GLU
GLY
GLY
ALA
SER
PRO
LEU
ASP
PHE
ASP

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	341427	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	33.992	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	22500	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.656	Depositor
Minimum map value	-1.597	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.058	Depositor
Recommended contour level	0.3	Depositor
Map size ( $\text{\AA}$ )	322.224, 322.224, 322.224	wwPDB
Map dimensions	294, 294, 294	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.096, 1.096, 1.096	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	0.25	0/535	0.35	0/711
1	C	0.57	0/525	0.81	0/699
2	B	0.25	0/562	0.42	0/753
2	D	0.23	0/562	0.39	0/753
3	E	0.25	0/2238	0.38	0/3007
3	F	0.19	0/2238	0.32	0/3007
3	G	0.21	0/2242	0.38	0/3012
3	H	0.19	0/2289	0.32	0/3075
4	J	0.20	0/1459	0.38	0/1967
4	K	0.19	0/1459	0.37	0/1967
All	All	0.23	0/14109	0.39	0/18951

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	528	513	513	7	0
1	C	519	508	504	23	0
2	B	556	544	544	14	0
2	D	556	506	544	12	0
3	E	2202	2170	2168	34	0
3	F	2202	2168	2168	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	2206	2171	2171	33	0
3	H	2245	2205	2193	21	0
4	J	1435	1435	1437	42	0
4	K	1435	1435	1437	47	0
5	B	3	0	0	0	0
5	C	5	0	0	0	0
5	D	2	0	0	0	0
5	E	4	0	0	0	0
5	F	4	0	0	0	0
5	G	2	0	0	0	0
5	H	4	0	0	0	0
All	All	13908	13655	13679	238	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 9.

All (238) 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)
2:D:192:LEU:HD23	2:D:195:ILE:HD12	1.38	1.05
2:D:192:LEU:HA	2:D:195:ILE:HD12	1.52	0.91
4:J:200:LYS:O	4:J:201:THR:OG1	1.95	0.83
2:B:241:VAL:HG22	1:C:67:ILE:HD11	1.64	0.80
4:K:200:LYS:O	4:K:201:THR:OG1	2.00	0.79
1:C:49:MET:HE1	3:G:197:LEU:HD22	1.61	0.79
2:D:191:ALA:O	2:D:195:ILE:HG13	1.84	0.77
4:J:100:ASP:OD1	4:J:101:PHE:N	2.20	0.75
4:K:97:ILE:HD12	4:K:183:VAL:HG11	1.69	0.74
2:D:192:LEU:HA	2:D:195:ILE:CD1	2.17	0.73
3:H:139:GLU:N	3:H:139:GLU:OE1	2.22	0.73
2:B:241:VAL:HA	1:C:67:ILE:HD11	1.72	0.71
4:J:135:GLN:N	4:J:135:GLN:OE1	2.24	0.71
4:K:128:GLN:O	4:K:177:VAL:HG12	1.93	0.69
3:E:76:GLN:OE1	3:E:76:GLN:N	2.26	0.68
4:K:77:GLU:OE1	4:K:77:GLU:N	2.27	0.68
3:G:251:HIS:CG	3:G:251:HIS:O	2.48	0.67
4:J:95:MET:SD	4:J:95:MET:N	2.68	0.67
3:E:174:GLN:O	3:E:174:GLN:NE2	2.29	0.66
3:G:1:MET:SD	3:G:2:ASP:N	2.69	0.65
3:E:193:MET:HE2	3:E:232:PHE:CD1	2.32	0.65
4:K:186:GLU:N	4:K:186:GLU:OE2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:LYS:HD2	1:A:70:ASP:N	2.12	0.64
2:B:241:VAL:HG22	1:C:67:ILE:CD1	2.27	0.64
3:G:134:GLU:OE1	3:G:135:LEU:N	2.31	0.64
4:K:141:ASN:OD1	4:K:141:ASN:O	2.16	0.64
4:J:35:VAL:HG13	4:J:49:LEU:HD11	1.81	0.63
1:C:69:LYS:HE2	3:E:116:ARG:HD2	1.79	0.63
3:G:57:ASN:OD1	3:G:58:TRP:N	2.32	0.63
3:H:240:GLU:OE1	3:H:240:GLU:N	2.30	0.62
2:D:192:LEU:HD23	2:D:195:ILE:CD1	2.23	0.62
3:E:251:HIS:O	3:E:251:HIS:ND1	2.33	0.61
3:G:255:ASN:ND2	3:G:257:ASP:OD1	2.34	0.60
3:G:231:LEU:HD23	3:G:231:LEU:O	2.01	0.60
1:A:56:GLN:NE2	2:D:231:ASP:OD1	2.33	0.60
3:E:240:GLU:OE1	3:E:240:GLU:N	2.30	0.60
3:E:193:MET:HE1	3:E:231:LEU:CD2	2.31	0.59
3:E:219:LEU:HD23	4:K:67:ARG:NH1	2.18	0.59
4:K:36:ILE:HG23	4:K:36:ILE:O	2.02	0.59
4:K:46:ILE:HG21	4:K:174:VAL:CG2	2.33	0.59
3:E:231:LEU:HD23	3:E:231:LEU:O	2.03	0.59
4:J:86:ASP:N	4:J:90:GLN:OE1	2.36	0.58
3:G:257:ASP:OD1	3:G:257:ASP:N	2.34	0.58
4:K:153:GLU:N	4:K:153:GLU:OE1	2.36	0.58
4:K:95:MET:HB3	4:K:152:ILE:HD12	1.84	0.58
2:B:241:VAL:CG2	1:C:67:ILE:HD11	2.34	0.57
3:E:249:GLU:OE2	3:E:249:GLU:HA	2.05	0.56
3:F:38:ILE:HD12	3:F:38:ILE:H	1.69	0.56
4:K:70:ALA:HB3	4:K:72:LEU:HD12	1.87	0.56
4:J:140:PHE:CD2	4:J:141:ASN:OD1	2.58	0.56
3:H:112:THR:CG2	3:G:54:MET:HE1	2.36	0.56
4:J:37:VAL:HG21	4:J:78:ILE:HD12	1.88	0.56
4:K:95:MET:SD	4:K:97:ILE:HD11	2.45	0.55
3:F:182:ILE:HD11	3:F:212:CYS:HB3	1.88	0.55
4:K:138:PHE:HB2	4:K:147:LEU:HD11	1.89	0.55
1:C:65:ASP:O	1:C:66:GLN:C	2.50	0.55
3:G:269:ILE:HD12	3:G:269:ILE:H	1.71	0.55
2:B:237:VAL:O	2:B:241:VAL:HG23	2.07	0.54
3:G:136:VAL:HG12	3:G:136:VAL:O	2.07	0.54
4:K:95:MET:HG3	4:K:183:VAL:HG22	1.89	0.54
4:K:151:ASP:OD1	4:K:152:ILE:N	2.40	0.54
4:K:82:LEU:HD23	4:K:83:TYR:N	2.22	0.54
4:K:46:ILE:HG21	4:K:174:VAL:HG21	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:178:TYR:O	3:F:182:ILE:HD12	2.08	0.54
3:E:6:LYS:HD3	3:E:51:MET:HE1	1.90	0.53
3:E:69:ALA:HB2	3:E:84:CYS:HB2	1.90	0.53
2:B:241:VAL:HG22	1:C:67:ILE:CG1	2.38	0.53
3:G:134:GLU:CD	3:G:135:LEU:HD23	2.34	0.53
3:E:101:ILE:HD11	3:E:130:ILE:HG21	1.90	0.53
3:F:1:MET:SD	3:F:2:ASP:N	2.82	0.52
3:H:46:ALA:O	3:H:50:ASN:ND2	2.43	0.52
4:J:23:VAL:HG12	4:J:55:VAL:HG21	1.92	0.52
1:C:27:GLU:O	1:C:31:ARG:HG3	2.09	0.52
4:K:92:ILE:O	4:K:178:VAL:HG22	2.10	0.52
3:E:287:ILE:HG23	3:E:287:ILE:O	2.10	0.51
3:F:231:LEU:O	3:F:231:LEU:HD23	2.10	0.51
1:A:75:GLU:OE1	1:A:76:LYS:N	2.43	0.51
4:J:63:SER:OG	4:J:66:GLN:NE2	2.44	0.51
3:G:186:GLU:OE2	3:G:228:TYR:OH	2.29	0.51
3:H:193:MET:HE1	3:H:231:LEU:CD2	2.41	0.50
4:K:34:HIS:HB3	4:K:46:ILE:HD11	1.93	0.50
4:K:35:VAL:HG22	4:K:49:LEU:HD11	1.93	0.50
3:F:285:LYS:HD2	3:F:285:LYS:C	2.36	0.50
3:H:193:MET:HE1	3:H:231:LEU:HD21	1.93	0.50
3:F:253:GLU:O	3:F:253:GLU:HG2	2.11	0.50
4:K:200:LYS:O	4:K:201:THR:CB	2.60	0.50
3:E:7:GLN:HB3	3:E:11:MET:HE1	1.94	0.50
3:F:285:LYS:O	3:F:287:ILE:HG22	2.11	0.50
4:K:49:LEU:N	4:K:49:LEU:HD12	2.26	0.50
4:K:92:ILE:HG23	4:K:152:ILE:HD11	1.93	0.50
4:K:79:GLU:HA	4:K:79:GLU:OE2	2.11	0.50
4:J:200:LYS:O	4:J:201:THR:CB	2.60	0.50
4:J:102:LEU:C	4:J:102:LEU:HD23	2.37	0.49
3:E:101:ILE:HD11	3:E:130:ILE:CG2	2.42	0.49
3:E:230:GLU:C	3:E:230:GLU:OE2	2.55	0.49
4:J:41:PRO:O	4:J:44:LYS:NZ	2.45	0.49
4:K:86:ASP:HB3	4:K:90:GLN:HG2	1.94	0.49
2:D:192:LEU:HA	2:D:195:ILE:CG1	2.41	0.49
4:K:185:PHE:C	4:K:186:GLU:OE2	2.56	0.49
3:F:38:ILE:HD12	3:F:38:ILE:N	2.26	0.49
3:H:231:LEU:HD23	3:H:231:LEU:O	2.13	0.49
4:J:187:LYS:HD3	4:J:193:LEU:O	2.13	0.49
4:K:95:MET:HE1	4:K:130:PHE:HD2	1.78	0.49
4:J:24:VAL:HG22	4:J:25:SER:N	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:241:VAL:CA	1:C:67:ILE:HD11	2.43	0.49
3:F:256:VAL:HB	3:F:287:ILE:HD13	1.95	0.48
4:J:97:ILE:HD12	4:J:183:VAL:HG13	1.94	0.48
3:F:286:THR:O	3:F:287:ILE:C	2.56	0.48
4:J:37:VAL:CG2	4:J:78:ILE:HD12	2.43	0.48
1:C:25:SER:O	1:C:29:THR:HG23	2.14	0.48
2:B:250:ASP:C	2:B:250:ASP:OD1	2.56	0.48
3:G:253:GLU:N	3:G:253:GLU:OE1	2.47	0.48
3:H:255:ASN:OD1	3:H:255:ASN:O	2.32	0.48
4:J:97:ILE:HD12	4:J:183:VAL:CG1	2.43	0.48
4:J:4:ARG:NH2	4:J:28:ASP:OD2	2.47	0.48
4:J:95:MET:HB3	4:J:152:ILE:HD13	1.95	0.48
2:D:201:GLU:OE2	2:D:201:GLU:HA	2.14	0.48
3:G:251:HIS:O	3:G:251:HIS:ND1	2.47	0.47
4:K:24:VAL:HG11	4:K:49:LEU:HD23	1.96	0.47
4:J:11:CYS:HA	4:J:61:ALA:HB1	1.95	0.47
3:H:133:THR:HG23	3:H:134:GLU:HG2	1.96	0.47
4:J:111:PRO:HB2	4:J:196:ILE:HG21	1.96	0.47
3:H:112:THR:HG21	3:G:54:MET:HE1	1.96	0.47
3:E:231:LEU:HD23	3:E:231:LEU:C	2.39	0.47
1:C:24:GLU:OE1	1:C:25:SER:N	2.47	0.47
4:J:102:LEU:HD13	4:J:137:VAL:HG13	1.97	0.47
1:A:74:ALA:HB2	2:D:248:VAL:HG21	1.97	0.47
4:J:95:MET:HE1	4:J:181:SER:HB3	1.95	0.47
3:F:40:GLU:OE1	3:F:44:ILE:HG23	2.16	0.46
4:J:102:LEU:CD1	4:J:137:VAL:HG22	2.46	0.46
3:H:23:ASN:OD1	3:H:23:ASN:C	2.58	0.46
1:C:69:LYS:O	1:C:70:ASP:C	2.57	0.46
3:F:255:ASN:C	3:F:255:ASN:OD1	2.59	0.46
3:G:40:GLU:OE1	3:G:40:GLU:C	2.58	0.46
4:K:94:THR:HG22	4:K:95:MET:N	2.30	0.46
1:C:49:MET:CE	3:G:197:LEU:HD22	2.39	0.46
3:F:40:GLU:O	3:F:44:ILE:HG12	2.15	0.46
3:G:283:ILE:O	3:G:287:ILE:HG22	2.16	0.46
3:H:20:LYS:HD2	3:H:37:LYS:HE2	1.97	0.46
4:J:12:PRO:HB2	4:J:52:HIS:CE1	2.50	0.46
4:K:127:ASN:OD1	4:K:127:ASN:O	2.33	0.46
4:J:15:GLU:HG3	4:J:16:LEU:HD22	1.97	0.45
3:G:1:MET:O	3:G:2:ASP:HB2	2.17	0.45
4:J:35:VAL:HG12	4:J:82:LEU:HA	1.98	0.45
4:J:20:ASN:HB2	4:J:136:LEU:HD11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:28:SER:HA	1:C:31:ARG:HD3	1.99	0.45
2:D:192:LEU:CA	2:D:195:ILE:HD12	2.34	0.45
3:E:0:GLY:O	3:E:1:MET:HE2	2.16	0.45
3:F:287:ILE:HG23	3:F:287:ILE:O	2.17	0.45
1:C:28:SER:O	1:C:32:MET:HG2	2.17	0.45
3:E:101:ILE:HD12	3:E:127:ILE:HG23	1.99	0.45
4:K:127:ASN:O	4:K:127:ASN:CG	2.60	0.44
1:C:71:MET:SD	1:C:71:MET:C	3.01	0.44
3:E:1:MET:HE2	3:E:1:MET:HA	1.99	0.44
4:K:53:PRO:O	4:K:54:SER:HB2	2.18	0.44
4:J:200:LYS:C	4:J:201:THR:HG1	2.12	0.44
4:K:46:ILE:HG21	4:K:174:VAL:HG23	1.99	0.44
2:B:231:ASP:OD2	2:B:231:ASP:C	2.60	0.44
4:J:27:LYS:HD2	4:J:27:LYS:C	2.43	0.44
4:J:153:GLU:CD	4:J:171:LYS:HZ2	2.25	0.44
4:J:148:LEU:HD23	4:J:149:VAL:N	2.33	0.44
3:G:1:MET:SD	3:G:1:MET:C	3.01	0.43
3:G:251:HIS:CE1	3:G:287:ILE:HG23	2.53	0.43
4:J:24:VAL:HG22	4:J:25:SER:H	1.82	0.43
4:K:138:PHE:CZ	4:K:140:PHE:HB2	2.52	0.43
1:C:65:ASP:HB3	3:E:116:ARG:NH2	2.33	0.43
1:A:31:ARG:O	1:A:35:LEU:HD23	2.19	0.43
4:K:83:TYR:CD1	4:K:83:TYR:C	2.95	0.43
2:B:216:PHE:CZ	2:D:216:PHE:CZ	3.05	0.43
3:H:116:ARG:N	3:H:116:ARG:HD2	2.32	0.43
3:G:38:ILE:HD12	3:G:75:LEU:HD12	1.98	0.43
4:K:92:ILE:CG2	4:K:152:ILE:HD11	2.48	0.43
4:K:104:LYS:O	4:K:107:ILE:HG12	2.19	0.43
3:E:37:LYS:O	3:E:40:GLU:HG2	2.18	0.43
3:G:38:ILE:CD1	3:G:75:LEU:HD12	2.49	0.43
4:K:95:MET:O	4:K:183:VAL:HG13	2.18	0.43
4:K:189:GLU:OE2	4:K:189:GLU:HA	2.17	0.43
2:B:241:VAL:HG22	1:C:67:ILE:HG12	2.01	0.43
3:F:34:GLY:O	3:F:38:ILE:HD12	2.19	0.43
3:F:17:ALA:HA	3:F:44:ILE:HD11	2.00	0.43
1:C:62:GLU:OE2	3:E:122:LYS:NZ	2.38	0.42
4:K:70:ALA:HB3	4:K:72:LEU:CD1	2.49	0.42
1:C:21:LEU:HD12	1:C:21:LEU:H	1.84	0.42
3:H:112:THR:HG22	3:G:54:MET:HE1	2.01	0.42
3:G:75:LEU:HD23	3:G:76:GLN:N	2.35	0.42
2:B:248:VAL:CG1	2:B:249:SER:N	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:193:MET:HE1	3:F:231:LEU:HD22	2.01	0.42
2:D:245:GLU:O	2:D:248:VAL:HG12	2.19	0.42
3:E:146:GLU:OE2	3:E:168:VAL:HG11	2.19	0.42
3:E:193:MET:HE1	3:E:231:LEU:HD23	2.00	0.42
3:F:253:GLU:O	3:F:253:GLU:CG	2.68	0.42
4:K:136:LEU:HD23	4:K:136:LEU:N	2.34	0.42
4:K:113:ASP:OD2	4:K:113:ASP:C	2.63	0.42
3:H:218:MET:SD	3:H:218:MET:C	3.03	0.42
1:C:77:ASN:HD22	1:C:78:LEU:N	2.18	0.42
3:H:13:LEU:HD21	3:H:44:ILE:CD1	2.49	0.42
3:F:75:LEU:HD12	3:F:76:GLN:H	1.85	0.42
4:J:33:GLN:HB2	4:J:49:LEU:HD13	2.02	0.42
4:K:126:ASN:O	4:K:127:ASN:HB3	2.18	0.42
4:J:95:MET:SD	4:J:182:GLN:O	2.78	0.41
2:B:194:GLU:HA	2:B:194:GLU:OE1	2.19	0.41
4:J:109:SER:O	4:J:194:ASN:OD1	2.37	0.41
1:C:66:GLN:O	1:C:67:ILE:C	2.60	0.41
3:H:130:ILE:HA	3:H:133:THR:HG22	2.02	0.41
3:E:198:LEU:N	3:E:198:LEU:HD12	2.35	0.41
3:G:71:LEU:O	3:G:74:GLN:HG2	2.20	0.41
3:H:255:ASN:OD1	3:H:258:SER:CB	2.68	0.41
3:E:10:ALA:HB1	3:E:52:PHE:CE2	2.55	0.41
3:E:251:HIS:NE2	3:E:287:ILE:HG22	2.35	0.41
3:F:96:ASP:OD1	3:F:96:ASP:O	2.38	0.41
3:G:238:SER:O	3:G:242:LYS:NZ	2.46	0.41
4:J:95:MET:CB	4:J:152:ILE:HD13	2.51	0.41
2:B:191:ALA:O	2:B:192:LEU:C	2.64	0.41
3:G:40:GLU:OE2	3:G:44:ILE:HD11	2.20	0.41
4:J:102:LEU:HD23	4:J:102:LEU:O	2.19	0.41
4:J:46:ILE:HD12	4:J:46:ILE:N	2.35	0.41
3:E:182:ILE:CD1	3:E:213:HIS:NE2	2.83	0.41
3:F:17:ALA:O	3:F:21:VAL:HG12	2.21	0.41
3:G:240:GLU:OE1	3:G:240:GLU:N	2.47	0.41
3:H:253:GLU:O	3:H:254:GLN:HB2	2.20	0.41
3:F:18:GLU:HA	3:F:21:VAL:HG12	2.02	0.41
3:G:269:ILE:HD12	3:G:269:ILE:N	2.34	0.41
4:J:140:PHE:CE2	4:J:141:ASN:OD1	2.74	0.41
3:E:42:CYS:SG	3:E:43:GLU:N	2.94	0.40
1:A:22:ALA:O	1:A:25:SER:HB2	2.22	0.40
3:E:103:CYS:SG	3:E:104:LEU:N	2.94	0.40
3:E:243:LEU:HD21	3:E:247:LEU:HD11	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:134:GLU:OE2	3:G:135:LEU:HD23	2.21	0.40
3:G:214:PHE:O	3:G:214:PHE:CD1	2.74	0.40
3:H:198:LEU:HD12	3:H:198:LEU:N	2.37	0.40
4:J:13:THR:HG22	4:J:14:ASP:N	2.35	0.40
4:K:40:SER:HB2	4:K:43:HIS:HB2	2.03	0.40
4:K:138:PHE:HB2	4:K:147:LEU:CD1	2.52	0.40
1:A:76:LYS:O	1:A:79:THR:OG1	2.37	0.40
3:H:243:LEU:HD12	3:H:247:LEU:HD13	2.03	0.40
3:E:19:ARG:HD2	3:E:19:ARG:C	2.47	0.40
3:F:136:VAL:O	3:F:136:VAL:HG12	2.22	0.40
4:K:4:ARG:HA	4:K:4:ARG:NE	2.36	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	65/84 (77%)	64 (98%)	1 (2%)	0	100	100
1	C	64/84 (76%)	64 (100%)	0	0	100	100
2	B	66/78 (85%)	64 (97%)	2 (3%)	0	100	100
2	D	66/78 (85%)	64 (97%)	2 (3%)	0	100	100
3	E	276/296 (93%)	271 (98%)	5 (2%)	0	100	100
3	F	276/296 (93%)	269 (98%)	7 (2%)	0	100	100
3	G	277/296 (94%)	273 (99%)	4 (1%)	0	100	100
3	H	282/296 (95%)	276 (98%)	6 (2%)	0	100	100
4	J	181/747 (24%)	173 (96%)	7 (4%)	1 (1%)	22	55
4	K	181/747 (24%)	173 (96%)	7 (4%)	1 (1%)	22	55
All	All	1734/3002 (58%)	1691 (98%)	41 (2%)	2 (0%)	50	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	J	13	THR
4	K	55	VAL

### 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	60/74 (81%)	59 (98%)	1 (2%)	56	76
1	C	59/74 (80%)	56 (95%)	3 (5%)	20	49
2	B	62/71 (87%)	61 (98%)	1 (2%)	58	77
2	D	62/71 (87%)	62 (100%)	0	100	100
3	E	230/243 (95%)	229 (100%)	1 (0%)	89	95
3	F	230/243 (95%)	230 (100%)	0	100	100
3	G	230/243 (95%)	228 (99%)	2 (1%)	75	87
3	H	236/243 (97%)	236 (100%)	0	100	100
4	J	159/638 (25%)	158 (99%)	1 (1%)	84	92
4	K	159/638 (25%)	157 (99%)	2 (1%)	65	82
All	All	1487/2538 (59%)	1476 (99%)	11 (1%)	80	90

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	ASP
2	B	228	GLU
1	C	72	LYS
1	C	73	GLU
1	C	77	ASN
3	E	119	ILE
3	G	79	HIS
3	G	272	LEU
4	J	30	GLN
4	K	38	ARG

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Mol	Chain	Res	Type
4	K	141	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	77	ASN
2	D	213	HIS
2	D	236	ASN
3	H	123	HIS
3	E	98	GLN
3	E	124	HIS
3	E	144	HIS
3	F	50	ASN
3	G	63	ASN
3	G	123	HIS
3	G	179	GLN
4	J	34	HIS
4	J	52	HIS
4	J	141	ASN
4	J	180	ASN
4	K	141	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

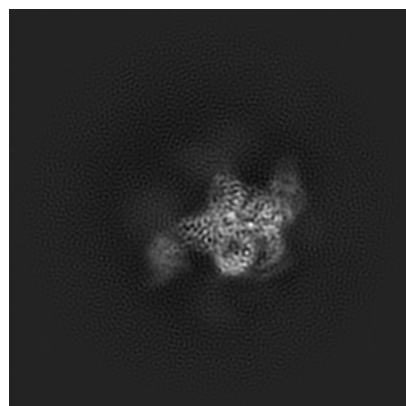
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71601. These allow visual inspection of the internal detail of the map and identification of artifacts.

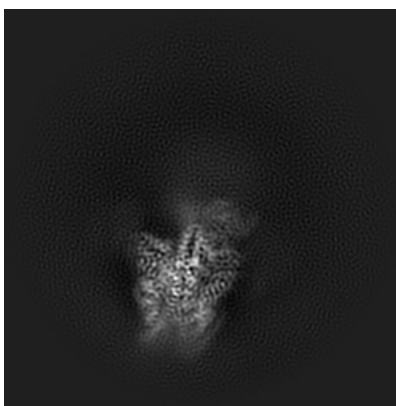
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

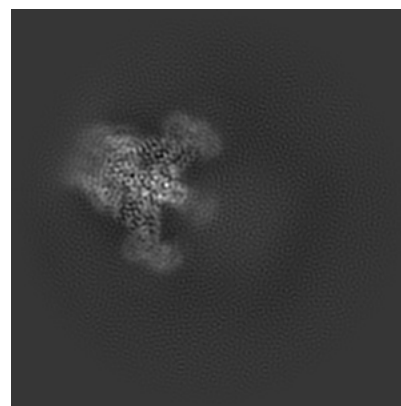
#### 6.1.1 Primary map



X

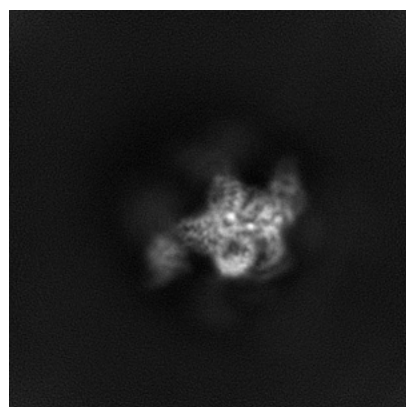


Y

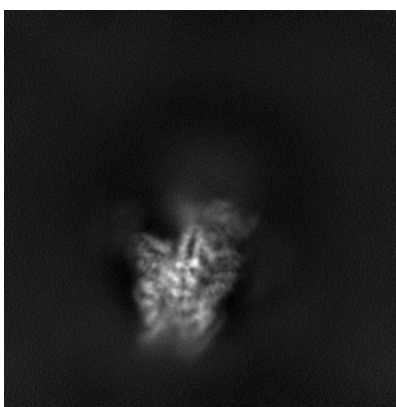


Z

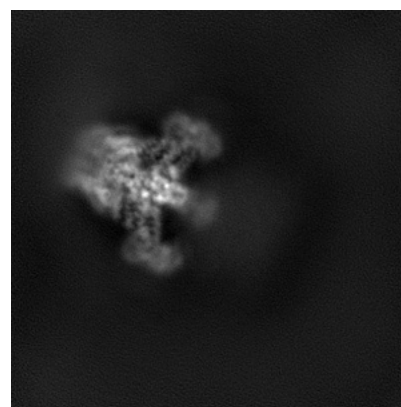
#### 6.1.2 Raw map



X



Y

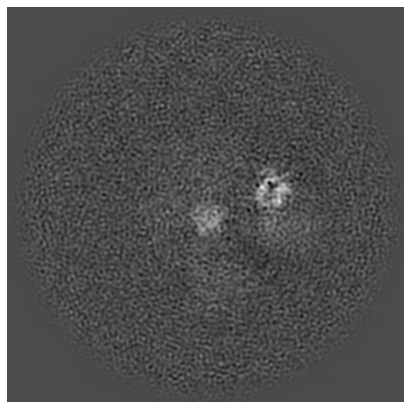


Z

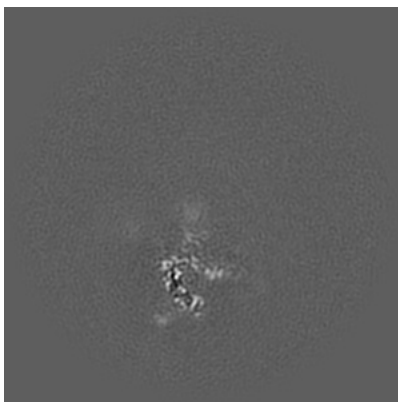
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

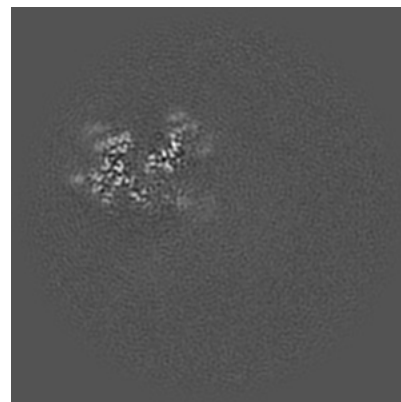
### 6.2.1 Primary map



X Index: 147

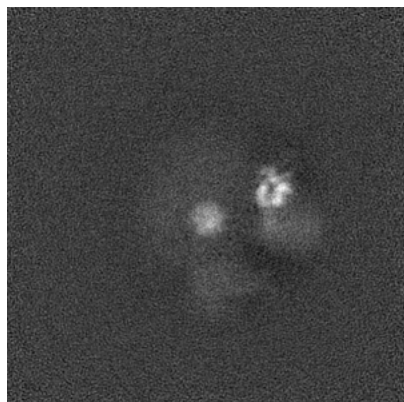


Y Index: 147

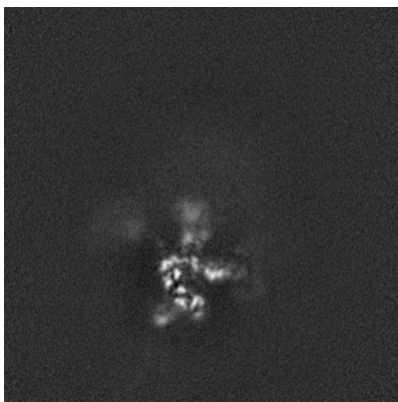


Z Index: 147

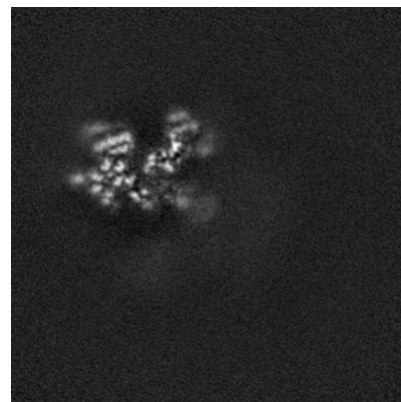
### 6.2.2 Raw map



X Index: 147



Y Index: 147



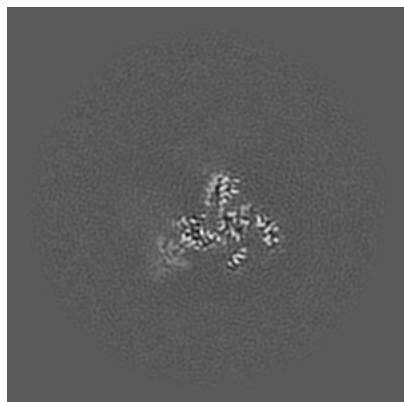
Z Index: 147

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

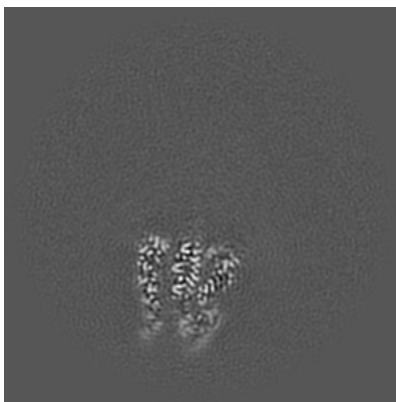


## 6.3 Largest variance slices [i](#)

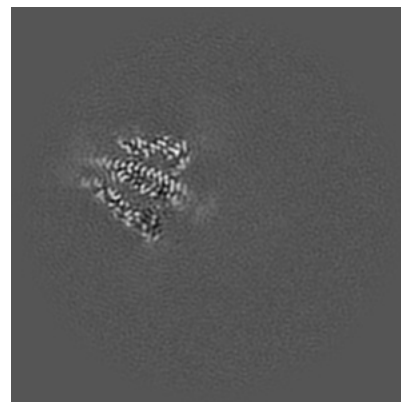
### 6.3.1 Primary map



X Index: 99

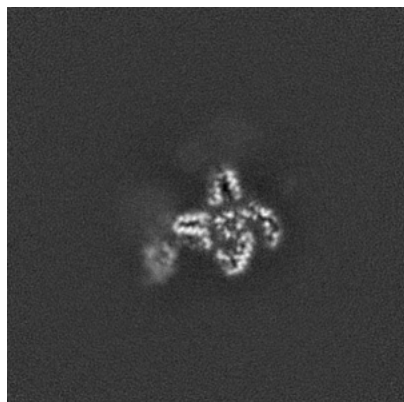


Y Index: 165

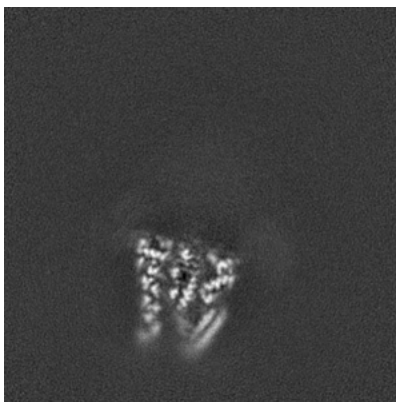


Z Index: 133

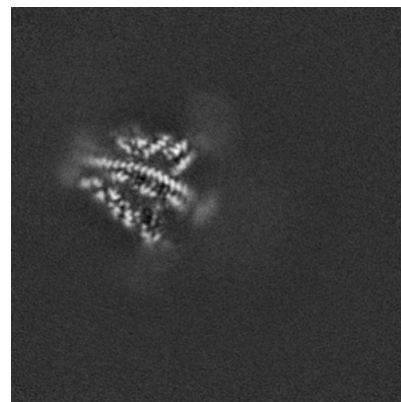
### 6.3.2 Raw map



X Index: 106



Y Index: 168

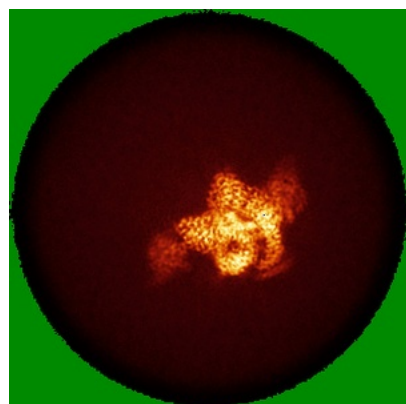


Z Index: 133

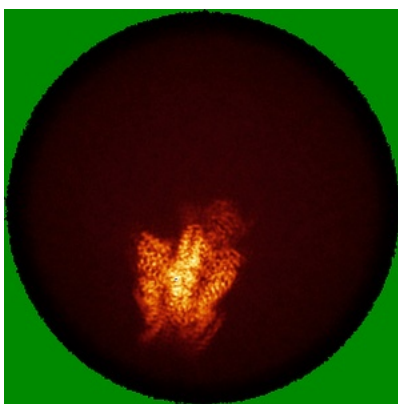
The images above show the largest variance slices of the map in three orthogonal directions.

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

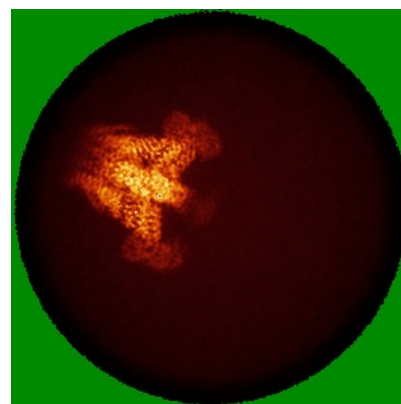
### 6.4.1 Primary map



X

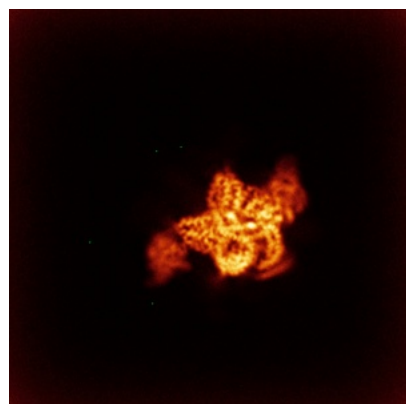


Y

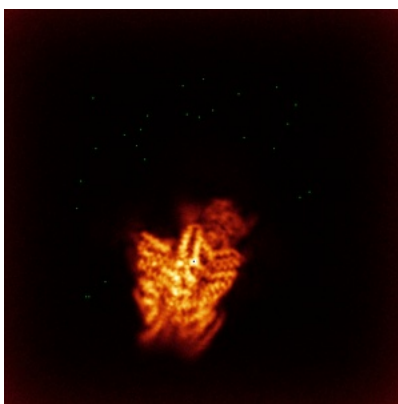


Z

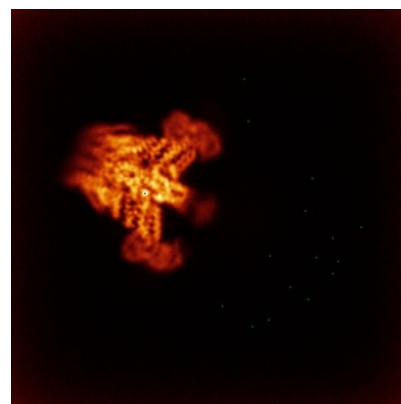
### 6.4.2 Raw map



X



Y

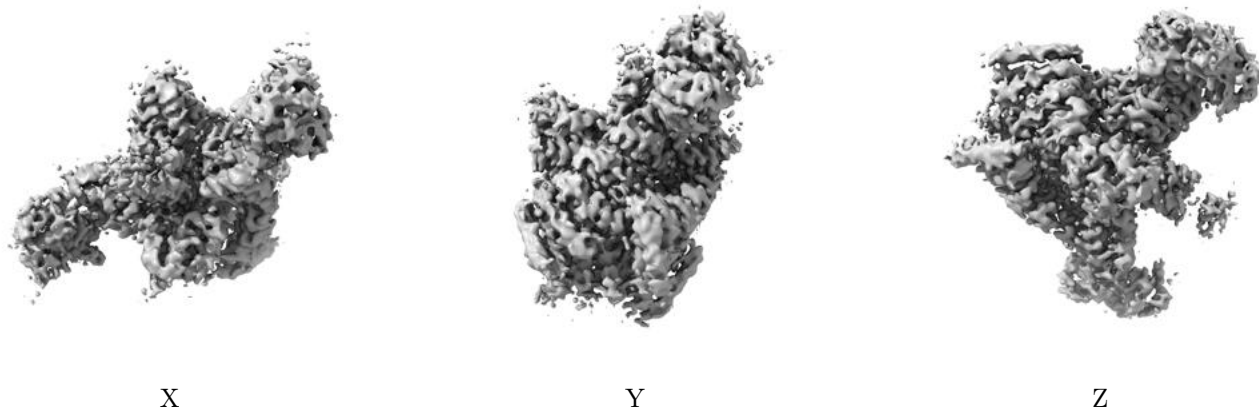


Z

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.

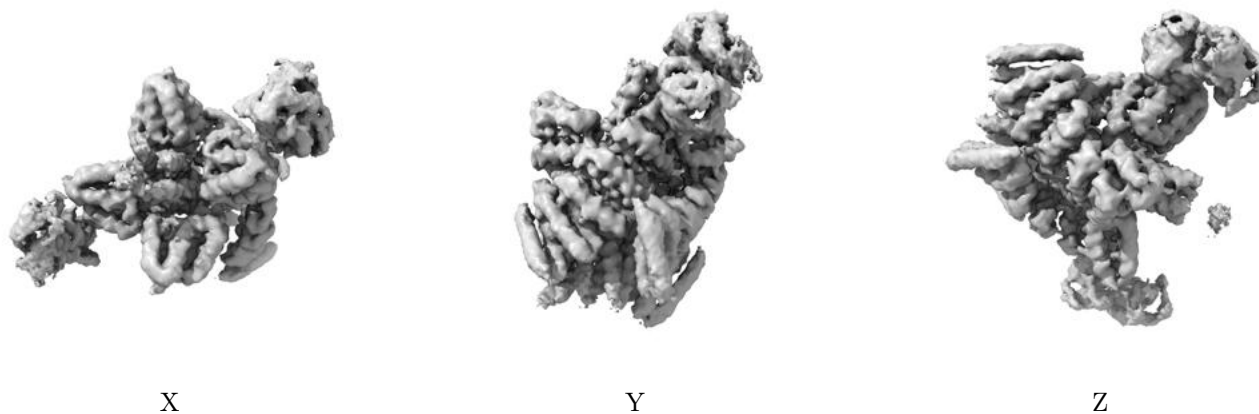
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. 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.

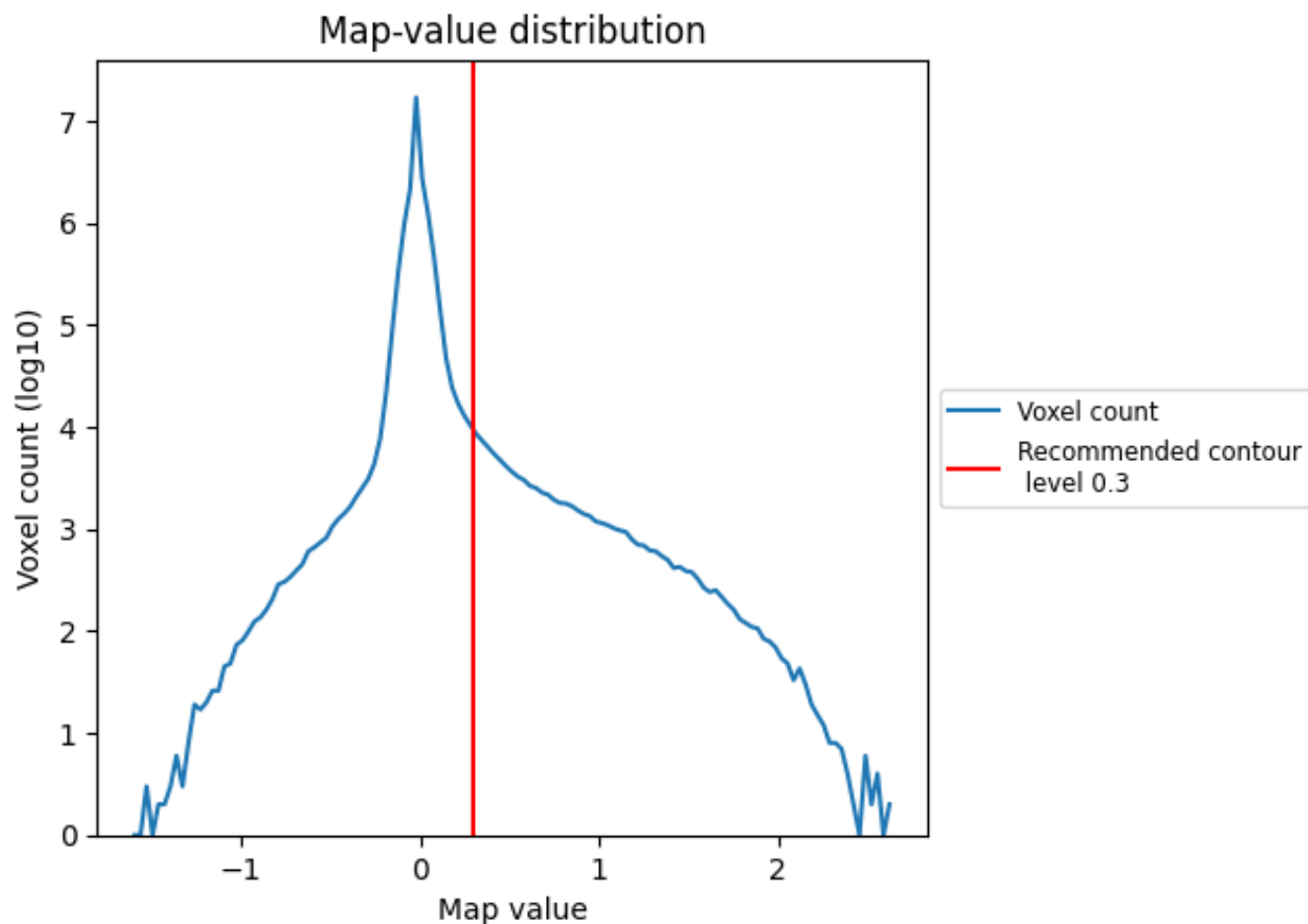
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

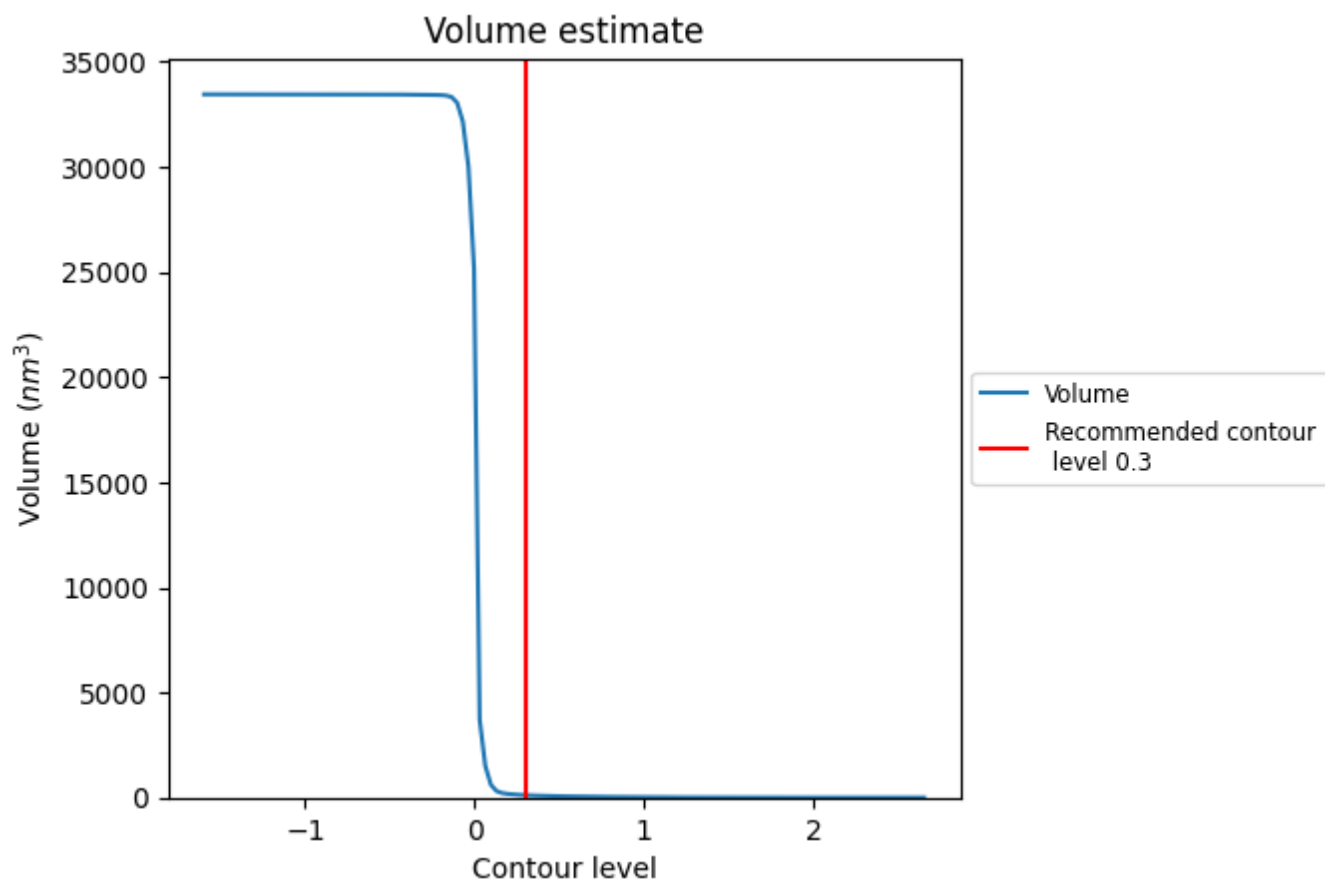
This section contains the results of statistical analysis of the map.

### 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.

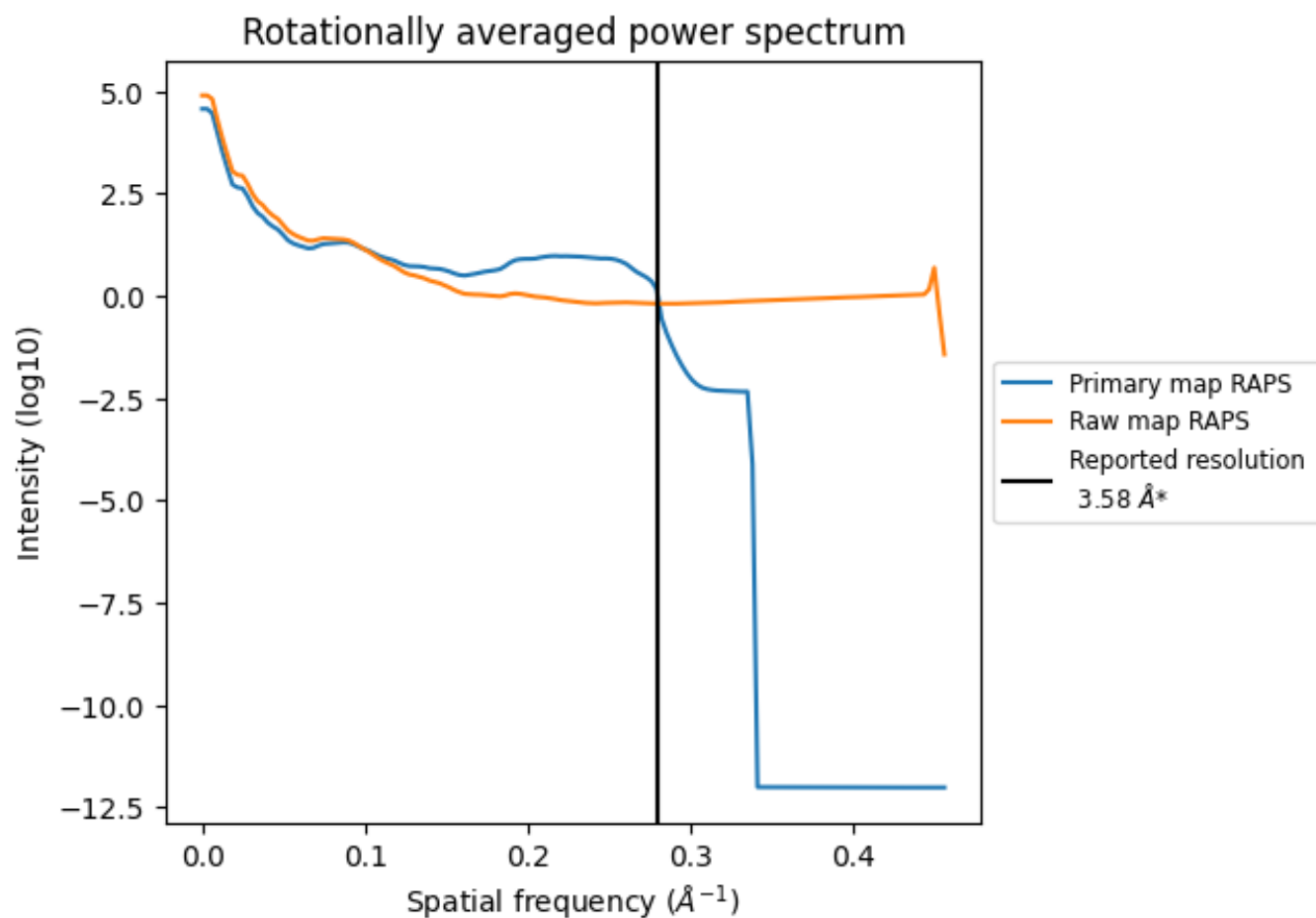
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 114 nm<sup>3</sup>; this corresponds to an approximate mass of 103 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 ⓘ

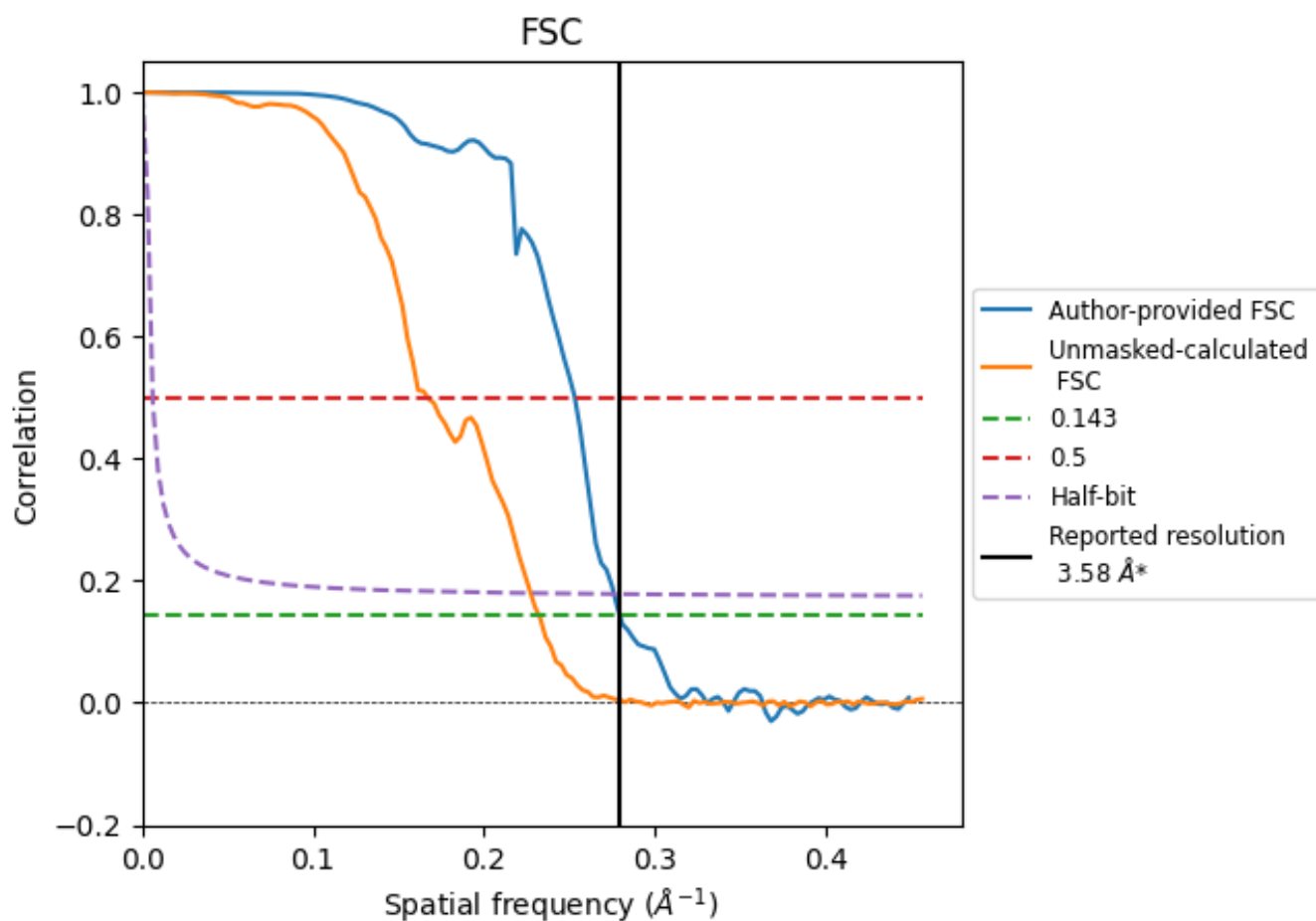


\*Reported resolution corresponds to spatial frequency of 0.279 Å<sup>-1</sup>

## 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 0.279  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.58	-	-
Author-provided FSC curve	3.58	3.95	3.62
Unmasked-calculated*	4.31	5.98	4.40

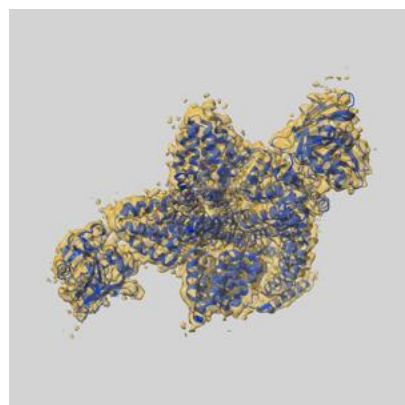
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.31 differs from the reported value 3.58 by more than 10 %



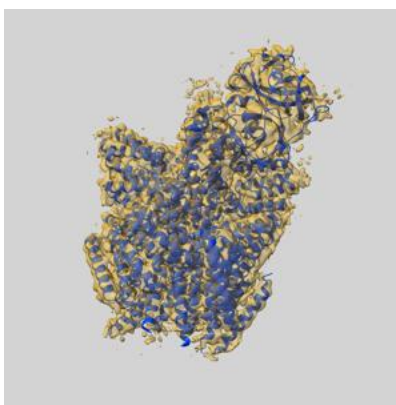
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-71601 and PDB model 9PFG. Per-residue inclusion information can be found in section 3 on page 7.

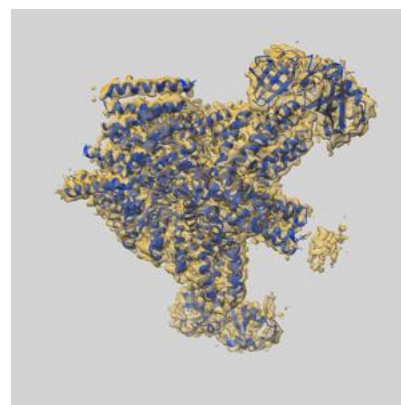
### 9.1 Map-model overlay [i](#)



X



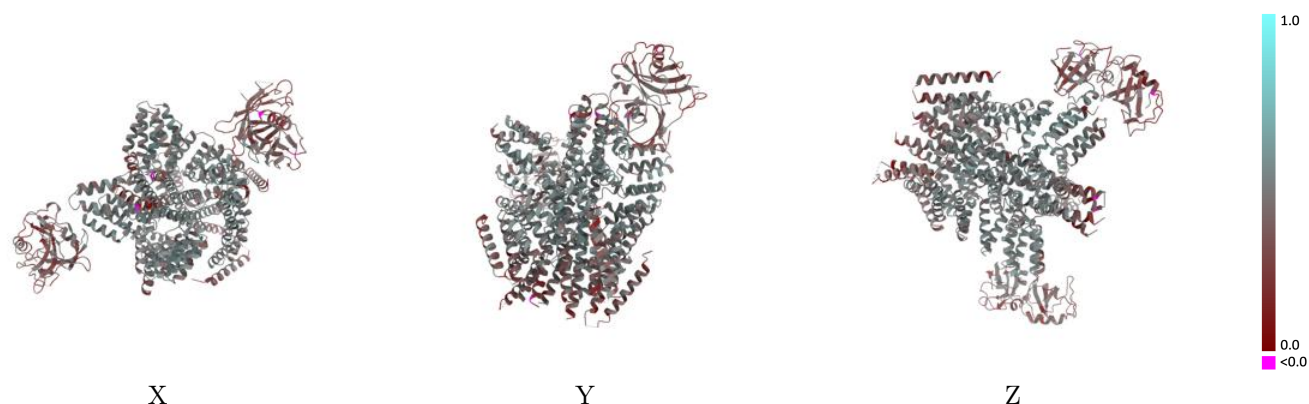
Y



Z

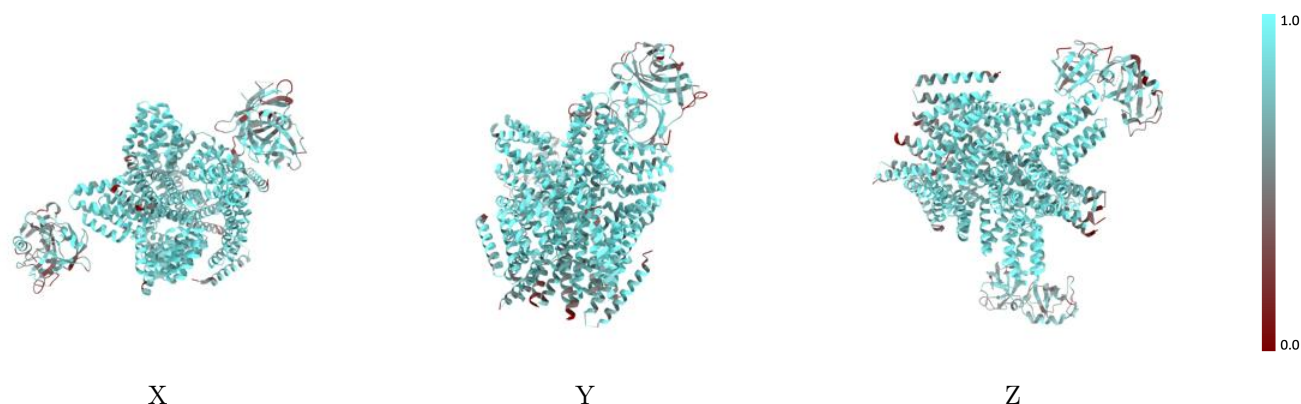
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



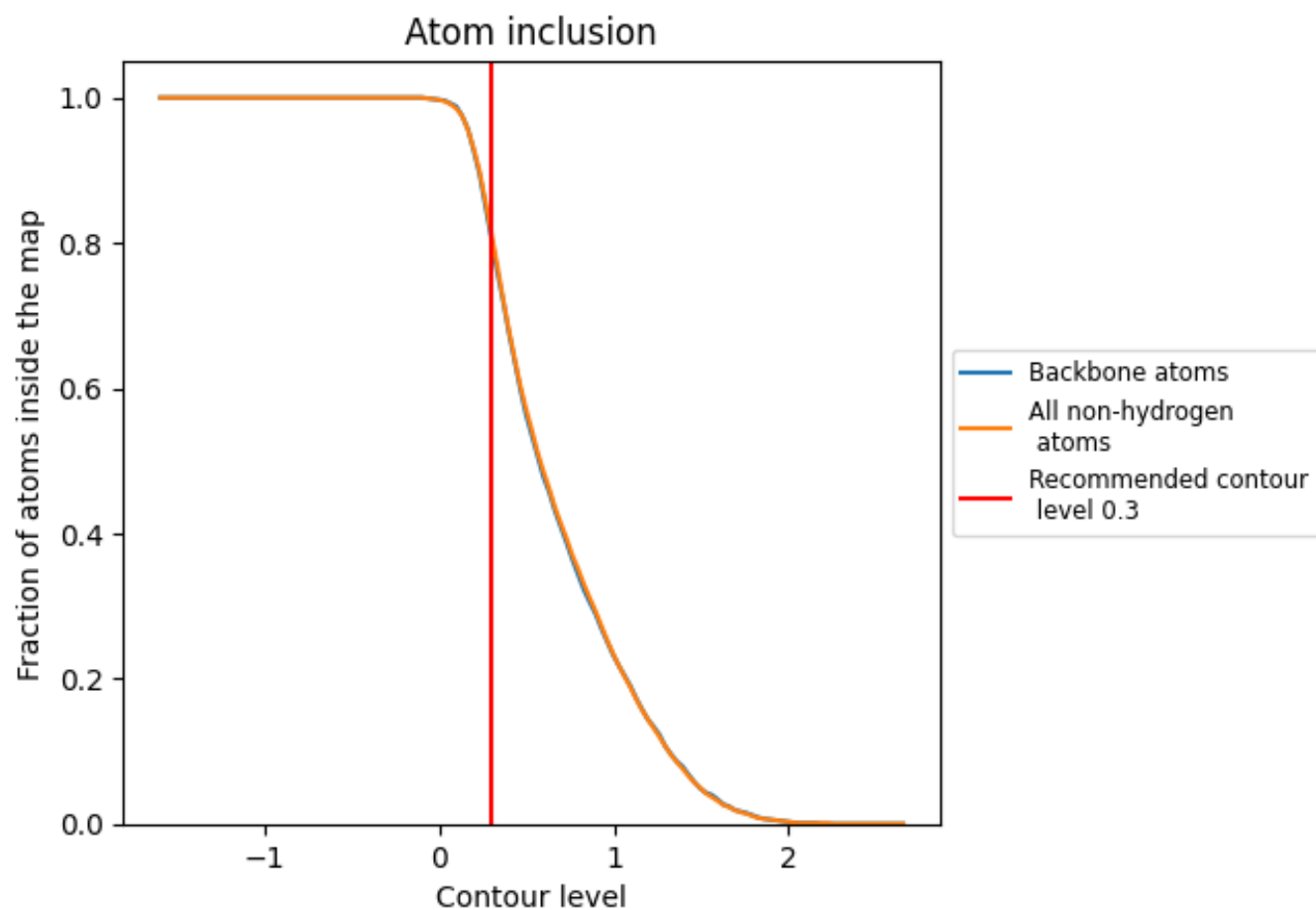
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 81% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8110	<div></div> 0.4430
A	<div></div> 0.7620	<div></div> 0.4420
B	<div></div> 0.7580	<div></div> 0.4290
C	<div></div> 0.7860	<div></div> 0.4400
D	<div></div> 0.7520	<div></div> 0.4300
E	<div></div> 0.8970	<div></div> 0.4810
F	<div></div> 0.8890	<div></div> 0.4760
G	<div></div> 0.8960	<div></div> 0.4790
H	<div></div> 0.8760	<div></div> 0.4710
J	<div></div> 0.6530	<div></div> 0.3430
K	<div></div> 0.6030	<div></div> 0.3430

