



## wwPDB EM Validation Summary Report ⓘ

Jan 7, 2025 – 12:48 pm GMT

PDB ID : 9FSQ  
EMDB ID : EMD-50732  
Title : RNA Polymerase III Class III Melting Pre-Initiation Complex (MC)  
Authors : Shah, S.Z.; Ramsay, E.P.; Cecatiello, V.; Perry, T.N.; Vannini, A.  
Deposited on : 2024-06-21  
Resolution : 3.51 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.dev113  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

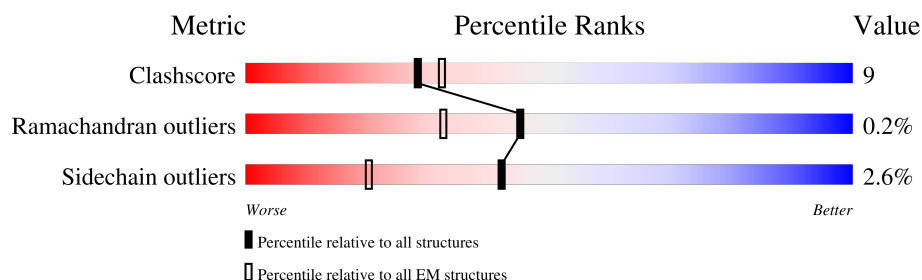
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.51 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	1390	
2	B	1133	
3	C	534	
4	D	398	
5	E	708	
6	F	316	
7	G	223	
8	H	204	

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Mol	Chain	Length	Quality of chain
9	I	148	
10	J	108	
11	K	346	
12	L	133	
13	M	210	
14	N	127	
15	O	150	
16	P	58	
17	Q	67	
18	R	200	
19	S	419	
20	T	484	
21	U	368	
22	W	1519	
23	X	98	
24	Y	98	
25	Z	411	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
28	SF4	F	401	-	-	X	-

## 2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 56541 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 DNA-directed RNA polymerase III subunit RPC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1381	Total	C	N	O	S	0	0
			10848	6876	1891	2008	73		

- Molecule 2 is a protein called DNA-directed RNA polymerase III subunit RPC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1097	Total	C	N	O	S	0	0
			8680	5499	1516	1597	68		

- Molecule 3 is a protein called DNA-directed RNA polymerase III subunit RPC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	512	Total	C	N	O	S	0	0
			4075	2565	712	774	24		

- Molecule 4 is a protein called DNA-directed RNA polymerase III subunit RPC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	186	Total	C	N	O	S	0	0
			1448	907	251	281	9		

- Molecule 5 is a protein called DNA-directed RNA polymerase III subunit RPC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	400	Total	C	N	O	S	0	0
			3211	2038	557	596	20		

- Molecule 6 is a protein called DNA-directed RNA polymerase III subunit RPC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	302	Total	C	N	O	S	0	0
			2395	1512	410	457	16		

- Molecule 7 is a protein called DNA-directed RNA polymerase III subunit RPC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	82	Total	C	N	O	S	0	0
			717	463	121	127	6		

- Molecule 8 is a protein called DNA-directed RNA polymerase III subunit RPC8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	189	Total	C	N	O	S	0	0
			1509	979	237	286	7		

- Molecule 9 is a protein called DNA-directed RNA polymerase III subunit RPC9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	124	Total	C	N	O	S	0	0
			1001	626	174	198	3		

- Molecule 10 is a protein called DNA-directed RNA polymerase III subunit RPC10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	107	Total	C	N	O	S	0	0
			849	525	157	154	13		

- Molecule 11 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	343	Total	C	N	O	S	0	0
			2736	1723	488	514	11		

- Molecule 12 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	107	Total	C	N	O	S	0	0
			856	531	153	165	7		

- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	209	Total	C	N	O	S	0	0
			1715	1083	300	324	8		

- Molecule 14 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	78	Total	C	N	O	S	0	0
			627	402	106	114	5		

- Molecule 15 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

- Molecule 16 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	46	Total	C	N	O	S	0	0
			388	241	75	66	6		

- Molecule 17 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	66	Total	C	N	O	S	0	0
			524	339	88	91	6		

- Molecule 18 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	178	Total	C	N	O	S	0	0
			1402	909	246	240	7		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	140	MET	-	initiating methionine	UNP P20226
R	141	ALA	-	expression tag	UNP P20226
R	142	HIS	-	expression tag	UNP P20226
R	143	HIS	-	expression tag	UNP P20226
R	144	HIS	-	expression tag	UNP P20226
R	145	HIS	-	expression tag	UNP P20226
R	146	HIS	-	expression tag	UNP P20226
R	147	HIS	-	expression tag	UNP P20226
R	148	VAL	-	expression tag	UNP P20226
R	149	GLY	-	expression tag	UNP P20226
R	150	THR	-	expression tag	UNP P20226
R	151	LEU	-	expression tag	UNP P20226

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Chain	Residue	Modelled	Actual	Comment	Reference
R	152	GLU	-	expression tag	UNP P20226
R	153	VAL	-	expression tag	UNP P20226
R	154	LEU	-	expression tag	UNP P20226
R	155	PHE	-	expression tag	UNP P20226
R	156	GLN	-	expression tag	UNP P20226
R	157	GLY	-	expression tag	UNP P20226
R	158	PRO	-	expression tag	UNP P20226

- Molecule 19 is a protein called Transcription factor IIIB 50 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	361	Total	C	N	O	S	0	0
			2847	1789	506	530	22		

- Molecule 20 is a protein called Transcription factor TFIIB component B'' homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	78	Total	C	N	O	S	0	0
			665	430	117	115	3		

- Molecule 21 is a protein called snRNA-activating protein complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	141	Total	C	N	O	S	0	0
			1183	770	203	202	8		

- Molecule 22 is a protein called snRNA-activating protein complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	242	Total	C	N	O	S	0	0
			2018	1264	370	378	6		

There are 51 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	-38	MET	-	initiating methionine	UNP Q5SXM2
W	-37	ALA	-	expression tag	UNP Q5SXM2
W	-36	SER	-	expression tag	UNP Q5SXM2
W	-35	TRP	-	expression tag	UNP Q5SXM2
W	-34	SER	-	expression tag	UNP Q5SXM2
W	-33	HIS	-	expression tag	UNP Q5SXM2

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Chain	Residue	Modelled	Actual	Comment	Reference
W	-32	PRO	-	expression tag	UNP Q5SXM2
W	-31	GLN	-	expression tag	UNP Q5SXM2
W	-30	PHE	-	expression tag	UNP Q5SXM2
W	-29	GLU	-	expression tag	UNP Q5SXM2
W	-28	LYS	-	expression tag	UNP Q5SXM2
W	-27	GLY	-	expression tag	UNP Q5SXM2
W	-26	GLY	-	expression tag	UNP Q5SXM2
W	-25	GLY	-	expression tag	UNP Q5SXM2
W	-24	SER	-	expression tag	UNP Q5SXM2
W	-23	GLY	-	expression tag	UNP Q5SXM2
W	-22	GLY	-	expression tag	UNP Q5SXM2
W	-21	GLY	-	expression tag	UNP Q5SXM2
W	-20	SER	-	expression tag	UNP Q5SXM2
W	-19	TRP	-	expression tag	UNP Q5SXM2
W	-18	SER	-	expression tag	UNP Q5SXM2
W	-17	HIS	-	expression tag	UNP Q5SXM2
W	-16	PRO	-	expression tag	UNP Q5SXM2
W	-15	GLN	-	expression tag	UNP Q5SXM2
W	-14	PHE	-	expression tag	UNP Q5SXM2
W	-13	GLU	-	expression tag	UNP Q5SXM2
W	-12	LYS	-	expression tag	UNP Q5SXM2
W	-11	GLY	-	expression tag	UNP Q5SXM2
W	-10	GLY	-	expression tag	UNP Q5SXM2
W	-9	GLY	-	expression tag	UNP Q5SXM2
W	-8	SER	-	expression tag	UNP Q5SXM2
W	-7	GLU	-	expression tag	UNP Q5SXM2
W	-6	ASN	-	expression tag	UNP Q5SXM2
W	-5	LEU	-	expression tag	UNP Q5SXM2
W	-4	TYR	-	expression tag	UNP Q5SXM2
W	-3	PHE	-	expression tag	UNP Q5SXM2
W	-2	GLN	-	expression tag	UNP Q5SXM2
W	-1	GLY	-	expression tag	UNP Q5SXM2
W	0	SER	-	expression tag	UNP Q5SXM2
W	1	ALA	-	expression tag	UNP Q5SXM2
W	1470	ALA	-	expression tag	UNP Q5SXM2
W	1471	HIS	-	expression tag	UNP Q5SXM2
W	1472	HIS	-	expression tag	UNP Q5SXM2
W	1473	HIS	-	expression tag	UNP Q5SXM2
W	1474	HIS	-	expression tag	UNP Q5SXM2
W	1475	HIS	-	expression tag	UNP Q5SXM2
W	1476	HIS	-	expression tag	UNP Q5SXM2
W	1477	HIS	-	expression tag	UNP Q5SXM2

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Chain	Residue	Modelled	Actual	Comment	Reference
W	1478	HIS	-	expression tag	UNP Q5SXM2
W	1479	HIS	-	expression tag	UNP Q5SXM2
W	1480	HIS	-	expression tag	UNP Q5SXM2

- Molecule 23 is a DNA chain called U6\_2\_Template.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	61	Total	C	N	O	P	0	0
			1237	595	209	372	61		

- Molecule 24 is a DNA chain called U6\_2\_Non template.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	62	Total	C	N	O	P	0	0
			1283	611	244	366	62		

- Molecule 25 is a protein called snRNA-activating protein complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	385	Total	C	N	O	S	0	0
			3123	1977	533	591	22		

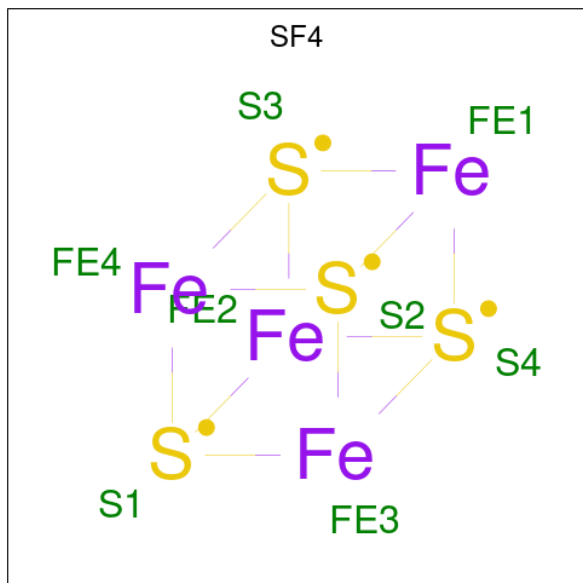
- Molecule 26 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
26	A	2	Total	Zn	0
			2	2	
26	B	1	Total	Zn	0
			1	1	
26	J	1	Total	Zn	0
			1	1	
26	P	1	Total	Zn	0
			1	1	
26	Q	1	Total	Zn	0
			1	1	
26	S	1	Total	Zn	0
			1	1	
26	Z	2	Total	Zn	0
			2	2	

- Molecule 27 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
27	A	1	Total	Mg	0
			1	1	

- Molecule 28 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula:  $\text{Fe}_4\text{S}_4$ ).

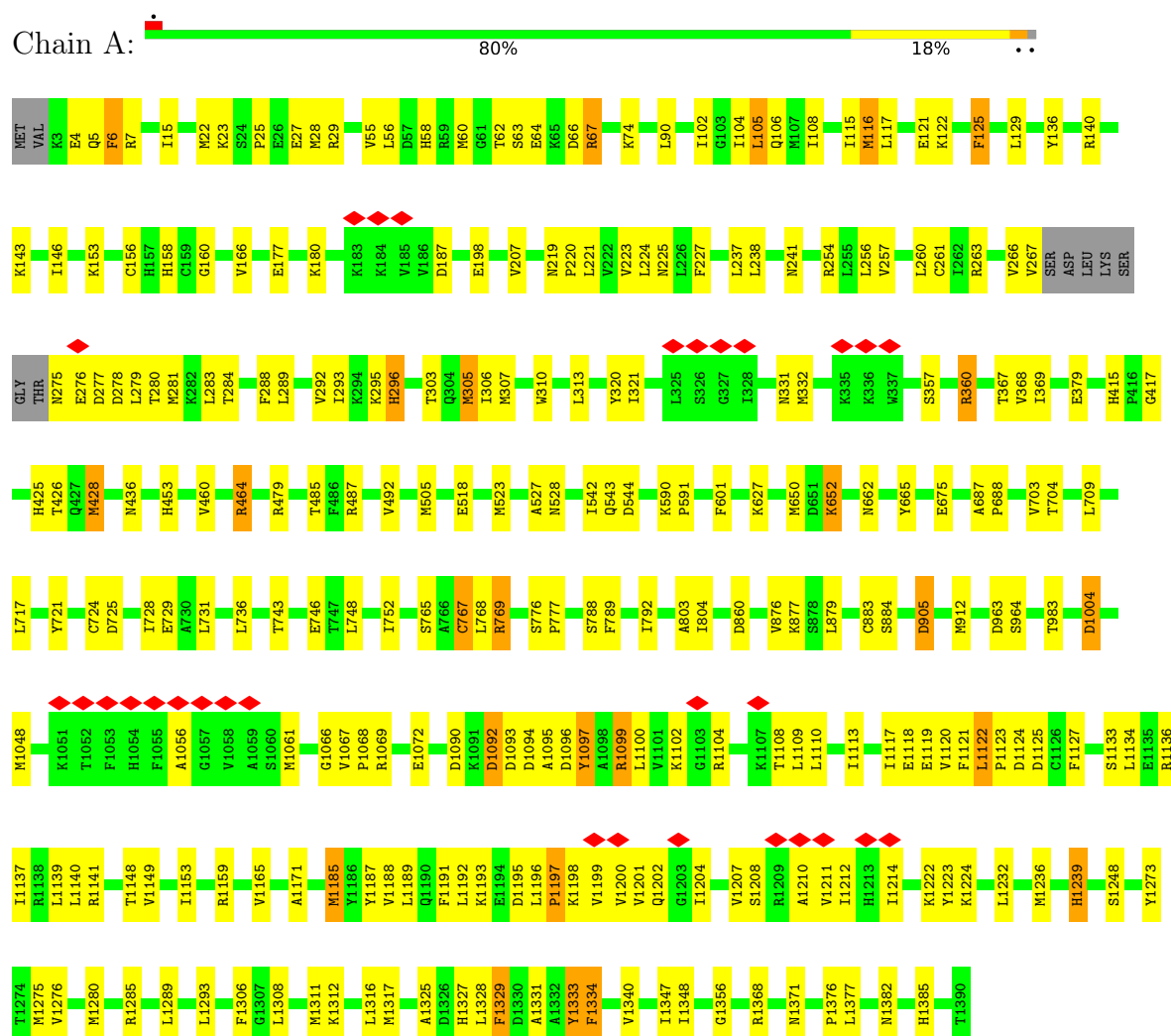


Mol	Chain	Residues	Atoms			AltConf
28	F	1	Total	Fe	S	0
			8	4	4	

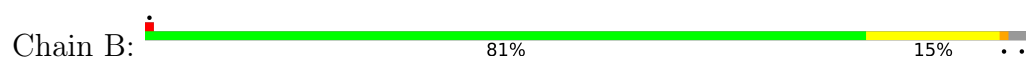
### 3 Residue-property plots

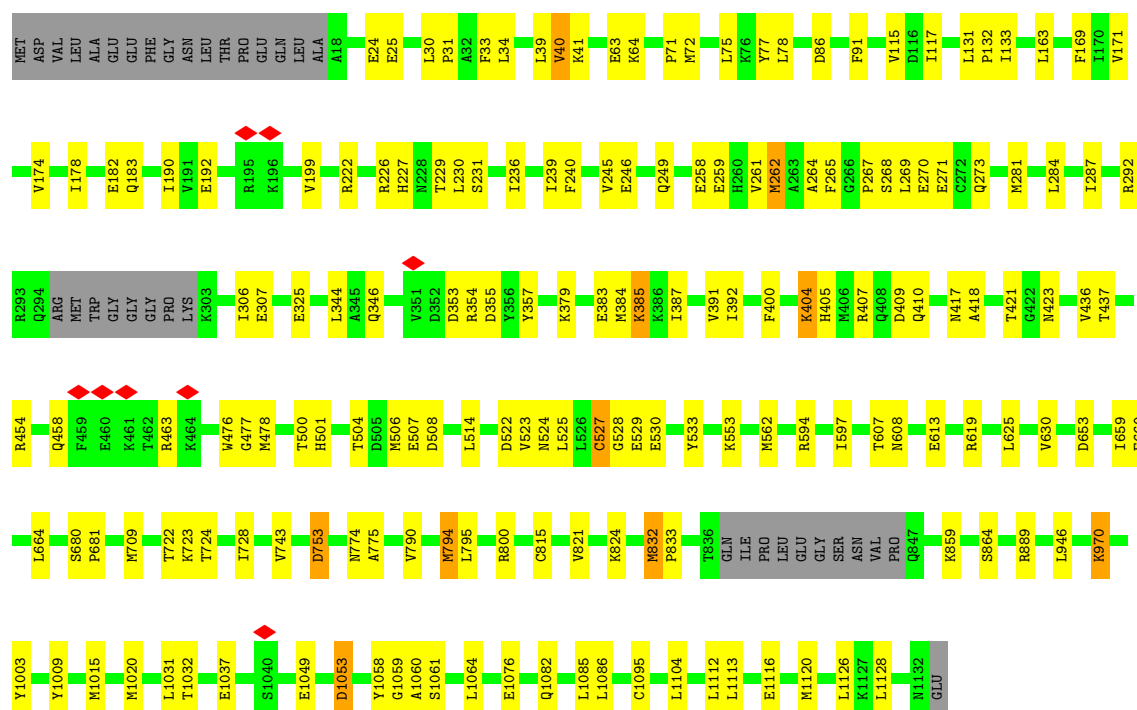
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: DNA-directed RNA polymerase III subunit RPC1

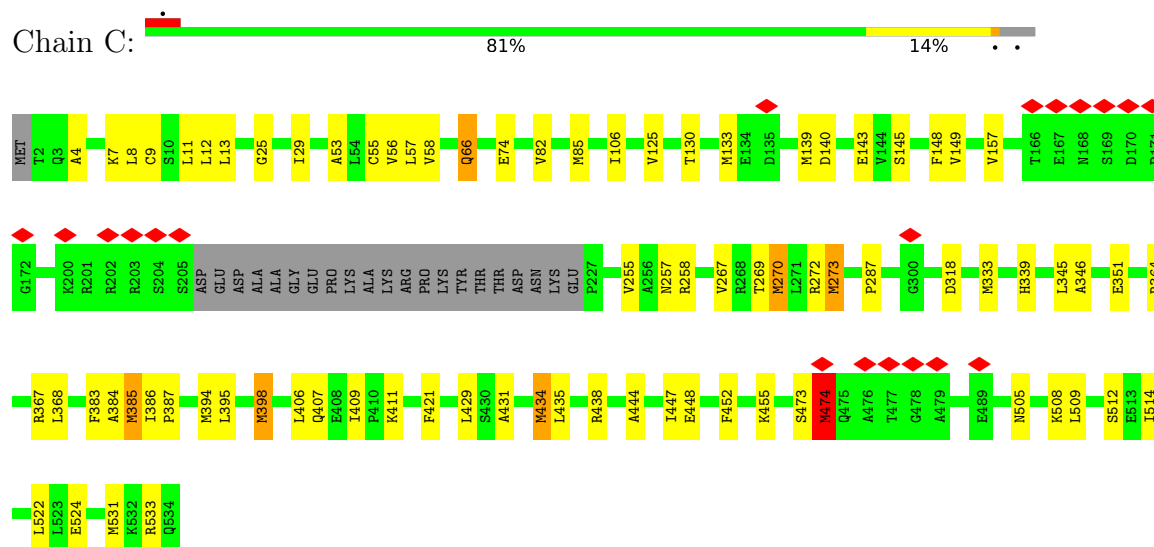


#### • Molecule 2: DNA-directed RNA polymerase III subunit RPC2

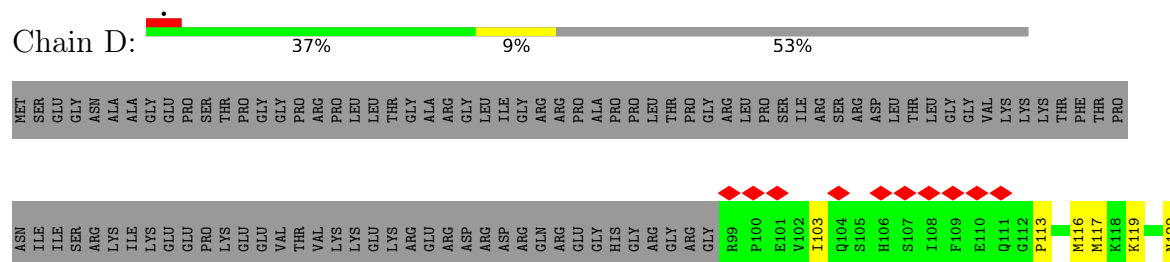




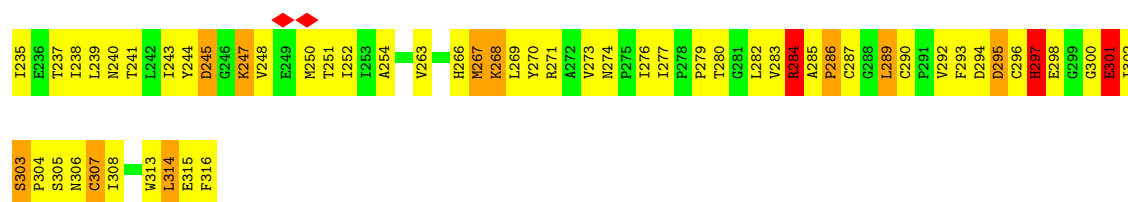
- Molecule 3: DNA-directed RNA polymerase III subunit RPC3



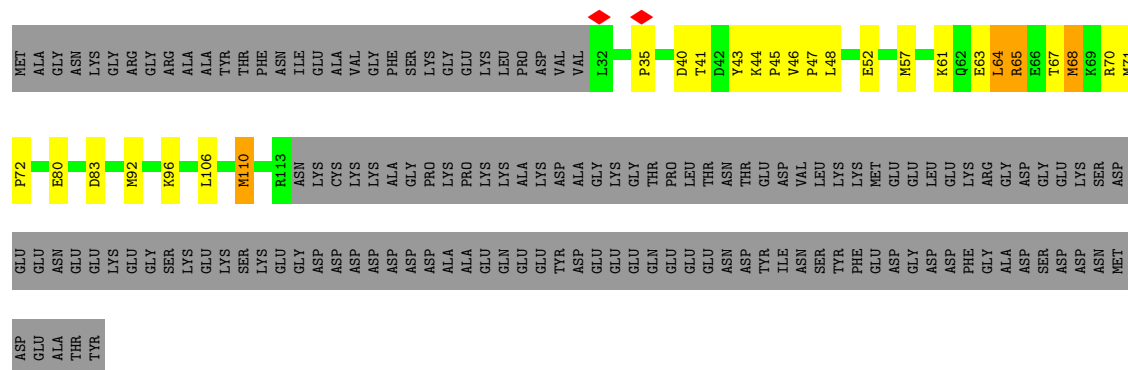
- Molecule 4: DNA-directed RNA polymerase III subunit RPC4



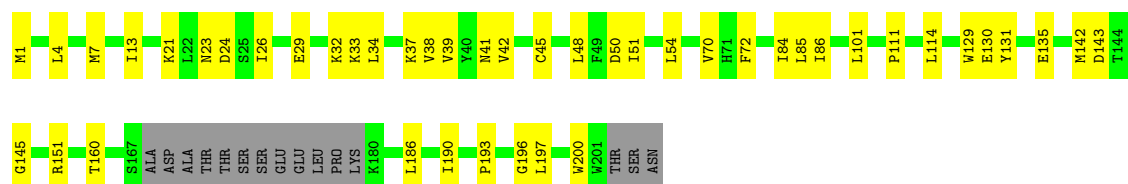




• Molecule 7: DNA-directed RNA polymerase III subunit RPC7



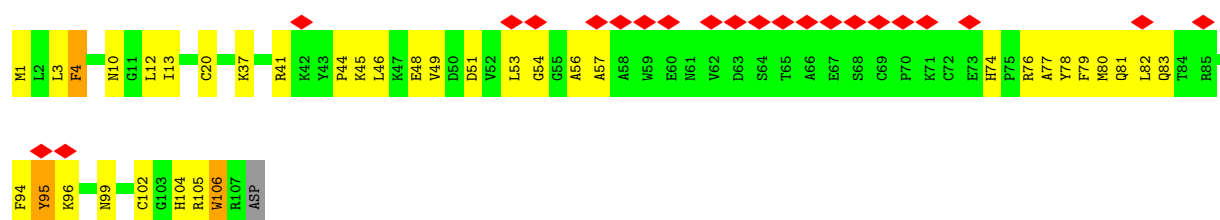
• Molecule 8: DNA-directed RNA polymerase III subunit RPC8



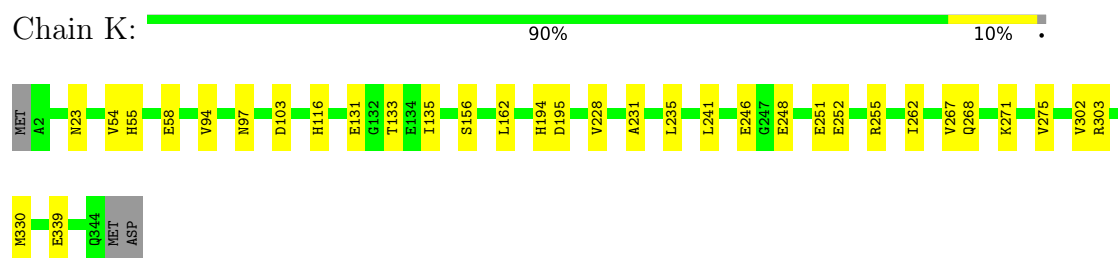
• Molecule 9: DNA-directed RNA polymerase III subunit RPC9



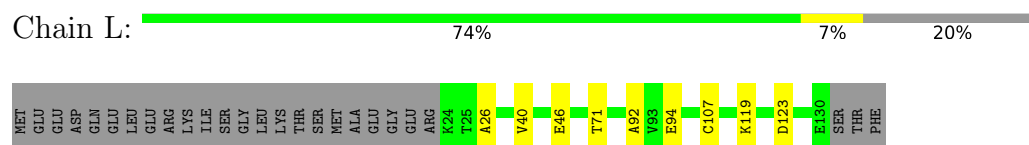
• Molecule 10: DNA-directed RNA polymerase III subunit RPC10



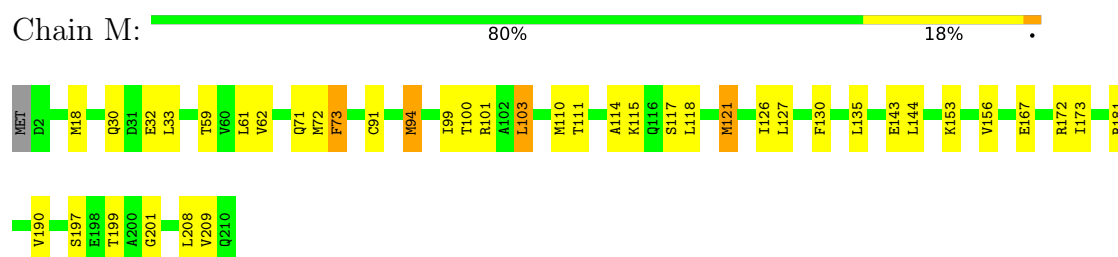
- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC1



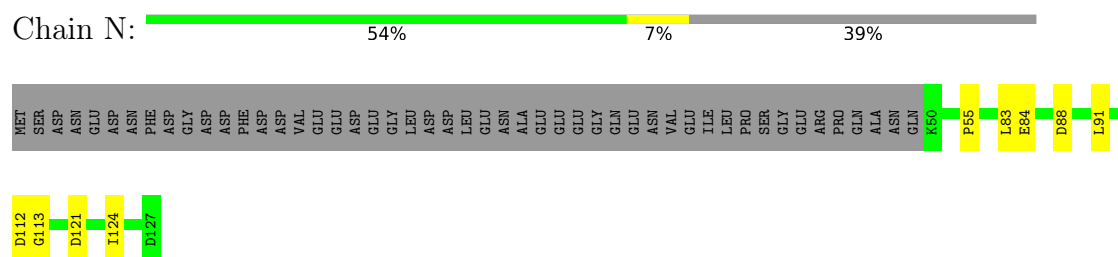
- Molecule 12: DNA-directed RNA polymerases I and III subunit RPAC2



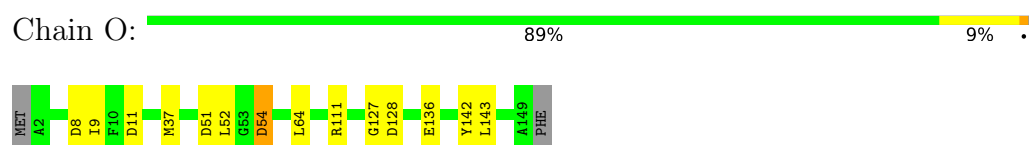
- Molecule 13: DNA-directed RNA polymerases I, II, and III subunit RPABC1



- Molecule 14: DNA-directed RNA polymerases I, II, and III subunit RPABC2



- Molecule 15: DNA-directed RNA polymerases I, II, and III subunit RPABC3



- Molecule 16: DNA-directed RNA polymerases I, II, and III subunit RPABC4



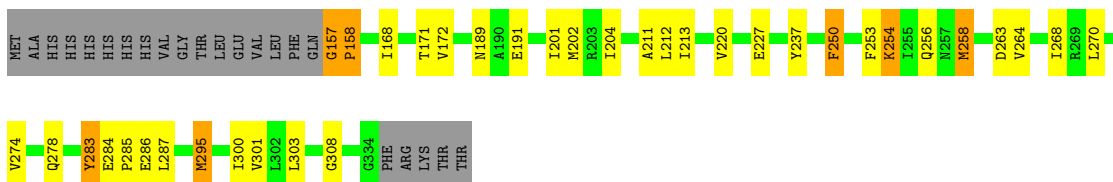
- Molecule 17: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain Q:  91% 7%



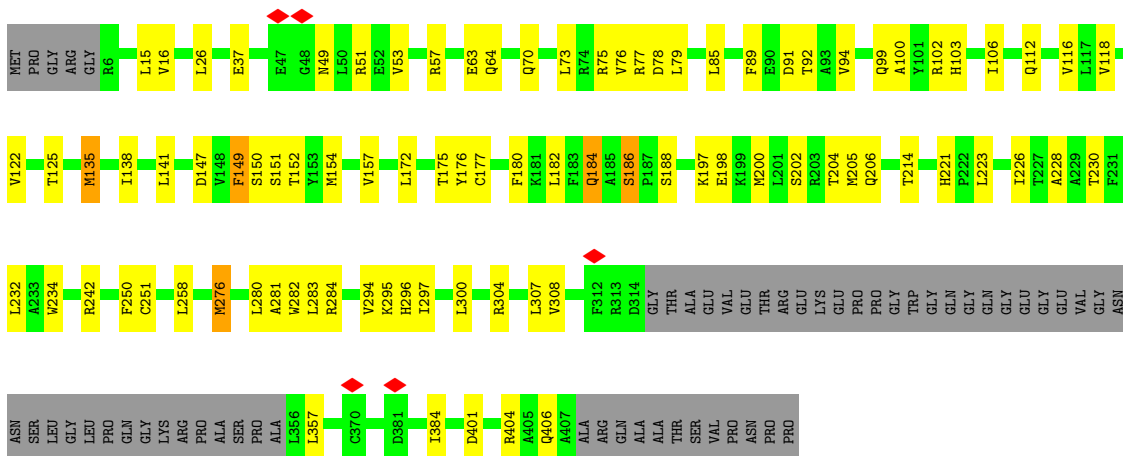
- Molecule 18: TATA-box-binding protein

Chain R:  70% 15% 5% 10%



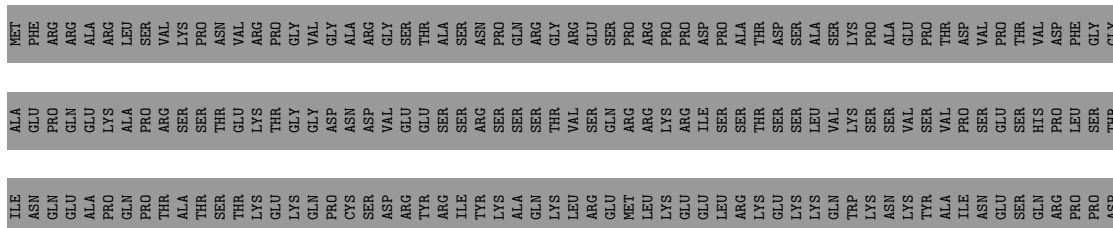
- Molecule 19: Transcription factor IIB 50 kDa subunit

Chain S:  65% 20% 14%



- Molecule 20: Transcription factor TFIIB component B" homolog

Chain T:  11% 5% 84%







- Molecule 23: U6\_2\_Template





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9476	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	130000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	2.320	Depositor
Minimum map value	-1.264	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	401.1, 401.1, 401.1	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95500004, 0.95500004, 0.95500004	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SF4, MG

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	0.37	0/11044	0.60	1/14893 (0.0%)
2	B	0.42	0/8845	0.60	0/11930
3	C	0.29	0/4141	0.59	1/5592 (0.0%)
4	D	0.33	0/1466	0.61	0/1972
5	E	0.29	0/3282	0.54	0/4439
6	F	0.39	0/2438	0.64	0/3289
7	G	1.07	4/739 (0.5%)	1.05	5/996 (0.5%)
8	H	0.32	0/1551	0.53	0/2110
9	I	0.28	0/1013	0.52	0/1365
10	J	0.33	0/870	0.65	0/1175
11	K	0.45	0/2790	0.60	0/3782
12	L	0.46	0/871	0.60	0/1174
13	M	0.31	0/1745	0.58	0/2358
14	N	0.40	0/637	0.61	0/861
15	O	0.41	0/1207	0.58	0/1628
16	P	0.41	0/394	0.61	0/524
17	Q	0.51	0/533	0.59	0/719
18	R	0.82	3/1428 (0.2%)	0.97	5/1924 (0.3%)
19	S	0.31	0/2898	0.59	0/3933
20	T	0.34	0/680	0.65	0/904
21	U	0.32	0/1215	0.58	0/1640
22	W	0.29	0/2058	0.54	0/2760
23	X	0.60	0/1381	1.51	70/2124 (3.3%)
24	Y	0.60	0/1442	1.43	67/2223 (3.0%)
25	Z	0.29	0/3203	0.53	0/4335
All	All	0.41	7/57871 (0.0%)	0.68	149/78650 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
6	F	0	5
7	G	0	1
All	All	0	8

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	R	158	PRO	CB-CG	23.81	2.69	1.50
7	G	35	PRO	CG-CD	-21.44	0.79	1.50
18	R	158	PRO	CG-CD	-12.82	1.08	1.50
7	G	35	PRO	N-CD	12.63	1.65	1.47
7	G	35	PRO	CB-CG	9.20	1.96	1.50

The worst 5 of 149 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	R	158	PRO	CB-CG-CD	-27.30	0.02	106.50
7	G	35	PRO	N-CD-CG	-20.18	72.92	103.20
18	R	158	PRO	CA-N-CD	-13.94	91.99	111.50
7	G	35	PRO	CA-CB-CG	-10.93	83.23	104.00
18	R	158	PRO	CA-CB-CG	-10.33	84.37	104.00

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1092	ASP	Peptide
1	A	1198	LYS	Peptide
6	F	84	LYS	Peptide
6	F	85	MET	Peptide
6	F	86	LYS	Peptide

## 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	10848	0	11089	261	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	8680	0	8805	142	0
3	C	4075	0	4149	73	0
4	D	1448	0	1489	33	0
5	E	3211	0	3227	49	0
6	F	2395	0	2404	131	0
7	G	717	0	719	24	0
8	H	1509	0	1461	31	0
9	I	1001	0	1028	15	0
10	J	849	0	813	62	0
11	K	2736	0	2712	22	0
12	L	856	0	840	9	0
13	M	1715	0	1733	37	0
14	N	627	0	659	8	0
15	O	1186	0	1147	13	0
16	P	388	0	393	8	0
17	Q	524	0	540	4	0
18	R	1402	0	1489	30	0
19	S	2847	0	2887	83	0
20	T	665	0	665	21	0
21	U	1183	0	1175	26	0
22	W	2018	0	1997	22	0
23	X	1237	0	695	23	0
24	Y	1283	0	700	25	0
25	Z	3123	0	2983	32	0
26	A	2	0	0	0	0
26	B	1	0	0	0	0
26	J	1	0	0	0	0
26	P	1	0	0	0	0
26	Q	1	0	0	0	0
26	S	1	0	0	0	0
26	Z	2	0	0	0	0
27	A	1	0	0	0	0
28	F	8	0	0	6	0
All	All	56541	0	55799	1033	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.

The worst 5 of 1033 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)
15:O:51:ASP:OD1	15:O:52:LEU:N	1.98	0.97
21:U:37:LYS:HE3	21:U:40:THR:HG23	1.57	0.87
6:F:293:PHE:HA	28:F:401:SF4:S2	2.18	0.82
1:A:1094:ASP:OD1	1:A:1095:ALA:N	2.13	0.82
2:B:410:GLN:N	2:B:410:GLN:OE1	2.13	0.82

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	1377/1390 (99%)	1274 (92%)	101 (7%)	2 (0%)	48	79
2	B	1091/1133 (96%)	1031 (94%)	59 (5%)	1 (0%)	48	79
3	C	508/534 (95%)	489 (96%)	19 (4%)	0	100	100
4	D	180/398 (45%)	170 (94%)	10 (6%)	0	100	100
5	E	396/708 (56%)	378 (96%)	18 (4%)	0	100	100
6	F	300/316 (95%)	241 (80%)	46 (15%)	13 (4%)	2	18
7	G	80/223 (36%)	70 (88%)	10 (12%)	0	100	100
8	H	185/204 (91%)	178 (96%)	7 (4%)	0	100	100
9	I	122/148 (82%)	120 (98%)	2 (2%)	0	100	100
10	J	105/108 (97%)	87 (83%)	18 (17%)	0	100	100
11	K	341/346 (99%)	327 (96%)	14 (4%)	0	100	100
12	L	105/133 (79%)	99 (94%)	6 (6%)	0	100	100
13	M	207/210 (99%)	201 (97%)	6 (3%)	0	100	100
14	N	76/127 (60%)	72 (95%)	4 (5%)	0	100	100
15	O	146/150 (97%)	141 (97%)	5 (3%)	0	100	100
16	P	44/58 (76%)	38 (86%)	6 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Q	64/67 (96%)	64 (100%)	0	0	100	100
18	R	176/200 (88%)	170 (97%)	6 (3%)	0	100	100
19	S	357/419 (85%)	347 (97%)	10 (3%)	0	100	100
20	T	76/484 (16%)	72 (95%)	4 (5%)	0	100	100
21	U	139/368 (38%)	137 (99%)	2 (1%)	0	100	100
22	W	240/1519 (16%)	235 (98%)	5 (2%)	0	100	100
25	Z	383/411 (93%)	370 (97%)	13 (3%)	0	100	100
All	All	6698/9654 (69%)	6311 (94%)	371 (6%)	16 (0%)	45	75

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	40	VAL
6	F	86	LYS
6	F	160	SER
6	F	232	MET
6	F	245	ASP

### 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	1204/1212 (99%)	1167 (97%)	37 (3%)	35	62
2	B	959/988 (97%)	935 (98%)	24 (2%)	42	67
3	C	458/476 (96%)	448 (98%)	10 (2%)	47	69
4	D	167/347 (48%)	164 (98%)	3 (2%)	54	74
5	E	358/622 (58%)	346 (97%)	12 (3%)	32	60
6	F	268/280 (96%)	250 (93%)	18 (7%)	13	40
7	G	79/195 (40%)	73 (92%)	6 (8%)	11	35
8	H	168/181 (93%)	165 (98%)	3 (2%)	54	74
9	I	116/136 (85%)	115 (99%)	1 (1%)	75	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	J	93/94 (99%)	90 (97%)	3 (3%)	34	61
11	K	299/302 (99%)	298 (100%)	1 (0%)	91	96
12	L	96/119 (81%)	96 (100%)	0	100	100
13	M	191/192 (100%)	183 (96%)	8 (4%)	25	54
14	N	68/111 (61%)	68 (100%)	0	100	100
15	O	129/131 (98%)	128 (99%)	1 (1%)	79	87
16	P	43/55 (78%)	42 (98%)	1 (2%)	45	69
17	Q	55/56 (98%)	54 (98%)	1 (2%)	54	74
18	R	152/172 (88%)	147 (97%)	5 (3%)	33	60
19	S	324/365 (89%)	317 (98%)	7 (2%)	47	69
20	T	70/440 (16%)	67 (96%)	3 (4%)	25	53
21	U	124/334 (37%)	118 (95%)	6 (5%)	21	50
22	W	215/1250 (17%)	211 (98%)	4 (2%)	52	73
25	Z	340/356 (96%)	337 (99%)	3 (1%)	75	86
All	All	5976/8414 (71%)	5819 (97%)	157 (3%)	42	65

5 of 157 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	J	95	TYR
20	T	367	PHE
13	M	73	PHE
18	R	254	LYS
22	W	186	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
6	F	214	HIS
6	F	297	HIS
25	Z	289	GLN
22	W	306	GLN
3	C	457	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](#)

Of 11 ligands modelled in this entry, 10 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
28	SF4	F	401	6	0,12,12	-	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	SF4	F	401	6	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	F	401	SF4	6	0

## 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.

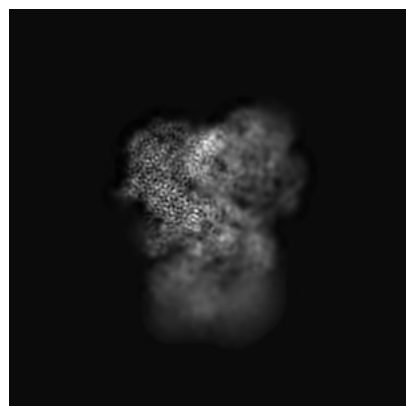
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50732. These allow visual inspection of the internal detail of the map and identification of artifacts.

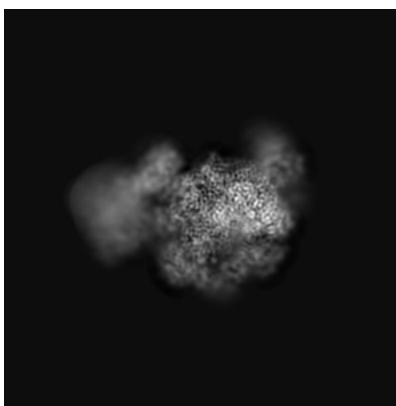
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

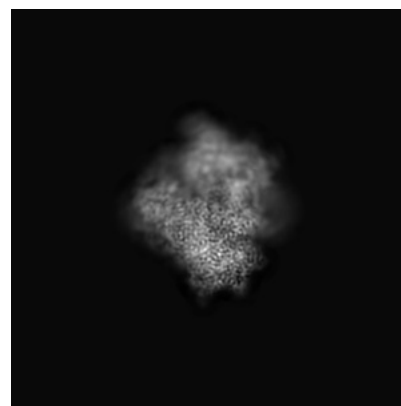
#### 6.1.1 Primary map



X

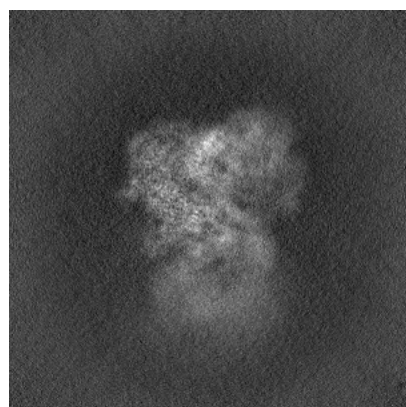


Y

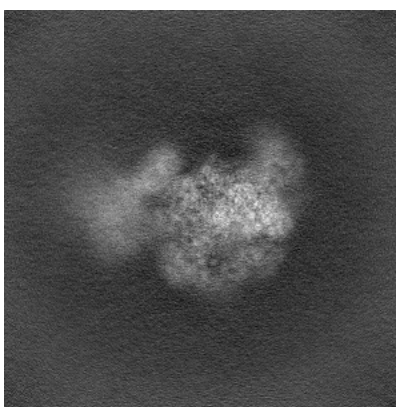


Z

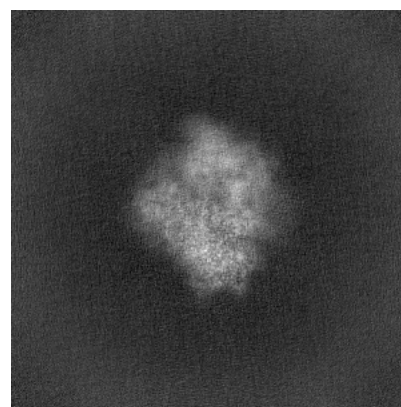
#### 6.1.2 Raw map



X



Y

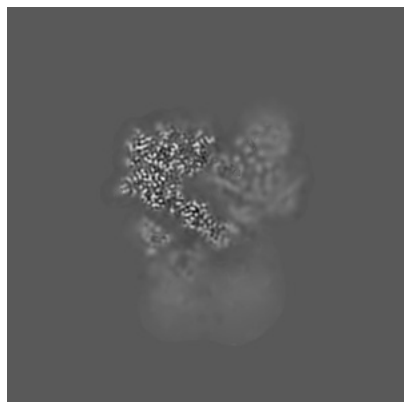


Z

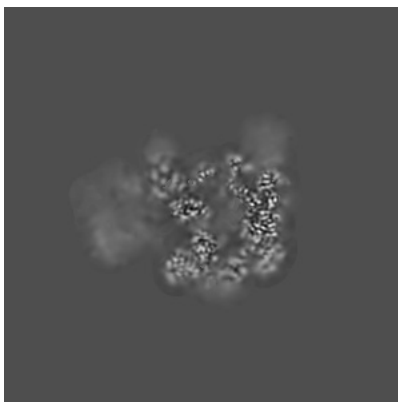
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

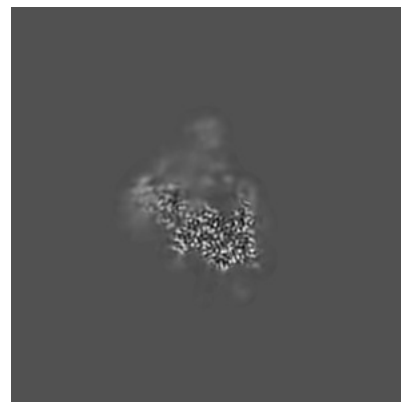
### 6.2.1 Primary map



X Index: 210

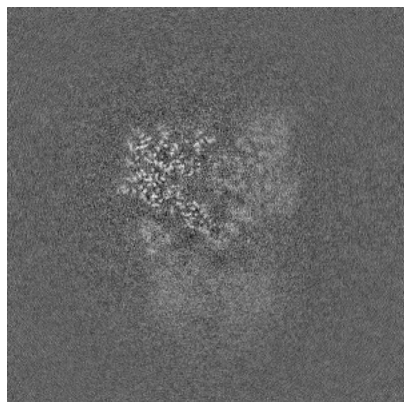


Y Index: 210

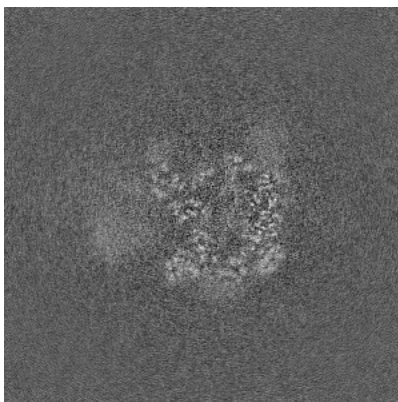


Z Index: 210

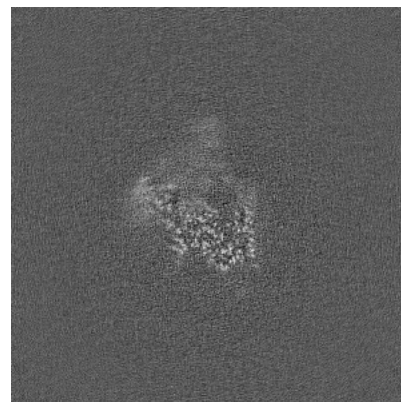
### 6.2.2 Raw map



X Index: 210



Y Index: 210

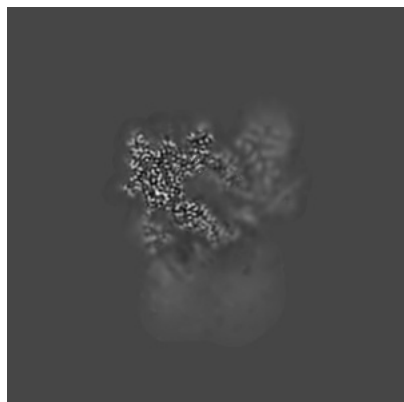


Z Index: 210

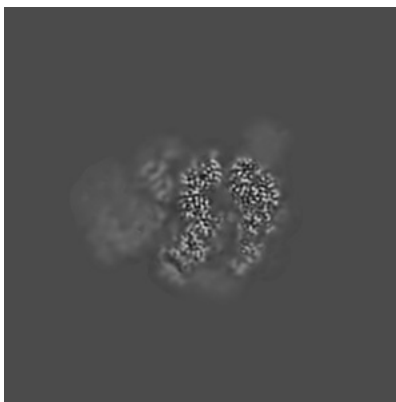
The images above show central slices of the map in three orthogonal directions.

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

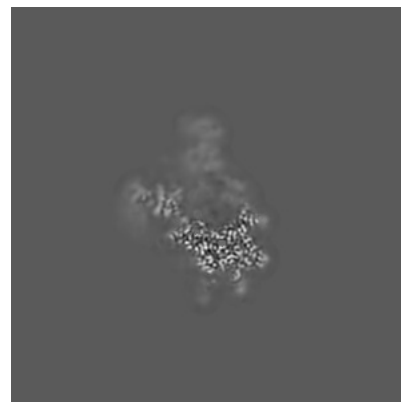
### 6.3.1 Primary map



X Index: 214

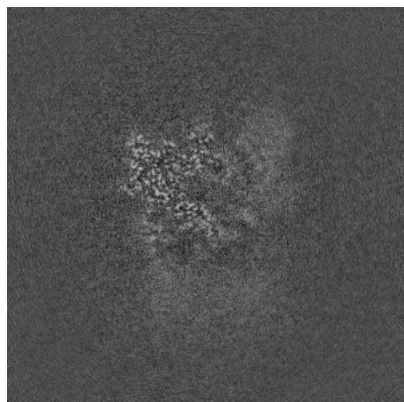


Y Index: 195

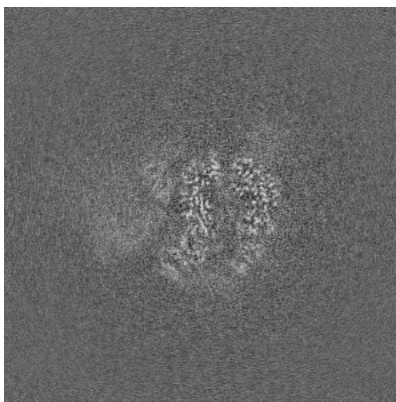


Z Index: 220

### 6.3.2 Raw map



X Index: 214



Y Index: 196



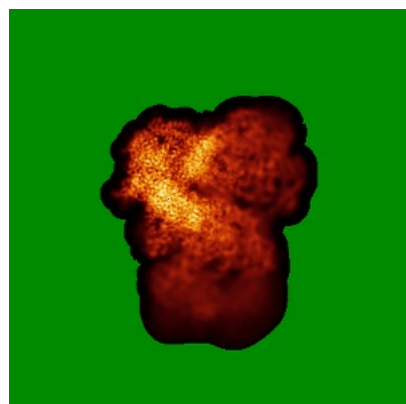
Z Index: 220

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

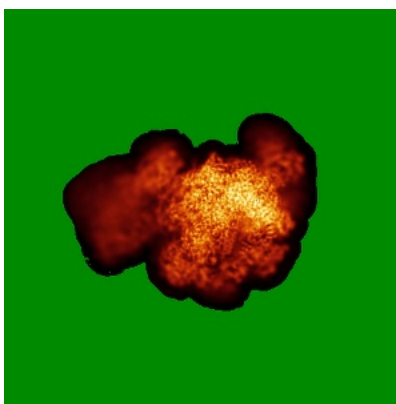


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

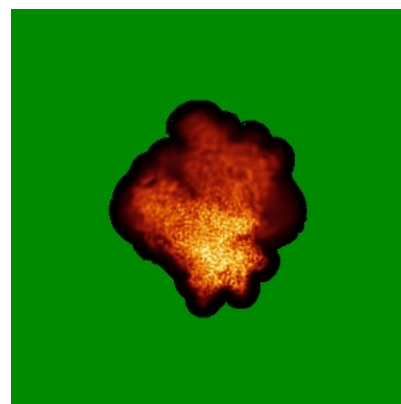
### 6.4.1 Primary map



X

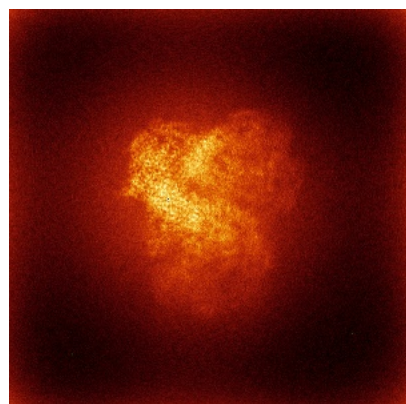


Y

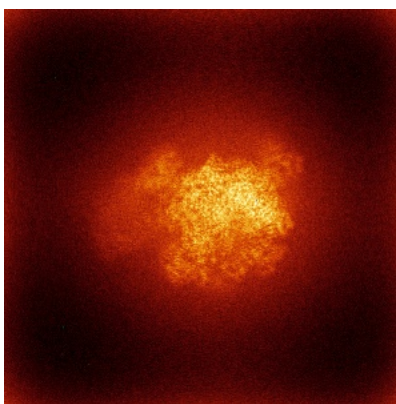


Z

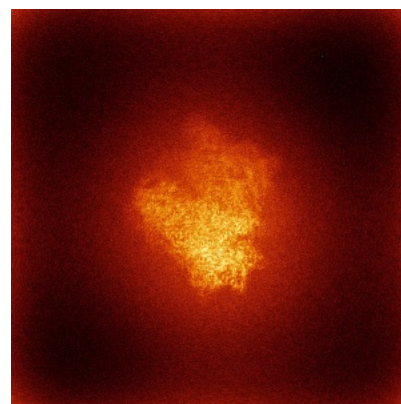
### 6.4.2 Raw map



X



Y



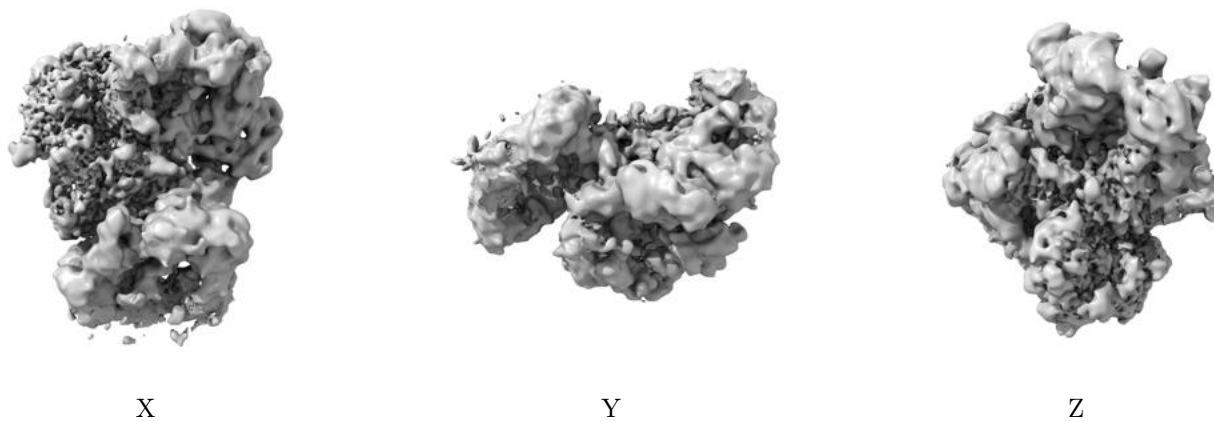
Z

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.



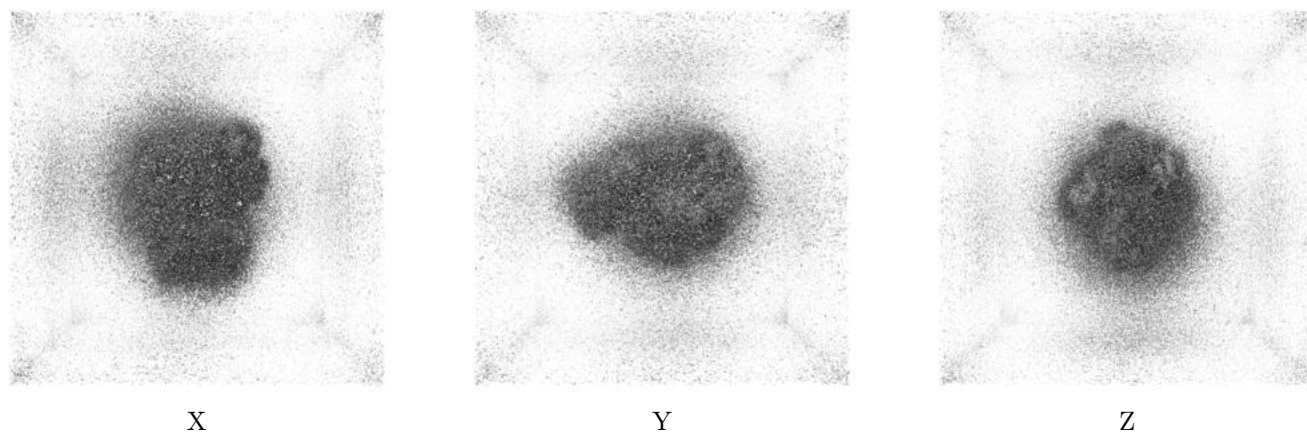
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

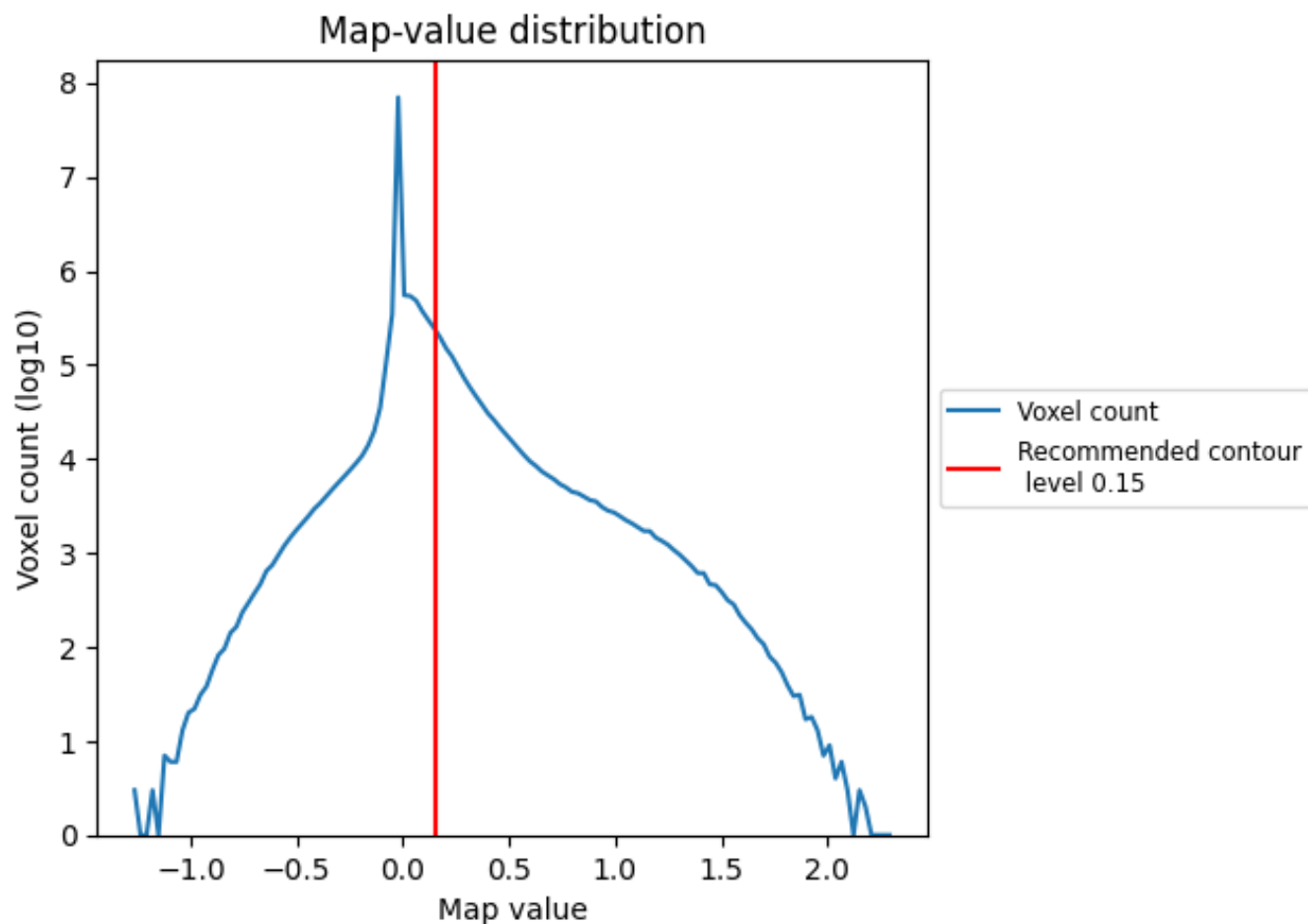
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

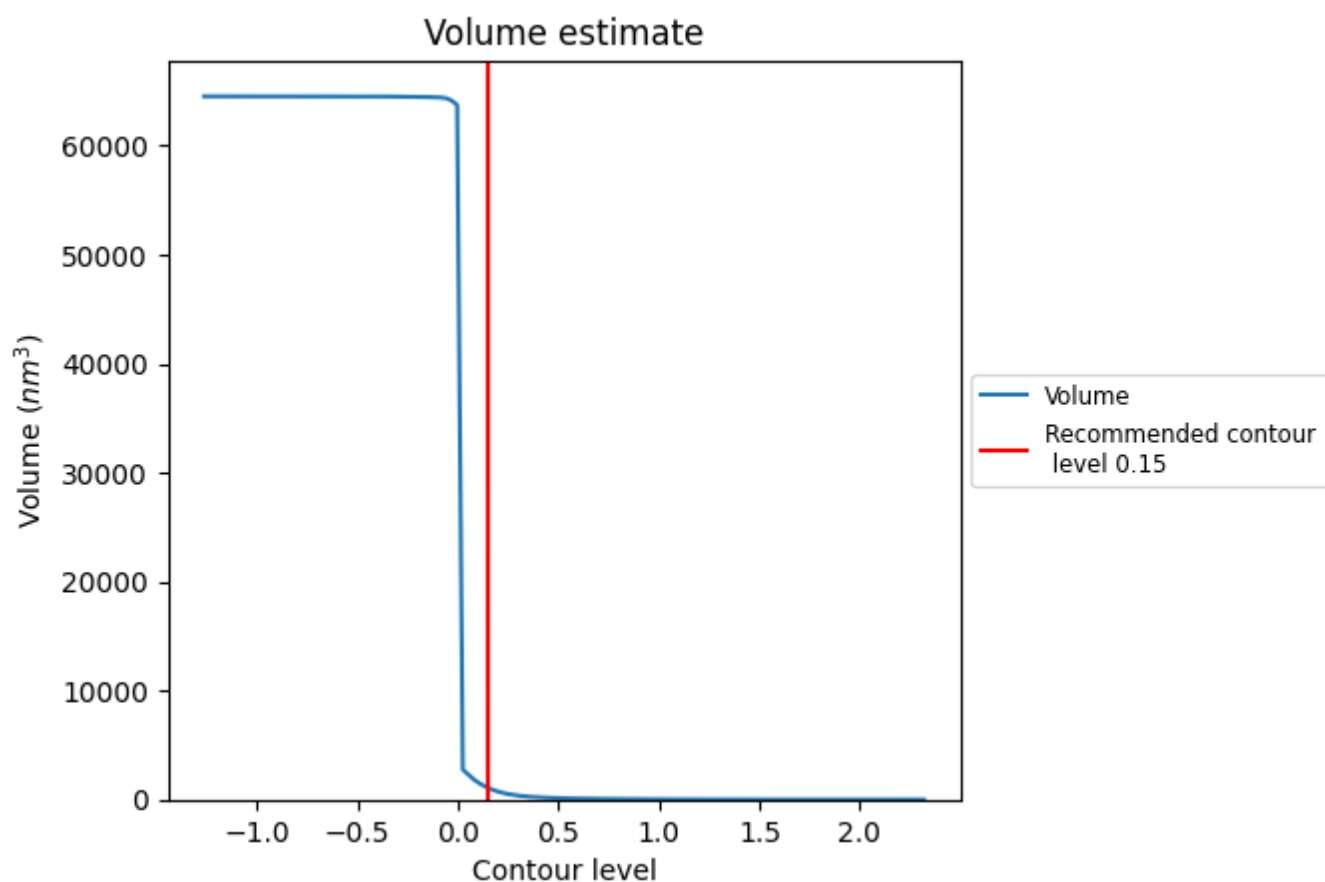
This section contains the results of statistical analysis of the map.

### 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.

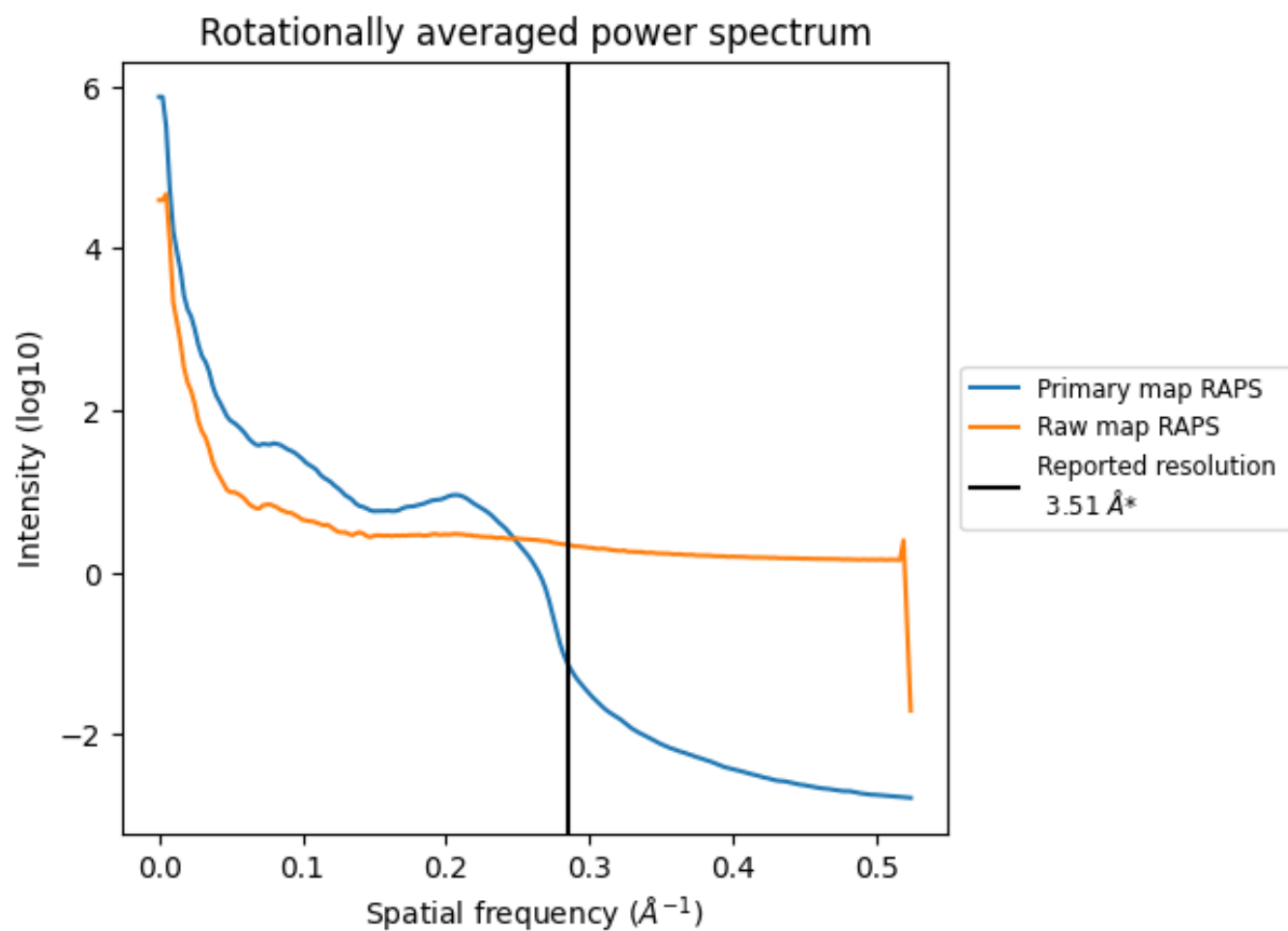
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1080 nm<sup>3</sup>; this corresponds to an approximate mass of 976 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 ⓘ

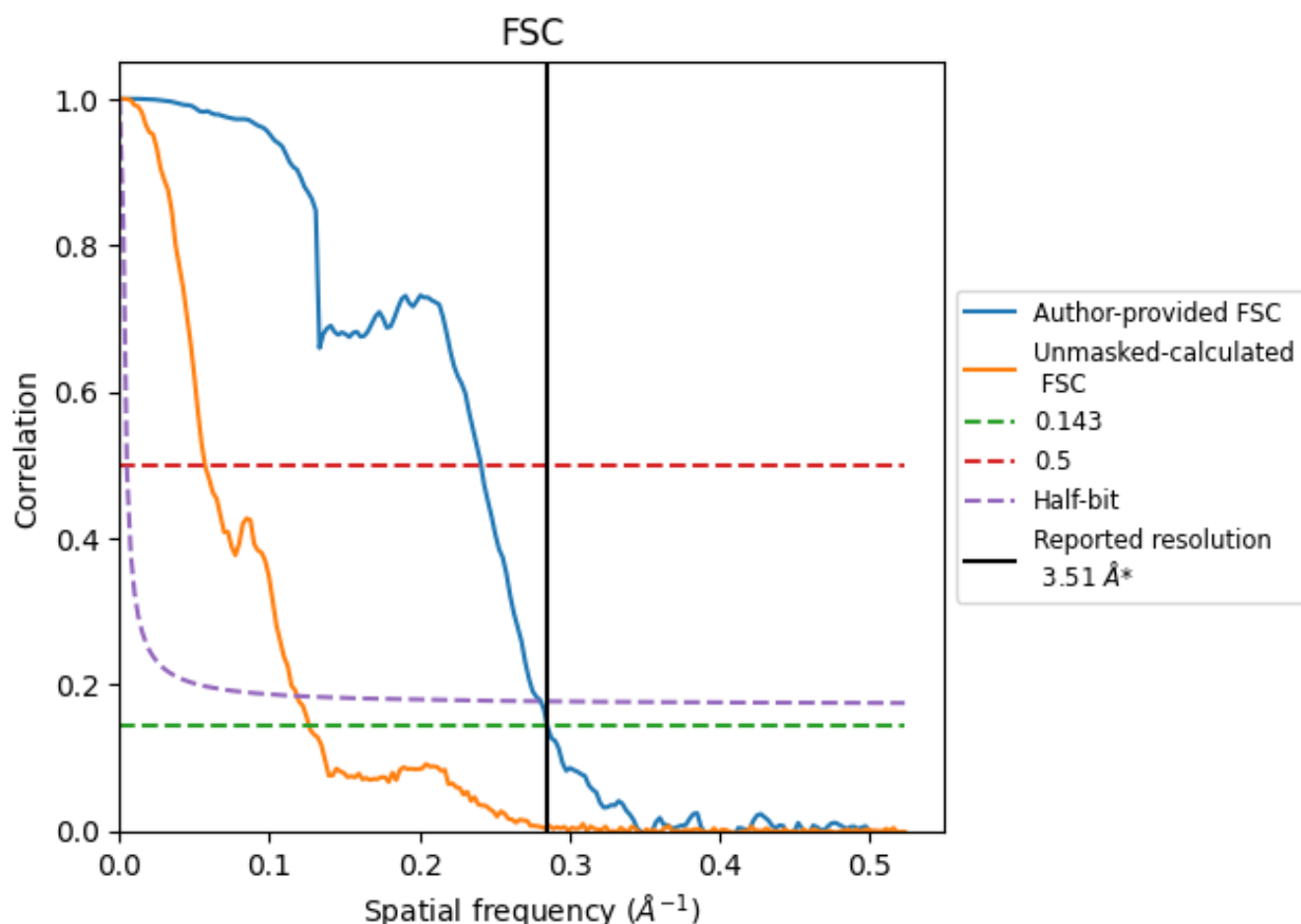


\*Reported resolution corresponds to spatial frequency of 0.285  $\text{\AA}^{-1}$

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

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.285  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

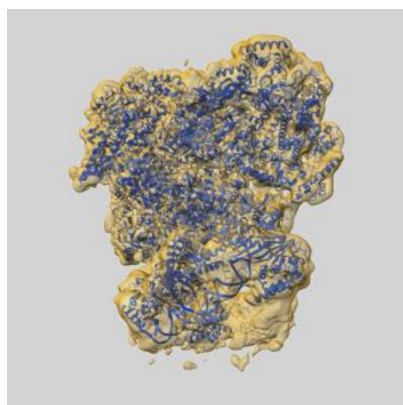
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.51	-	-
Author-provided FSC curve	3.51	4.15	3.56
Unmasked-calculated*	7.91	17.51	8.45

\*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 7.91 differs from the reported value 3.51 by more than 10 %

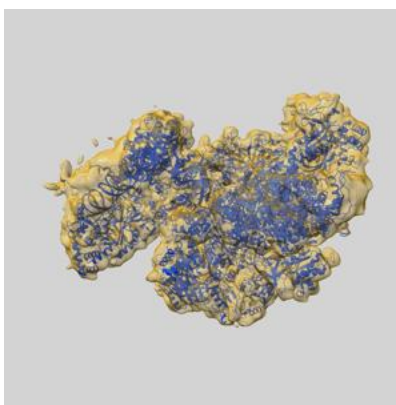
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-50732 and PDB model 9FSQ. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

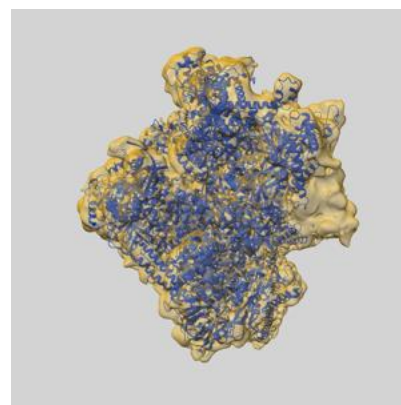
### 9.1 Map-model overlay [i](#)



X



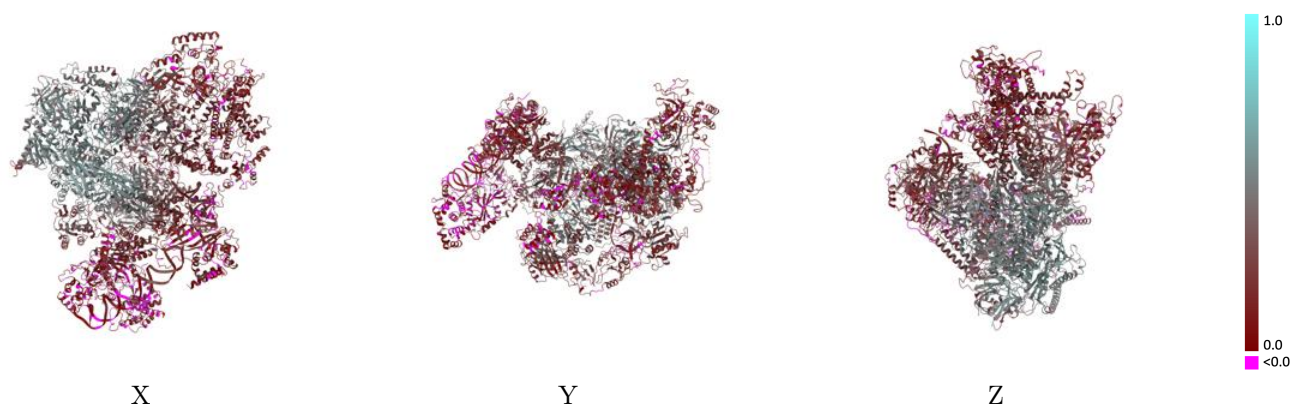
Y



Z

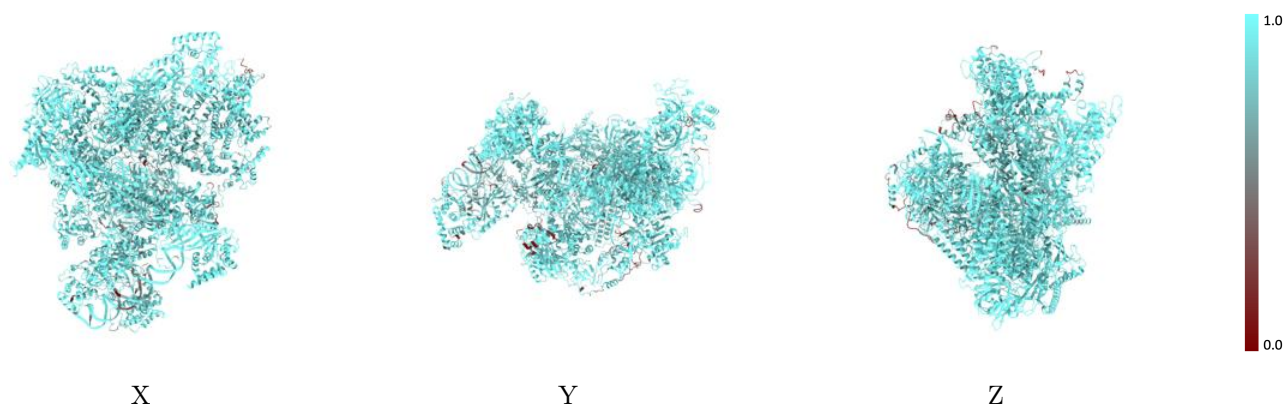
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

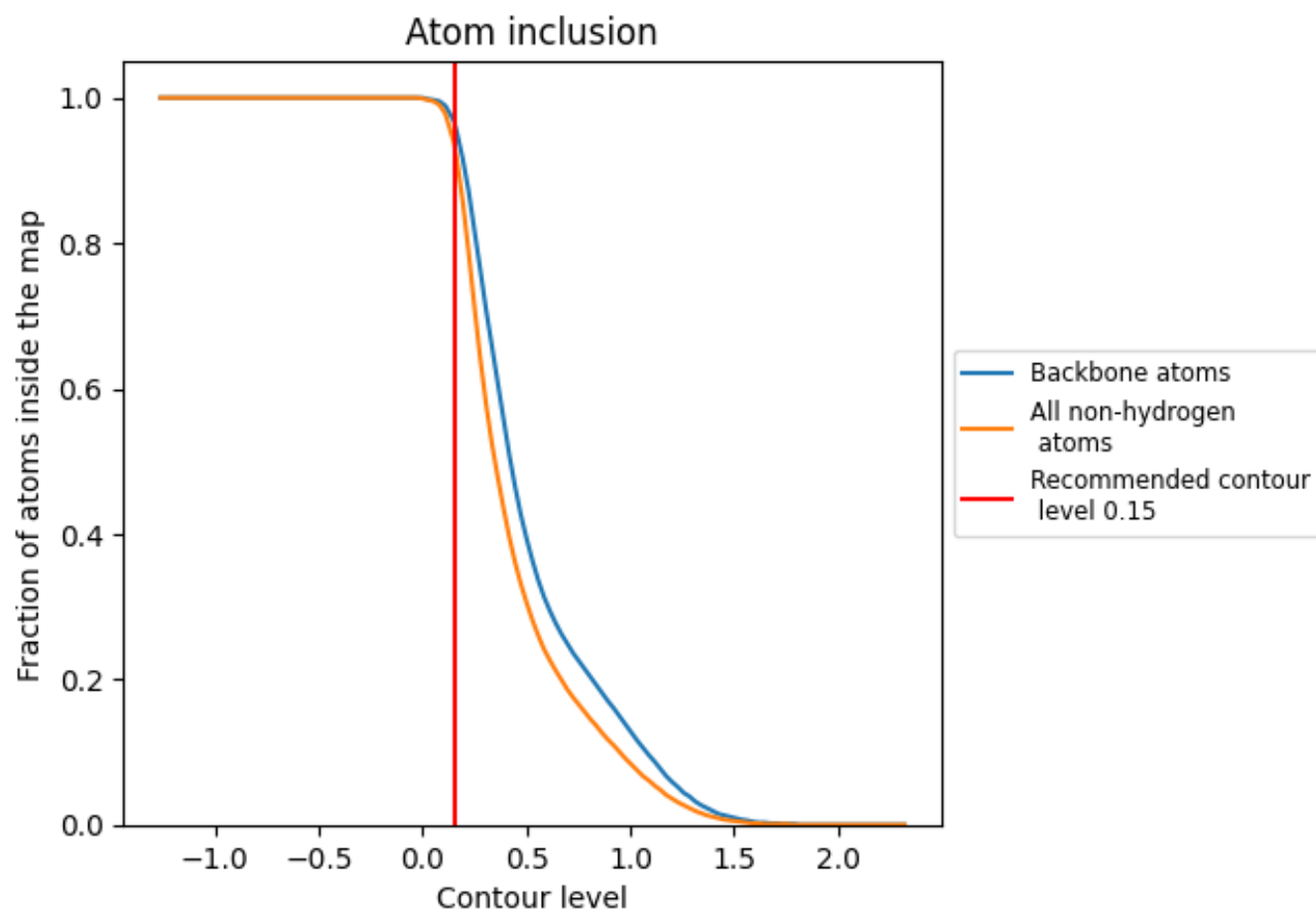
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.15).























































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9380	 0.2940
A	 0.9390	 0.3690
B	 0.9690	 0.4640
C	 0.9190	 0.1590
D	 0.8690	 0.2560
E	 0.9290	 0.2740
F	 0.8680	 0.1080
G	 0.9510	 0.1950
H	 0.9810	 0.2610
I	 0.9820	 0.1970
J	 0.7550	 0.1290
K	 0.9880	 0.4980
L	 0.9960	 0.4860
M	 0.9800	 0.3040
N	 0.9920	 0.5030
O	 0.9890	 0.4650
P	 0.9920	 0.4540
Q	 0.9940	 0.5310
R	 0.9850	 0.1650
S	 0.9080	 0.2430
T	 0.9970	 0.1370
U	 0.9440	 0.0550
W	 0.8880	 0.1200
X	 0.9160	 0.1710
Y	 0.8900	 0.1520
Z	 0.9030	 0.0800

