



wwPDB EM Validation Summary Report ⓘ

Nov 21, 2022 – 09:03 PM JST

PDB ID : 7DN3
EMDB ID : EMD-30779
Title : Structure of Human RNA Polymerase III elongation complex
Authors : Li, L.; Yu, Z.; Zhao, D.; Ren, Y.; Hou, H.; Xu, Y.
Deposited on : 2020-12-08
Resolution : 3.50 Å(reported)

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A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
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) : 2.31.3

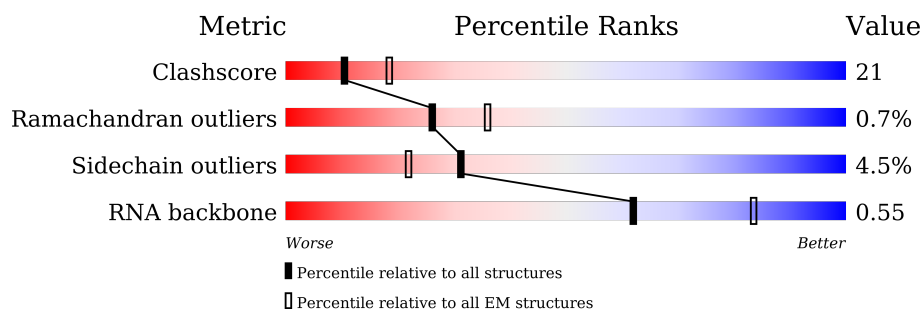
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



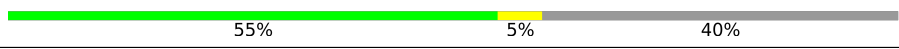

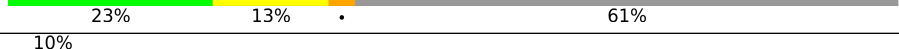

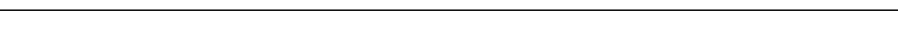
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A	1390	
2	B	1133	
3	C	346	
4	G	204	
5	I	108	
6	K	133	
7	L	58	

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Mol	Chain	Length	Quality of chain
8	P	316	
9	E	210	
10	F	127	
11	H	150	
12	J	67	
13	O	534	
14	Q	223	
15	D	148	
16	M	708	
17	N	398	
18	X	16	
19	Y	23	
20	R	6	

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
23	SF4	P	401	-	-	X	-

2 Entry composition [i](#)

There are 23 unique types of molecules in this entry. The entry contains 36856 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	1293	Total	C	N	O	S	0	0
			10152	6430	1776	1875	71		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1044	Total	C	N	O	S	0	0
			8254	5238	1434	1514	68		

- Molecule 3 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	330	Total	C	N	O	S	0	0
			2641	1667	469	494	11		

- Molecule 4 is a protein called DNA-directed RNA polymerase III subunit RPC8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	166	Total	C	N	O	S	0	0
			1337	876	211	245	5		

- Molecule 5 is a protein called DNA-directed RNA polymerase III subunit RPC10.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	58	Total	C	N	O	S	0	0
			393	241	76	71	5		

- Molecule 6 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	103	Total	C	N	O	S	0	0
			822	513	145	157	7		

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	44	Total	C	N	O	S	0	0
			372	231	72	63	6		

- Molecule 8 is a protein called DNA-directed RNA polymerase III subunit RPC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	130	Total	C	N	O	S	0	0
			1008	636	166	196	10		

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	194	Total	C	N	O	S	0	0
			1590	1014	276	292	8		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	76	Total	C	N	O	S	0	0
			610	392	103	110	5		

- Molecule 11 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	122	Total	C	N	O	S	0	0
			1002	645	167	185	5		

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	64	Total	C	N	O	S	0	0
			507	328	86	87	6		

- Molecule 13 is a protein called DNA-directed RNA polymerase III subunit RPC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	443	Total	C	N	O	S	0	0
			3546	2233	620	673	20		

- Molecule 14 is a protein called DNA-directed RNA polymerase III subunit RPC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	86	Total	C	N	O	S	0	0
			724	463	124	131	6		

- Molecule 15 is a protein called DNA-directed RNA polymerase III subunit RPC9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	D	122	Total	C	N	O	S	0	0
			985	614	172	196	3		

- Molecule 16 is a protein called DNA-directed RNA polymerase III subunit RPC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	154	Total	C	N	O	S	0	0
			1272	809	226	232	5		

- Molecule 17 is a protein called DNA-directed RNA polymerase III subunit RPC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	92	Total	C	N	O	S	0	0
			697	445	117	131	4		

- Molecule 18 is a DNA chain called DNA (5'-D(P*TP*CP*GP*TP*CP*TP*GP*AP*TP*C P*TP*CP*GP*GP*AP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
18	X	16	Total	C	N	O	P	0	0
			327	156	57	98	16		

- Molecule 19 is a DNA chain called DNA (5'-D(P*TP*TP*CP*CP*GP*AP*GP*AP*TP*C P*AP*GP*AP*CP*GP*AP*GP*AP*TP*CP*GP*GP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Y	23	Total	C	N	O	P	0	0
			477	225	93	136	23		

- Molecule 20 is a RNA chain called RNA (5'-R(P*CP*CP*CP*GP*AP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	6	Total	C	N	O	P	0	0
			125	56	21	42	6		

- Molecule 21 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Lig-

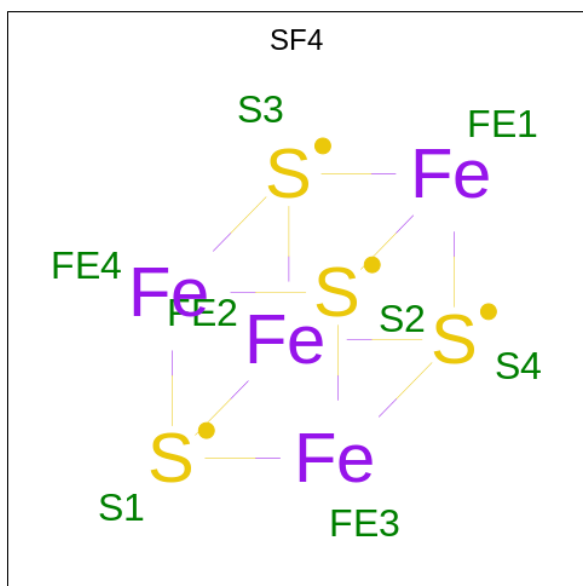
and of Interest" by depositor).

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

- Molecule 22 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
22	A	2	Total	Zn	0
			2	2	
22	B	1	Total	Zn	0
			1	1	
22	I	1	Total	Zn	0
			1	1	
22	L	1	Total	Zn	0
			1	1	
22	J	1	Total	Zn	0
			1	1	

- Molecule 23 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).

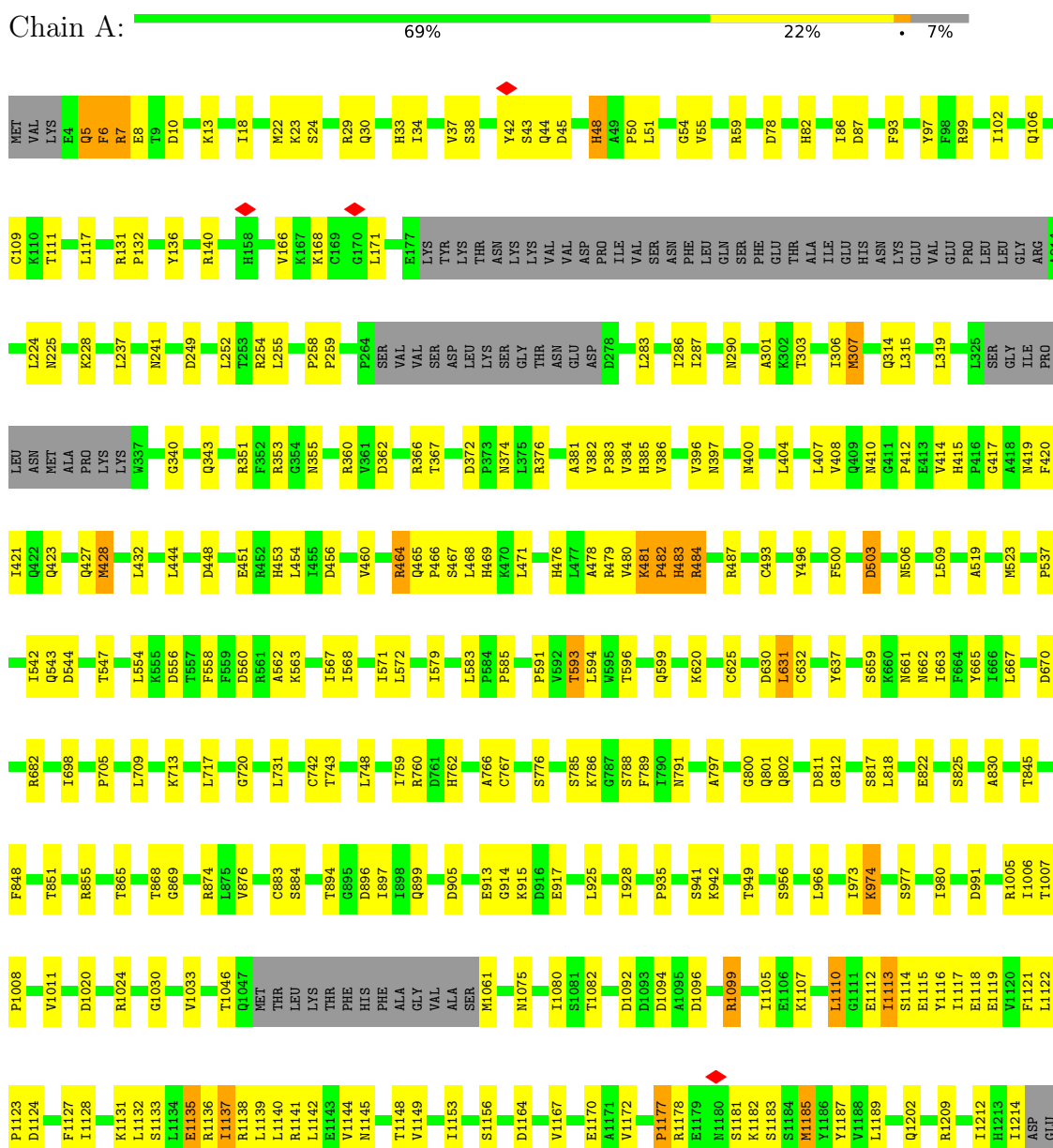


Mol	Chain	Residues	Atoms			AltConf
23	P	1	Total	Fe	S	0
			8	4	4	

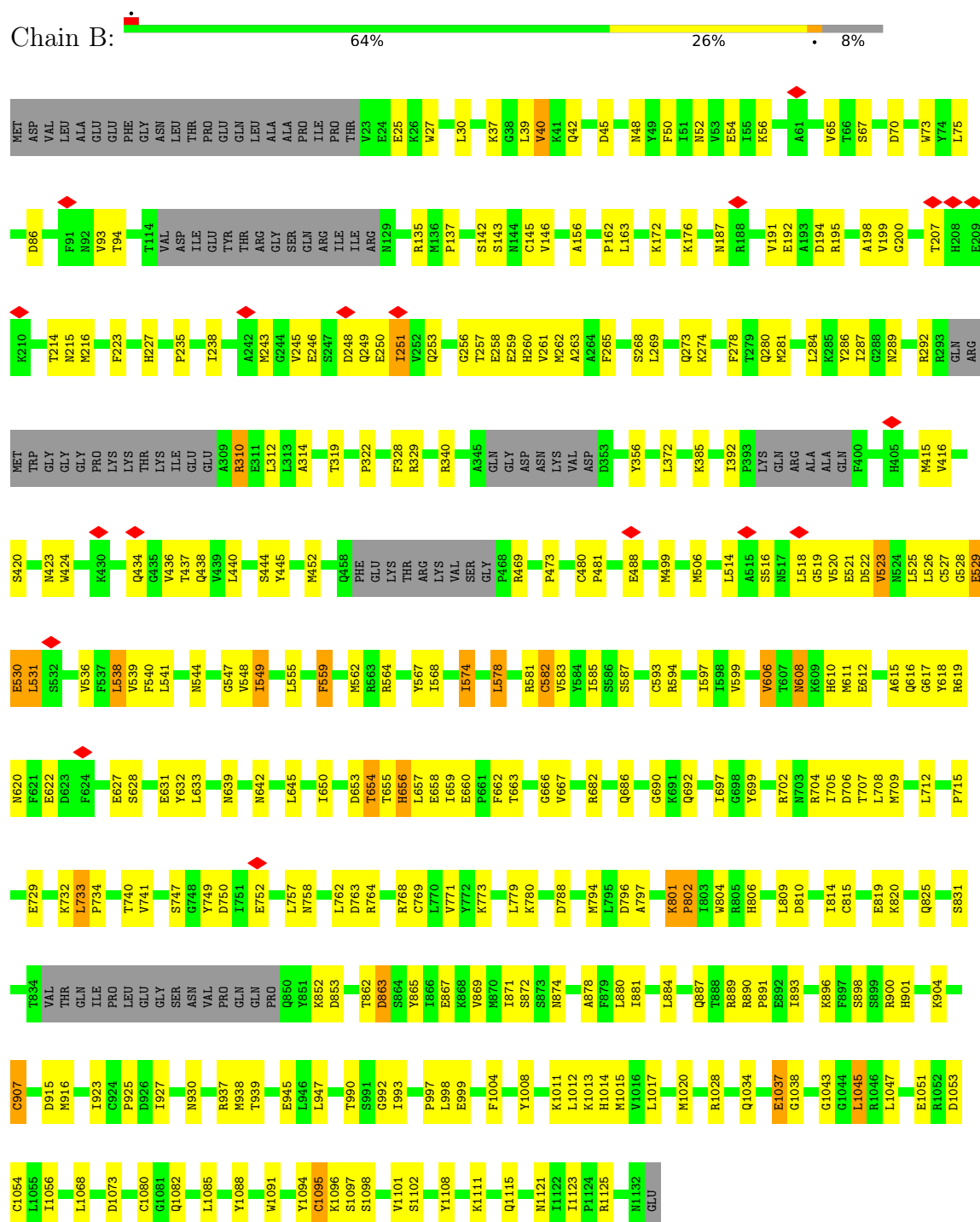
3 Residue-property plots

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.

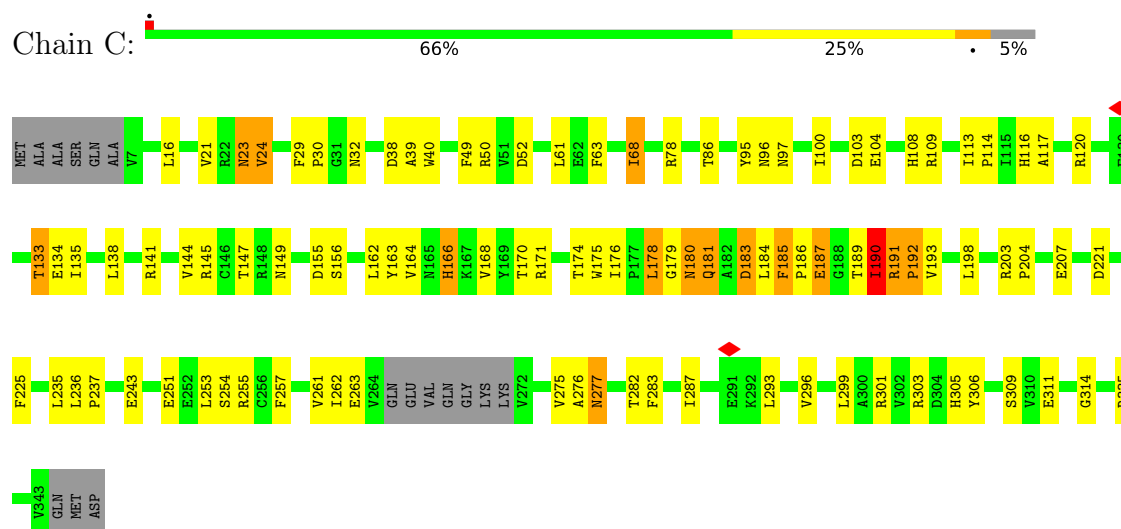
- Molecule 1: DNA-directed RNA polymerase III subunit RPC1



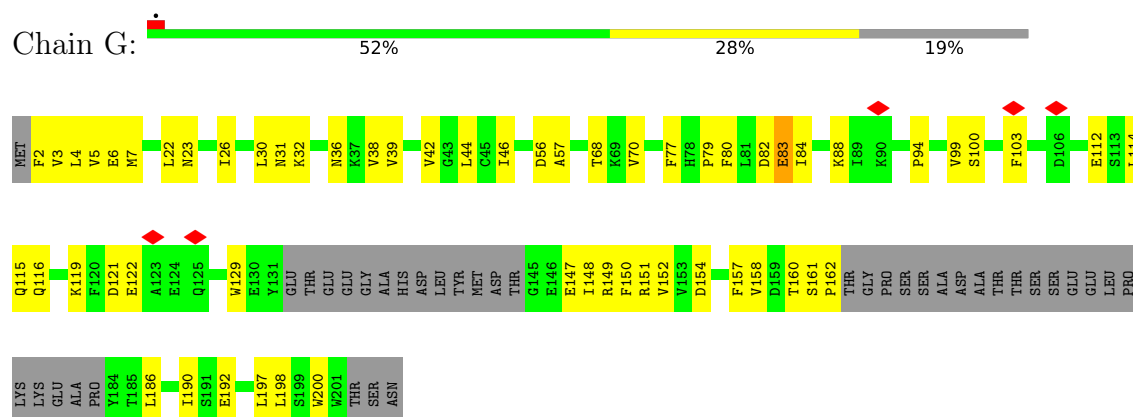
- Molecule 2: DNA-directed RNA polymerase III subunit RPC2



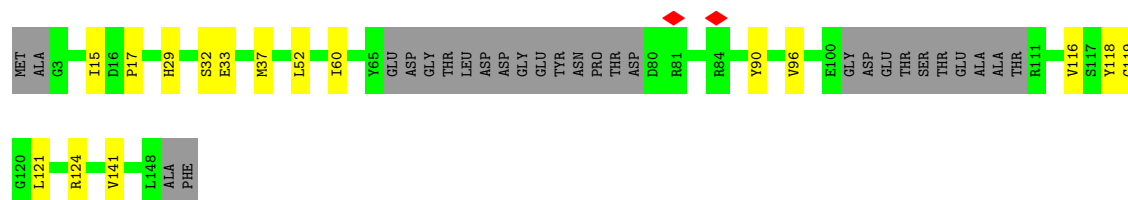
- Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1



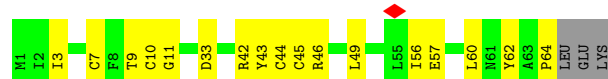
• Molecule 4: DNA-directed RNA polymerase III subunit RPC8



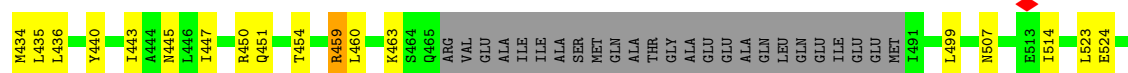
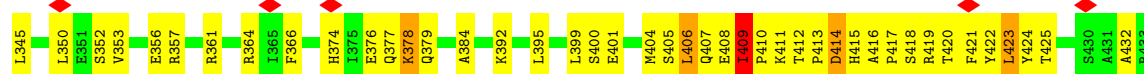
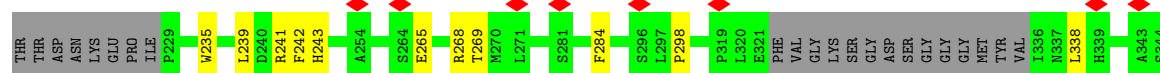
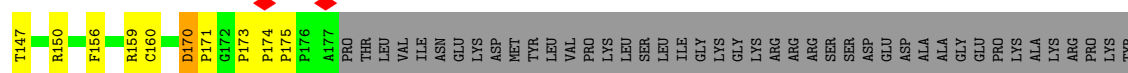
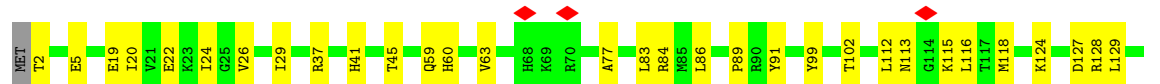
- Chain H:  71% 11% 19%



- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC5



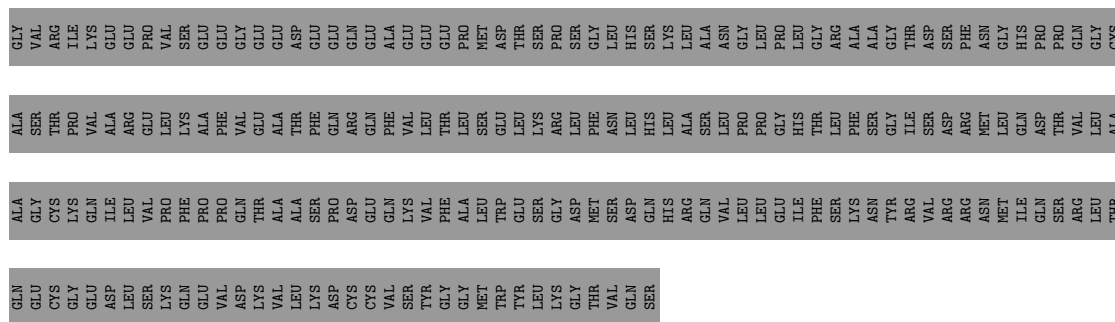
- Molecule 13: DNA-directed RNA polymerase III subunit RPC3



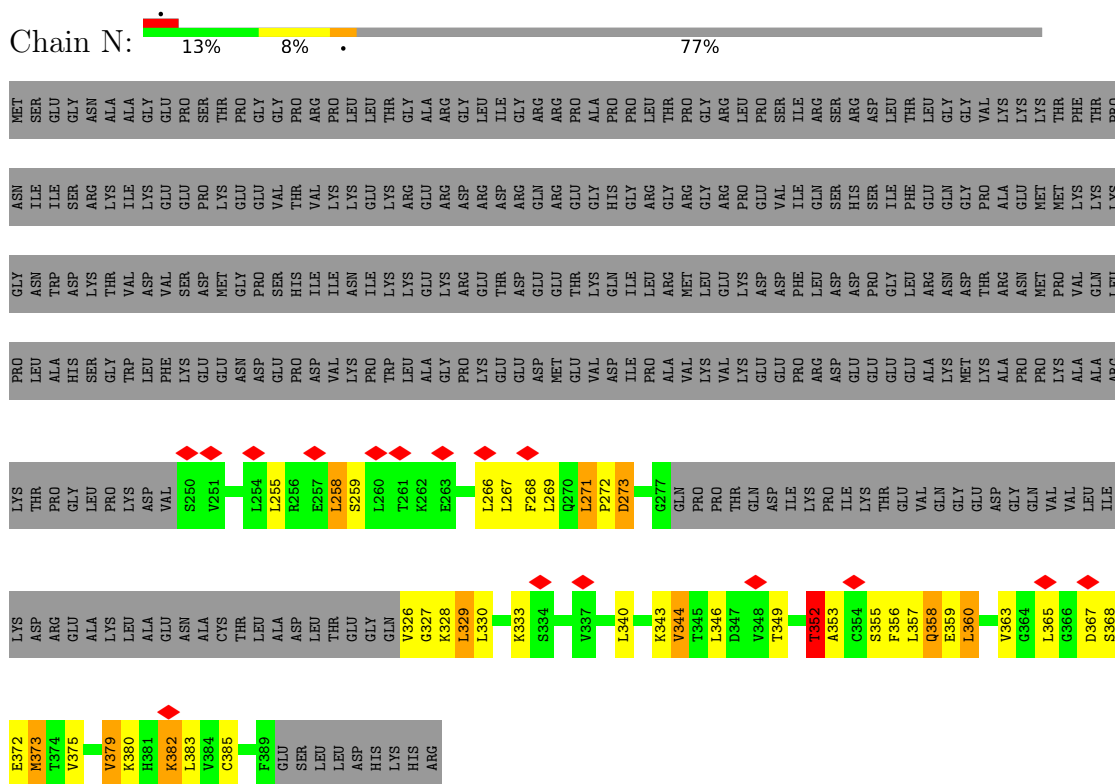
- Molecule 14: DNA-directed RNA polymerase III subunit RPC7







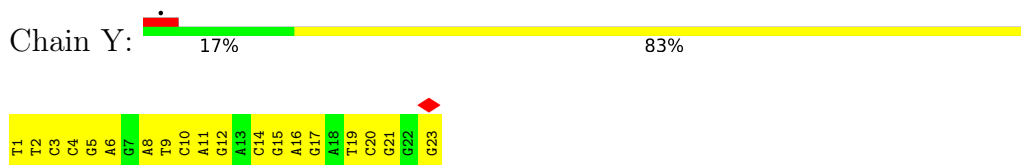
- Molecule 17: DNA-directed RNA polymerase III subunit RPC4



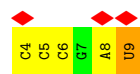
- Molecule 18: DNA (5'-D(P*TP*CP*GP*TP*CP*TP*GP*AP*TP*CP*TP*CP*GP*GP*AP*A)-3')



- Molecule 19: DNA (5'-D(P*TP*TP*CP*CP*GP*AP*GP*AP*TP*CP*AP*GP*AP*CP*GP*AP*GP*AP*TP*CP*GP*GP*G)-3')



- Molecule 20: RNA (5'-R(P*CP*CP*CP*GP*AP*U)-3')



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	98293	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.594	Depositor
Minimum map value	-0.377	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.049	Depositor
Recommended contour level	0.2	Depositor
Map size (\AA)	339.2, 339.2, 339.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.0600001, 1.0600001, 1.0600001	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.54	0/10329	0.65	0/13920
2	B	0.61	0/8410	0.68	0/11338
3	C	0.63	0/2694	0.69	0/3653
4	G	0.50	0/1374	0.69	0/1868
5	I	0.58	0/399	0.96	1/542 (0.2%)
6	K	0.63	0/837	0.67	0/1129
7	L	0.60	0/377	0.64	0/500
8	P	0.44	0/1028	0.72	0/1391
9	E	0.53	0/1616	0.61	0/2180
10	F	0.60	0/620	0.64	0/839
11	H	0.60	0/1019	0.68	0/1366
12	J	0.68	0/516	0.70	0/696
13	O	0.40	0/3604	0.60	0/4872
14	Q	0.45	0/742	0.69	0/996
15	D	0.57	0/997	0.79	0/1343
16	M	0.63	0/1301	0.95	0/1754
17	N	0.59	0/703	0.90	0/946
18	X	0.53	0/365	1.02	0/561
19	Y	0.68	0/536	0.84	0/826
20	R	0.26	0/138	0.75	0/212
All	All	0.56	0/37605	0.69	1/50932 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	44	PRO	N-CA-CB	6.12	110.65	103.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	10152	0	10382	338	0
2	B	8254	0	8364	324	0
3	C	2641	0	2615	148	0
4	G	1337	0	1306	107	0
5	I	393	0	339	68	0
6	K	822	0	810	61	0
7	L	372	0	382	20	0
8	P	1008	0	998	64	0
9	E	1590	0	1630	64	0
10	F	610	0	642	3	0
11	H	1002	0	999	11	0
12	J	507	0	524	24	0
13	O	3546	0	3585	145	0
14	Q	724	0	734	47	0
15	D	985	0	1006	118	0
16	M	1272	0	1264	151	0
17	N	697	0	742	69	0
18	X	327	0	182	40	0
19	Y	477	0	258	58	0
20	R	125	0	65	11	0
21	A	1	0	0	0	0
22	A	2	0	0	0	0
22	B	1	0	0	0	0
22	I	1	0	0	0	0
22	J	1	0	0	0	0
22	L	1	0	0	0	0
23	P	8	0	0	4	0
All	All	36856	0	36827	1547	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 21.

The worst 5 of 1547 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)
16:M:31:PRO:HG2	16:M:136:ARG:CD	1.57	1.34
17:N:357:LEU:HD23	17:N:358:GLN:NE2	1.43	1.30
13:O:356:GLU:OE1	14:Q:39:PRO:HD3	1.33	1.29
6:K:40:VAL:CG2	6:K:92:ALA:HB1	1.64	1.27
1:A:484:ARG:HH21	2:B:1017:LEU:CD2	1.48	1.26

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	1281/1390 (92%)	1153 (90%)	125 (10%)	3 (0%)	47	81
2	B	1030/1133 (91%)	926 (90%)	99 (10%)	5 (0%)	29	68
3	C	326/346 (94%)	293 (90%)	30 (9%)	3 (1%)	17	56
4	G	160/204 (78%)	137 (86%)	23 (14%)	0	100	100
5	I	56/108 (52%)	40 (71%)	12 (21%)	4 (7%)	1	12
6	K	101/133 (76%)	91 (90%)	8 (8%)	2 (2%)	7	39
7	L	42/58 (72%)	40 (95%)	1 (2%)	1 (2%)	6	35
8	P	128/316 (40%)	102 (80%)	25 (20%)	1 (1%)	19	58
9	E	188/210 (90%)	172 (92%)	15 (8%)	1 (0%)	29	68
10	F	74/127 (58%)	68 (92%)	6 (8%)	0	100	100
11	H	116/150 (77%)	101 (87%)	15 (13%)	0	100	100
12	J	62/67 (92%)	58 (94%)	4 (6%)	0	100	100
13	O	435/534 (82%)	416 (96%)	18 (4%)	1 (0%)	47	81
14	Q	82/223 (37%)	72 (88%)	9 (11%)	1 (1%)	13	50
15	D	120/148 (81%)	109 (91%)	10 (8%)	1 (1%)	19	58
16	M	148/708 (21%)	110 (74%)	33 (22%)	5 (3%)	3	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	N	88/398 (22%)	80 (91%)	6 (7%)	2 (2%)	6	36
All	All	4437/6253 (71%)	3968 (89%)	439 (10%)	30 (1%)	26	61

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	523	VAL
2	B	802	PRO
3	C	190	ILE
3	C	191	ARG
5	I	34	ILE

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	1124/1212 (93%)	1095 (97%)	29 (3%)	46	74
2	B	912/988 (92%)	880 (96%)	32 (4%)	36	67
3	C	290/302 (96%)	274 (94%)	16 (6%)	21	54
4	G	149/181 (82%)	146 (98%)	3 (2%)	55	79
5	I	34/94 (36%)	26 (76%)	8 (24%)	1	4
6	K	92/119 (77%)	91 (99%)	1 (1%)	73	88
7	L	41/55 (74%)	39 (95%)	2 (5%)	25	59
8	P	114/280 (41%)	110 (96%)	4 (4%)	36	67
9	E	177/192 (92%)	174 (98%)	3 (2%)	60	82
10	F	66/111 (60%)	66 (100%)	0	100	100
11	H	110/131 (84%)	110 (100%)	0	100	100
12	J	53/56 (95%)	53 (100%)	0	100	100
13	O	400/476 (84%)	390 (98%)	10 (2%)	47	75
14	Q	81/195 (42%)	72 (89%)	9 (11%)	6	28
15	D	114/136 (84%)	88 (77%)	26 (23%)	1	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	M	138/622 (22%)	115 (83%)	23 (17%)	2	12
17	N	81/347 (23%)	67 (83%)	14 (17%)	2	11
All	All	3976/5497 (72%)	3796 (96%)	180 (4%)	31	61

5 of 180 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	Q	86	ARG
16	M	42	ILE
15	D	11	LEU
15	D	59	ARG
16	M	77	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
15	D	43	ASN
15	D	85	GLN
17	N	358	GLN
2	B	887	GLN
2	B	825	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	R	5/6 (83%)	2 (40%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	R	5	C
20	R	9	U

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 7 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	$\# Z > 2$
23	SF4	P	401	8	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
23	SF4	P	401	8	-	-	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.

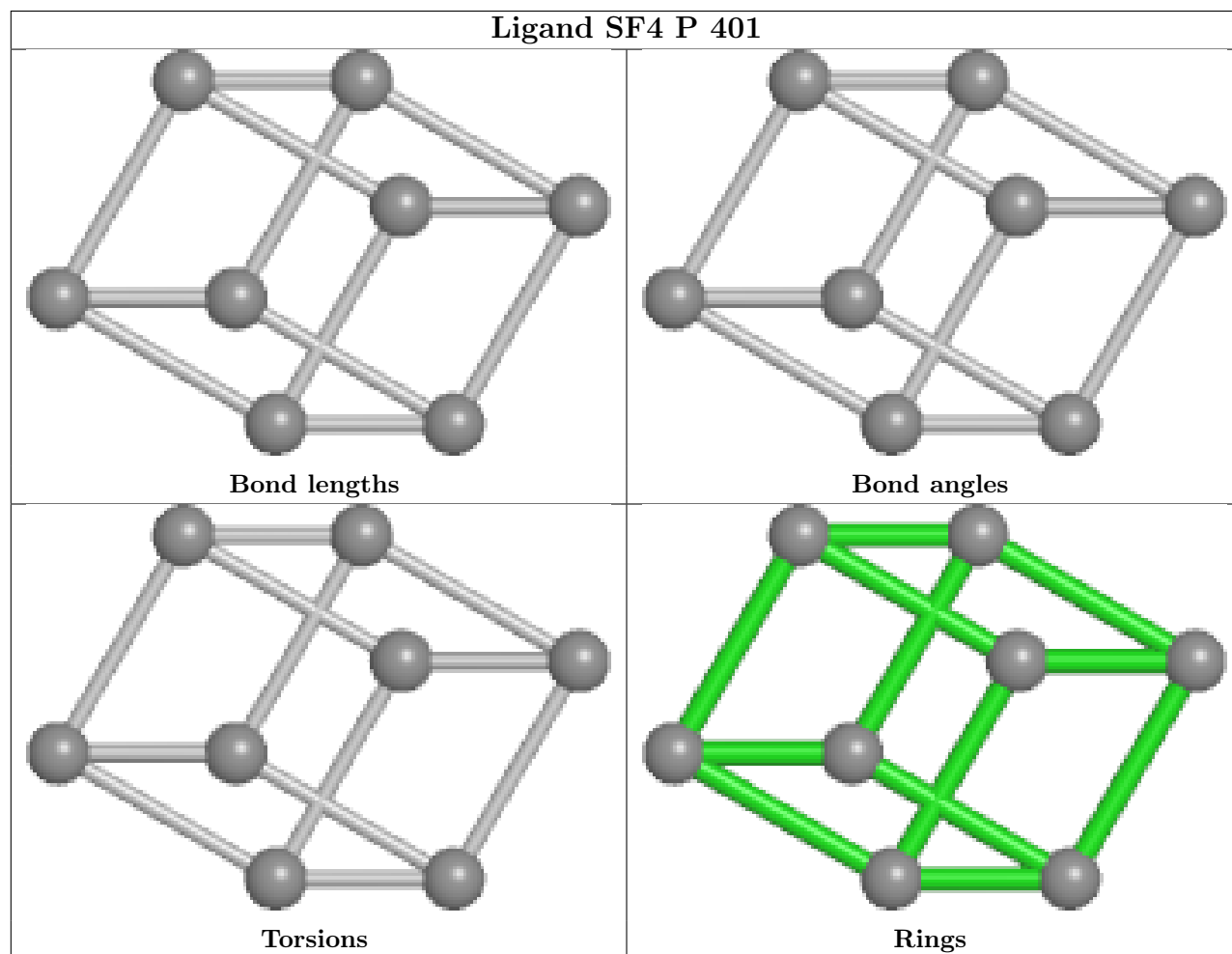
There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	P	401	SF4	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

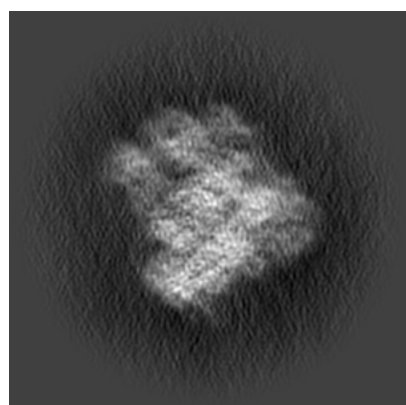
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30779. These allow visual inspection of the internal detail of the map and identification of artifacts.

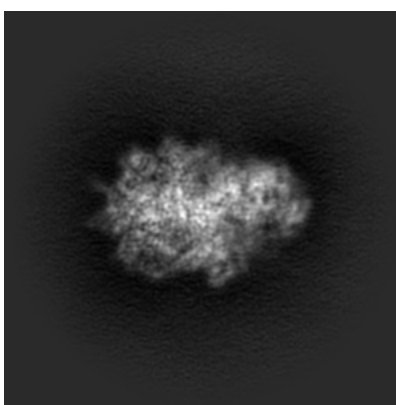
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

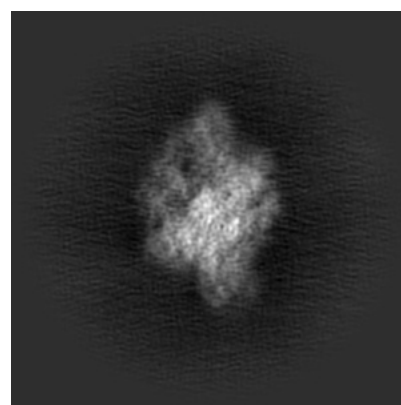
6.1.1 Primary map



X



Y

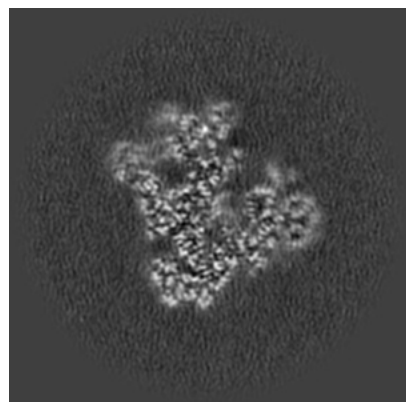


Z

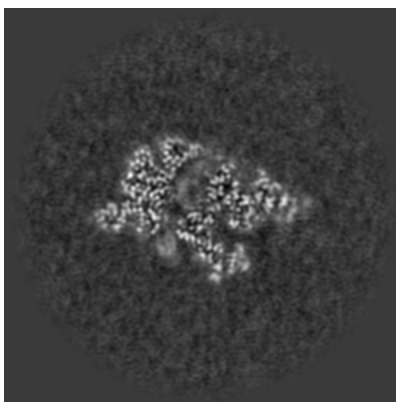
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

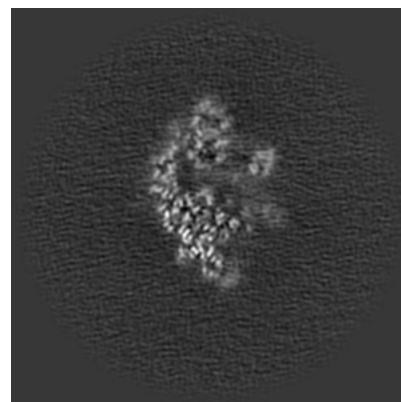
6.2.1 Primary map



X Index: 160



Y Index: 160

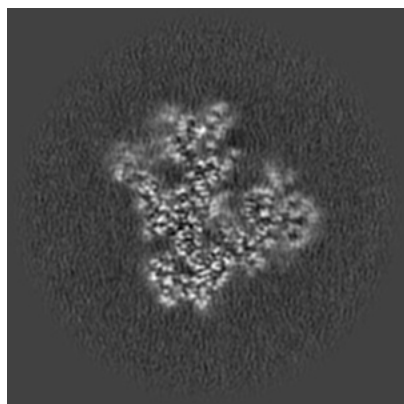


Z Index: 160

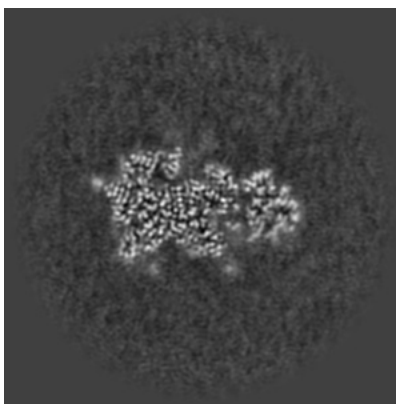
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

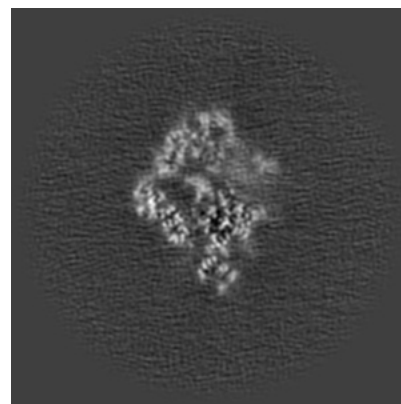
6.3.1 Primary map



X Index: 159



Y Index: 145

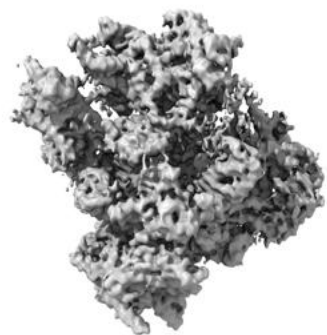


Z Index: 170

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

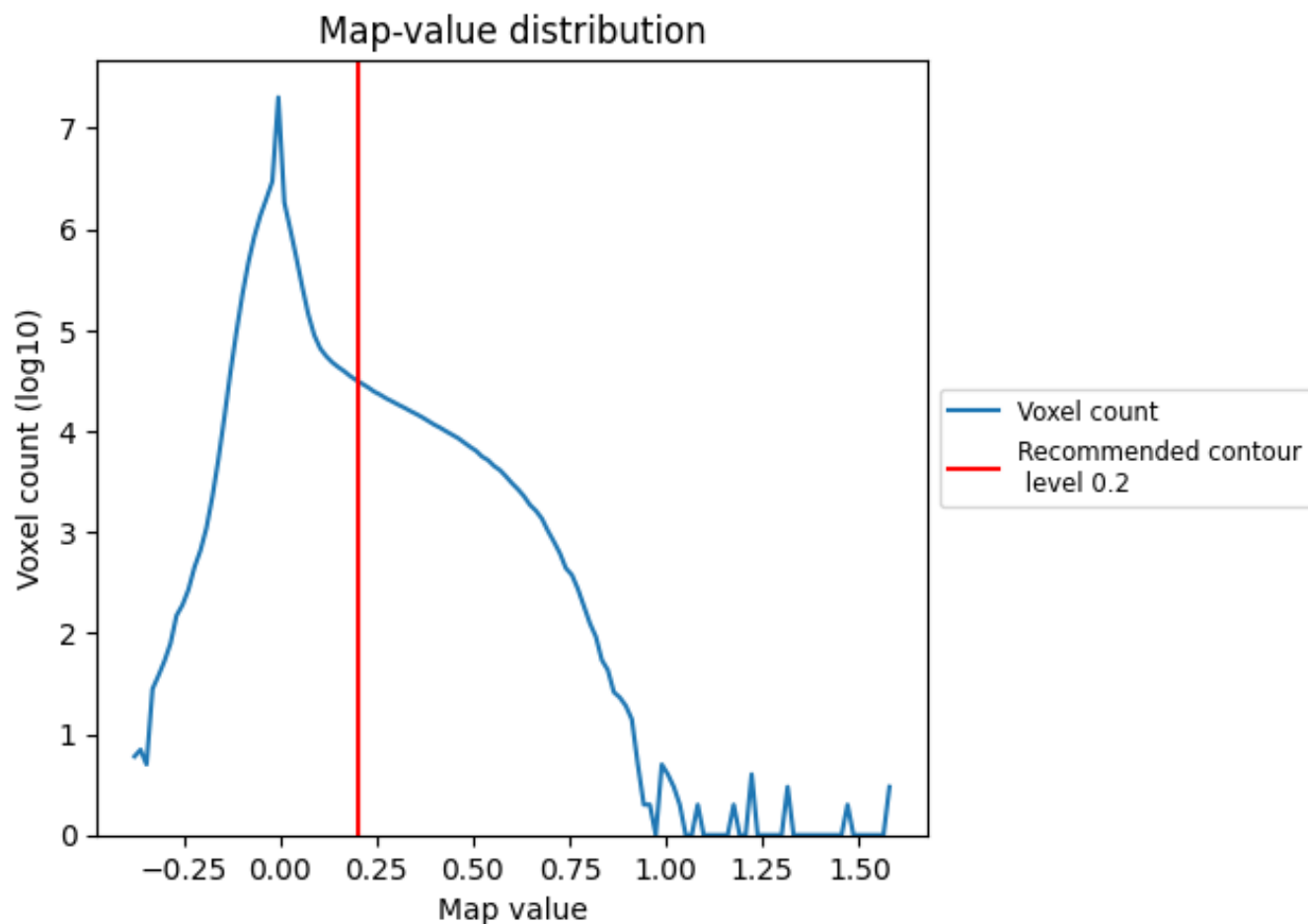
6.5 Mask visualisation

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

7 Map analysis [i](#)

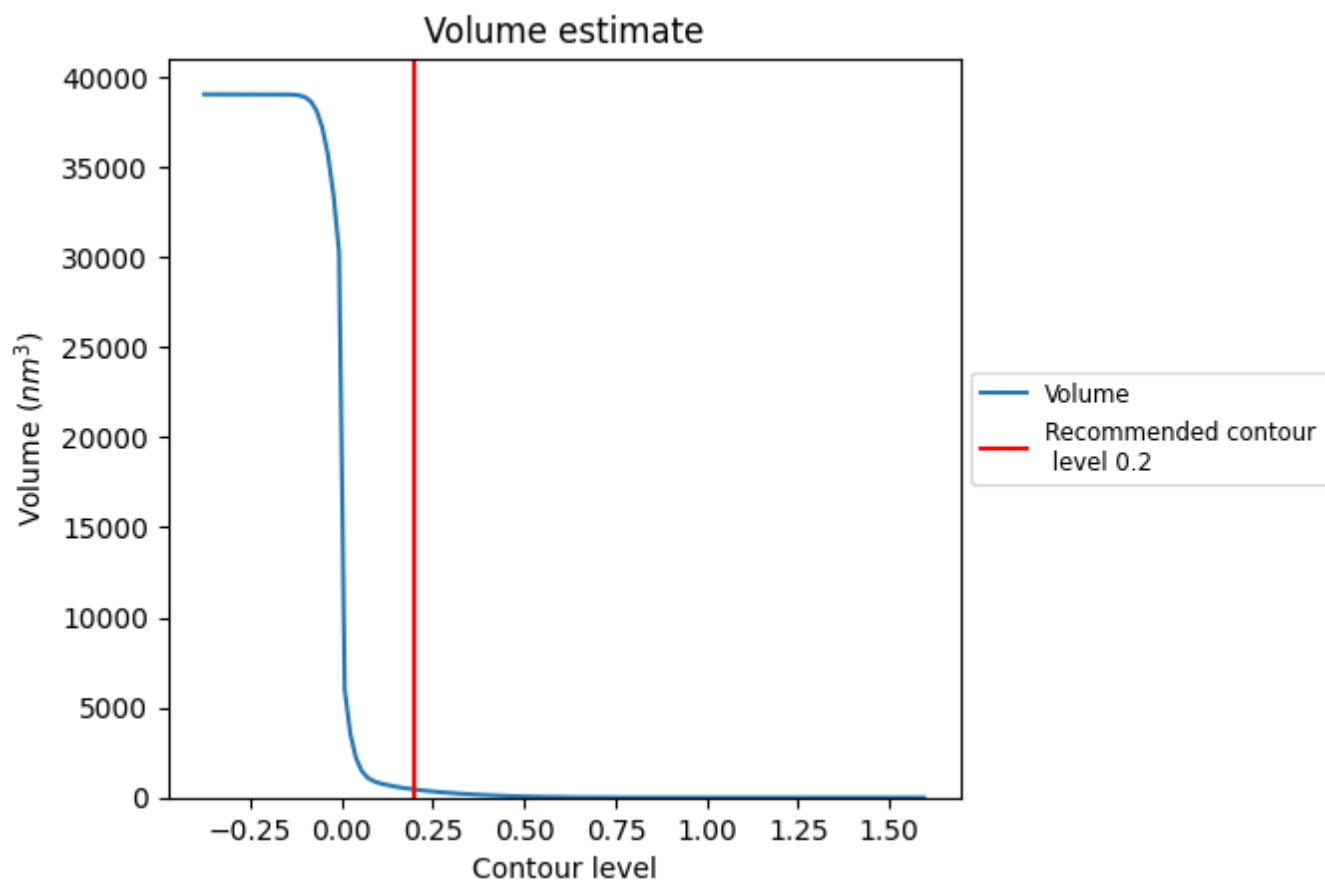
This section contains the results of statistical analysis of the map.

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.

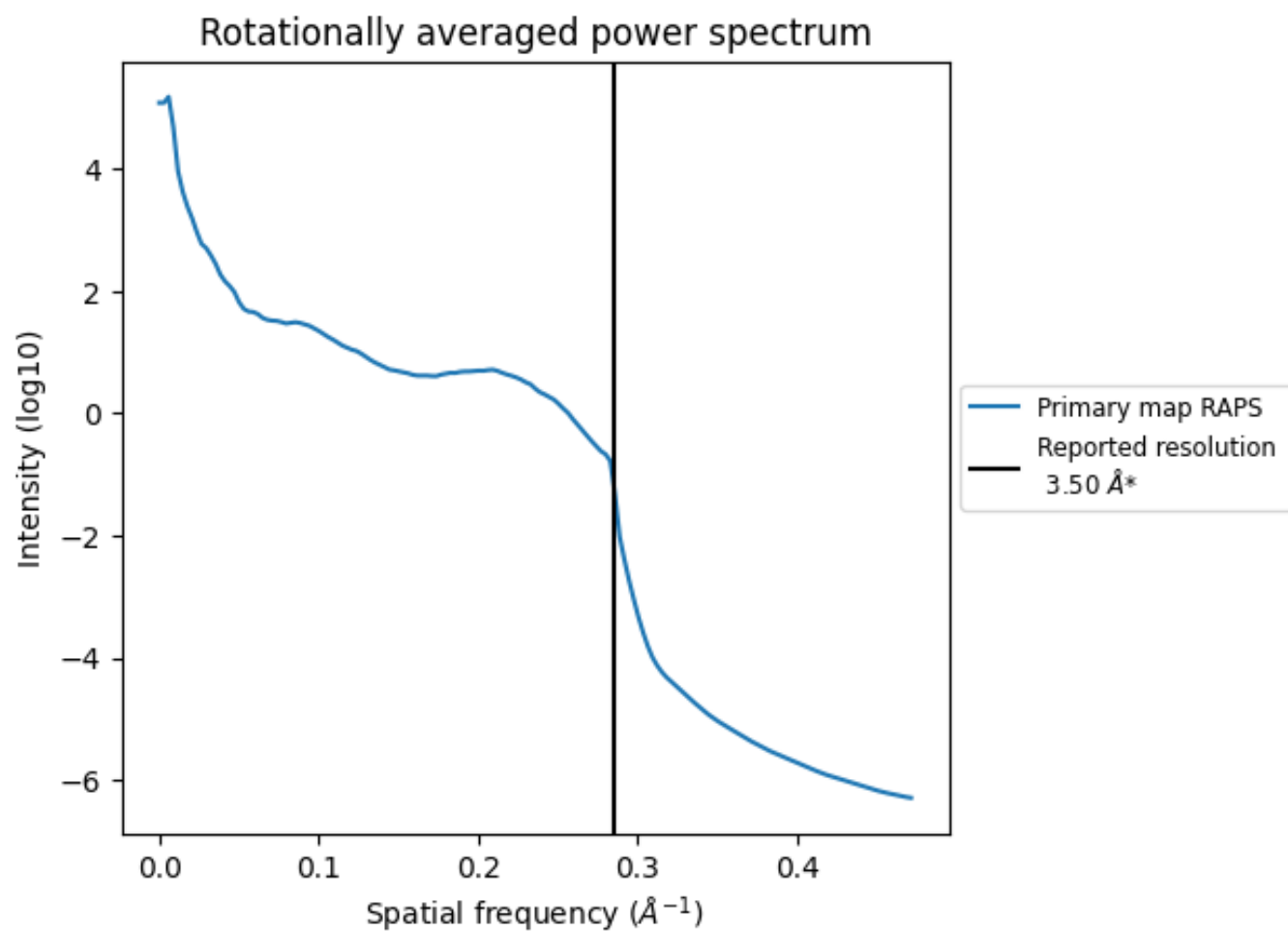
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 447 nm^3 ; this corresponds to an approximate mass of 404 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 0.286 Å⁻¹

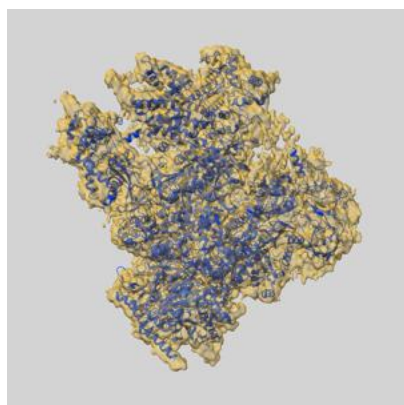
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

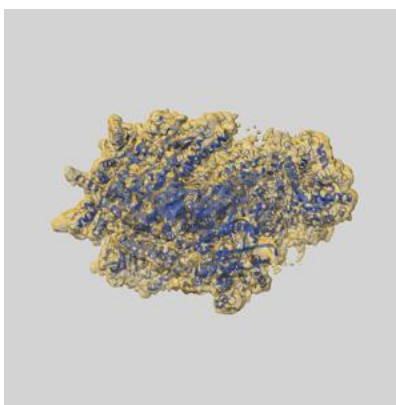
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30779 and PDB model 7DN3. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

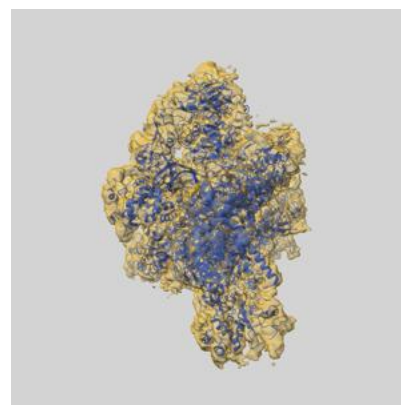
9.1 Map-model overlay [i](#)



X



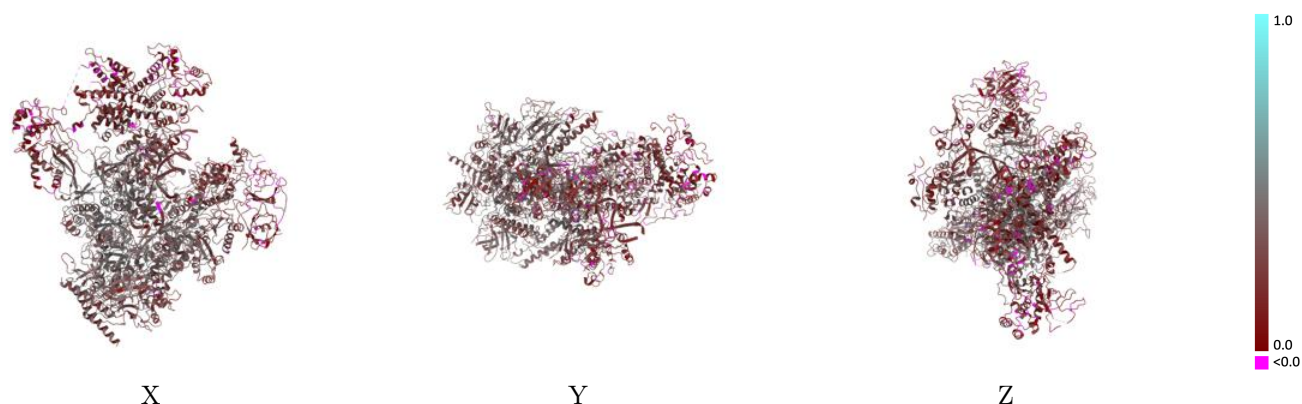
Y



Z

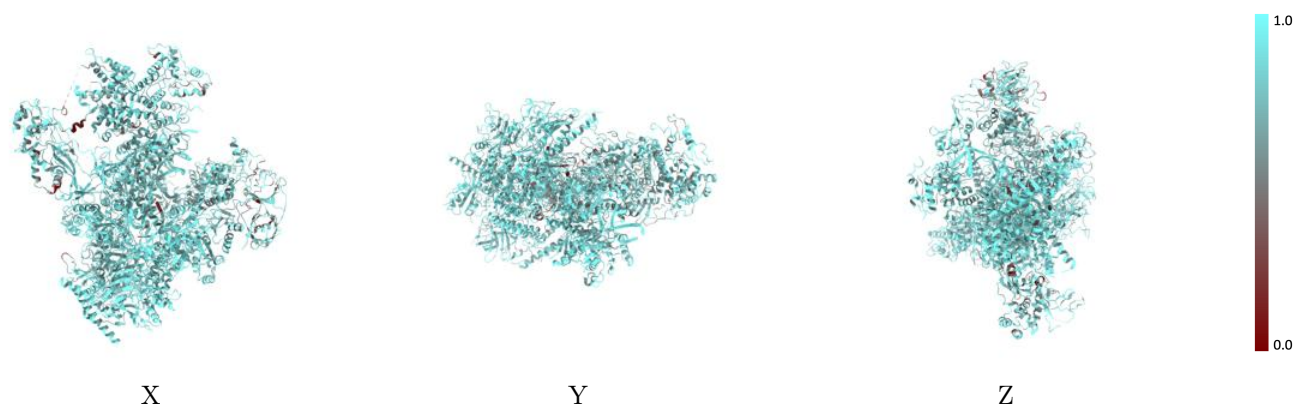
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



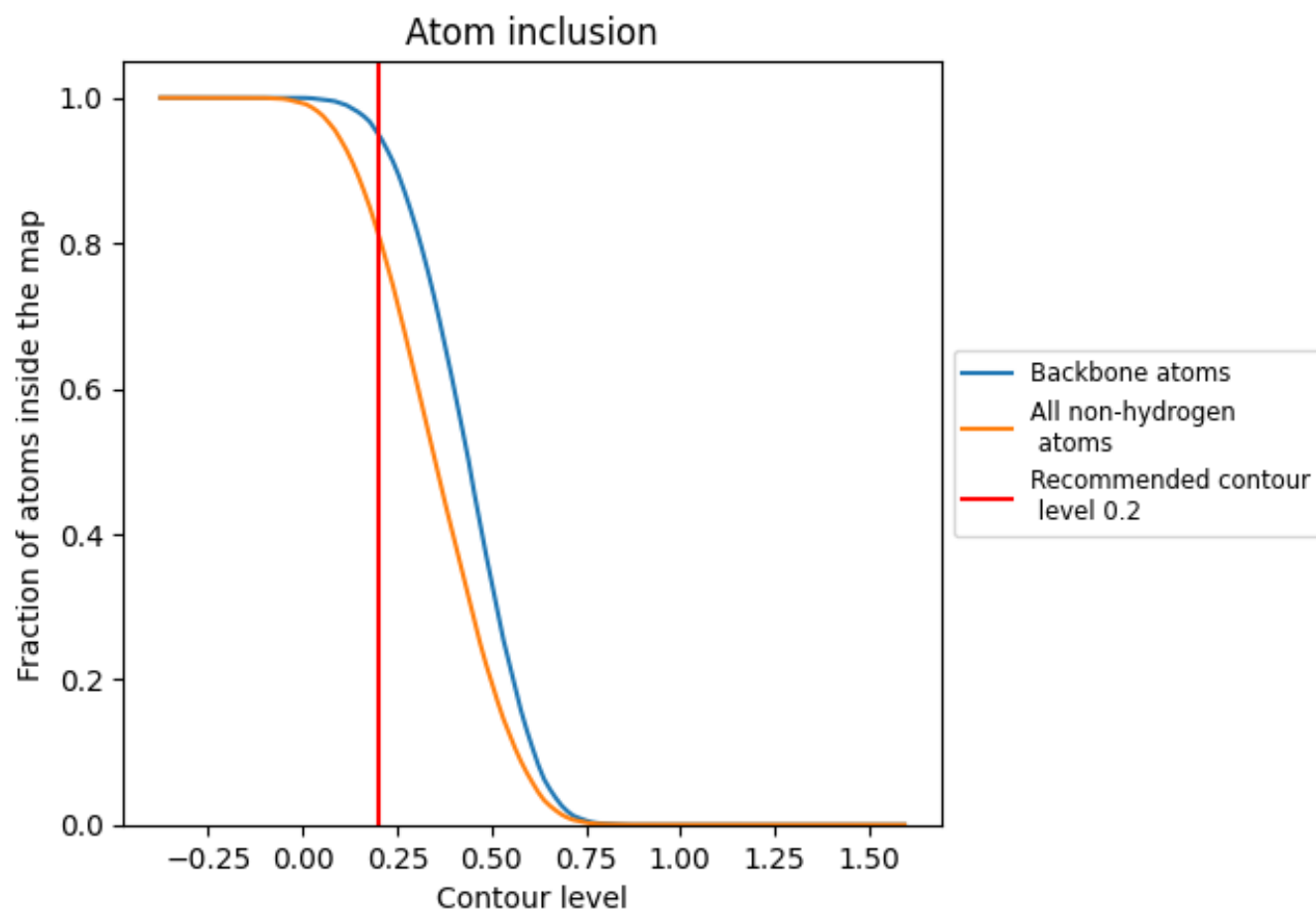
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).











































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8133	 0.3070
A	 0.8414	 0.3690
B	 0.8203	 0.3550
C	 0.8498	 0.3290
D	 0.7099	 0.1770
E	 0.8109	 0.2710
F	 0.8731	 0.4090
G	 0.8156	 0.2350
H	 0.8330	 0.3350
I	 0.8527	 0.2630
J	 0.8525	 0.3450
K	 0.8578	 0.3530
L	 0.8596	 0.3590
M	 0.7250	 0.1520
N	 0.6676	 0.1450
O	 0.7785	 0.2020
P	 0.7725	 0.1600
Q	 0.6671	 0.1680
R	 0.4400	 0.2550
X	 0.8654	 0.2370
Y	 0.8805	 0.2880

