



wwPDB EM Validation Summary Report ⓘ

Jun 29, 2026 – 02:27 PM JST

PDB ID : 9UZ9 / pdb_00009uz9
EMDB ID : EMD-64642
Title : RNA polymerase II elongation complex stalled at SHL(-6) in the hexasome of the overlapping dinucleosome
Authors : Chen, Z.; Ho, C.; Tanaka, H.; Kujirai, T.; Ogasawara, M.; Ehara, H.; Sekine, S.; Takizawa, Y.; Kurumizaka, H.
Deposited on : 2025-05-16
Resolution : 6.74 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

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:

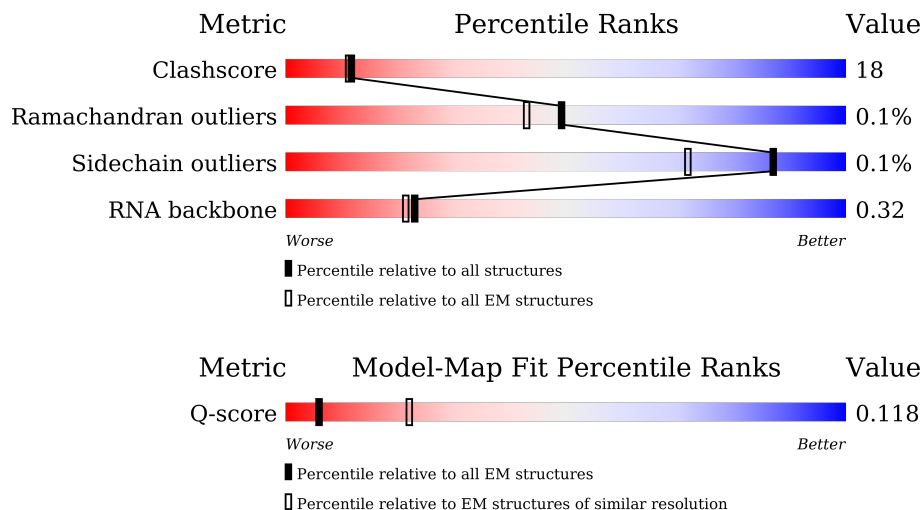
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 6.74 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	480 (6.24 - 7.24)

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	1743	
2	B	1227	
3	C	304	

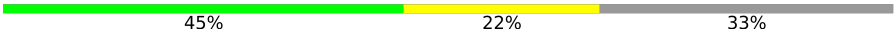
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Mol	Chain	Length	Quality of chain
4	D	186	61% 77% 6% 16%
5	E	214	63% 36%
6	F	155	33% 21% 46%
7	G	171	47% 74% 26%
8	H	145	66% 26% 8%
9	I	115	69% 28%
10	J	72	51% 40% 8%
11	K	118	66% 30%
12	L	72	42% 21% 38%
13	N	279	34% 63%
14	P	11	45% 36% 18%
15	T	279	46% 54%
16	a	139	52% 17% 32%
16	e	139	49% 19% 32%
16	k	139	35% 17% 47%
16	m	139	40% 29% 32%
17	b	106	47% 26% 26%
17	f	106	59% 14% 26%
17	l	106	37% 30% 33%
17	n	106	53% 21% 26%
18	c	133	53% 20% 26%
18	g	133	51% 22% 26%
18	o	133	57% 16% 27%
19	d	129	52% 18% 30%
19	h	129	53% 16% 31%

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Mol	Chain	Length	Quality of chain
19	p	129	 45% 22% 33%

2 Entry composition [i](#)

There are 21 unique types of molecules in this entry. The entry contains 52384 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 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1408	11095	6997	1935	2093	70	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1161	9261	5835	1636	1732	58	0	0

- Molecule 3 is a protein called RNA polymerase II third largest subunit B44, part of central core.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	263	2098	1319	354	413	12	0	0

- Molecule 4 is a protein called RNA polymerase II subunit B32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	156	1210	753	210	245	2	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	213	1740	1094	312	324	10	0	0

- Molecule 6 is a protein called RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	84	Total	C	N	O	S	0	0
			677	429	114	131	3		

- Molecule 7 is a protein called RNA polymerase II subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1324	858	214	247	5		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	133	Total	C	N	O	S	0	0
			1052	671	169	208	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	111	Total	C	N	O	S	0	0
			917	565	161	180	11		

- Molecule 10 is a protein called RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	66	Total	C	N	O	S	0	0
			545	349	95	95	6		

- Molecule 11 is a protein called RNA polymerase II subunit B12.5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	113	Total	C	N	O	S	0	0
			932	599	160	169	4		

- Molecule 12 is a protein called RNA polymerase subunit ABC10-alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	45	Total	C	N	O	S	0	0
			359	221	72	61	5		

- Molecule 13 is a DNA chain called DNA (270-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
13	N	270	5497	2616	963	1648	270	0	0

- Molecule 14 is a RNA chain called RNA (5'-R(P*UP*GP*UP*GP*UP*UP*UP*GP*GP*G P*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
14	P	11	235	104	37	83	11	0	0

- Molecule 15 is a DNA chain called DNA (279-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
15	T	279	5752	2717	1114	1642	279	0	0

- Molecule 16 is a protein called Histone H3.3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	a	95	779	492	150	135	2	0	0
16	e	95	779	492	150	135	2	0	0
16	k	73	587	373	109	103	2	0	0
16	m	95	779	492	150	135	2	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	-3	GLY	-	expression tag	UNP P84243
a	-2	SER	-	expression tag	UNP P84243
a	-1	HIS	-	expression tag	UNP P84243
e	-3	GLY	-	expression tag	UNP P84243
e	-2	SER	-	expression tag	UNP P84243
e	-1	HIS	-	expression tag	UNP P84243
k	-3	GLY	-	expression tag	UNP P84243
k	-2	SER	-	expression tag	UNP P84243
k	-1	HIS	-	expression tag	UNP P84243
m	-3	GLY	-	expression tag	UNP P84243
m	-2	SER	-	expression tag	UNP P84243
m	-1	HIS	-	expression tag	UNP P84243

- Molecule 17 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	b	78	Total	C	N	O	S	0	0
			619	391	120	107	1		
17	f	78	Total	C	N	O	S	0	0
			619	391	120	107	1		
17	l	71	Total	C	N	O	S	0	0
			568	357	113	97	1		
17	n	78	Total	C	N	O	S	0	0
			619	391	120	107	1		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	-3	GLY	-	expression tag	UNP P62805
b	-2	SER	-	expression tag	UNP P62805
b	-1	HIS	-	expression tag	UNP P62805
f	-3	GLY	-	expression tag	UNP P62805
f	-2	SER	-	expression tag	UNP P62805
f	-1	HIS	-	expression tag	UNP P62805
l	-3	GLY	-	expression tag	UNP P62805
l	-2	SER	-	expression tag	UNP P62805
l	-1	HIS	-	expression tag	UNP P62805
n	-3	GLY	-	expression tag	UNP P62805
n	-2	SER	-	expression tag	UNP P62805
n	-1	HIS	-	expression tag	UNP P62805

- Molecule 18 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	c	98	Total	C	N	O	0	0
			757	475	149	133		
18	g	98	Total	C	N	O	0	0
			757	475	149	133		
18	o	97	Total	C	N	O	0	0
			752	472	148	132		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	-3	GLY	-	expression tag	UNP P04908
c	-2	SER	-	expression tag	UNP P04908
c	-1	HIS	-	expression tag	UNP P04908

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Chain	Residue	Modelled	Actual	Comment	Reference
g	-3	GLY	-	expression tag	UNP P04908
g	-2	SER	-	expression tag	UNP P04908
g	-1	HIS	-	expression tag	UNP P04908
o	-3	GLY	-	expression tag	UNP P04908
o	-2	SER	-	expression tag	UNP P04908
o	-1	HIS	-	expression tag	UNP P04908

- Molecule 19 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	d	90	Total	C	N	O	S	0	0
			698	440	123	133	2		
19	h	89	Total	C	N	O	S	0	0
			689	435	122	130	2		
19	p	87	Total	C	N	O	S	0	0
			679	430	120	127	2		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	-3	GLY	-	expression tag	UNP P06899
d	-2	SER	-	expression tag	UNP P06899
d	-1	HIS	-	expression tag	UNP P06899
h	-3	GLY	-	expression tag	UNP P06899
h	-2	SER	-	expression tag	UNP P06899
h	-1	HIS	-	expression tag	UNP P06899
p	-3	GLY	-	expression tag	UNP P06899
p	-2	SER	-	expression tag	UNP P06899
p	-1	HIS	-	expression tag	UNP P06899

- Molecule 20 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
20	A	2	Total	Zn	0
			2	2	
20	B	1	Total	Zn	0
			1	1	
20	C	1	Total	Zn	0
			1	1	
20	I	2	Total	Zn	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
20	J	1	Total 1	Zn 1	0
20	L	1	Total 1	Zn 1	0

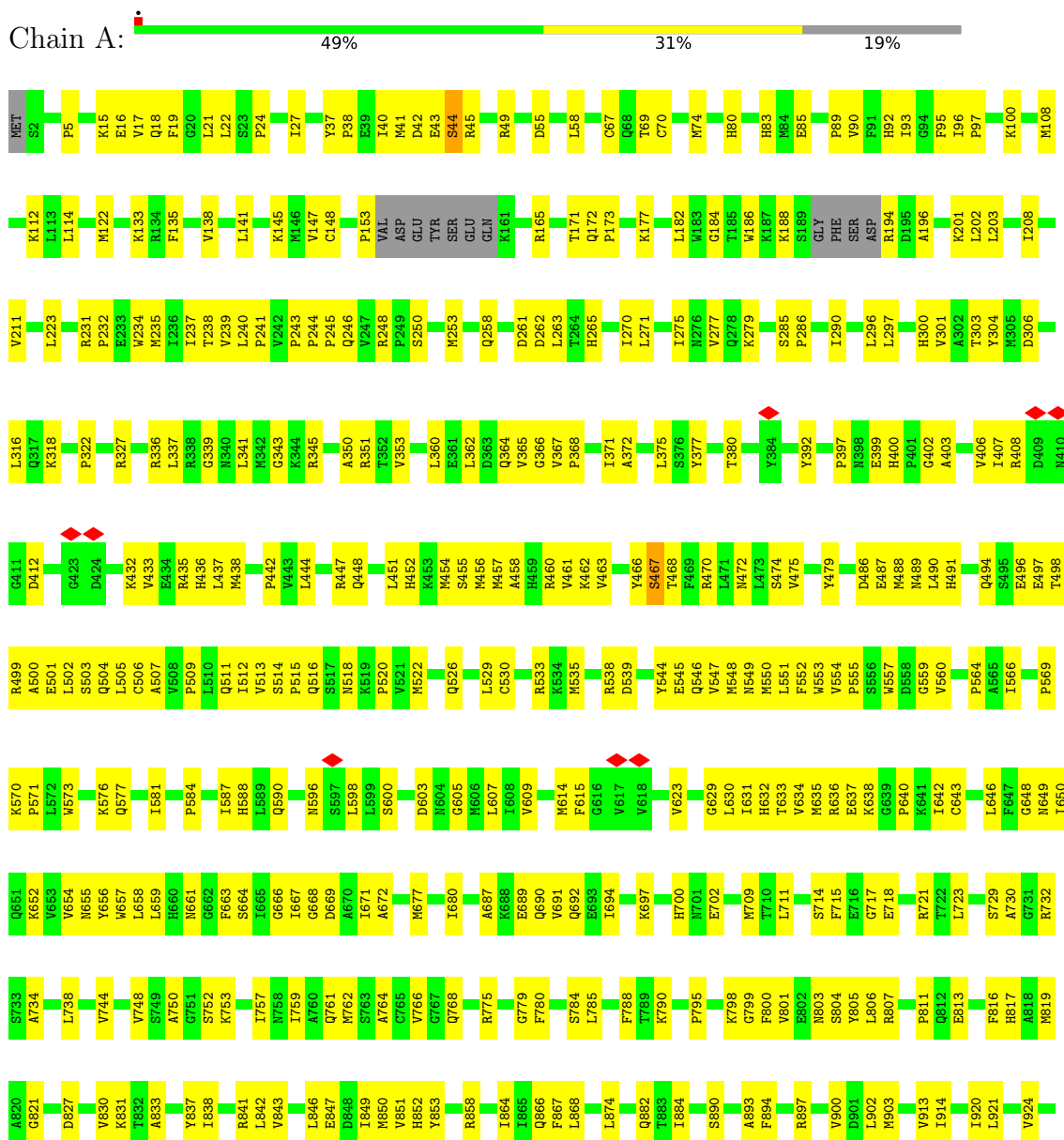
- Molecule 21 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

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 subunit



Q927	A1026	G1099	I1197	Y1301	T1408	ASP	ALA	PRO	PRO	GLN	V268
K928	R1027	V1100	E1198	Y1306	V1409	GLU	PRO	THR	THR	TYR	K269
E929	L1028	P1101	L1199	L1306	A1417	PHE	THR	SER	SER	PRO	I272
L930	R1031	R1102	R1203	L1309	L1421	ASN	PRO	PRO	GLN	ASP	K182
D940	R1032	I1106	M211	L1309	L1421	HIS	PRO	TYR	TYR	PRO	M183
F943	L1033	L1107	M212	E1310	D1422	ASP	PRO	SER	GLN	TYR	G192
L944	L1034	L1113	Q1213	T1311	D1423	VAL	PRO	PRO	PRO	ILE	F194
R945	E1035	I1113	Q1213	L1316	C1424	ALA	PRO	THR	THR	D9	V277
R947	L1039	A1117	V1214	L1316	V1427	ASP	THR	SER	ASN	Y110	R278
V948	L1039	A1117	A1215	A1317	S1428	VAL	SER	PRO	GLY	Y111	R279
F949	D1042	L1118	D1216	E1318	S1428	MET	PRO	GLN	GLU	S112	F286
V950	A1043	L1119	K1217	V1319	M1429	PHE	GLY	TYR	TYR	S113	V288
L958	F1044	V1120	I1218	M1320	M1430	SER	TYR	SER	LYS	Y114	V284
P959	W1045	Y1121	I1222	A1321	V1431	PRO	PRO	PRO	GLY	Y116	P286
V960	W1046	L1122	L1122	V1322	M1432	MET	PRO	THR	GLU	L117	G287
R961	W1047	I1136	L1226	S1328	L1436	ALA	THR	THR	GLU	D118	E288
L962	I1051	I1140	L1230	R1329	M1439	GLU	PRO	PRO	GLN	M119	A210
R963	Q1054	E1141	W1230	T1330	F1444	GLY	THR	THR	TYR	T19	A210
R964	F1055	E1141	S1231	Y1331	F1444	GLY	SER	PRO	GLN	T19	A210
R965	Q1056	Y1142	I1239	Y1331	D1449	ASP	PRO	GLM	THR	I127	S122
R966	Q1056	T1143	I1240	F1335	D1449	ASP	THR	THR	THR	I127	S122
Y972	L1059	K1146	R1243	E1337	L1452	ARG	PRO	SER	PRO	A128	ASP
F973	V1060	M1147	V1244	I1338	L1452	SER	PRO	SER	GLN	GLU	GLU
H974	V1060	V1148	V1245	I1339	L1453	GLY	THR	THR	TYR	GLY	GLY
L975	P1062	T1149	I1245	S1340	T1454	GLY	SER	SER	SER	ASN	ASN
D976	G1063	Y1153	ARG	V1341	L1455	LEU	PRO	GLN	PRO	PRO	PRO
S981	ASP	E1153	PRO	L1342	L1456	THR	PRO	GLM	THR	ASN	ASN
L989	E1064	T1154	LYS	G1343	P1457	GLU	THR	THR	SER	ALA	ALA
V1000	M1065	Y1155	ALA	T1347	ALA	TYR	PRO	PRO	SER	THR	THR
L1001	V1066	Y1156	ALA	Y1352	ASP	GLY	PRO	PRO	PRO	GLN	GLN
R1002	G1067	D1157	MET	K1353	TYR	ILE	THR	THR	THR	TYR	TYR
G1004	I1068	T1163	ASP	E1354	ALA	ILE	TYR	TYR	TYR	SER	SER
E1005	I1069	T1163	GLU	E1354	PRO	GLN	PRO	PRO	PRO	GLN	GLN
M1006	A1070	D1168	LEU	I1355	THR	PRO	THR	THR	THR	TYR	TYR
I1009	S1073	S1177	ALA	L1356	MET	TYR	PRO	PRO	PRO	PRO	PRO
F1020	THR	ILE	E1259	M1357	PRO	TYR	PRO	PRO	PRO	PRO	PRO
F1021	LEU	PRO	M1262	V1358	LEU	PRO	PRO	PRO	PRO	PRO	PRO
Q1021	ASN	ASP	L1263	H1370	LYS	GLY	THR	THR	THR	THR	THR
Q1013	THR	GLU	M1270	M1371	LYS	ALA	THR	THR	THR	THR	THR
Q1014	THR	VAL	L1271	A1372	ALA	ALA	THR	THR	THR	THR	THR
S1018	THR	GLY	M1278	V1375	THR	THR	THR	THR	THR	THR	THR
L1019	ALA	ASP	I1279	R1381	ALA	GLY	THR	THR	THR	THR	THR
F1020	VAL	ASP	I1282	A1395	TYR	GLY	THR	THR	THR	THR	THR
Q1021	SER	ASP	S1283	L1400	ASP	PHE	THR	THR	THR	THR	THR
Q1022	SER	VAL	V1285	L1401	ASN	ALA	PRO	PRO	PRO	PRO	PRO
G1022	LYS	Q1190	V1285	R1402	ASN	THR	TYR	TYR	TYR	TYR	TYR
V1024	M1095	W1193	K1289	C1403	ALA	ALA	PRO	PRO	PRO	PRO	PRO
R1025	L1098	L1194	P1295	E1407	THR	GLY	THR	THR	THR	THR	THR
		R1196			ASP	PHE	SER	SER	SER	SER	SER

• Molecule 2: DNA-directed RNA polymerase subunit beta

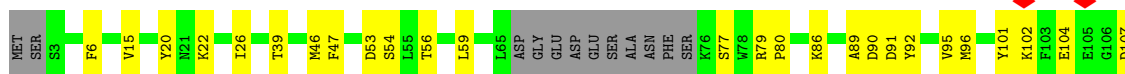


MET	P101	D179	V268
SER	Q102	L180	K269
TYR	E103	Y181	I272
ASP	A104	K182	P273
PRO	R105	M183	I274
TYR	L106	G192	V275
SER	R107	F193	I276
ILE	M108	F194	V277
D9	L109	V278	R279
I12	Y110	K201	F286
T13	Y111	V202	G287
T14	S112	L203	E288
E15	S113	I204	V283
D16	Y116	R208	V284
C17	L117	S209	P286
W18	D118	G287	G287
T19	M119	A210	E288
V20	E120	I213	K300
I21	K121	V214	Q301
S22	S122	Q215	K302
A23	I127	K218	L303
F24	I127	A221	E304
V31	ASP	A221	K305
S32	GLU	P222	L306
Q33	GLY	S223	K307
Q34	ASN	P224	P308
L35	PRO	I225	E311
D36	ASN	S226	I316
Q47	ALA	H227	Q317
D48	THR	V228	V321
L49	LEU	A229	L323
V50	ASP	S233	D324
W51	TRP	A234	F325
L53	GLN	L235	I326
M66	VAL	L241	G327
N66	HIS	L242	R328
D69	GLU	S243	R329
N70	ILE	T244	A332
I71	LYS	K245	I336
R74	ASP	Q246	R337
R74	GLY	I247	K340
E76	VAL	K248	R341
I77	GLU	R252	I342
R78	G153	E253	Q343
F79	I158	S254	Q350
G80	G159	K255	L354
K81	K160	R259	P355
Y83	R173	A263	H356
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M99	L175	D176	
F100	E177	P266	
	V178	Y267	



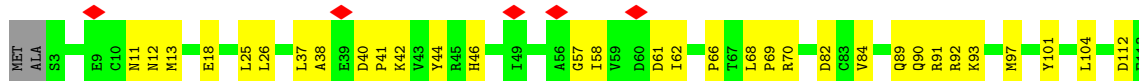
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H: 66% 26% 8%



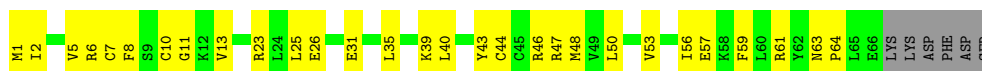
- Molecule 9: DNA-directed RNA polymerase subunit

Chain I: 69% 28%



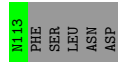
- Molecule 10: RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III

Chain J: 51% 40% 8%



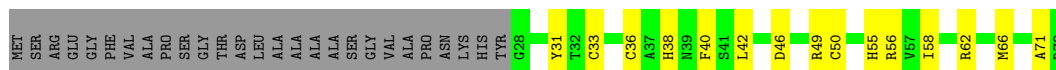
- Molecule 11: RNA polymerase II subunit B12.5

Chain K: 66% 30%

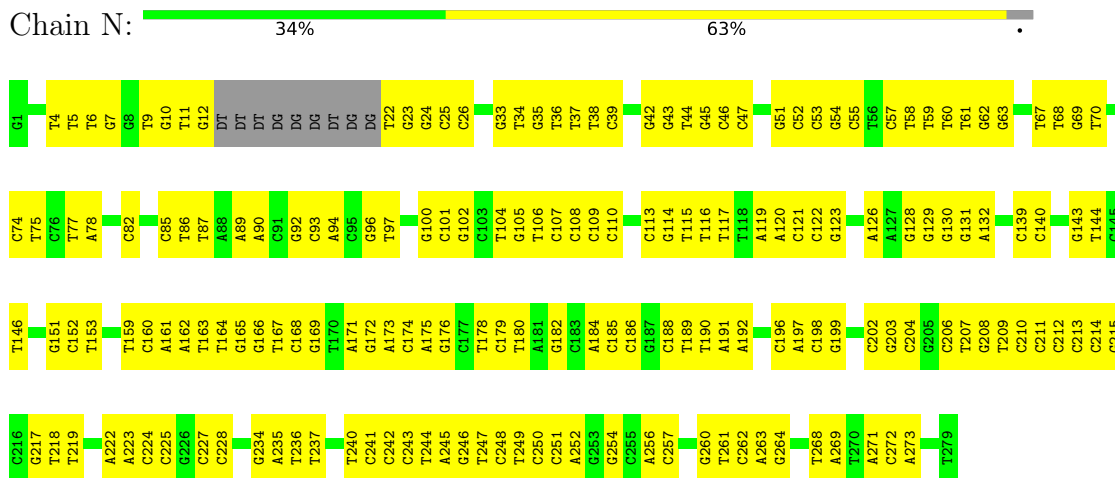


- Molecule 12: RNA polymerase subunit ABC10-alpha

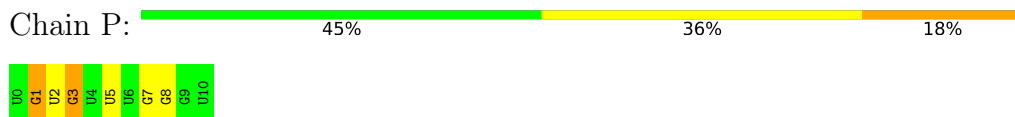
Chain L: 42% 21% 38%



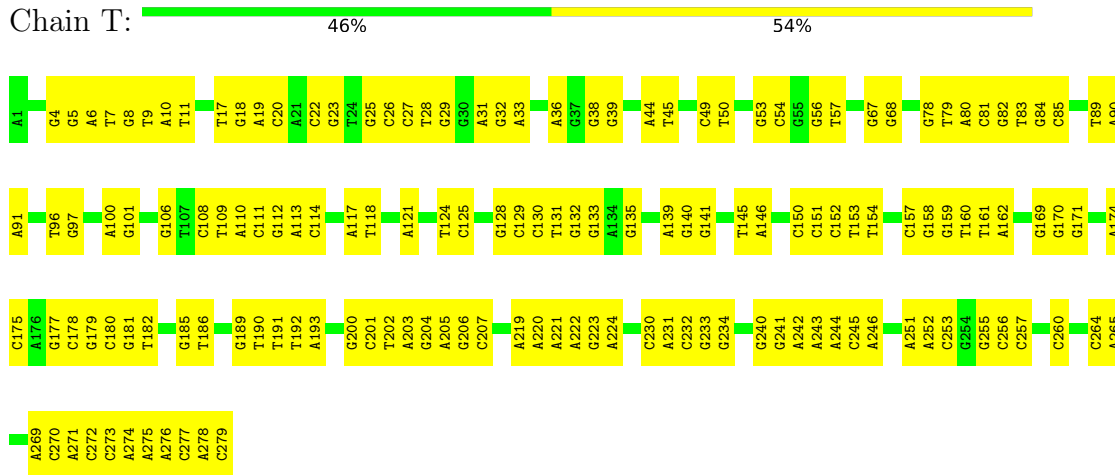
- Molecule 13: DNA (270-MER)



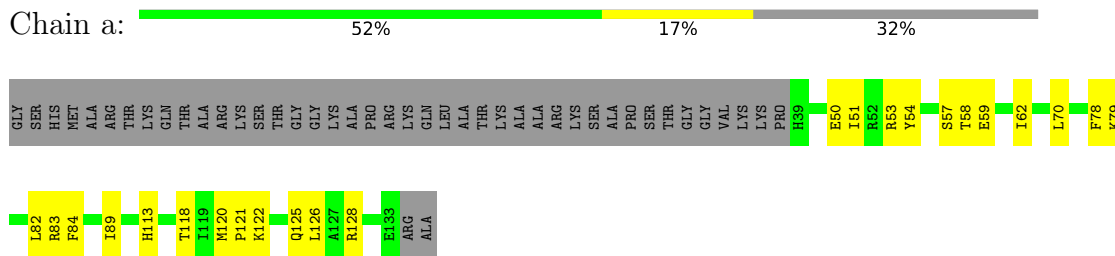
- Molecule 14: RNA (5'-R(P*UP*GP*UP*GP*UP*UP*UP*GP*GP*GP*U)-3')



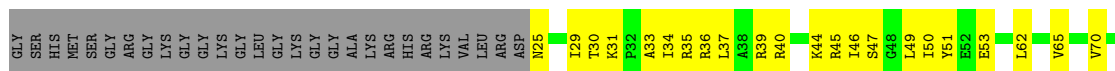
- Molecule 15: DNA (279-MER)



- Molecule 16: Histone H3.3



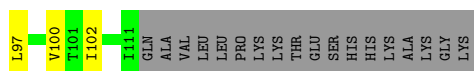
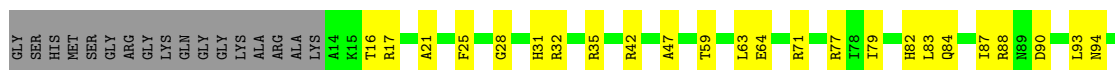
- Molecule 16: Histone H3.3



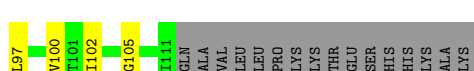
• Molecule 17: Histone H4



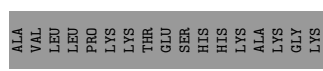
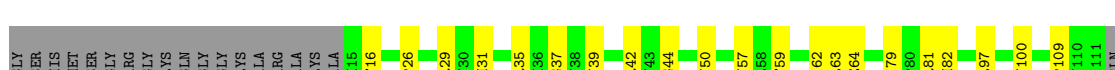
• Molecule 18: Histone H2A type 1-B/E



• Molecule 18: Histone H2A type 1-B/E

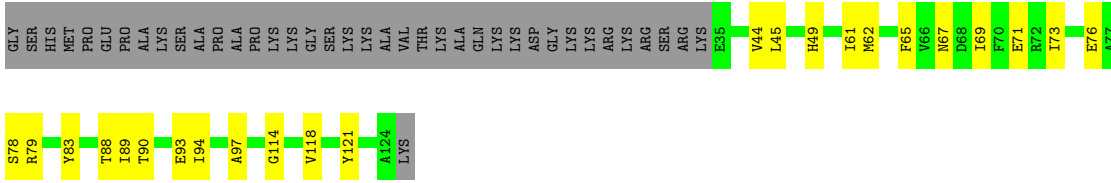


• Molecule 18: Histone H2A type 1-B/E

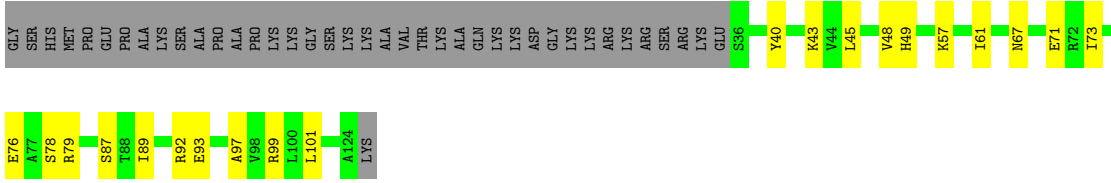


• Molecule 19: Histone H2B type 1-J

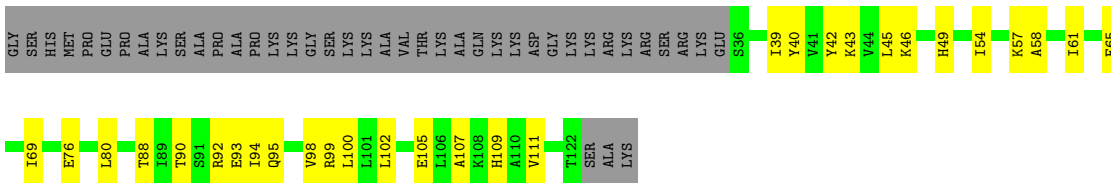




• Molecule 19: Histone H2B type 1-J



• Molecule 19: Histone H2B type 1-J



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	34000	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 ($e^-/\text{\AA}^2$)	60.9	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	0.028	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.000666	Depositor
Map size (\AA)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.23	0/11299	0.48	0/15266
2	B	0.21	0/9441	0.47	0/12732
3	C	0.24	0/2139	0.49	0/2895
4	D	0.15	0/1221	0.35	0/1648
5	E	0.22	0/1772	0.47	0/2385
6	F	0.18	0/687	0.48	0/931
7	G	0.22	0/1353	0.38	0/1837
8	H	0.19	0/1069	0.42	0/1444
9	I	0.14	0/934	0.39	0/1257
10	J	0.18	0/554	0.50	0/742
11	K	0.14	0/953	0.36	0/1291
12	L	0.12	0/365	0.35	0/484
13	N	0.54	0/6148	0.74	0/9479
14	P	0.63	0/261	0.82	0/405
15	T	0.57	0/6470	0.77	0/9987
16	a	0.34	0/790	0.49	0/1060
16	e	0.27	0/790	0.47	0/1060
16	k	0.33	0/594	0.59	0/797
16	m	0.31	0/790	0.53	0/1060
17	b	0.16	0/626	0.36	0/837
17	f	0.14	0/626	0.32	0/837
17	l	0.15	0/573	0.39	0/767
17	n	0.16	0/626	0.39	0/837
18	c	0.13	0/766	0.28	0/1033
18	g	0.21	0/766	0.36	0/1033
18	o	0.13	0/761	0.33	0/1026
19	d	0.14	0/709	0.33	0/955
19	h	0.14	0/700	0.33	0/943
19	p	0.14	0/690	0.33	0/930
All	All	0.33	0/54473	0.55	0/75958

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	11095	0	11132	472	0
2	B	9261	0	9265	385	0
3	C	2098	0	2059	79	0
4	D	1210	0	1205	9	0
5	E	1740	0	1754	61	0
6	F	677	0	693	34	0
7	G	1324	0	1342	28	0
8	H	1052	0	1050	30	0
9	I	917	0	869	30	0
10	J	545	0	561	35	0
11	K	932	0	944	27	0
12	L	359	0	359	13	0
13	N	5497	0	3045	288	0
14	P	235	0	116	5	0
15	T	5752	0	3115	178	0
16	a	779	0	814	21	0
16	e	779	0	814	21	0
16	k	587	0	615	26	0
16	m	779	0	814	41	0
17	b	619	0	659	27	0
17	f	619	0	659	14	0
17	l	568	0	614	27	0
17	n	619	0	659	21	0
18	c	757	0	802	26	0
18	g	757	0	802	26	0
18	o	752	0	797	16	0
19	d	698	0	710	20	0
19	h	689	0	704	16	0
19	p	679	0	698	24	0
20	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	B	1	0	0	0	0
20	C	1	0	0	0	0
20	I	2	0	0	0	0
20	J	1	0	0	0	0
20	L	1	0	0	0	0
21	A	1	0	0	0	0
All	All	52384	0	47670	1739	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 18.

The worst 5 of 1739 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)
13:N:248:DC:H2''	13:N:249:DT:C7	1.16	1.59
13:N:115:DT:C2'	13:N:116:DT:H72	1.50	1.41
15:T:191:DT:H2''	15:T:192:DT:C7	1.52	1.37
13:N:248:DC:C2'	13:N:249:DT:H73	1.60	1.31
15:T:191:DT:C2'	15:T:192:DT:H73	1.60	1.30

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	1396/1743 (80%)	1324 (95%)	70 (5%)	2 (0%)	48 83
2	B	1151/1227 (94%)	1089 (95%)	61 (5%)	1 (0%)	48 83
3	C	261/304 (86%)	244 (94%)	17 (6%)	0	100 100
4	D	148/186 (80%)	143 (97%)	5 (3%)	0	100 100
5	E	211/214 (99%)	205 (97%)	6 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	82/155 (53%)	77 (94%)	5 (6%)	0	100	100
7	G	169/171 (99%)	165 (98%)	3 (2%)	1 (1%)	21	59
8	H	129/145 (89%)	123 (95%)	6 (5%)	0	100	100
9	I	109/115 (95%)	101 (93%)	8 (7%)	0	100	100
10	J	64/72 (89%)	63 (98%)	1 (2%)	0	100	100
11	K	111/118 (94%)	103 (93%)	8 (7%)	0	100	100
12	L	43/72 (60%)	39 (91%)	4 (9%)	0	100	100
16	a	93/139 (67%)	93 (100%)	0	0	100	100
16	e	93/139 (67%)	90 (97%)	3 (3%)	0	100	100
16	k	71/139 (51%)	69 (97%)	2 (3%)	0	100	100
16	m	93/139 (67%)	92 (99%)	1 (1%)	0	100	100
17	b	76/106 (72%)	76 (100%)	0	0	100	100
17	f	76/106 (72%)	76 (100%)	0	0	100	100
17	l	69/106 (65%)	68 (99%)	1 (1%)	0	100	100
17	n	76/106 (72%)	75 (99%)	1 (1%)	0	100	100
18	c	96/133 (72%)	95 (99%)	1 (1%)	0	100	100
18	g	96/133 (72%)	95 (99%)	1 (1%)	0	100	100
18	o	95/133 (71%)	95 (100%)	0	0	100	100
19	d	88/129 (68%)	87 (99%)	1 (1%)	0	100	100
19	h	87/129 (67%)	86 (99%)	1 (1%)	0	100	100
19	p	85/129 (66%)	84 (99%)	1 (1%)	0	100	100
All	All	5068/6288 (81%)	4857 (96%)	207 (4%)	4 (0%)	49	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	G	154	VAL
1	A	467	SER
1	A	960	VAL
2	B	222	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1223/1528 (80%)	1219 (100%)	4 (0%)	86	86
2	B	1016/1077 (94%)	1016 (100%)	0	100	100
3	C	236/264 (89%)	236 (100%)	0	100	100
4	D	133/160 (83%)	133 (100%)	0	100	100
5	E	196/197 (100%)	196 (100%)	0	100	100
6	F	75/137 (55%)	75 (100%)	0	100	100
7	G	148/148 (100%)	148 (100%)	0	100	100
8	H	120/130 (92%)	120 (100%)	0	100	100
9	I	106/109 (97%)	106 (100%)	0	100	100
10	J	60/66 (91%)	60 (100%)	0	100	100
11	K	104/109 (95%)	104 (100%)	0	100	100
12	L	38/56 (68%)	38 (100%)	0	100	100
16	a	81/112 (72%)	81 (100%)	0	100	100
16	e	81/112 (72%)	81 (100%)	0	100	100
16	k	61/112 (54%)	61 (100%)	0	100	100
16	m	81/112 (72%)	81 (100%)	0	100	100
17	b	63/81 (78%)	63 (100%)	0	100	100
17	f	63/81 (78%)	63 (100%)	0	100	100
17	l	59/81 (73%)	59 (100%)	0	100	100
17	n	63/81 (78%)	63 (100%)	0	100	100
18	c	77/102 (76%)	77 (100%)	0	100	100
18	g	77/102 (76%)	76 (99%)	1 (1%)	61	74
18	o	77/102 (76%)	77 (100%)	0	100	100
19	d	76/107 (71%)	76 (100%)	0	100	100
19	h	75/107 (70%)	75 (100%)	0	100	100
19	p	74/107 (69%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4463/5380 (83%)	4458 (100%)	5 (0%)	87 89

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	SER
1	A	399	GLU
1	A	448	GLN
1	A	468	THR
18	g	64	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
9	I	46	HIS
16	m	39	HIS
9	I	90	GLN
16	e	39	HIS
16	m	76	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	P	10/11 (90%)	3 (30%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
14	P	1	G
14	P	3	G
14	P	5	U

There are no RNA pucker outliers to report.

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 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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.

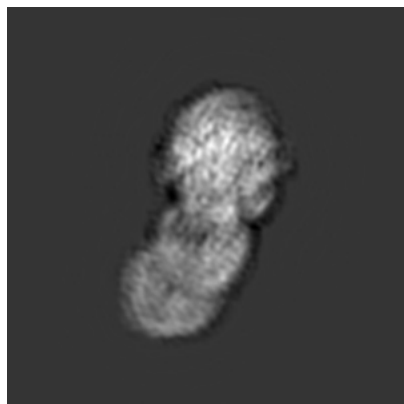
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64642. These allow visual inspection of the internal detail of the map and identification of artifacts.

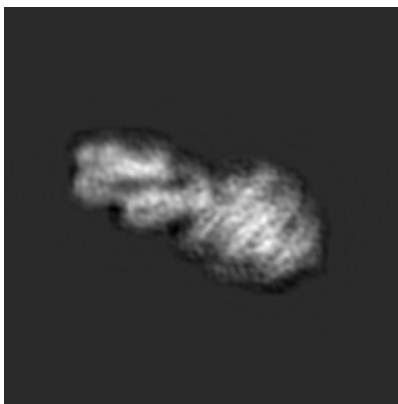
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

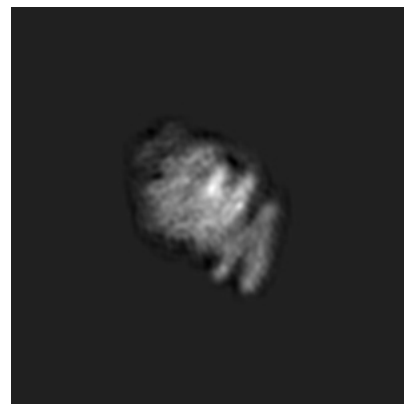
6.1.1 Primary map



X

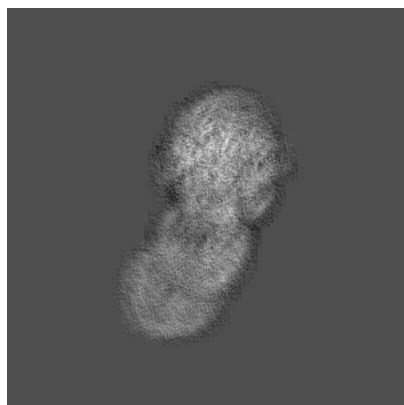


Y

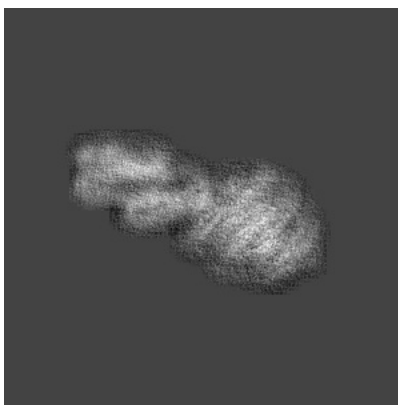


Z

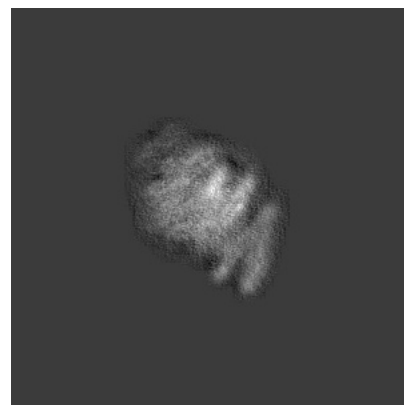
6.1.2 Raw map



X



Y

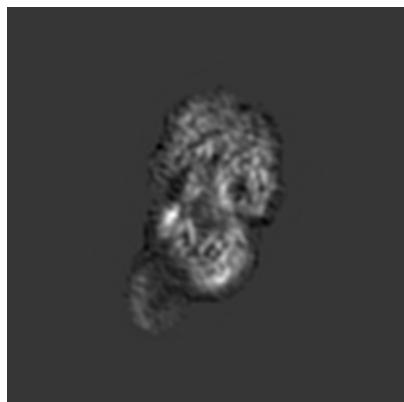


Z

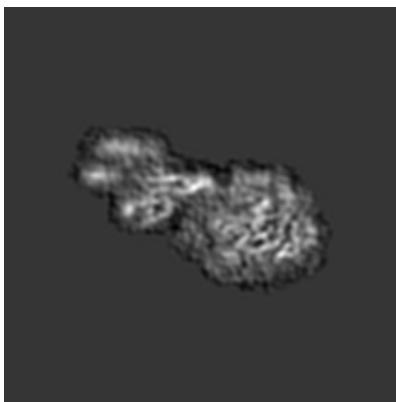
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 200

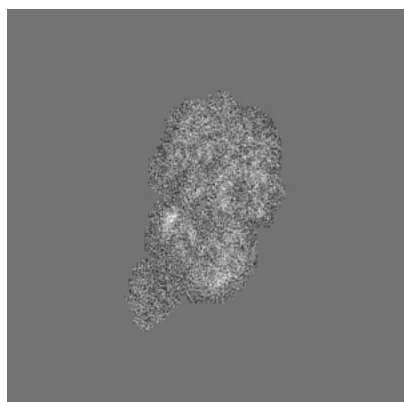


Y Index: 200

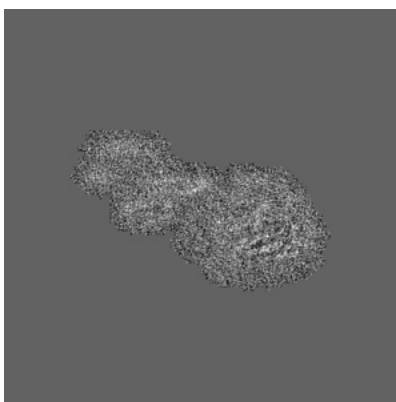


Z Index: 200

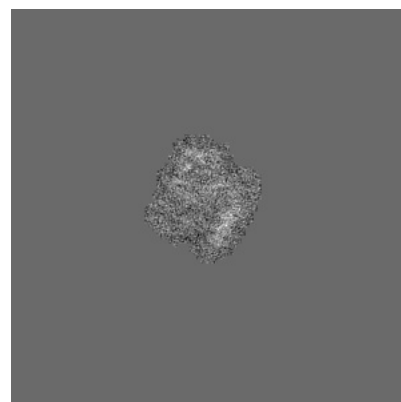
6.2.2 Raw map



X Index: 200



Y Index: 200

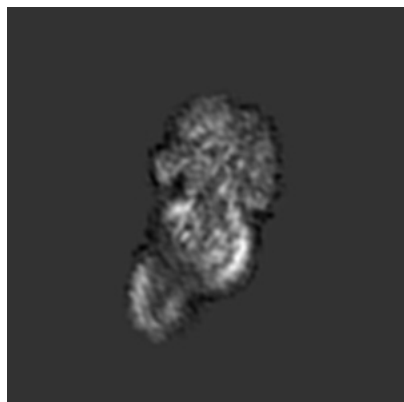


Z Index: 200

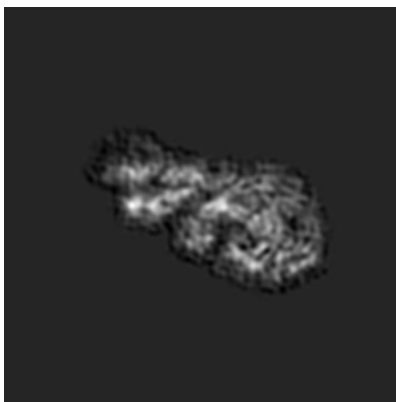
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

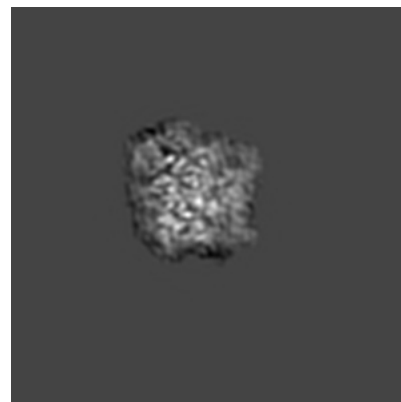
6.3.1 Primary map



X Index: 207

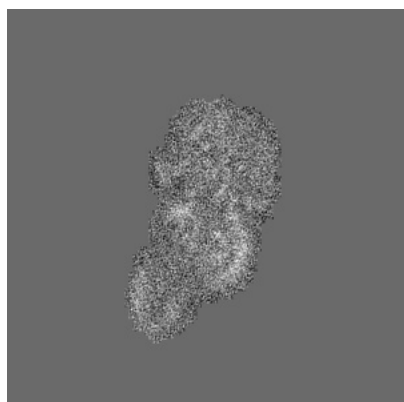


Y Index: 216

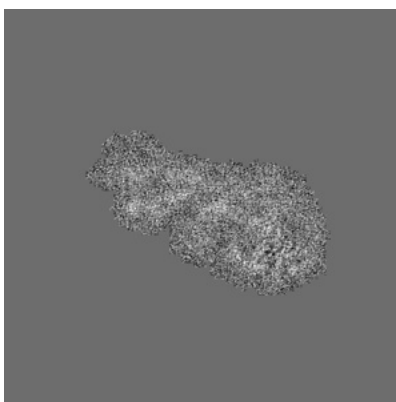


Z Index: 259

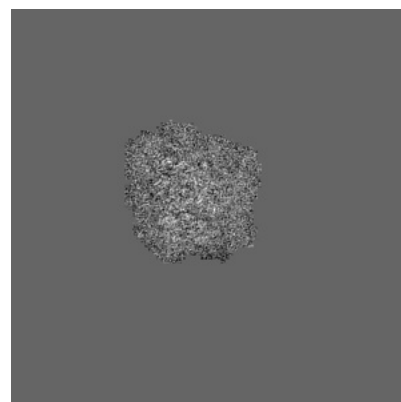
6.3.2 Raw map



X Index: 207



Y Index: 216

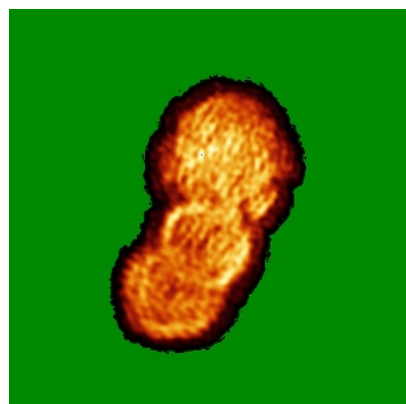


Z Index: 261

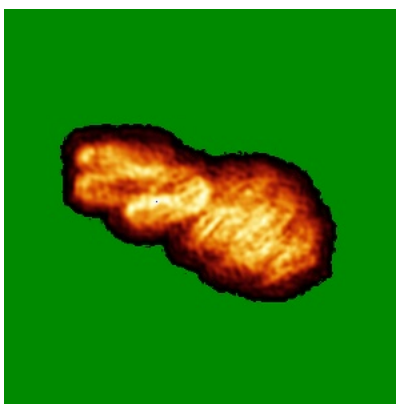
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

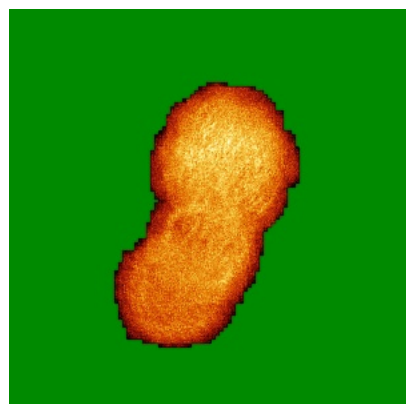


Y

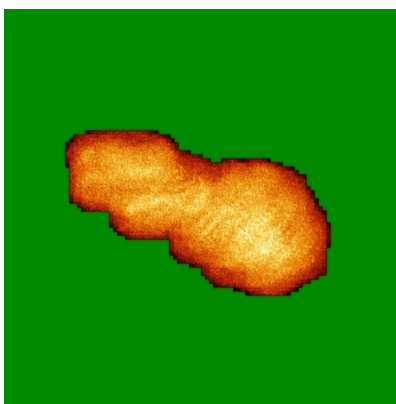


Z

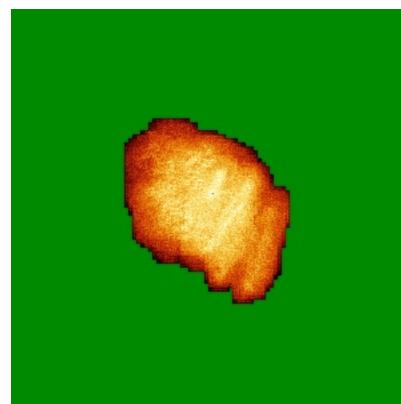
6.4.2 Raw map



X



Y

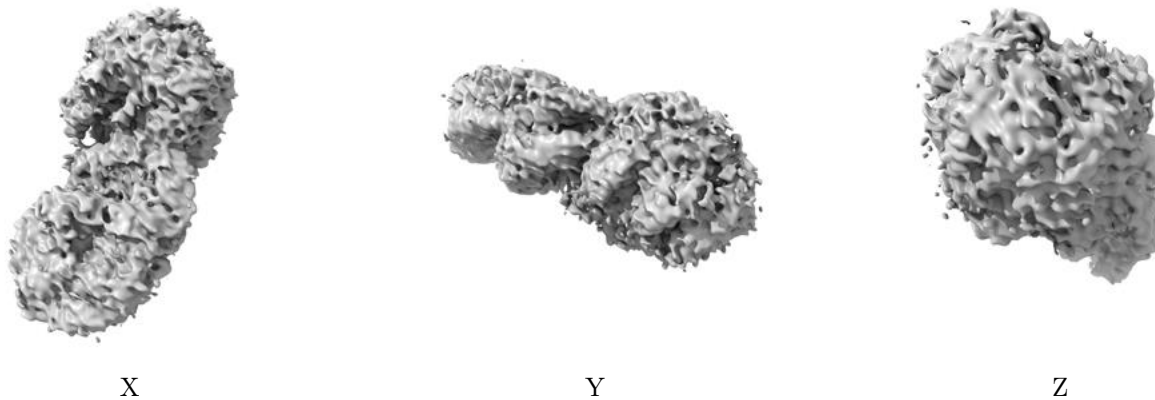


Z

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.

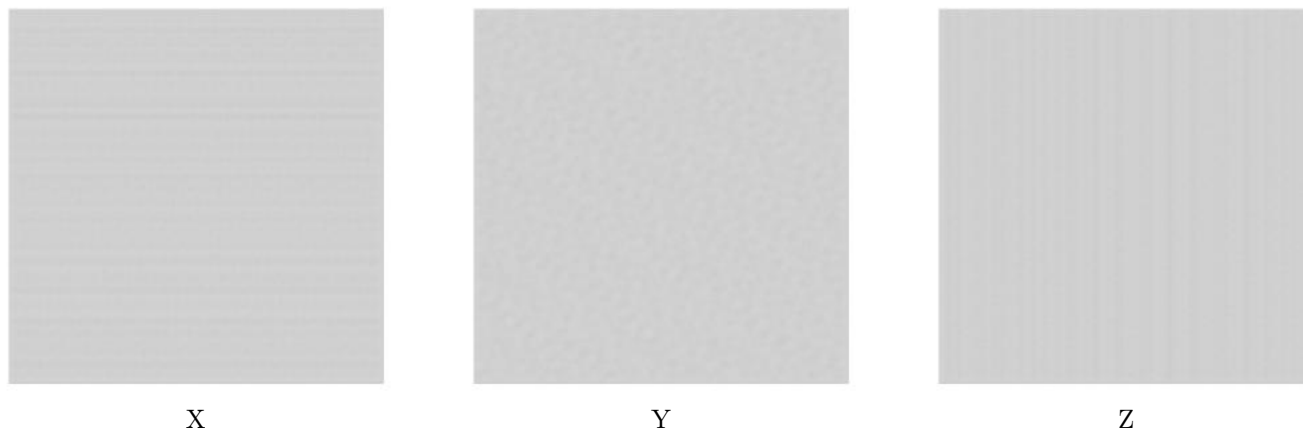
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.000666. 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.

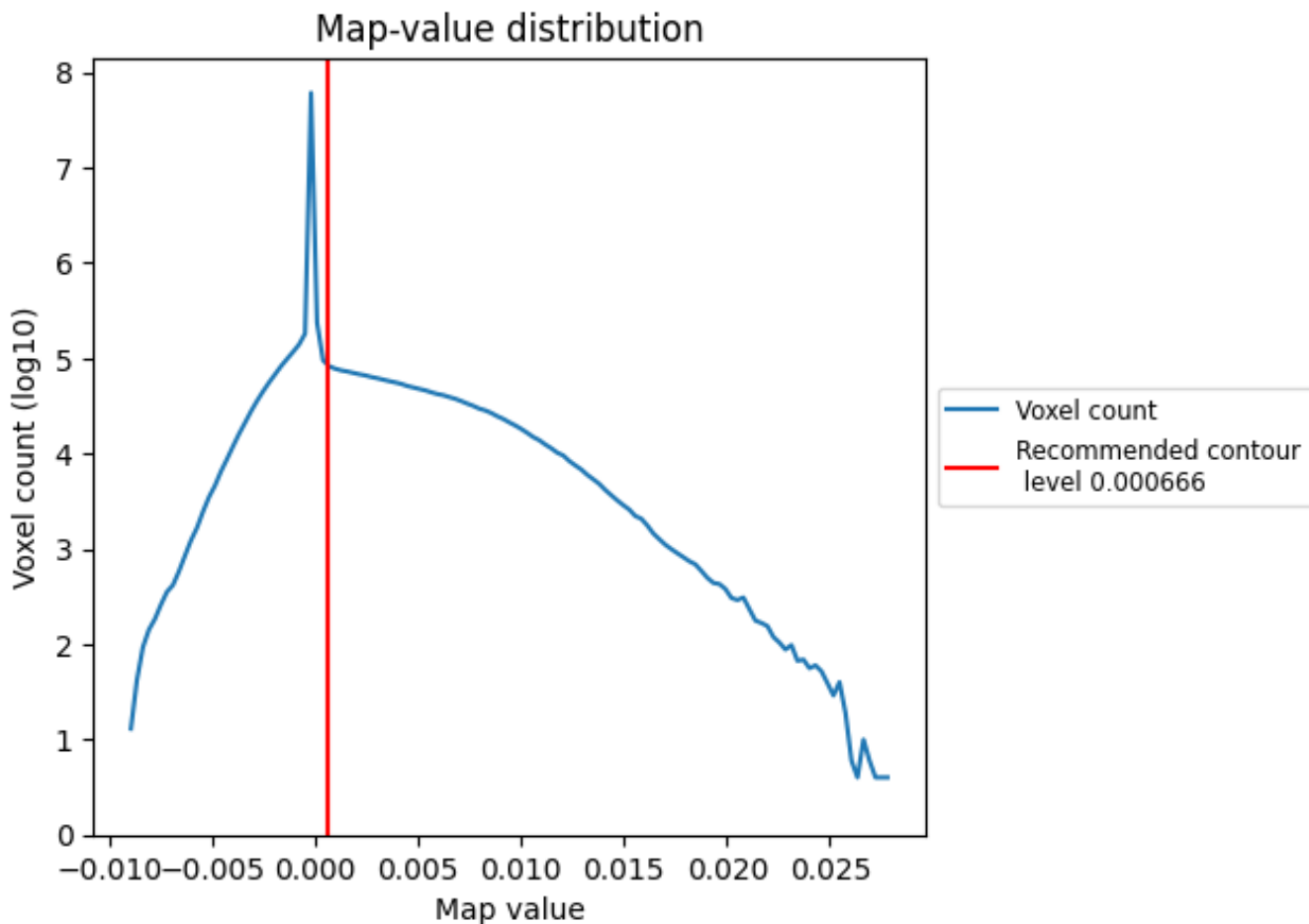
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

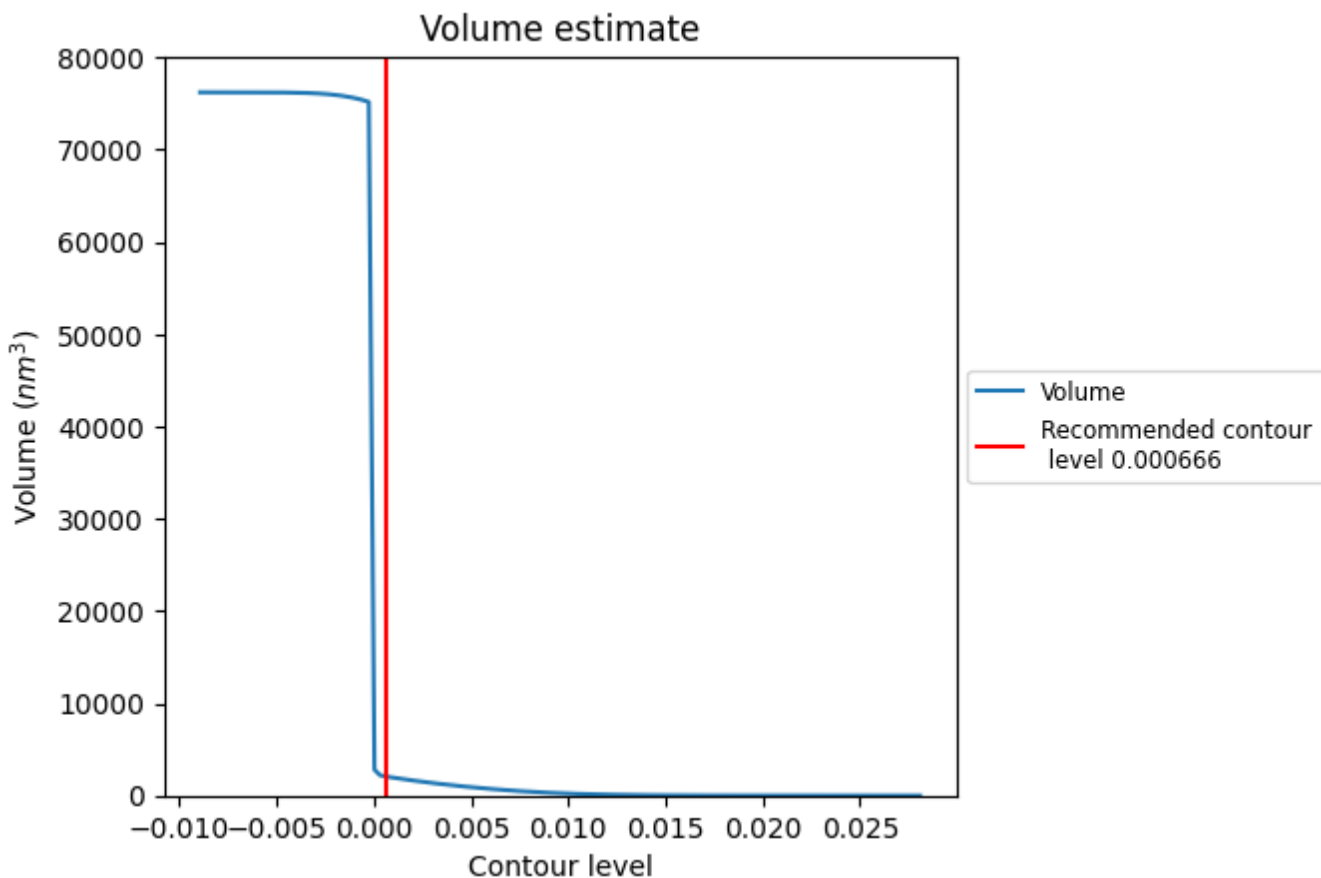
This section contains the results of statistical analysis of the map.

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.

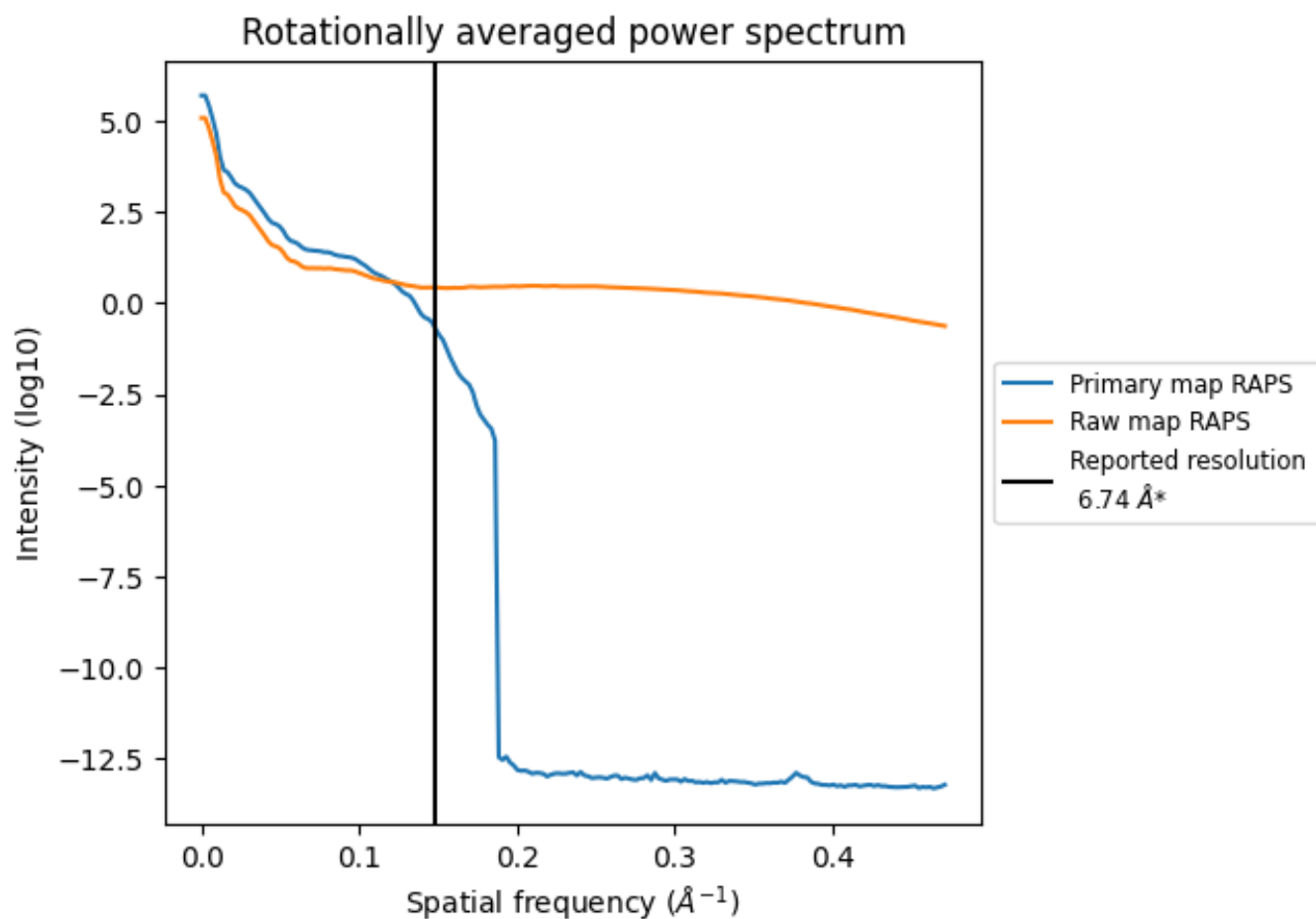
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2056 nm^3 ; this corresponds to an approximate mass of 1858 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

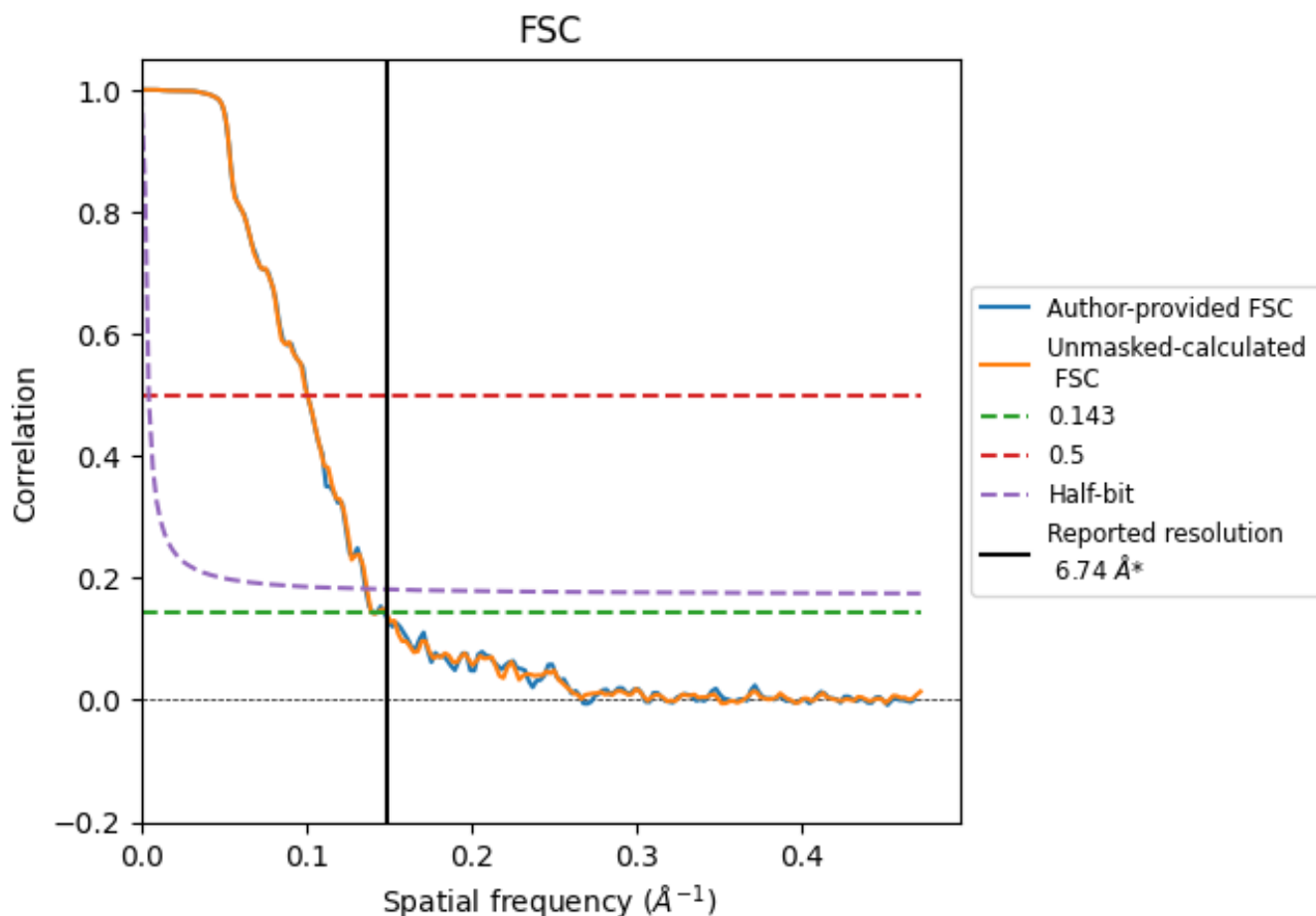


*Reported resolution corresponds to spatial frequency of 0.148 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.148 Å⁻¹

8.2 Resolution estimates [i](#)

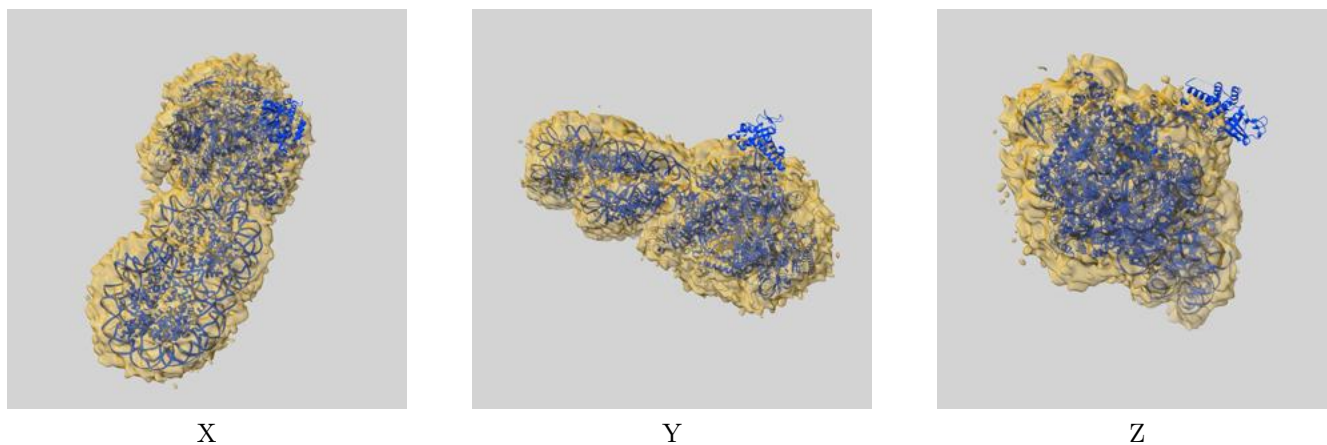
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.74	-	-
Author-provided FSC curve	7.13	9.95	7.36
Unmasked-calculated*	7.15	9.94	7.32

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

9 Map-model fit [i](#)

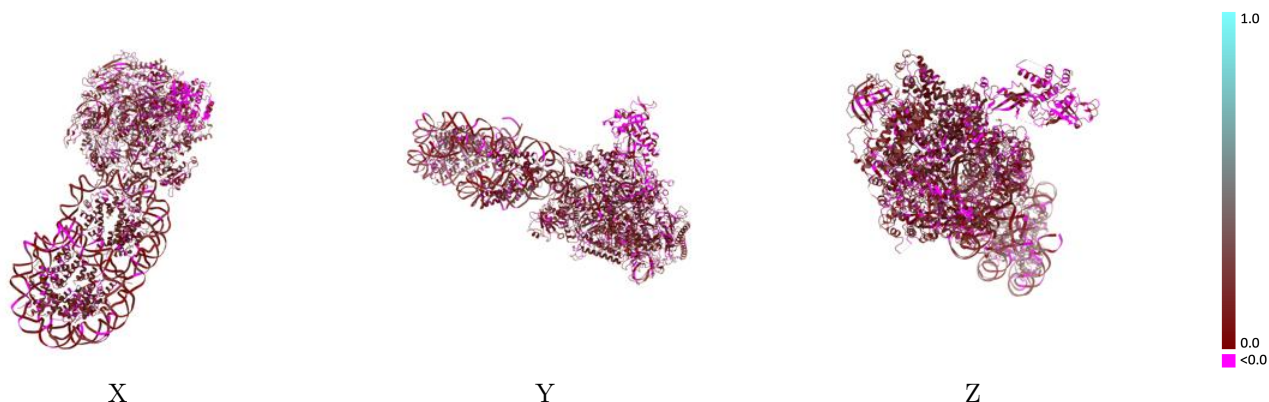
This section contains information regarding the fit between EMDB map EMD-64642 and PDB model 9UZ9. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



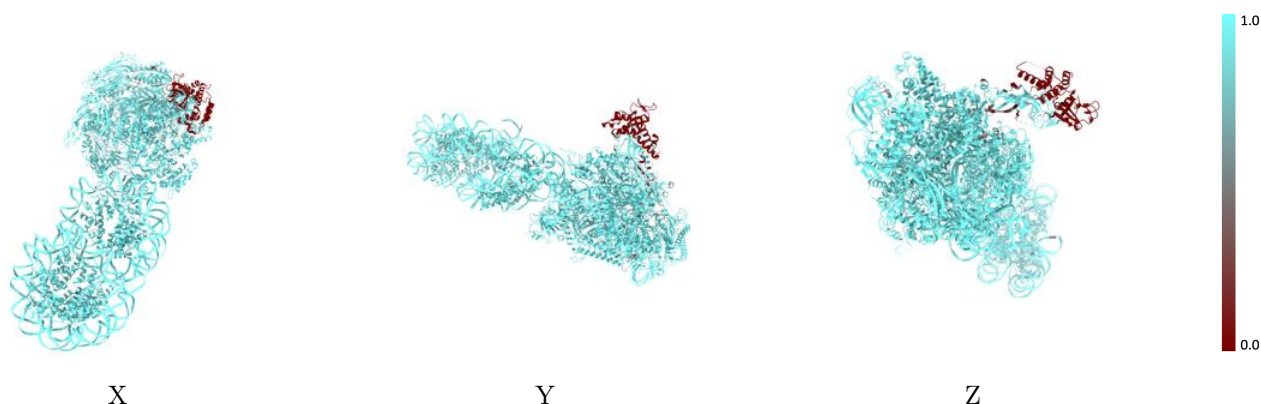
The images above show the 3D surface view of the map at the recommended contour level 0.000666 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



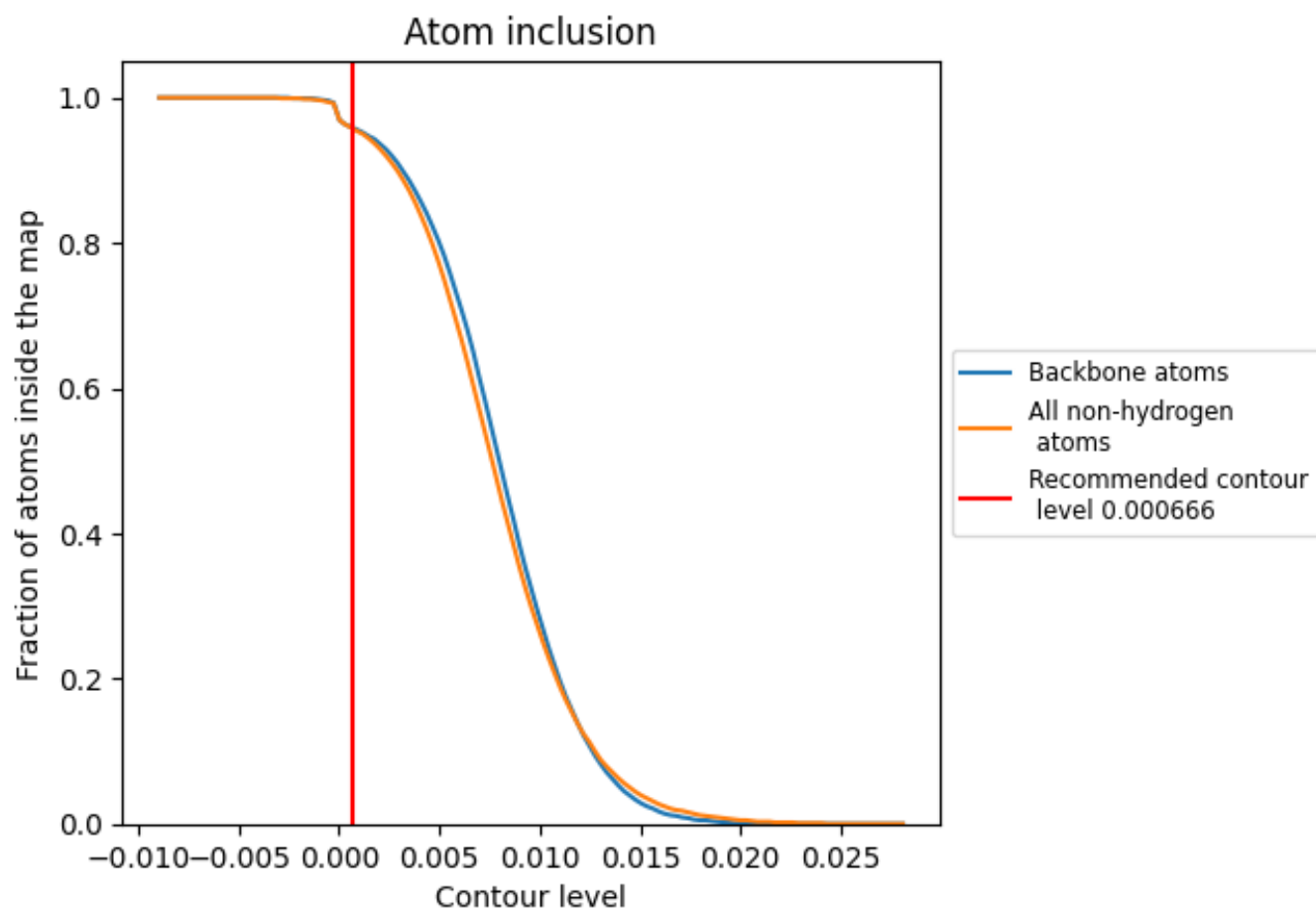
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.000666).





























































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.000666) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9580	 0.1180
A	 0.9850	 0.1310
B	 0.9920	 0.1230
C	 0.9880	 0.1290
D	 0.2450	 0.0070
E	 0.9940	 0.1480
F	 0.9530	 0.1180
G	 0.5160	 0.0210
H	 0.9470	 0.1300
I	 0.9300	 0.0700
J	 0.9910	 0.1160
K	 0.9610	 0.1060
L	 0.9940	 0.1080
N	 0.9910	 0.1140
P	 1.0000	 0.1670
T	 0.9880	 0.1140
a	 1.0000	 0.1150
b	 0.9970	 0.1260
c	 0.9890	 0.1280
d	 0.9900	 0.1320
e	 1.0000	 0.1360
f	 1.0000	 0.0770
g	 0.9740	 0.1120
h	 1.0000	 0.1300
k	 1.0000	 0.1330
l	 0.9980	 0.1480
m	 0.9990	 0.1320
n	 1.0000	 0.1190
o	 0.9960	 0.1380
p	 0.9990	 0.1480

