wwPDB EM Validation Summary Report

Mar 8, 2026 – 01:26 PM UTC

PDB ID	:	7AOC / pdb_00007aoc
EMDB ID	:	EMD-11840
Title	:	Schizosaccharomyces pombe RNA polymerase I (monomer)
Authors	:	Heiss, F.; Daiss, J.; Becker, P.; Engel, C.
Deposited on	:	2020-10-14
Resolution	:	3.84 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:

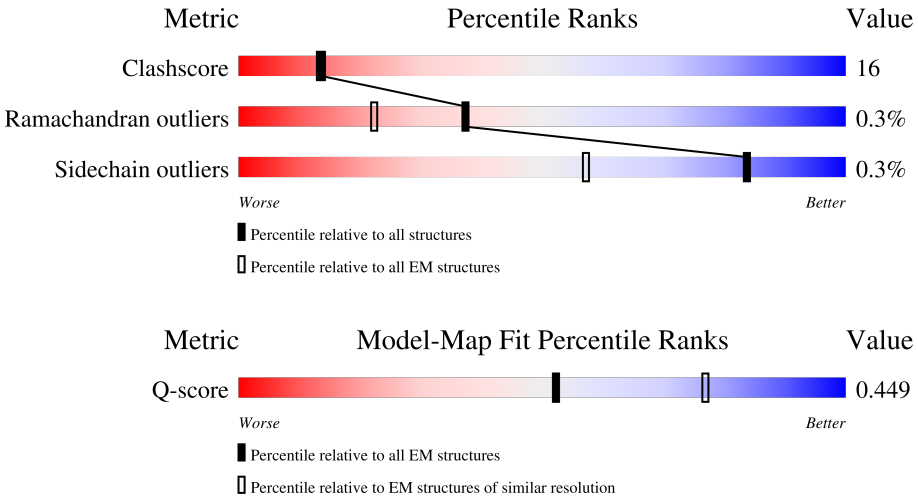
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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 3.84 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.



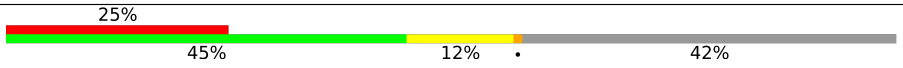
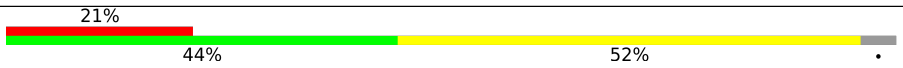
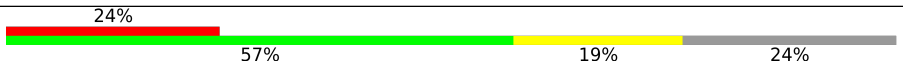
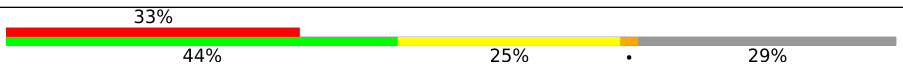
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	9033 (3.34 - 4.34)

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 <=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	1689	46% 54% 28% • 17%
2	B	1174	37% 65% 34% •
3	C	348	39% 64% 26% • 9%
4	D	147	27% 16% 10% 73%

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Mol	Chain	Length	Quality of chain
5	E	210	
6	F	142	
7	G	173	
8	H	125	
9	I	119	
10	J	71	
11	K	125	
12	L	63	

2 Entry composition (i)

There are 13 unique types of molecules in this entry. The entry contains 29724 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 I subunit rpa1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1394	11051	7009	1907	2076	59	0	0

- Molecule 2 is a protein called Probable DNA-directed RNA polymerase I subunit RPA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1159	9148	5803	1595	1691	59	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	317	2533	1621	430	475	7	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase I subunit rpa14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	39	322	203	57	61	1	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	207	1663	1050	301	306	6	0	0

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	82	650	413	111	123	3	0	0

- Molecule 7 is a protein called DNA-directed RNA polymerase I subunit rpa43.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	160	Total	C	N	O	S	0	0
			1267	817	210	236	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	123	Total	C	N	O	S	0	0
			990	628	166	193	3		

- Molecule 9 is a protein called DNA-directed RNA polymerase I subunit RPA12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	57	Total	C	N	O	S	0	0
			431	269	69	89	4		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	68	Total	C	N	O	S	0	0
			550	350	93	100	7		

- Molecule 11 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	95	Total	C	N	O	S	0	0
			745	472	123	146	4		

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	45	Total	C	N	O	S	0	0
			368	225	74	61	8		

- Molecule 13 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
13	A	2	Total	Zn	0
			2	2	
13	B	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
13	I	1	Total Zn 1 1	0
13	J	1	Total Zn 1 1	0
13	L	1	Total Zn 1 1	0

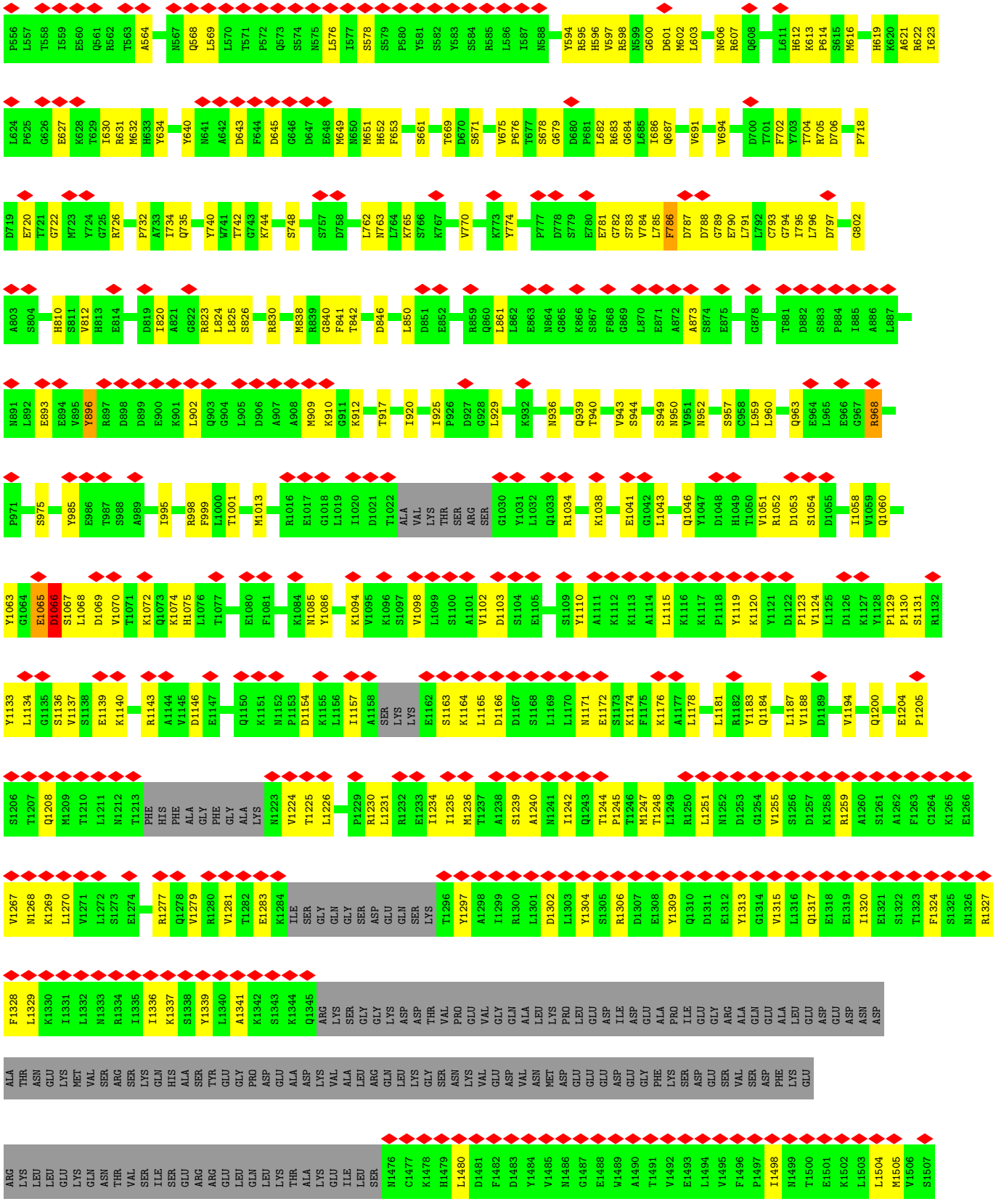
3 Residue-property plots (i)

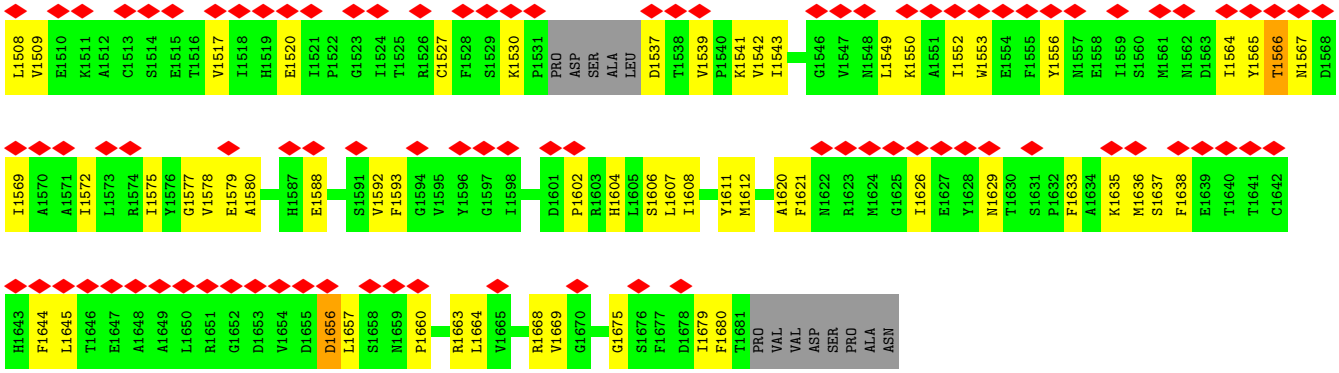
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: DNA-directed RNA polymerase I subunit rpa1

Chain A:



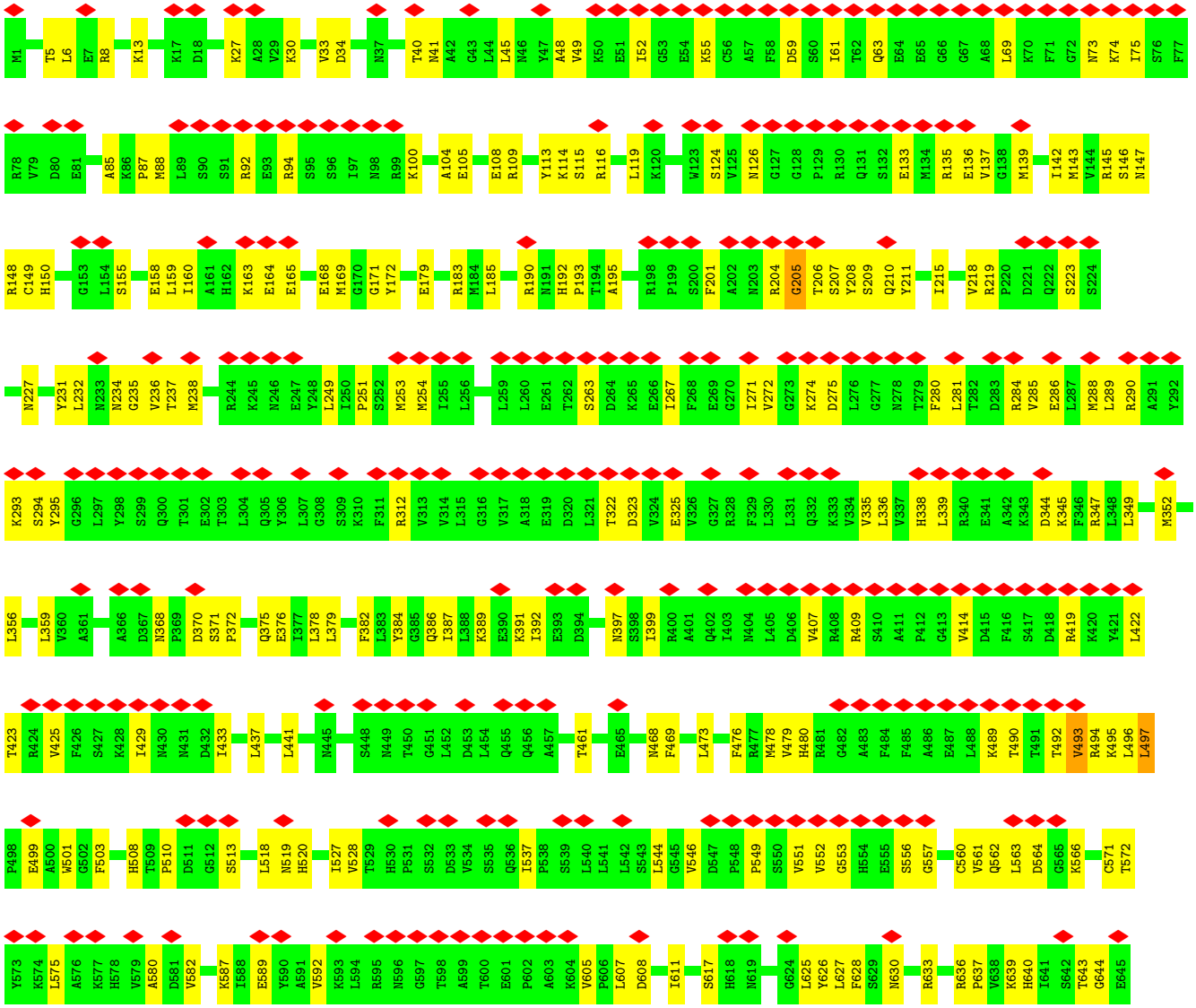

P556 L557 T558 I559 E560 Q561 R562 T563 A564 N567 Q568 L569 L570 T571 P572 Q573 S574 N575 L576 I577 S578 S579 P580 Y581 S582 Y583 S584 R585 L586 I587 N588 Y594 R595 H596 V597 R598 N599 G600 D601 M602 L603 N606 R607 Q608 L611 H612 K613 P614 S615 M616 H619 K620 A621 R622 I623
L624 P625 G626 E627 K628 T629 I630 R631 M632 H633 Y634 Y640 N641 A642 D643 F644 D645 G646 D647 E648 M649 N650 M651 H652 F653 S661 T669 D670 S671 V675 P676 T677 S678 G679 D680 P681 L682 R683 G684 L685 I686 Q687 V691 V694 D700 T701 F702 Y703 T704 R705 D706 P718
D719 E720 T721 G722 M723 Y724 G725 R726 P732 A733 I734 Q735 Y740 W741 T742 G743 K744 S748 S757 D758 L762 N763 L764 K765 S766 K767 V770 K773 Y774 P777 D778 S779 E780 E781 G782 S783 V784 L785 F786 D787 D788 G789 E790 L791 L792 C793 G794 I795 L796 D797 G802
A803 S804 H810 S811 V812 H813 E814 D819 I820 A821 G822 R823 L824 L825 S826 R830 M838 R839 G840 F841 T842 D846 L850 D851 E852 R859 Q860 L861 L862 E863 N864 G865 K866 S867 F868 G869 L870 E871 A872 A873 S874 E875 G878 T881 D882 S883 P884 I885 A886 L887
N891 L892 E893 E894 V895 Y896 R897 D898 D899 E900 K901 L902 Q903 G904 L905 D906 A907 A908 M909 K910 G911 K912 T917 I920 I925 P926 D927 G928 L929 K932 N936 Q939 T940 V943 S944 S949 N950 V951 N952 S957 C958 L959 L960 Q963 E964 L965 E966 G967 R968
P971 S975 Y985 E986 T987 S988 A989 I995 R998 F999 L1000 T1001 M1013 R1016 E1017 G1018 L1019 I1020 D1021 T1022 ALA VAL LYS THR SER ARG SER G1030 Y1031 L1032 Q1033 R1034 K1038 E1041 G1042 L1043 Q1046 Y1047 D1048 H1049 T1050 V1051 R1052 D1053 S1054 D1055 I1058 V1059 Q1060
Y1063 G1064 E1065 D1066 S1067 L1068 D1069 V1070 T1071 K1072 Q1073 K1074 H1075 L1076 T1077 E1080 F1081 K1084 N1085 Y1086 K1094 V1095 K1096 S1097 V1098 L1099 S1100 A1101 V1102 D1103 S1104 E1105 S1109 Y1110 A1111 K1112 K1113 A1114 L1115 K1116 K1117 P1118 Y1119 K1120 Y1121 D1122 P1123 V1124 L1125 D1126 K1127 Y1128 P1129 P1130 S1131 R1132
Y1133 L1134 G1135 S1136 V1137 S1138 E1139 K1140 R1143 A1144 V1145 D1146 E1147 Q1150 K1151 N1152 P1153 D1154 K1155 L1156 I1157 A1158 SER LYS LYS E1162 S1163 K1164 L1165 D1166 D1167 S1168 L1169 L1170 N1171 E1172 S1173 K1174 F1175 K1176 A1177 L1178 L1181 R1182 Y1183 Q1184 L1187 V1188 D1189 V1194 Q1200 E1204 P1205
S1206 T1207 Q1208 M1209 T1210 L1211 N1212 T1213 PHE HIS PHE ALA GLY PHE GLY ALA LYS N1223 V1224 T1225 L1226 P1229 R1230 L1231 R1232 E1233 I1234 I1235 M1236 T1237 A1238 S1239 A1240 N1241 I1242 Q1243 T1244 P1245 T1246 M1247 T1248 L1249 R1250 L1251 N1252 D1253 G1254 V1255 S1256 D1257 K1258 R1259 A1260 S1261 A1262 F1263 C1264 K1265 E1266
V1267 N1268 K1269 L1270 V1271 L1272 S1273 E1274 R1277 Q1278 V1279 R1280 V1281 T1282 E1283 K1284 ILE SER GLY GLN GLY SER ASP GLU GLN SER LYS T1296 Y1297 A1298 I1299 R1300 L1301 D1302 L1303 Y1304 S1305 R1306 D1307 E1308 Y1309 Q1310 D1311 E1312 Y1313 G1314 V1315 L1316 Q1317 E1318 E1319 I1320 E1321 S1322 T1323 F1324 S1325 N1326 R1327
F1328 L1329 K1330 I1331 L1332 N1333 R1334 I1335 I1336 K1337 S1338 Y1339 L1340 A1341 K1342 S1343 K1344 Q1345 ARG LYS SER GLY GLY LYS ASP ASP THR VAL PRO GLU VAL GLY GLN ALA LEU LYS PRO LEU GLU ASP ILE ASP GLU ALA PRO ILE GLU GLY GLY ARG ALA GLN GLU ASP GLU ALA LEU GLU ASP GLU ASP ASN ASP
ALA THR ASN GLU LYS MET VAL SER ARG SER LYS GLN HIS ALA SER TYR GLU GLY PRO ASP GLU ALA ASP LYS VAL ALA LEU ARG GLN LEU LYS GLY SER ASN LYS VAL GLU ASP VAL ASN MET ASP GLU GLU GLU ASP GLY GLY PHE LYS SER ASP GLU GLY SER VAL SER ASP PHE LYS GLU
ARG LYS LEU LEU GLU LYS LYS GLN ASN THR VAL SER SER ILE SER GLU GLU ARG ARG GLU GLU LEU GLN LEU LYS THR ALA LYS LYS GLU ILE LEU LEU SER N1476 C1477 K1478 H1479 L1480 D1481 F1482 D1483 Y1484 V1485 N1486 G1487 E1488 W1489 A1490 T1491 V1492 E1493 L1494 E1495 F1496 P1497 I1498 N1499 T1500 E1501 K1502 L1503 L1504 M1505 V1506 S1507

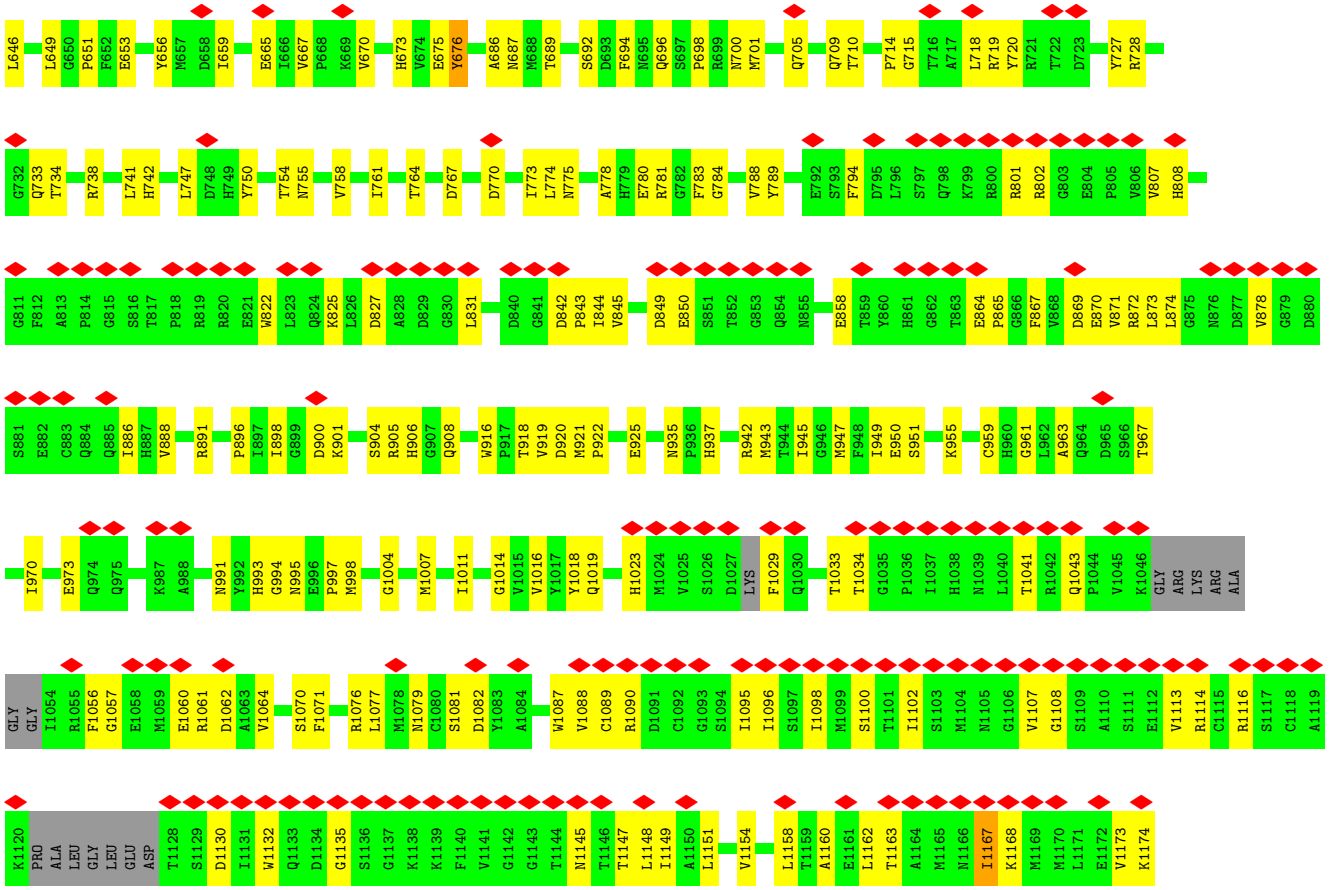


• Molecule 2: Probable DNA-directed RNA polymerase I subunit RPA2

Chain B:



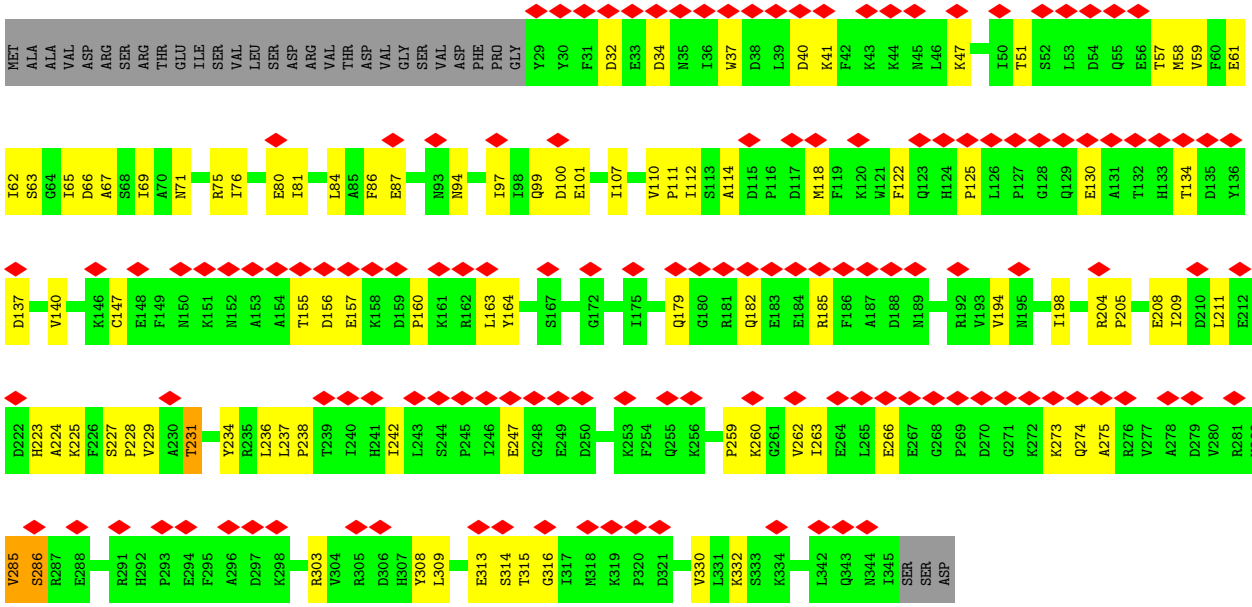




• Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1

Chain C:

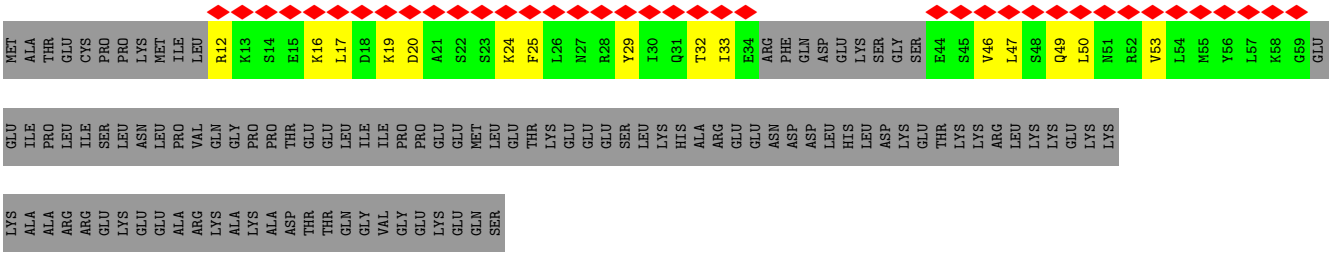




• Molecule 4: DNA-directed RNA polymerase I subunit rpa14

Chain D:

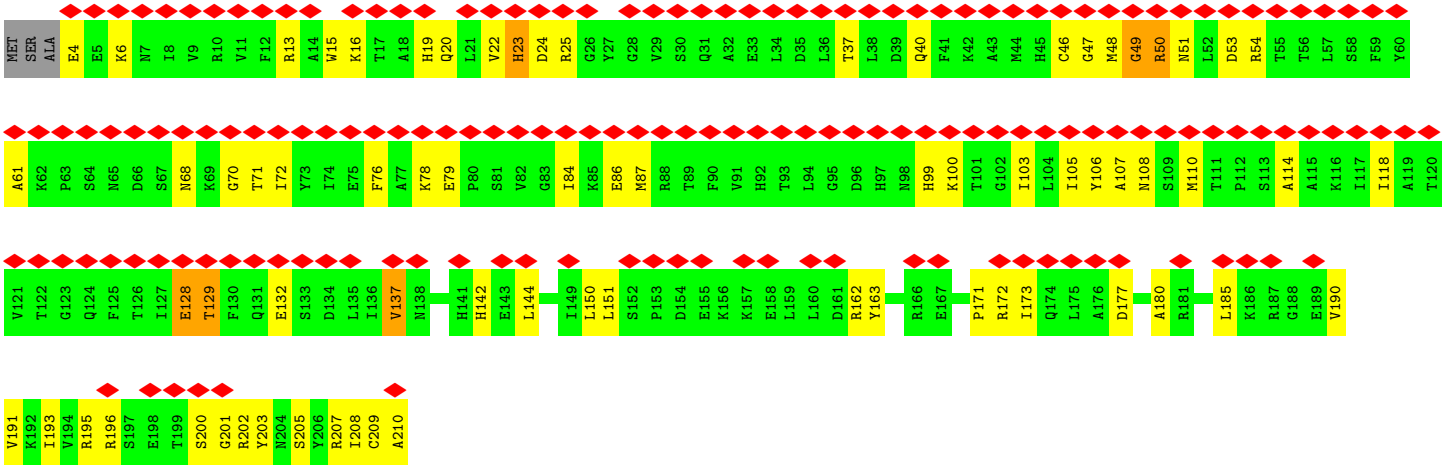




- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

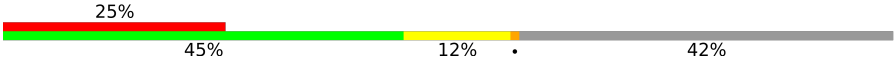
Chain E:

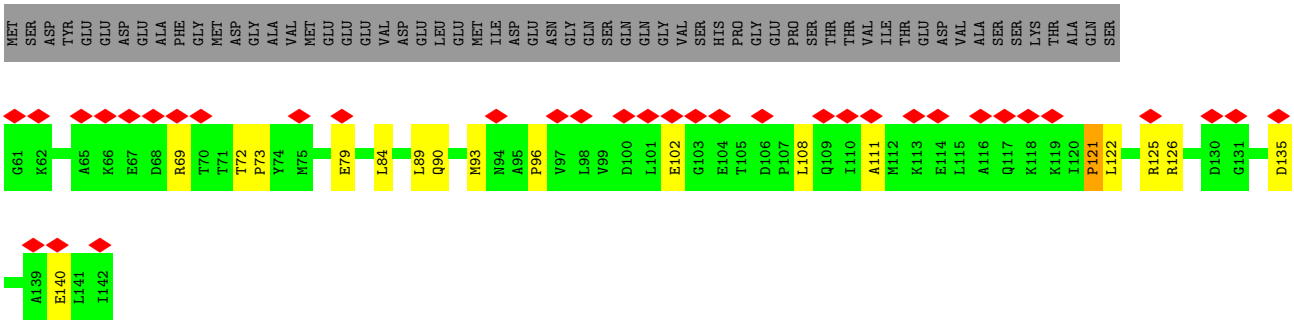




- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

Chain F:

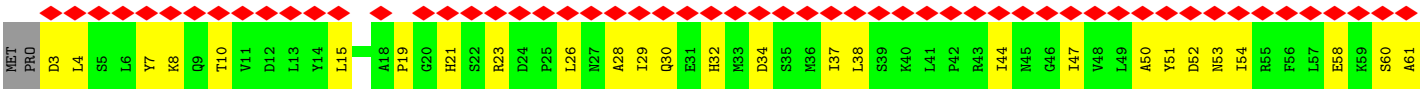


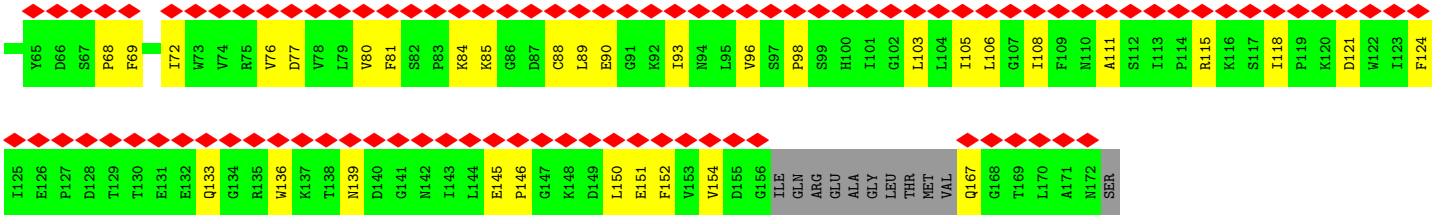


- Molecule 7: DNA-directed RNA polymerase I subunit rpa43

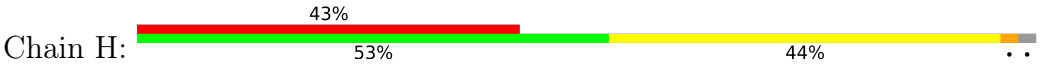
Chain G:



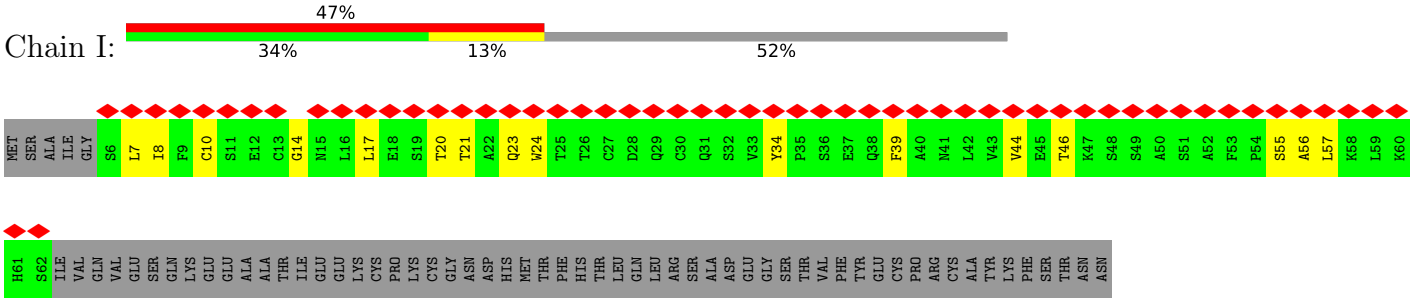




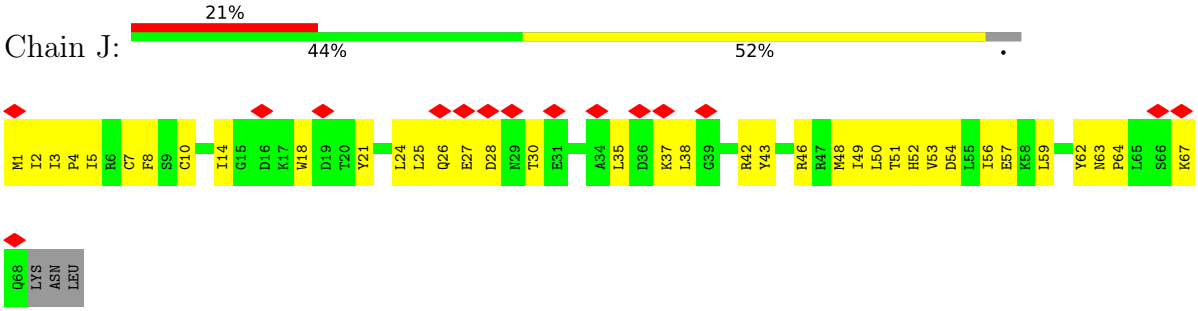
• Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



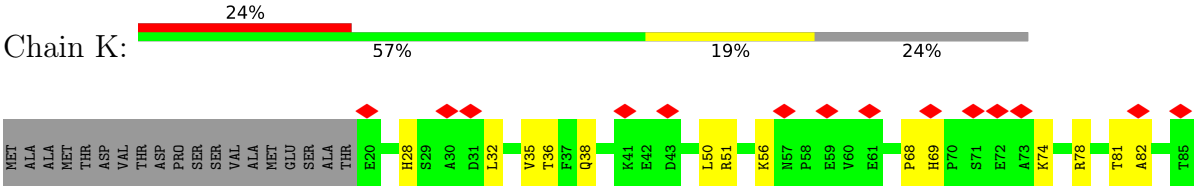
• Molecule 9: DNA-directed RNA polymerase I subunit RPA12

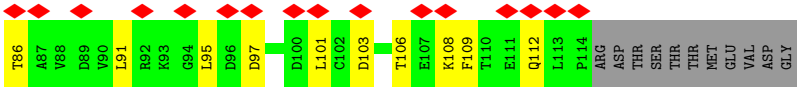


• Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



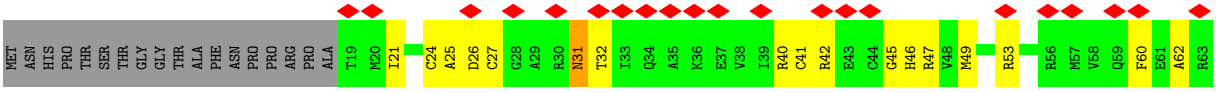
• Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2





• Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	79313	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	86.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.501	Depositor
Minimum map value	-0.291	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	233.97002, 233.97002, 233.97002	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0635, 1.0635, 1.0635	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.32	0/11271	0.53	1/15226 (0.0%)
2	B	0.36	0/9353	0.53	0/12644
3	C	0.32	0/2588	0.49	0/3505
4	D	0.18	0/323	0.41	0/427
5	E	0.26	0/1695	0.63	3/2287 (0.1%)
6	F	0.32	0/660	0.47	0/893
7	G	0.20	0/1295	0.46	0/1755
8	H	0.30	0/1004	0.63	2/1355 (0.1%)
9	I	0.22	0/439	0.53	0/596
10	J	0.41	0/558	0.55	0/751
11	K	0.36	0/759	0.42	0/1030
12	L	0.30	0/371	0.55	0/491
All	All	0.33	0/30316	0.53	6/40960 (0.0%)

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	7
2	B	0	2
5	E	0	5
All	All	0	14

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	E	24	ASP	N-CA-C	7.23	126.20	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	E	49	GLY	CA-C-N	5.87	132.26	121.70
5	E	49	GLY	C-N-CA	5.87	132.26	121.70
1	A	1066	ASP	N-CA-C	5.33	122.16	110.80
8	H	17	ASP	CA-C-N	5.11	130.90	121.70

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1065	GLU	Peptide
1	A	1066	ASP	Peptide
1	A	246	ILE	Peptide
1	A	84	ILE	Peptide
1	A	896	TYR	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	11051	0	11047	391	0
2	B	9148	0	9109	328	0
3	C	2533	0	2540	74	0
4	D	322	0	338	19	0
5	E	1663	0	1684	60	0
6	F	650	0	674	19	0
7	G	1267	0	1278	53	0
8	H	990	0	1001	44	0
9	I	431	0	410	14	0
10	J	550	0	566	38	0
11	K	745	0	745	22	0
12	L	368	0	377	17	0
13	A	2	0	0	0	0
13	B	1	0	0	0	0
13	I	1	0	0	0	0
13	J	1	0	0	0	0
13	L	1	0	0	0	0
All	All	29724	0	29769	944	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 16.

The worst 5 of 944 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)
5:E:23:HIS:HA	5:E:25:ARG:H	1.27	0.97
1:A:1324:PHE:O	1:A:1328:PHE:HB3	1.72	0.90
1:A:103:CYS:SG	1:A:106:CYS:HB3	1.86	0.90
8:H:17:ASP:HA	8:H:18:LYS:HB2	1.58	0.84
1:A:56:PRO:HG3	1:A:63:CYS:HB2	1.58	0.84

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	1368/1689 (81%)	1235 (90%)	130 (10%)	3 (0%)	43 74
2	B	1151/1174 (98%)	993 (86%)	155 (14%)	3 (0%)	36 69
3	C	315/348 (90%)	290 (92%)	23 (7%)	2 (1%)	21 55
4	D	35/147 (24%)	35 (100%)	0	0	100 100
5	E	205/210 (98%)	176 (86%)	29 (14%)	0	100 100
6	F	80/142 (56%)	74 (92%)	5 (6%)	1 (1%)	9 40
7	G	156/173 (90%)	141 (90%)	15 (10%)	0	100 100
8	H	121/125 (97%)	94 (78%)	26 (22%)	1 (1%)	16 50
9	I	55/119 (46%)	51 (93%)	4 (7%)	0	100 100
10	J	66/71 (93%)	50 (76%)	16 (24%)	0	100 100
11	K	93/125 (74%)	84 (90%)	9 (10%)	0	100 100
12	L	43/63 (68%)	42 (98%)	1 (2%)	0	100 100
All	All	3688/4386 (84%)	3265 (88%)	413 (11%)	10 (0%)	37 69

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	206	THR
2	B	493	VAL
1	A	782	GLY
3	C	286	SER
1	A	968	ARG

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	1233/1484 (83%)	1232 (100%)	1 (0%)	88 89
2	B	1004/1013 (99%)	999 (100%)	5 (0%)	81 81
3	C	281/308 (91%)	279 (99%)	2 (1%)	76 78
4	D	37/134 (28%)	37 (100%)	0	100 100
5	E	182/184 (99%)	181 (100%)	1 (0%)	81 81
6	F	70/121 (58%)	70 (100%)	0	100 100
7	G	143/154 (93%)	143 (100%)	0	100 100
8	H	112/114 (98%)	112 (100%)	0	100 100
9	I	51/105 (49%)	51 (100%)	0	100 100
10	J	63/66 (96%)	63 (100%)	0	100 100
11	K	86/111 (78%)	86 (100%)	0	100 100
12	L	39/53 (74%)	37 (95%)	2 (5%)	21 47
All	All	3301/3847 (86%)	3290 (100%)	11 (0%)	84 85

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	231	THR
5	E	137	VAL
12	L	31	ASN
12	L	26	ASP

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Mol	Chain	Res	Type
2	B	676	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 85 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1043	GLN
5	E	142	HIS
2	B	1145	ASN
3	C	300	GLN
7	G	133	GLN

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 6 ligands modelled in this entry, 6 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.

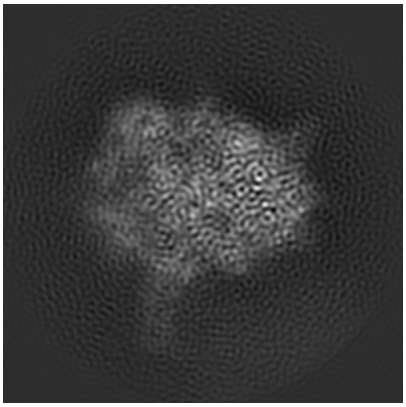
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-11840. These allow visual inspection of the internal detail of the map and identification of artifacts.

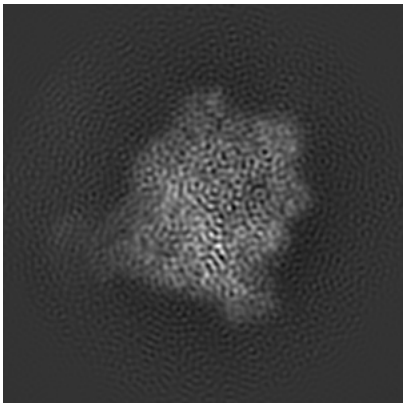
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

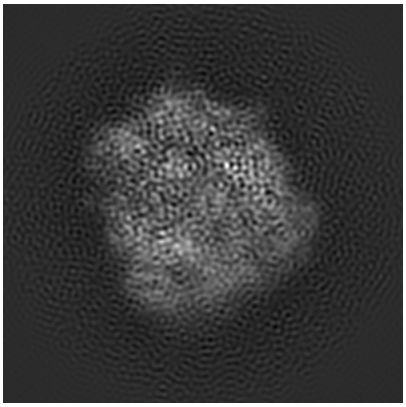
6.1.1 Primary map



X



Y

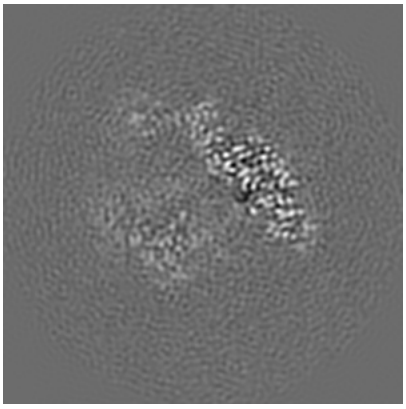


Z

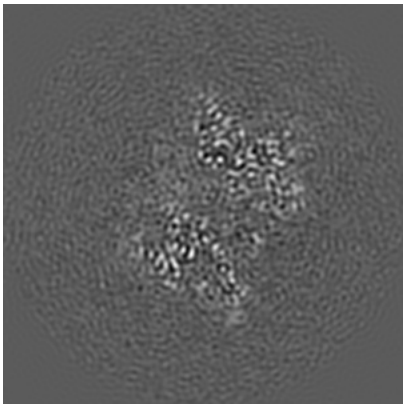
The images above show the map projected in three orthogonal directions.

6.2 Central slices

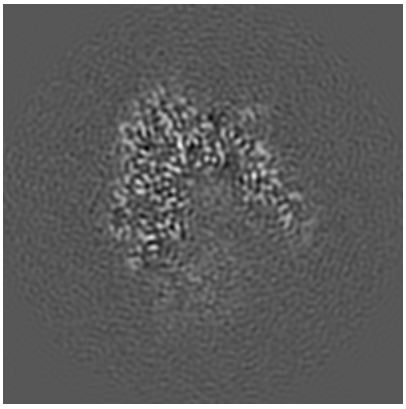
6.2.1 Primary map



X Index: 110



Y Index: 110

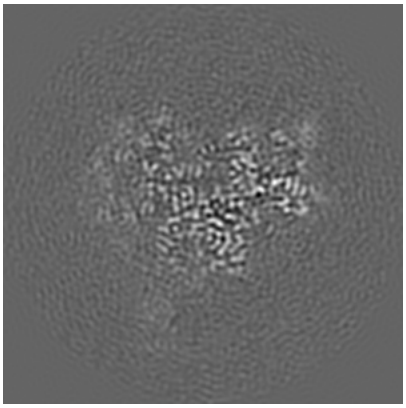


Z Index: 110

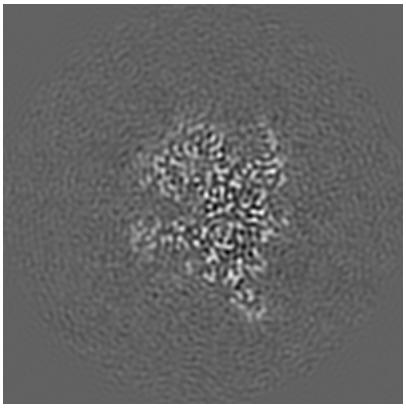
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

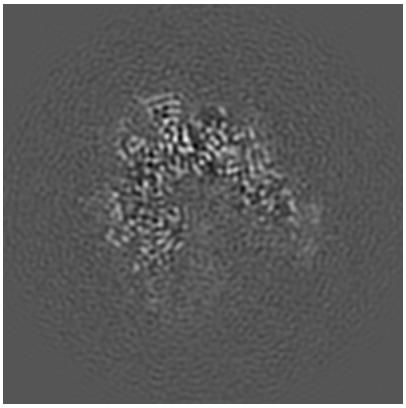
6.3.1 Primary map



X Index: 91



Y Index: 129

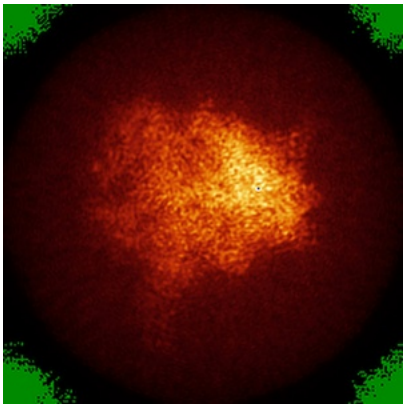


Z Index: 118

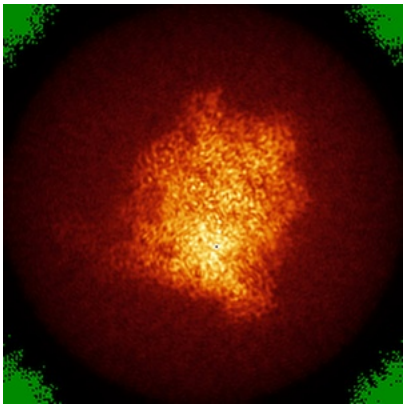
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

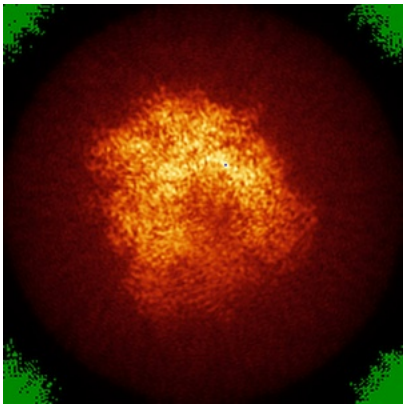
6.4.1 Primary map



X



Y

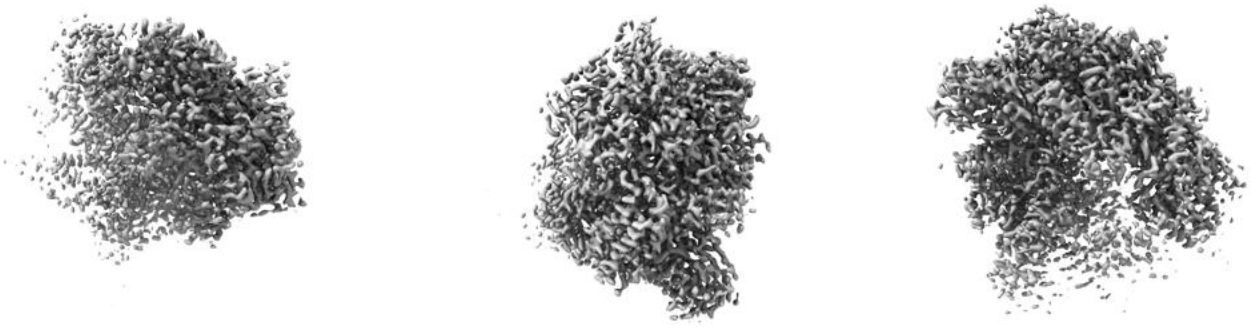


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

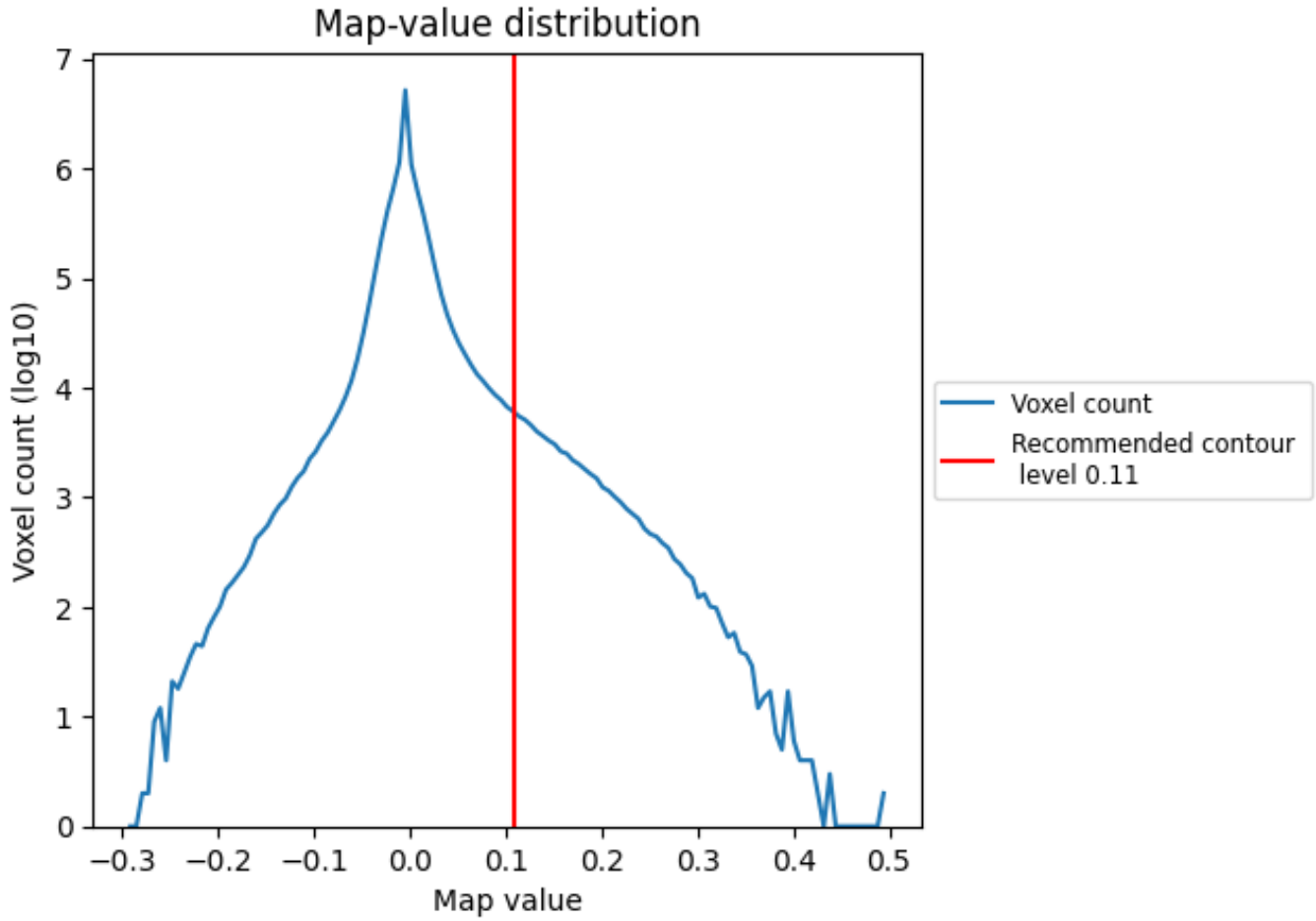
6.6 Mask visualisation (i)

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

7 Map analysis

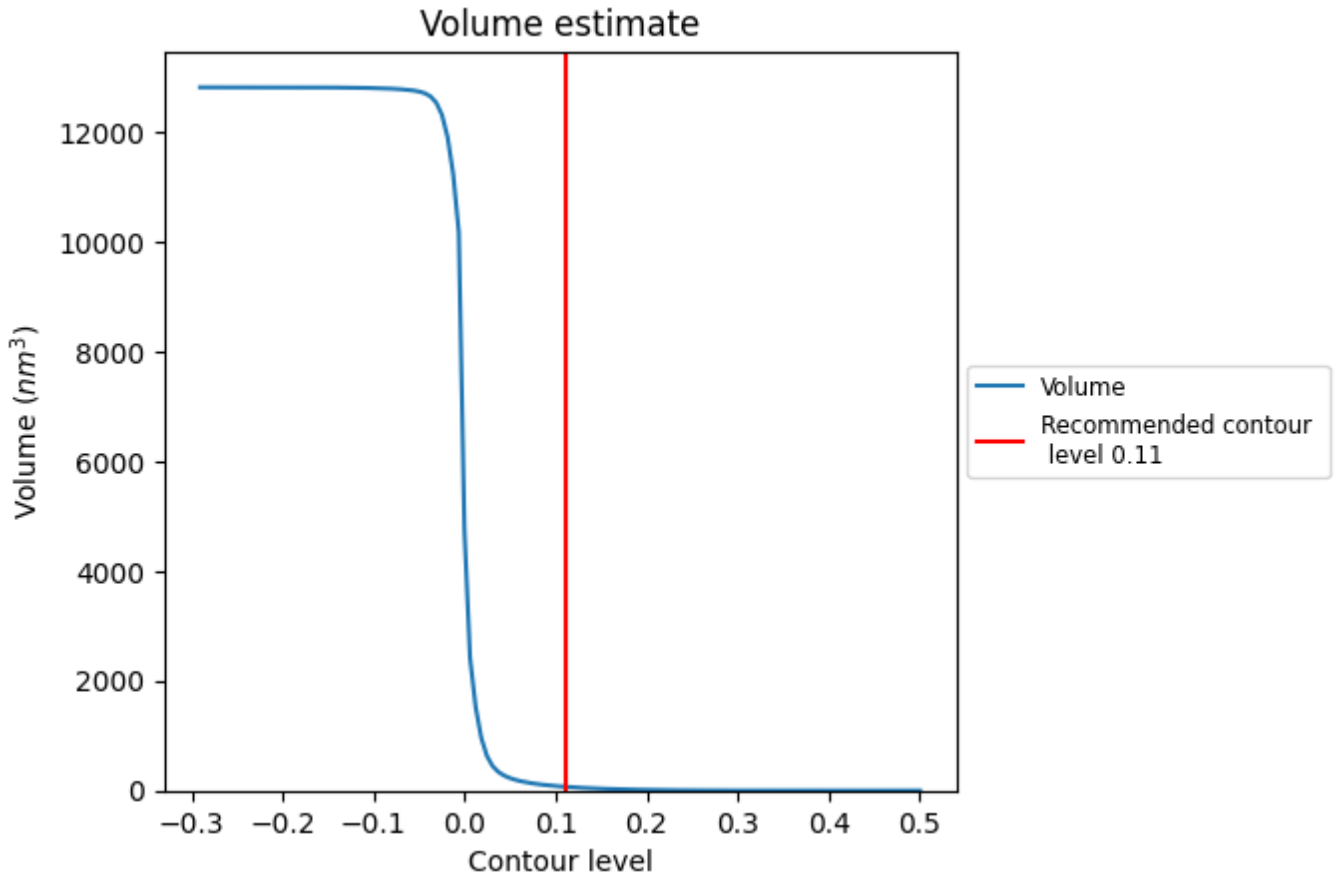
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

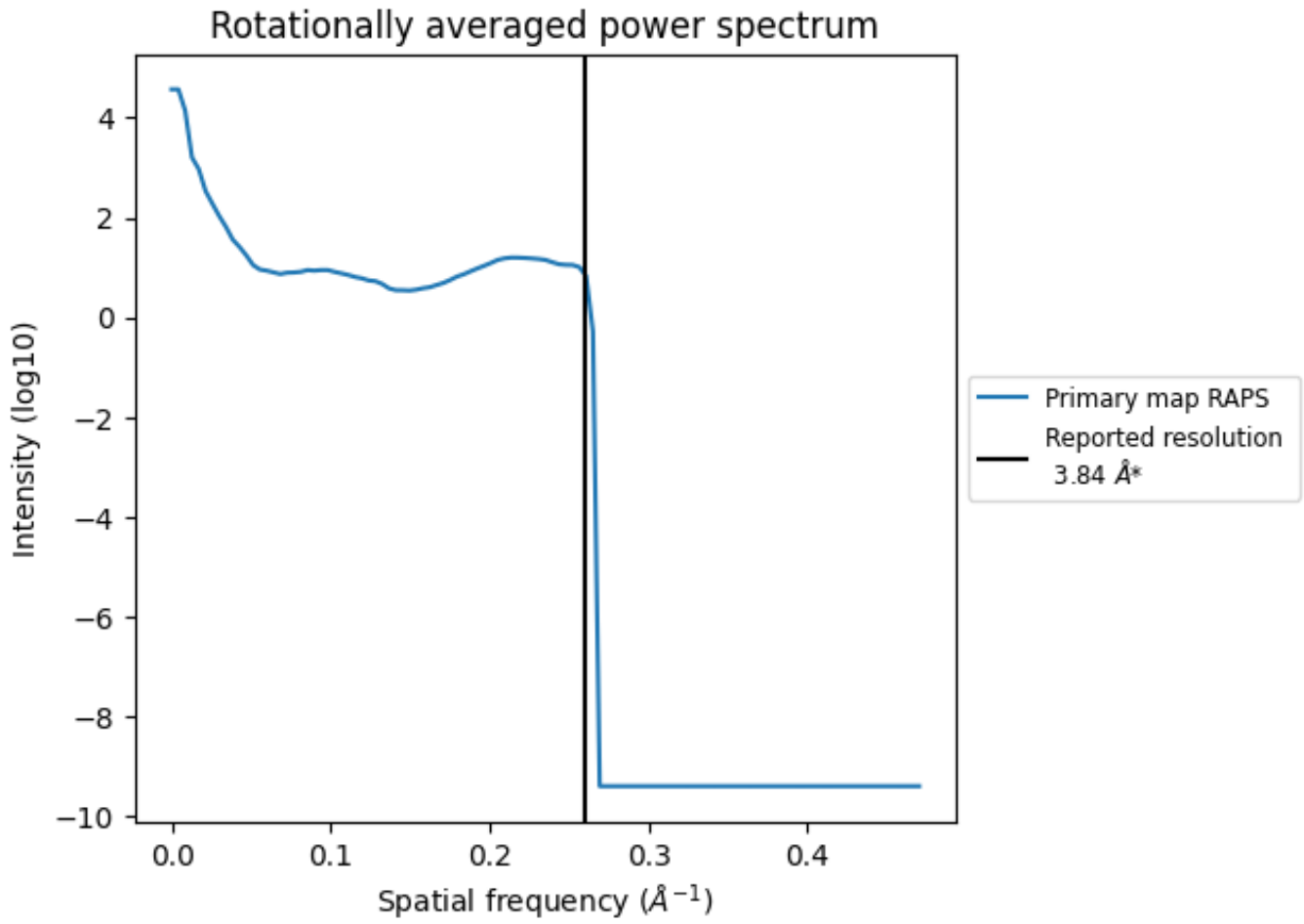
7.2 Volume estimate (i)



The volume at the recommended contour level is 69 nm^3; this corresponds to an approximate mass of 63 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 0.260 Å^{-1}

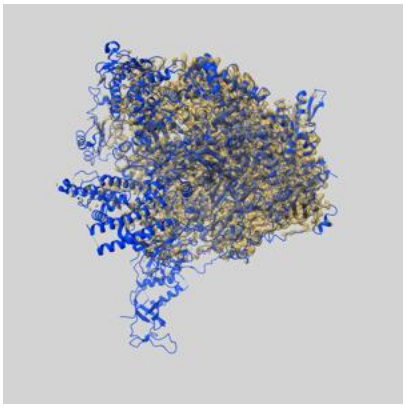
8 Fourier-Shell correlation (i)

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

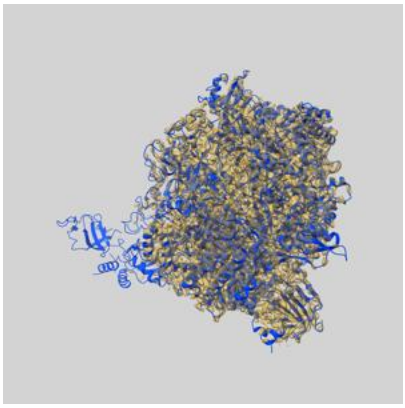
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-11840 and PDB model 7AOC. Per-residue inclusion information can be found in section 3 on page 7.

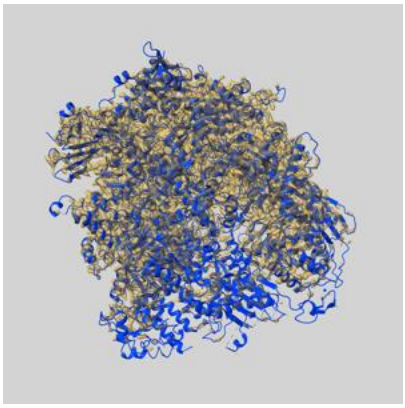
9.1 Map-model overlay



X



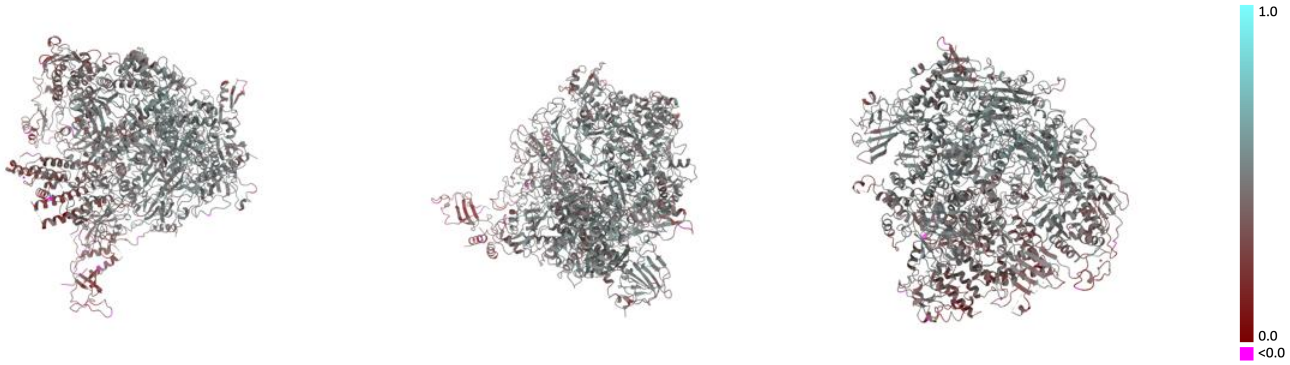
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.11 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.

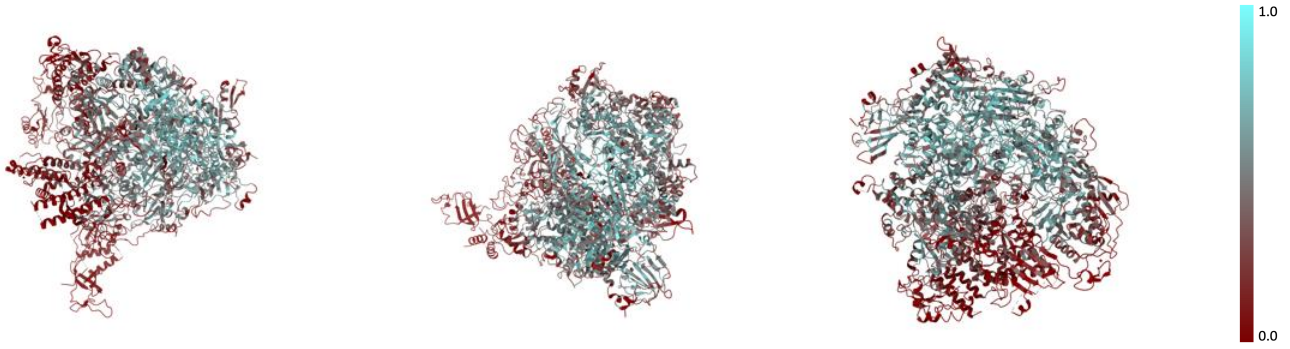
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

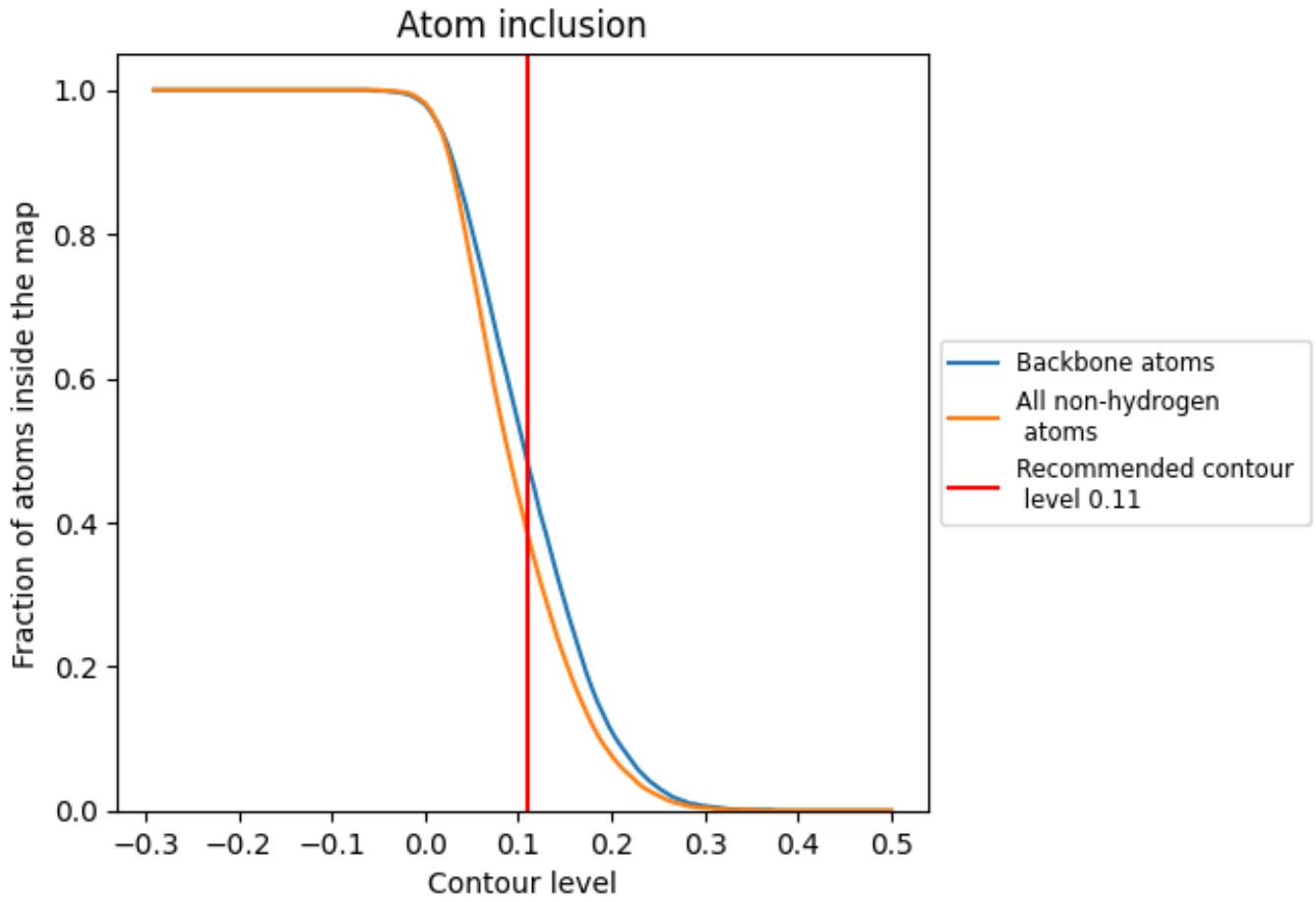
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.11).

9.4 Atom inclusion (i)



At the recommended contour level, 48% of all backbone atoms, 38% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3830	0.4490
A	0.3510	0.4410
B	0.4770	0.4760
C	0.4280	0.4710
D	0.0000	0.2440
E	0.2120	0.4140
F	0.4690	0.4850
G	0.0660	0.3150
H	0.4210	0.4760
I	0.0280	0.3530
J	0.5830	0.5020
K	0.5320	0.4940
L	0.4420	0.4940

