wwPDB EM Validation Summary Report (i)

Mar 19, 2024 – 08:45 PM JST

PDB ID	:	6JNX
EMDB ID	:	EMD-9852
Title	:	Cryo-EM structure of a Q-engaged arrested complex
Authors	:	Feng, Y.; Shi, J.
Deposited on	:	2019-03-18
Resolution	:	4.08 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 (i) 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 (i)) were used in the production of this report:

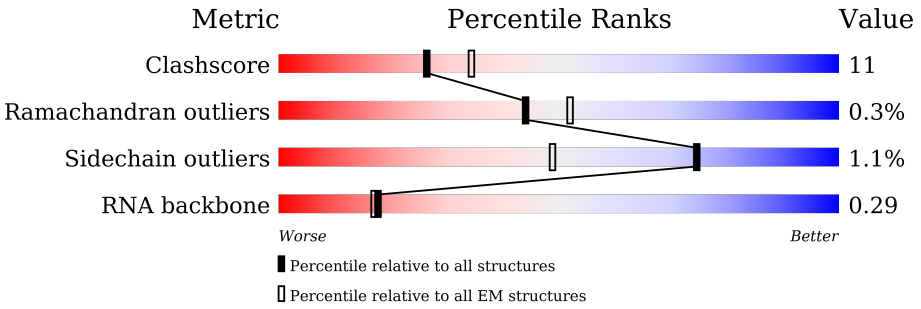
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.08 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 <=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	329	5%, 53%, 13%, 33%
1	B	329	15%, 51%, 15%, •, 34%
2	C	1342	17%, 77%, 23%, •
3	D	1407	21%, 69%, 25%, • 5%
4	E	91	16%, 68%, 19%, 13%
5	F	613	31%, 34%, 16%, 50%
6	N	63	8%, 71%, 29%

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Mol	Chain	Length	Quality of chain
7	R	18	22% 28% 56% 17%
8	T	63	13% 57% 43%
9	P	162	29% 69% 20% 9%
9	Q	162	40% 57% 19% 22%

2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 32639 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 alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	219	1686	1056	298	326	6	0	0
1	B	218	1681	1050	297	328	6	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	C	1340	10567	6631	1841	2052	43	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	1335	10388	6526	1854	1958	50	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	79	627	382	118	126	1	0	0

- Molecule 5 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	307	2513	1583	442	473	15	0	0

- Molecule 6 is a DNA chain called DNA (63-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	N	63	1303	620	247	373	63	0	0

- Molecule 7 is a RNA chain called RNA (5'-R(P*AP*UP*AP*AP*GP*GP*UP*GP*GP*GP*GP*UP*UP*AP*GP*UP*GP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	R	18	394	175	75	126	18	0	0

- Molecule 8 is a DNA chain called DNA (63-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	T	63	1281	614	223	381	63	0	0

- Molecule 9 is a protein called Antiterminator Q protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	P	147	1179	750	210	208	11	0	0
			Total	C	N	O	S		
9	Q	126	1017	651	179	179	8	0	0

- Molecule 10 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
10	D	1	1	1	0

- Molecule 11 is ZINC ION (three-letter code: ZN) (formula: Zn).

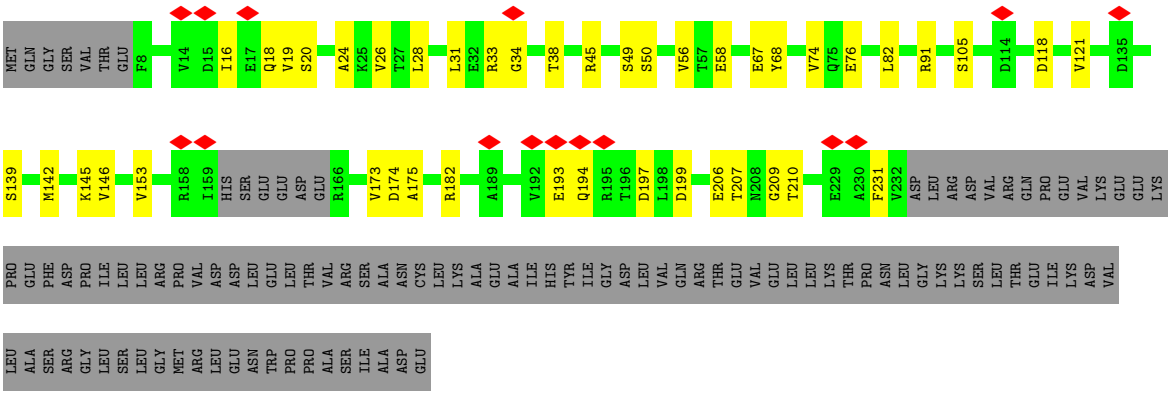
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
11	D	2	2	2	0

3 Residue-property plots (i)

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

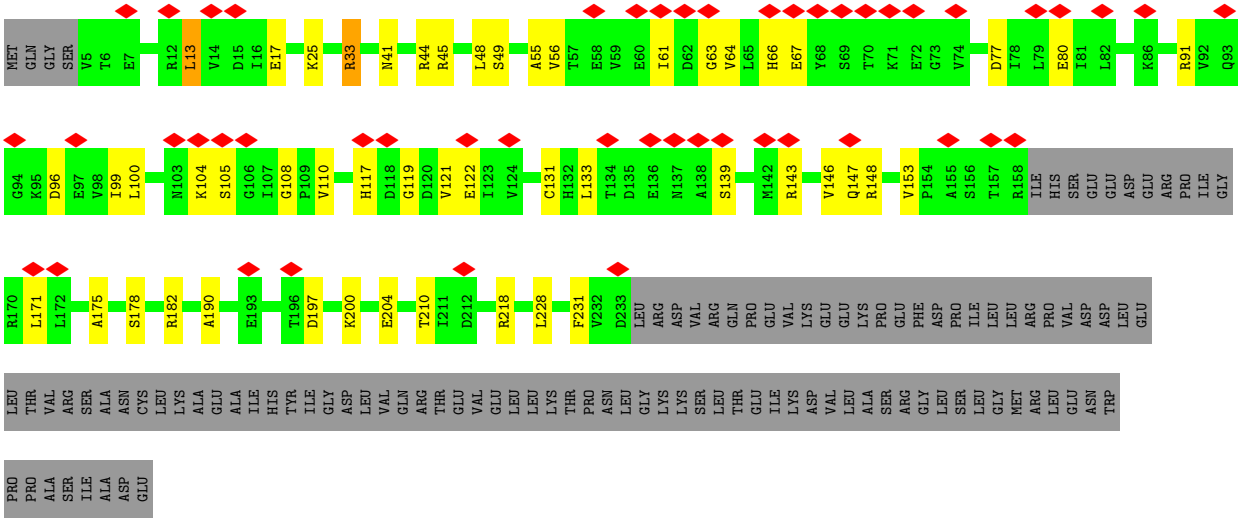
- Molecule 1: DNA-directed RNA polymerase subunit alpha

Chain A:



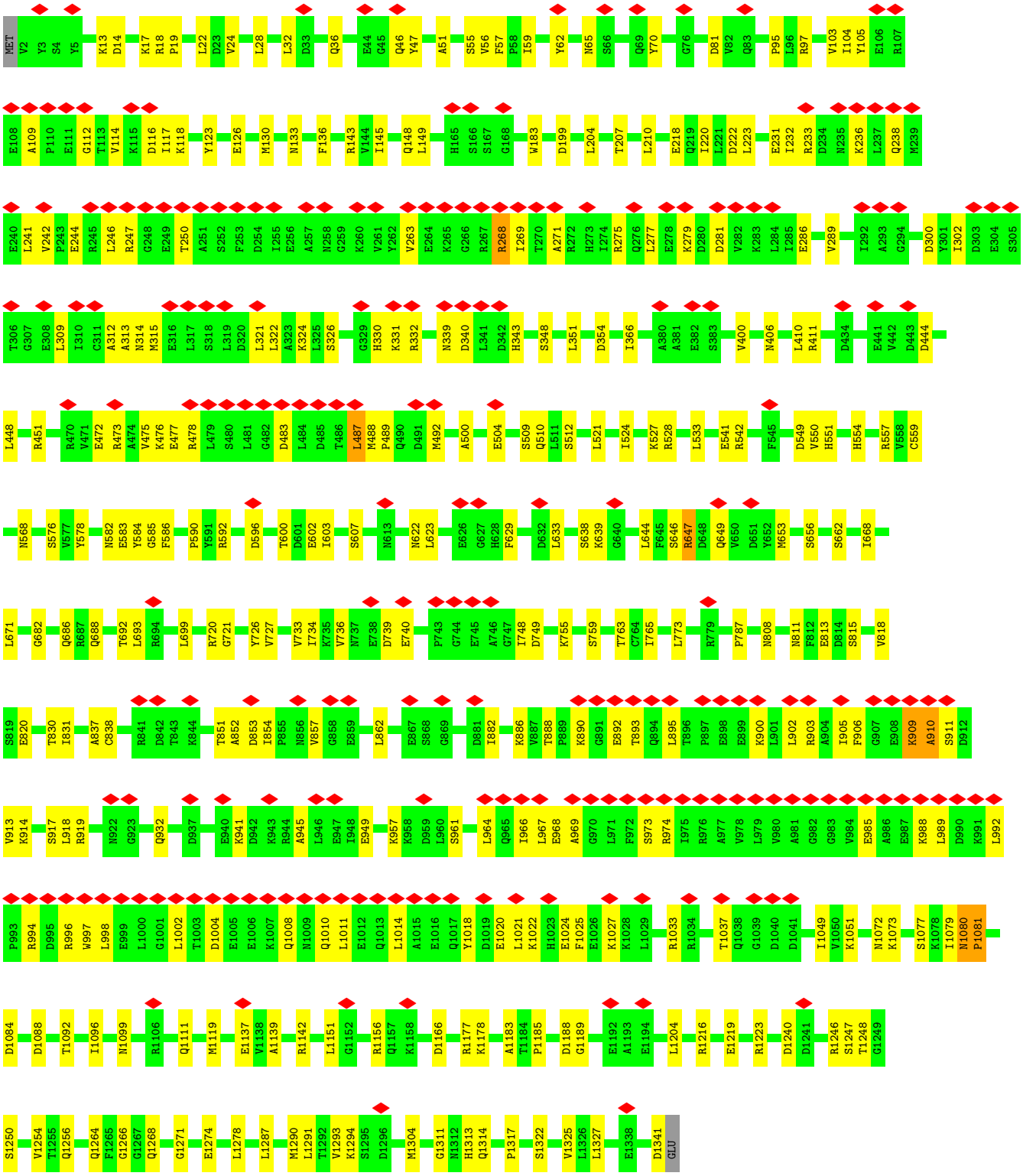
- Molecule 1: DNA-directed RNA polymerase subunit alpha

Chain B:



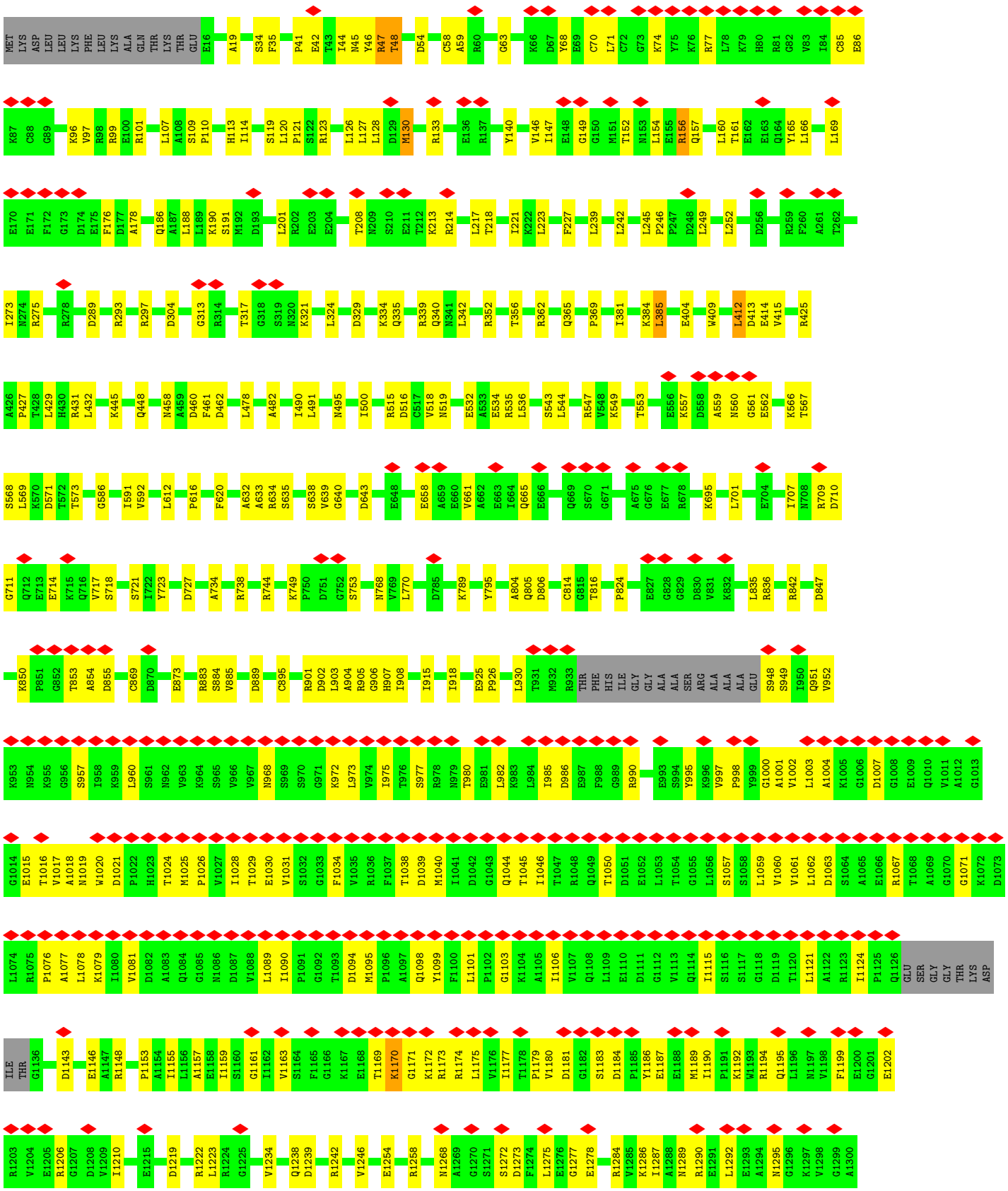
- Molecule 2: DNA-directed RNA polymerase subunit beta

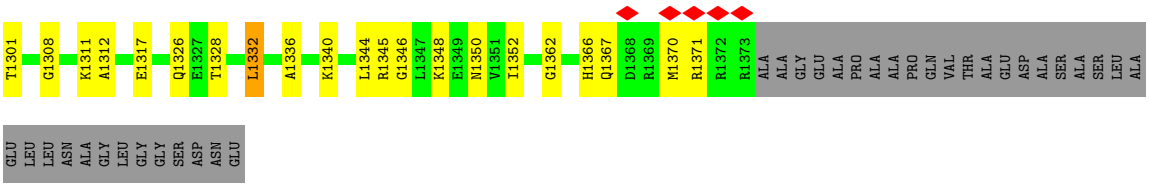
Chain C: 17% 77% 23%



- Molecule 3: DNA-directed RNA polymerase subunit beta'

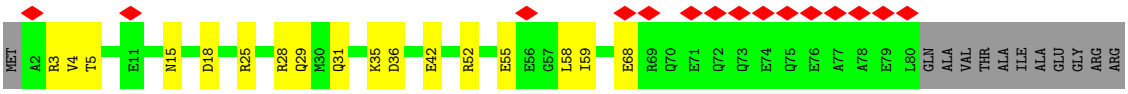
Chain D: 21% 69% 25% 5%


MET LYS ASP LEU LEU LYS PHE LEU LYS ALA GLN THR LYS THR GLU E16 A19 S34 F35 P41 E42 T43 I44 N45 Y46 R47 T48 D54 C58 A59 R60 G63 K66 D67 Y68 E69 C70 L71 C72 G73 K74 Y75 K76 R77 L78 K79 H80 R81 G82 V83 I84 C85 E86
K87 C88 G89 K96 V97 R98 R99 E100 R101 L107 A108 S109 P110 H113 I114 S119 L120 P121 S122 R123 L126 L127 L128 D129 M130 R133 E136 R137 Y140 V146 I147 E148 G149 G150 M151 T152 N153 L154 E155 R156 Q157 L160 T161 E162 E163 Q164 Y165 L166 L169
E170 E171 F172 G173 D174 E175 F176 D177 A178 Q186 A187 L188 L189 K190 S191 M192 D193 L201 R202 E203 E204 T208 N209 S210 E211 T212 K213 R214 L217 T218 I221 K222 L223 F227 L239 L242 L245 P246 P247 D248 L249 L252 D256 R259 F260 A261 T262
I273 N274 R275 R278 D289 R293 R297 D304 G313 R314 T317 G318 S319 N320 K321 L324 D329 K334 Q335 R339 Q340 N341 L342 R352 T356 R362 Q365 P369 I381 K384 L385 E404 W409 L412 D413 E414 V415 R425
A426 P427 T428 L429 H430 R431 L432 K445 Q448 N458 A459 D460 F461 D462 L478 A482 I490 L491 N495 I500 R515 D516 C517 V518 N519 E532 A533 E534 R535 L536 S543 L544 R547 V548 K549 T553 E556 K557 D558 A559 N560 G561 E562 K566 T567
S568 L569 K570 D571 T572 T573 G586 I591 V592 L612 P616 F620 A632 A633 R634 S635 S638 V639 G640 D643 E648 E658 A659 E660 V661 A662 E663 I664 Q665 E666 Q669 S670 G671 A675 G676 E677 R678 K695 L701 E704 I707 N708 R709 D710
G711 Q712 E713 E714 K715 Q716 V717 S718 S721 I722 Y723 D727 A734 R738 R744 K749 P750 D751 G752 S753 N768 V769 L770 D785 K789 Y795 A804 Q805 D806 C814 G815 T816 P824 E827 G828 G829 D830 V831 K832 L835 R836 R842 D847
K850 P851 G852 T853 A854 D855 C869 D870 E873 R883 S884 V885 D889 C895 R901 D902 L903 A904 R905 G906 H907 I908 I915 I918 E925 P926 L930 T931 M932 R933 THR PHE HIS ILE GLY GLY ALA ALA SER ARG ALA ALA ALA GLU S948 S949 I950 Q951 V952
K953 N954 K955 G956 S957 I958 K959 L960 S961 N962 V963 K964 S965 V966 V967 N968 S969 S970 G971 K972 L973 V974 I975 T976 S977 R978 N979 T980 E981 L982 K983 L984 I985 D986 E987 F988 G989 R990 E993 S994 Y995 K996 V997 P998 Y999 G1000 A1001 V1002 L1003 A1004 K1005 G1006 D1007 G1008 E1009 Q1010 V1011 A1012 G1013
G1014 E1015 T1016 V1017 A1018 N1019 W1020 D1021 P1022 H1023 T1024 M1025 P1026 V1027 I1028 T1029 E1030 V1031 S1032 G1033 F1034 V1035 R1036 F1037 T1038 D1039 M1040 I1041 D1042 G1043 Q1044 T1045 I1046 T1047 R1048 Q1049 T1050 D1051 E1052 L1053 T1054 G1055 L1056 S1057 S1058 L1059 V1060 V1061 L1062 D1063 S1064 A1065 E1066 R1067 T1068 A1069 G1070 G1071 K1072 D1073
L1074 R1075 P1076 A1077 L1078 K1079 I1080 V1081 D1082 A1083 Q1084 G1085 N1086 D1087 V1088 L1089 I1090 P1091 G1092 T1093 D1094 M1095 P1096 A1097 Q1098 Y1099 F1100 L1101 P1102 G1103 K1104 A1105 I1106 V1107 Q1108 L1109 E1110 D1111 G1112 V1113 Q1114 I1115 S1116 S1117 G1118 D1119 T1120 L1121 A1122 R1123 I1124 P1125 Q1126 GLU SER GLY GLY THR LYS ASP
ILE THR G1136 D1143 E1146 A1147 R1148 P1153 A1154 I1155 L1156 A1157 E1158 I1159 S1160 G1161 I1162 V1163 S1164 F1165 G1166 K1167 E1168 T1169 K1170 G1171 K1172 R1173 R1174 L1175 V1176 I1177 T1178 P1179 V1180 D1181 G1182 S1183 D1184 P1185 Y1186 E1187 E1188 M1189 I1190 P1191 K1192 W1193 R1194 Q1195 L1196 N1197 V1198 F1199 E1200 G1201 E1202
R1203 V1204 E1205 R1206 G1207 D1208 V1209 I1210 E1215 D1219 R1222 L1223 R1224 G1225 V1234 Q1238 D1239 R1242 V1246 E1254 R1258 N1268 A1269 G1270 S1271 S1272 D1273 F1274 L1275 E1276 G1277 E1278 R1284 V1285 K1286 I1287 A1288 N1289 R1290 E1291 L1292 E1293 A1294 N1295 G1296 K1297 V1298 G1299 A1300



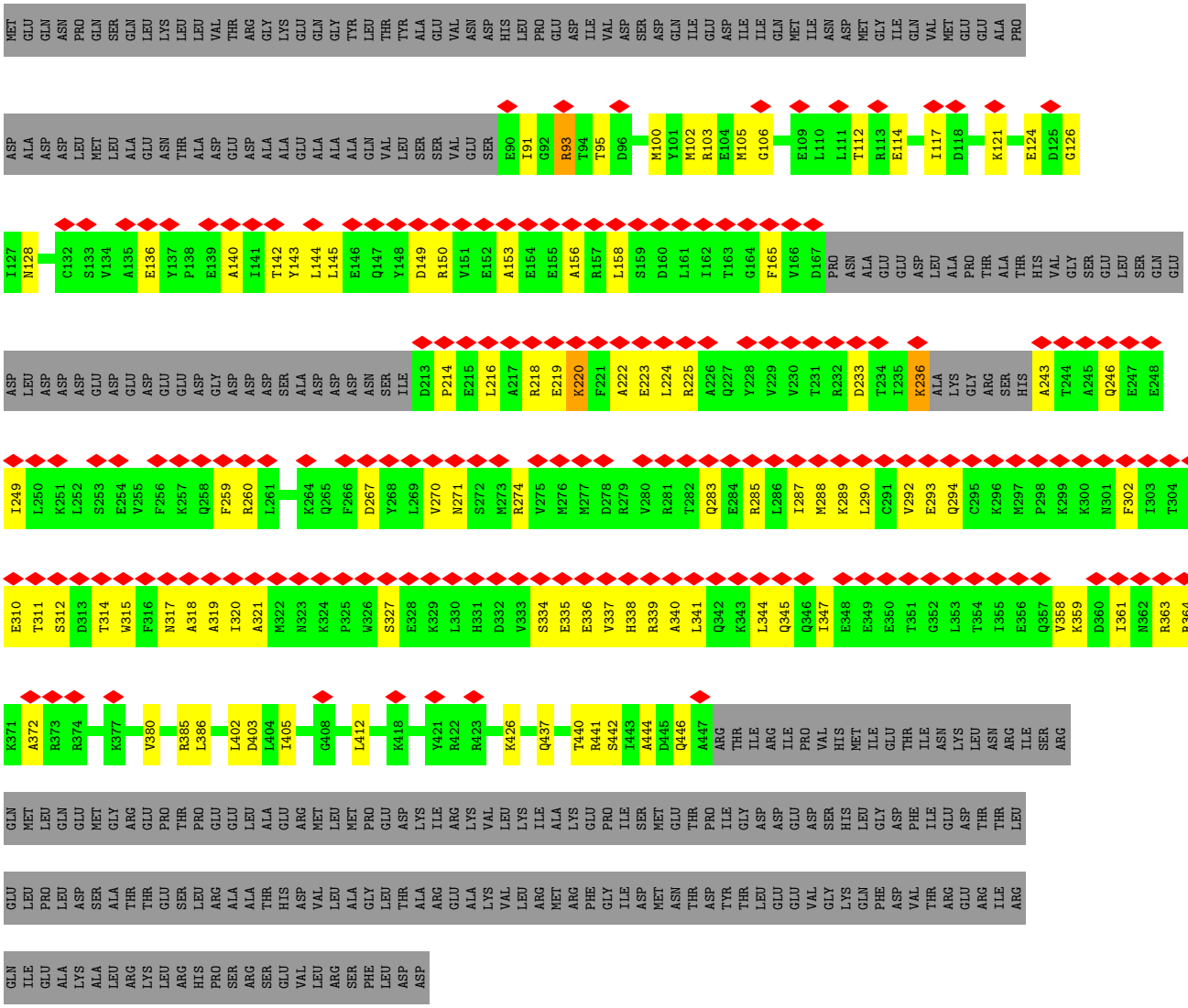
• Molecule 4: DNA-directed RNA polymerase subunit omega

Chain E:



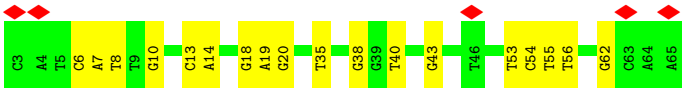
• Molecule 5: RNA polymerase sigma factor RpoD

Chain F:



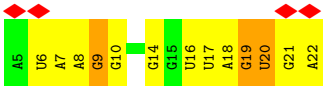
• Molecule 6: DNA (63-MER)

Chain N: 8% 71% 29%



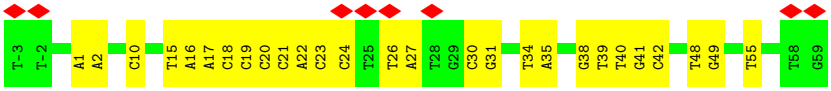
• Molecule 7: RNA (5'-R(P*AP*UP*AP*AP*GP*GP*UP*GP*GP*GP*GP*UP*UP*AP*GP*UP*GP*A)-3')

Chain R: 22% 28% 56% 17%



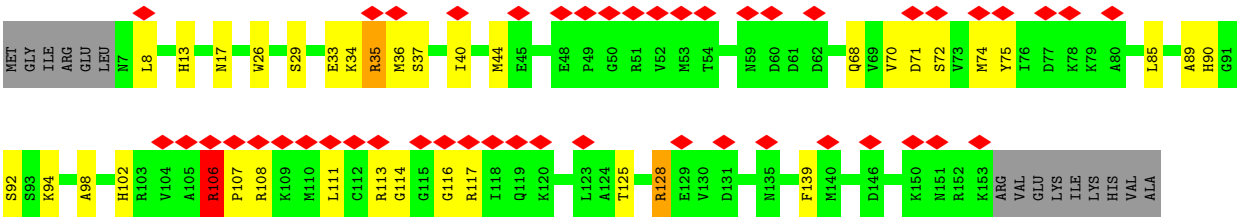
• Molecule 8: DNA (63-MER)

Chain T: 13% 57% 43%



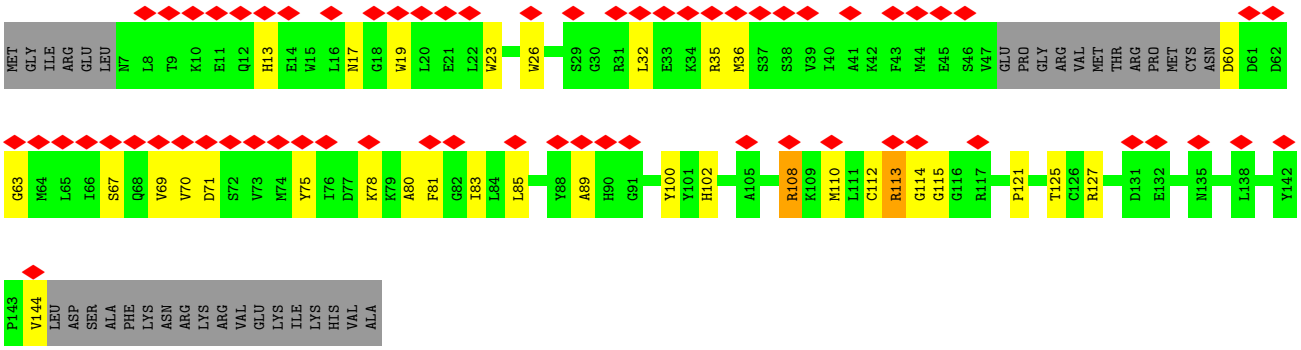
• Molecule 9: Antiterminator Q protein

Chain P: 29% 69% 20% 9%



• Molecule 9: Antiterminator Q protein

Chain Q: 40% 57% 19% 22%



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	64497	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 ($e^-/Å^2$)	56	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.151	Depositor
Minimum map value	-0.093	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.026	Depositor
Map size (Å)	261.4, 261.4, 261.4	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3069999, 1.3069999, 1.3069999	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0/1706	0.68	0/2312
1	B	0.49	0/1700	0.67	0/2304
2	C	0.60	0/10736	0.66	0/14487
3	D	0.56	0/10545	0.69	0/14236
4	E	0.46	0/629	0.65	0/847
5	F	0.45	0/2547	0.59	0/3421
6	N	1.43	0/1465	1.08	0/2261
7	R	1.18	0/442	1.19	0/689
8	T	1.46	0/1433	1.09	0/2207
9	P	0.54	0/1206	0.62	0/1623
9	Q	0.44	0/1040	0.59	0/1399
All	All	0.69	0/33449	0.73	0/45786

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	1686	0	1726	24	0
1	B	1681	0	1714	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	10567	0	10585	235	0
3	D	10388	0	10611	271	0
4	E	627	0	634	14	0
5	F	2513	0	2546	73	0
6	N	1303	0	710	18	0
7	R	394	0	194	7	0
8	T	1281	0	714	23	0
9	P	1179	0	1180	35	0
9	Q	1017	0	1017	34	0
10	D	1	0	0	0	0
11	D	2	0	0	0	0
All	All	32639	0	31631	707	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 11.

The worst 5 of 707 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:890:LYS:CD	2:C:914:LYS:HE3	1.58	1.30
2:C:890:LYS:HD2	2:C:914:LYS:CE	1.61	1.28
3:D:1171:GLY:O	3:D:1172:LYS:HD3	1.05	1.20
3:D:146:VAL:HG12	3:D:178:ALA:CB	1.79	1.11
8:T:26:DT:H2"	8:T:27:DA:OP1	1.45	1.11

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	215/329 (65%)	196 (91%)	19 (9%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	214/329 (65%)	198 (92%)	16 (8%)	0	100	100
2	C	1338/1342 (100%)	1224 (92%)	111 (8%)	3 (0%)	47	80
3	D	1329/1407 (94%)	1209 (91%)	114 (9%)	6 (0%)	29	67
4	E	77/91 (85%)	72 (94%)	5 (6%)	0	100	100
5	F	301/613 (49%)	293 (97%)	8 (3%)	0	100	100
9	P	145/162 (90%)	133 (92%)	9 (6%)	3 (2%)	7	38
9	Q	122/162 (75%)	117 (96%)	5 (4%)	0	100	100
All	All	3741/4435 (84%)	3442 (92%)	287 (8%)	12 (0%)	44	75

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	910	ALA
3	D	1345	ARG
3	D	1169	THR
9	P	107	PRO
2	C	1081	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	186/286 (65%)	186 (100%)	0	100	100
1	B	186/286 (65%)	184 (99%)	2 (1%)	73	84
2	C	1155/1157 (100%)	1147 (99%)	8 (1%)	84	90
3	D	1120/1168 (96%)	1106 (99%)	14 (1%)	69	82
4	E	67/75 (89%)	67 (100%)	0	100	100
5	F	271/540 (50%)	268 (99%)	3 (1%)	73	84
9	P	126/140 (90%)	122 (97%)	4 (3%)	39	62
9	Q	108/140 (77%)	105 (97%)	3 (3%)	43	65
All	All	3219/3792 (85%)	3185 (99%)	34 (1%)	74	84

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	P	113	ARG
9	P	117	ARG
9	Q	108	ARG
3	D	156	ARG
3	D	130	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	805	GLN
3	D	1326	GLN
3	D	1295	ASN
4	E	15	ASN
2	C	1268	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
7	R	17/18 (94%)	9 (52%)	0

5 of 9 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	R	6	U
7	R	7	A
7	R	8	A
7	R	9	G
7	R	10	G

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 3 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.

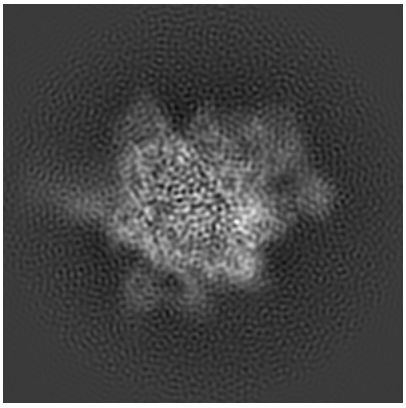
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-9852. These allow visual inspection of the internal detail of the map and identification of artifacts.

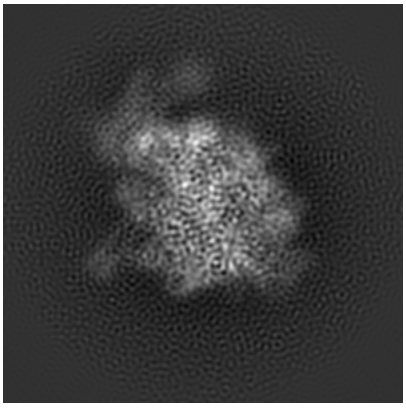
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

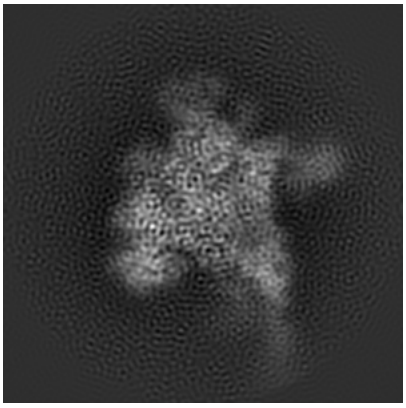
6.1.1 Primary map



X



Y

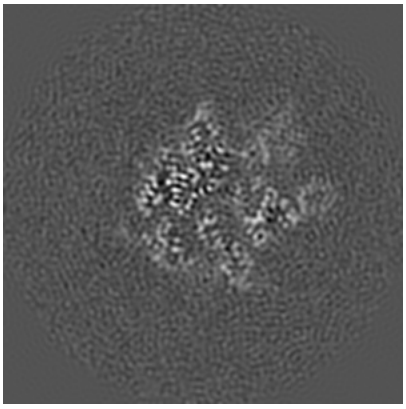


Z

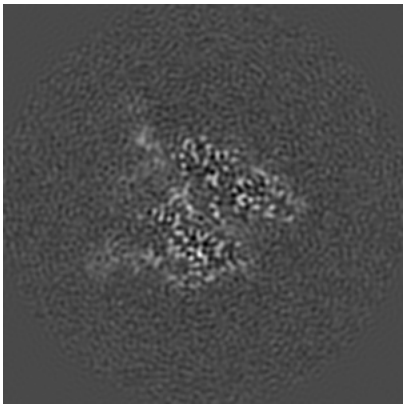
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

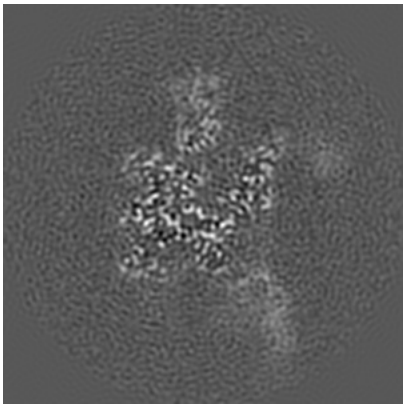
6.2.1 Primary map



X Index: 100



Y Index: 100

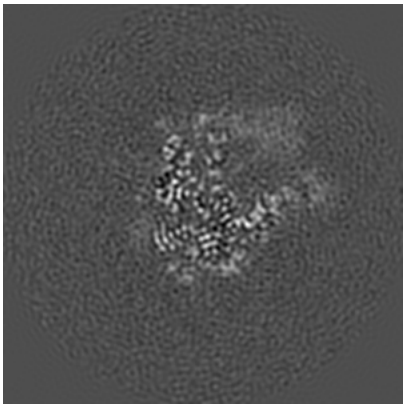


Z Index: 100

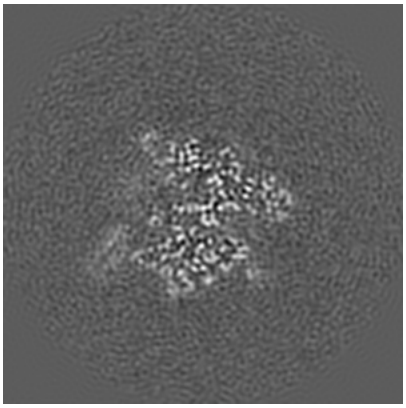
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

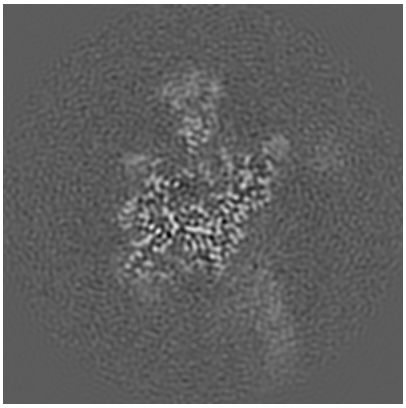
6.3.1 Primary map



X Index: 92



Y Index: 96

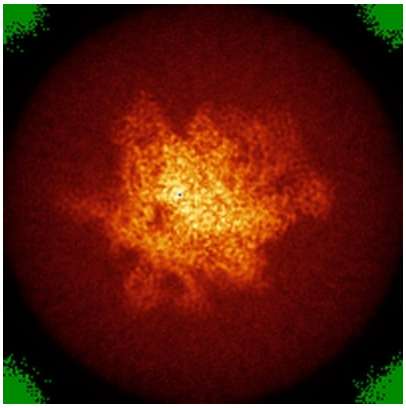


Z Index: 103

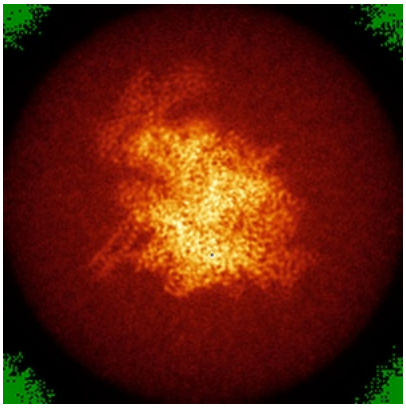
The images above show the largest variance slices of the map in three orthogonal directions.

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

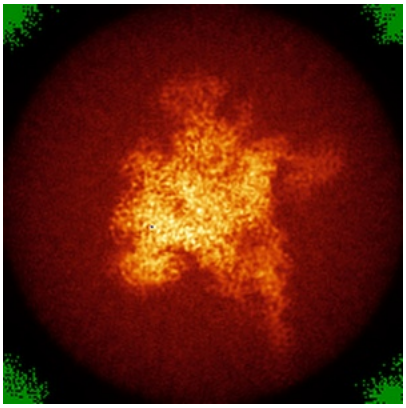
6.4.1 Primary map



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 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

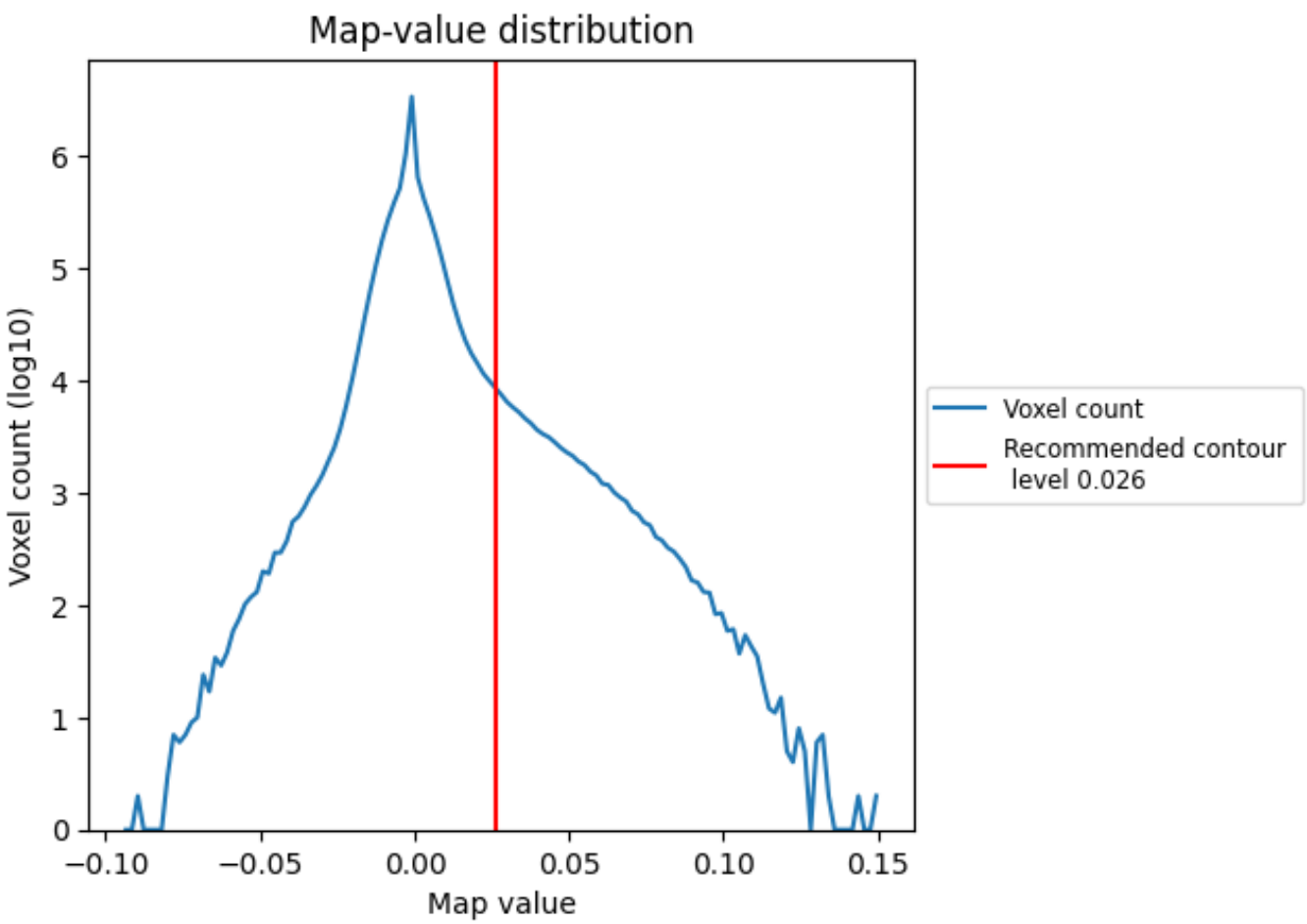
6.6 Mask visualisation (i)

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

7 Map analysis (i)

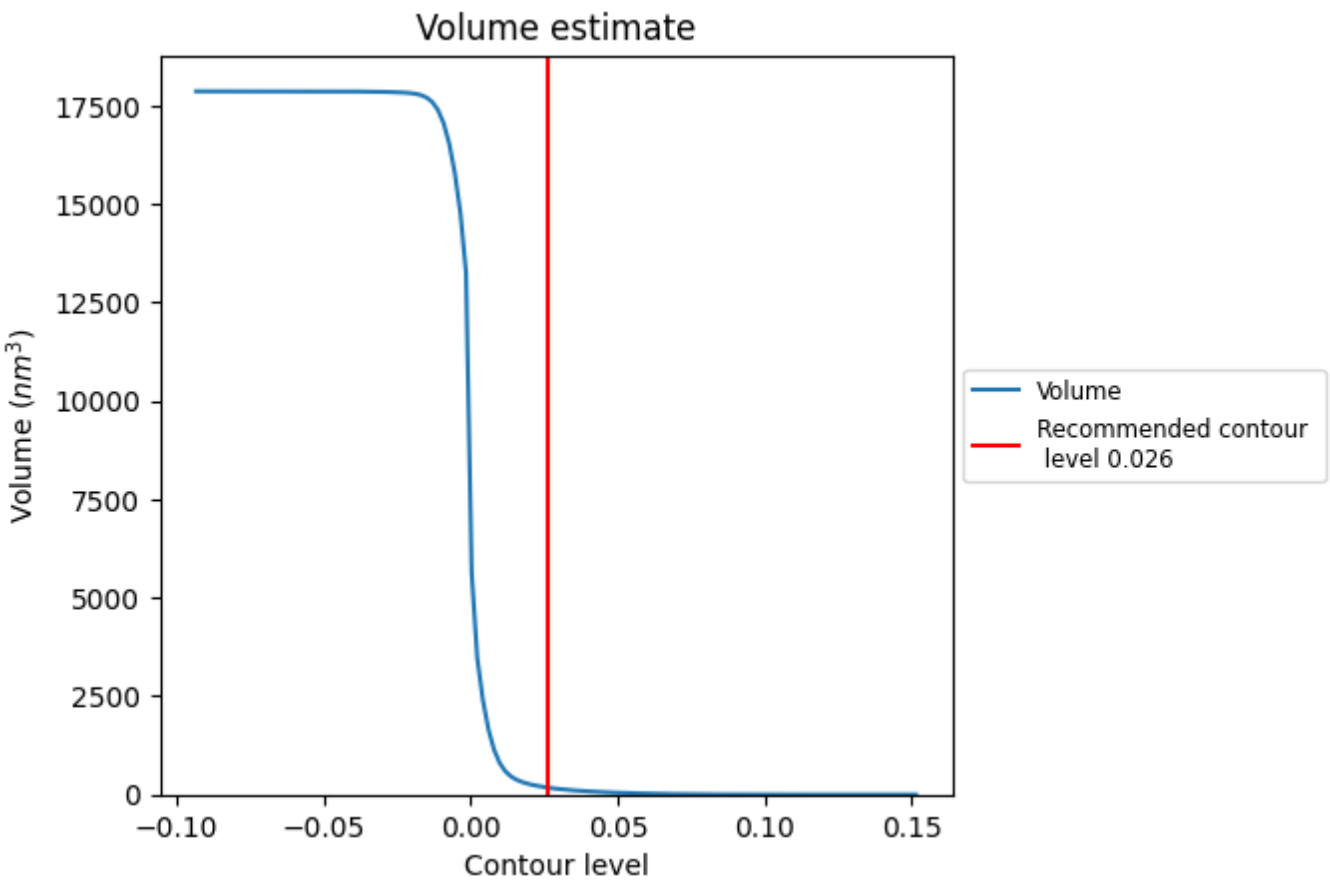
This section contains the results of statistical analysis of the map.

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.

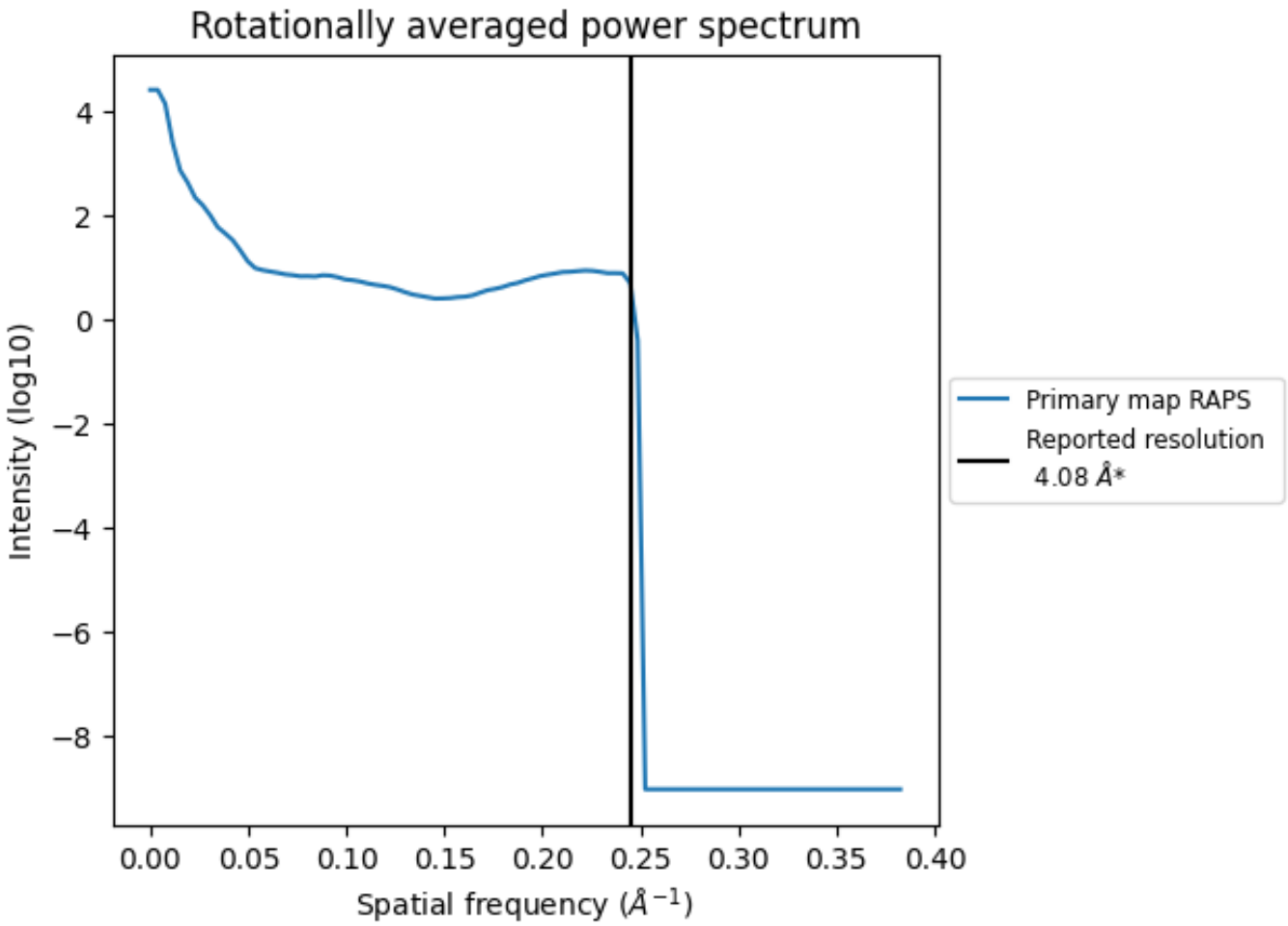
7.2 Volume estimate (i)



The volume at the recommended contour level is 179 nm^3; this corresponds to an approximate mass of 161 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 0.245 Å^{-1}

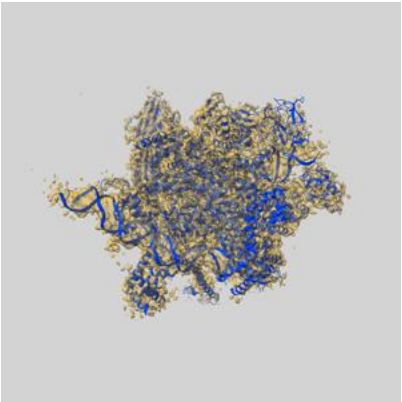
8 Fourier-Shell correlation (i)

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

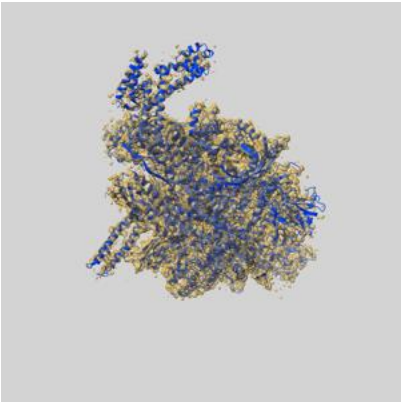
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-9852 and PDB model 6JNX. Per-residue inclusion information can be found in section 3 on page 6.

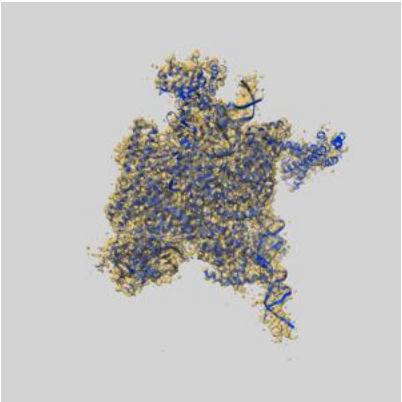
9.1 Map-model overlay (i)



X



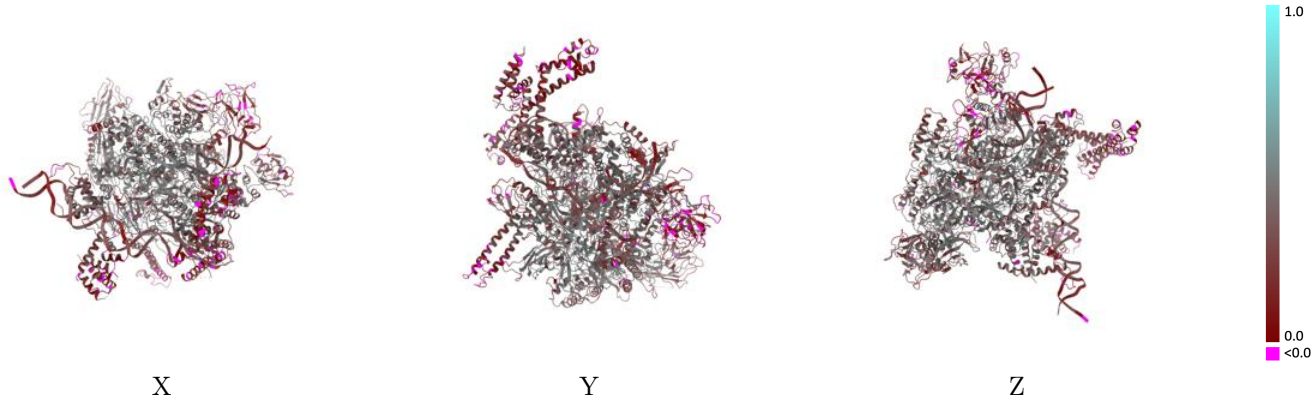
Y



Z

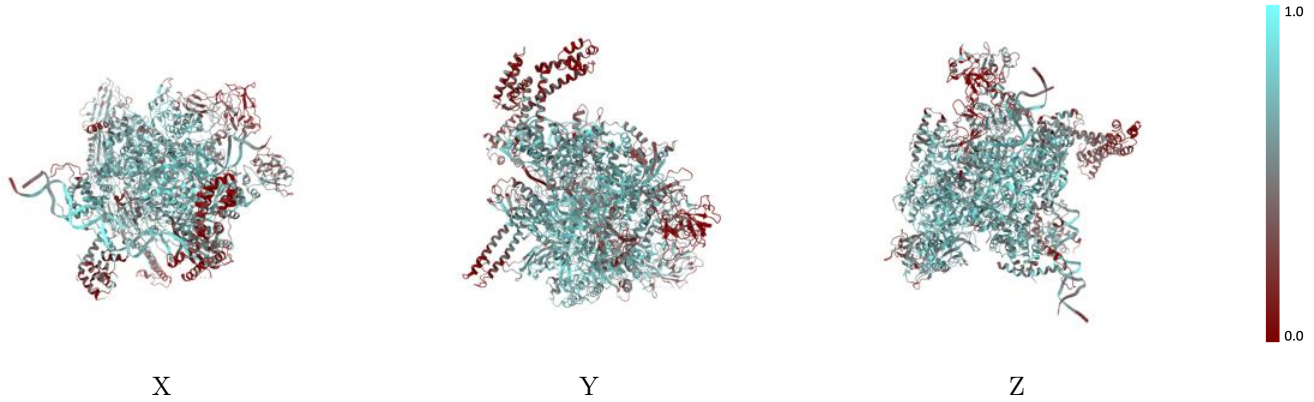
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



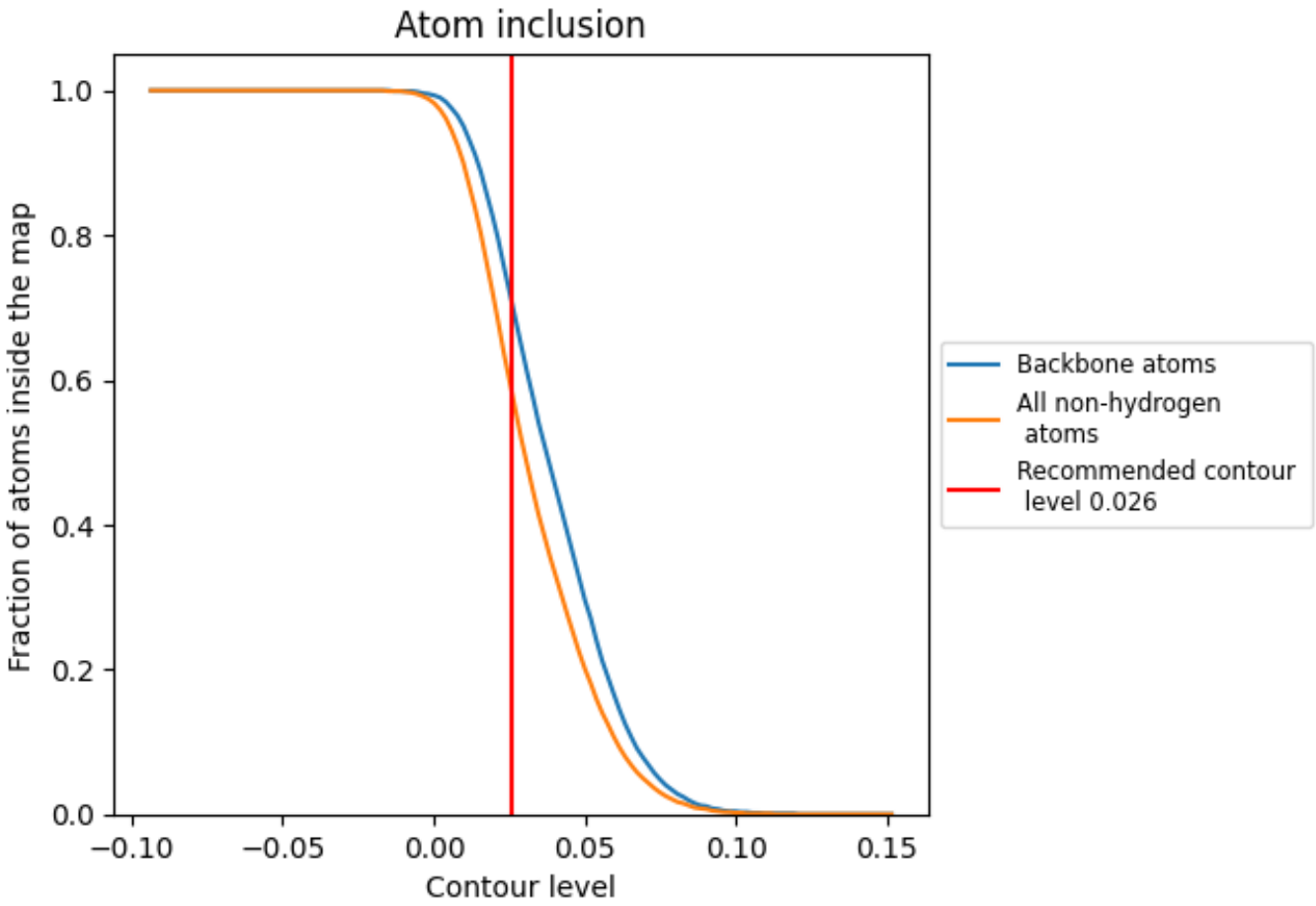
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.026).

9.4 Atom inclusion (i)



At the recommended contour level, 70% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5800	0.3500
A	0.6600	0.4130
B	0.5540	0.3490
C	0.6220	0.3800
D	0.5860	0.3650
E	0.5370	0.3550
F	0.3210	0.2220
N	0.6950	0.2920
P	0.5350	0.3160
Q	0.4080	0.2260
R	0.6240	0.3830
T	0.6710	0.3130