



## wwPDB EM Validation Summary Report ⓘ

Nov 15, 2022 – 01:12 AM 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

---

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

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

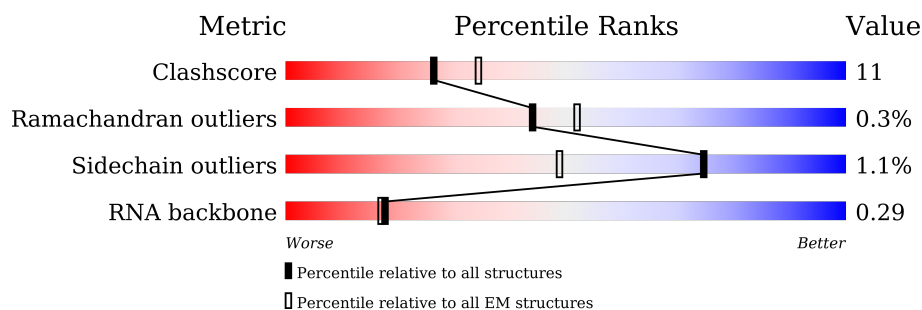
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	329	<div> <div>5%</div> <div>53%</div> <div>13%</div> <div>33%</div> </div>
1	B	329	<div> <div>15%</div> <div>51%</div> <div>15%</div> <div>34%</div> </div>
2	C	1342	<div> <div>17%</div> <div>77%</div> <div>23%</div> </div>
3	D	1407	<div> <div>21%</div> <div>69%</div> <div>25%</div> <div>5%</div> </div>
4	E	91	<div> <div>16%</div> <div>68%</div> <div>19%</div> <div>13%</div> </div>
5	F	613	<div> <div>31%</div> <div>34%</div> <div>16%</div> <div>50%</div> </div>
6	N	63	<div> <div>8%</div> <div>71%</div> <div>29%</div> </div>

Continued on next page...

Continued from previous page...

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

## 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
1	A	219	Total	C	N	O	S	0	0
			1686	1056	298	326	6		
1	B	218	Total	C	N	O	S	0	0
			1681	1050	297	328	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1340	Total	C	N	O	S	0	0
			10567	6631	1841	2052	43		

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

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

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

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

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

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

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

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

- 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
7	R	18	Total	C	N	O	P	0	0
			394	175	75	126	18		

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

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

- Molecule 9 is a protein called Antiterminator Q protein.

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

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

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

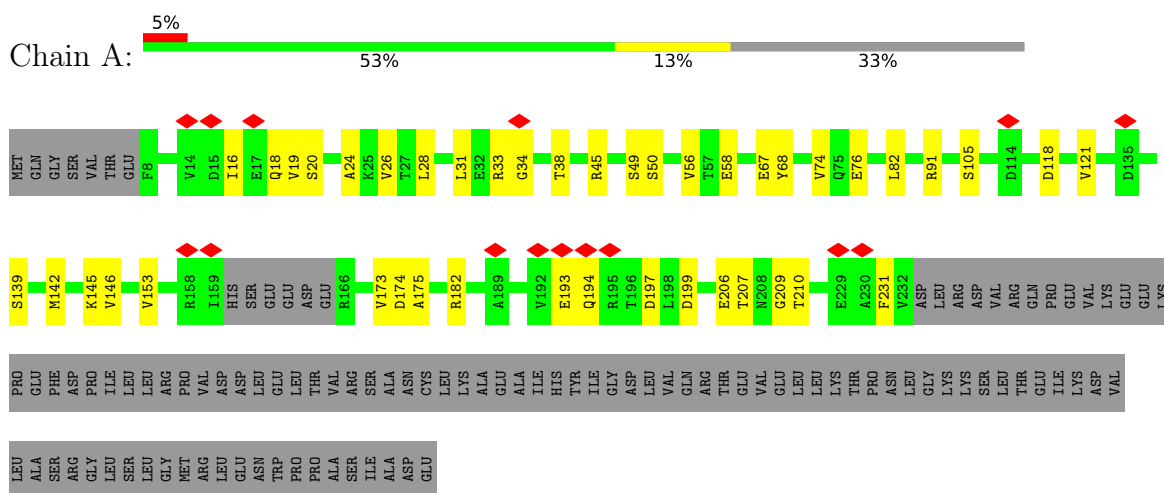
- Molecule 11 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

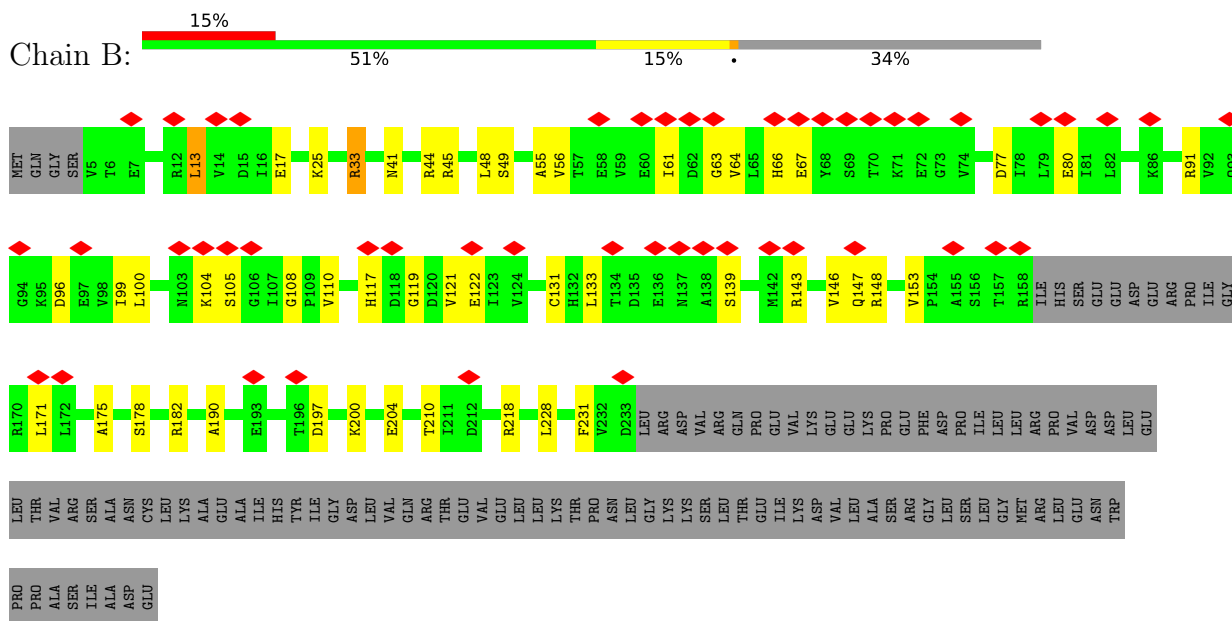
### 3 Residue-property plots [i](#)

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.

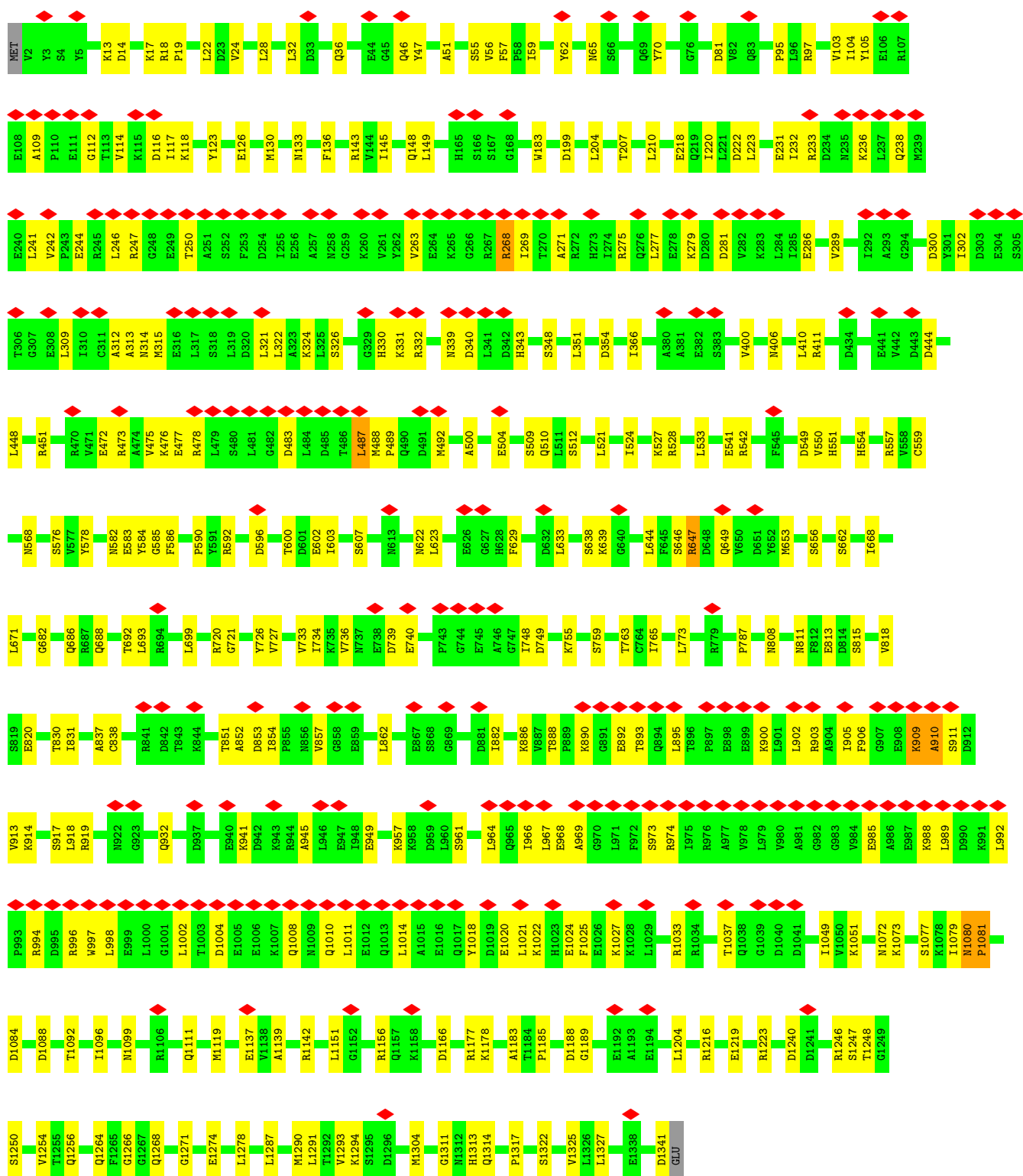
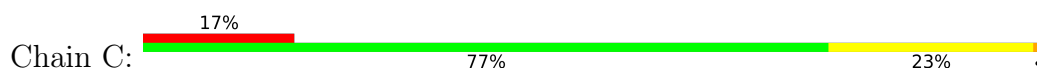
- Molecule 1: DNA-directed RNA polymerase subunit alpha



- Molecule 1: DNA-directed RNA polymerase subunit alpha



- Molecule 2: DNA-directed RNA polymerase subunit beta

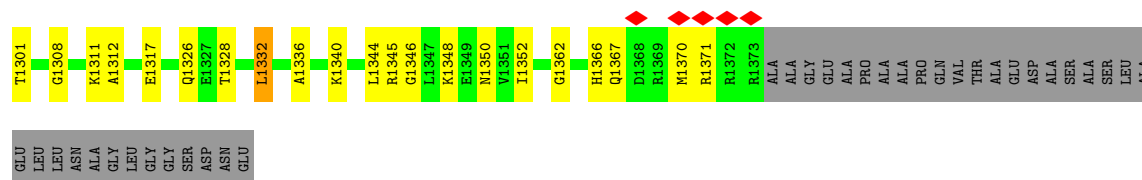


• Molecule 3: DNA-directed RNA polymerase subunit beta'



R1203	V1204	E1205	L1206	G1207	D1208	V1209	I1210	E1215	D1219	R1222	L1223	R1224	G1225	V1234	Q1238	D1239	R1242	V1246	E1254	R1258	A1269	G1270	S1271	S1272	L1275	F1274	L1276	G1277	E1278	R1284	V1285	K1286	I1287	A1288	N1289	R1290	L1291	L1292	E1293	A1294	N1295	G1296	K1297	V1298	G1299	A1300																																																																																																				
ILE	THR	G1136		D1143	E1146	A1147	R1148	P1153	A1154	I1155	A1156	A1157	E1158	I1159	S1160	G1161	I1162	V1163	S1164	F1165	G1166	K1167	E1168	T1169	O1170	K1170	G1171	K1172	R1173	R1174	L1175	V1176	I1177	T1178	P1179	V1180	D1181	G1182	S1183	D1184	P1185	Y1186	E1187	E1188	M1189	I1190	P1191	K1192	M1193	R1194	Q1195	L1196	N1197	V1198	F1199	G1201	E1202																																																																																									
L1074	R1075	P1076	A1077	L1078	N1079	I1080	V1081	D1082	A1083	Q1084	G1085	M1086	D1087	V1088	L1089	I1090	P1091	G1092	T1093	D1094	M1095	P1096	A1097	Q1098	Y1099	F1100	L1101	P1102	G1103	K1104	A1105	I1106	V1107	Q1108	L1109	D1110	E1111	G1112	G1113	D1114	S1115	P1116	S1117	G1118	D1119	T1120	L1121	A1122	R1123	T1124	P1125	Q1126	GLU	SER	GLY	GLY	THR	LYS	ASP																																																																																							
G1014	E1015	T1016	V1017	A1018	N1019	V1020	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																																																																																							
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	E981	L982	K983	L984	I985	D986	E987	F988	G989	R990	E993	S994	I995	K996	V997	P998	G999	G1000	A1001	V1002	L1003	A1004	K1005	G1006	D1007	G1008	E1009	Q1010	V1011	A1012	G1013																																																																																									
G711	Q712	E713	E714	K715	W716	V717	S718	S721	I722	Y723	D727	A734	R738	R744	K749	P750	D751	G752	S753	N768	W769	L770	D785	K789	Y795	A804	D805	D806	C814	G815	T816	P824	E827	G828	G829	D830	V831	K832	L835	R836	R842	D847																																																																																																								
S868	L869	E870	D871	T872	H873	T874	D875	G876	S877	F878	A879	G880	S881	S882	S883	S884	S885	C886	D887	E888	E889	C890	R891	D892	L893	A894	R895	G896	H897	I898	I899	T900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	G1000	A1001	S949	V1002	L1003	A1004	K1005	G1006	D1007	G1008	E1009	Q1010	V1011	A1012	G1013
A426	P427	T428	L429	H430	R431	L432	K445	Q448	M458	A459	D460	F461	D462	L478	A482	I490	L491	M495	I500	R515	D516	G517	V518	N519	E532	A533	E534	R535	L536	S543	L544	R547	V548	K549	T553	E556	K557	D558	A559	N560	G561	E562	K566	T567																																																																																																						
L273	R274	R275	R276	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																																																																																																													
E170	E171	F172	G173	D174	E175	F176	D177	A178	Q186	A187	L188	D189	K190	S191	D193	L201	R202	E203	E204	T208	N209	S210	E211	T212	K213	R214	L217	T218	K222	L223	F227	L239	L242	L245	P246	P247	D248	L249	L252	D256	R259	F260	A261	T262																																																																																																						
K37	C38	G39	K36	V37	R38	R39	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	N153	L154	E155	R156	Q157	L160	T161	E162	E163	Q164	Y165	L166	L169																																																																																																			
MET	LYS	ASP	LEU	LEU	LYS	PHE	LEU	LYS	ALA	GLN	THR	LYS	THR	E16	A19	S34	F35	P41	E42	T43	I44	M45	Y46	R47	T48	D54	C58	A59	R60	G63	K66	D67	Y68	E69	C70	L71	C72	G73	K74	Y75	R76	R77	L78	K79	H80	R81	G82	V83	I84	C85	E86																																																																																															

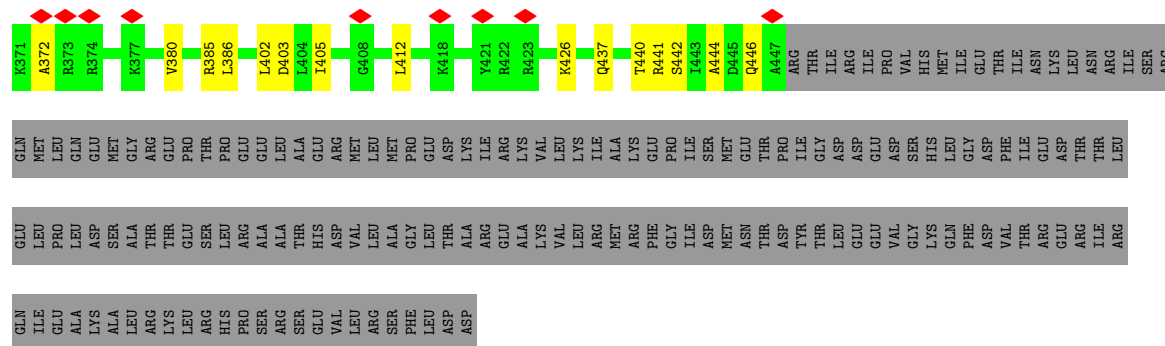
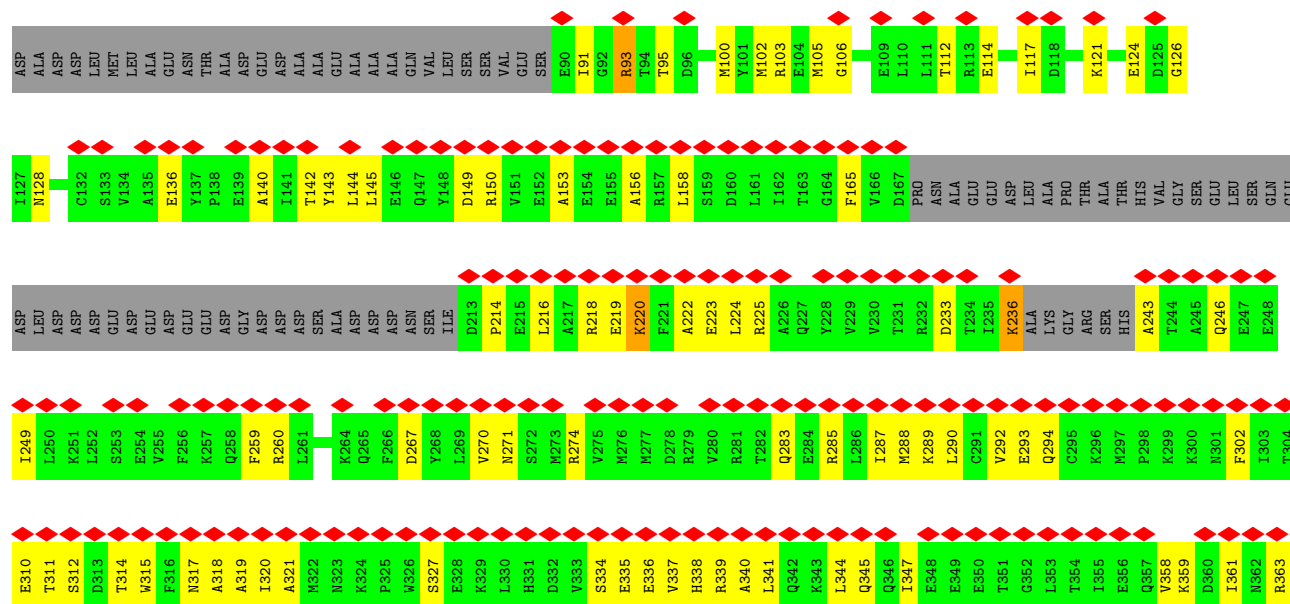
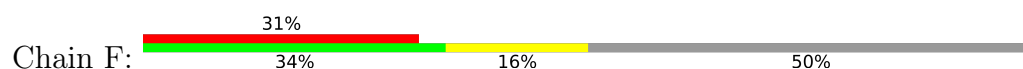




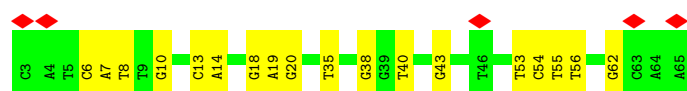
• Molecule 4: DNA-directed RNA polymerase subunit omega



• Molecule 5: RNA polymerase sigma factor RpoD



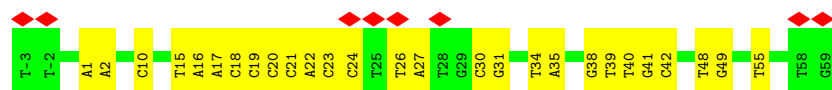
• Molecule 6: DNA (63-MER)



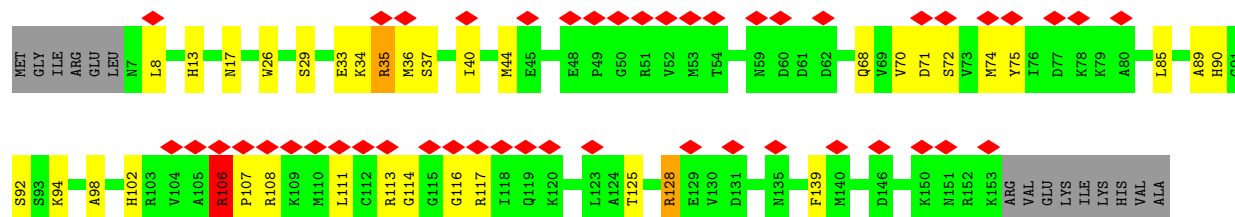
- Molecule 7: RNA (5'-R(P\*AP\*UP\*AP\*AP\*GP\*GP\*UP\*GP\*GP\*GP\*GP\*UP\*UP\*AP\*GP\*UP\*GP\*A)-3')



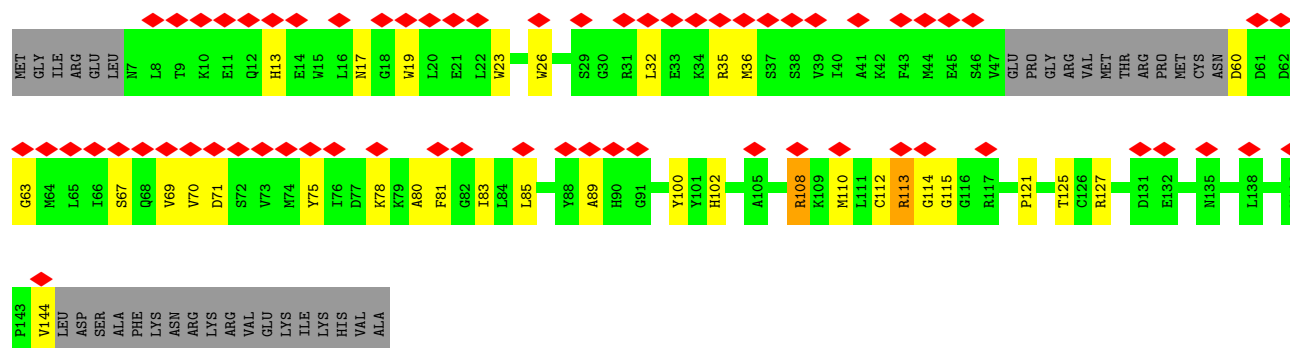
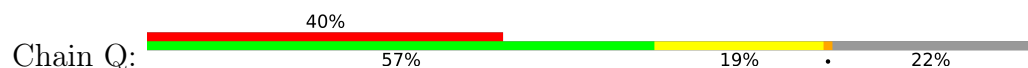
- Molecule 8: DNA (63-MER)



- Molecule 9: Antiterminator Q protein



- Molecule 9: Antiterminator Q protein



## 4 Experimental information

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 ( $e^-/\text{\AA}^2$ )	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 ( $\text{\AA}$ )	261.4, 261.4, 261.4	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	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

*Continued on next page...*

*Continued from previous page...*

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 ⓘ

### 5.3.1 Protein backbone ⓘ

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

*Continued on next page...*

Continued from previous page...

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 ⓘ

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 ⓘ

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 ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



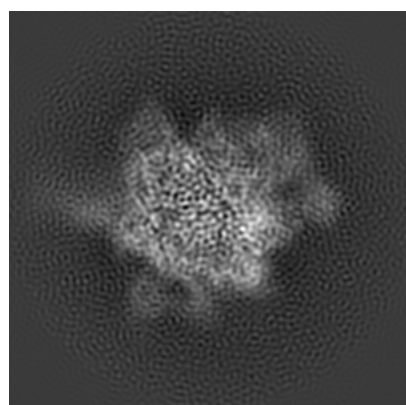
## 6 Map visualisation [i](#)

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.

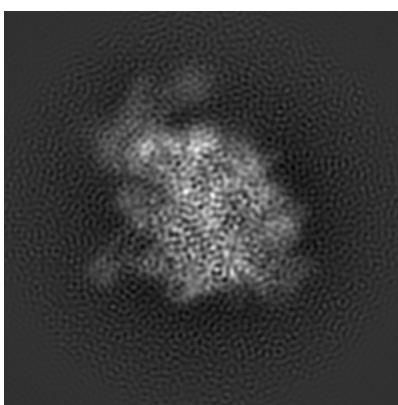
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

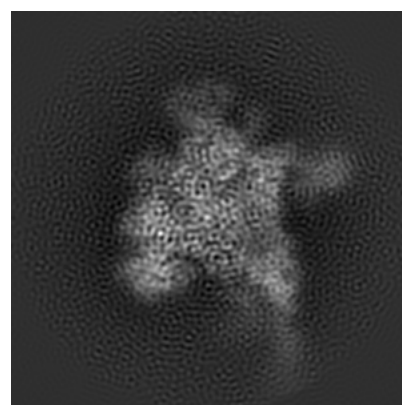
#### 6.1.1 Primary map



X



Y

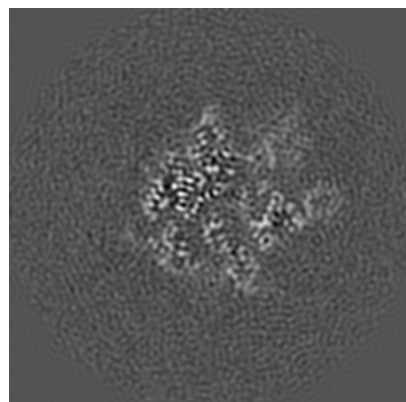


Z

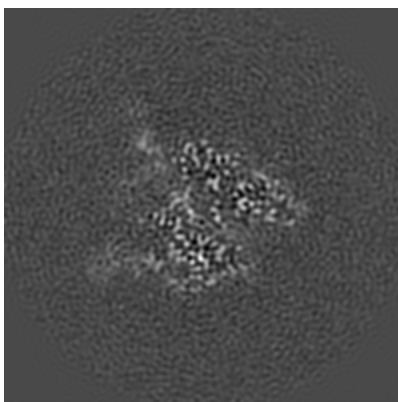
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

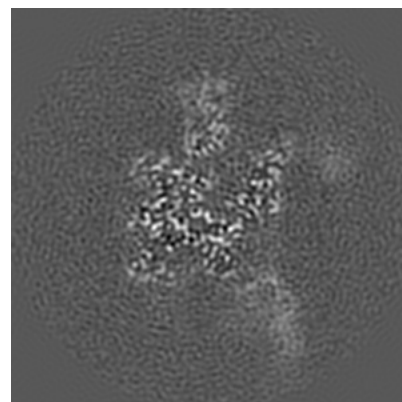
#### 6.2.1 Primary map



X Index: 100



Y Index: 100

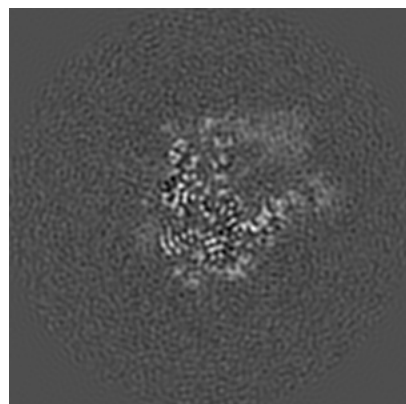


Z Index: 100

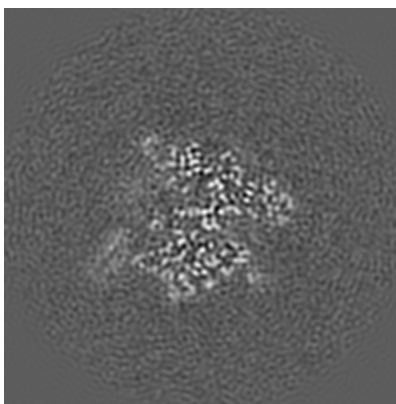
The images above show central slices of the map in three orthogonal directions.

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

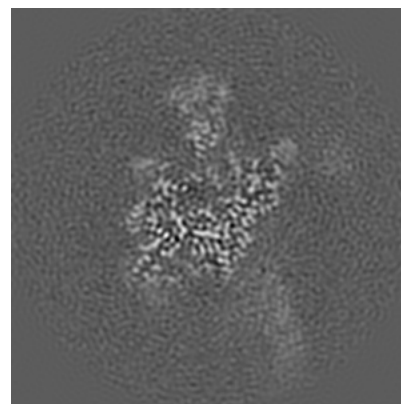
### 6.3.1 Primary map



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 surface views [i](#)

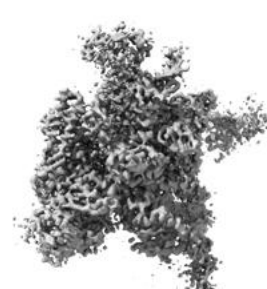
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

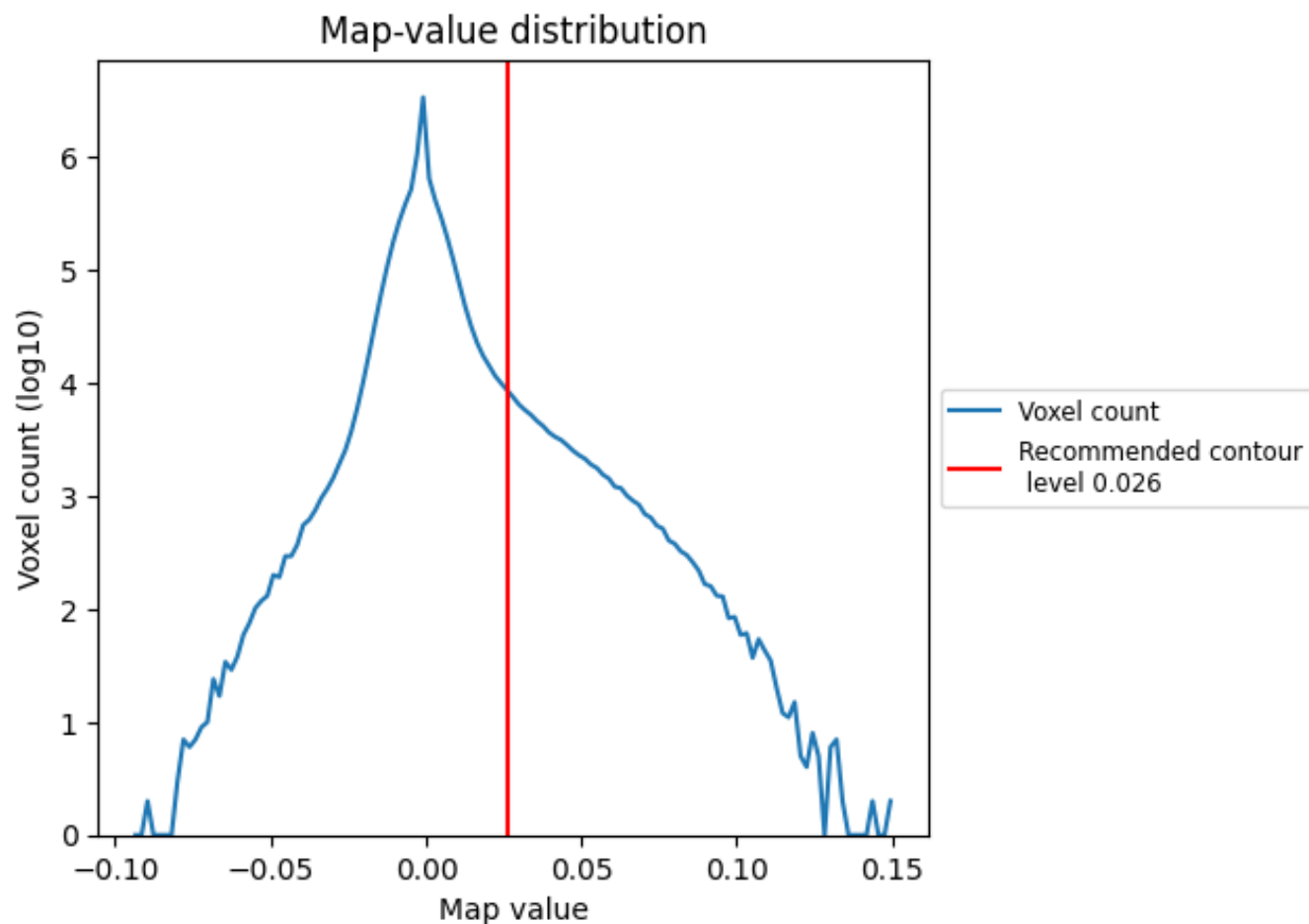
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

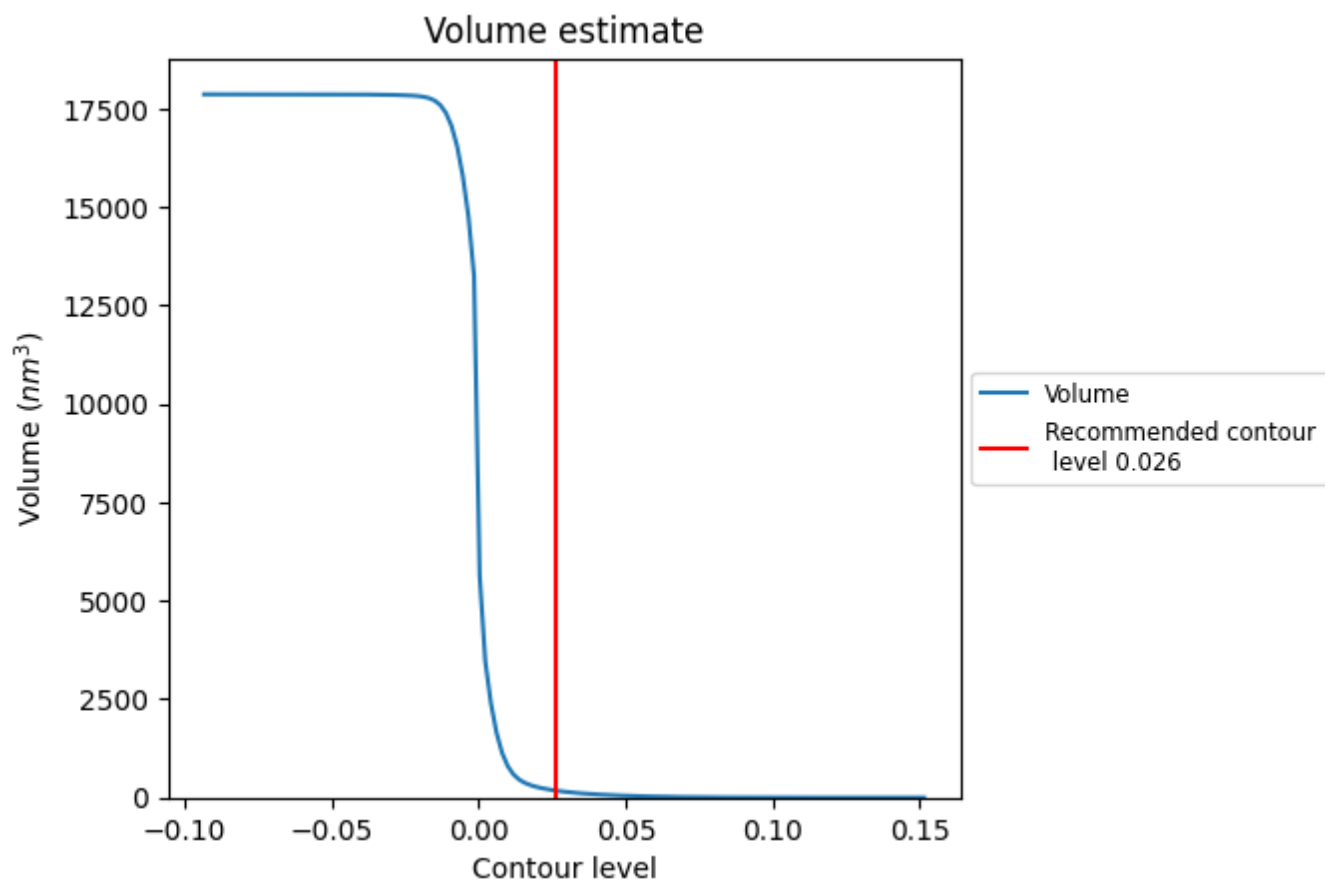
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

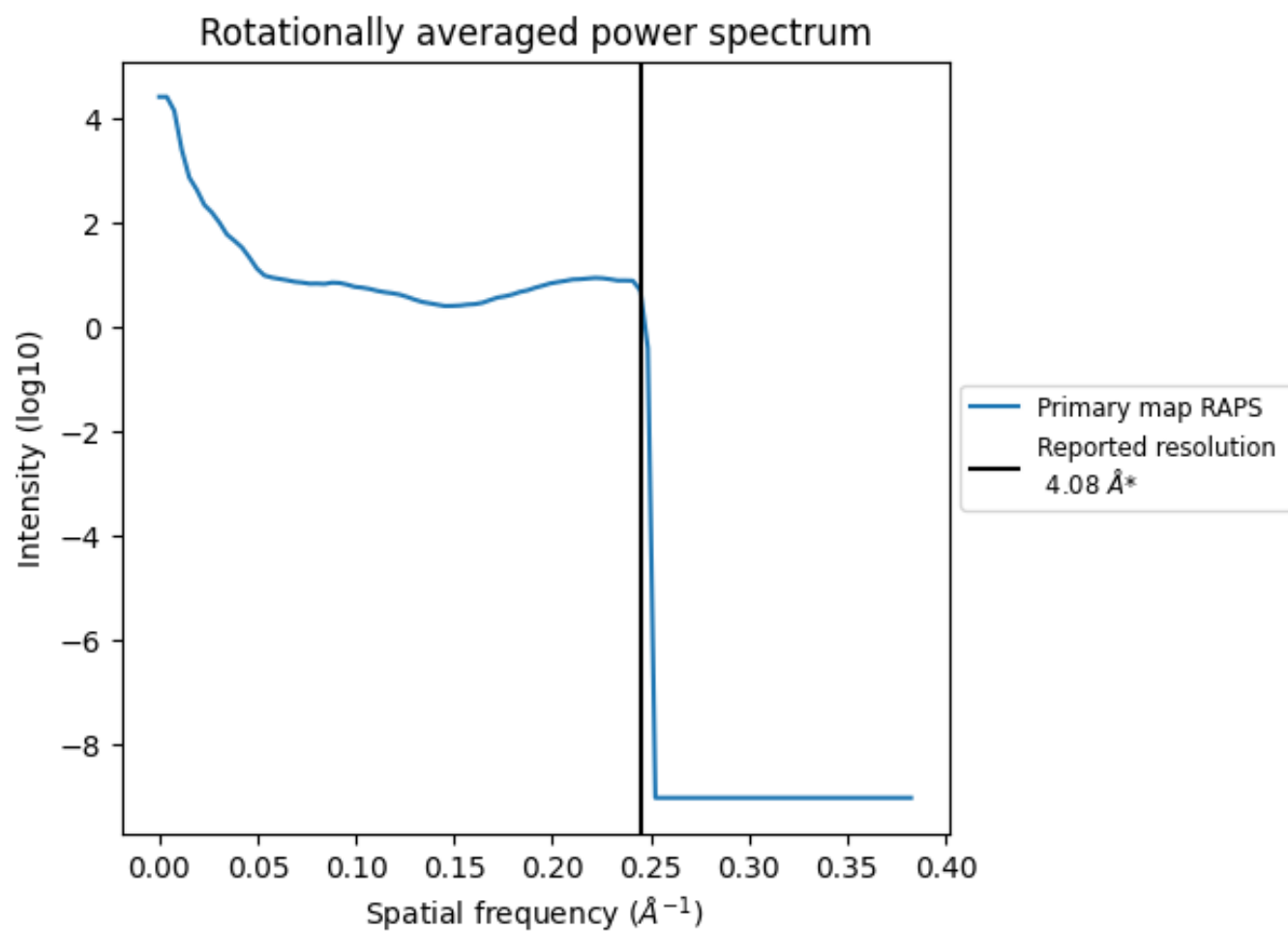
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 179 nm<sup>3</sup>; 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 ⓘ



\*Reported resolution corresponds to spatial frequency of 0.245 Å<sup>-1</sup>

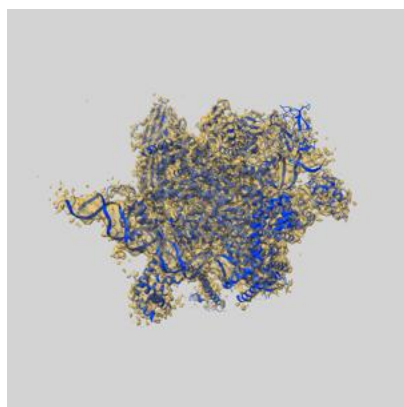
## 8 Fourier-Shell correlation

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

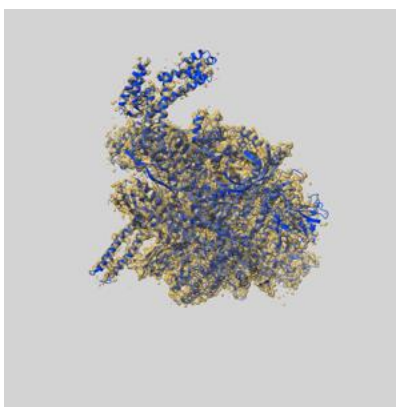
## 9 Map-model fit [i](#)

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

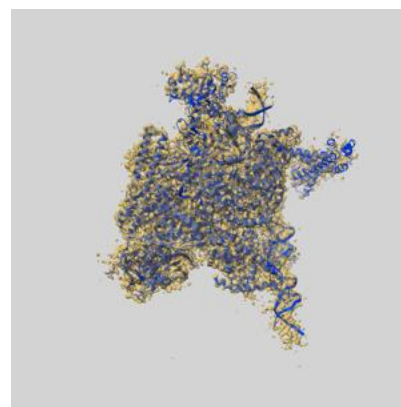
### 9.1 Map-model overlay [i](#)



X



Y

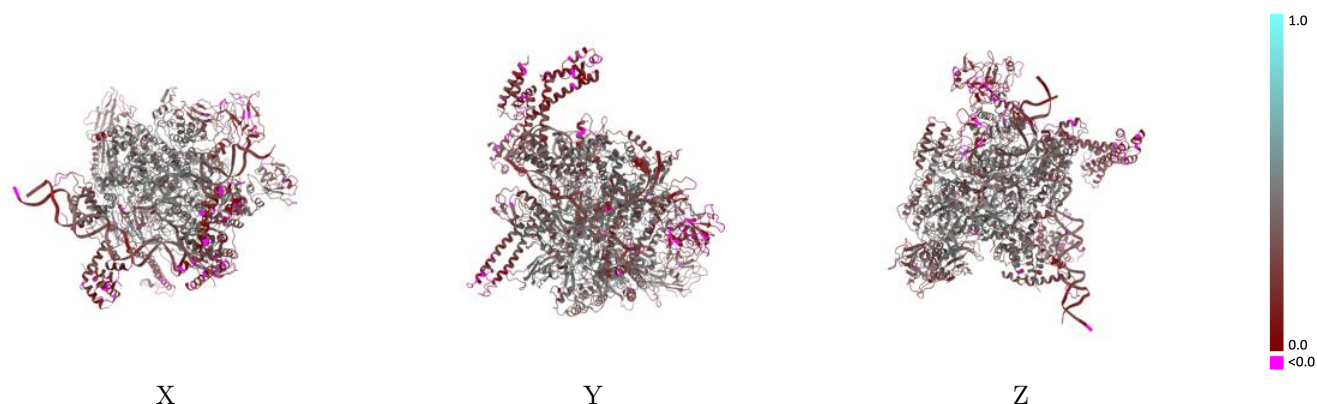


Z

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.

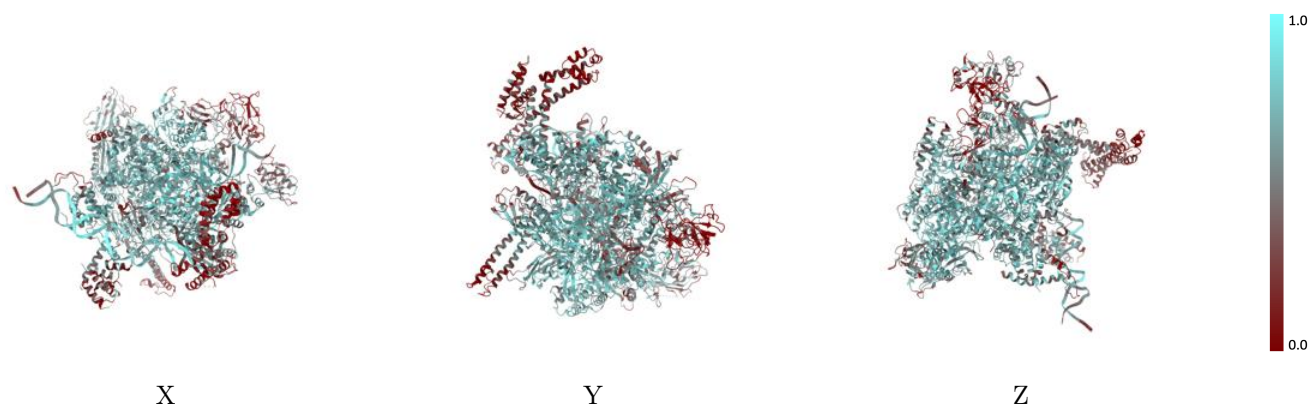


## 9.2 Q-score mapped to coordinate model [i](#)



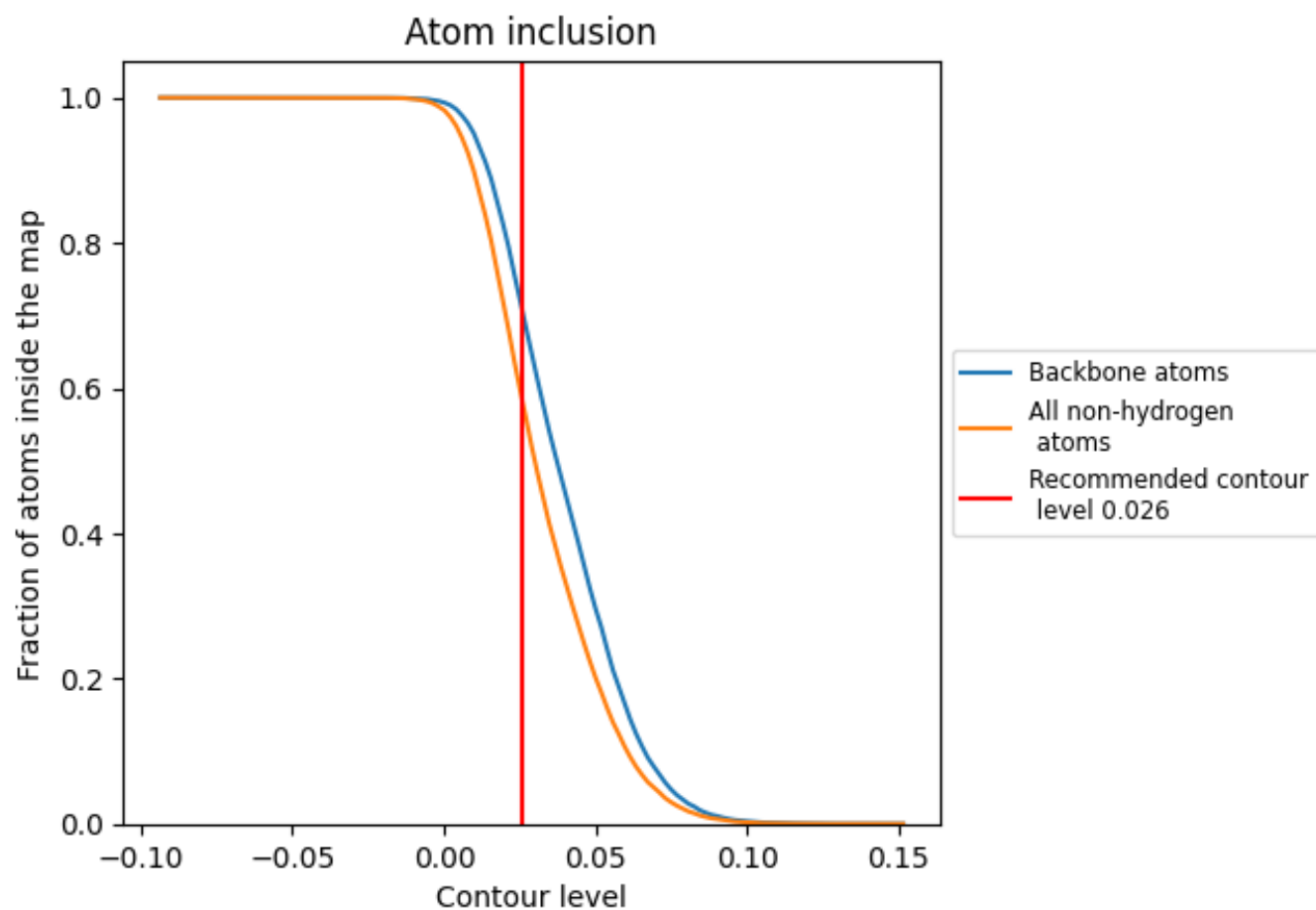
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

























## 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

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	 0.5797	 0.3500
A	 0.6598	 0.4130
B	 0.5537	 0.3490
C	 0.6223	 0.3800
D	 0.5861	 0.3650
E	 0.5368	 0.3550
F	 0.3212	 0.2220
N	 0.6953	 0.2920
P	 0.5349	 0.3160
Q	 0.4079	 0.2260
R	 0.6244	 0.3830
T	 0.6714	 0.3130

