



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:53 AM UTC

PDB ID : 6X2F / pdb_00006x2f
EMDB ID : EMD-22006
Title : Mfd-bound E.coli RNA polymerase elongation complex - L2 state
Authors : Llewellyn, E.; Chen, J.; Kang, J.Y.; Darst, S.A.
Deposited on : 2020-05-20
Resolution : 4.00 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:

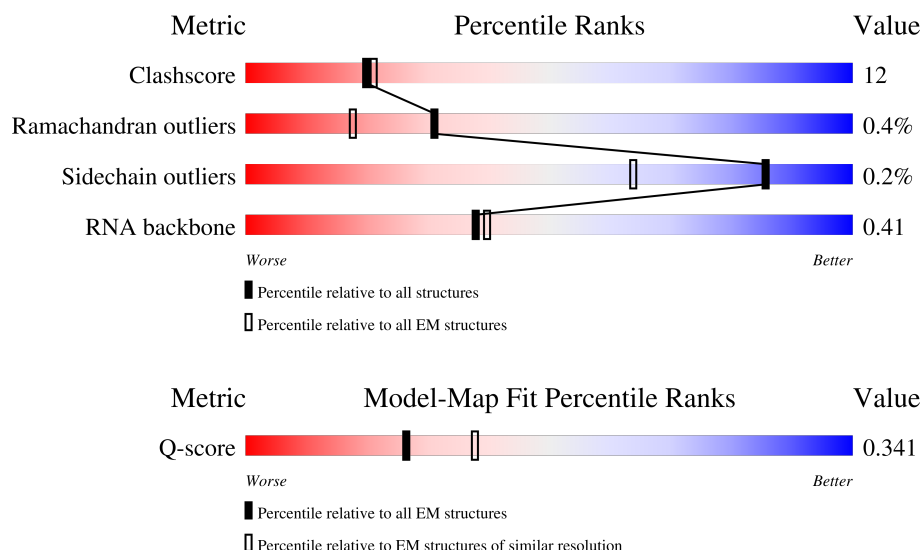
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 4.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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

Mol	Chain	Length	Quality of chain
1	A	1148	5% 58% 41% .
2	G	329	55% 13% 32%
2	H	329	5% 50% 16% 34%

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Mol	Chain	Length	Quality of chain
3	I	1342	
4	J	1407	
5	K	91	
6	R	21	
7	P	64	
8	Q	64	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 36054 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 Transcription-repair-coupling factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1144	Total	C	N	O	S	0	0
			8934	5654	1594	1651	35		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	224	Total	C	N	O	S	0	0
			1721	1078	303	334	6		
2	H	217	Total	C	N	O	S	0	0
			1667	1043	293	325	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	1316	Total	C	N	O	S	0	0
			10368	6507	1808	2010	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	1336	Total	C	N	O	S	0	0
			10383	6524	1852	1957	50		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	1384	VAL	MET	conflict	UNP A0A4S1NBU2

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

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

- Molecule 6 is a RNA chain called RNA (20-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	R	9	Total	C	N	O	P	0	0
			201	89	42	61	9		

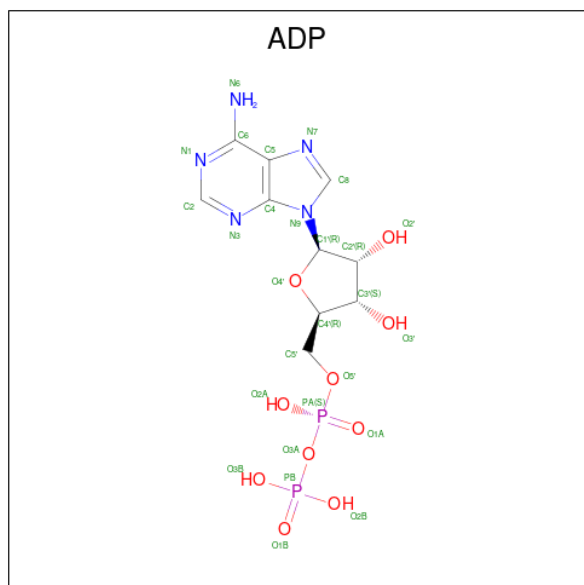
- Molecule 7 is a DNA chain called DNA (64-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	P	55	Total	C	N	O	P	0	0
			1112	531	192	335	54		

- Molecule 8 is a DNA chain called DNA (64-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Q	49	Total	C	N	O	P	0	0
			1011	478	194	290	49		

- Molecule 9 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
9	A	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

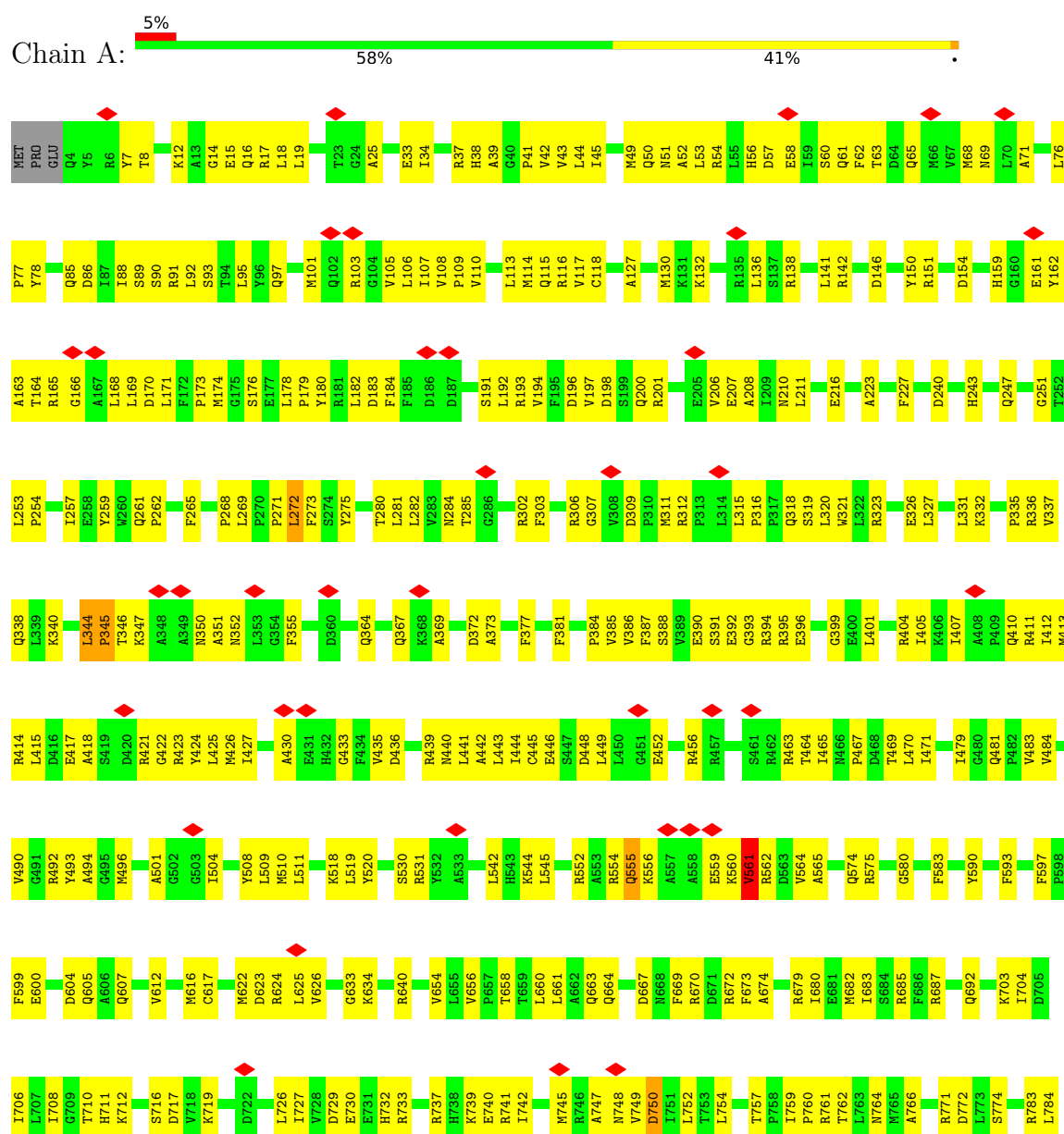
- Molecule 11 is ZINC ION (CCD ID: ZN) (formula: Zn).

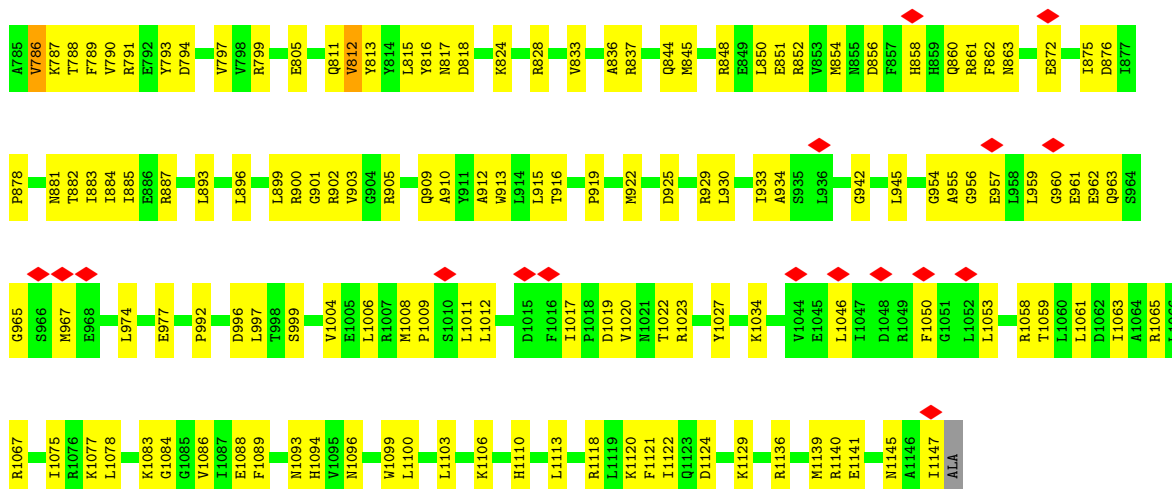
Mol	Chain	Residues	Atoms		AltConf
11	J	2	Total 2	Zn 2	0

3 Residue-property plots

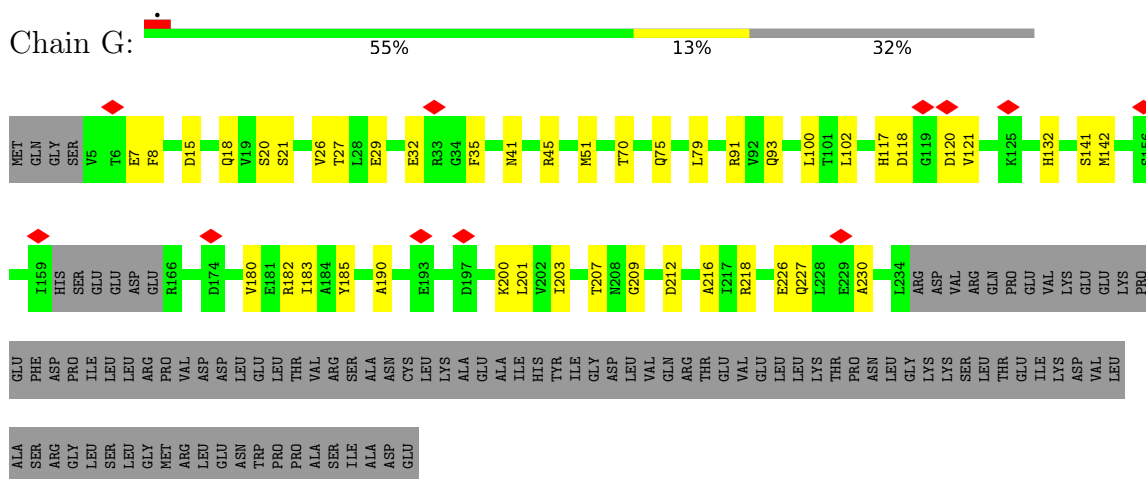
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Transcription-repair-coupling factor

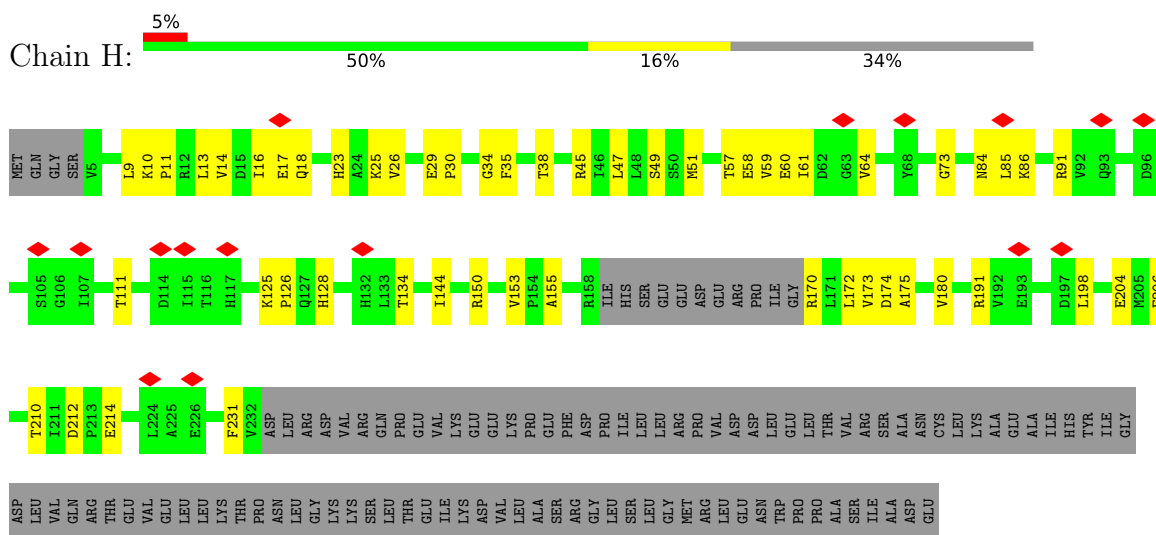




- Molecule 2: DNA-directed RNA polymerase subunit alpha

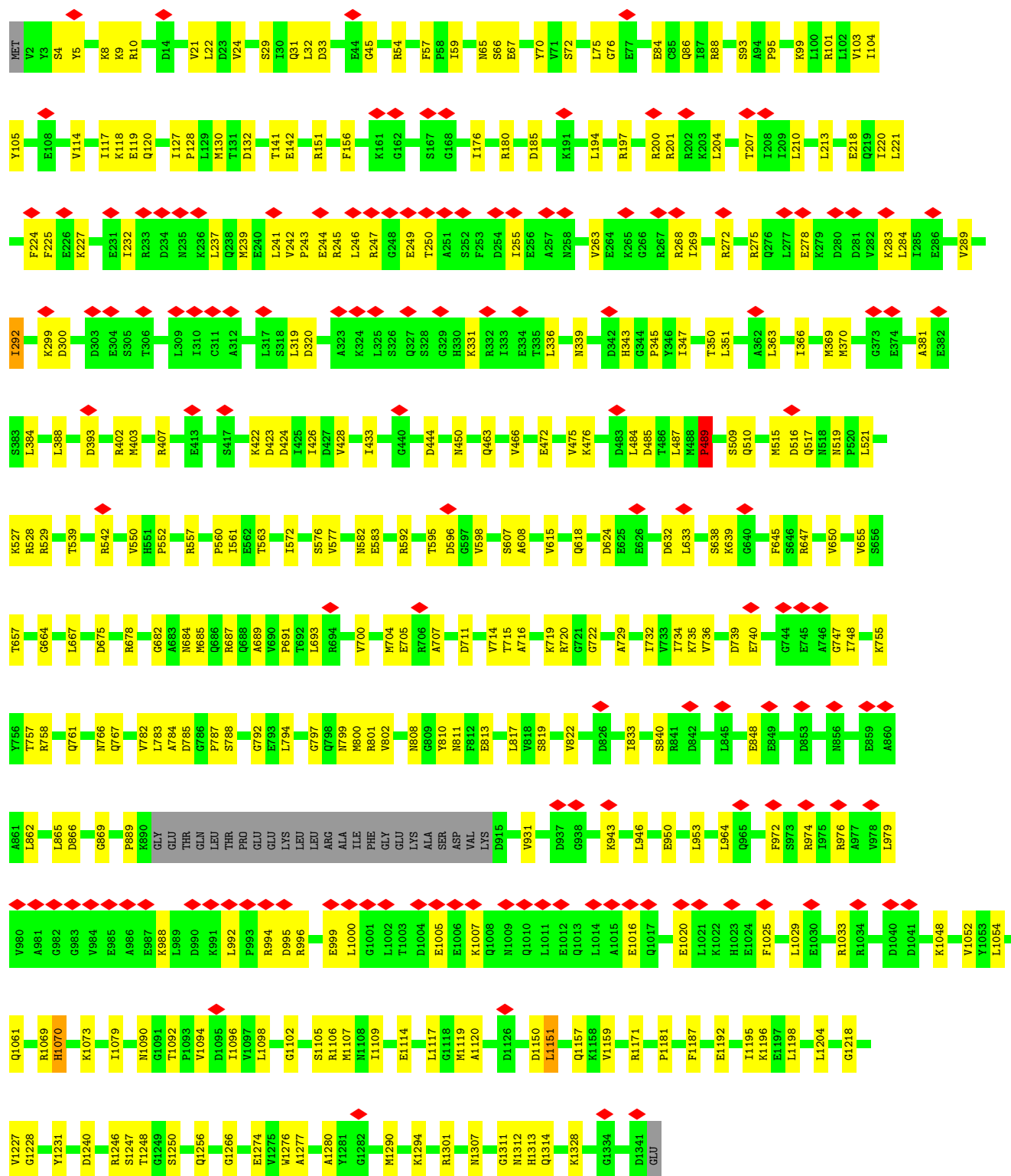


- Molecule 2: DNA-directed RNA polymerase subunit alpha



- Molecule 3: DNA-directed RNA polymerase subunit beta

Chain I:

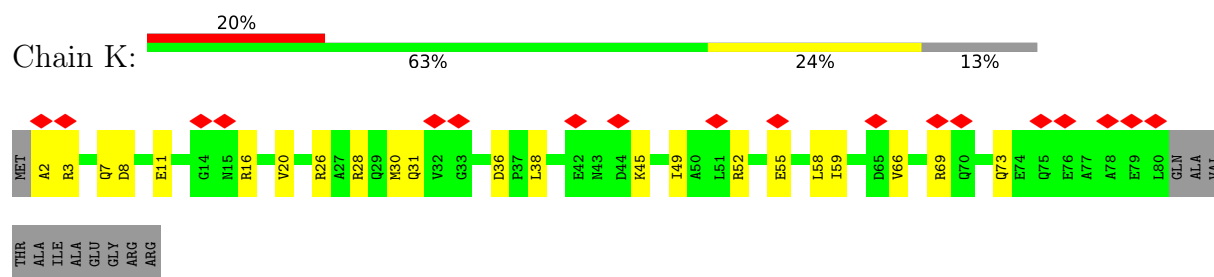


Chain J:

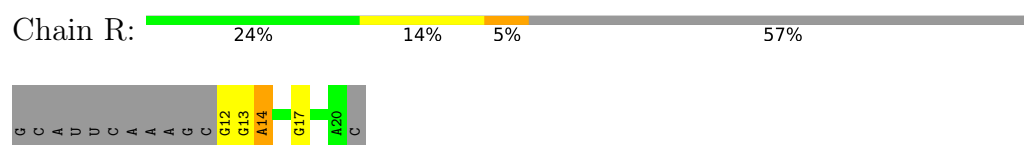


ALA	SER	ALA	SER	LEU	LEU	ALA	GLU	LEU	LEU	LEU	LEU	PHE	LEU	LYS	LYS	GLN	THR	LYS	THR	THR	GLU	E16	K21	G36	K40	R47	R83	D54	G55	L56	A59	R60	I61	F82	G83	P84	D87	C70	L71	Y75	L78	R81	I84	C85	E86	V90	T93	R98	M102	G103									
W1295	G1296	G1299	A1300	R1304	F1199	E1200	L1306	L1307	R1203	T1310	K1311	A1312	R1206	ASP	T1316	E1317	S1318	F1325	Q1326	E1327	L1332	A1336	R1342	E1343	L1344	R1345	G1346	L1347	V1351	I1357	F1358	A1359	M1370	R1371	R1372	R1373	ALA	ALA	GLY	GLU	ALA	PRO	ALA	ALA	PRO	GLN	VAL	THR	ALA	GLU	ASP								
P1096	A1097	Q1098	Y1099	F1100	L1101	A1105	T1106	V1107	Q1108	L1109	E1110	D1111	G1112	V1113	Q1114	I1115	S1116	S1117	G1118	L1121	A1122	R1123	Q1126	GLU	SER	GLY	GLY	THR	LYS	ASP	ILE	T1135	K1151	L1156	I1159	S1160	S1164	F1165	G1166	T1169	K1170	G1171	K1172	R1173	L1174	L1175	D1181	D1184	P1185										
Y1186	E1187	E1188	M1189	V1198	F1199	E1200	G1201	E1202	R1203	V1204	R1205	R1206	G1207	S1211	D1212	A1216	P1217	R1224	R1231	D1239	R1242	L1243	Q1244	G1245	V1246	M1249	D1250	K1251	R1258	R1262	K1263	A1264	T1265	D1273	E1276	Q1279	V1280	E1281	R1284	M1289	L1292	E1293	A1294																
R1036	F1037	T1038	D1039	M1040	I1041	D1042	G1043	Q1044	T1045	I1046	T1047	R1048	Q1049	T1050	D1051	E1052	L1053	T1054	G1055	L1056	S1057	G1058	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
C869	D870	L871	N875	D878	K881	V882	R883	S884	W885	V886	C895	C898	R901	N910	X911	G912	I918	P926	G927	T928	T931	N932	R933	THR	PHE	HIS	ILE	GLY	GLY	ALA	ALA	SER	ARG	ALA	ALA	ALA	S948	S949	I950	Q951	V952	R953	R954	K955	G956	S957	I958	K959											
L960	S961	N962	V963	K964	S965	V966	V967	N968	S969	S970	G971	K972	L973	S977	R978	T980	E981	L982	K983	L984	I985	D986	E987	F988	G989	R990	E993	K996	V997	A1004	K1005	G1006	D1007	K1008	E1009	Q1010	G1014	E1015	T1016	D1021	T1024	M1025	I1028	T1029	E1030	V1031	S1032	G1033	F1034	V1035									
D751	I754	I755	I759	N762	F763	R764	L770	Q771	Y772	T776	K789	R799	L800	V801	D806	V809	G815	T816	H817	E818	R820	P824	E827	G828	V831	L835	R836	V839	A845	F846	D847	V848	L849	K850	A854	D855	V858	L863																					
A633	S638	V639	G640	I641	D642	D643	M644	K649	T653	V661	T664	F668	L672	V673	R678	Y679	S694	M697	E704	T705	V706	R709	D710	G711	Q712	K715	S718	S721	I722	Y723	M724	S733	A734	Q736	I737	R738	Q739	L740	A741	K749	P750																		
L478	E479	M485	D505	V506	L510	T514	R515	D516	C517	V518	G522	L527	E532	R535	R547	V550	Y555	E556	D558	E562	D571	K585	G586	L587	I591	L596	M604	L614	V618	I619	F620	A621	D622	Q623	L624	G628	F629																						
R312	G313	R314	N320	K321	R322	K325	M330	I331	K334	R339	Y349	L363	H364	T381	R388	T393	A396	E402	R403	L412	D413	E414	V415	R417	E418	H419	M424	R425	A426	I434	P439	H450	P451	L452	F461	L472	T473	Q477																					
E199	Q200	L201	R202	N206	N209	S210	E211	T212	K213	R214	L217	T218	K219	R220	I221	L224	E225	V228	L239	L242	P243	P246	L255	D256	G257	G258	R259	T262	S263	D264	L265	N266	R278	L279	K280	R281	L282	L285	A286	A287	M298	E301	D304																
H104	L107	A108	T111	A112	S119	L120	P121	S122	R123	I124	G125	L126	L127	D134	I135	E136	Y140	F141	E142	S143	Y144	G150	M151	T152	N153	L154	E155	L156	Q157	Q158	I159	L160	T161	E162	E163	L166	E170	E171	F172	G173	D174	E175	D177	A178	M192	L194	C198												
MET	LYS	ASP	LEU	LEU	LYS	PHE	LEU	LYS	LYS	GLN	THR	LYS	THR	GLU	E16	K21	G36	K40	R47	R83	D54	G55	L56	A59	R60	I61	F82	G83	P84	D87	C70	L71	Y75	L78	R81	I84	C85	E86	V90	T93	R98	M102	G103																

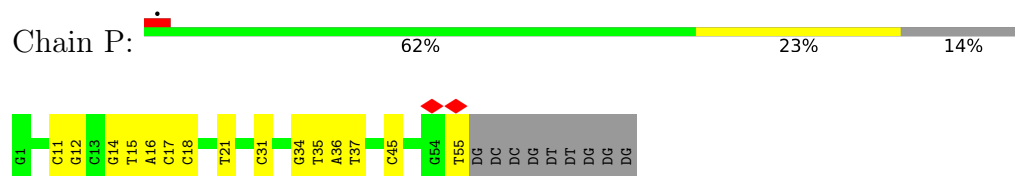
- Molecule 5: DNA-directed RNA polymerase subunit omega



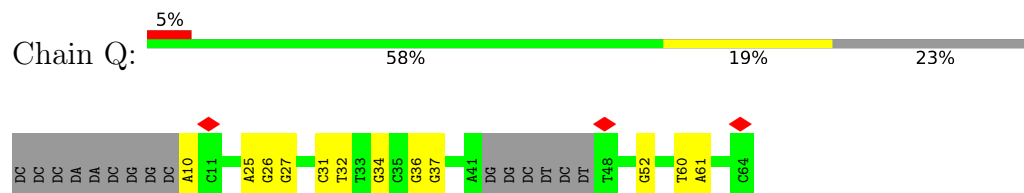
- Molecule 6: RNA (20-MER)



- Molecule 7: DNA (64-MER)



- Molecule 8: DNA (64-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	16000	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 ($e^-/\text{\AA}^2$)	60	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	24.221	Depositor
Minimum map value	-12.069	Depositor
Average map value	0.008	Depositor
Map value standard deviation	1.068	Depositor
Recommended contour level	4.5	Depositor
Map size (Å)	390.0, 390.0, 390.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	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: ZN, MG, ADP

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	0.34	0/9112	0.83	10/12359 (0.1%)
2	G	0.33	0/1741	0.66	0/2361
2	H	0.33	0/1686	0.73	2/2286 (0.1%)
3	I	0.39	1/10533 (0.0%)	0.69	3/14214 (0.0%)
4	J	0.36	0/10540	0.69	2/14231 (0.0%)
5	K	0.37	0/629	0.82	0/847
6	R	0.45	0/226	0.43	0/352
7	P	0.40	0/1242	0.52	0/1913
8	Q	0.36	0/1135	0.50	0/1748
All	All	0.37	1/36844 (0.0%)	0.72	17/50311 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	489	PRO	N-CD	5.21	1.55	1.47

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	344	LEU	CA-C-N	8.87	130.93	119.84
1	A	344	LEU	C-N-CA	8.87	130.93	119.84
1	A	617	CYS	CA-C-N	7.89	131.36	120.39
1	A	617	CYS	C-N-CA	7.89	131.36	120.39
1	A	564	VAL	N-CA-C	-7.05	106.43	113.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8934	0	8813	362	0
2	G	1721	0	1759	34	0
2	H	1667	0	1699	39	0
3	I	10368	0	10379	215	0
4	J	10383	0	10598	229	0
5	K	627	0	634	21	0
6	R	201	0	98	4	0
7	P	1112	0	622	16	0
8	Q	1011	0	550	10	0
9	A	27	0	12	5	0
10	J	1	0	0	0	0
11	J	2	0	0	0	0
All	All	36054	0	35164	879	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 12.

The worst 5 of 879 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)
1:A:786:VAL:HG12	1:A:910:ALA:CB	1.25	1.62
1:A:786:VAL:CG1	1:A:910:ALA:HB3	1.43	1.46
4:J:264:ASP:OD2	4:J:325:LYS:HG2	1.26	1.27
1:A:281:LEU:HA	1:A:335:PRO:HG2	1.23	1.18
1:A:812:VAL:CG2	1:A:882:THR:HB	1.81	1.10

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	1142/1148 (100%)	1030 (90%)	103 (9%)	9 (1%)	16	52
2	G	220/329 (67%)	205 (93%)	15 (7%)	0	100	100
2	H	213/329 (65%)	193 (91%)	19 (9%)	1 (0%)	24	60
3	I	1312/1342 (98%)	1215 (93%)	94 (7%)	3 (0%)	43	75
4	J	1330/1407 (94%)	1230 (92%)	97 (7%)	3 (0%)	43	75
5	K	77/91 (85%)	72 (94%)	5 (6%)	0	100	100
All	All	4294/4646 (92%)	3945 (92%)	333 (8%)	16 (0%)	31	65

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	345	PRO
1	A	786	VAL
2	H	13	LEU
4	J	417	ARG
1	A	85	GLN

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	923/973 (95%)	919 (100%)	4 (0%)	84	84
2	G	190/286 (66%)	190 (100%)	0	100	100
2	H	184/286 (64%)	184 (100%)	0	100	100
3	I	1132/1157 (98%)	1131 (100%)	1 (0%)	88	89
4	J	1118/1168 (96%)	1114 (100%)	4 (0%)	84	84
5	K	67/75 (89%)	67 (100%)	0	100	100
All	All	3614/3945 (92%)	3605 (100%)	9 (0%)	85	87

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	J	710	ASP
4	J	1170	LYS
1	A	812	VAL
3	I	1151	LEU
4	J	263	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
3	I	235	ASN
4	J	1244	GLN
4	J	209	ASN
5	K	75	GLN
4	J	1023	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	R	8/21 (38%)	2 (25%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	R	14	A
6	R	17	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
9	ADP	A	2000	-	28,29,29	1.38	5 (17%)	43,45,45	1.90	8 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	ADP	A	2000	-	-	4/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	2000	ADP	C5-C4	4.43	1.47	1.39
9	A	2000	ADP	C5-N7	-2.58	1.34	1.39
9	A	2000	ADP	C5-C6	2.45	1.47	1.41
9	A	2000	ADP	C8-N7	2.24	1.36	1.31
9	A	2000	ADP	C4-N9	-2.01	1.33	1.37

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	2000	ADP	C5-C4-N3	-5.84	118.67	126.72
9	A	2000	ADP	N3-C4-N9	4.62	135.03	127.17
9	A	2000	ADP	C2-N3-C4	3.58	120.57	111.83
9	A	2000	ADP	C4-C5-N7	-3.49	106.59	110.58
9	A	2000	ADP	N3-C2-N1	-3.09	123.91	128.58

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	2000	ADP	C5'-O5'-PA-O1A

Continued on next page...

Continued from previous page...

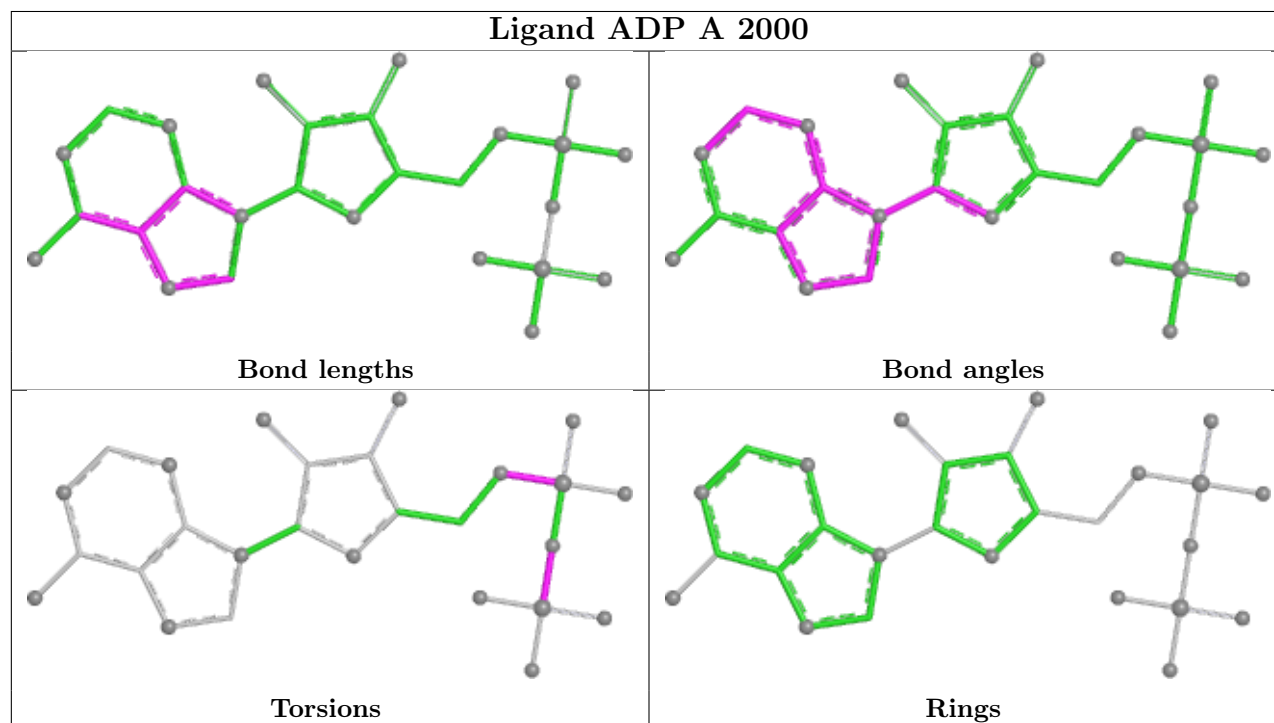
Mol	Chain	Res	Type	Atoms
9	A	2000	ADP	C5'-O5'-PA-O2A
9	A	2000	ADP	C5'-O5'-PA-O3A
9	A	2000	ADP	PA-O3A-PB-O2B

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	2000	ADP	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

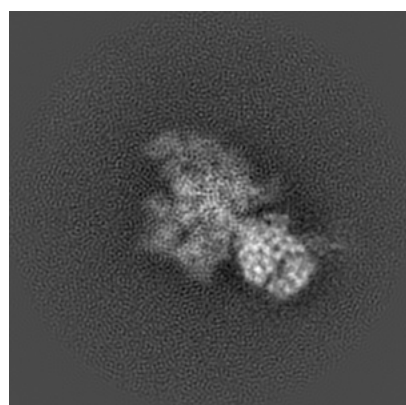
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22006. These allow visual inspection of the internal detail of the map and identification of artifacts.

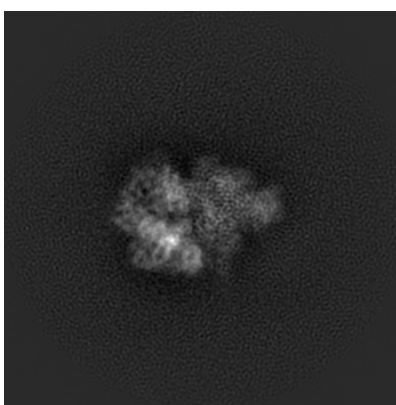
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

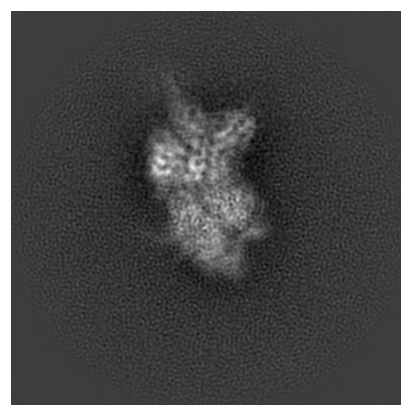
6.1.1 Primary map



X



Y

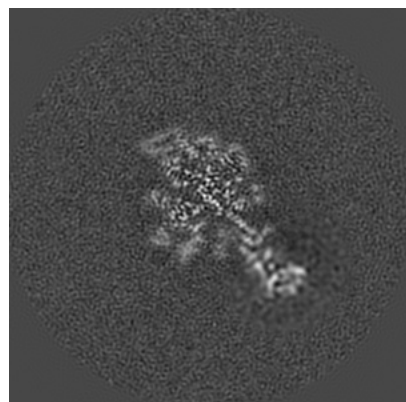


Z

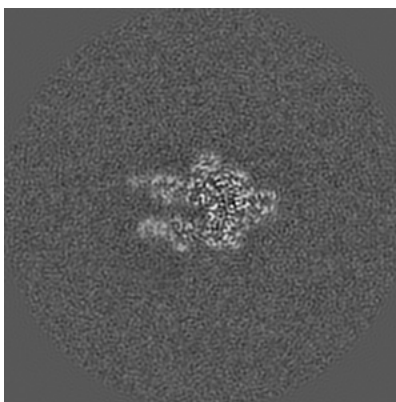
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

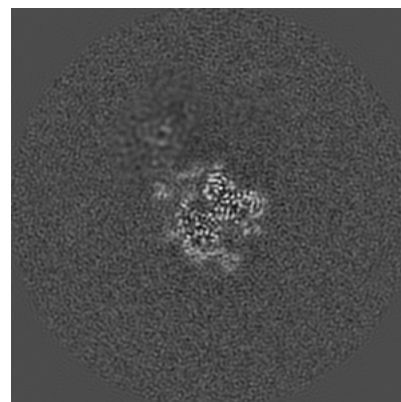
6.2.1 Primary map



X Index: 150



Y Index: 150

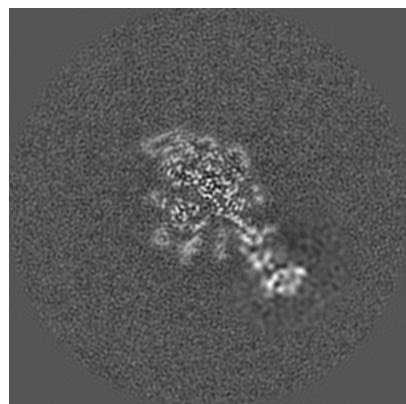


Z Index: 150

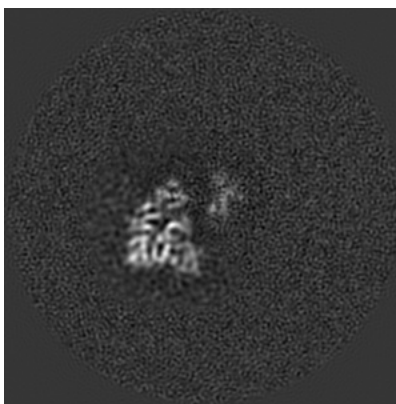
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

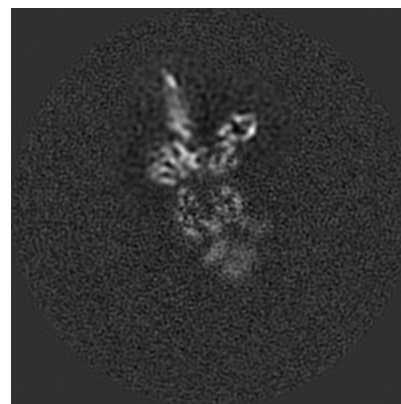
6.3.1 Primary map



X Index: 151



Y Index: 186

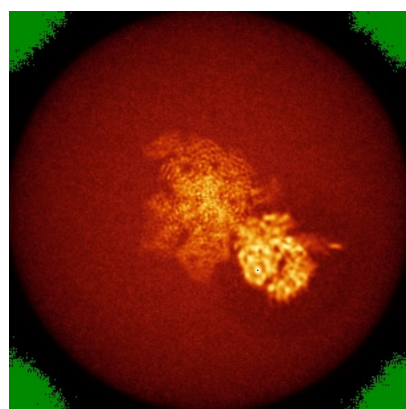


Z Index: 123

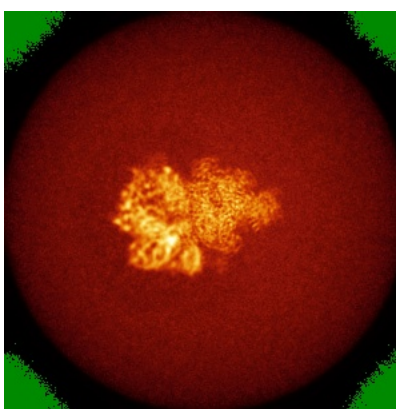
The images above show the largest variance slices of the map in three orthogonal directions.

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

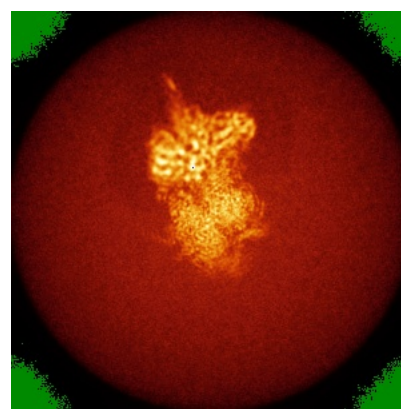
6.4.1 Primary map



X



Y

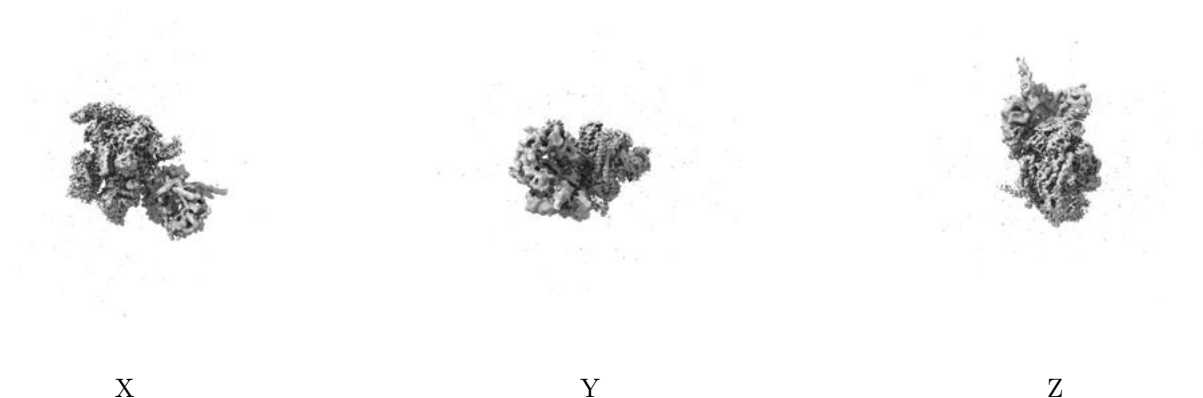


Z

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



The images above show the 3D surface view of the map at the recommended contour level 4.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

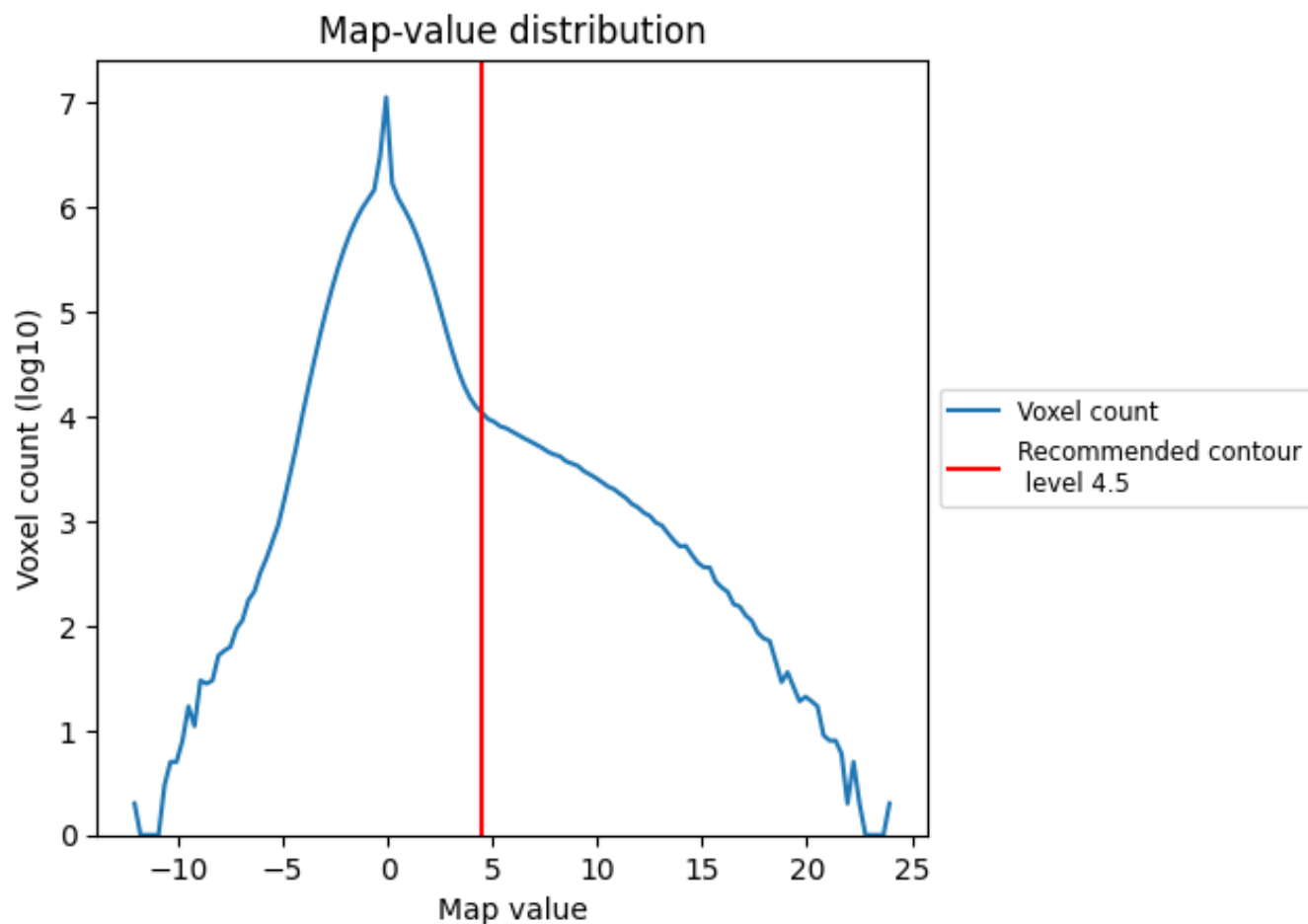
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

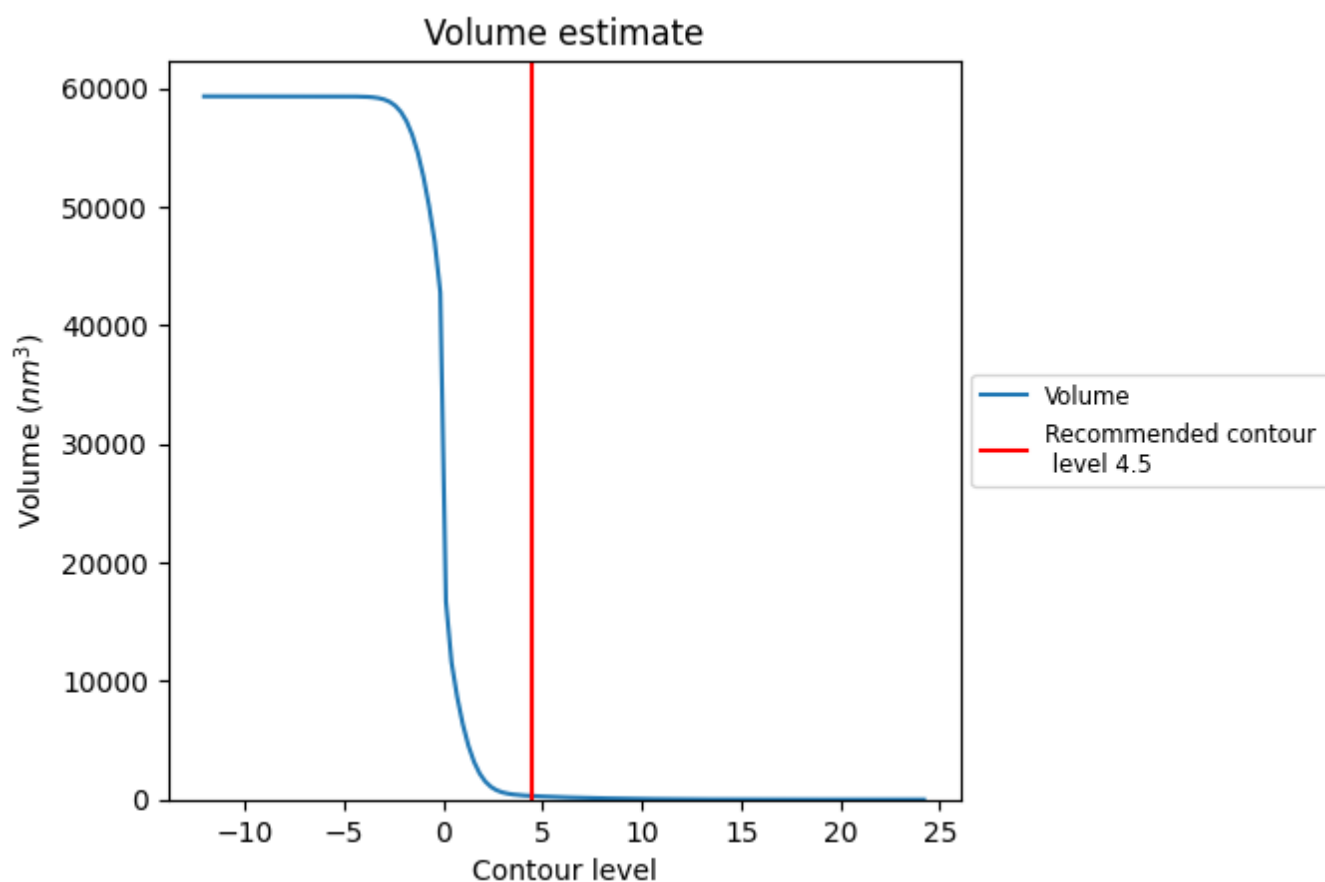
This section contains the results of statistical analysis of the map.

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.

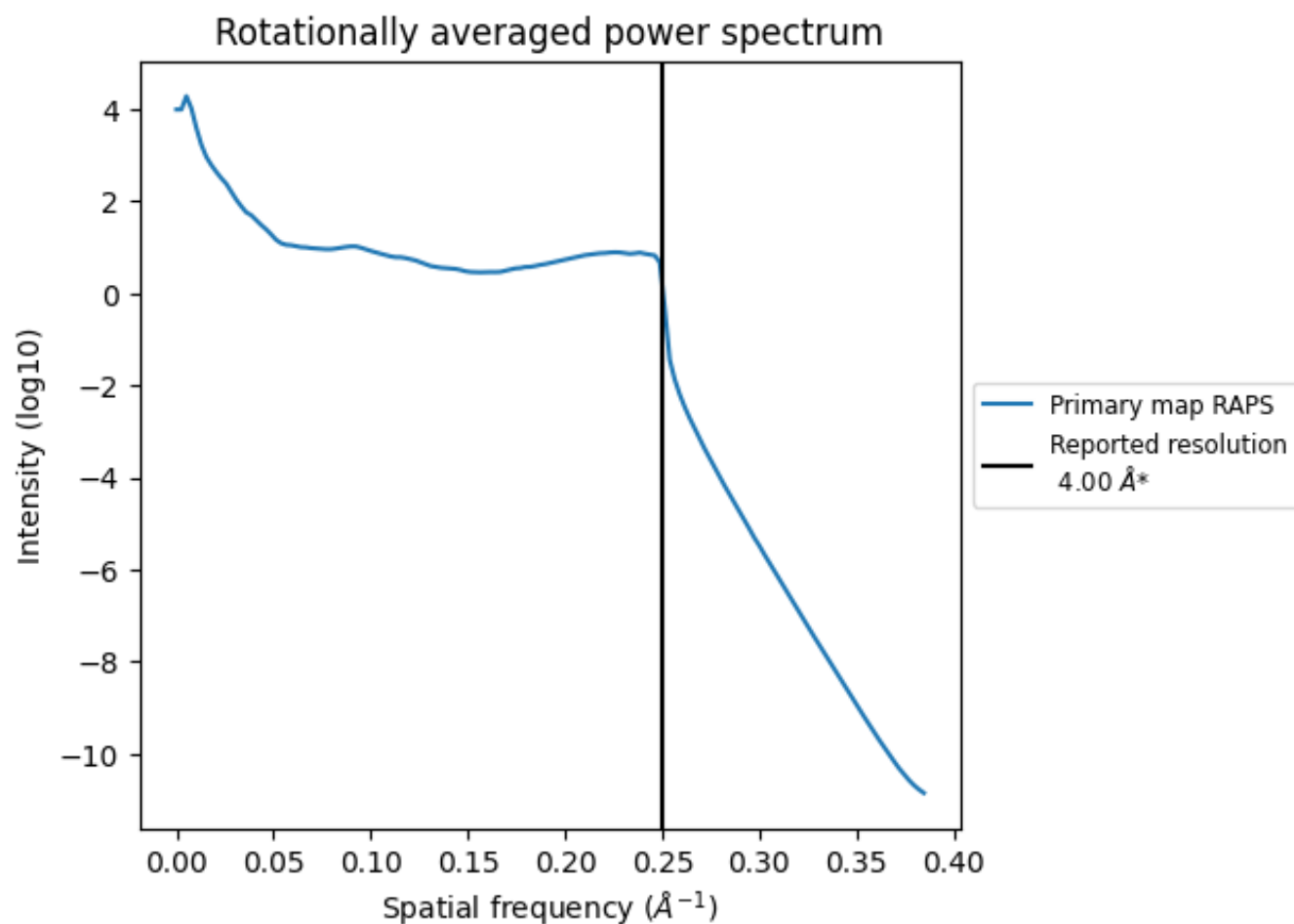
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 302 nm³; this corresponds to an approximate mass of 272 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 0.250 Å⁻¹

8 Fourier-Shell correlation

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

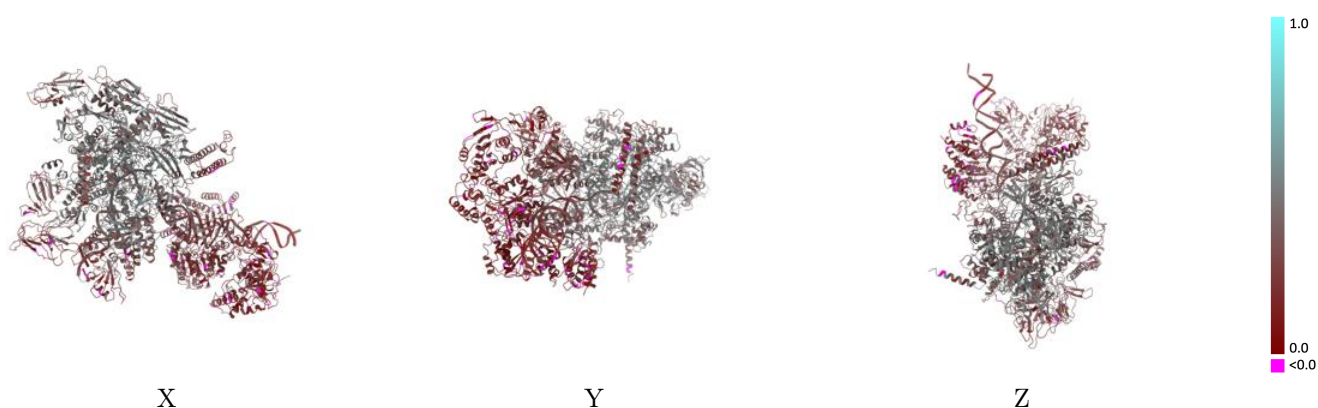
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22006 and PDB model 6X2F. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

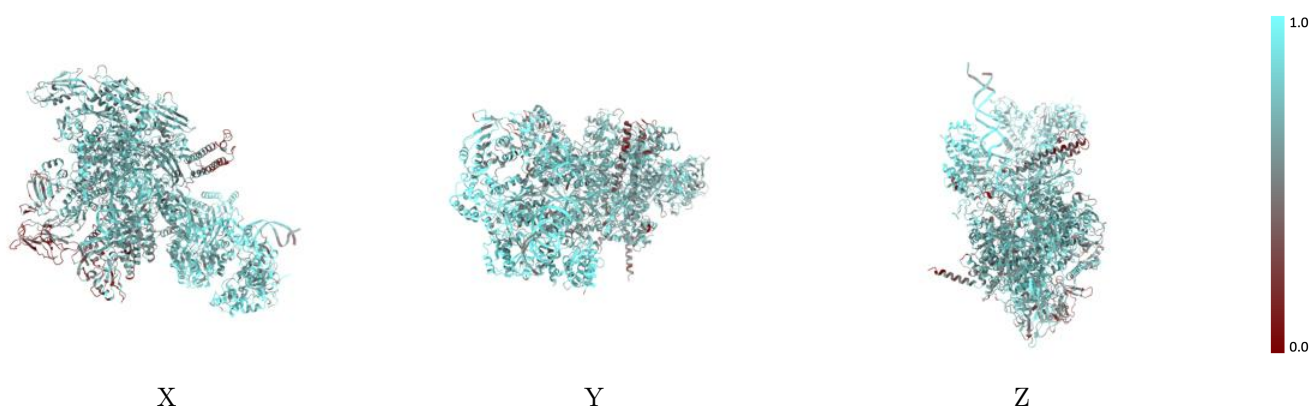
This section was not generated.

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



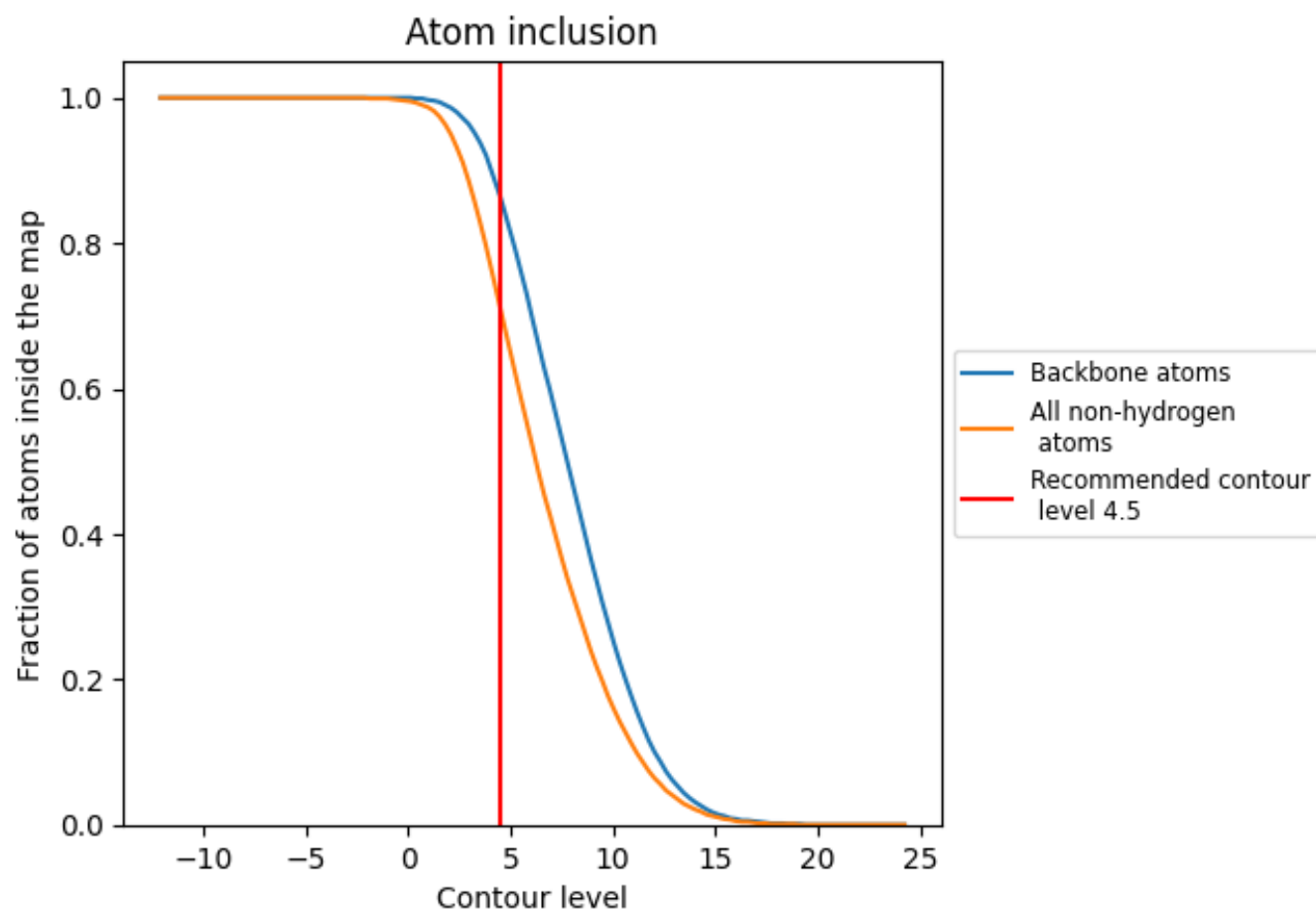
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.5).

9.4 Atom inclusion ⓘ



At the recommended contour level, 86% of all backbone atoms, 71% 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 (4.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7110	0.3410
A	0.8160	0.1940
G	0.6940	0.4310
H	0.6610	0.3800
I	0.6750	0.4040
J	0.6450	0.3920
K	0.5430	0.3680
P	0.8710	0.2870
Q	0.8350	0.2820
R	0.9050	0.4170

1.0

0.0

<0.0