



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 09:35 PM UTC

PDB ID : 6FLQ / pdb_00006flq
EMDB ID : EMD-4275
Title : CryoEM structure of E.coli RNA polymerase paused elongation complex bound to NusA
Authors : Guo, X.; Weixlbaumer, A.
Deposited on : 2018-01-26
Resolution : 3.60 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:

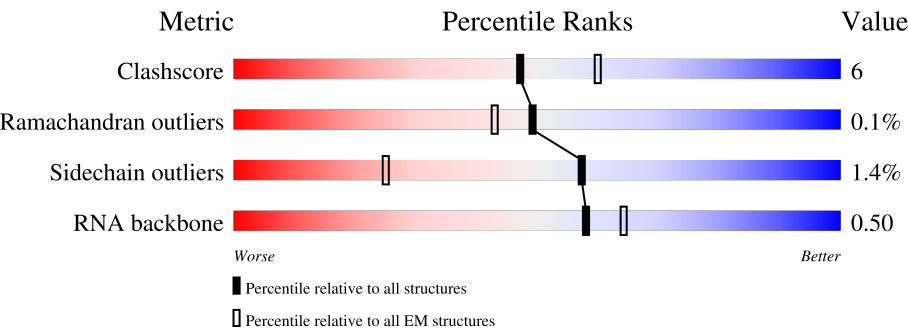
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.60 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	329	88% 79%14%6%
1	B	329	86% 76%14%9%
2	C	1342	85% 82%17%
3	D	1407	81% 80%14%5%
4	E	91	92% 93%5%
5	F	495	100% 95%5%
6	N	31	94% 81%19%

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Mol	Chain	Length	Quality of chain
7	R	21	95% 38% 38% 24%
8	T	39	79% 77% 23%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 30201 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	310	Total	C	N	O	S	0	0
			2168	1339	394	429	6		
1	B	298	Total	C	N	O	S	0	0
			2068	1280	374	408	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1341	Total	C	N	O	S	0	0
			10573	6634	1841	2055	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1334	Total	C	N	O	S	0	0
			10357	6510	1846	1952	49		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	90	Total	C	N	O	S	0	0
			709	430	136	142	1		

- Molecule 5 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	F	495	Total	C	N	O	0	0
			2447	1457	495	495		

- Molecule 6 is a DNA chain called DNA (31-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	31	Total	C	N	O	P	0	0
			647	304	131	181	31		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	R	21	Total	C	N	O	P	0	0
			444	199	77	148	20		

- Molecule 8 is a DNA chain called DNA (39-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	T	39	Total	C	N	O	P	0	0
			785	375	135	236	39		

- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

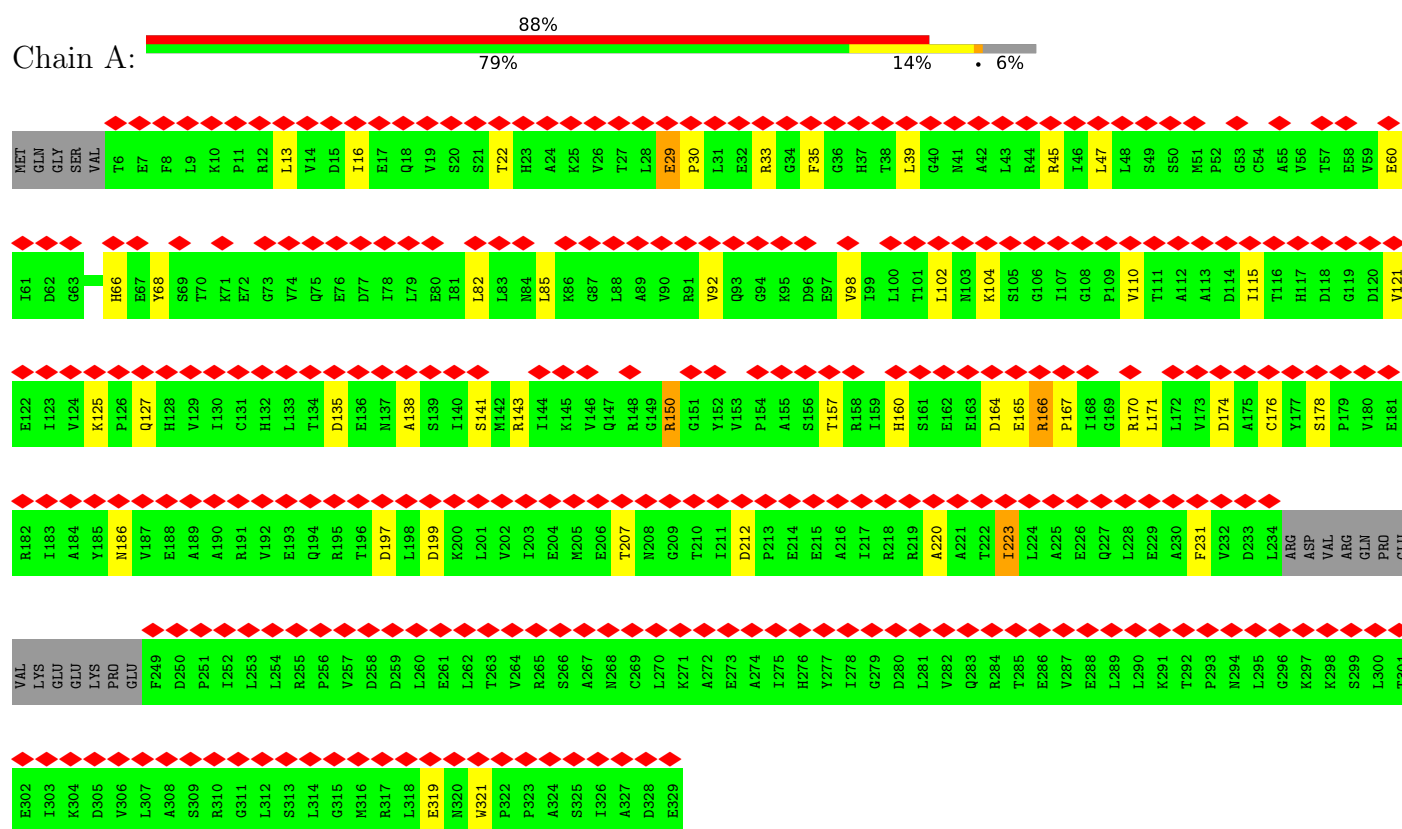
- Molecule 10 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

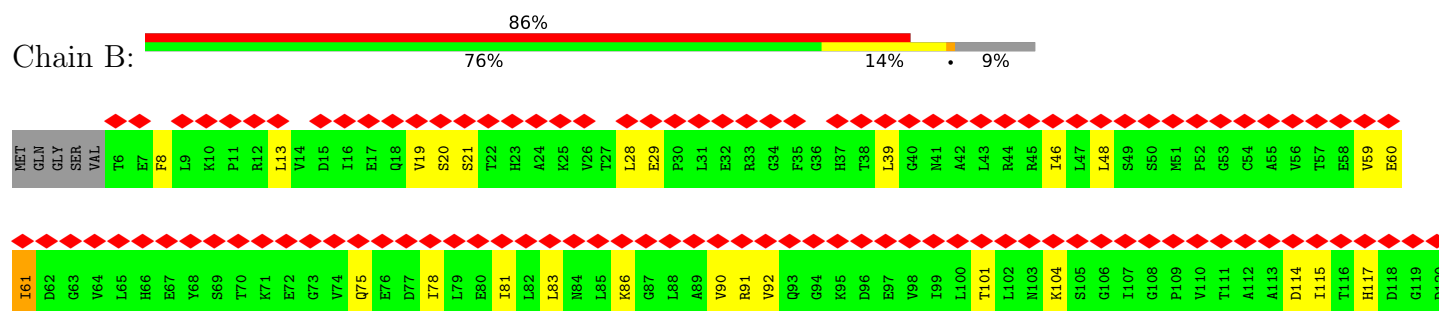
3 Residue-property plots

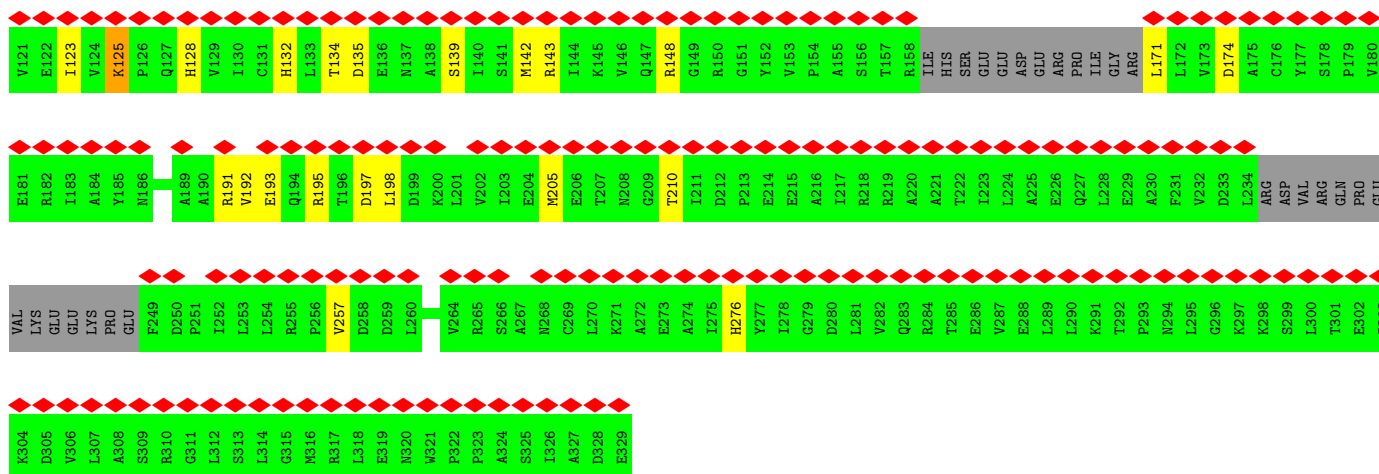
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: DNA-directed RNA polymerase subunit alpha

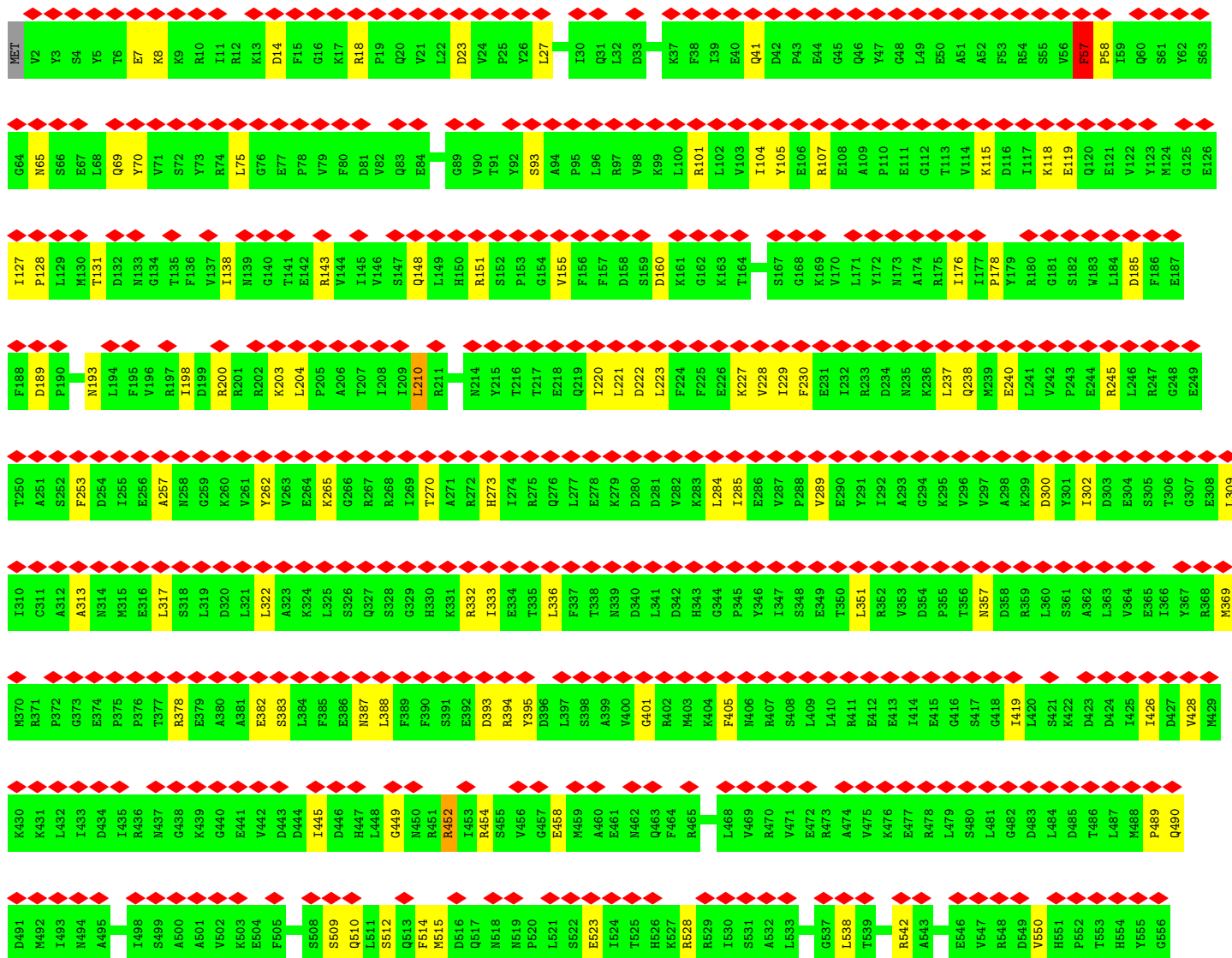
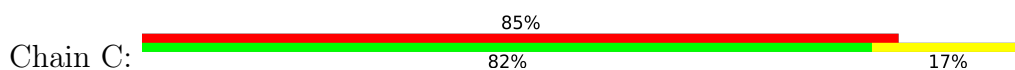


- Molecule 1: DNA-directed RNA polymerase subunit alpha



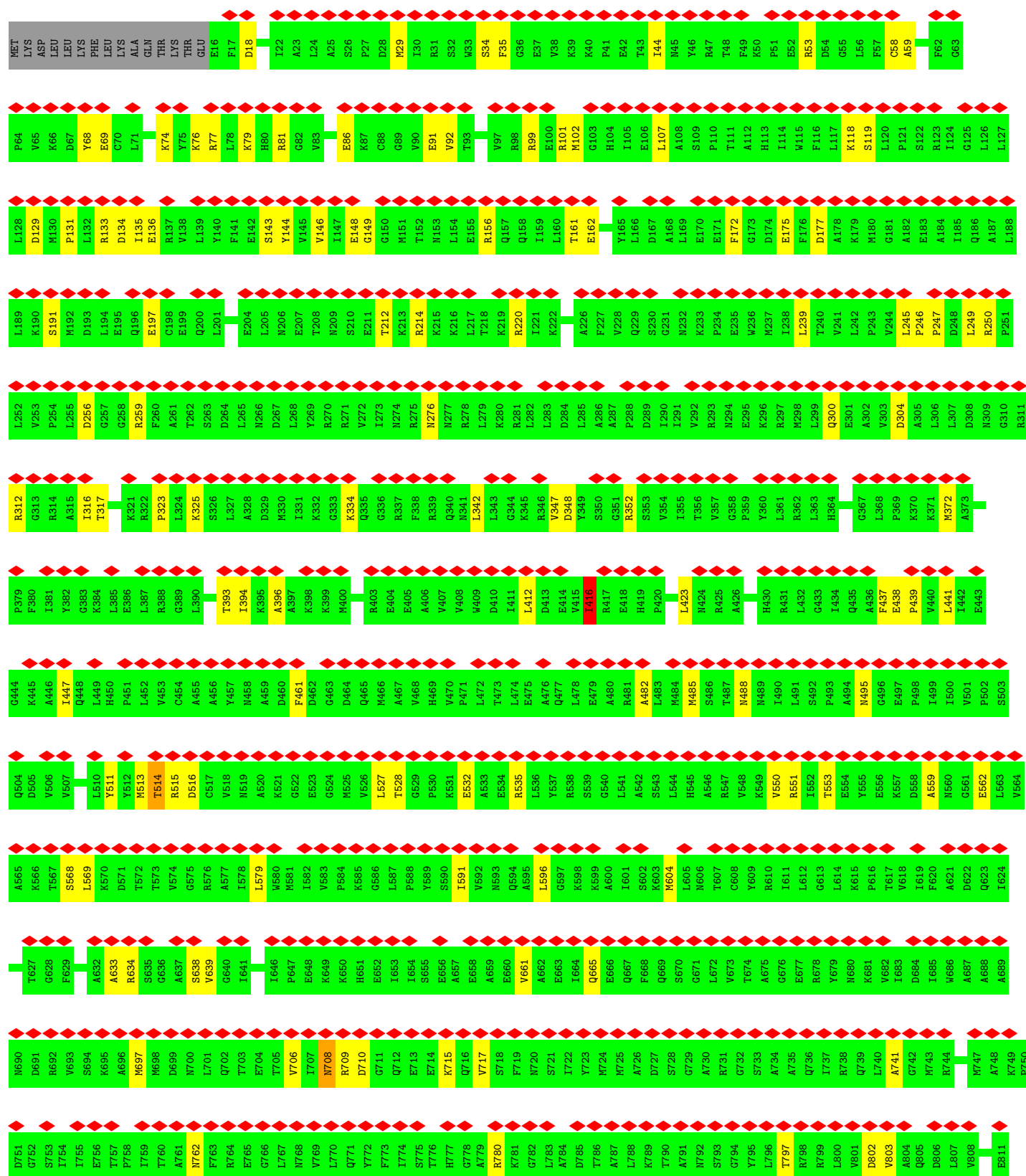
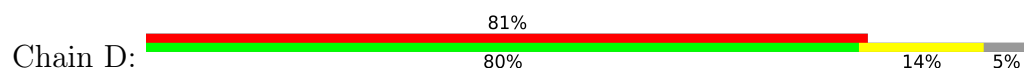


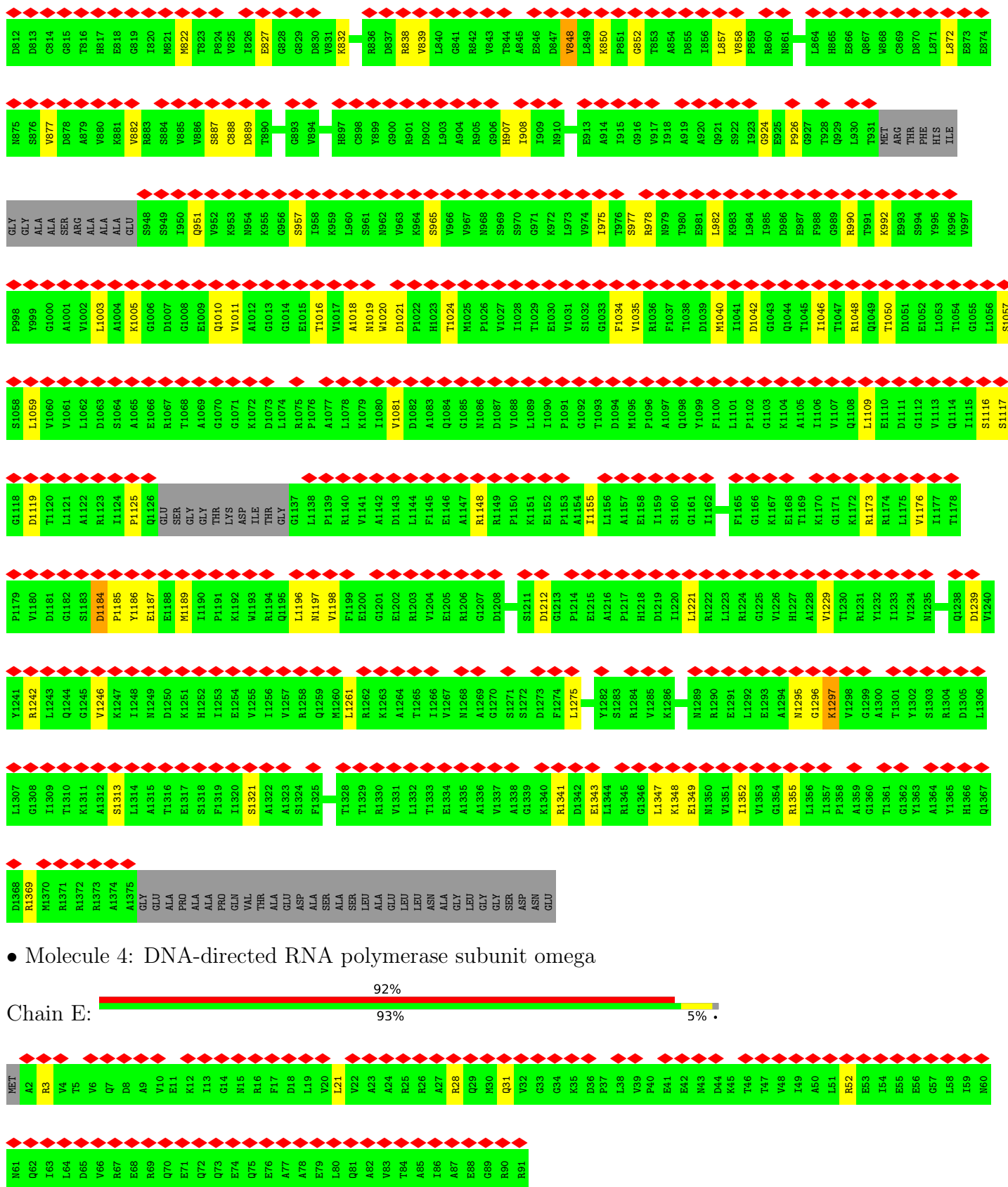
• Molecule 2: DNA-directed RNA polymerase subunit beta

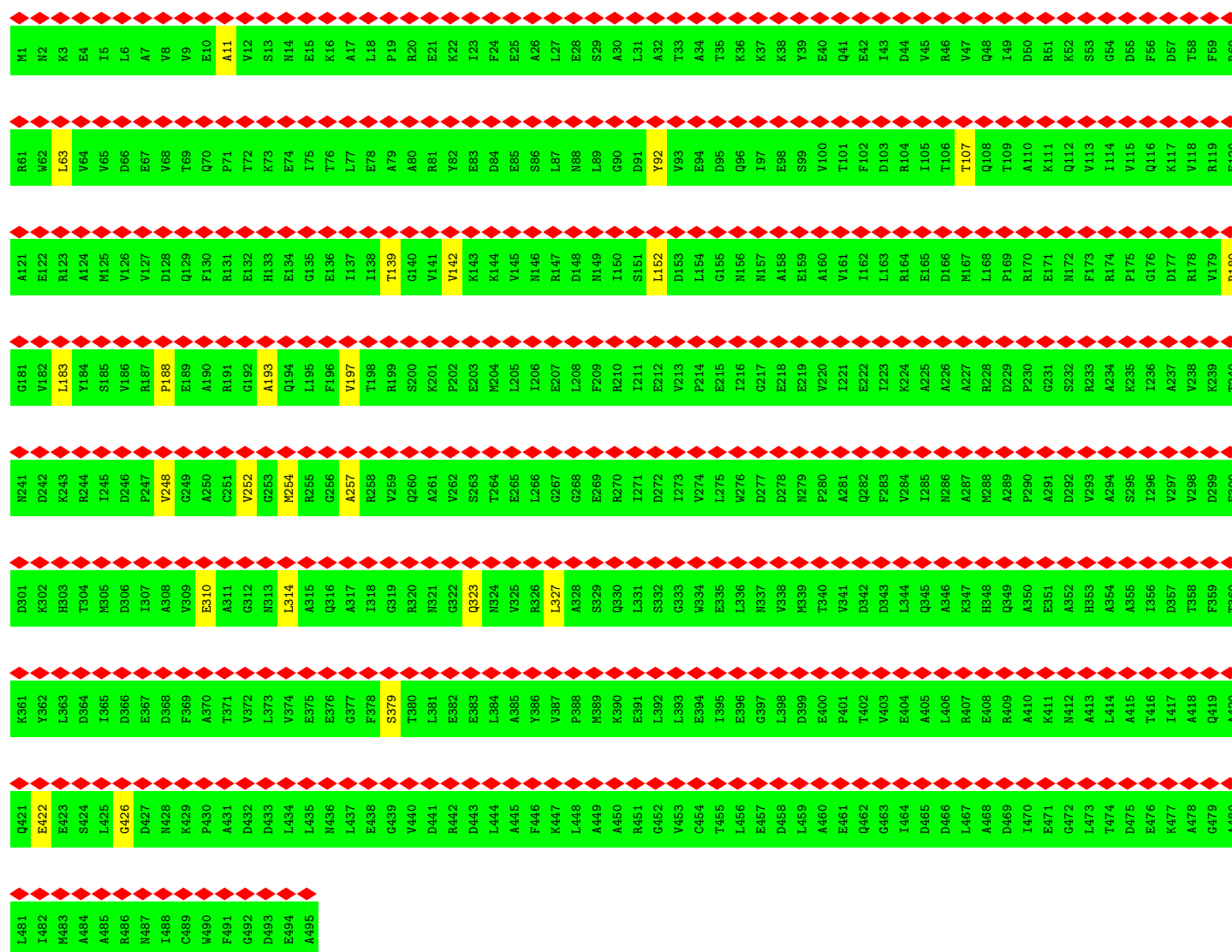


M1304	Y1305	K1306	N1307	I1308	V1309	D1310	G1311	N1312	H1313	Q1314	M1315	P1320	E1321	S1322	P1323	N1324	V1325	L1326	L1327	K1328	E1329	F1330	R1331	S1332	L1333	G1334	I1335	N1336	I1337	E1338	L1339	E1340	D1341	E1342																								
K1242	M1243	H1244	A1245	R1246	S1247	T1248	G1249	S1250	Y1251	L1253	V1254	T1255	Q1256	Q1257	P1258	L1259	G1260	G1261	K1262	A1263	Q1264	F1265	G1266	G1267	Q1268	R1269	F1270	G1271	E1272	M1273	E1274	V1275	A1276	L1277	L1278	E1279	Y1281	G1282	A1283	A1284																		
K1178	A1183	T1184	P1185	D1188	G1189	A1190	K1191	E1192	A1193	E1194	I1195	K1196	E1197	L1198	L1199	K1200	L1201	G1202	D1203	F1204	P1205	T1206	S1207	R1208	Q1209	I1210	R1211	L1212	Y1213	D1214	G1215	R1216	T1217	G1218	E1219	Q1220	F1221	E1222	R1223	P1224	V1225	T1226	V1227	G1228	Y1229	M1230	Y1231	M1232	L1233	K1234	L1235	N1236	H1237	L1238	V1239	D1240	D1241	
G1118	M1119	A1120	I1121	K1122	G1123	I1124	G1125	D1126	K1127	I1128	A1129	M1130	L1132	K1133	Q1134	Q1135	Q1136	E1137	V1138	A1139	K1140	L1141	R1142	E1143	F1144	I1145	Q1146	R1147	A1148	Y1149	L1150	L1151	G1152	A1153	D1154	V1155	R1156	Q1157	K1158	V1159	D1160	L1161	S1162	T1163	F1164	S1165	D1166	E1167	E1168	V1169	M1170	R1171	L1172	L1173	A1174	E1175	N1176	R1177
V1056	K1057	R1058	R1059	I1060	Q1061	P1062	G1063	D1064	K1065	M1066	A1067	K1068	R1069	H1070	G1071	N1072	K1073	G1074	V1075	I1076	S1077	K1078	I1079	N1080	P1081	I1082	E1083	D1084	M1085	P1086	Y1087	E1088	M1089	N1090	G1091	T1092	P1093	V1094	D1095	L1096	V1097	L1098	N1099	P1100	L1101	G1102	R1106	M1107	M1108	I1109	G1110	Q1111	I1112	L1113	E1114	T1115	H1116	L1117
D995	R996	W997	L998	E999	L1000	G1001	L1002	T1003	D1004	E1005	E1006	K1007	Q1008	N1009	Q1010	L1011	E1012	Q1013	L1014	A1015	E1016	Q1017	Y1018	D1019	E1020	L1021	K1022	H1023	E1024	F1025	E1026	K1027	K1028	L1029	E1030	A1031	K1032	R1033	I1036	T1037	Q1038	G1039	D1040	D1041	L1042	A1043	P1044	G1045	V1046	K1047	K1048	L1049	V1050	K1051	V1052	Y1053	L1054	A1055
Q932	V933	F934	T935	R936	K941	D942	K943	R944	A945	L946	E947	T948	E949	E950	H951	Q952	L953	K954	Q955	A956	K957	K958	D959	L960	S961	E962	E963	L964	Q965	L966	L967	E968	A969	G970	L971	F972	S973	R974	T975	R976	A977	L978	V980	A981	G982	G983	V984	E985	A986	E987	K988	L989	D990	K991	L992	P993	R994	
G869	T870	V871	Y872	T873	G874	A875	T878	D881	T882	L883	V884	G885	K886	P889	K890	G891	E892	T893	Q894	L895	T896	P897	E898	E899	K900	L901	L902	R903	A904	I905	F906	G907	E908	K909	A910	S911	D912	V913	K914	D915	S916	S917	L918	R919	V920	P921	N922	G923	V924	S925	G926	T927	V928	I929	D930	V931		
N808	G809	Y810	N811	F812	E813	D814	S815	I816	L817	V818	S819	E820	R821	V822	V823	Q824	E825	D826	R827	F828	T829	T830	I831	H832	I833	Q834	E835	L836	V839	S840	R841	D842	T843	K844	L845	G846	P847	E848	E849	I850	T851	A852	D853	I854	P855	N856	G858	E859	A860	A861	G862	S863	K864	L865	D866	E867	S868	
A746	G747	I748	D749	T750	Y751	N752	L753	T754	K755	Y756	S759	N760	Q761	N762	T763	C764	I765	N766	Q767	N768	P769	C770	V771	S772	L773	G774	E775	F776	V777	E778	K779	G780	L783	A784	D785	G786	P787	S788	T789	D790	L791	G792	E793	L794	A795	L796	G797	Q798	N799	M800	R801	A803	F804	M805	P806	N807		
M681	G682	Q686	R687	Q688	A689	T692	L693	R694	A695	D696	K697	L699	V700	G703	M704	E705	R706	A707	P708	S712	G713	V714	T715	A716	V717	A718	K719	R720	G721	G722	V723	V724	Q725	Q726	V727	D728	A729	S730	R731	I732	V733	I734	K735	P736	N737	E738	D739	E740	M741	V742	P743	G744	E745					
N620	S621	N622	L623	D624	E625	E626	G627	H628	F629	V630	E631	D632	L633	V634	T635	C636	R637	S638	K639	G640	N641	S642	S643	L644	F645	S646	R647	D648	Q649	V650	R651	Y652	M653	D654	V655	S656	T657	Q658	Q659	V660	V661	S662	A665	S666	L667	I668	P669	F670	L671	E672	H673	D674	V675	A676	N677	R678	L680	

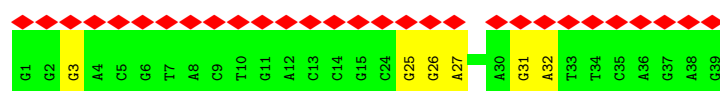
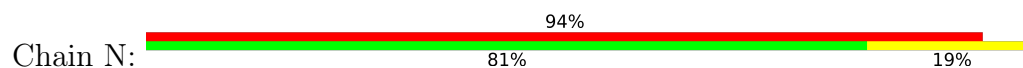
- Molecule 3: DNA-directed RNA polymerase subunit beta'







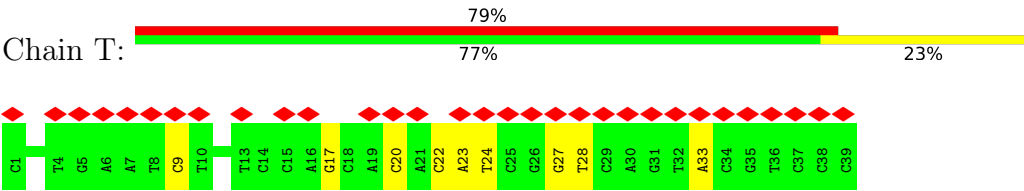
• Molecule 6: DNA (31-MER)



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



● Molecule 8: DNA (39-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	157100	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 ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.869	Depositor
Minimum map value	-1.326	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.086	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	308.0, 308.0, 308.0	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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

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	0.63	0/2189	0.76	1/2981 (0.0%)
1	B	0.58	0/2086	0.83	1/2841 (0.0%)
2	C	0.74	1/10742 (0.0%)	0.81	6/14494 (0.0%)
3	D	0.69	0/10514	0.80	2/14199 (0.0%)
4	E	0.55	0/711	0.70	0/956
5	F	0.23	0/2446	0.63	2/3406 (0.1%)
6	N	0.43	0/728	0.57	0/1121
7	R	0.49	0/494	0.70	0/766
8	T	0.55	0/876	0.61	0/1346
All	All	0.66	1/30786 (0.0%)	0.78	12/42110 (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	4
1	B	0	4
2	C	0	4
3	D	0	5
5	F	0	1
All	All	0	18

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1084	ASP	C-N	-15.66	1.08	1.33

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	135	ILE	N-CA-C	-8.60	104.36	112.96
2	C	1084	ASP	CA-C-N	7.11	130.59	120.49
2	C	1084	ASP	C-N-CA	7.11	130.59	120.49
2	C	910	ALA	CA-C-N	5.92	132.35	121.70
2	C	910	ALA	C-N-CA	5.92	132.35	121.70

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	166	ARG	Peptide
1	A	29	GLU	Peptide
1	A	319	GLU	Peptide
1	A	321	TRP	Peptide
1	B	19	VAL	Peptide

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	2168	0	1960	31	0
1	B	2068	0	1867	26	0
2	C	10573	0	10584	151	0
3	D	10357	0	10571	138	0
4	E	709	0	719	7	0
5	F	2447	0	1180	11	0
6	N	647	0	347	6	0
7	R	444	0	228	9	0
8	T	785	0	440	8	0
9	D	1	0	0	0	0
10	D	2	0	0	0	0
All	All	30201	0	27896	347	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 6.

The worst 5 of 347 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:393:ASP:OD2	2:C:394:ARG:NH1	1.90	1.04
3:D:1341:ARG:NH1	3:D:1343:GLU:OE2	1.98	0.97
3:D:129:ASP:OD2	3:D:220:ARG:NH1	1.98	0.96
1:A:33:ARG:NH1	1:A:199:ASP:OD2	2.02	0.91
3:D:832:LYS:HZ2	3:D:1242:ARG:HH12	1.12	0.90

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	306/329 (93%)	262 (86%)	44 (14%)	0	100	100
1	B	292/329 (89%)	243 (83%)	47 (16%)	2 (1%)	18	51
2	C	1339/1342 (100%)	1190 (89%)	147 (11%)	2 (0%)	48	79
3	D	1328/1407 (94%)	1191 (90%)	136 (10%)	1 (0%)	48	79
4	E	88/91 (97%)	82 (93%)	6 (7%)	0	100	100
5	F	493/495 (100%)	458 (93%)	35 (7%)	0	100	100
All	All	3846/3993 (96%)	3426 (89%)	415 (11%)	5 (0%)	49	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	57	PHE
2	C	58	PRO
1	B	61	ILE
1	B	117	HIS
3	D	1185	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	194/286 (68%)	191 (98%)	3 (2%)	57	70
1	B	183/286 (64%)	180 (98%)	3 (2%)	55	69
2	C	1155/1157 (100%)	1135 (98%)	20 (2%)	53	69
3	D	1114/1168 (95%)	1102 (99%)	12 (1%)	65	74
4	E	74/75 (99%)	74 (100%)	0	100	100
All	All	2720/2972 (92%)	2682 (99%)	38 (1%)	57	71

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	212	THR
3	D	882	VAL
3	D	239	LEU
3	D	708	ASN
3	D	1261	LEU

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	469	HIS
3	D	1019	ASN
3	D	1010	GLN
3	D	1023	HIS
2	C	604	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
7	R	19/21 (90%)	6 (31%)	1 (5%)

5 of 6 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	R	18	G
7	R	19	C
7	R	20	G
7	R	21	A
7	R	25	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	R	20	G

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 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
6	N	1
7	R	1
2	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	N	15:DG	O3'	24:DC	P	28.78
1	R	5:A	O3'	14:U	P	17.75
1	C	1084:ASP	C	1085:MET	N	1.08

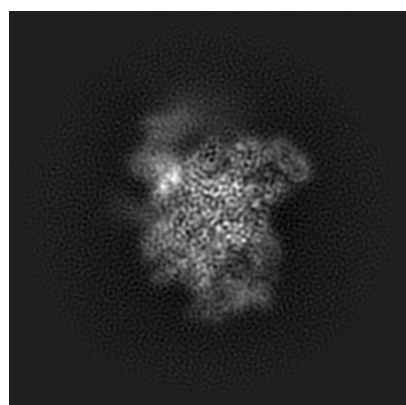
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4275. These allow visual inspection of the internal detail of the map and identification of artifacts.

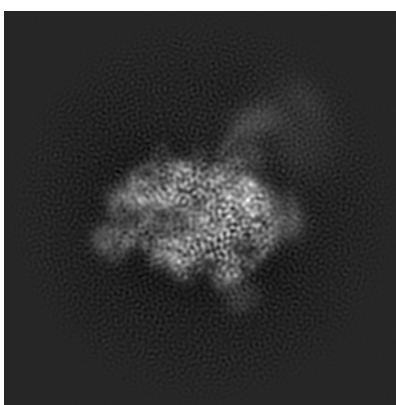
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

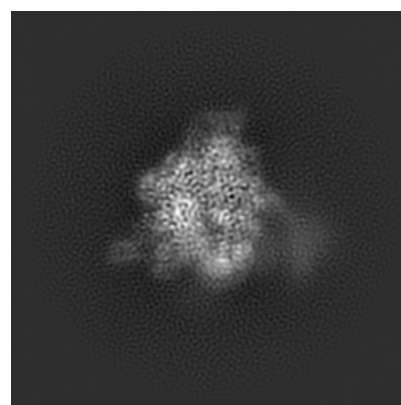
6.1.1 Primary map



X



Y

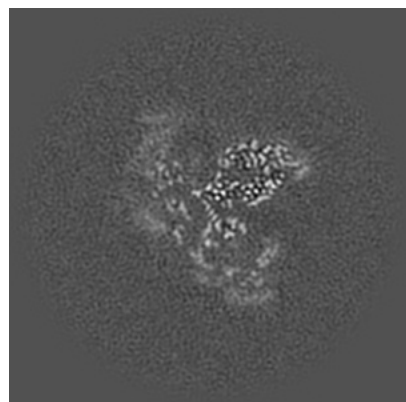


Z

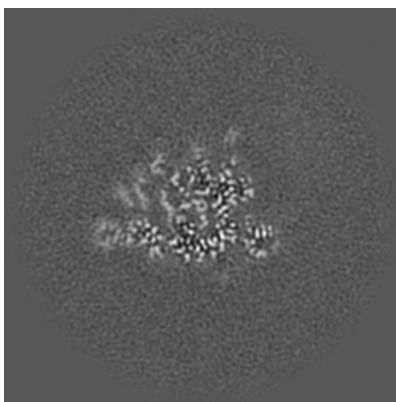
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

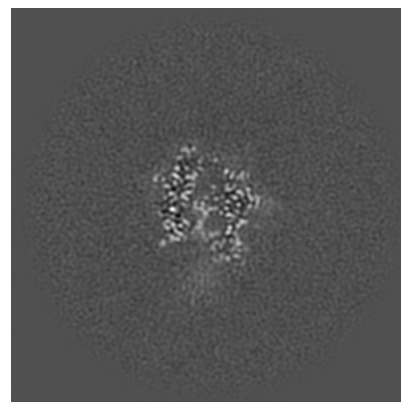
6.2.1 Primary map



X Index: 140



Y Index: 140

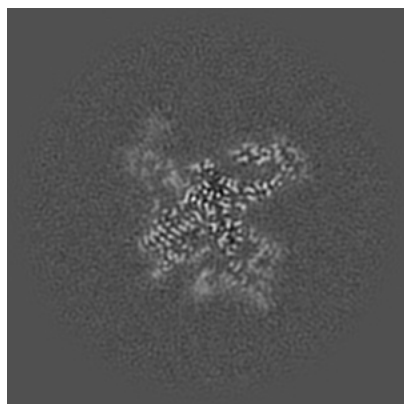


Z Index: 140

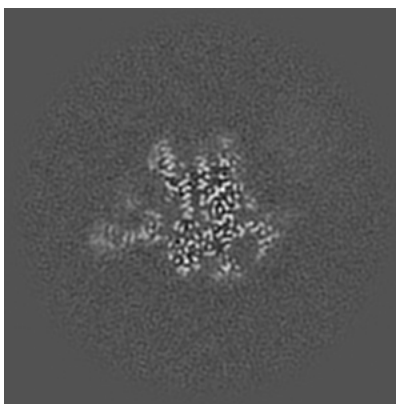
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

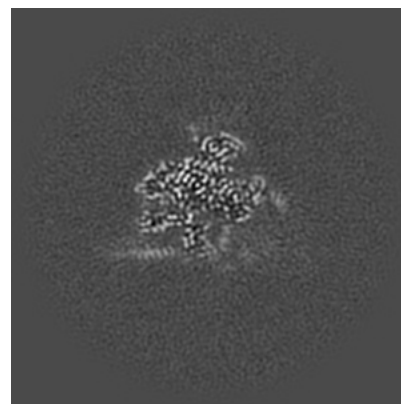
6.3.1 Primary map



X Index: 150



Y Index: 147

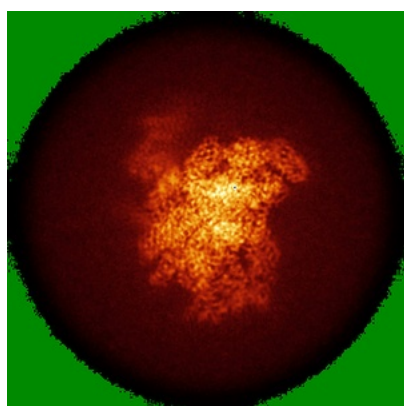


Z Index: 156

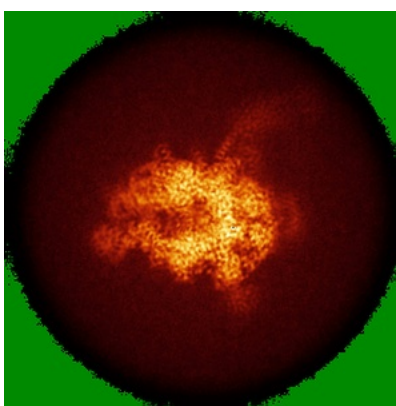
The images above show the largest variance slices of the map in three orthogonal directions.

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

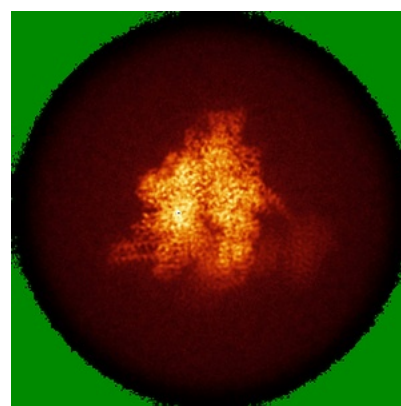
6.4.1 Primary map



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

This section was not generated.

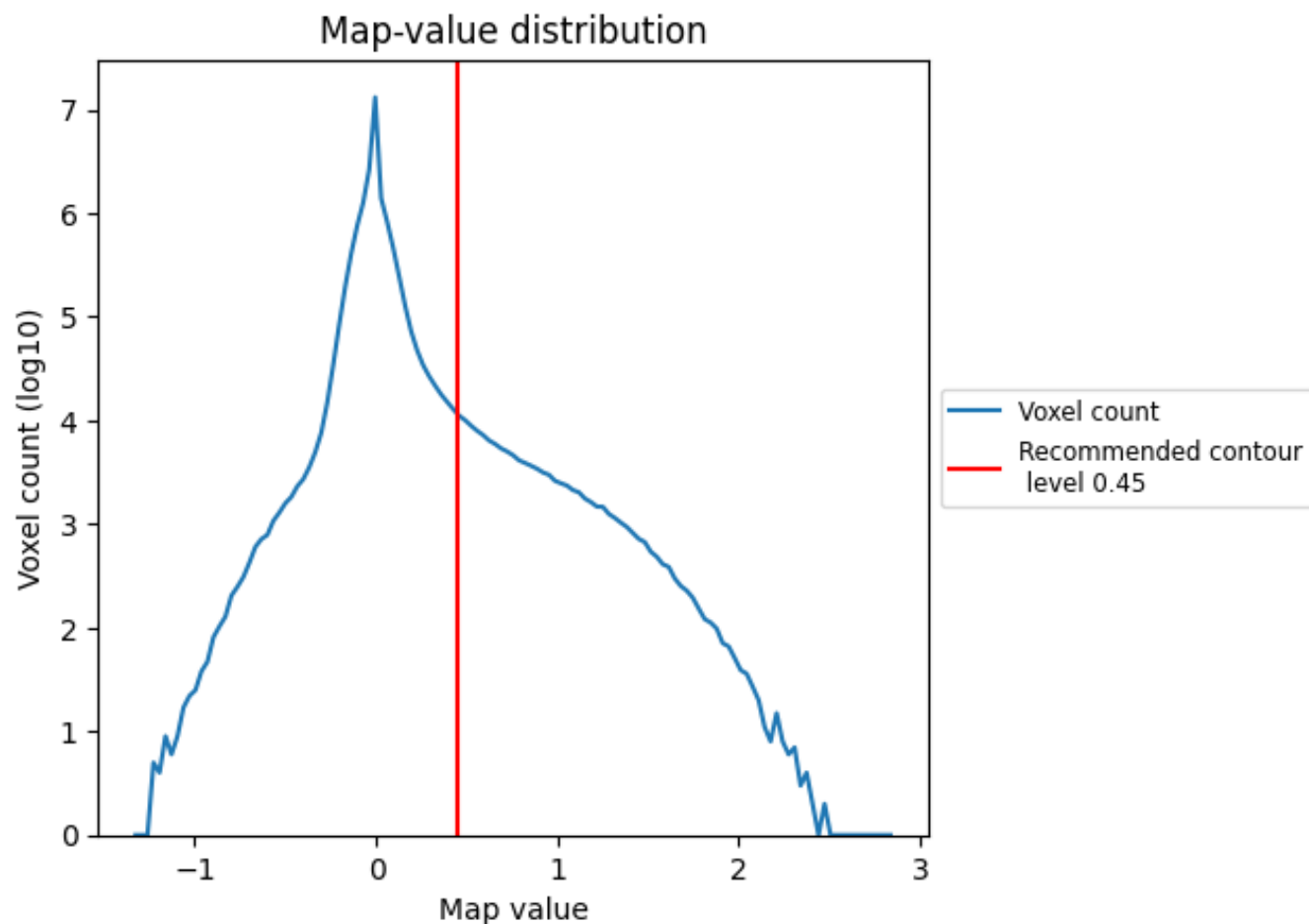
6.6 Mask visualisation

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

7 Map analysis [i](#)

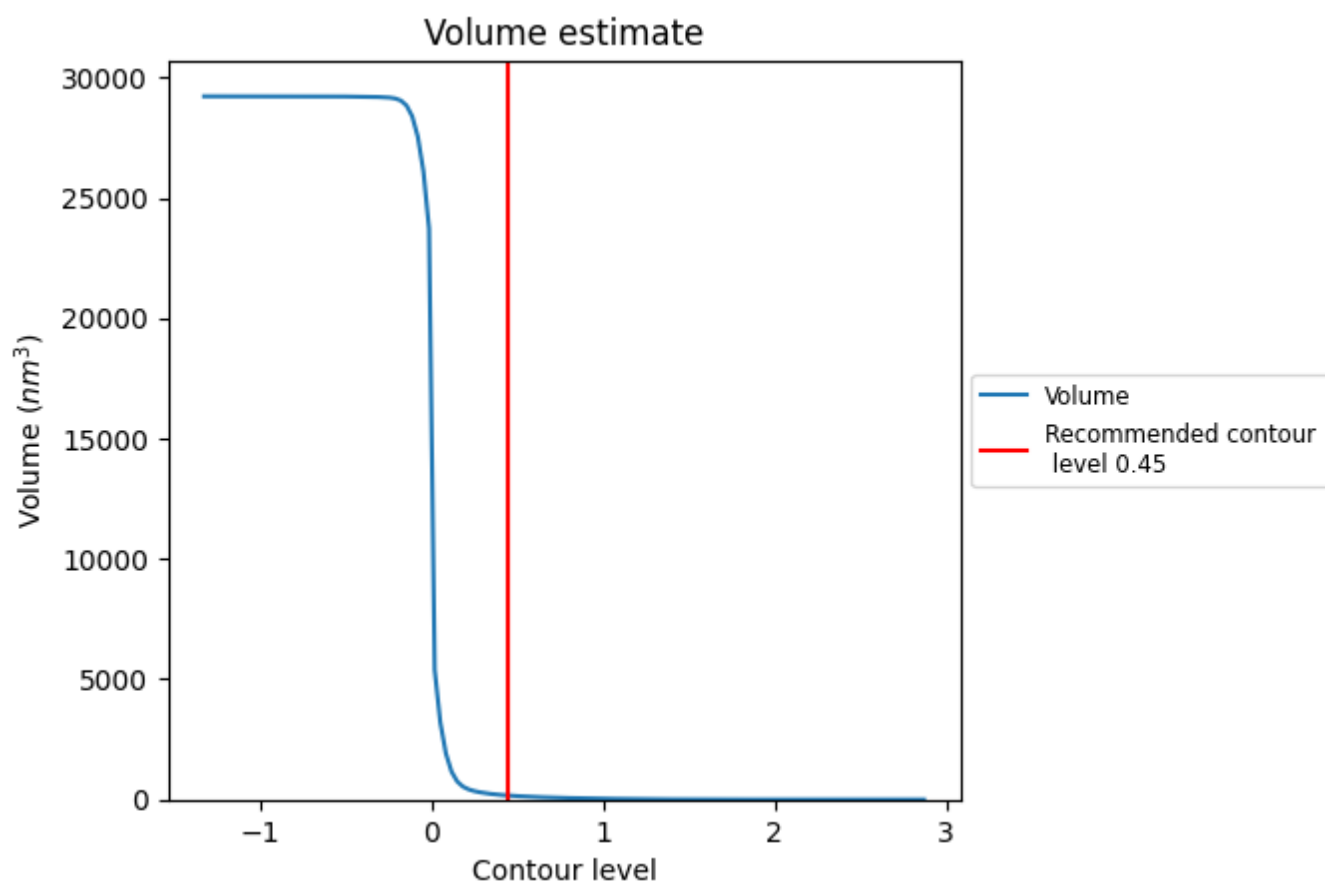
This section contains the results of statistical analysis of the map.

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.

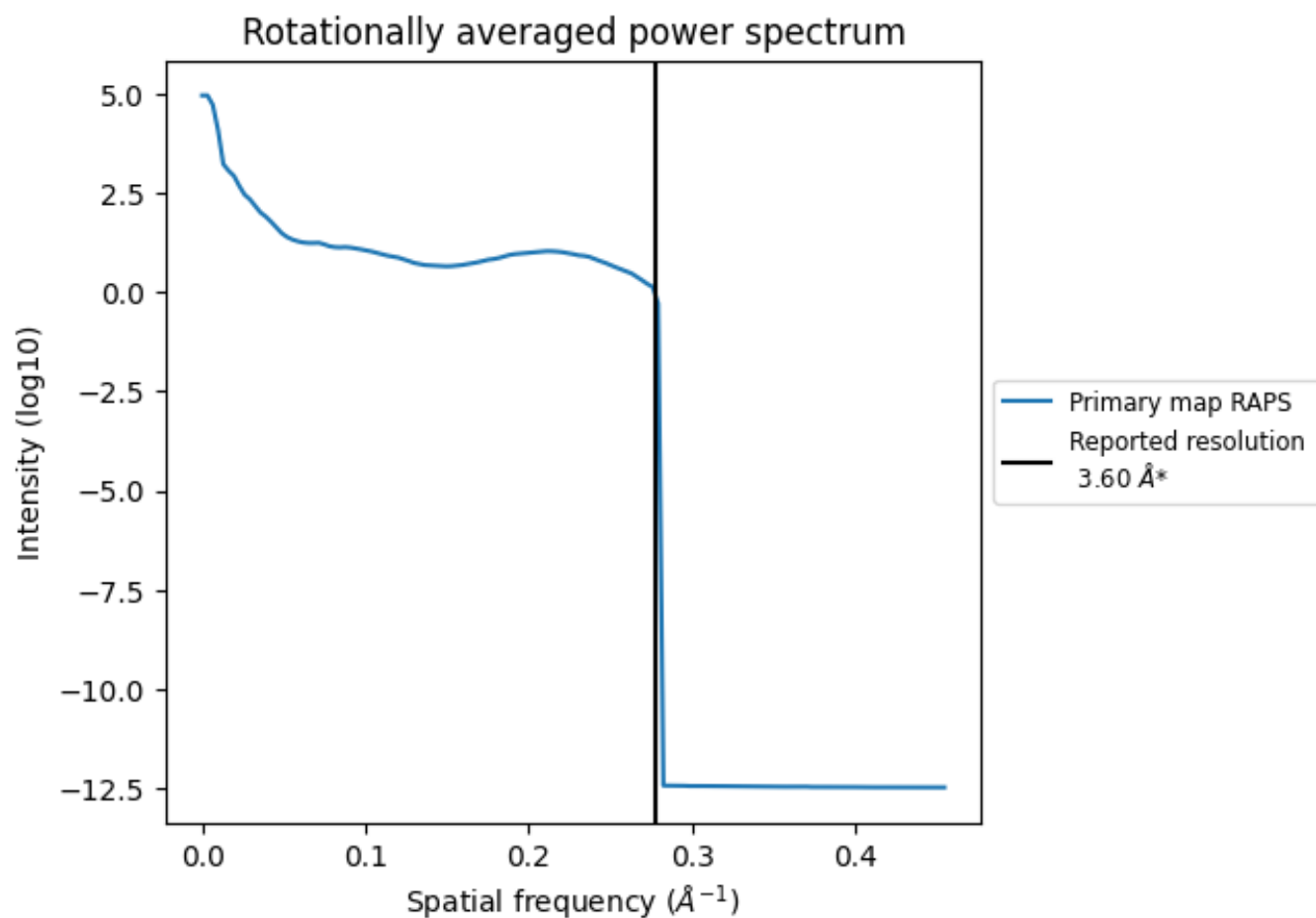
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 166 nm³; this corresponds to an approximate mass of 150 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 0.278 Å⁻¹

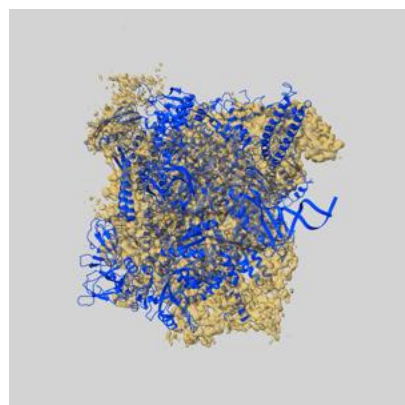
8 Fourier-Shell correlation

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

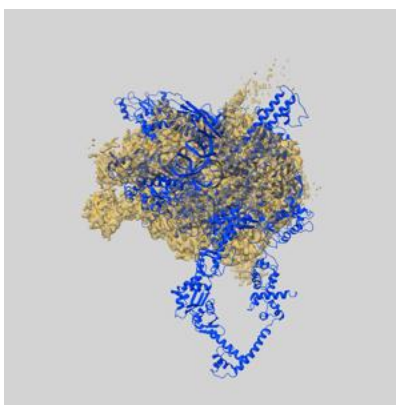
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4275 and PDB model 6FLQ. Per-residue inclusion information can be found in section 3 on page 6.

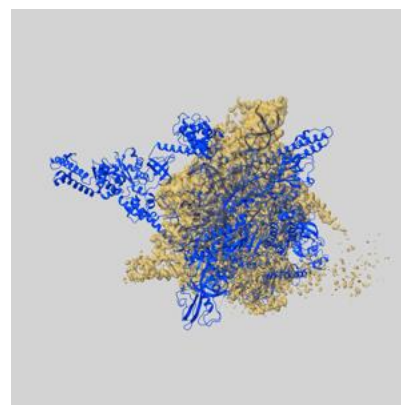
9.1 Map-model overlay [i](#)



X



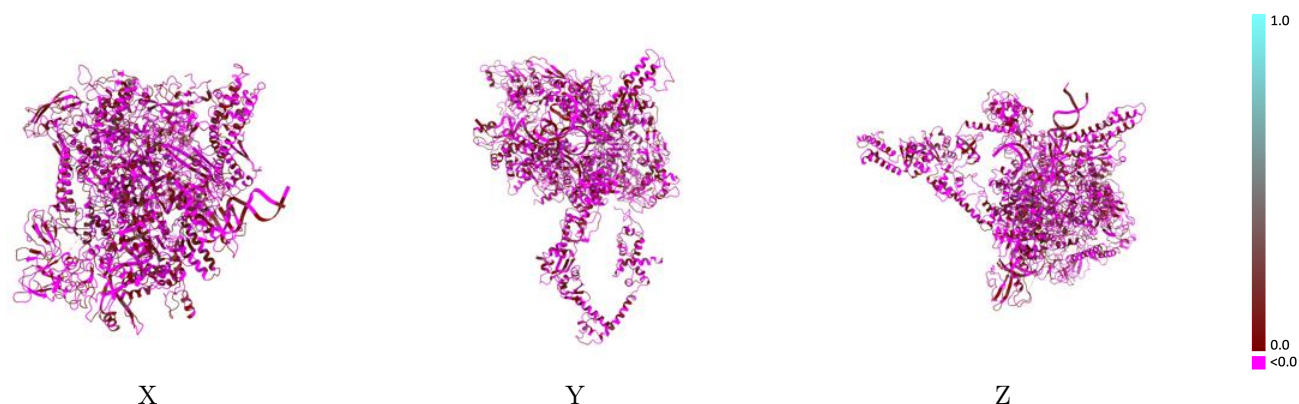
Y



Z

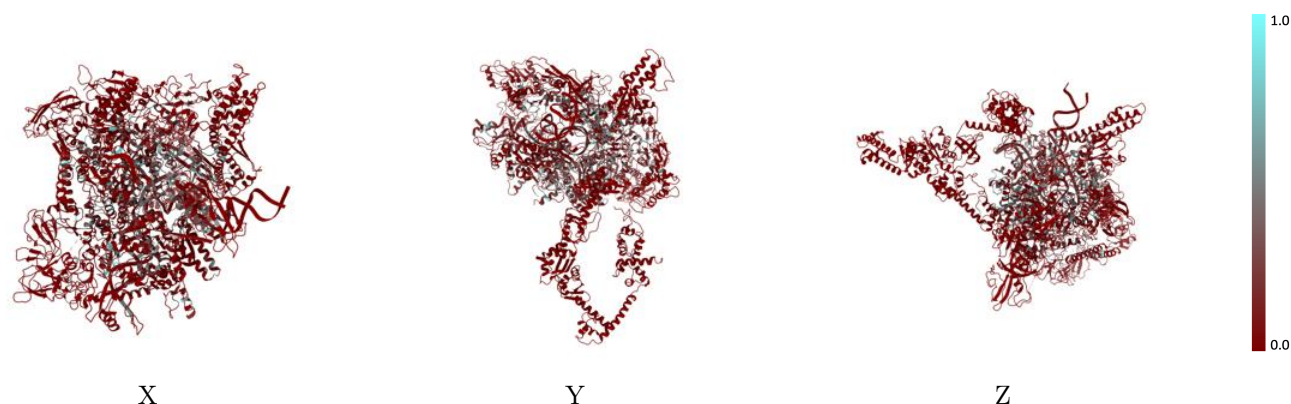
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



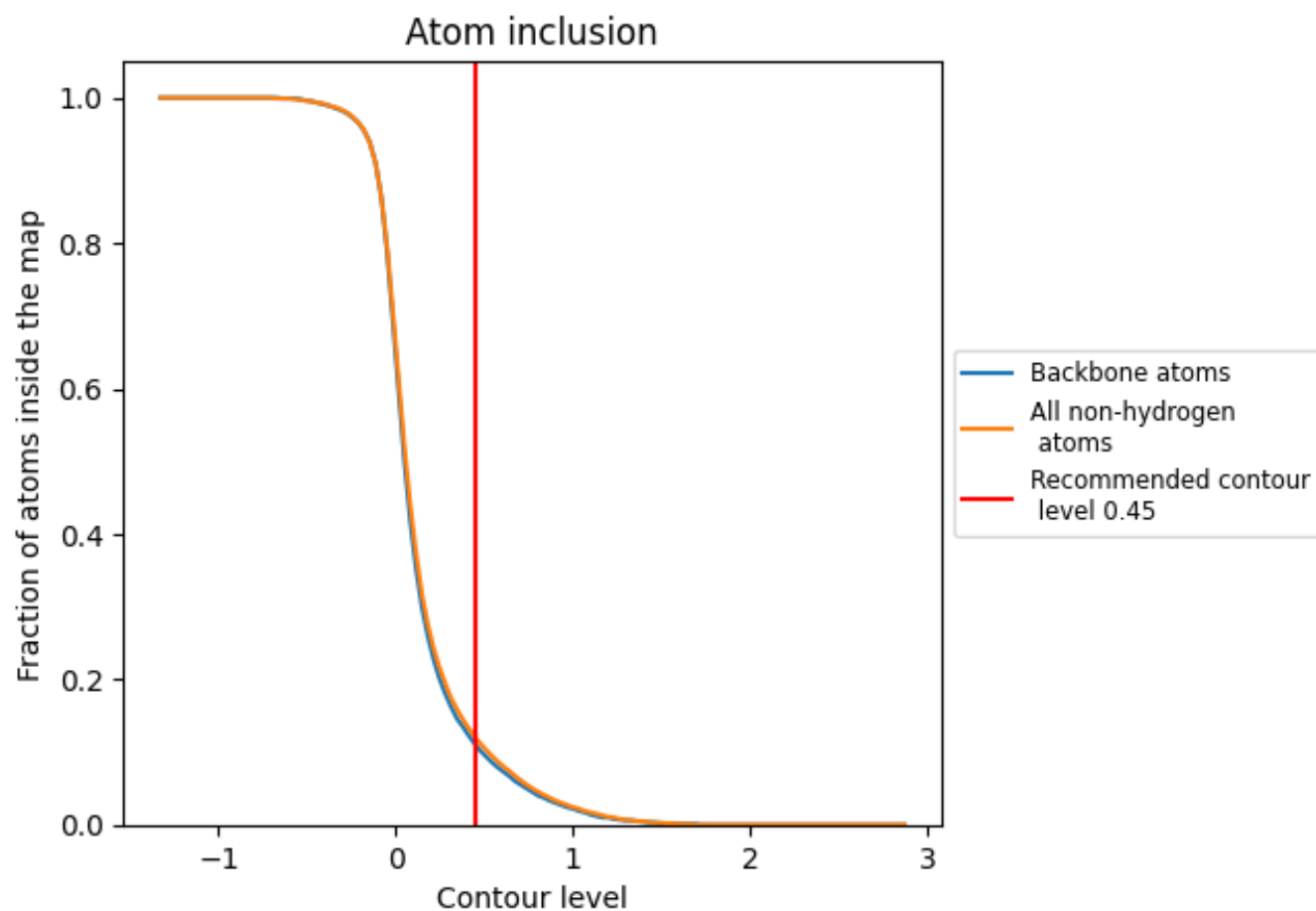
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion ⓘ



At the recommended contour level, 11% of all backbone atoms, 12% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.1200	-0.0110
A	0.0840	-0.0070
B	0.0490	-0.0030
C	0.1390	-0.0150
D	0.1490	-0.0060
E	0.0680	-0.0180
F	0.0010	-0.0220
N	0.1130	-0.0070
R	0.2280	-0.0290
T	0.1530	-0.0050

1.0

0.0

<0.0