



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:18 PM UTC

PDB ID : 6CNF / pdb_00006cnf
EMDB ID : EMD-7533
Title : Yeast RNA polymerase III elongation complex
Authors : Han, Y.; He, Y.
Deposited on : 2018-03-08
Resolution : 4.50 Å (reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

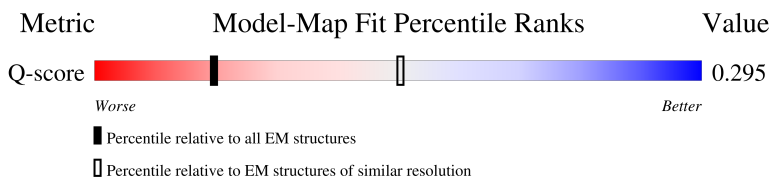
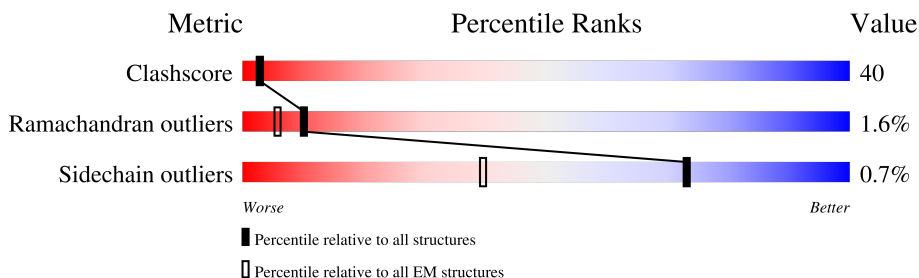
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.50 Å.

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





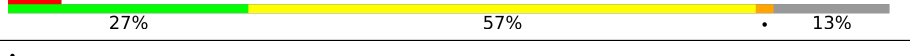
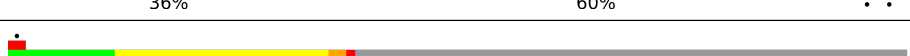

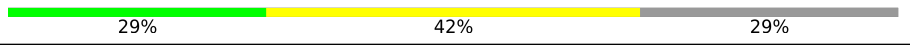
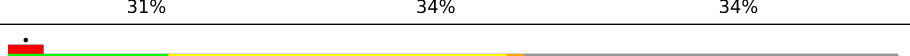
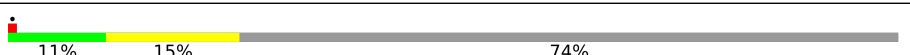
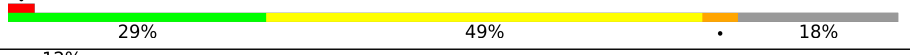
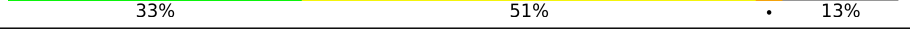
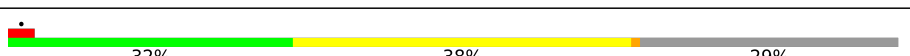






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	1460	 38% 57%
2	B	1149	 35% 59%
3	C	335	 39% 56%
4	D	161	 30% 41% 26%

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Mol	Chain	Length	Quality of chain
5	E	215	
6	F	155	
7	G	212	
8	H	146	
9	I	110	
10	J	70	
11	K	142	
12	L	70	
13	M	282	
14	N	422	
15	O	654	
16	P	317	
17	Q	251	
18	R	736	
19	S	594	
20	X	79	
21	Y	79	

2 Entry composition [i](#)

There are 22 unique types of molecules in this entry. The entry contains 47675 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 III subunit RPC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1428	11159	7029	1972	2099	59	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase III subunit RPC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1114	8788	5558	1516	1654	60	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	335	2655	1681	454	511	9	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase III subunit RPC9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	119	977	628	156	187	6	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	215	1759	1116	310	321	12	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	83	671	429	114	125	3	0	0

- Molecule 7 is a protein called DNA-directed RNA polymerase III subunit RPC8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	184	Total	C	N	O	S	0	0
			1484	972	239	267	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	140	Total	C	N	O	S	0	0
			1120	703	188	224	5		

- Molecule 9 is a protein called DNA-directed RNA polymerase III subunit RPC10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	42	Total	C	N	O	S	0	0
			321	204	47	64	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	67	Total	C	N	O	S	0	0
			549	350	95	98	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	101	Total	C	N	O	S	0	0
			792	496	130	161	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	46	Total	C	N	O	S	0	0
			363	224	72	63	4		

- Molecule 13 is a protein called DNA-directed RNA polymerase III subunit RPC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	164	Total	C	N	O	S	0	0
			1338	857	227	253	1		

- Molecule 14 is a protein called DNA-directed RNA polymerase III subunit RPC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	N	110	845	536	152	154	3	0	0

- Molecule 15 is a protein called DNA-directed RNA polymerase III subunit RPC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	O	539	4329	2756	741	813	19	0	0

- Molecule 16 is a protein called DNA-directed RNA polymerase III subunit RPC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	P	277	2242	1438	368	425	11	0	0

- Molecule 17 is a protein called DNA-directed RNA polymerase III subunit RPC7,DNA-directed RNA polymerase III subunit RPC7,DNA-directed RNA polymerase III subunit RPC7,DNA-directed RNA polymerase III subunit RPC7,DNA-directed RNA polymerase III subunit RPC7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	Q	54	368	238	64	66	0	0

- Molecule 18 is a protein called Transcription factor IIIB 70 kDa subunit,TATA-box-binding protein,Transcription factor IIIB 70 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	R	522	4131	2621	733	757	20	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	383	ALA	-	linker	UNP P29056
R	384	MET	-	linker	UNP P29056
R	385	PRO	-	linker	UNP P29056
R	386	TRP	-	linker	UNP P29056
R	567	GLY	-	linker	UNP P13393
R	568	SER	-	linker	UNP P13393
R	569	GLY	-	linker	UNP P13393
R	570	SER	-	linker	UNP P13393
R	571	GLY	-	linker	UNP P13393

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Chain	Residue	Modelled	Actual	Comment	Reference
R	572	SER	-	linker	UNP P13393
R	573	GLY	-	linker	UNP P13393
R	574	SER	-	linker	UNP P13393
R	575	GLY	-	linker	UNP P13393
R	576	SER	-	linker	UNP P13393
R	577	GLY	-	linker	UNP P13393
R	578	SER	CYS	engineered mutation	UNP P29056

- Molecule 19 is a protein called Transcription factor TFIIB component B",Transcription factor TFIIB component B",Transcription factor TFIIB component B",Transcription factor TFIIB component B",Transcription factor TFIIB component B",Transcription factor TFIIB component B".

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	S	217	1649	1035	286	321	7	0	0

- Molecule 20 is a DNA chain called DNA (79-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
20	X	47	959	463	164	286	46	0	0

- Molecule 21 is a DNA chain called DNA (79-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
21	Y	57	1169	560	220	333	56	0	0

- Molecule 22 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
22	A	2	Total	Zn	0
			2	2	
22	B	1	Total	Zn	0
			1	1	
22	I	1	Total	Zn	0
			1	1	
22	J	1	Total	Zn	0
			1	1	
22	L	1	Total	Zn	0
			1	1	

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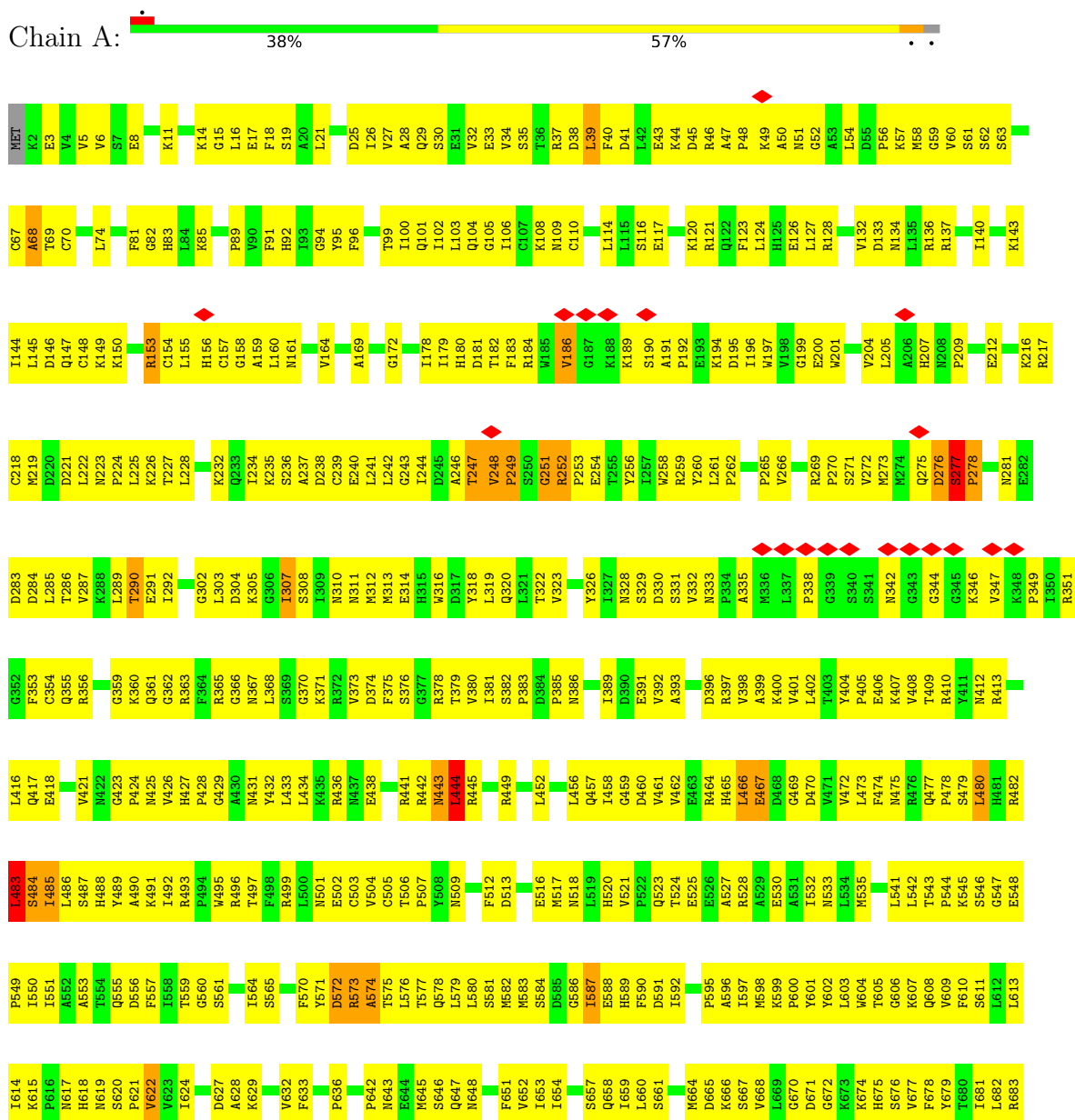
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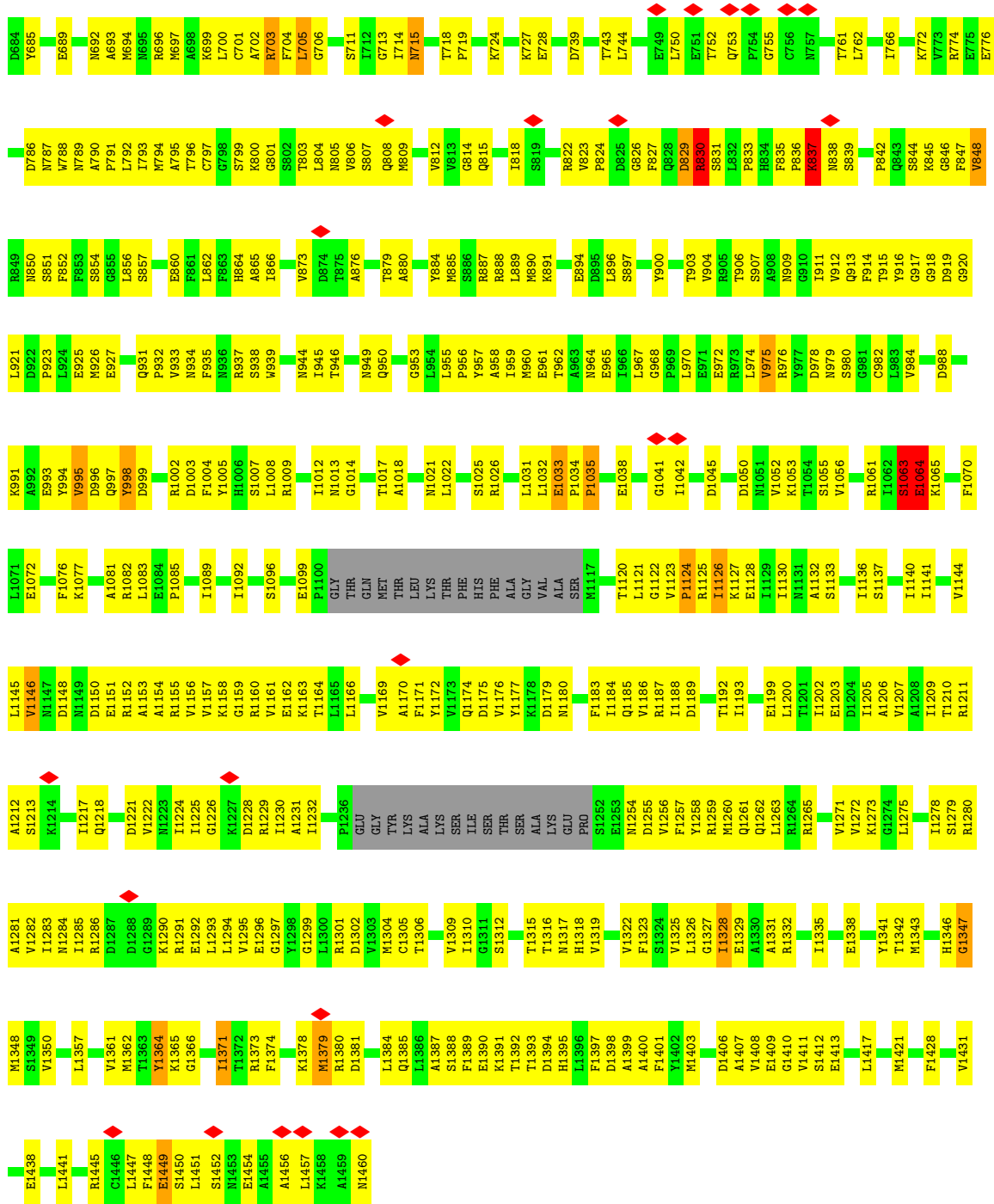
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
22	R	1	1	1	0

3 Residue-property plots

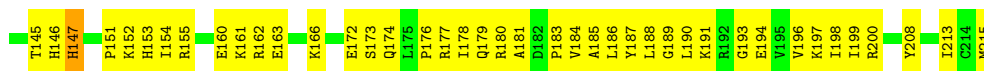
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: DNA-directed RNA polymerase III subunit RPC1

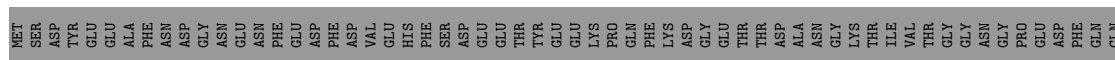
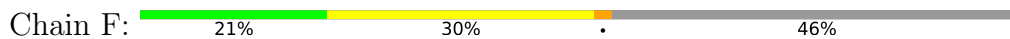




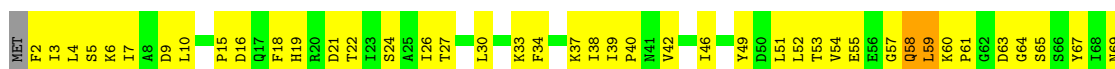
L1046	E974	R904	Q822	D747	L881	R610	D545	S480	K408	E338	E267	N203	G138	D63
Q1049	G976	R905	S823	P750	G882	P611	S546	R481	K409	A339	I268	R204	R139	S64
P1050	G975	G909	L824	G754	A683	I613	L549	S484	M410	L340	L271	I205	M140	M66
R1054	G981	D910	G825	N754	A685	I614	H550	G485	M411	D341	G274	I207	M141	F68
S1055	S982	K911	E831	Q754	G886	V615	L551	P486	R412	F342	E208	E208	M143	F67
R1056	D986	F912	V832	A755	G887	S616	N552	R487	M414	E344	A209	V207	H444	F68
D1057	S913	S913	Q619	T756	I888	Q619	Y553	A488	M414	K345	A210	D210	K145	D72
G1058	S914	R989	R620	V757	P889	S620	G554	L488	E415	A346	D211	E211	K146	I76
G1059	S987	R915	Y842	F758	A690	R621	V555	Q490	Y416	L347	K212	K212	E148	I77
R1060	S988	H916	I843	V759	P691	R622	V556	Q490	D417	Q280	G214	G214	E149	I77
L1061	K989	G917	N844	M760	H692	V622	L557	Q493	A418	Y348	G214	G214	G150	Q81
L1062	R990	Q918	H623	S761	H693	K623	N558	L419	L419	I349	I349	I349	G150	Q81
G1063	L991	K919	V647	Y762	N694	D624	F494	L420	L420	M552	V216	V216	R151	L82
E1064	V992	G920	P848	S763	Q895	I625	G495	F495	S421	T953	Q217	Q217	M152	L83
G1065	D993	R921	T849	Q764	S696	H626	M496	L497	I422	A284	A284	A284	M153	L84
M1065	Q994	C922	N850	V765	L561	L627	T562	C498	M426	V255	V255	V255	P153	L84
E1066	K1001	G923	S851	D766	R697	R628	G563	T499	S426	R355	R355	R355	M155	S85
R1067	L1002	R930	P855	I767	H698	K629	S664	D501	M428	N362	S222	S222	M156	D86
D1068	M1003	D930	V637	D768	R698	L630	I565	D501	I429	F363	E288	E288	R157	V87
C1069	L1004	R931	F637	E768	N699	L631	T569	F504	T430	K364	E289	E289	L156	D88
I1070	L1005	M858	D636	A770	Q702	L635	E504	C508	M434	I366	K292	K292	L163	D89
I1071	Y1005	V860	F637	L771	M705	G635	F571	G509	R435	D367	I295	I295	Y164	D90
A1072	G1006	M861	D638	L772	A709	F637	R570	F571	R435	R369	T297	T297	Y165	D91
Y1073	S1007	I710	D639	M774	I710	D638	F571	C508	R435	D370	Q299	Q299	L166	D92
S1076	T1009	I713	F640	K775	I713	F640	Q574	G509	S438	D370	Q299	Q299	A166	D93
I1077	G1010	A714	L643	F575	A714	L643	R575	L510	T439	Y371	Y371	Y371	D167	D94
L1078	E1011	T864	G644	R576	T864	G644	H577	V511	M442	V372	Q300	Q300	E168	D95
L1079	C1012	Q717	L645	H577	N716	L645	L514	L514	M442	K375	A301	A301	E169	D96
L1080	L1013	Q717	L646	L578	Q717	L646	A515	F450	M449	R376	L302	L302	K170	D97
E1081	I1017	R780	V646	R580	R718	V646	L516	L516	M449	L377	L302	L302	A171	D98
R1082	F1018	F782	E647	R580	R718	V646	L516	L516	M449	E378	E303	E303	A172	D99
L1083	F1019	R720	E647	R580	R718	V646	L516	L516	M449	L379	G306	G306	A173	D100
I1085	R945	R720	E648	R580	R718	V646	L516	L516	M449	L379	K308	K308	A174	D101
S1086	I1022	I721	D722	T787	I721	D722	T518	T518	V454	G381	A380	A380	N175	D102
S1087	Y1023	D722	T723	L788	D722	T723	H519	H519	T455	G382	Q822	Q822	E176	D103
D1088	Y1024	L724	L724	R788	L724	L724	I520	I520	T455	L383	H244	H244	G177	D104
E1091	Q1025	L725	L725	R789	L725	L725	T521	T521	H456	L384	N245	N245	L178	D105
V1092	L1026	L795	L795	K790	L725	L725	D523	D523	R314	L384	N245	N245	L179	D106
V1093	L1027	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D107
D1093	L1028	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D108
V1094	H1029	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D109
C1095	H1030	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D110
G1099	V1031	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D111
L1100	D1032	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D112
M1101	D1033	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D113
G1102	K1034	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D114
Y1103	M1035	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D115
S1104	H1036	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D116
G1105	A1037	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D117
W1106	R1038	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D118
C1107	A1039	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D119
T1108	R1040	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D120
T1109	G1041	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D121
C1110	F1042	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D122
S1111	R1043	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D123
	A1044	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D124
	V1045	L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D125
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D126
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D127
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D128
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D129
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D130
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D131
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D132
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D133
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D134
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D135
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D136
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D137
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D138
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D139
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D140
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D141
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D142
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D143
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D144
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D145
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D146
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D147
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D148
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D149
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D150
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D151
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D152
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D153
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D154
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D155
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D156
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D157
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D158
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D159
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D160
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D161
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D162
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D163
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D164
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D165
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D166
		L796	L796	K790	L725	L725	D524	D524	R314	L384	N245	N245	L181	D167
		L796	L796	K790	L725	L725	D524	D524	R314	L384				



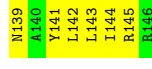
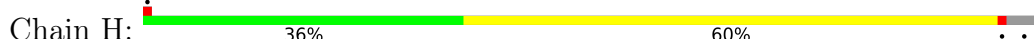
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2



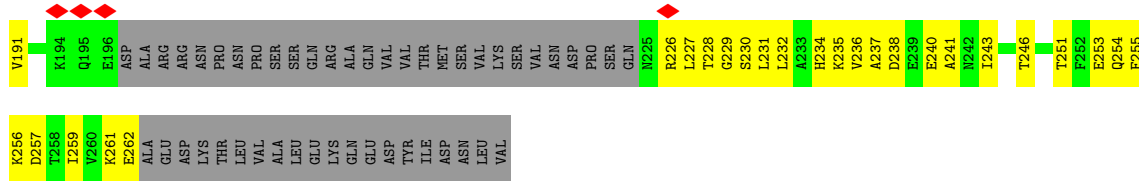
- Molecule 7: DNA-directed RNA polymerase III subunit RPC8



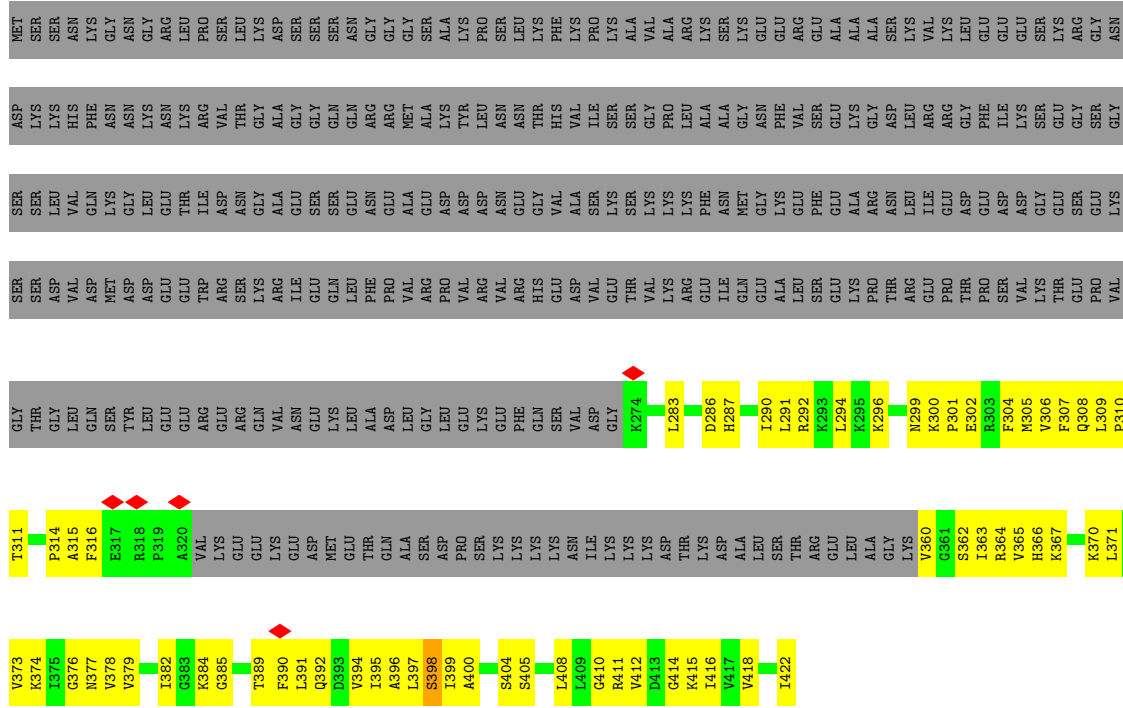
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



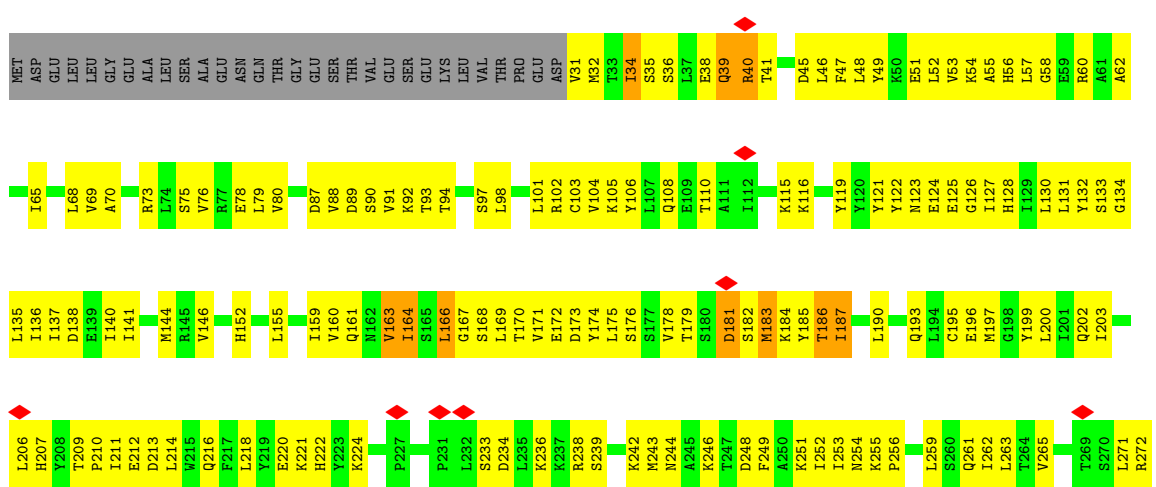
- Molecule 9: DNA-directed RNA polymerase III subunit RPC10

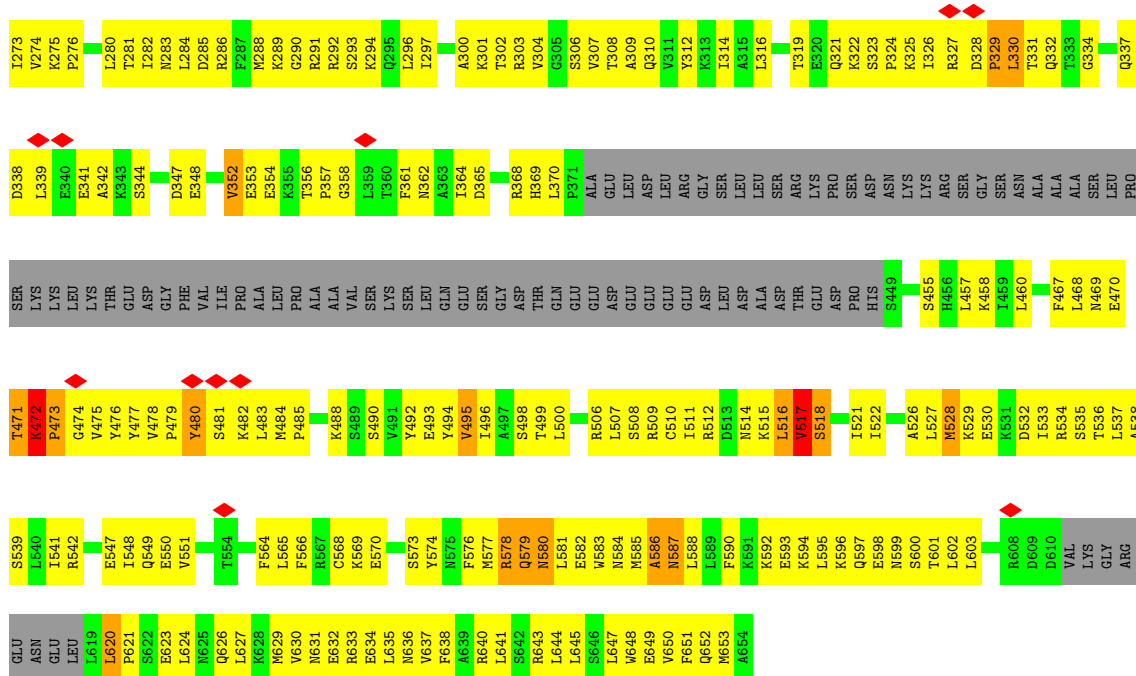


• Molecule 14: DNA-directed RNA polymerase III subunit RPC4

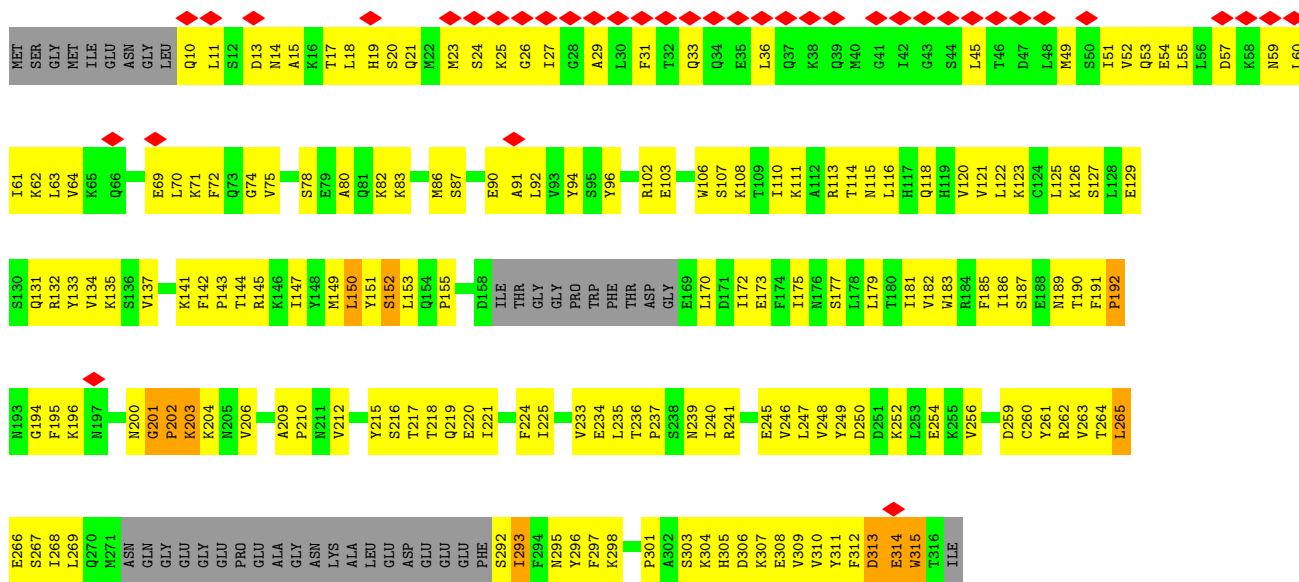


• Molecule 15: DNA-directed RNA polymerase III subunit RPC3





• Molecule 16: DNA-directed RNA polymerase III subunit RPC6



• Molecule 17: DNA-directed RNA polymerase III subunit RPC7, DNA-directed RNA polymerase III subunit RPC7, DNA-directed RNA polymerase III subunit RPC7, DNA-directed RNA polymerase III subunit RPC7, DNA-directed RNA polymerase III subunit RPC7



A64
C66
T66
A67
A68
T69
A70
T71
A72
T73
G74
T75
T76
G77
A78
A79

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	47141	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY; CTF amplitude correction was performed following 3D auto refinement in relion.	Depositor
Microscope	JEOL 3200FS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	68.9	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	0.197	Depositor
Minimum map value	-0.096	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.035	Depositor
Map size (\AA)	339.84, 339.84, 339.84	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.18, 1.18, 1.18	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

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	2/11358 (0.0%)	0.79	30/15345 (0.2%)
2	B	0.35	2/8943 (0.0%)	0.81	24/12068 (0.2%)
3	C	0.32	0/2711	0.78	7/3676 (0.2%)
4	D	0.20	0/991	0.69	2/1328 (0.2%)
5	E	0.28	0/1795	0.71	4/2416 (0.2%)
6	F	0.29	0/683	0.66	0/923
7	G	0.24	0/1523	0.65	2/2066 (0.1%)
8	H	0.28	0/1138	0.69	0/1540
9	I	0.30	0/328	0.89	0/445
10	J	0.44	1/558 (0.2%)	0.72	0/750
11	K	0.31	0/803	0.70	0/1083
12	L	0.28	0/365	0.75	1/485 (0.2%)
13	M	0.26	0/1369	0.84	9/1851 (0.5%)
14	N	0.24	0/855	0.77	3/1149 (0.3%)
15	O	0.30	0/4394	0.83	14/5928 (0.2%)
16	P	0.25	0/2282	0.70	5/3075 (0.2%)
17	Q	0.28	0/281	0.63	0/381
18	R	0.27	2/4200 (0.0%)	0.63	7/5659 (0.1%)
19	S	0.23	0/1464	0.60	2/1971 (0.1%)
20	X	0.30	0/1072	0.56	0/1651
21	Y	0.26	0/1313	0.47	0/2022
All	All	0.31	7/48426 (0.0%)	0.75	110/65812 (0.2%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	R	151	GLN	CA-C	7.58	1.63	1.52
18	R	173	LEU	C-N	7.15	1.50	1.33
10	J	63	TYR	C-N	-6.36	1.25	1.33
2	B	550	HIS	CA-C	6.29	1.60	1.52
1	A	829	ASP	CA-C	6.08	1.60	1.52

The worst 5 of 110 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	O	587	ASN	N-CA-C	12.08	124.44	111.03
15	O	472	LYS	CA-C-N	9.37	131.55	119.84
15	O	472	LYS	C-N-CA	9.37	131.55	119.84
2	B	824	LEU	N-CA-C	9.32	119.21	108.49
18	R	211	LYS	N-CA-C	9.19	121.30	111.28

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	11159	0	11285	1043	0
2	B	8788	0	8901	797	0
3	C	2655	0	2628	227	0
4	D	977	0	983	92	0
5	E	1759	0	1788	122	0
6	F	671	0	692	57	0
7	G	1484	0	1485	144	0
8	H	1120	0	1089	95	0
9	I	321	0	303	41	0
10	J	549	0	559	53	0
11	K	792	0	790	80	0
12	L	363	0	387	26	0
13	M	1338	0	1307	144	0
14	N	845	0	891	77	0
15	O	4329	0	4497	456	0
16	P	2242	0	2265	239	0
17	Q	368	0	308	28	0
18	R	4131	0	4230	280	0
19	S	1649	0	1455	111	0
20	X	959	0	539	59	0
21	Y	1169	0	645	66	0
22	A	2	0	0	0	0
22	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	I	1	0	0	0	0
22	J	1	0	0	0	0
22	L	1	0	0	0	0
22	R	1	0	0	0	0
All	All	47675	0	47027	3766	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 40.

The worst 5 of 3766 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:484:SER:HB2	2:B:1069:CYS:SG	1.40	1.58
15:O:330:LEU:CD1	15:O:331:THR:HG23	1.27	1.58
15:O:330:LEU:CD1	15:O:331:THR:H	1.20	1.54
1:A:1145:LEU:CD1	1:A:1146:VAL:H	1.20	1.52
2:B:590:ILE:HA	2:B:601:ILE:CD1	1.45	1.45

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	1422/1460 (97%)	1106 (78%)	292 (20%)	24 (2%)	7	35
2	B	1112/1149 (97%)	901 (81%)	194 (17%)	17 (2%)	8	38
3	C	333/335 (99%)	282 (85%)	44 (13%)	7 (2%)	5	30
4	D	113/161 (70%)	87 (77%)	24 (21%)	2 (2%)	6	33
5	E	213/215 (99%)	182 (85%)	29 (14%)	2 (1%)	14	49
6	F	81/155 (52%)	66 (82%)	13 (16%)	2 (2%)	4	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	178/212 (84%)	145 (82%)	30 (17%)	3 (2%)	7	35
8	H	136/146 (93%)	112 (82%)	23 (17%)	1 (1%)	18	55
9	I	40/110 (36%)	30 (75%)	7 (18%)	3 (8%)	1	10
10	J	65/70 (93%)	54 (83%)	11 (17%)	0	100	100
11	K	99/142 (70%)	77 (78%)	22 (22%)	0	100	100
12	L	44/70 (63%)	33 (75%)	11 (25%)	0	100	100
13	M	160/282 (57%)	127 (79%)	31 (19%)	2 (1%)	9	41
14	N	106/422 (25%)	82 (77%)	24 (23%)	0	100	100
15	O	533/654 (82%)	401 (75%)	116 (22%)	16 (3%)	3	22
16	P	271/317 (86%)	219 (81%)	47 (17%)	5 (2%)	6	33
17	Q	33/251 (13%)	28 (85%)	5 (15%)	0	100	100
18	R	514/736 (70%)	439 (85%)	72 (14%)	3 (1%)	21	58
19	S	172/594 (29%)	157 (91%)	14 (8%)	1 (1%)	21	58
All	All	5625/7481 (75%)	4528 (80%)	1009 (18%)	88 (2%)	10	37

5 of 88 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	249	PRO
1	A	252	ARG
1	A	587	ILE
1	A	837	LYS
1	A	1033	GLU

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	1232/1257 (98%)	1217 (99%)	15 (1%)	63	73
2	B	975/1006 (97%)	969 (99%)	6 (1%)	78	80
3	C	296/296 (100%)	294 (99%)	2 (1%)	76	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	110/145 (76%)	109 (99%)	1 (1%)	70	76
5	E	197/197 (100%)	197 (100%)	0	100	100
6	F	73/137 (53%)	72 (99%)	1 (1%)	59	71
7	G	164/190 (86%)	161 (98%)	3 (2%)	51	67
8	H	123/128 (96%)	122 (99%)	1 (1%)	73	77
9	I	38/98 (39%)	37 (97%)	1 (3%)	40	60
10	J	62/65 (95%)	62 (100%)	0	100	100
11	K	91/130 (70%)	91 (100%)	0	100	100
12	L	40/57 (70%)	40 (100%)	0	100	100
13	M	142/249 (57%)	142 (100%)	0	100	100
14	N	92/360 (26%)	92 (100%)	0	100	100
15	O	495/593 (84%)	491 (99%)	4 (1%)	73	77
16	P	255/285 (90%)	252 (99%)	3 (1%)	63	73
17	Q	31/195 (16%)	31 (100%)	0	100	100
18	R	450/623 (72%)	450 (100%)	0	100	100
19	S	157/494 (32%)	157 (100%)	0	100	100
All	All	5023/6505 (77%)	4986 (99%)	37 (1%)	73	79

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	H	130	ARG
16	P	293	ILE
9	I	35	ILE
15	O	516	LEU
1	A	848	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 113 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	69	ASN
19	S	444	GLN
13	M	86	HIS
18	R	631	ASN
16	P	118	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 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
19	S	1
17	Q	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S	319:UNK	C	360:THR	N	39.73

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Q	70:PHE	C	1070:UNK	N	13.87

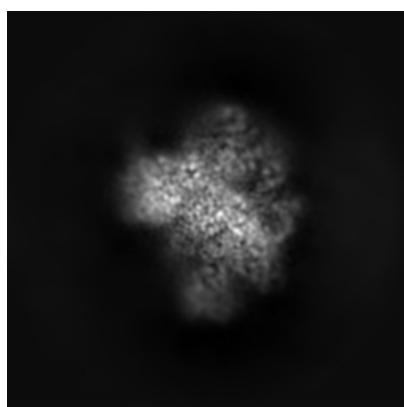
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7533. These allow visual inspection of the internal detail of the map and identification of artifacts.

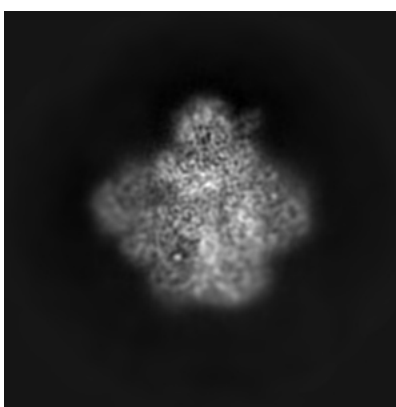
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

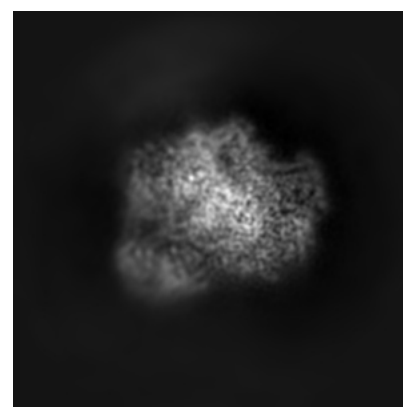
6.1.1 Primary map



X



Y

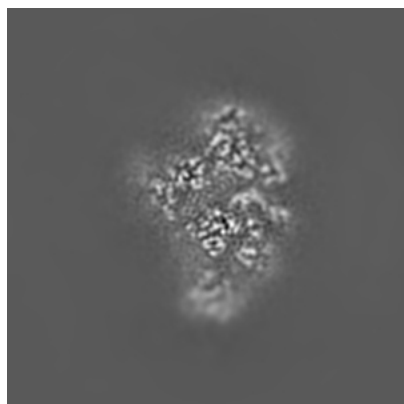


Z

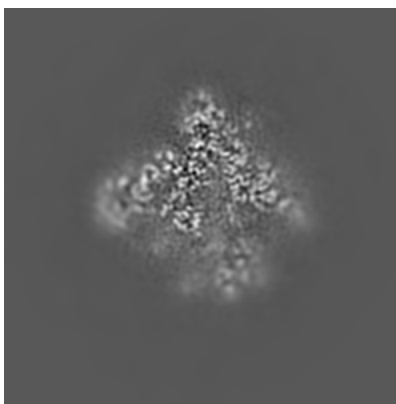
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

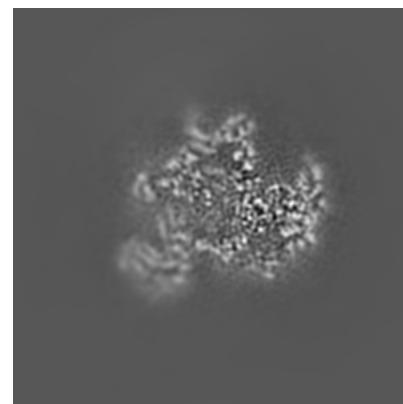
6.2.1 Primary map



X Index: 144



Y Index: 144

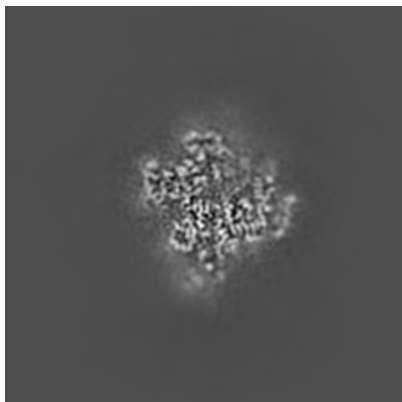


Z Index: 144

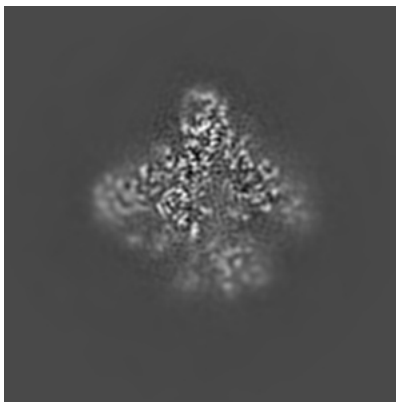
The images above show central slices of the map in three orthogonal directions.

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

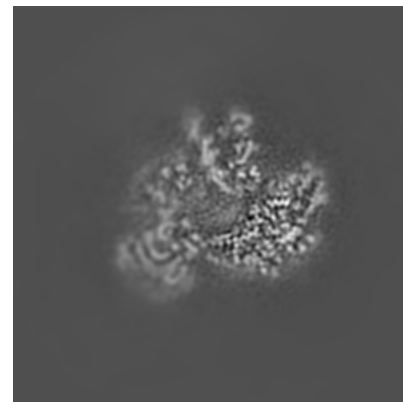
6.3.1 Primary map



X Index: 169



Y Index: 147

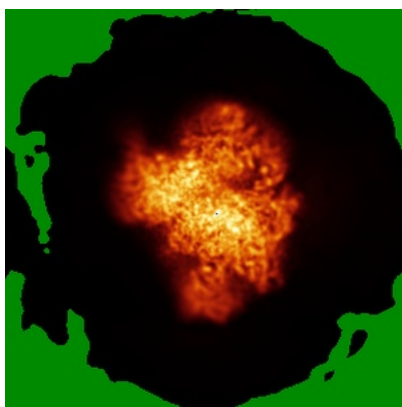


Z Index: 150

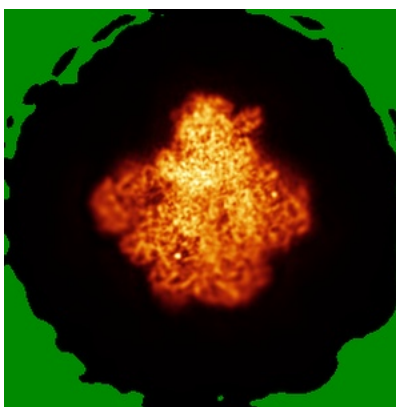
The images above show the largest variance slices of the map in three orthogonal directions.

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

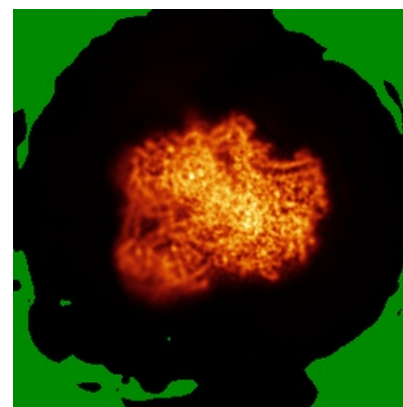
6.4.1 Primary map



X



Y

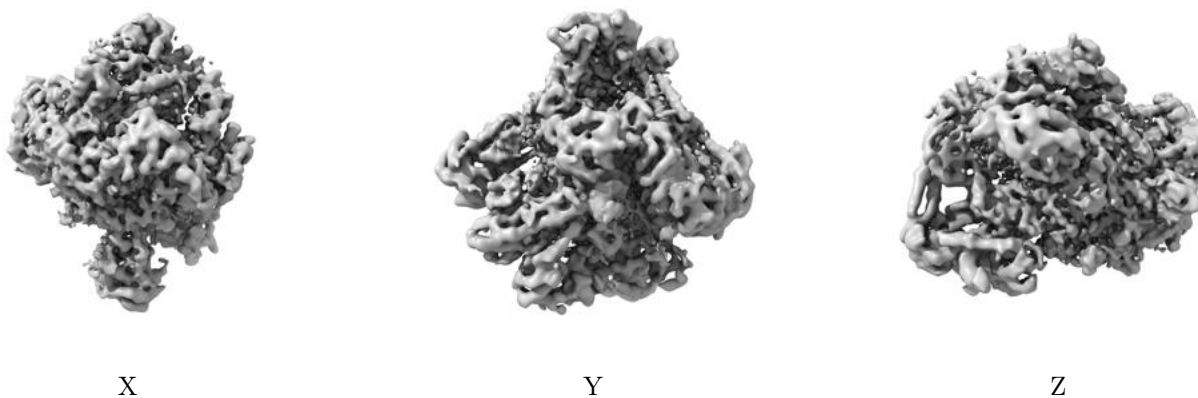


Z

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

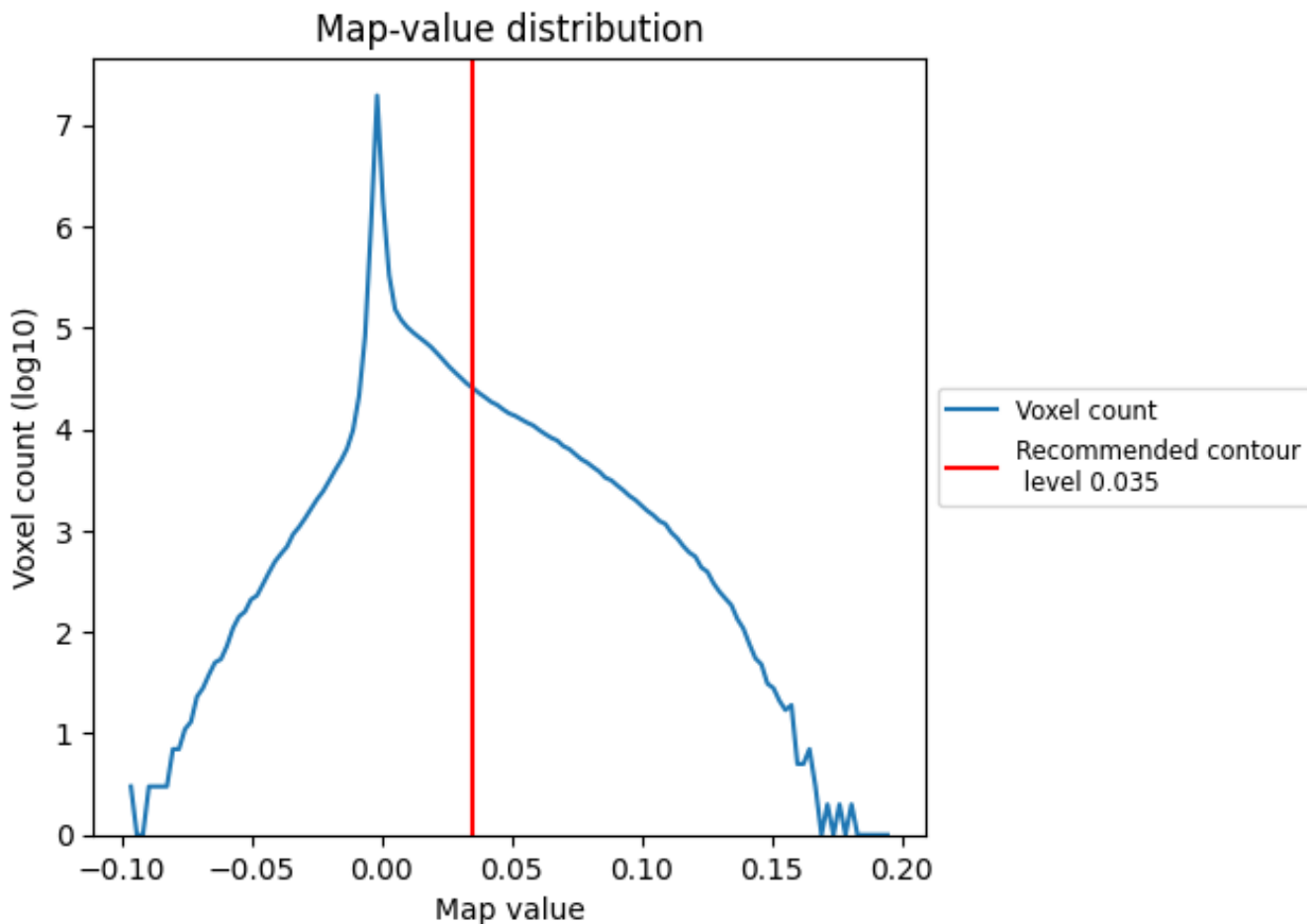
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

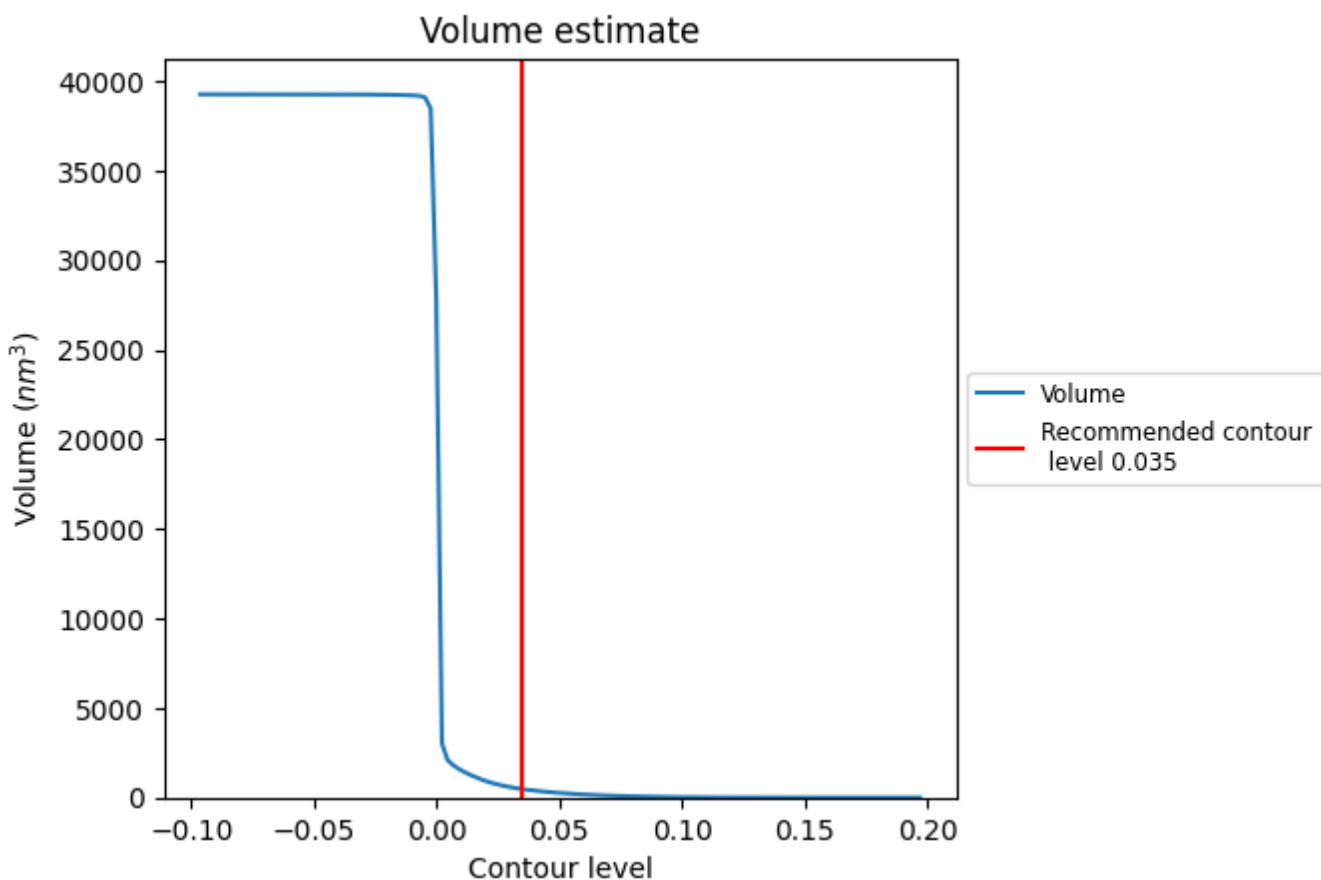
This section contains the results of statistical analysis of the map.

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.

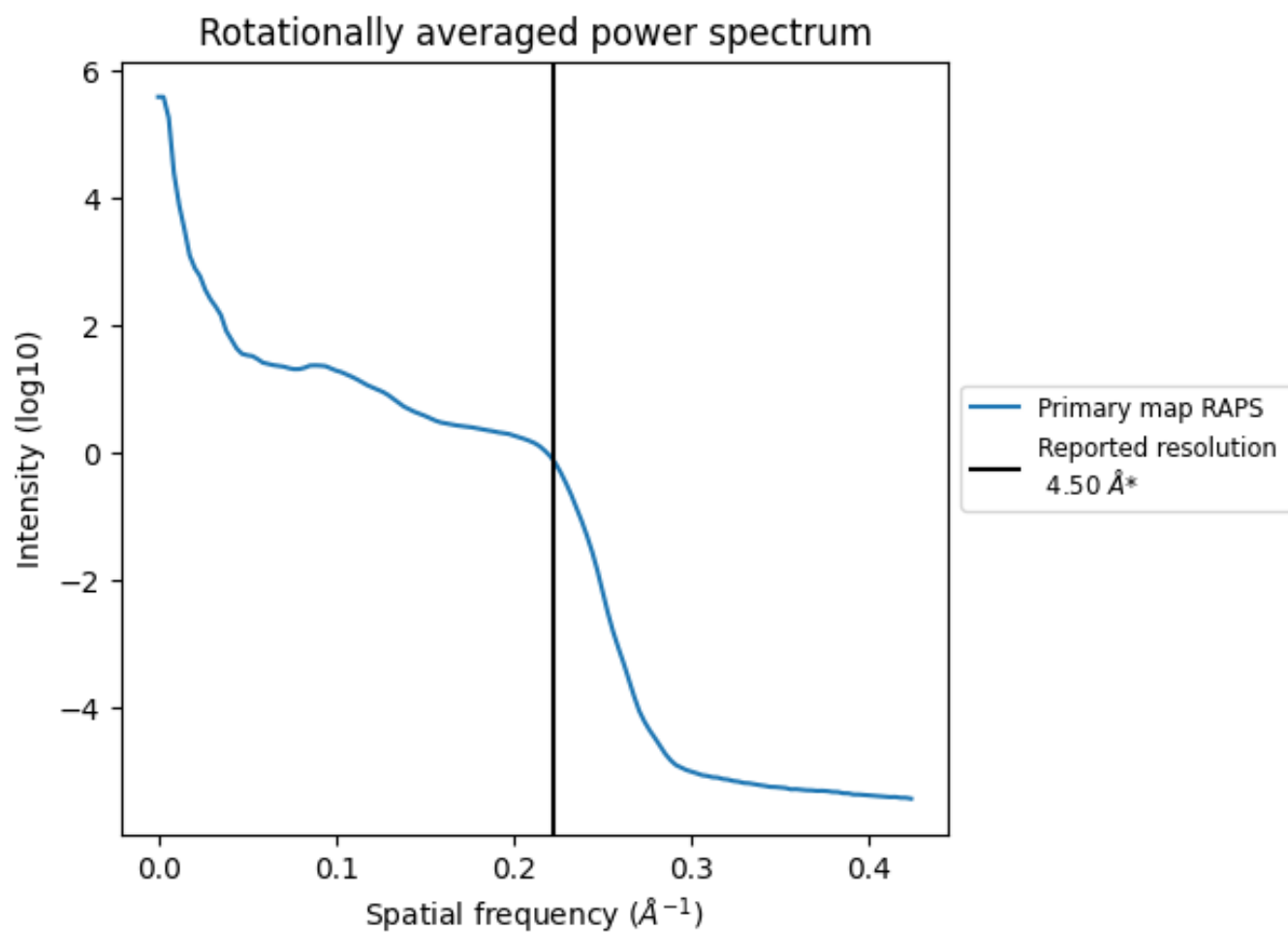
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 470 nm³; this corresponds to an approximate mass of 424 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](#)

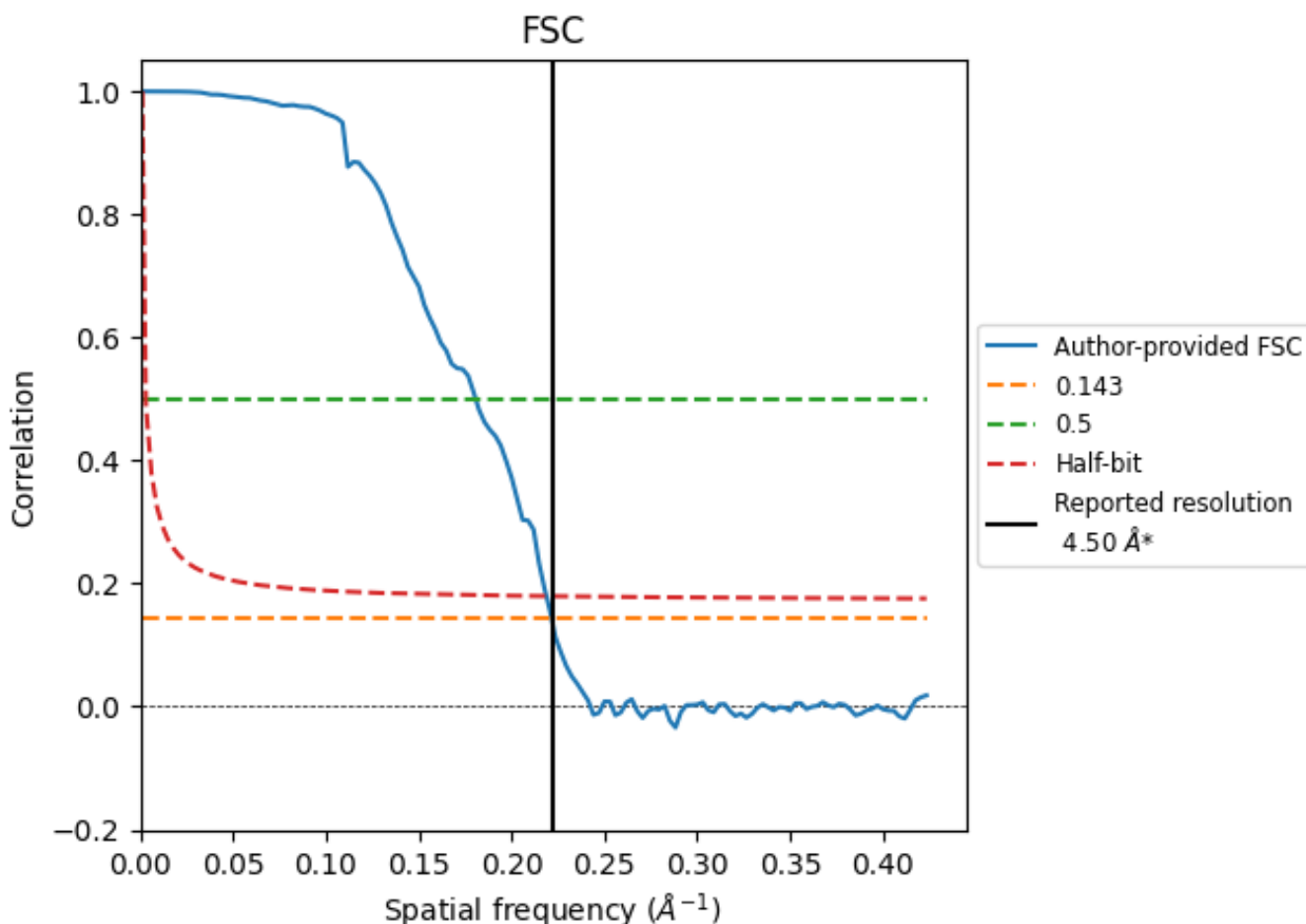


*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.51	5.53	4.57
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

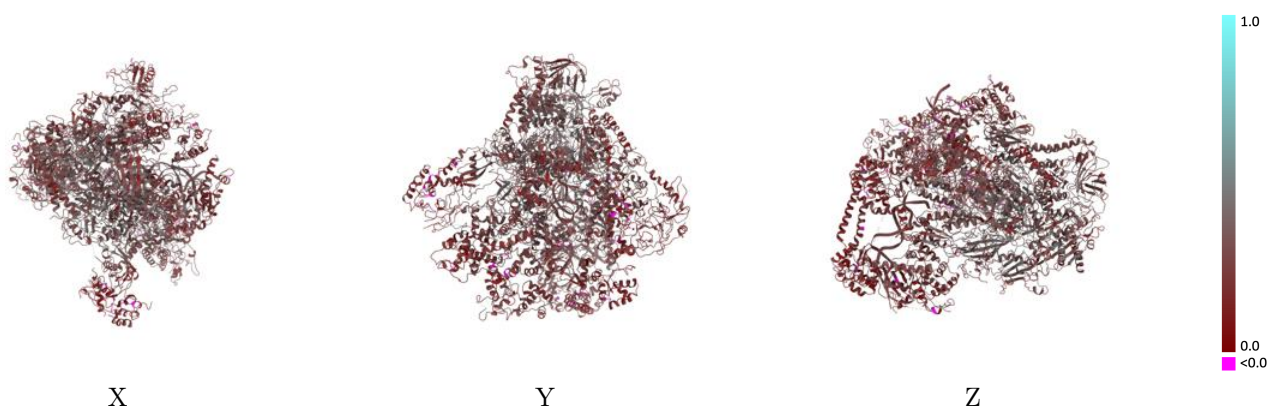
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7533 and PDB model 6CNF. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

This section was not generated.

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

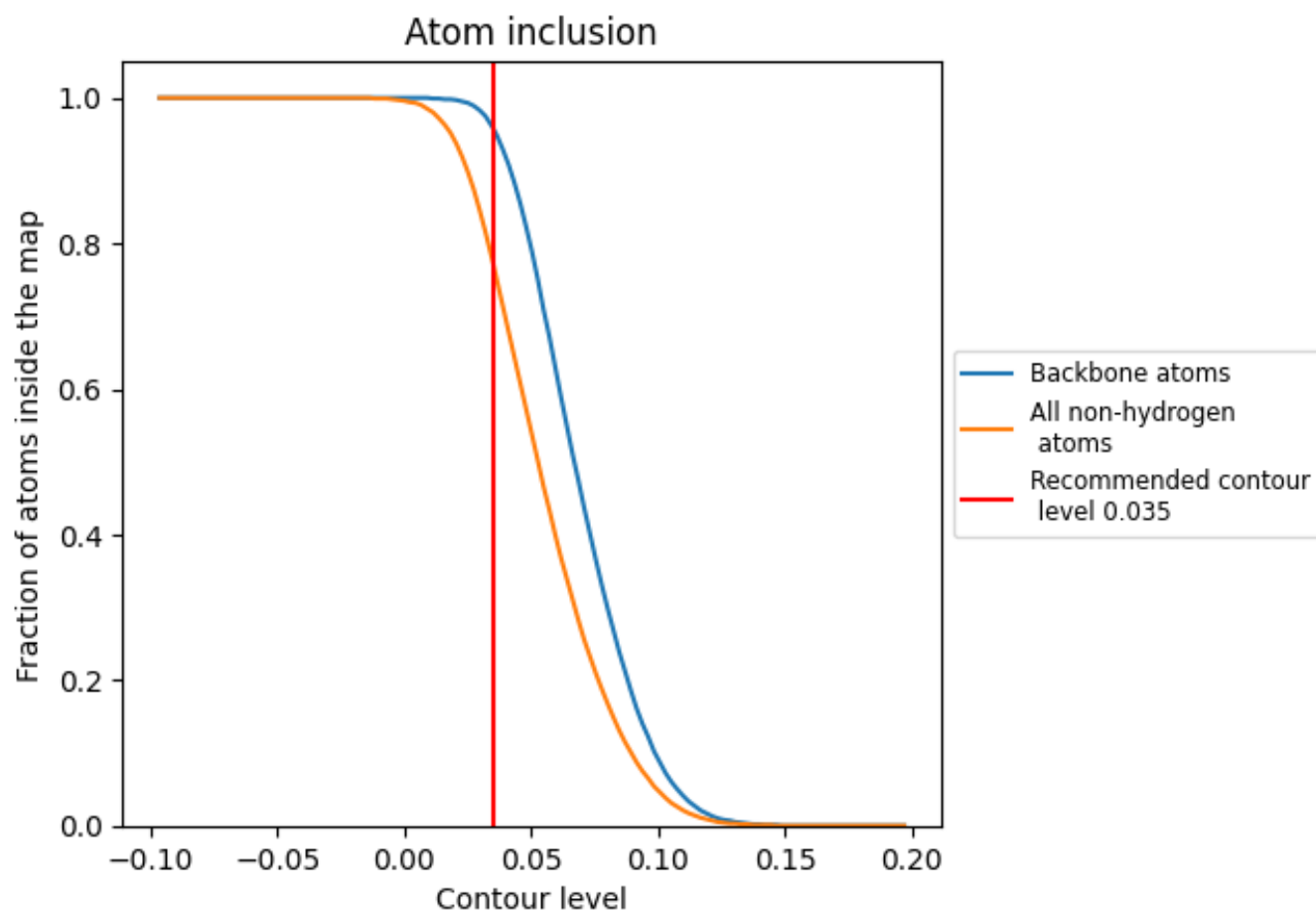


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.













































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 77% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7720	 0.2950
A	 0.7880	 0.3320
B	 0.7870	 0.3390
C	 0.8500	 0.3350
D	 0.7270	 0.1820
E	 0.7870	 0.2910
F	 0.8640	 0.3640
G	 0.7800	 0.2340
H	 0.8340	 0.3170
I	 0.7760	 0.2400
J	 0.8410	 0.3440
K	 0.8290	 0.3360
L	 0.8380	 0.3490
M	 0.7080	 0.2280
N	 0.7530	 0.2430
O	 0.7260	 0.2560
P	 0.6670	 0.2290
Q	 0.8790	 0.3320
R	 0.7000	 0.2270
S	 0.6270	 0.2160
X	 0.9200	 0.2960
Y	 0.8920	 0.3150

