



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:54 AM UTC

PDB ID : 6TNN / pdb_00006tnn
EMDB ID : EMD-10535
Title : Mini-RNase III (Mini-III) bound to 50S ribosome with precursor 23S rRNA
Authors : Oerum, S.; Dendooven, T.; Gilet, L.; Catala, M.; Degut, C.; Trinquier, A.; Barraud, P.; Luisi, B.; Condon, C.; Tisne, C.
Deposited on : 2019-12-09
Resolution : 3.07 Å(reported)
Based on initial model : 3J3V

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:

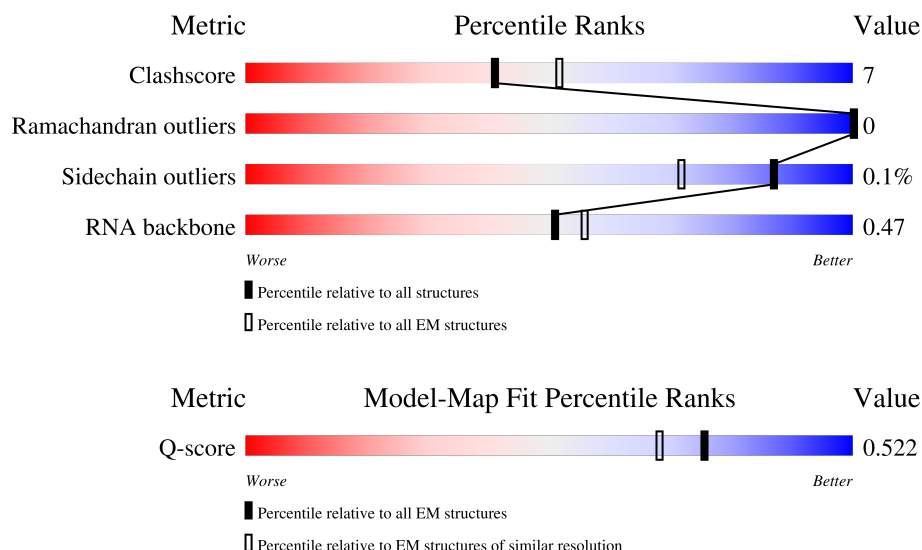
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.07 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.



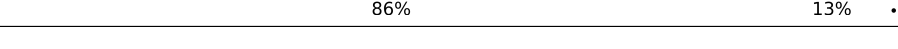
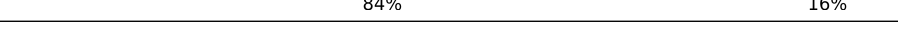
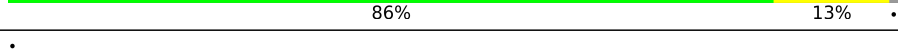
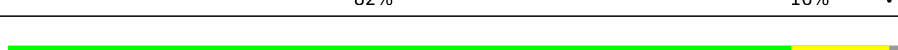
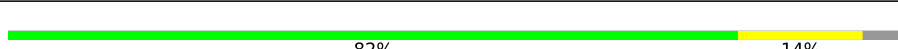
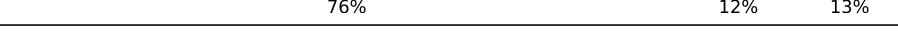
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13977 (2.57 - 3.57)

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	b	166	
2	H	143	
2	I	143	

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Mol	Chain	Length	Quality of chain
3	U	2930	
4	V	116	
5	W	277	
6	X	209	
7	Y	207	
8	Z	179	
9	a	179	
10	c	145	
11	d	122	
12	e	146	
13	f	144	
14	g	120	
15	h	120	
16	i	115	
17	j	119	
18	k	102	
19	l	113	
20	m	95	
21	n	103	
22	o	94	
23	p	59	
24	q	49	
25	r	44	
26	s	66	
27	t	37	

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Mol	Chain	Length	Quality of chain
28	u	62	 77% 16% 6%
29	v	66	 73% 26% .
30	w	59	 73% 25% .

2 Entry composition [i](#)

There are 32 unique types of molecules in this entry. The entry contains 91840 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 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	123	Total	C	N	O	S	0	0
			955	602	163	189	1		

- Molecule 2 is a protein called Mini-ribonuclease 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	132	Total	C	N	O		0	0
			1063	680	182	201			
2	I	134	Total	C	N	O	S	0	0
			1079	691	184	203	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	23	ASN	ASP	conflict	UNP O31418
I	23	ASN	ASP	conflict	UNP O31418

- Molecule 3 is a RNA chain called pre-23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	U	2930	Total	C	N	O	P	0	0
			62920	28070	11619	20301	2930		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	V	116	Total	C	N	O	P	0	0
			2475	1105	447	808	115		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	W	275	Total	C	N	O	S	0	0
			2110	1312	416	376	6		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	X	207	Total	C	N	O	S	0	0
			1574	988	290	291	5		

- Molecule 7 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Y	205	Total	C	N	O	S	0	0
			1560	980	289	289	2		

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Z	178	Total	C	N	O	S	0	0
			1403	893	245	258	7		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	175	Total	C	N	O	S	0	0
			1341	835	248	256	2		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	c	142	Total	C	N	O	S	0	0
			1122	710	206	201	5		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	d	122	Total	C	N	O	S	0	0
			919	571	173	171	4		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	e	146	Total	C	N	O	S	0	0
			1080	671	207	200	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	f	138	Total	C	N	O	S	0	0
			1096	703	208	180	5		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	g	119	Total	C	N	O	S	0	0
			952	583	186	179	4		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	h	120	Total	C	N	O	S	0	0
			911	564	176	170	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	i	114	Total	C	N	O	0	0
			935	595	184	156		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	j	117	Total	C	N	O	S	0	0
			939	591	189	155	4		

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	k	101	Total	C	N	O	0	0
			785	501	139	145		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	l	109	Total	C	N	O	S	0	0
			841	525	164	149	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	m	93	Total	C	N	O	S	0	0
			751	472	137	138	4		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	n	101	Total	C	N	O	S	0	0
			761	478	142	137	4		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	o	82	Total	C	N	O		0	0
			629	390	123	116			

- Molecule 23 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	p	54	Total	C	N	O	S	0	0
			425	262	86	70	7		

- Molecule 24 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	q	48	Total	C	N	O	S	0	0
			400	244	80	72	4		

- Molecule 25 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	44	Total	C	N	O	S	0	0
			366	222	89	53	2		

- Molecule 26 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	s	64	Total	C	N	O	S	0	0
			511	321	107	81	2		

- Molecule 27 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	36	Total	C	N	O	S	0	0
			287	181	59	43	4		

- Molecule 28 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	u	58	Total	C	N	O	S	0	0
			443	275	92	74	2		

- Molecule 29 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	v	65	Total	C	N	O	S	0	0
			529	328	102	97	2		

- Molecule 30 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	w	58	Total	C	N	O	S	0	0
			454	281	89	83	1		

- Molecule 31 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
31	I	1	Total	Mg	0
			1	1	
31	U	214	Total	Mg	0
			214	214	
31	V	1	Total	Mg	0
			1	1	
31	W	2	Total	Mg	0
			2	2	
31	e	2	Total	Mg	0
			2	2	
31	u	1	Total	Mg	0
			1	1	

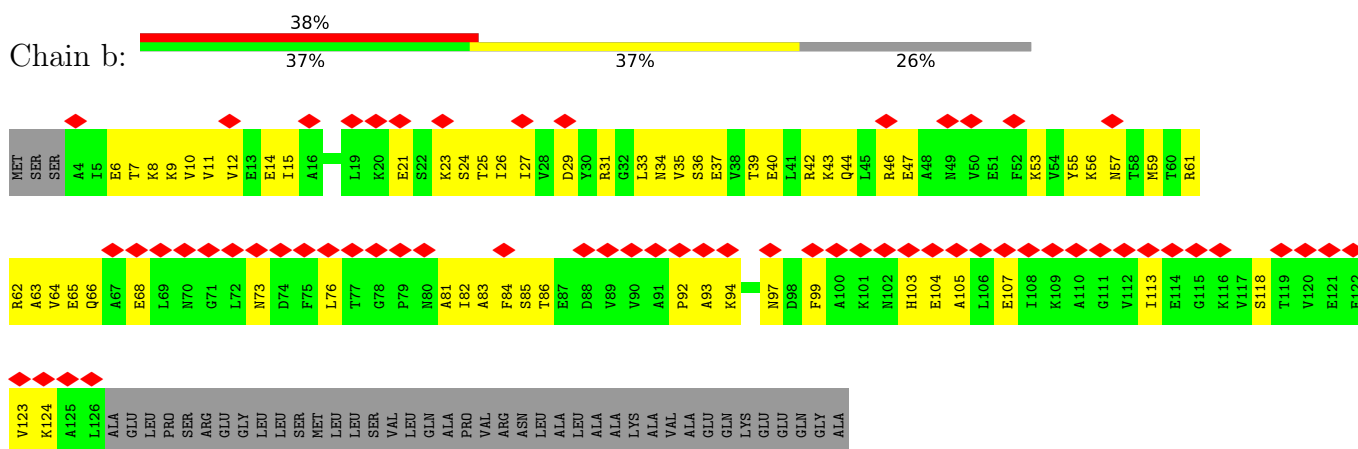
- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
32	p	1	Total 1	Zn 1	0
32	q	1	Total 1	Zn 1	0
32	t	1	Total 1	Zn 1	0

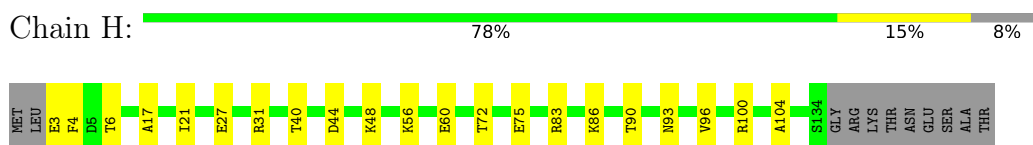
3 Residue-property plots [i](#)

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

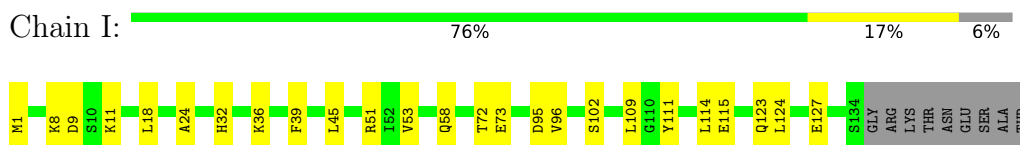
- Molecule 1: 50S ribosomal protein L10



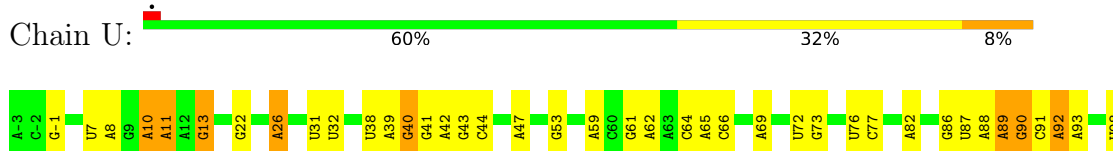
- Molecule 2: Mini-ribonuclease 3



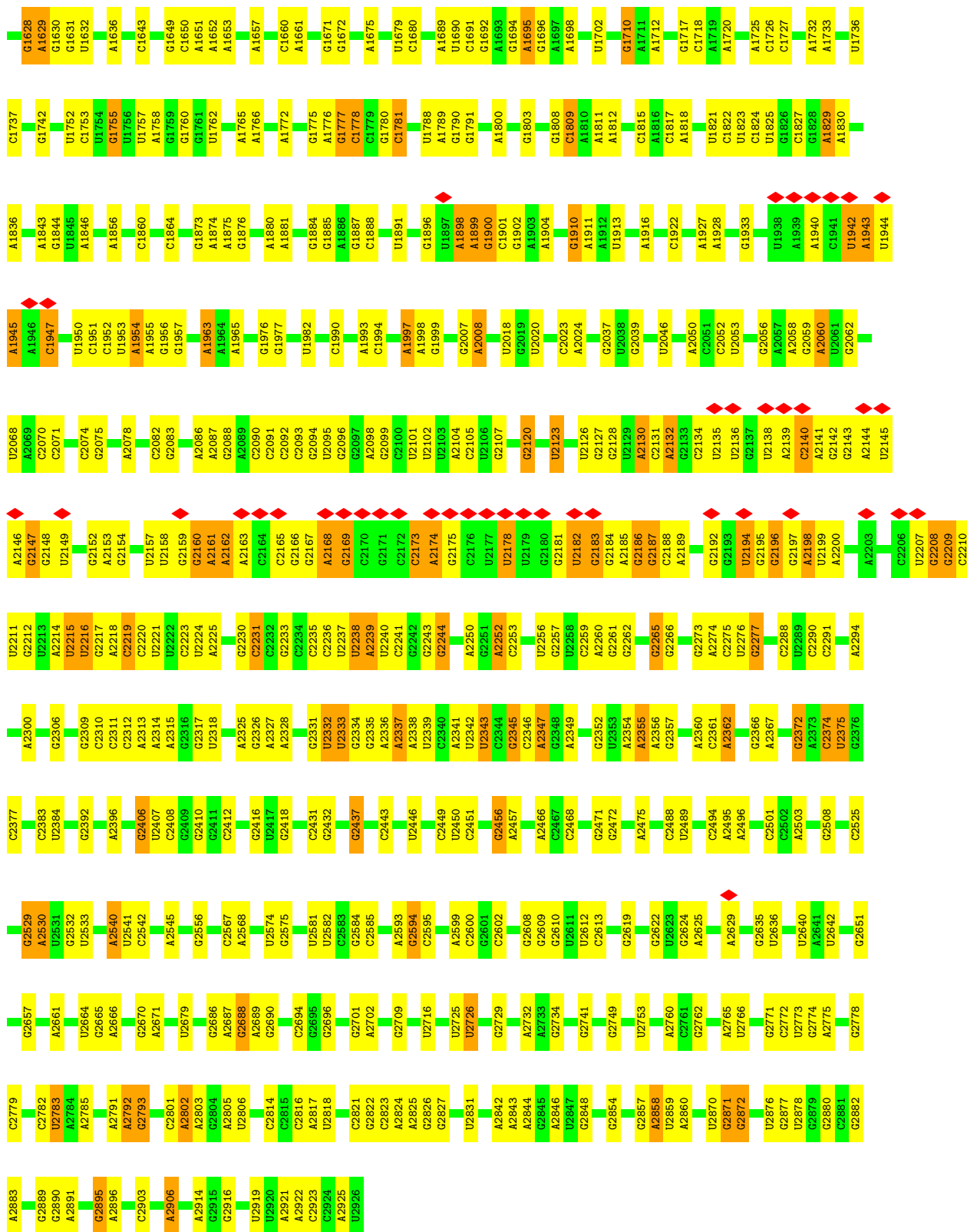
- Molecule 2: Mini-ribonuclease 3

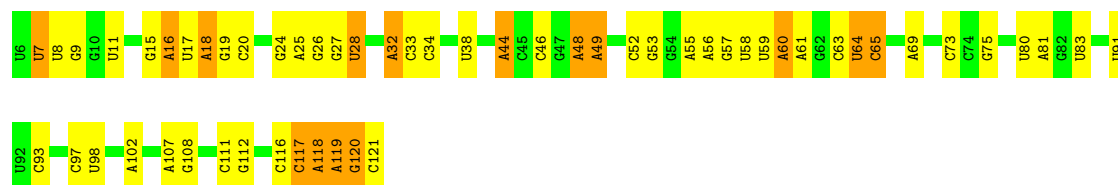


- Molecule 3: pre-23S rRNA



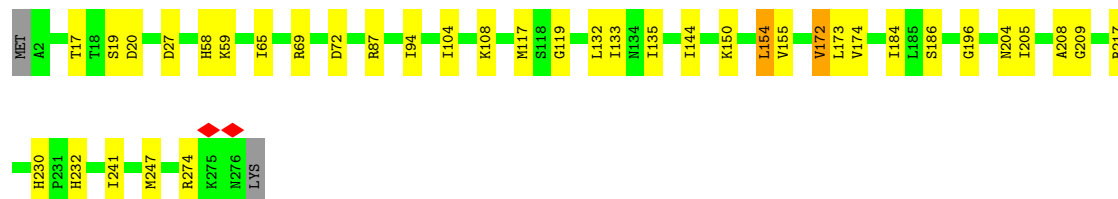
G1537	G1465	C1368	C1246	G1143	G1076	A963	A892	C762	A665	G566	A446	G314	C232	G99
A1540	G1469	G1375	G1250	U1145	U1079	U970	G893	A763	G669	A572	A447	G315	G233	A100
C1543	G1470	G1376	C1254	A1147	U1085	G971	G895	G771	C670	A573	U448	A316	A234	
C1544	A1471	U1377		U1148	G1086	A972	U896	A772	A671	G574	G451	U319	U235	A115
U1545	G1473		A1258	U1149	U1087	C973	C897	G773	G672	U575	G452		U236	A116
U1546	C1474	C1382		G1150	U1088		G903	G774	C673	A576		A322	G243	U117
U1547	A1475	G1383	G1261	G1151	U1089	U977	G904	C775	G674	C577	C459		U244	A128
	G1476				A1090		G909	C787	A675	A460		G325	U245	C129
	G1477	U1389	A1267	G1154	G1091	A985	G909	A788	A676	C579	U461	G329	G246	C130
		A1390		A1155	A1092	A989	C910		G677	A582	U463	G330	G249	
		A1391	G1276	U1156	A1093	G990	A911	U792	C579	A590	A335	G339	C250	A148
				U1157				G793	G680		G336	G320	C251	U149
	C1394	G1395	A1285	G1158	C1097	G996	U916	G803	A681	G593		G342	A256	C151
	A1396		G1288	U1171	A1098	G1005	U917	A809	G682	U596	A468	G344	A257	A152
	G1397	A1171	A1172	A1177	G1099	A1006	G918	G810	U683	C597			A258	A154
		A1173	G1290	C1173	A1101	U1007	G919		G686				C259	
	G1401	U1174	A1291	U1175	U1102	C1008	U922	G820	A687	C602		C347	G260	G158
	A1402	G1175		G1176	G1103		A923		G688			U348	G260	
	A1403	U1176	G1294	A1017	U1104	A1017	G924	G825	U689	G605			C265	
	A1404	A1177	G1302	A1018	G1105	A1018	G925	A826		C501		A353	A266	U161
	G1412	C1178		A1025	G1106	A1026	G926	A827	G692	G501			C267	U162
		U1416	A1306	C1026	G1107	A1027	C927	A828	G693	A614		A364	A273	
	U1416		G1307	A1027	C1108	A1027	C928	U829	G615	A511		G365	A273	
	A1421	C1183		A1032	U1109	A1032	C929	G830	U698	G512		G366	C274	G173
	A1422	U1185	A1310	A1032	U1110	A1032	C930	G837	G699	G513			C275	A174
	A1423	A1186	A1311	G1037	A1111	G1037	C931	U932	U702	G514		U370	A276	G175
	C1423	A1312	A1312	C1038	A1112	C1038	U932	A839	A703	G514		A371	A277	A176
	A1424	G1313	A1314	C1039	A1113	C1039	A933	A839	G714	G518		A372	A278	A177
	G1425	A1314		G1115	A1114	A1040	C934	A847	A715				G279	
	G1426	G1315	G1315	C1116	A1115	A1040	C934		C716	A522		G380	G280	C184
			G1316	U1117	A1117	G1041	C935		C717	G526		U381	G281	
	A1432	G1317		G1211	A1118	C1042	G936	G850	C717	C527		A382	G281	G188
	U1433	U1317	U1319	C1119	G1118	U1043	G937		C718	C527			U283	
		U1319	U1319	C1120	C1120	A1044	G938	C857		A628		A386	U284	A192
	C1436	U1320	G1320	U1213	C1121	A1045	U939	U858	G729	G533		A387	G285	C193
	U1437			U1216	A1121	A1045	U940	C859	A730	G534		A388	G286	
	G1438		A1323	C1217	C1122	A1053	U940	C859	U731	U631		A389	C287	A197
	U1439			G1218	C1123	A1053	U941	C862	C732	A632		C390	U288	A198
		C1329	C1219	A1219	U1124	U1056	C942	G863	U733				U288	A199
	A1442	U1330	U1330	A1220	U1125	U1056	C942	A864		C639		U400	U290	A200
	A1443			C1221	U1126	A1057	C943		A738			C401	U291	U201
	U1446	A1337	A1337	A1222	U1127	U1058	G944			U543		C402	G292	
	C1447	A1338	G1223	A1222	A1128	A1059	A945	U872	U741	G643		C403	G292	
	C1448	U1339	G1223	G1223	A1129	C1060	A946	U873	C742	A545		U403	G293	A214
		G1341	G1226	G1226	A1130	G1061	U947	U879		A546		G404		
	A1451	C1342	U1227	U1227	G1131	U1062	U948	G876	G745	A547			U296	
	U1526	U1343		U1237	A1132	U1063	A950	G877		G548		G408	U296	A217
	C1452	C1342	C1342	U1334	U1134	U1063	G951	U879		A549		G409	U299	G219
	C1453	A1344	A1344	G1238	U1135	G1066	U952	U879	U748	G550			U299	
	A1454	A1345	C1239	C1239	G1135	G1066	U952	G879	G749	A650		G415	A300	A223
			U1240	C1239	G1136	G1069	C953			A651		A416	A301	A224
			A1241	U1240	G1137	A1070	A954	C883	A756	U552		G417	G301	A225
	U1457	G1356	A1242	A1240	U1137	A1070	A955	U884	G757	C553			G302	G225
	G1458	G1357	A1242	A1241	U1138	A1071	A956	C885		C554		G431	G310	C226
			G1243	A1242	U1139	A1072	A956	A886		G555		U432	G310	A227
			G1244	A1243	A1140	A1073	C957		U759	C662			A312	A228
	A1463	C1362	U1244	G1244	U1141	A1073	U958	U890	A760	G663			A312	
	U1464	U1363	G1245	G1245	U1141	U1077	C959	A891	A761	G664			C313	G231
					A1142		C960							
							G961							
								</						





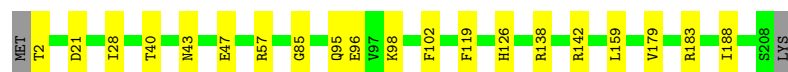
- Molecule 5: 50S ribosomal protein L2

Chain W: 86% 13% ..



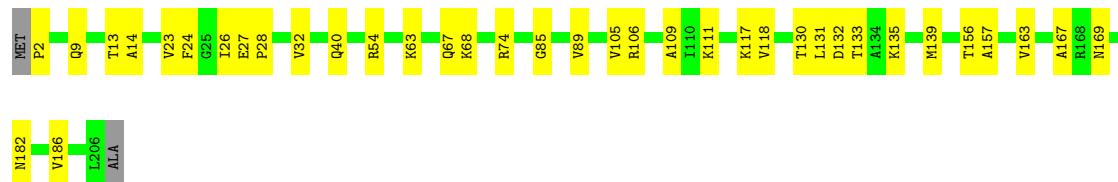
- Molecule 6: 50S ribosomal protein L3

Chain X: 89% 10% .



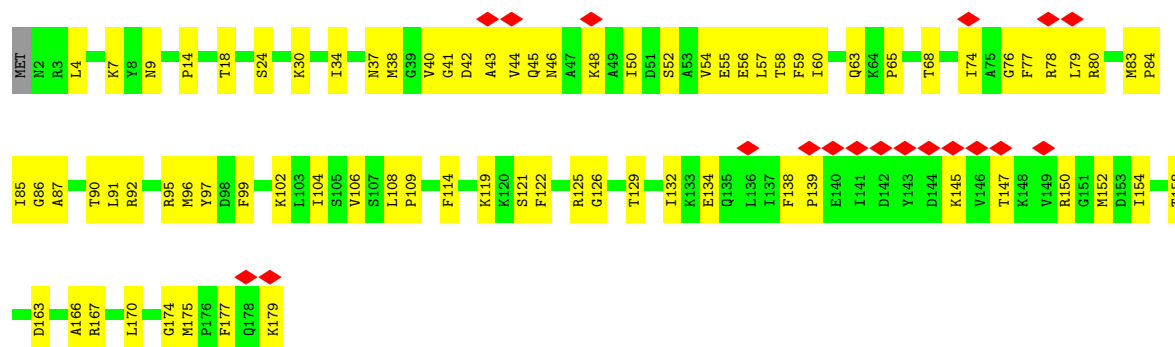
- Molecule 7: 50S ribosomal protein L4

Chain Y: 81% 18% .



- Molecule 8: 50S ribosomal protein L5

Chain Z: 11% 56% 44% .



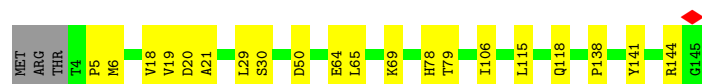
- Molecule 9: 50S ribosomal protein L6

Chain a:  79% 18%



- Molecule 10: 50S ribosomal protein L13

Chain c:  84% 14%



- Molecule 11: 50S ribosomal protein L14

Chain d:  84% 16%



- Molecule 12: 50S ribosomal protein L15

Chain e:  90% 10%



- Molecule 13: 50S ribosomal protein L16

Chain f:  81% 15%



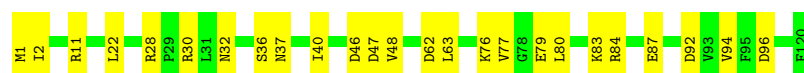
- Molecule 14: 50S ribosomal protein L17

Chain g:  79% 20%



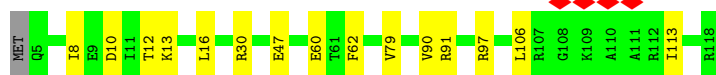
- Molecule 15: 50S ribosomal protein L18

Chain h:  79% 21%



- Molecule 16: 50S ribosomal protein L19

Chain i:  86% 13%



- Molecule 17: 50S ribosomal protein L20

Chain j:  82% 16%



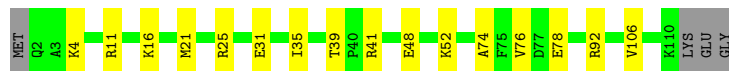
- Molecule 18: 50S ribosomal protein L21

Chain k:  88% 11%



- Molecule 19: 50S ribosomal protein L22

Chain l:  82% 14%



- Molecule 20: 50S ribosomal protein L23

Chain m:  86% 12%



- Molecule 21: 50S ribosomal protein L24

Chain n:  83% 16%



- Molecule 22: 50S ribosomal protein L27

Chain o:  76% 12% 13%



- Molecule 23: 50S ribosomal protein L32

Chain p:  80% 12% 8%



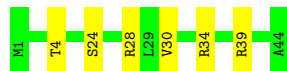
- Molecule 24: 50S ribosomal protein L33 1

Chain q:  84% 14% .



- Molecule 25: 50S ribosomal protein L34

Chain r:  86% 14%



- Molecule 26: 50S ribosomal protein L35

Chain s:  76% 21% .



- Molecule 27: 50S ribosomal protein L36

Chain t:  78% 19% .



- Molecule 28: 50S ribosomal protein L28

Chain u:  77% 16% 6%

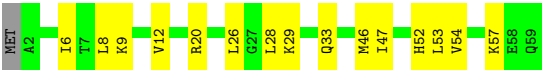


- Molecule 29: 50S ribosomal protein L29

Chain v:  73% 26% .



- Molecule 30: 50S ribosomal protein L30



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	57683	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	23.94	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	9.780	Depositor
Minimum map value	-5.441	Depositor
Average map value	0.014	Depositor
Map value standard deviation	0.220	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	406.8, 406.8, 406.8	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.13, 1.13, 1.13	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	b	0.16	0/963	0.51	0/1298
2	H	0.13	0/1082	0.32	0/1454
2	I	0.14	0/1098	0.35	0/1475
3	U	0.19	0/70479	0.31	0/109956
4	V	0.13	0/2767	0.30	0/4313
5	W	0.19	0/2147	0.42	0/2880
6	X	0.20	0/1596	0.40	0/2139
7	Y	0.24	1/1579 (0.1%)	0.38	0/2131
8	Z	0.16	0/1422	0.47	0/1909
9	a	0.16	0/1359	0.36	0/1831
10	c	0.20	0/1145	0.40	0/1541
11	d	0.17	0/926	0.41	0/1244
12	e	0.18	0/1092	0.43	1/1456 (0.1%)
13	f	0.15	0/1119	0.34	0/1495
14	g	0.19	0/959	0.45	1/1283 (0.1%)
15	h	0.13	0/920	0.39	0/1235
16	i	0.19	0/948	0.42	0/1268
17	j	0.22	0/951	0.41	0/1265
18	k	0.18	0/796	0.43	0/1069
19	l	0.21	0/850	0.42	0/1145
20	m	0.18	0/758	0.42	0/1010
21	n	0.17	0/771	0.39	0/1031
22	o	0.20	0/637	0.46	0/846
23	p	0.20	0/432	0.42	0/573
24	q	0.15	0/405	0.38	0/539
25	r	0.21	0/369	0.44	0/482
26	s	0.19	0/518	0.44	0/679
27	t	0.17	0/290	0.32	0/382
28	u	0.18	0/447	0.46	0/595
29	v	0.16	0/530	0.37	0/706
30	w	0.19	0/456	0.36	0/612
All	All	0.18	1/99811 (0.0%)	0.33	2/149842 (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	b	0	1
5	W	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	Y	85	GLY	C-O	6.53	1.28	1.24

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	e	94	GLU	N-CA-C	-6.15	107.61	114.62
14	g	43	VAL	N-CA-C	-5.37	107.59	112.96

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	W	154	LEU	Peptide
1	b	57	ASN	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	b	955	0	990	57	0
2	H	1063	0	1065	16	0
2	I	1079	0	1088	17	0
3	U	62920	0	31659	626	0
4	V	2475	0	1255	35	0
5	W	2110	0	2200	30	0
6	X	1574	0	1642	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	Y	1560	0	1647	24	0
8	Z	1403	0	1467	65	0
9	a	1341	0	1388	24	0
10	c	1122	0	1162	12	0
11	d	919	0	977	13	0
12	e	1080	0	1132	9	0
13	f	1096	0	1165	12	0
14	g	952	0	983	14	0
15	h	911	0	947	22	0
16	i	935	0	1008	10	0
17	j	939	0	1005	18	0
18	k	785	0	826	10	0
19	l	841	0	899	12	0
20	m	751	0	802	7	0
21	n	761	0	821	13	0
22	o	629	0	644	7	0
23	p	425	0	442	6	0
24	q	400	0	410	5	0
25	r	366	0	410	6	0
26	s	511	0	564	13	0
27	t	287	0	327	4	0
28	u	443	0	487	9	0
29	v	529	0	568	12	0
30	w	454	0	491	11	0
31	I	1	0	0	0	0
31	U	214	0	0	0	0
31	V	1	0	0	0	0
31	W	2	0	0	0	0
31	e	2	0	0	0	0
31	u	1	0	0	0	0
32	p	1	0	0	0	0
32	q	1	0	0	0	0
32	t	1	0	0	0	0
All	All	91840	0	60471	1029	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 7.

The worst 5 of 1029 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)
3:U:2131:C:N4	3:U:2132:A:N6	2.04	1.04
3:U:2131:C:C4	3:U:2132:A:N6	2.35	0.92
3:U:1104:U:H3	3:U:1123:C:H42	1.01	0.92
3:U:927:G:H1	3:U:939:U:H3	1.23	0.87
3:U:1104:U:H3	3:U:1123:C:N4	1.73	0.86

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	b	121/166 (73%)	101 (84%)	20 (16%)	0	100	100
2	H	130/143 (91%)	127 (98%)	3 (2%)	0	100	100
2	I	132/143 (92%)	128 (97%)	4 (3%)	0	100	100
5	W	273/277 (99%)	252 (92%)	21 (8%)	0	100	100
6	X	205/209 (98%)	194 (95%)	11 (5%)	0	100	100
7	Y	203/207 (98%)	189 (93%)	14 (7%)	0	100	100
8	Z	176/179 (98%)	159 (90%)	17 (10%)	0	100	100
9	a	173/179 (97%)	160 (92%)	13 (8%)	0	100	100
10	c	140/145 (97%)	133 (95%)	7 (5%)	0	100	100
11	d	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
12	e	144/146 (99%)	132 (92%)	12 (8%)	0	100	100
13	f	136/144 (94%)	130 (96%)	6 (4%)	0	100	100
14	g	117/120 (98%)	107 (92%)	10 (8%)	0	100	100
15	h	118/120 (98%)	109 (92%)	9 (8%)	0	100	100
16	i	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
17	j	115/119 (97%)	107 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	k	99/102 (97%)	85 (86%)	14 (14%)	0	100	100
19	l	107/113 (95%)	103 (96%)	4 (4%)	0	100	100
20	m	91/95 (96%)	88 (97%)	3 (3%)	0	100	100
21	n	99/103 (96%)	88 (89%)	11 (11%)	0	100	100
22	o	80/94 (85%)	75 (94%)	5 (6%)	0	100	100
23	p	52/59 (88%)	47 (90%)	5 (10%)	0	100	100
24	q	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
25	r	42/44 (96%)	40 (95%)	2 (5%)	0	100	100
26	s	62/66 (94%)	60 (97%)	2 (3%)	0	100	100
27	t	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
28	u	56/62 (90%)	51 (91%)	5 (9%)	0	100	100
29	v	63/66 (96%)	60 (95%)	3 (5%)	0	100	100
30	w	56/59 (95%)	56 (100%)	0	0	100	100
All	All	3302/3483 (95%)	3080 (93%)	222 (7%)	0	100	100

There are no Ramachandran outliers to report.

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	b	105/138 (76%)	105 (100%)	0	100	100
2	H	114/123 (93%)	114 (100%)	0	100	100
2	I	116/123 (94%)	116 (100%)	0	100	100
5	W	223/225 (99%)	222 (100%)	1 (0%)	84	84
6	X	168/170 (99%)	168 (100%)	0	100	100
7	Y	169/170 (99%)	169 (100%)	0	100	100
8	Z	153/154 (99%)	153 (100%)	0	100	100
9	a	148/151 (98%)	148 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	c	120/123 (98%)	120 (100%)	0	100	100
11	d	101/101 (100%)	100 (99%)	1 (1%)	68	77
12	e	110/110 (100%)	110 (100%)	0	100	100
13	f	111/116 (96%)	111 (100%)	0	100	100
14	g	99/100 (99%)	99 (100%)	0	100	100
15	h	93/93 (100%)	93 (100%)	0	100	100
16	i	99/100 (99%)	99 (100%)	0	100	100
17	j	96/98 (98%)	96 (100%)	0	100	100
18	k	83/84 (99%)	83 (100%)	0	100	100
19	l	90/93 (97%)	90 (100%)	0	100	100
20	m	84/85 (99%)	84 (100%)	0	100	100
21	n	85/87 (98%)	85 (100%)	0	100	100
22	o	64/74 (86%)	64 (100%)	0	100	100
23	p	48/53 (91%)	48 (100%)	0	100	100
24	q	46/47 (98%)	45 (98%)	1 (2%)	45	68
25	r	39/39 (100%)	39 (100%)	0	100	100
26	s	54/56 (96%)	54 (100%)	0	100	100
27	t	34/35 (97%)	34 (100%)	0	100	100
28	u	47/50 (94%)	47 (100%)	0	100	100
29	v	56/57 (98%)	56 (100%)	0	100	100
30	w	52/53 (98%)	52 (100%)	0	100	100
All	All	2807/2908 (96%)	2804 (100%)	3 (0%)	87	89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	W	172	VAL
11	d	122	ILE
24	q	48	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
12	e	78	ASN

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Mol	Chain	Res	Type
17	j	107	ASN
30	w	33	GLN
13	f	123	HIS
17	j	29	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	U	2929/2930 (99%)	618 (21%)	29 (0%)
4	V	115/116 (99%)	30 (26%)	3 (2%)
All	All	3044/3046 (99%)	648 (21%)	32 (1%)

5 of 648 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	U	11	A
3	U	13	G
3	U	26	A
3	U	31	U
3	U	32	U

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	U	2871	G
4	V	24	G
3	U	681	A
3	U	646	G
4	V	52	C

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

Of 224 ligands modelled in this entry, 224 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

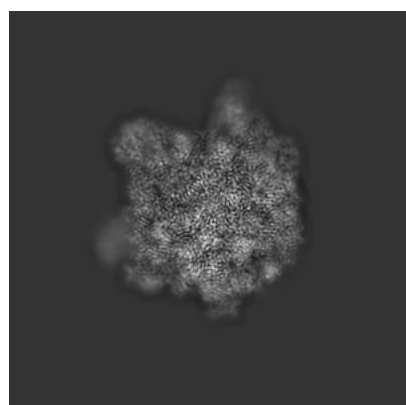
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10535. These allow visual inspection of the internal detail of the map and identification of artifacts.

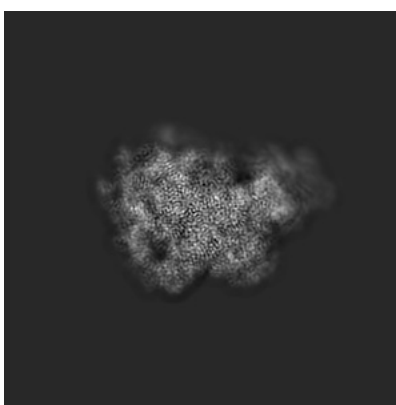
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

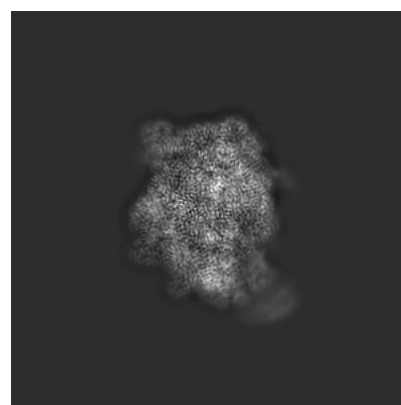
6.1.1 Primary map



X



Y

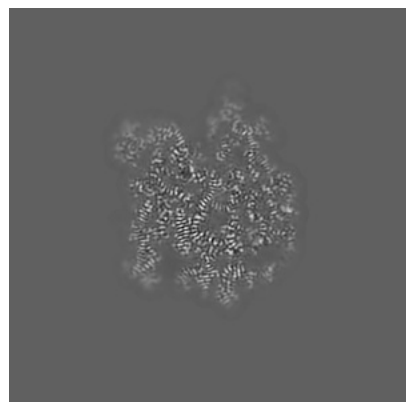


Z

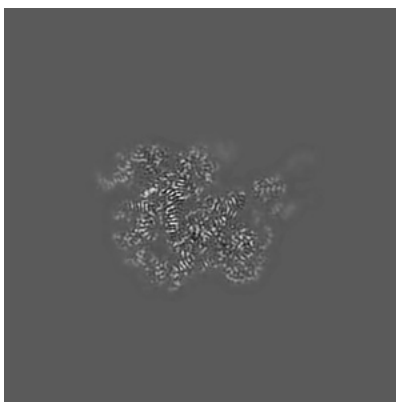
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

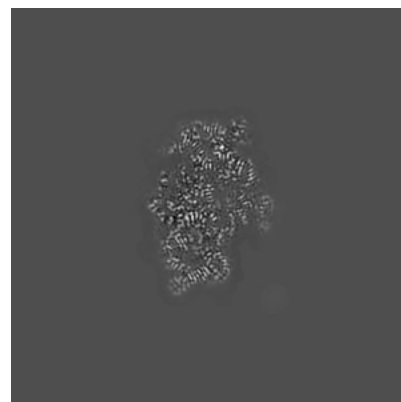
6.2.1 Primary map



X Index: 180



Y Index: 180

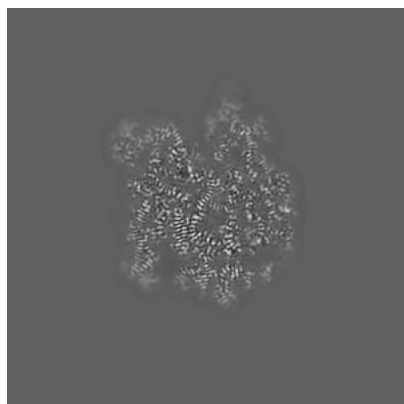


Z Index: 180

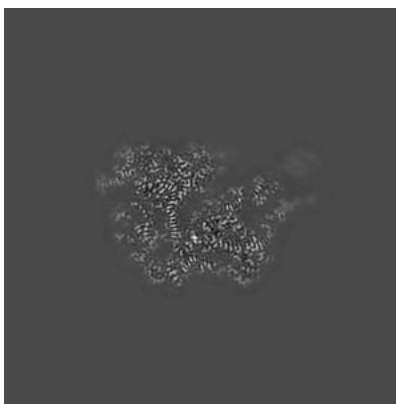
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

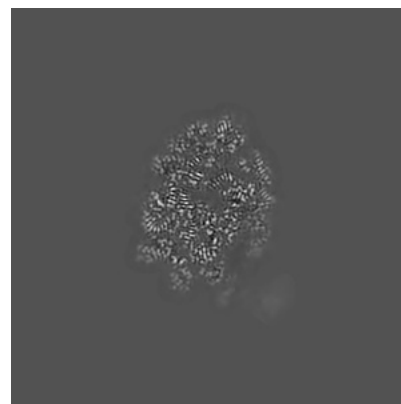
6.3.1 Primary map



X Index: 180



Y Index: 185

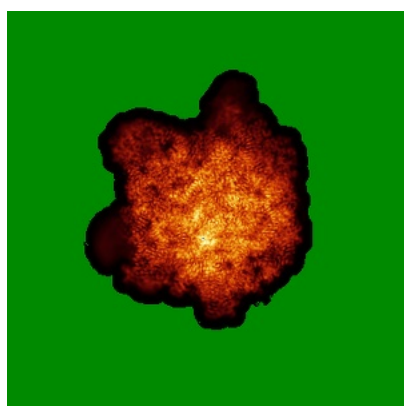


Z Index: 168

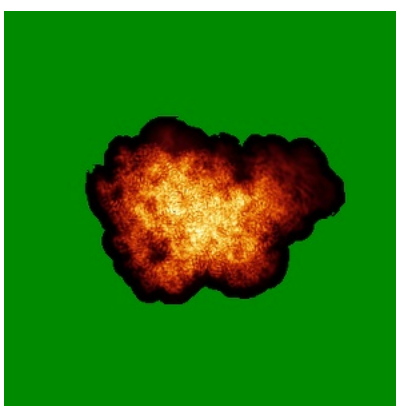
The images above show the largest variance slices of the map in three orthogonal directions.

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

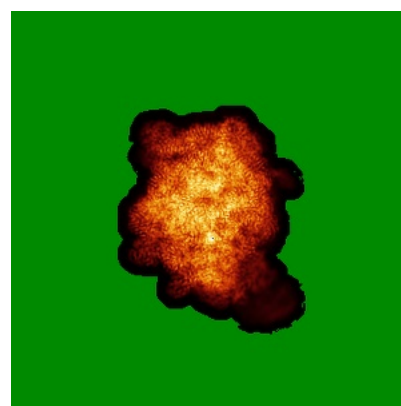
6.4.1 Primary map



X



Y

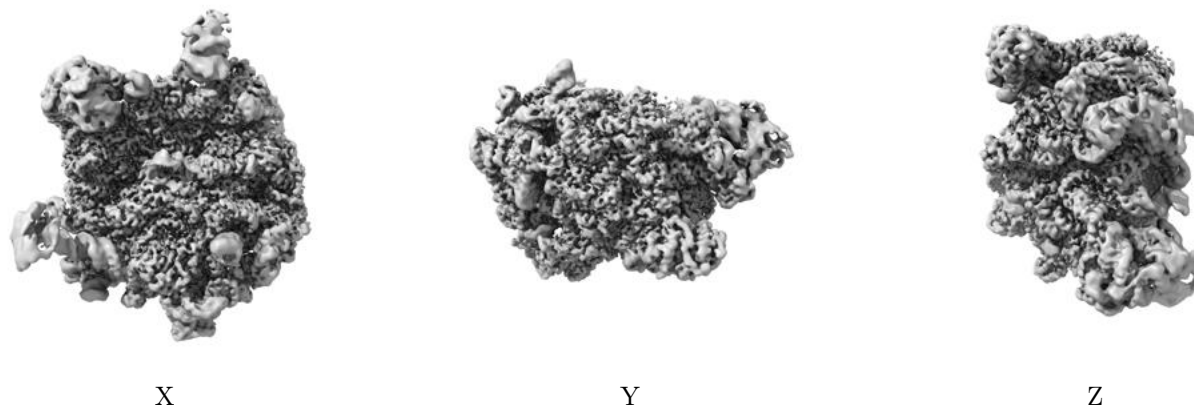


Z

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

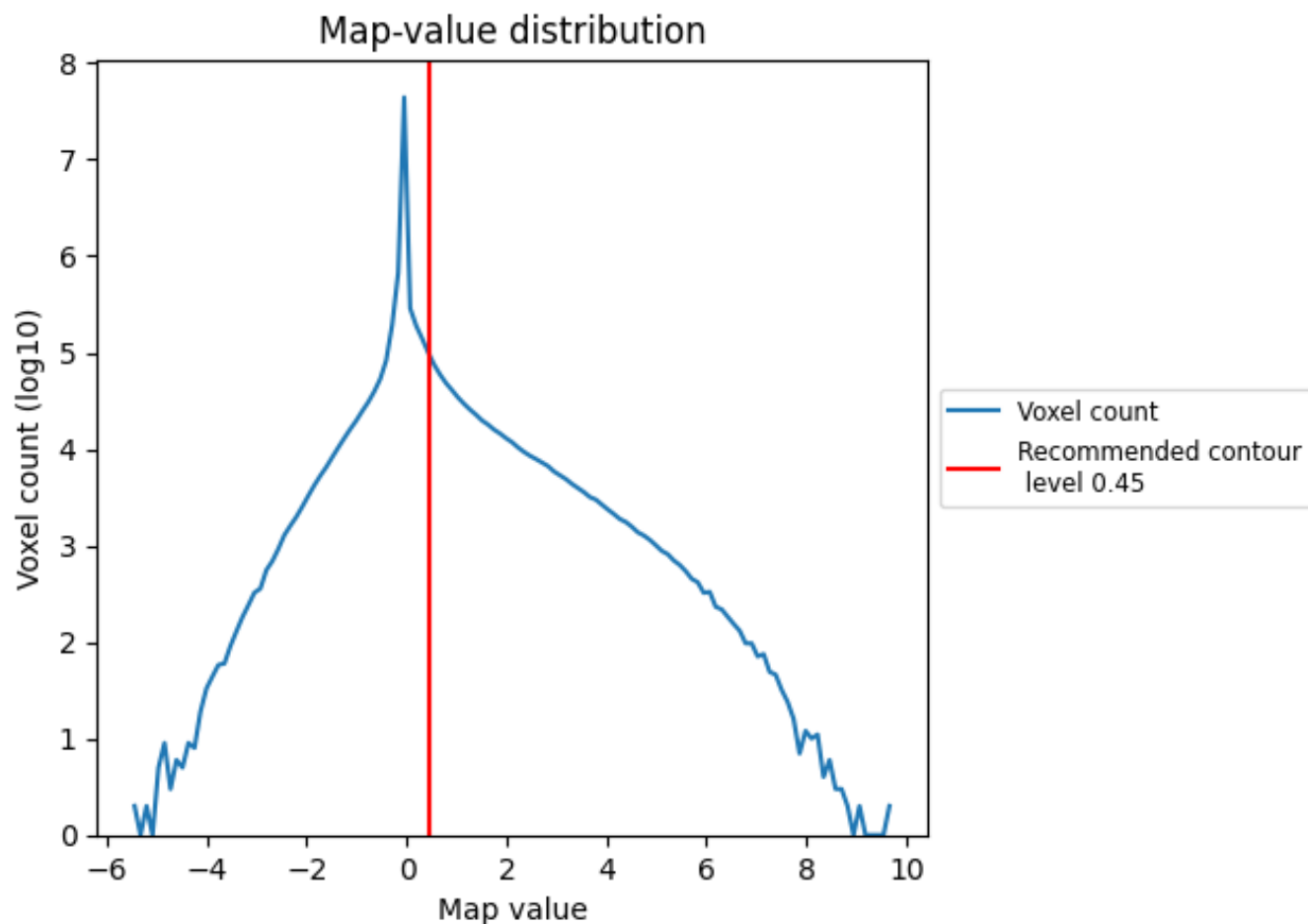
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

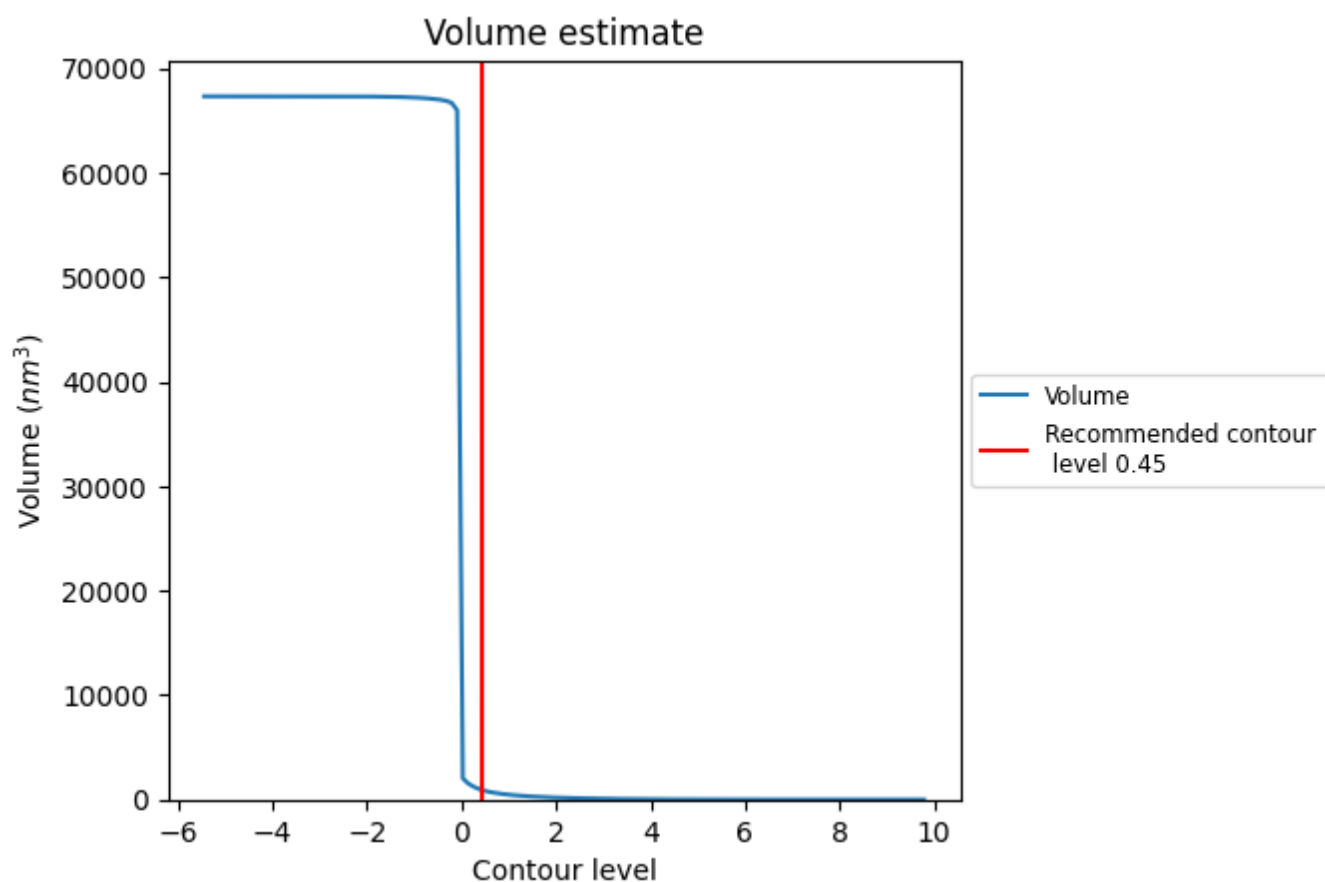
This section contains the results of statistical analysis of the map.

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.

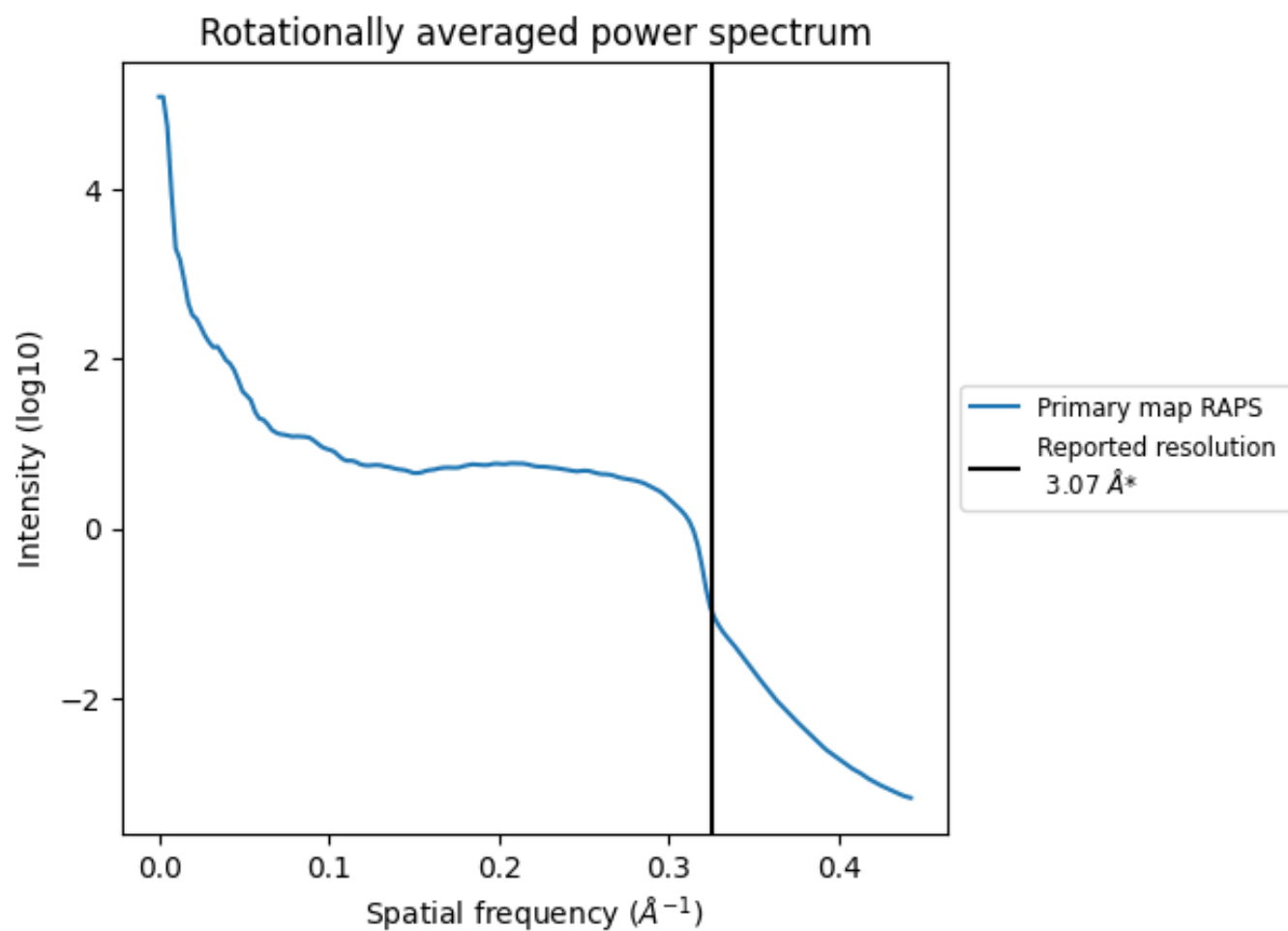
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 899 nm³; this corresponds to an approximate mass of 812 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 0.326 Å⁻¹

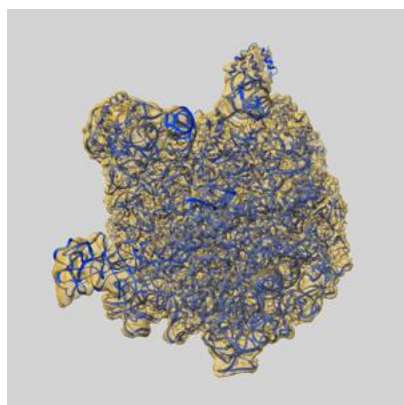
8 Fourier-Shell correlation

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

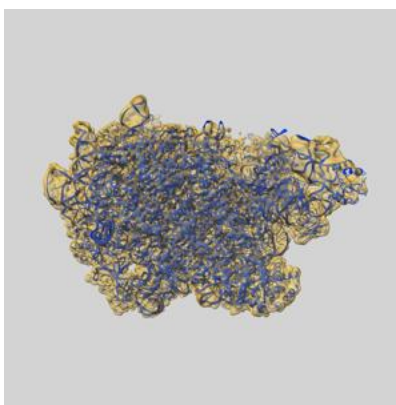
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10535 and PDB model 6TNN. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

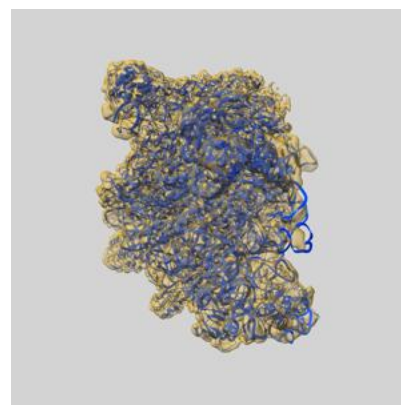
9.1 Map-model overlay [i](#)



X



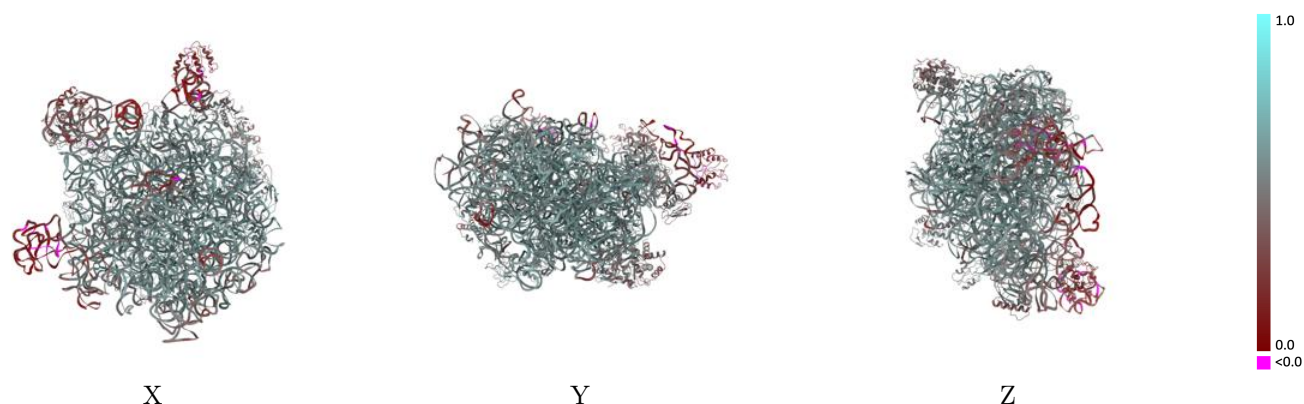
Y



Z

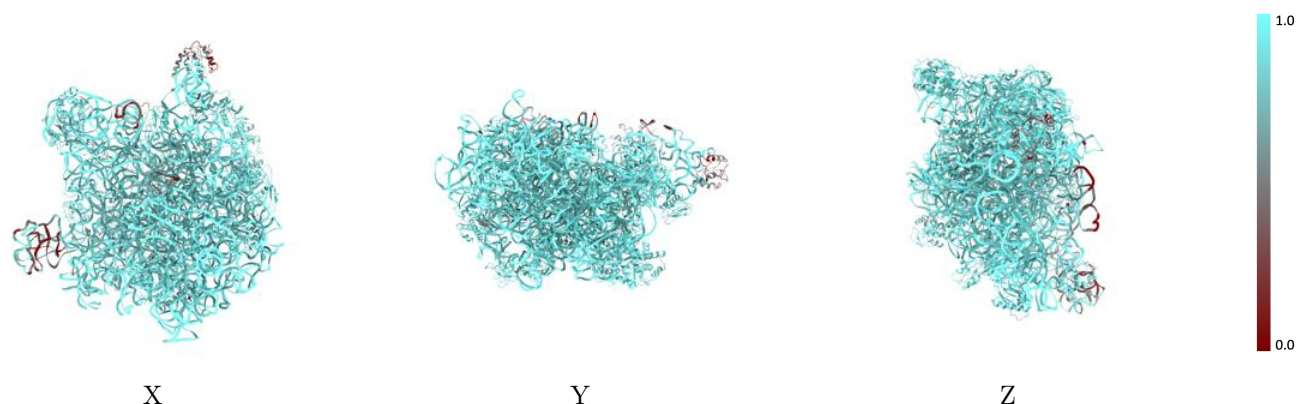
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



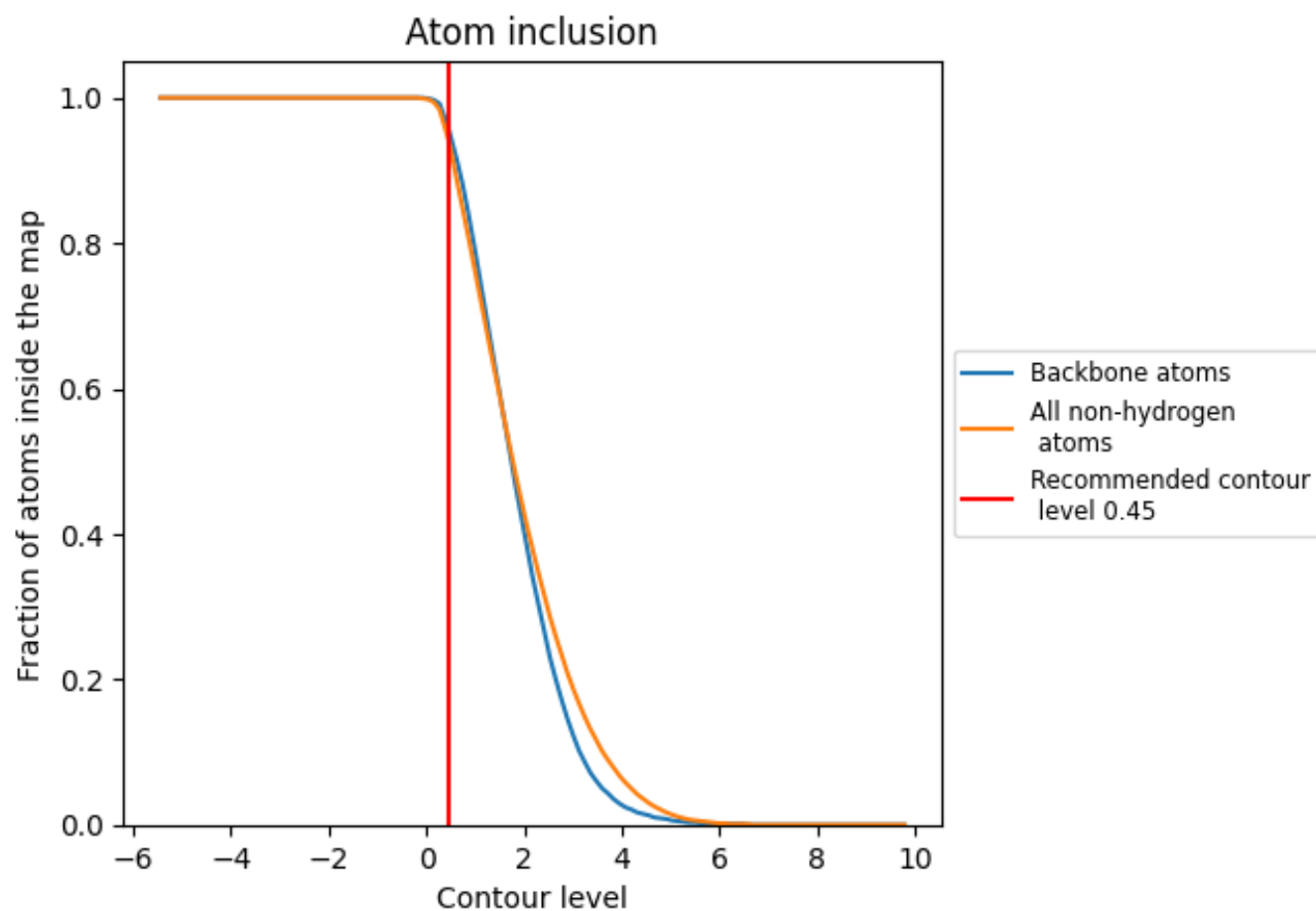
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 96% of all backbone atoms, 94% 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	 0.9420	 0.5220
H	 0.8810	 0.4300
I	 0.9110	 0.4700
U	 0.9560	 0.5300
V	 0.9820	 0.4600
W	 0.9440	 0.5680
X	 0.9570	 0.5680
Y	 0.9330	 0.5380
Z	 0.7670	 0.2910
a	 0.9120	 0.4560
b	 0.4060	 0.1490
c	 0.9340	 0.5690
d	 0.9420	 0.5490
e	 0.9430	 0.5440
f	 0.8960	 0.5390
g	 0.9360	 0.5570
h	 0.9090	 0.4700
i	 0.8960	 0.5160
j	 0.9530	 0.5710
k	 0.9510	 0.5470
l	 0.9500	 0.5670
m	 0.9040	 0.5290
n	 0.9220	 0.5050
o	 0.9140	 0.5620
p	 0.9560	 0.5760
q	 0.9410	 0.5360
r	 0.9800	 0.6060
s	 0.9660	 0.5920
t	 0.9220	 0.5670
u	 0.8890	 0.5460
v	 0.9220	 0.4900
w	 0.9350	 0.5530

