



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:51 PM UTC

PDB ID : 7PAU / pdb_00007pau
EMDB ID : EMD-13286
Title : free 50S in complex with ribosome recycling factor in untreated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-30
Resolution : 8.30 Å (reported)
Based on initial models : 1EH1, 7OOD

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:

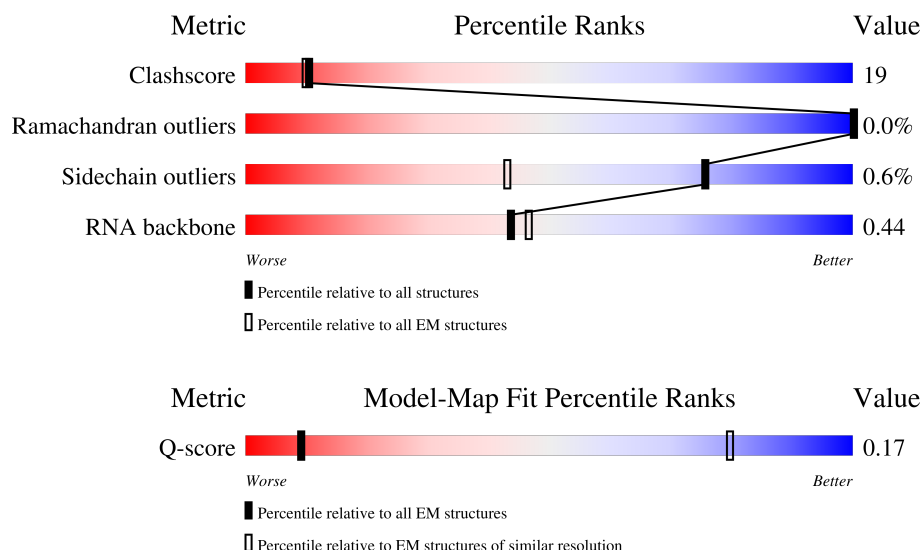
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

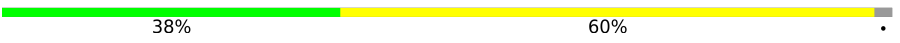
The reported resolution of this entry is 8.30 Å.

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	280 (7.82 - 8.80)

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	0	48	
2	1	59	
3	2	37	

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Mol	Chain	Length	Quality of chain
4	7	184	
5	a	287	
6	b	287	
7	c	212	
8	d	180	
9	e	184	
10	f	149	
11	g	161	
12	h	137	
13	i	146	
14	j	122	
15	k	151	
16	l	139	
17	m	124	
18	n	116	
19	o	119	
20	p	127	
21	q	100	
22	r	159	
23	s	237	
24	t	111	
25	u	104	
26	v	65	
27	w	111	
28	x	97	

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Mol	Chain	Length	Quality of chain
29	y	57	58% 37%
30	z	53	51% 43% 6%
31	3	2907	25% 57% 17%
32	4	108	32% 47% 18%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 92803 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 L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a protein called Ribosome-recycling factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	7	182	Total	C	N	O	S	0	0
			1510	960	262	283	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	e	176	Total	C	N	O	S	0	0
			1396	899	247	250			

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	f	145	Total	C	N	O	S	0	0
			1160	746	204	207	3		

- Molecule 11 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	g	126	Total	C	N	O	S	0	0
			960	612	167	178	3		

- Molecule 12 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	h	128	Total	C	N	O	S	0	0
			959	616	160	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	i	144	Total	C	N	O	S	0	0
			1164	737	213	209	5		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	k	148	Total	C	N	O		0	0
			1153	731	226	196			

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 18 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 19 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	p	114	Total	C	N	O	S	0	0
			947	603	188	154	2		

- Molecule 21 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 22 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	w	100	Total	C	N	O	0	0
			818	517	153	148		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 30 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 31 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

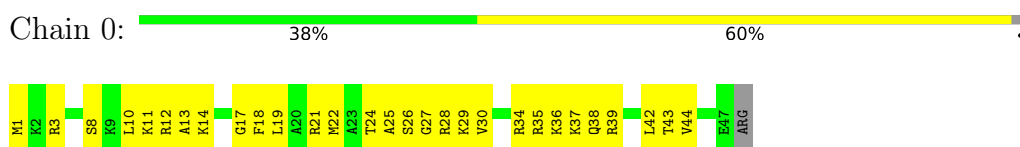
- Molecule 32 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

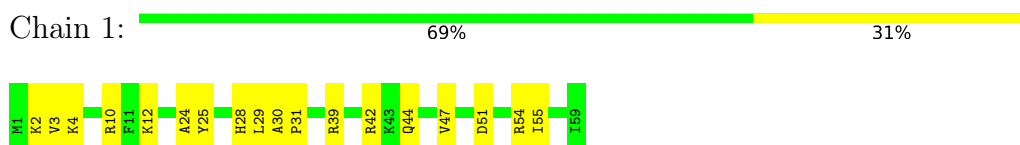
3 Residue-property plots [i](#)

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.

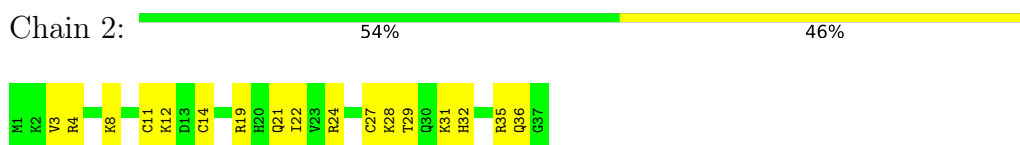
- Molecule 1: 50S ribosomal protein L34



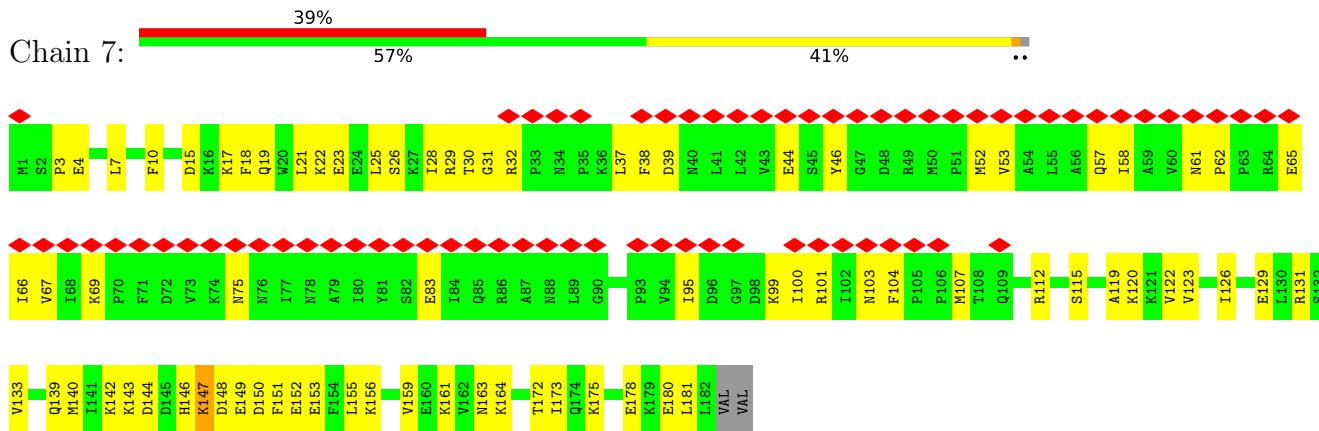
- Molecule 2: 50S ribosomal protein L35



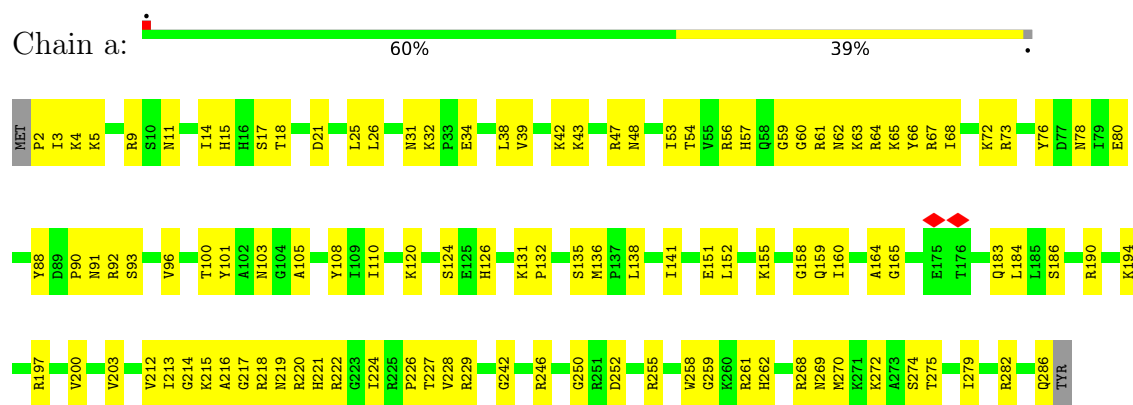
- Molecule 3: 50S ribosomal protein L36



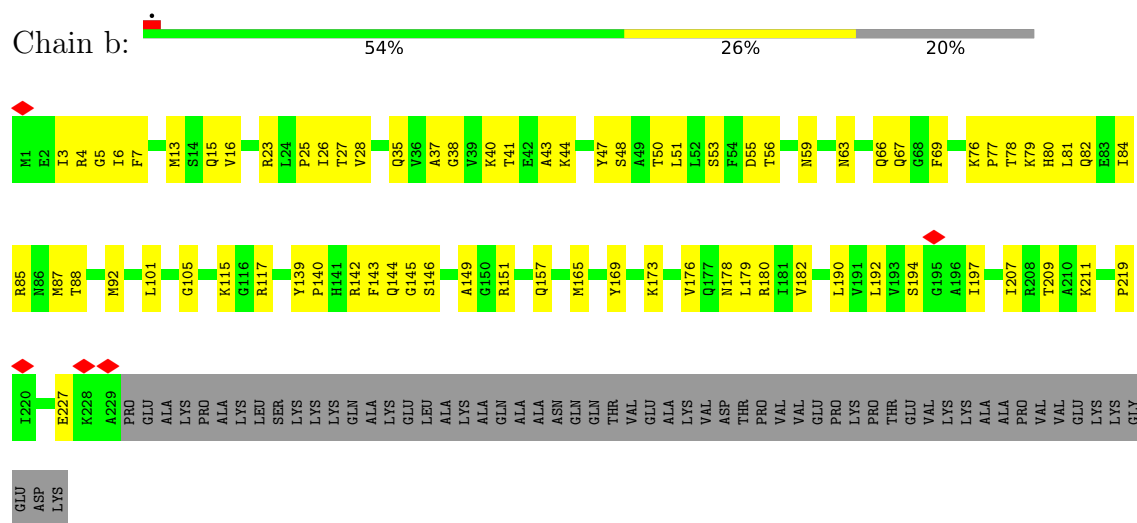
- Molecule 4: Ribosome-recycling factor



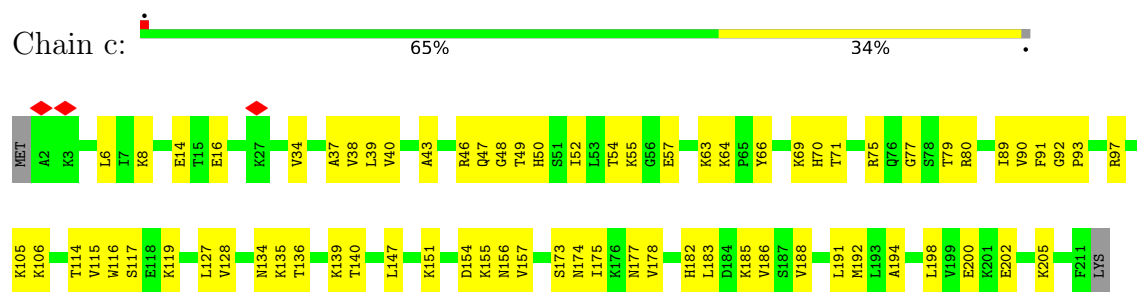
- Molecule 5: 50S ribosomal protein L2



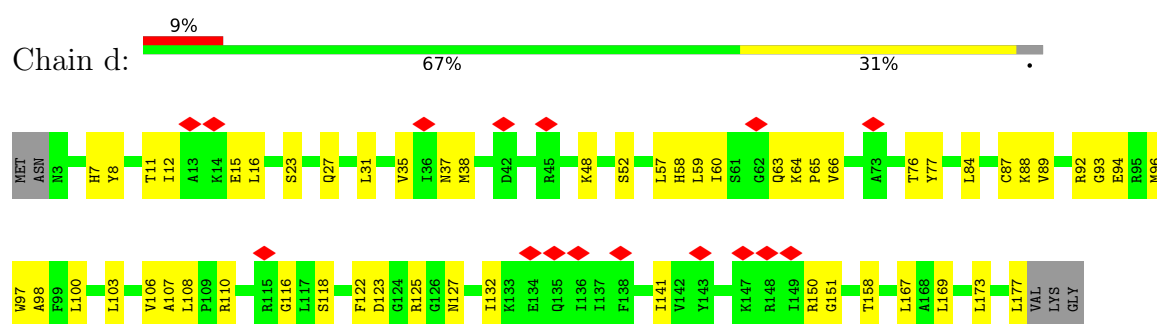
• Molecule 6: 50S ribosomal protein L3



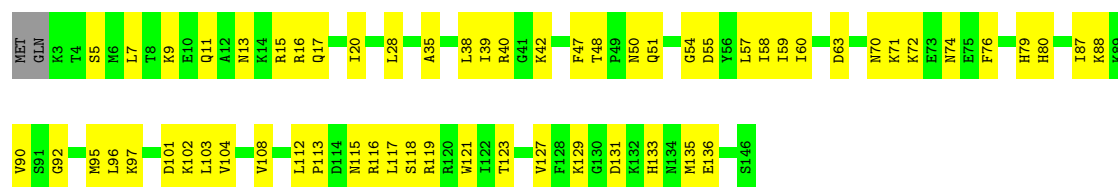
• Molecule 7: 50S ribosomal protein L4



• Molecule 8: 50S ribosomal protein L5

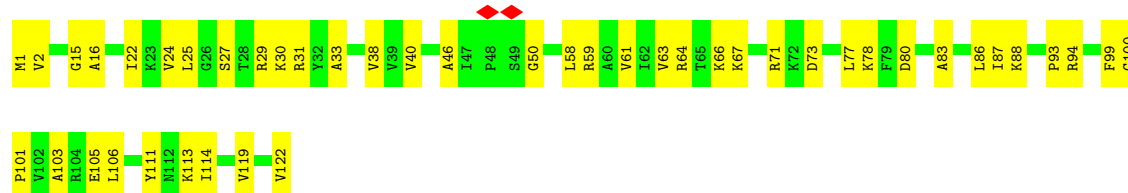


Chain i:  58% 41%



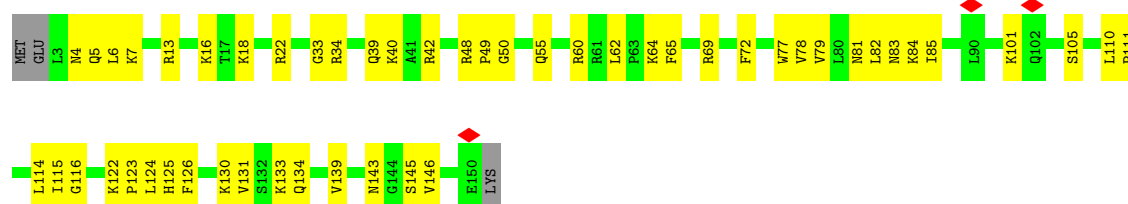
- Molecule 14: 50S ribosomal protein L14

Chain j:  63% 37%



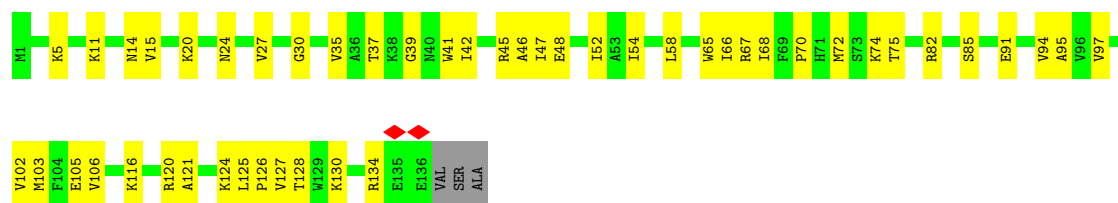
- Molecule 15: 50S ribosomal protein L15

Chain k:  64% 34%



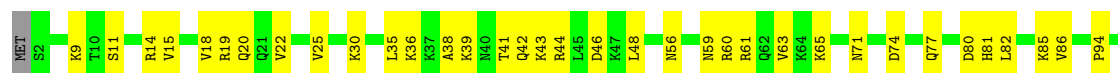
- Molecule 16: 50S ribosomal protein L16

Chain l:  63% 35%



- Molecule 17: 50S ribosomal protein L17

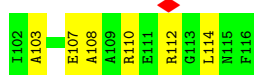
Chain m:  60% 36%





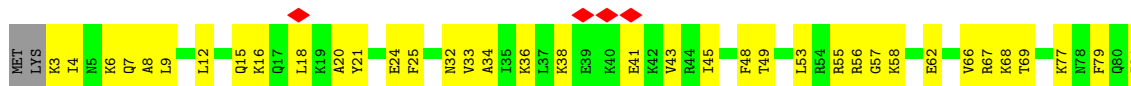
- Molecule 18: 50S ribosomal protein L18

Chain n: 63% 34%



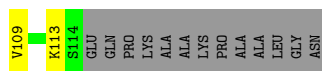
- Molecule 19: 50S ribosomal protein L19

Chain o: 59% 38%



- Molecule 20: 50S ribosomal protein L20

Chain p: 60% 30% 10%



- Molecule 21: 50S ribosomal protein L21

Chain q: 70% 29%



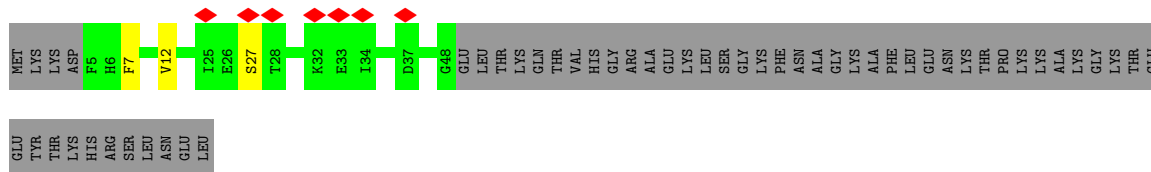
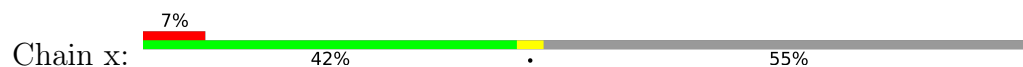
- Molecule 22: 50S ribosomal protein L22

Chain r: 51% 36% 13%

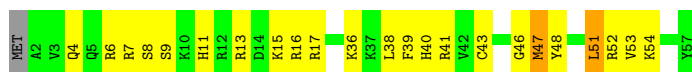




- Molecule 28: 50S ribosomal protein L31



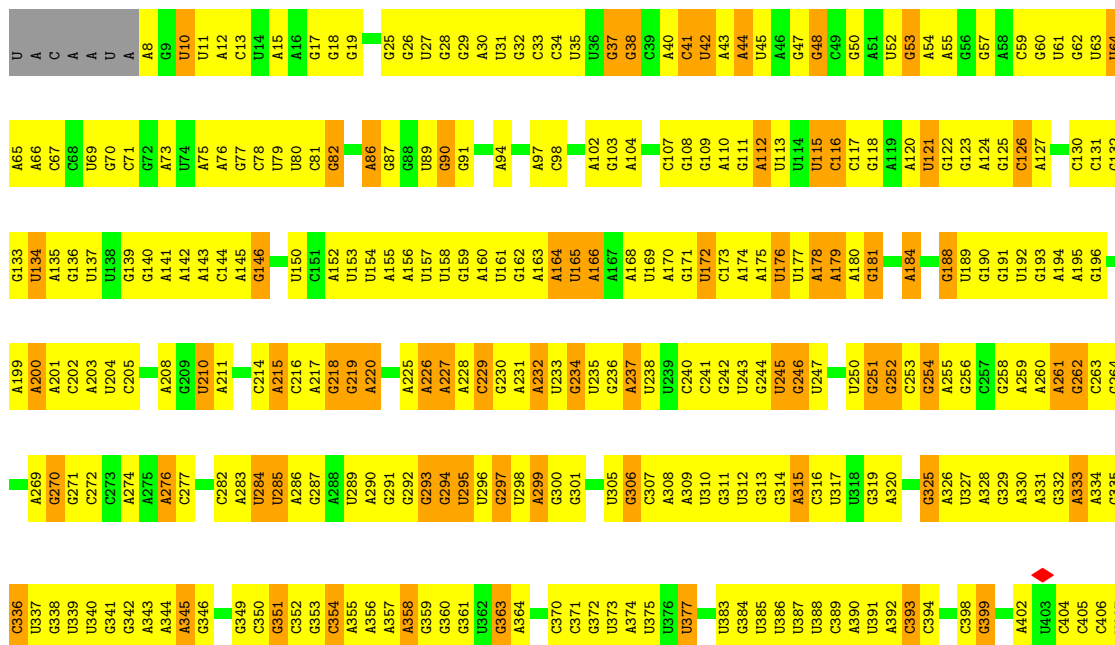
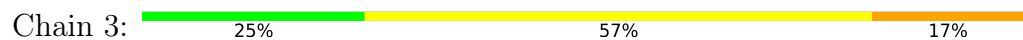
- Molecule 29: 50S ribosomal protein L32



- Molecule 30: 50S ribosomal protein L33 1



- Molecule 31: 23S ribosomal RNA

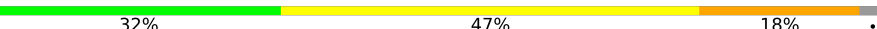


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C1139	U1140	U1141	G1142	U1143	A1146	G1147	U1148	G1149	U1150	U1151	U1154	C1155	C1156	C1157	C1158	C1159	G1160	A1161	A1162	G1163	A1164	U1165	G1166	U1167	A1168	A1169	C1170	G1171	G1174	C1175	U1176	A1177	A1178	G1179	A1183	A1186	C1187	C1188	G1189	A1190	A1191	U1192	U1193	U1194	A1195	U1196	G1197	G1198	A1199	U1200	A1201	A1202	C1137	A1203	A1204				
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G1065	G1066	U1067	U1068	G1069	U1070	G1071	U1072	A1073	A1074	G1075	U1076	G1077	C1078	A1081	A1082	A1085	G1086	C1087	A1088	G1089	G1090	G1091	A1092	U1093	G1094	U1095	U1096	G1097	G1098	G1099	U1100	U1101	U1102	A1103	A1104	A1105	G1106	C1111	A1112	U1113	C1114	G1115	U1116	A1123	G1124	U1125	G1126	A1131	C1132	A1133	U1136	C1137	A1138						
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U932	A933	C934	U935	G936	A937	A938	U939	A940	U944	U945	A946	A947	A948	U949	U950	C951	U952	G953	A954	A955	U956	G957	C958	U963	A964	U965	U966	U967	U968	A969	U970	U971	C972	U973	C974	G975	C976	A977	U978	U979	C980	A981	U982	A983	C984	A985	U986	G989	G990	U993	U994	A995	A996	U997	C998				
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G805	A806	U807	G810	G811	G812	G813	U814	G815	A816	A817	A818	U819	U820	C821	C822	A823	A824	U825	C826	C827	A828	A829	A830	U831	C832	C833	G834	U835	U836	A837	G840	C841	U842	G843	G844	C847	U848	C849	G850	U851	C852	A853	A854	A855	A856	C860	U861	U862	U863	A864	A865	U866	A867	U868	U869				
G732	C733	G735	U738	G739	A740	G742	U745	G746	A747	G748	C752	A753	U754	C755	A756	A757	U758	G759	U760	G761	A762	G763	G764	A765	U766	C767	G768	U769	A770	U774	C775	U781	U782	G783	A784	G788	A789	U790	G791	G792	C793	G794	U797	G798	A799	C800	U801	U802	G803	C805	U804								
A667	A668	C671	G672	A673	G674	U675	U676	U677	U678	A679	A680	A681	A682	A683	A684	G685	U689	U690	C692	G693	U694	G695	U696	A697	U700	A701	C702	A703	G704	A705	A638	C706	C707	G708	A710	A711	A712	C713	G714	G715	G716	G719	A720	G721	C722	C659	A724	G725	A728	U729	G730	A731							
G603	A604	A605	G606	U607	A608	U609	G610	A611	C613	G614	G615	G616	C617	U618	A619	G620	U621	U622	A623	G624	G625	A626	U627	A628	G629	C630	A631	A632	G633	C634	A635	U636	G637	A638	A646	A649	G650	A651	G655	G656	A657	G658	C659	U660	G661	U662	A663	G664	C665	G666									
C480	C481	A482	A483	U484	A485	G486	C487	A488	A489	A490	C491	A492	U493	G494	U495	C498	A499	U500	G501	A502	G503	G504	G505	A506	A507	A508	U509	C510	C511	G512	A513	A514	C515	A516	G517	A518	A519	C520	C521	A522	A523	G524	A525	G526	A527	U528	G529	G530	G531	C532	G533	U534	G535	A536	A537	A538	U539	A540	
G541	A542	U543	U544	C545	U546	G547	A548	A549	A550	C551	A552	U553	U554	A555	U556	G557	C558	C559	U560	A561	C562	A563	A564	C565	G566	U567	G568	U569	C570	A571	G572	A573	A574	C575	A576	C577	A578	U579	U580	A581	A582	U583	G584	U585	G586	U587	G588	A589	G590	G591	C592	G593	U594	U595	C596	C597	G598	U599	A600



A2386	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727	C2792	C2857	A2897	G2986	U2457	A2521	G2584	U2658	G2727
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• Molecule 32: 5S ribosomal RNA

Chain 4:  32% 47% 18% .

U1	U2	U3	G4	G5	U6	U7	C8	C9	C10	A11	U12	G13	G22	A23	A24	A25	C26	A27	C28	C29	U30	G31	G32	U33	U34	C35	C36	A37	U38	U39	U40	C41	G42	A43	A44	C45	C46	C47	A48	G49	C50	A51	U54	A55	A56	G57	C58	A59	C60	A61	G67	C68	C69	G74	U75
A76	G77	C78	U79	G80	U	U	C84	A85	G86	U87	G88	A89	G90	A91	A92	U93	A94	G95	A96	A97	A98	A99	G100	C101	A102	C103	C104	A105	A106	G107	C108																								

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	8203	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 ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.619	Depositor
Minimum map value	-0.546	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.104	Depositor
Recommended contour level	0.46	Depositor
Map size (Å)	480.00003, 480.00003, 480.00003	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.4, 2.4, 2.4	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0	0.12	0/383	0.37	0/504
2	1	0.11	0/484	0.42	0/637
3	2	0.13	0/306	0.39	0/401
4	7	0.23	0/1535	0.45	0/2061
5	a	0.14	0/2267	0.40	0/3044
6	b	0.16	0/1795	0.43	0/2412
7	c	0.14	0/1671	0.39	0/2246
8	d	0.14	0/1409	0.41	0/1894
9	e	0.15	0/1420	0.41	0/1912
10	f	0.14	0/1183	0.45	0/1587
11	g	0.49	0/969	0.78	0/1295
12	h	0.14	0/968	0.46	1/1298 (0.1%)
13	i	0.13	0/1186	0.34	0/1592
14	j	0.14	0/953	0.40	0/1275
15	k	0.13	0/1170	0.38	0/1559
16	l	0.14	0/1104	0.41	0/1481
17	m	0.13	0/973	0.39	0/1309
18	n	0.14	0/897	0.44	0/1198
19	o	0.15	0/948	0.45	0/1262
20	p	0.13	0/961	0.42	1/1278 (0.1%)
21	q	0.14	0/828	0.41	0/1111
22	r	0.15	0/1077	0.44	0/1441
23	s	0.12	0/732	0.42	0/988
24	t	0.15	0/879	0.38	0/1165
25	u	0.15	0/665	0.40	0/884
26	v	0.13	0/519	0.41	0/695
27	w	0.10	0/826	0.35	0/1104
28	x	0.15	0/353	0.47	0/474
29	y	0.35	0/457	0.61	0/601
30	z	0.13	0/412	0.42	0/547
31	3	0.09	0/69073	0.23	0/107710
32	4	0.09	0/2505	0.26	0/3902
All	All	0.12	0/100908	0.30	2/150867 (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
10	f	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	h	74	ILE	N-CA-C	-7.98	105.71	113.53
20	p	89	ILE	N-CA-C	-5.81	107.10	113.43

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	f	11	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	0	380	0	429	27	0
2	1	477	0	530	18	0
3	2	304	0	350	18	0
4	7	1510	0	1553	59	0
5	a	2225	0	2301	102	0
6	b	1762	0	1808	63	0
7	c	1644	0	1731	61	0
8	d	1388	0	1469	43	0
9	e	1396	0	1481	31	0
10	f	1160	0	1172	34	0
11	g	960	0	1014	5	0
12	h	959	0	1039	7	0
13	i	1164	0	1192	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	j	944	0	1019	37	0
15	k	1153	0	1256	45	0
16	l	1079	0	1134	39	0
17	m	958	0	1011	36	0
18	n	889	0	952	34	0
19	o	938	0	1008	36	0
20	p	947	0	1028	34	0
21	q	811	0	858	19	0
22	r	1068	0	1150	44	0
23	s	720	0	803	31	0
24	t	872	0	972	24	0
25	u	657	0	695	32	0
26	v	513	0	560	23	0
27	w	818	0	870	40	0
28	x	344	0	333	2	0
29	y	452	0	472	21	0
30	z	408	0	440	17	0
31	3	61664	0	30954	1980	0
32	4	2239	0	1137	71	0
All	All	92803	0	62721	2728	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 19.

The worst 5 of 2728 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)
9:e:16:VAL:HA	9:e:28:LYS:O	1.50	1.10
31:3:900:G:N2	31:3:903:A:H61	1.58	1.01
31:3:1807:C:H42	31:3:1824:G:N2	1.57	1.01
31:3:2299:U:H3	31:3:2349:G:H1	1.03	1.00
31:3:1746:U:H3	31:3:1753:G:H1	1.04	1.00

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	0	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
3	2	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
4	7	180/184 (98%)	168 (93%)	12 (7%)	0	100	100
5	a	283/287 (99%)	266 (94%)	17 (6%)	0	100	100
6	b	227/287 (79%)	209 (92%)	18 (8%)	0	100	100
7	c	208/212 (98%)	196 (94%)	12 (6%)	0	100	100
8	d	173/180 (96%)	163 (94%)	10 (6%)	0	100	100
9	e	174/184 (95%)	167 (96%)	7 (4%)	0	100	100
10	f	143/149 (96%)	130 (91%)	13 (9%)	0	100	100
11	g	124/161 (77%)	109 (88%)	14 (11%)	1 (1%)	16	54
12	h	126/137 (92%)	118 (94%)	8 (6%)	0	100	100
13	i	142/146 (97%)	135 (95%)	7 (5%)	0	100	100
14	j	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
15	k	146/151 (97%)	137 (94%)	9 (6%)	0	100	100
16	l	134/139 (96%)	126 (94%)	8 (6%)	0	100	100
17	m	117/124 (94%)	109 (93%)	8 (7%)	0	100	100
18	n	108/116 (93%)	98 (91%)	10 (9%)	0	100	100
19	o	113/119 (95%)	102 (90%)	11 (10%)	0	100	100
20	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
21	q	97/100 (97%)	86 (89%)	11 (11%)	0	100	100
22	r	137/159 (86%)	126 (92%)	11 (8%)	0	100	100
23	s	90/237 (38%)	84 (93%)	6 (7%)	0	100	100
24	t	109/111 (98%)	102 (94%)	7 (6%)	0	100	100
25	u	84/104 (81%)	79 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	v	61/65 (94%)	57 (93%)	4 (7%)	0	100	100
27	w	96/111 (86%)	92 (96%)	4 (4%)	0	100	100
28	x	42/97 (43%)	34 (81%)	8 (19%)	0	100	100
29	y	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
30	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	3585/4063 (88%)	3347 (93%)	237 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	g	45	PHE

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	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	7	170/172 (99%)	164 (96%)	6 (4%)	32	53
5	a	241/243 (99%)	241 (100%)	0	100	100
6	b	186/233 (80%)	186 (100%)	0	100	100
7	c	182/184 (99%)	182 (100%)	0	100	100
8	d	150/154 (97%)	150 (100%)	0	100	100
9	e	153/159 (96%)	153 (100%)	0	100	100
10	f	123/134 (92%)	123 (100%)	0	100	100
11	g	101/129 (78%)	91 (90%)	10 (10%)	7	24
12	h	102/110 (93%)	102 (100%)	0	100	100
13	i	126/128 (98%)	126 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	j	103/103 (100%)	103 (100%)	0	100	100
15	k	123/126 (98%)	123 (100%)	0	100	100
16	l	113/115 (98%)	113 (100%)	0	100	100
17	m	105/109 (96%)	105 (100%)	0	100	100
18	n	96/99 (97%)	96 (100%)	0	100	100
19	o	101/105 (96%)	101 (100%)	0	100	100
20	p	100/108 (93%)	100 (100%)	0	100	100
21	q	90/91 (99%)	90 (100%)	0	100	100
22	r	116/132 (88%)	116 (100%)	0	100	100
23	s	82/208 (39%)	82 (100%)	0	100	100
24	t	96/96 (100%)	96 (100%)	0	100	100
25	u	69/85 (81%)	69 (100%)	0	100	100
26	v	58/60 (97%)	58 (100%)	0	100	100
27	w	87/98 (89%)	87 (100%)	0	100	100
28	x	41/86 (48%)	41 (100%)	0	100	100
29	y	48/49 (98%)	45 (94%)	3 (6%)	16	37
30	z	47/50 (94%)	47 (100%)	0	100	100
All	All	3135/3493 (90%)	3116 (99%)	19 (1%)	76	83

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	g	88	GLU
29	y	51	LEU
29	y	52	ARG
29	y	47	MET
11	g	32	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
13	i	17	GLN
29	y	4	GLN
17	m	81	HIS
22	r	112	ASN

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Mol	Chain	Res	Type
13	i	82	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	3	2875/2907 (98%)	790 (27%)	28 (0%)
32	4	103/108 (95%)	25 (24%)	4 (3%)
All	All	2978/3015 (98%)	815 (27%)	32 (1%)

5 of 815 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
31	3	10	U
31	3	15	A
31	3	28	G
31	3	37	G
31	3	38	G

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
32	4	10	C
32	4	54	U
31	3	1216	U
31	3	1209	U
32	4	59	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

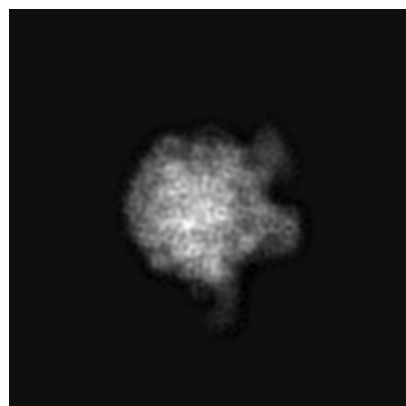
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13286. These allow visual inspection of the internal detail of the map and identification of artifacts.

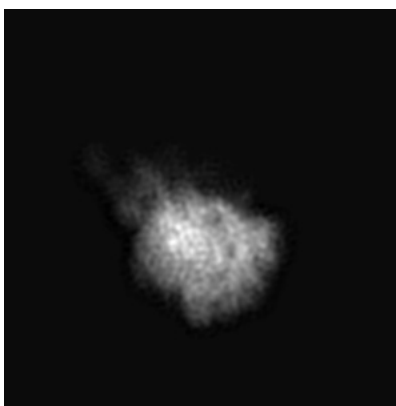
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

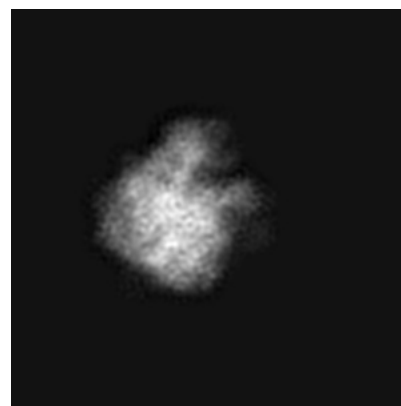
6.1.1 Primary map



X

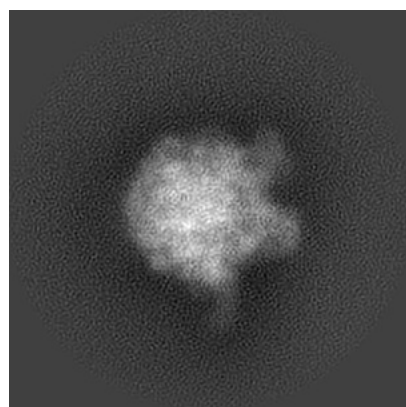


Y

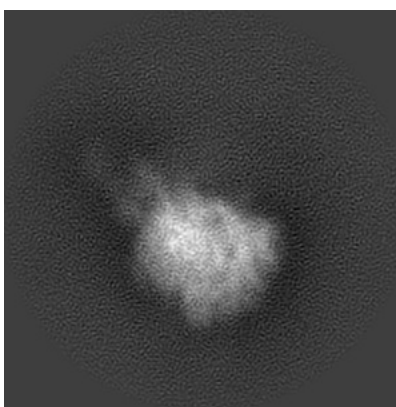


Z

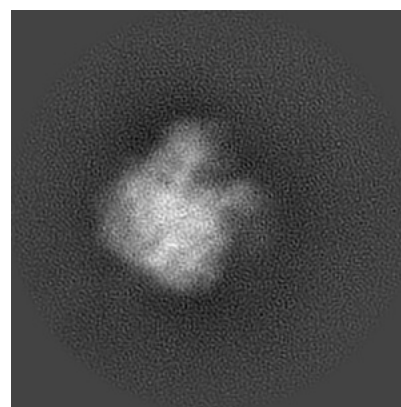
6.1.2 Raw map



X



Y

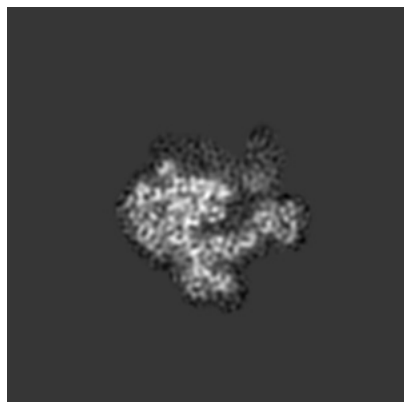


Z

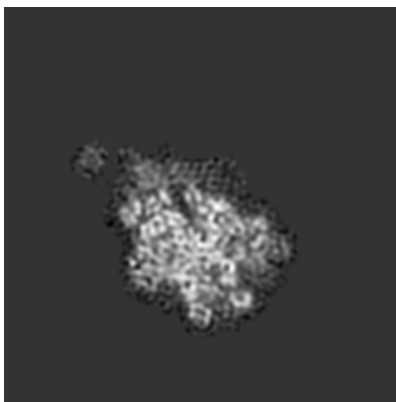
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

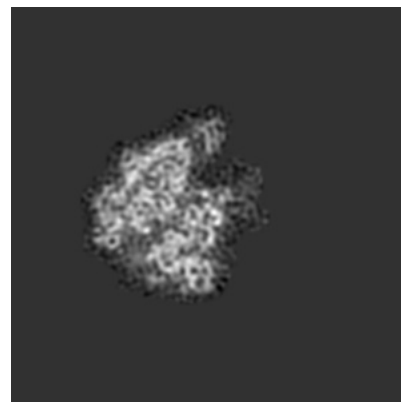
6.2.1 Primary map



X Index: 100

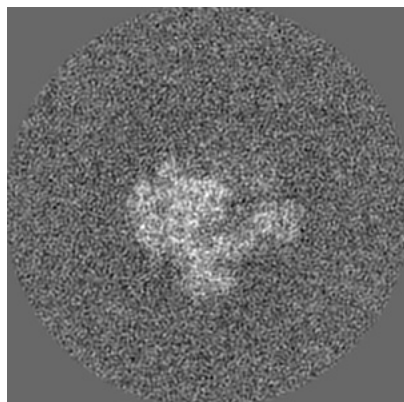


Y Index: 100

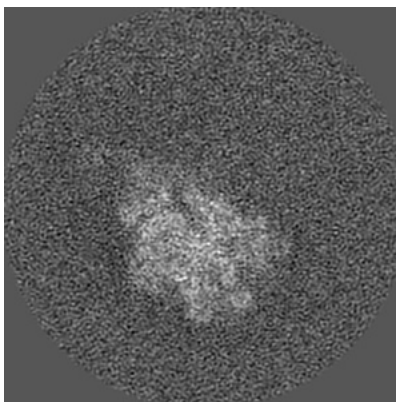


Z Index: 100

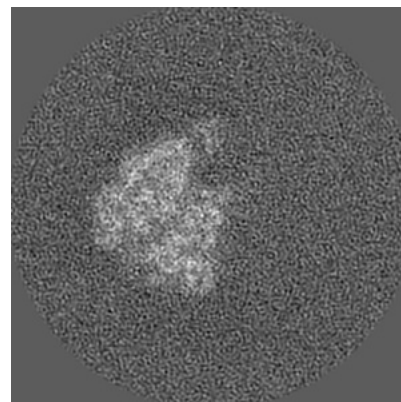
6.2.2 Raw map



X Index: 100



Y Index: 100

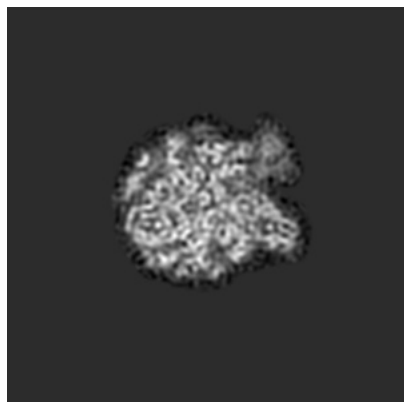


Z Index: 100

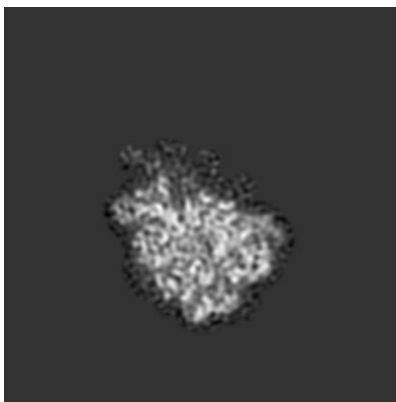
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

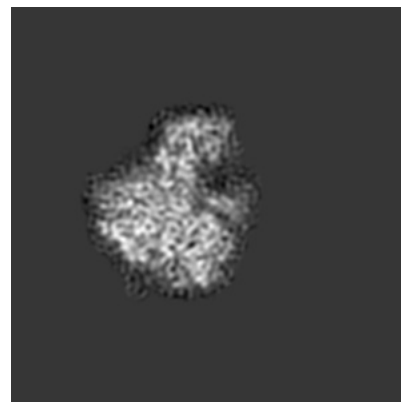
6.3.1 Primary map



X Index: 83

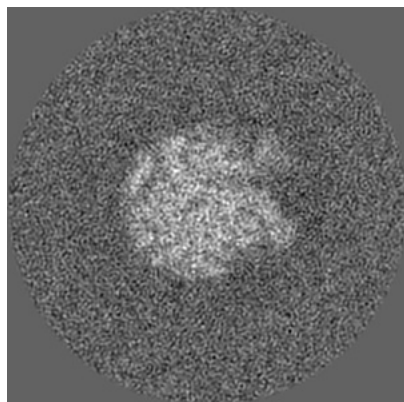


Y Index: 93

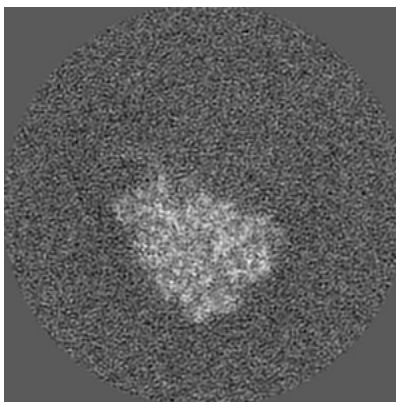


Z Index: 93

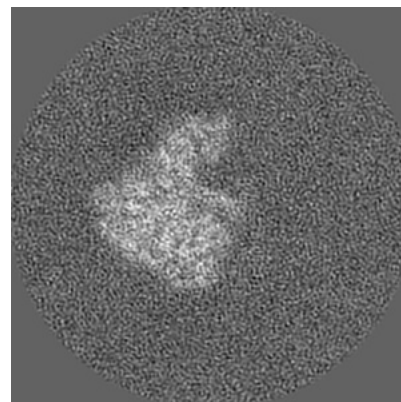
6.3.2 Raw map



X Index: 80



Y Index: 93



Z Index: 94

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

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

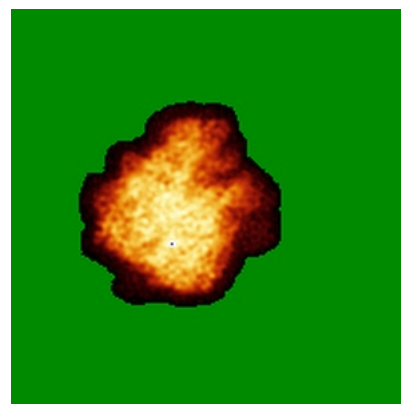
6.4.1 Primary map



X

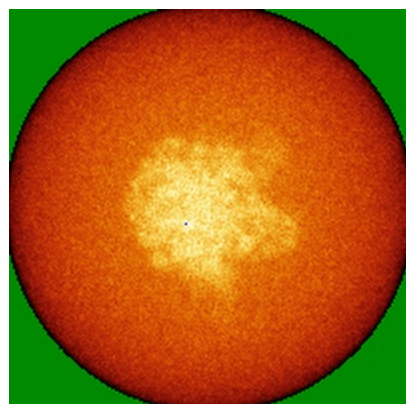


Y

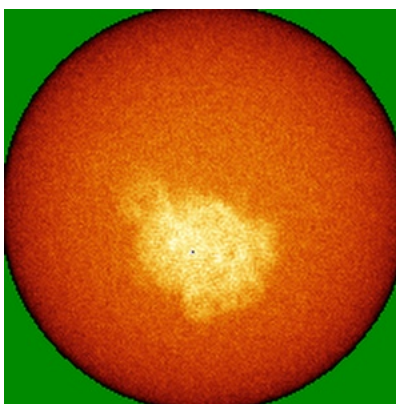


Z

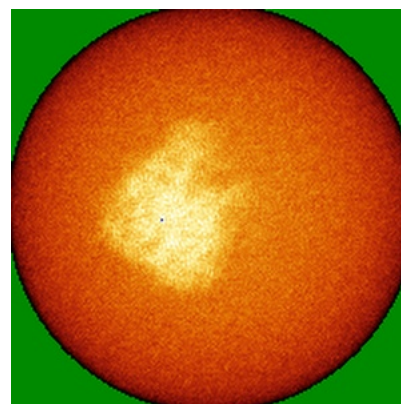
6.4.2 Raw map



X



Y

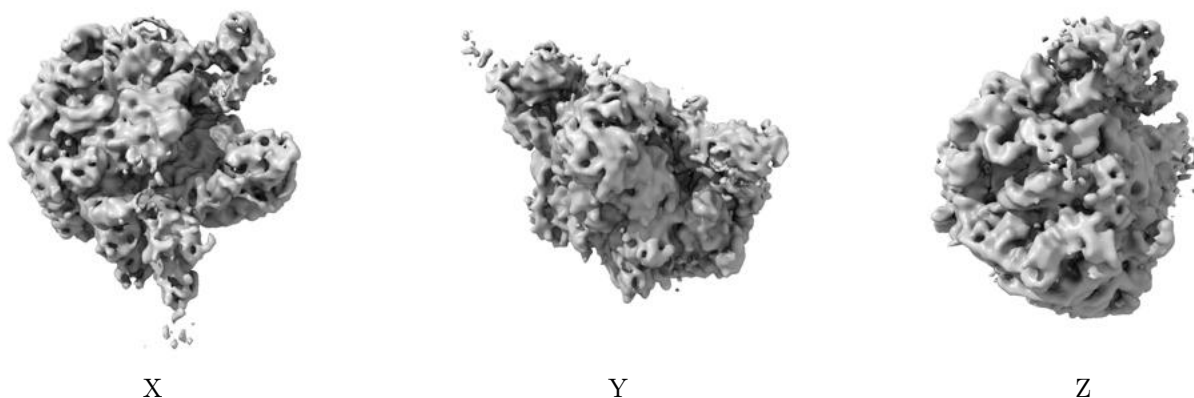


Z

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.

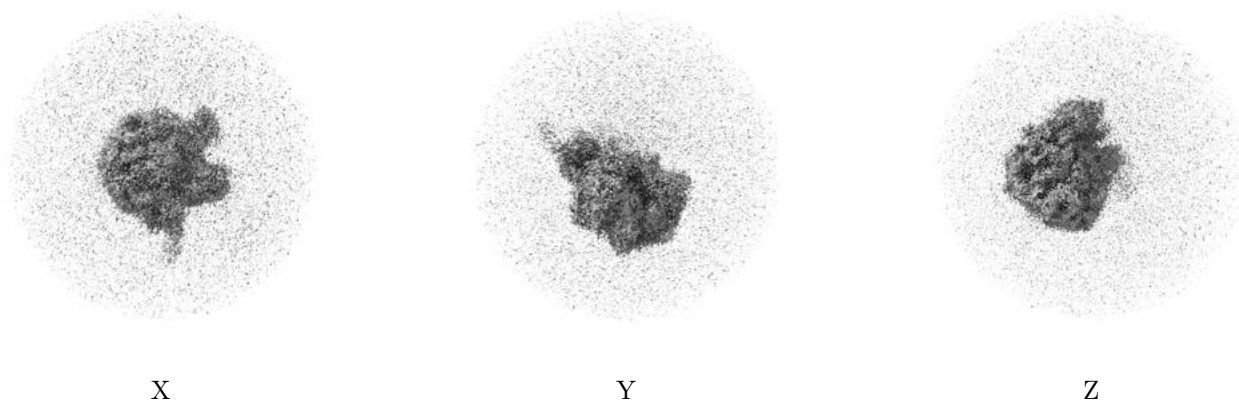
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.46. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

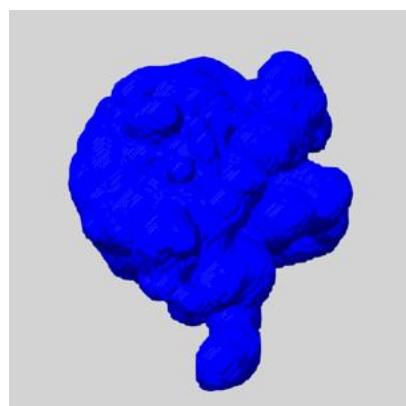
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

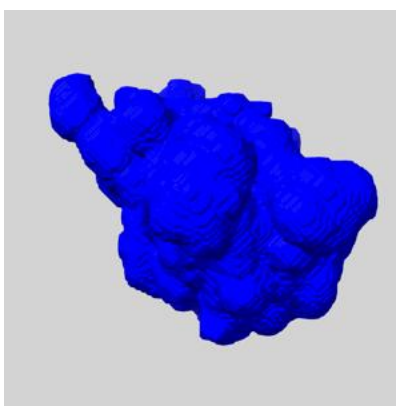
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

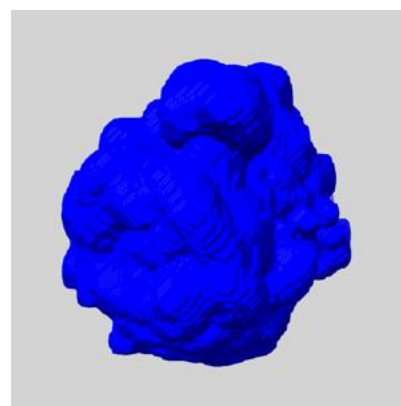
6.6.1 emd_13286_msk_1.map [i](#)



X



Y

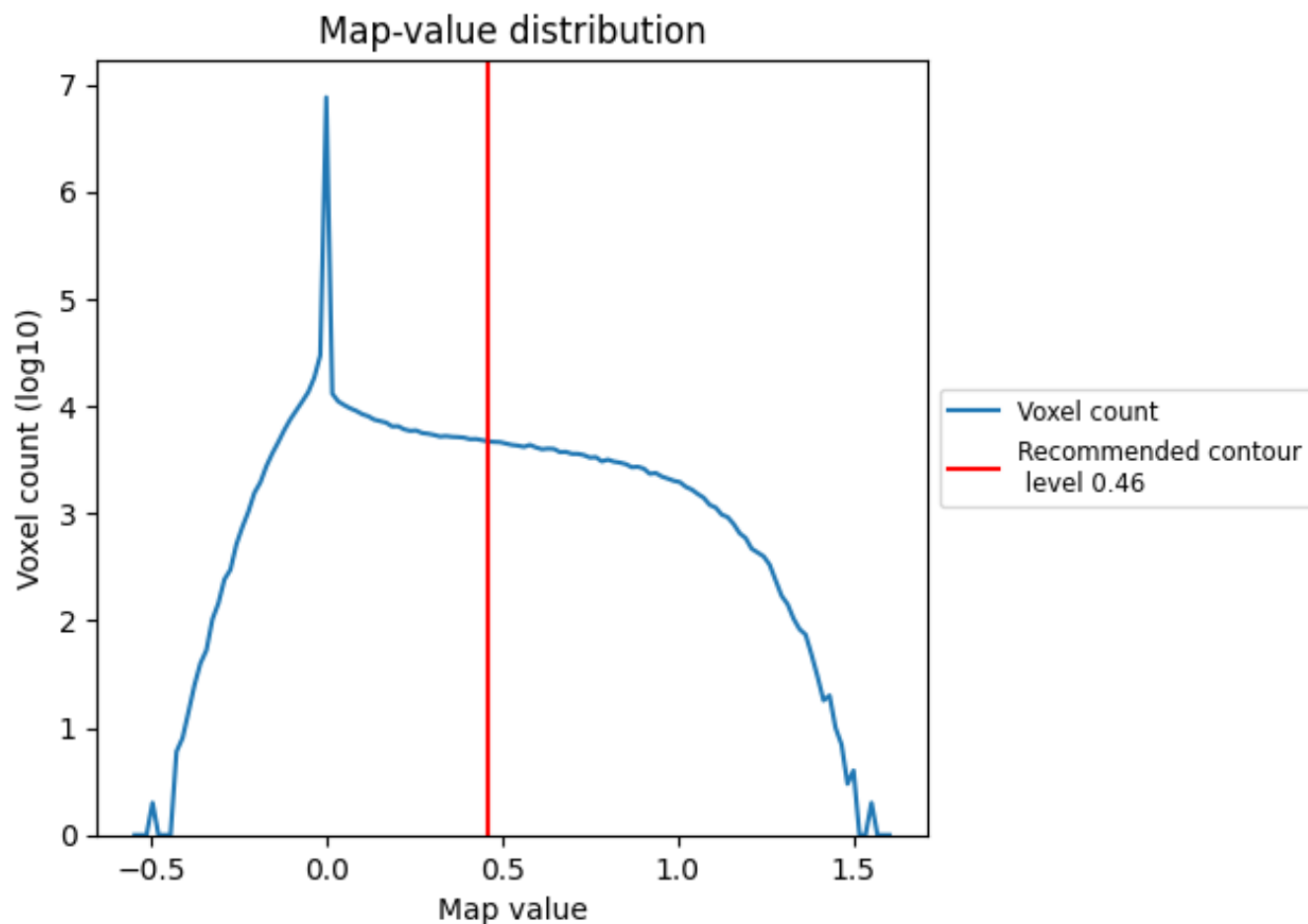


Z

7 Map analysis [i](#)

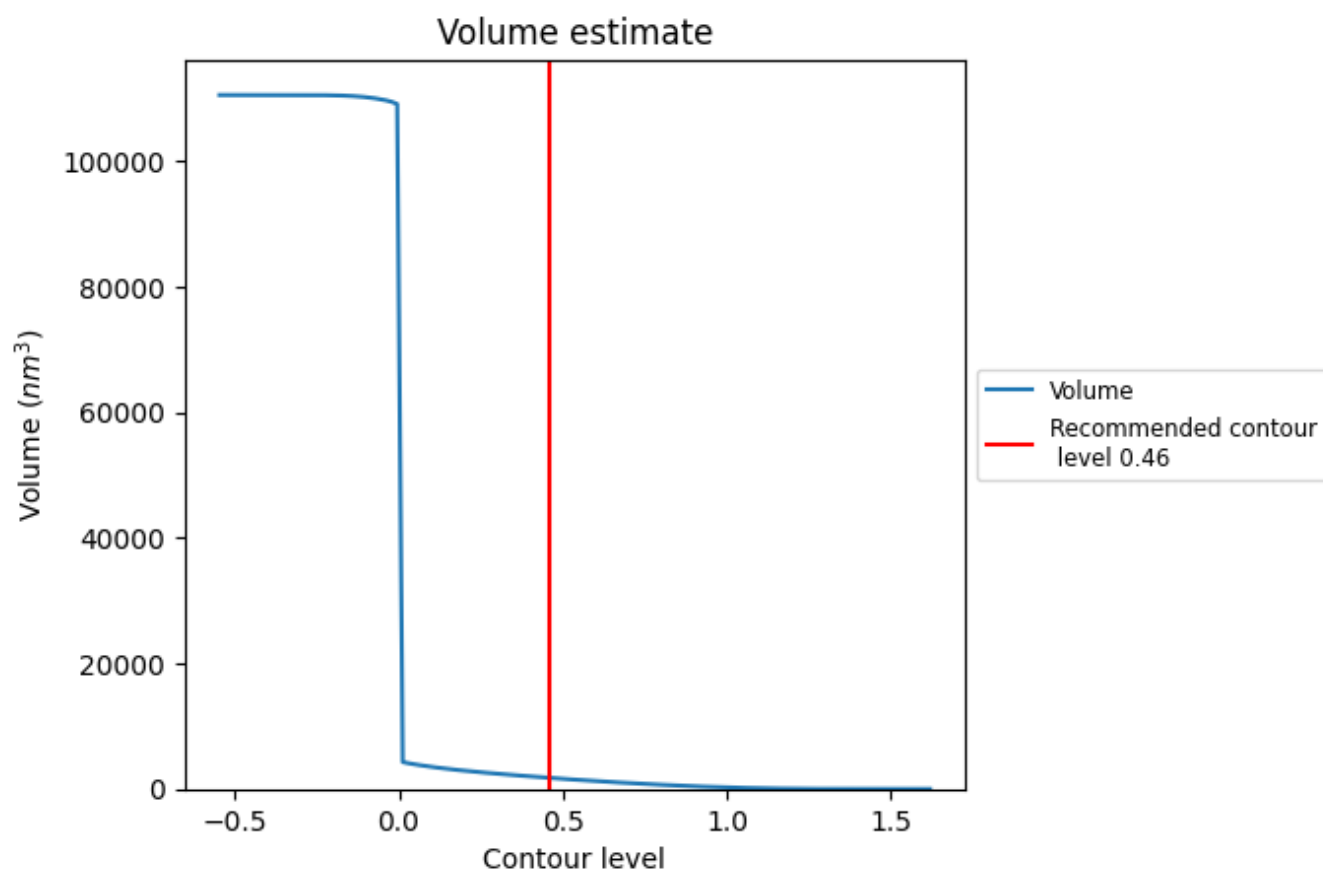
This section contains the results of statistical analysis of the map.

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.

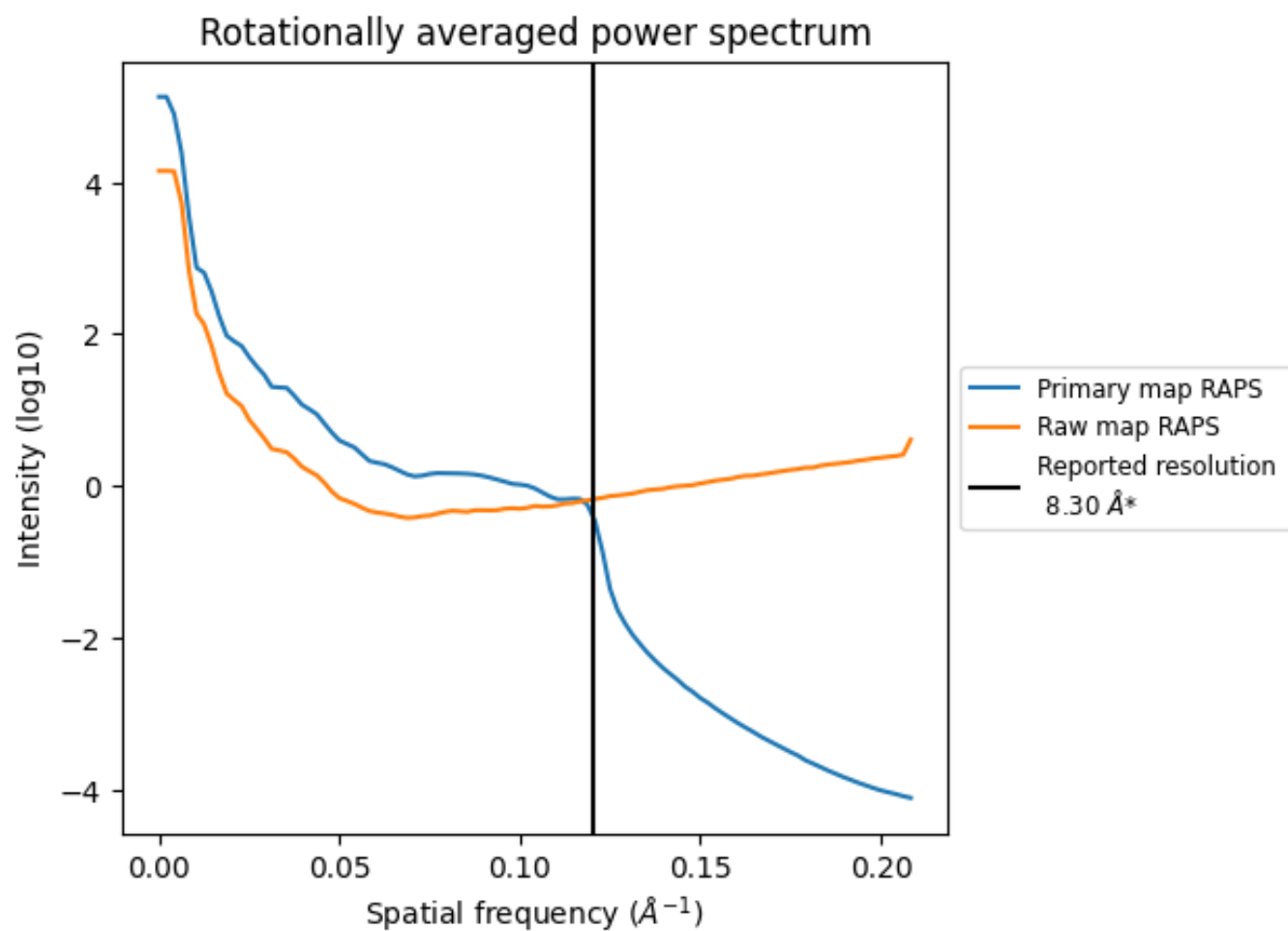
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1764 nm^3 ; this corresponds to an approximate mass of 1593 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 ⓘ

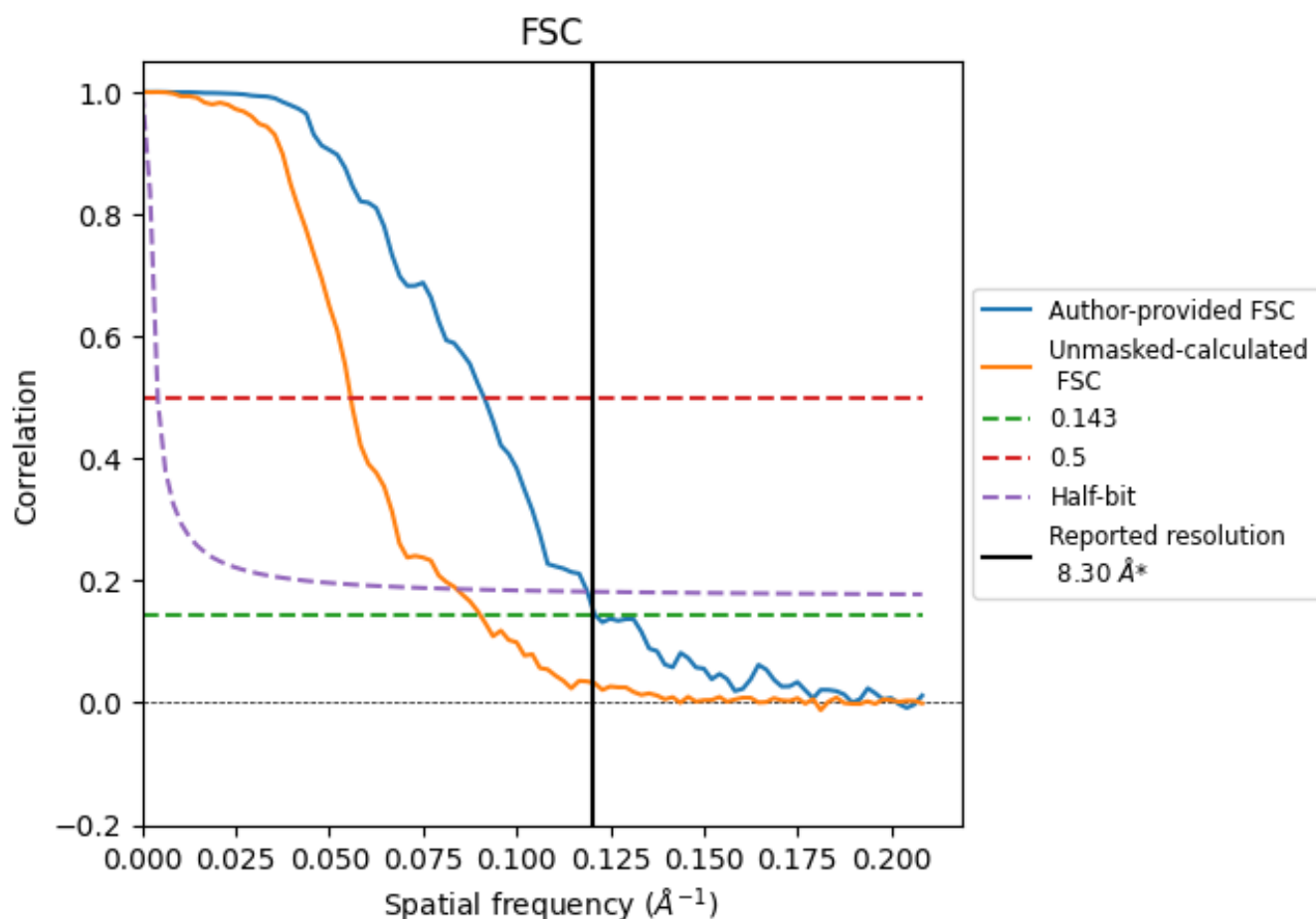


*Reported resolution corresponds to spatial frequency of 0.120 Å⁻¹

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 $0.120 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

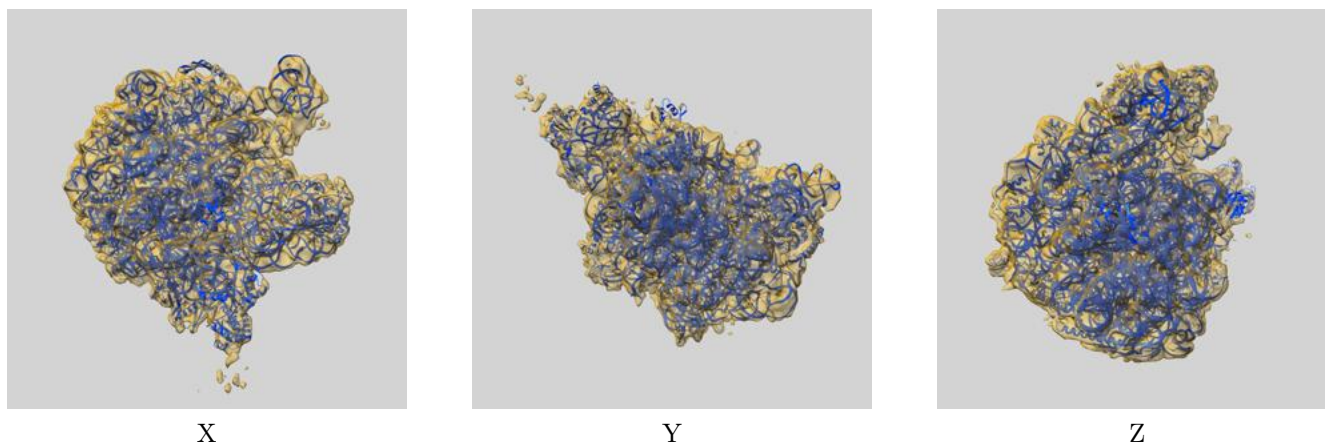
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.30	-	-
Author-provided FSC curve	8.26	10.96	8.42
Unmasked-calculated*	11.07	17.95	11.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 11.07 differs from the reported value 8.3 by more than 10 %

9 Map-model fit [i](#)

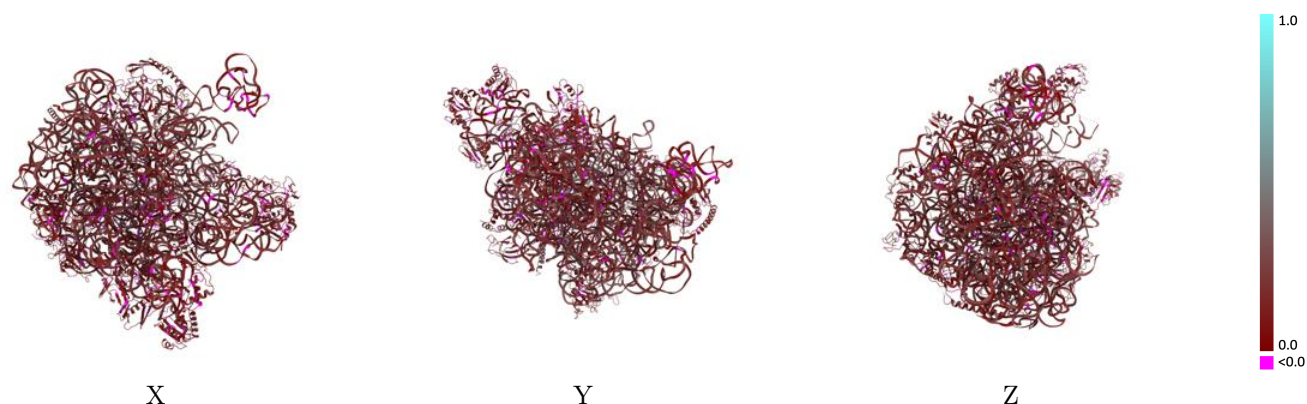
This section contains information regarding the fit between EMDB map EMD-13286 and PDB model 7PAU. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



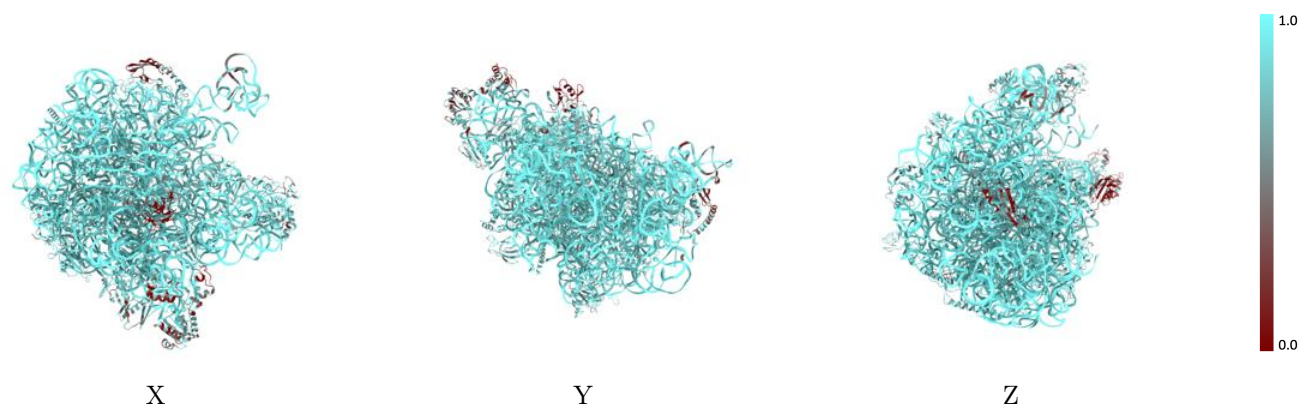
The images above show the 3D surface view of the map at the recommended contour level 0.46 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



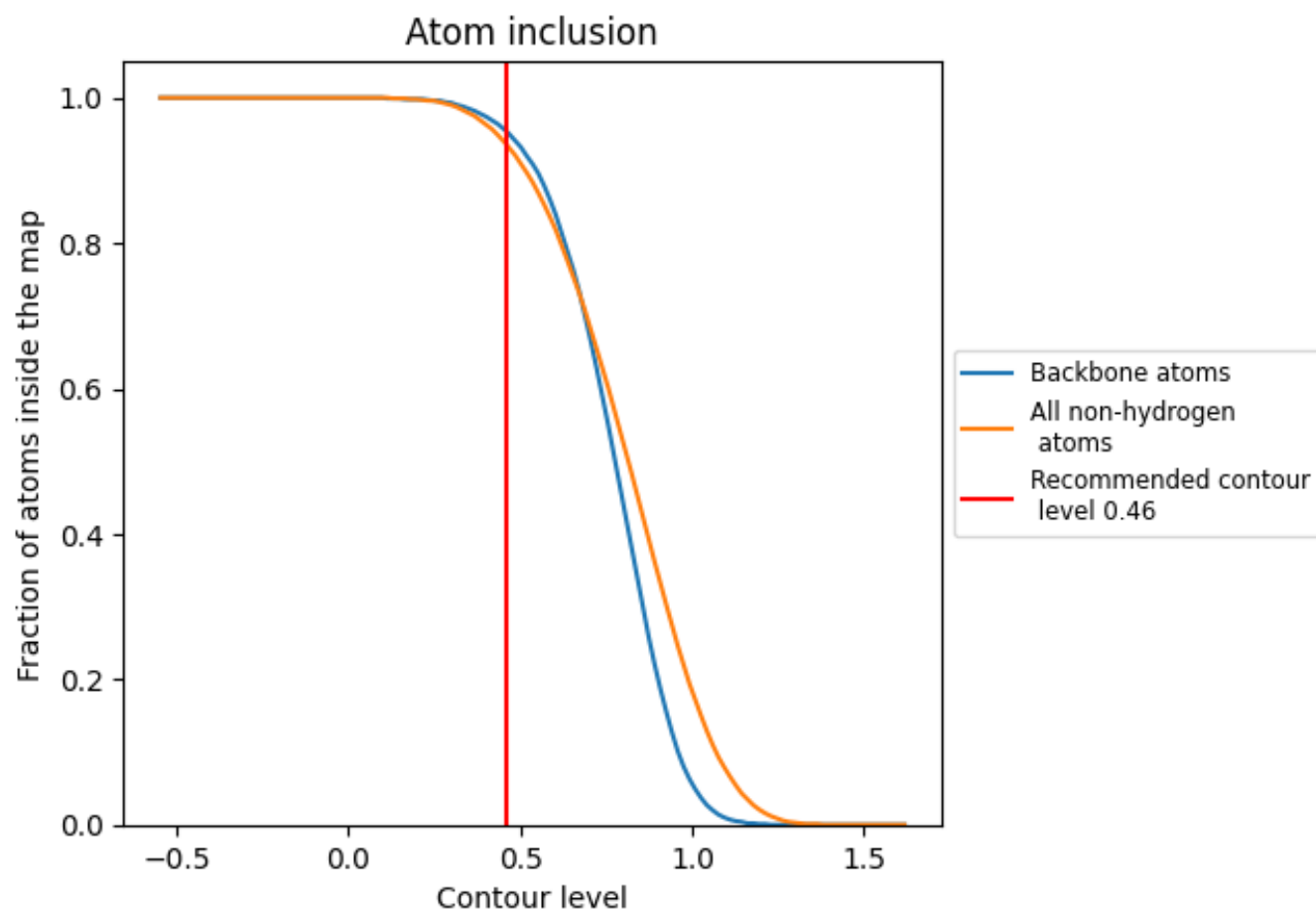
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.46).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% 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 (0.46) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9360	 0.1700
0	 0.9840	 0.1250
1	 0.9720	 0.1360
2	 0.9320	 0.0950
3	 0.9860	 0.1820
4	 0.9810	 0.1820
7	 0.5420	 0.1310
a	 0.9370	 0.1320
b	 0.8980	 0.1330
c	 0.8780	 0.1540
d	 0.7640	 0.1510
e	 0.7430	 0.1610
f	 0.4950	 0.1440
g	 0.5820	 0.1350
h	 0.4560	 0.1170
i	 0.9370	 0.1510
j	 0.8900	 0.1390
k	 0.9010	 0.1450
l	 0.9210	 0.1460
m	 0.9250	 0.1480
n	 0.8430	 0.1510
o	 0.8550	 0.1580
p	 0.9190	 0.1360
q	 0.8520	 0.1370
r	 0.9540	 0.1610
s	 0.9360	 0.1520
t	 0.7650	 0.1330
u	 0.9420	 0.1330
v	 0.9620	 0.1290
w	 0.8480	 0.1880
x	 0.6300	 0.1540
y	 0.9490	 0.1370
z	 0.9500	 0.1610

