



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:51 PM UTC

PDB ID : 8VKW / pdb_00008vkw
EMDB ID : EMD-43333
Title : Structure of Mycobacterium smegmatis 50S ribosomal subunit bound to delNTE-HflX
Authors : Majumdar, S.; Koripella, R.K.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.; Agrawal, R.K.
Deposited on : 2024-01-10
Resolution : 3.44 Å (reported)
Based on initial models : 5O61, 6DZI

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

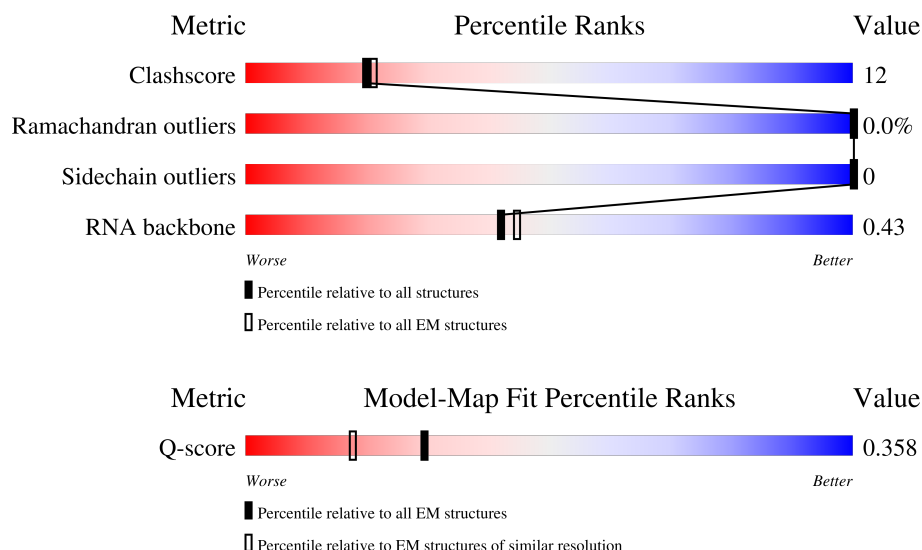
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.44 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.



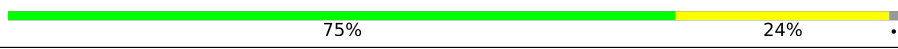
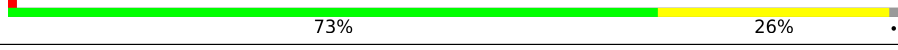
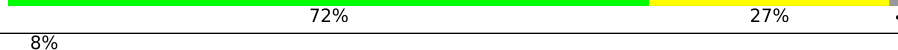
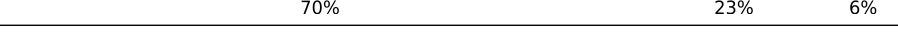
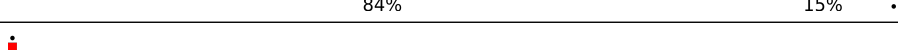
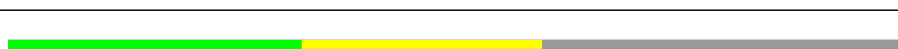
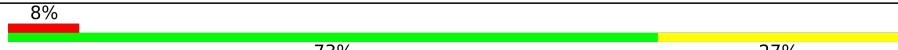
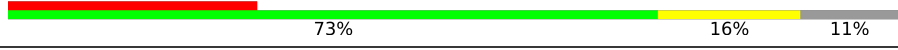
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13877 (2.94 - 3.94)

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	2	61	
2	3	24	
3	4	431	

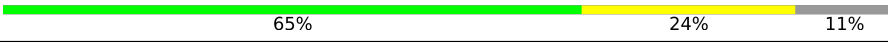
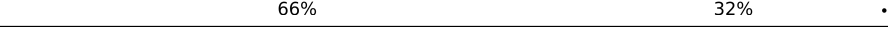
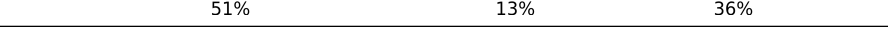
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Mol	Chain	Length	Quality of chain
4	A	3120	
5	B	118	
6	C	278	
7	D	217	
8	E	215	
9	F	187	
10	G	179	
11	H	151	
12	J	142	
13	K	147	
14	L	122	
15	M	147	
16	N	138	
17	O	199	
18	P	127	
19	Q	113	
20	R	129	
21	S	103	
22	T	153	
23	U	100	
24	V	105	
25	W	215	
26	X	88	
27	Y	64	
28	Z	77	

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Mol	Chain	Length	Quality of chain
29	b	57	
30	c	55	
31	d	47	
32	e	64	
33	f	37	
34	g	75	

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 97621 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 L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 2 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 3 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	426	Total	C	N	O	S	0	0
			3224	1995	599	623	7		

- Molecule 4 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	3043	Total	C	N	O	P	0	0
			65348	29127	12020	21158	3043		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 6 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	275	Total	C	N	O	S	0	0
			2106	1296	437	369	4		

- Molecule 7 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 8 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	209	Total	C	N	O	S	0	0
			1565	967	294	302	2		

- Molecule 9 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	182	Total	C	N	O	S	0	0
			1438	903	270	260	5		

- Molecule 10 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	176	Total	C	N	O	S	0	0
			1346	843	249	253	1		

- Molecule 11 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	53	Total	C	N	O	S	0	0
			367	230	67	69	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 13 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	146	Total	C	N	O	S	0	0
			1127	719	207	200	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 16 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	136	Total	C	N	O	S	0	0
			1089	689	212	186	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 18 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	126	Total	C	N	O		0	0
			941	576	197	168			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 20 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 21 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	S	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 22 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 23 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	U	97	Total	C	N	O	0	0
			756	479	138	139		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	97	Total	C	N	O	S	0	0
			729	455	136	136	2		

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	W	192	Total	C	N	O	0	0
			1420	877	253	290		

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 27 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	63	Total	C	N	O	S	0	0
			464	280	100	80	4		

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 30 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	49	Total	C	N	O	S	0	0
			397	244	79	70	4		

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	e	63	Total	C	N	O	0	0
			496	300	113	83		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

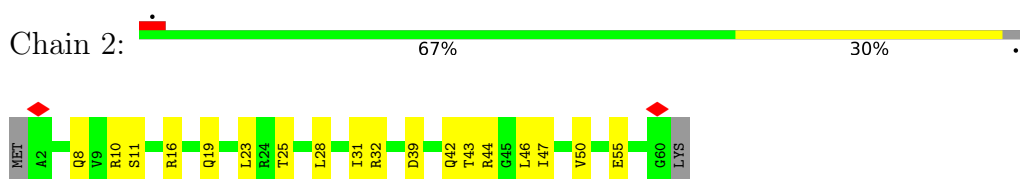
- Molecule 34 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

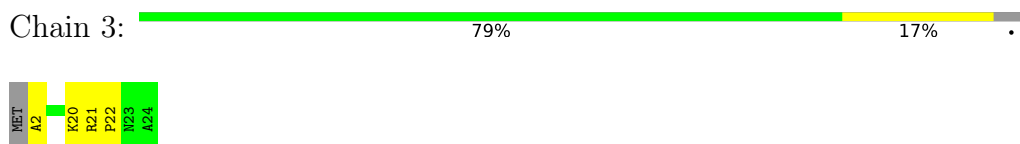
3 Residue-property plots

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.

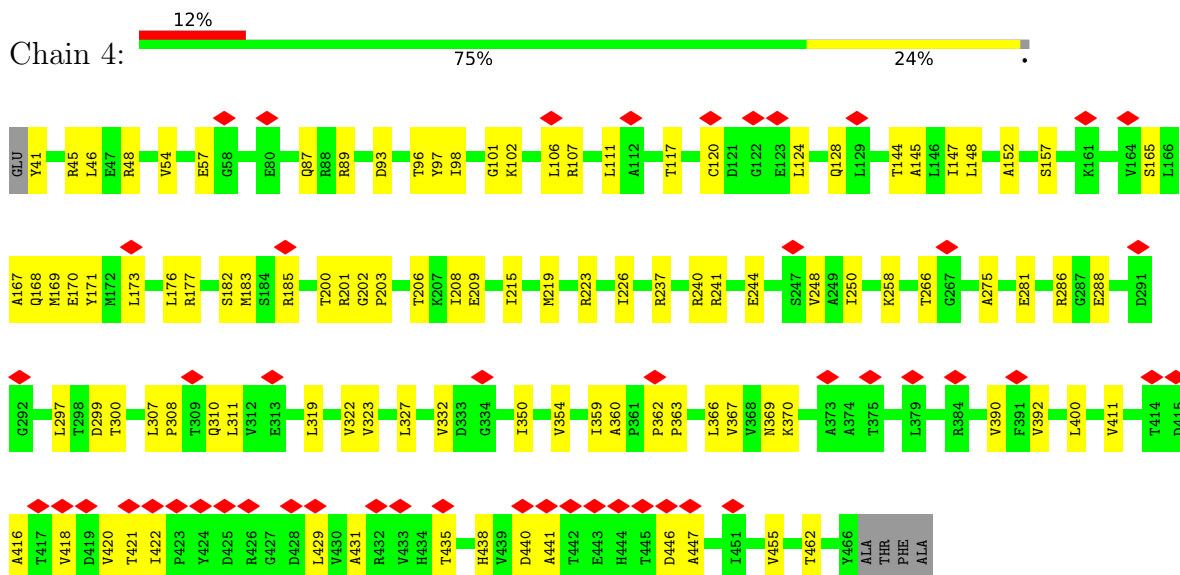
- Molecule 1: 50S ribosomal protein L30



- Molecule 2: 50S Ribosomal Protein L37



- Molecule 3: GTPase HflX

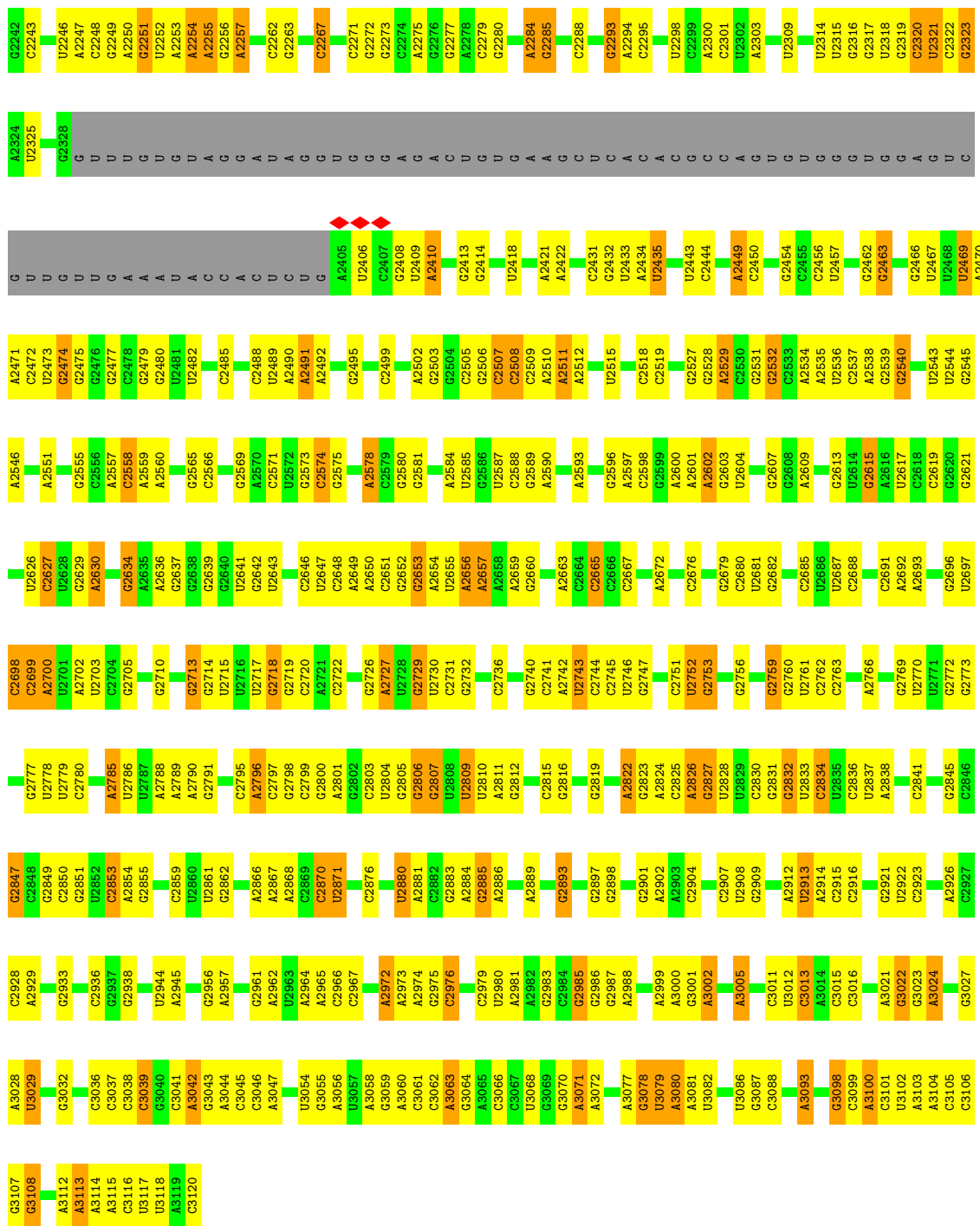


- Molecule 4: 23S ribosomal RNA

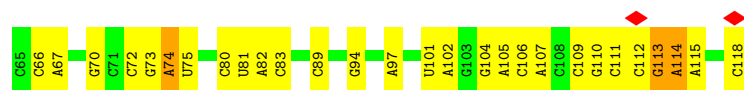


G1066	G1067	C1068	G1069	G1070	U1075	A1076	A1077	G1078	G1083	U1084	G1085	G1086	U1087	U1088	U1089	U1090	A1091	G1092	G1096	A1097	A1098	A1099	C1100	A1101	G1102	C1103	C1104	G1107	G1111	C1112	C1113	G1114	G1115	U1116	U1117	A1118	G1120	C1123	C1124	U1125	U1126	A1127	A1128	G1129	C1130	G1131	G1135	C1136	U1137	A1138	A1139						
G993	A994	U995	G996	G997	G998	C999	C1000	C1001	C1002	A1003	A1004	A1005	G1006	U1009	U1010	U1011	C1012	U1013	G1014	C1019	C1022	A1023	A1024	A1025	C1026	A1027	C1028	C1029	C1030	A1033	U1034	G1035	U1036	C1037	G1038	C1039	U1040	A1041	A1042	G1043	C1046	A1047	U1048	G1049	G1053	C1057	A1058	U1059	U1060	G1063	A1064	C1065					
A907	A908	U911	C912	G916	A917	A918	A919	A920	A921	C922	U926	C927	U928	C929	C932	G933	A934	U942	U943	A944	C949	A950	G953	U954	A958	U959	G960	U963	C964	U965	U966	A972	G973	G974	U975	A978	C979	C980	U981	A982	G986	A987	U988	U989	G990	C991	G992	A993	U994	U995							
G82	C87	A88	A93	G94	C95	G96	U97	C98	A99	C103	G104	A105	G106	C107	A108	U109	G110	A111	U112	U113	G114	A115	U116	G117	U118	G119	G120	G121	A122	A123	A124	G125	C126	G127	G128	U136	G137	A138	U139	A148	C149	U150	A151	C156	U157	C73	U158	A159	U160	U161	U162	U163	A164				
A241	G242	U243	A244	U245	G246	G247	G248	C249	G250	A251	G252	C253	G254	A255	A256	A257	G258	G261	A262	G263	G264	A265	U266	G267	G268	A271	A272	A273	C274	C275	U276	U277	U278	G279	G280	C281	A282	G286	A287	U288	A289	C290	G292	G293	G294	U295	A296	U297	U298	G299	G300	U301	U302	G303	U304		
G305	U306	G307	U308	A309	C310	G311	G312	G313	G314	U315	U318	G321	A322	C323	G324	U325	A326	U327	C328	U329	U330	G335	C336	U337	C338	U339	A340	C341	C342	U343	U347	G348	G349	A350	G351	G352	G353	C354	A355	G356	U357	G358	A359	G360	A361	A362	A363	U364	U365	G366	U370	G371	A375				
G376	A380	A381	A382	U383	G384	G385	C386	U387	U388	G389	G390	C391	A392	U393	G394	G399	A400	G401	G402	U403	A404	G405	A406	U410	A411	A412	G413	A414	A415	C416	C417	G420	U421	A422	A427	A428	A429	A430	G434	G437	U438	C439	U440	U441	U442	C443	U444	U445	G446	U447	A448	G449					
G450	U451	G452	U453	U454	C455	G458	A459	G460	U461	G468	G469	C472	C473	G474	U475	G476	A479	U485	G486	U487	G488	A489	U490	U491	G497	G498	G499	A500	C501	A503	C504	G507	G508	U509	A510	A511	G512	C514	U515	G516	A517	A518	U519	A520	C521	U522	U523	C524	U529								
G530	A531	C532	C533	U534	A535	U536	A537	U538	C539	U540	G541	A542	U543	U544	A545	C546	G551	U552	G553	A554	C555	U556	G557	G561	C562	U563	A564	A565	A566	A567	A568	G569	U570	A571	C572	C573	C574	C575	G576	G577	G578	A579	G580	G581	G585	U586	C587	A663	A664	G665	A666	A667	U668	G669	A670	U671	C672
G599	A600	C601	A602	U612	A613	A616	C619	G620	U621	A622	A623	G624	A625	G626	C631	U635	G636	G637	U638	C639	G640	U641	G642	G643	G644	G645	U646	G647	A648	U649	G650	G651	C652	G655	C656	C657	U658	U659	U660	U661	G662	A663	A664	G665	A666	A667	U668	G669	A670	U671	C672						
C673	U674	G679	A680	G684	A688	U689	C690	U691	G692	C693	C694	G695	U696	A697	A701	A702	C703	C704	C705	G706	G707	G708	G713	G719	C720	A721	G722	G723	U724	A725	A726	A727	G728	C729	G730	A731	G732	U733	C734	U735	G736	A737	U738	U739	A740	A741	G742	G745	U746	A747	C752	A753					
G754	A755	A756	G757	A758	G759	U760	G761	U762	G763	U764	G765	G766	U767	G768	U769	A770	G771	U772	G773	G776	U777	G778	G784	C787	G788	G789	A790	U796	G799	A800	U801	A804	C807	A808	U809	C813	A814	G815	G816	C817	U818	G819	A820	A821	G822	C823	G824	C901	G902	A903	U904	U905	U829				
A830	C834	C835	G836	G837	G838	U839	G840	A841	A842	G843	G844	C845	C846	C847	G848	A849	C852	U856	U857	A858	G859	G860	U861	G862	G863	G872	G875	A876	U877	G878	A879	G880	G885	A886	C887	U888	A889	G890	C891	U894	G895	A896	A897	A898	G899	G900	C901	G902	A903	U904	U905	C906					
A907	A908	U911	C912	G916	A917	A918	A919	A920	A921	C922	U926	C927	U928	C929	C932	G933	A934	U942	U943	A944	C949	A950	G953	U954	A958	U959	G960	U963	C964	U965	U966	A972	G973	U974	U975	A978	C979	C980	U981	A982	G986	A987	U988	U989	G990	C991	G992	A993	U994	U995	U996	U997	U998	G999	G1000		
G993	A994	U995	G996	G997	G998	C999	C1000	C1001	C1002	A1003	A1004	A1005	G1006	U1009	U1010	U1011	C1012	U1013	G1014	C1019	C1022	U1023	A1024	A1025	C1026	A1027	C1028	C1029	C1030	A1033	U1034	G1035	U1036	C1037	G1038	C1039	U1040	A1041	A1042	G1043	C1046	A1047	U1048	G1049	G1053	C1057	A1058	U1059	U1060	G1063	A1064	C1065					



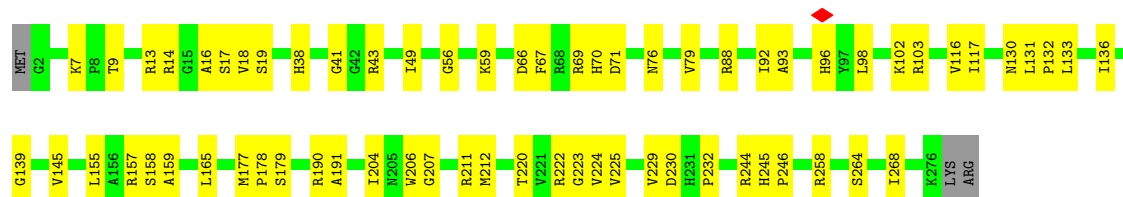


• Molecule 5: 5S ribosomal RNA



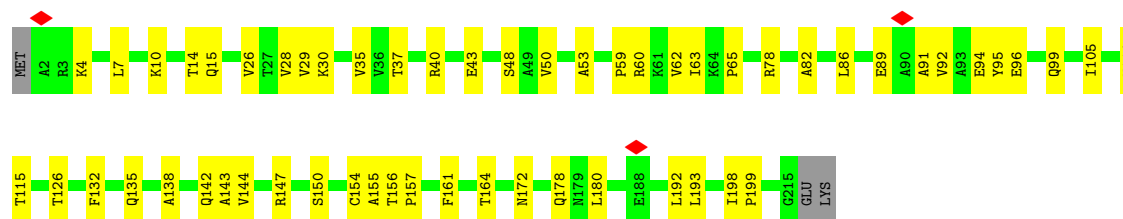
- Molecule 6: 50S ribosomal protein L2

Chain C: 75% 24%



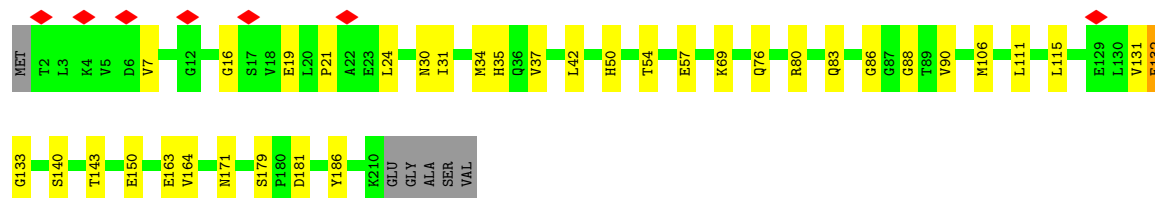
- Molecule 7: 50S ribosomal protein L3

Chain D: 73% 26%



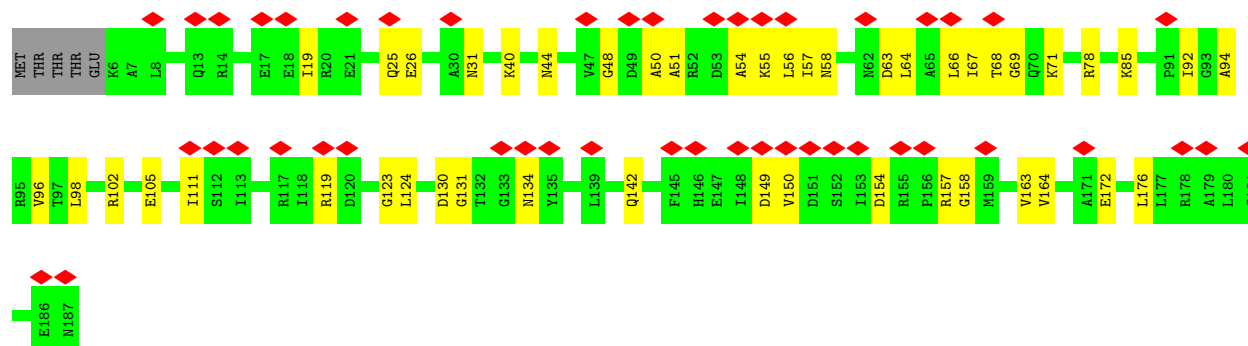
- Molecule 8: 50S Ribosomal Protein L4

Chain E: 80% 16%

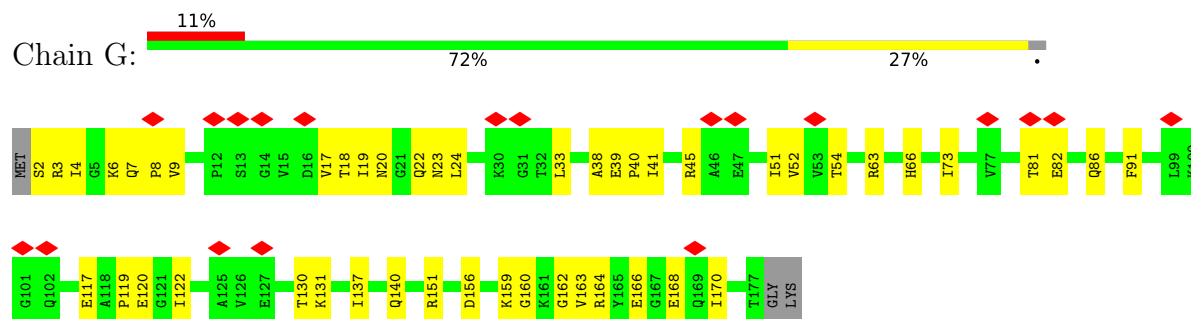


- Molecule 9: 50S Ribosomal Protein L5

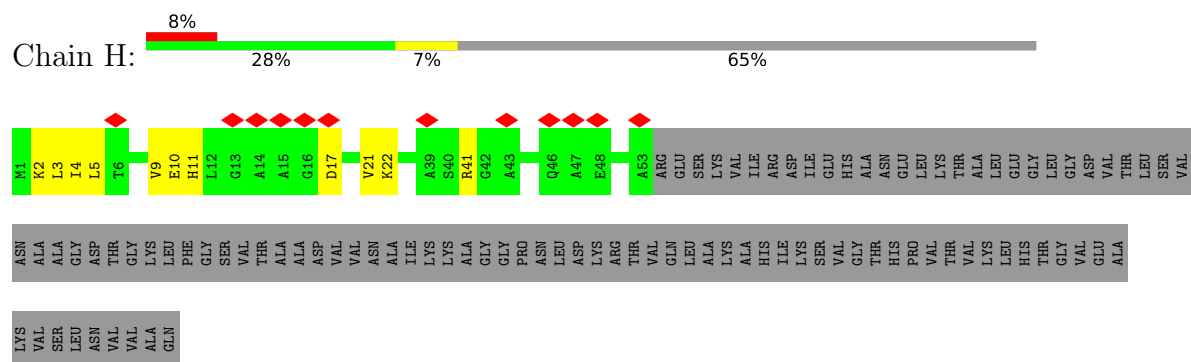
Chain F: 25% 73% 25%



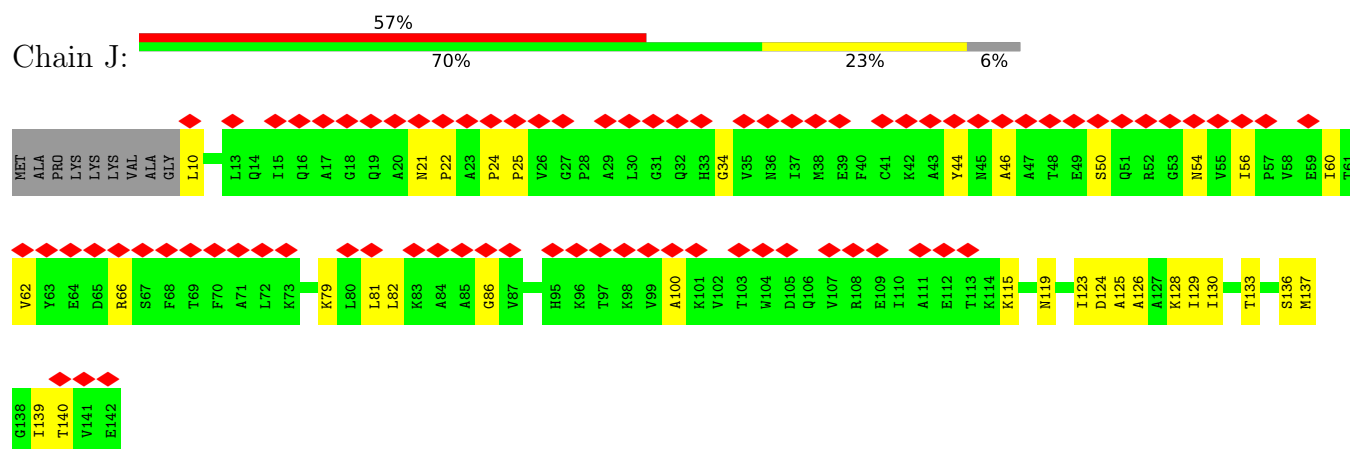
- Molecule 10: 50S ribosomal protein L6



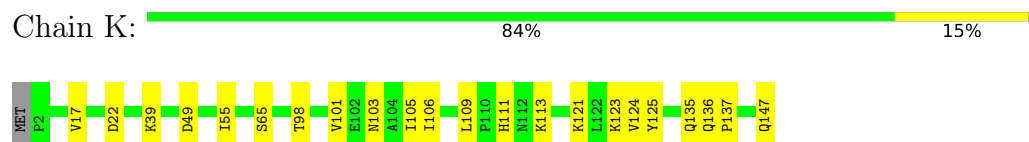
- Molecule 11: 50S ribosomal protein L9



- Molecule 12: 50S ribosomal protein L11

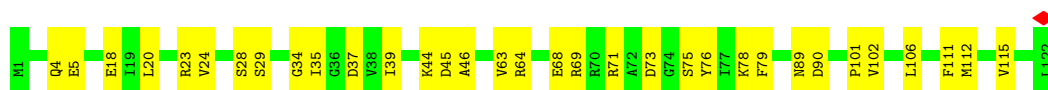


- Molecule 13: 50S Ribosomal Protein L13

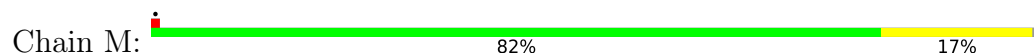


- Molecule 14: 50S ribosomal protein L14

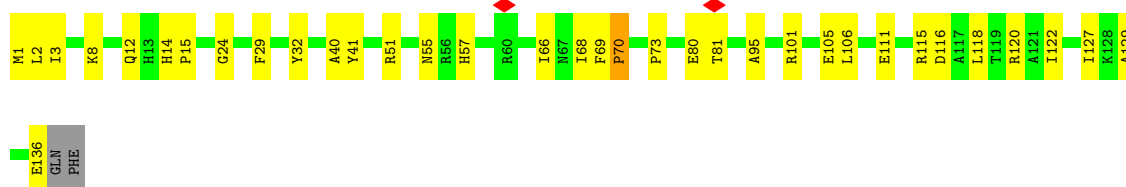




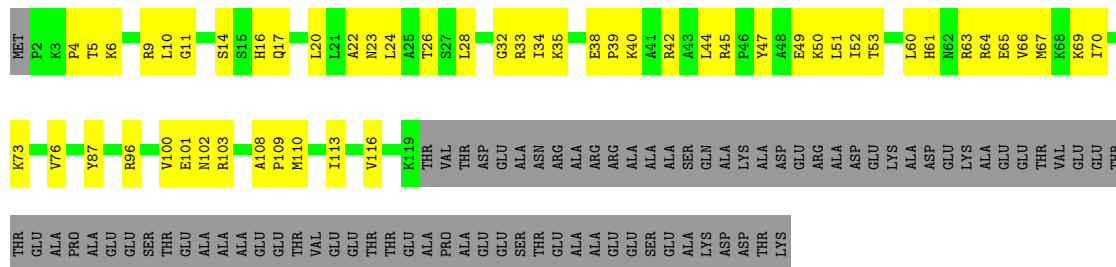
- Molecule 15: 50S ribosomal protein L15



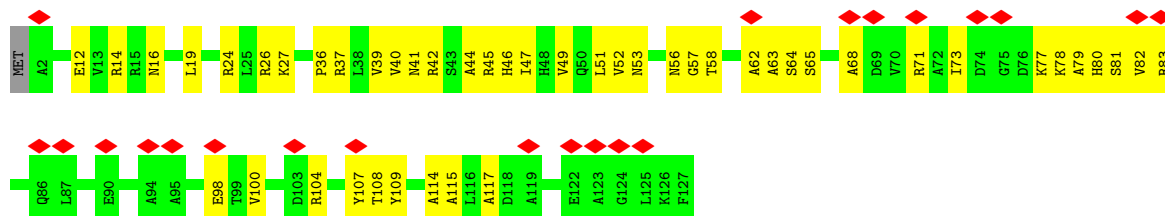
- Molecule 16: Large ribosomal subunit protein uL16



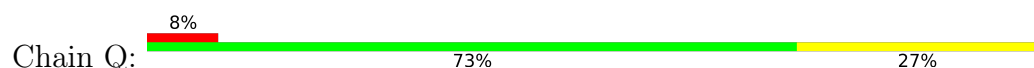
- Molecule 17: 50S ribosomal protein L17

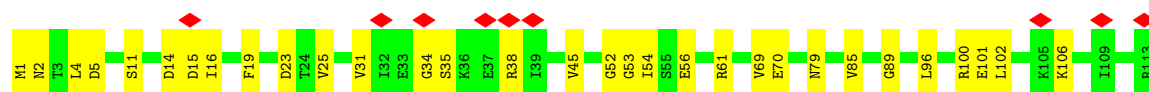


- Molecule 18: 50S Ribosomal Protein L18



- Molecule 19: 50S ribosomal protein L19

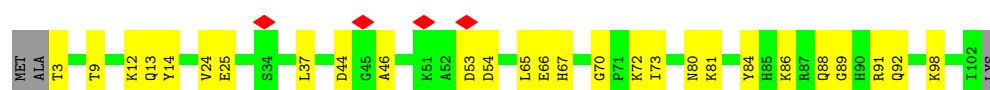




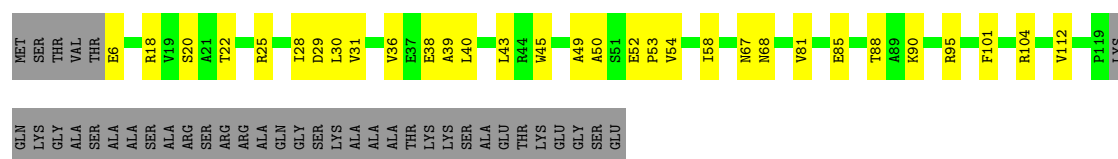
• Molecule 20: 50S Ribosomal Protein L20



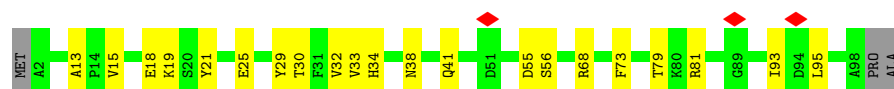
• Molecule 21: 50S Ribosomal Protein L21



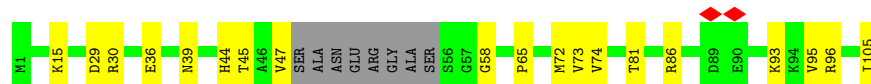
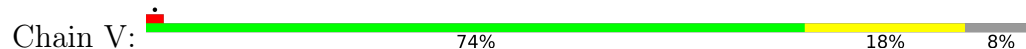
• Molecule 22: 50S Ribosomal Protein L22



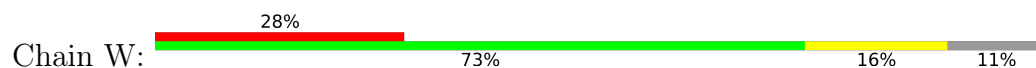
• Molecule 23: 50S Ribosomal Protein L23

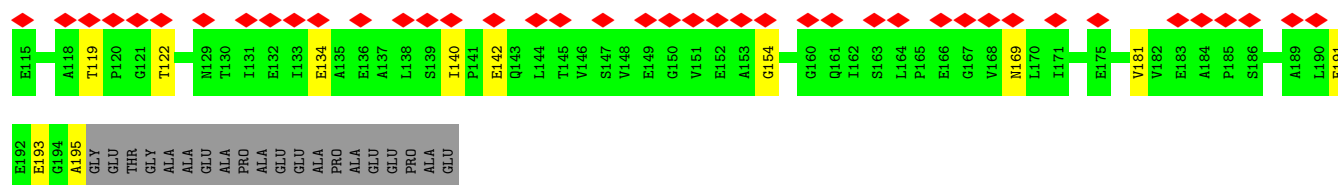


• Molecule 24: 50S ribosomal protein L24

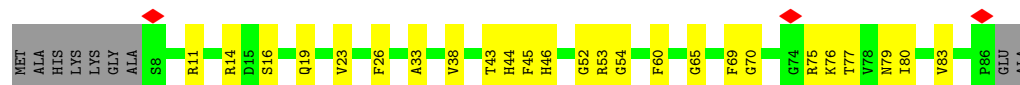


• Molecule 25: 50S ribosomal protein L25





- Molecule 26: 50S ribosomal protein L27



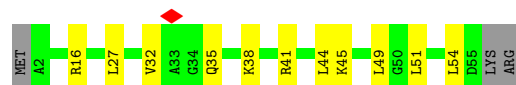
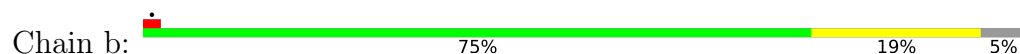
- Molecule 27: 50S Ribosomal Protein L28



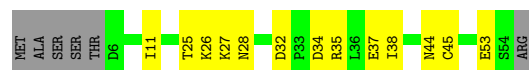
- Molecule 28: 50S ribosomal protein L29



- Molecule 29: 50S ribosomal protein L32



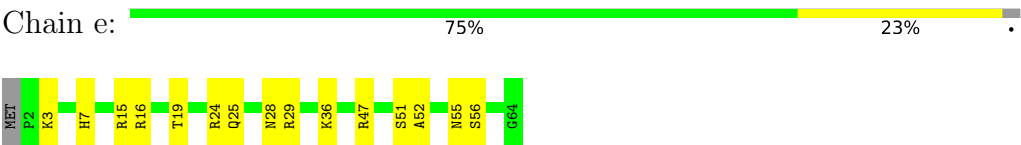
- Molecule 30: 50S Ribosomal Protein L33



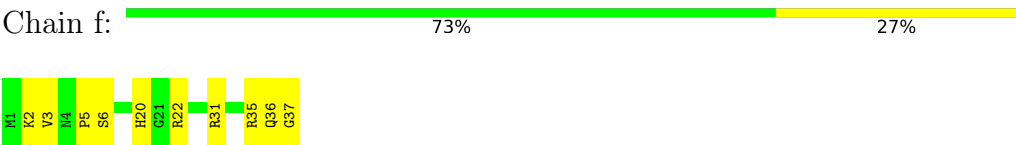
- Molecule 31: 50S ribosomal protein L34



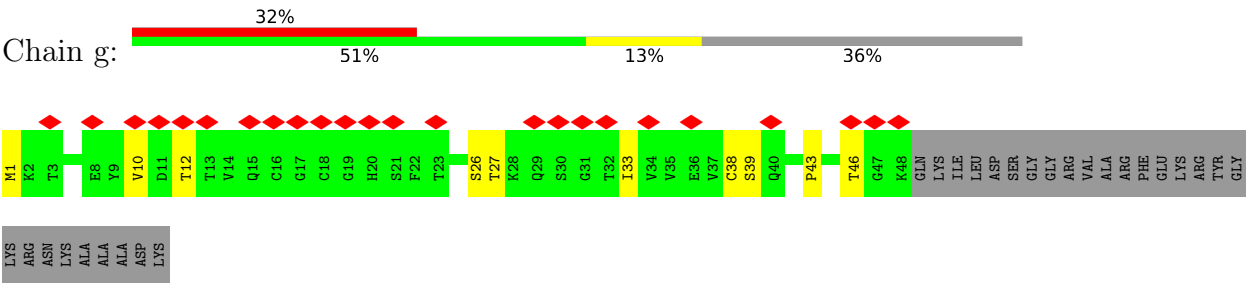
● Molecule 32: 50S ribosomal protein L35



● Molecule 33: 50S ribosomal protein L36



● Molecule 34: 50S Ribosomal Protein L31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	27550	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60.64	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.442	Depositor
Minimum map value	-0.335	Depositor
Average map value	0.030	Depositor
Map value standard deviation	0.091	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	338.4, 338.4, 338.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84599996, 0.84599996, 0.84599996	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	2	0.23	0/477	0.38	0/640
2	3	0.25	0/191	0.32	0/247
3	4	0.18	0/3264	0.35	0/4423
4	A	0.26	0/73172	0.28	0/114170
5	B	0.18	0/2821	0.29	0/4396
6	C	0.23	0/2149	0.36	0/2890
7	D	0.25	0/1609	0.37	0/2165
8	E	0.23	0/1588	0.34	0/2148
9	F	0.15	0/1460	0.35	0/1965
10	G	0.67	3/1367 (0.2%)	0.92	4/1845 (0.2%)
11	H	0.17	0/370	0.33	0/501
12	J	0.14	0/1006	0.38	0/1364
13	K	0.23	0/1154	0.30	0/1563
14	L	0.22	0/946	0.31	0/1268
15	M	0.24	0/1091	0.38	0/1457
16	N	0.33	1/1115 (0.1%)	0.36	0/1502
17	O	0.24	0/945	0.41	0/1267
18	P	0.29	0/950	0.46	0/1279
19	Q	0.20	0/921	0.30	0/1236
20	R	0.28	0/1000	0.34	0/1341
21	S	0.23	0/764	0.33	0/1030
22	T	0.25	0/887	0.34	0/1204
23	U	0.23	0/766	0.36	0/1030
24	V	0.18	0/735	0.31	0/983
25	W	0.16	0/1435	0.31	0/1960
26	X	0.25	0/595	0.38	0/798
27	Y	0.26	0/472	0.34	0/634
28	Z	0.18	0/534	0.31	0/713
29	b	0.26	0/427	0.32	0/572
30	c	0.20	0/404	0.32	0/541
31	d	0.30	0/380	0.34	0/500
32	e	0.25	0/501	0.33	0/664
33	f	0.24	0/303	0.37	0/401
34	g	0.16	0/372	0.33	0/503

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.26	4/106171 (0.0%)	0.32	4/159200 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	G	8	PRO	N-CD	18.27	1.73	1.47
10	G	8	PRO	CG-CD	-11.52	1.11	1.50
10	G	8	PRO	CB-CG	-7.02	1.14	1.49
16	N	70	PRO	N-CD	6.22	1.56	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	G	8	PRO	CB-CG-CD	23.07	179.91	106.10
10	G	8	PRO	N-CD-CG	-20.88	71.88	103.20
10	G	8	PRO	CA-CB-CG	-14.46	77.03	104.50
10	G	8	PRO	CA-N-CD	-10.76	96.94	112.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	474	0	500	21	0
2	3	189	0	205	4	0
3	4	3224	0	3281	76	0
4	A	65348	0	32886	1295	0
5	B	2522	0	1285	61	0
6	C	2106	0	2159	57	0
7	D	1587	0	1630	50	0
8	E	1565	0	1601	27	0
9	F	1438	0	1463	38	0
10	G	1346	0	1392	38	0
11	H	367	0	357	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	J	990	0	1021	22	0
13	K	1127	0	1158	17	0
14	L	938	0	1000	27	0
15	M	1078	0	1151	28	0
16	N	1089	0	1124	28	0
17	O	928	0	972	59	0
18	P	941	0	972	41	0
19	Q	907	0	938	23	0
20	R	988	0	1038	27	0
21	S	754	0	802	23	0
22	T	873	0	909	26	0
23	U	756	0	802	19	0
24	V	729	0	778	14	0
25	W	1420	0	1431	32	0
26	X	586	0	601	33	0
27	Y	464	0	471	21	0
28	Z	531	0	541	18	0
29	b	423	0	463	14	0
30	c	397	0	402	12	0
31	d	377	0	411	15	0
32	e	496	0	533	11	0
33	f	299	0	324	9	0
34	g	364	0	352	8	0
All	All	97621	0	64953	1958	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 1958 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)
4:A:250:G:H5'	15:M:59:MET:HE2	1.34	1.06
4:A:2718:G:O2'	16:N:80:GLU:OE2	1.78	1.00
4:A:2035:U:OP2	6:C:157:ARG:NH1	1.94	1.00
4:A:2796:A:OP2	7:D:156:THR:HG23	1.62	1.00
4:A:329:U:O2'	4:A:446:G:O6	1.82	0.97

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	2	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
2	3	21/24 (88%)	21 (100%)	0	0	100	100
3	4	424/431 (98%)	378 (89%)	46 (11%)	0	100	100
6	C	273/278 (98%)	250 (92%)	23 (8%)	0	100	100
7	D	212/217 (98%)	193 (91%)	19 (9%)	0	100	100
8	E	207/215 (96%)	190 (92%)	16 (8%)	1 (0%)	24	56
9	F	180/187 (96%)	148 (82%)	32 (18%)	0	100	100
10	G	174/179 (97%)	153 (88%)	21 (12%)	0	100	100
11	H	51/151 (34%)	41 (80%)	10 (20%)	0	100	100
12	J	131/142 (92%)	112 (86%)	19 (14%)	0	100	100
13	K	144/147 (98%)	137 (95%)	7 (5%)	0	100	100
14	L	120/122 (98%)	108 (90%)	12 (10%)	0	100	100
15	M	143/147 (97%)	129 (90%)	14 (10%)	0	100	100
16	N	134/138 (97%)	122 (91%)	12 (9%)	0	100	100
17	O	116/199 (58%)	106 (91%)	10 (9%)	0	100	100
18	P	124/127 (98%)	102 (82%)	22 (18%)	0	100	100
19	Q	111/113 (98%)	96 (86%)	15 (14%)	0	100	100
20	R	122/129 (95%)	116 (95%)	6 (5%)	0	100	100
21	S	98/103 (95%)	93 (95%)	5 (5%)	0	100	100
22	T	112/153 (73%)	106 (95%)	6 (5%)	0	100	100
23	U	95/100 (95%)	90 (95%)	5 (5%)	0	100	100
24	V	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
25	W	190/215 (88%)	179 (94%)	11 (6%)	0	100	100
26	X	77/88 (88%)	67 (87%)	10 (13%)	0	100	100
27	Y	61/64 (95%)	55 (90%)	6 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	Z	62/77 (80%)	61 (98%)	1 (2%)	0	100	100
29	b	52/57 (91%)	49 (94%)	3 (6%)	0	100	100
30	c	47/55 (86%)	43 (92%)	4 (8%)	0	100	100
31	d	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
32	e	61/64 (95%)	58 (95%)	3 (5%)	0	100	100
33	f	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
34	g	46/75 (61%)	41 (89%)	5 (11%)	0	100	100
All	All	3817/4247 (90%)	3460 (91%)	356 (9%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	E	132	GLU

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	2	52/54 (96%)	52 (100%)	0	100	100
2	3	18/19 (95%)	18 (100%)	0	100	100
3	4	336/340 (99%)	336 (100%)	0	100	100
6	C	214/218 (98%)	214 (100%)	0	100	100
7	D	160/163 (98%)	160 (100%)	0	100	100
8	E	168/173 (97%)	168 (100%)	0	100	100
9	F	149/156 (96%)	149 (100%)	0	100	100
10	G	147/150 (98%)	147 (100%)	0	100	100
11	H	31/116 (27%)	31 (100%)	0	100	100
12	J	102/108 (94%)	102 (100%)	0	100	100
13	K	118/120 (98%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	L	100/100 (100%)	100 (100%)	0	100	100
15	M	112/114 (98%)	112 (100%)	0	100	100
16	N	113/116 (97%)	113 (100%)	0	100	100
17	O	97/158 (61%)	97 (100%)	0	100	100
18	P	90/94 (96%)	90 (100%)	0	100	100
19	Q	100/100 (100%)	100 (100%)	0	100	100
20	R	97/99 (98%)	97 (100%)	0	100	100
21	S	81/83 (98%)	81 (100%)	0	100	100
22	T	90/117 (77%)	90 (100%)	0	100	100
23	U	83/85 (98%)	83 (100%)	0	100	100
24	V	80/86 (93%)	80 (100%)	0	100	100
25	W	153/168 (91%)	153 (100%)	0	100	100
26	X	58/63 (92%)	58 (100%)	0	100	100
27	Y	49/51 (96%)	49 (100%)	0	100	100
28	Z	58/66 (88%)	58 (100%)	0	100	100
29	b	43/46 (94%)	43 (100%)	0	100	100
30	c	45/52 (86%)	45 (100%)	0	100	100
31	d	35/36 (97%)	35 (100%)	0	100	100
32	e	51/54 (94%)	51 (100%)	0	100	100
33	f	35/35 (100%)	35 (100%)	0	100	100
34	g	43/63 (68%)	43 (100%)	0	100	100
All	All	3108/3403 (91%)	3108 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
20	R	94	ASN
25	W	61	HIS
31	d	36	ASN
25	W	126	GLN
21	S	85	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	A	3041/3120 (97%)	698 (22%)	29 (0%)
5	B	117/118 (99%)	36 (30%)	4 (3%)
All	All	3158/3238 (97%)	734 (23%)	33 (1%)

5 of 734 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	A	4	G
4	A	7	U
4	A	12	G
4	A	20	G
4	A	23	G

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	A	2826	A
5	B	10	G
5	B	66	C
4	A	974	G
4	A	919	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

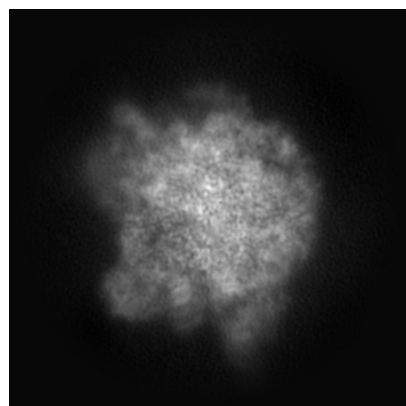
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43333. These allow visual inspection of the internal detail of the map and identification of artifacts.

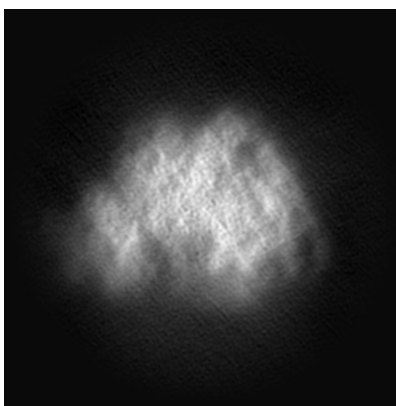
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

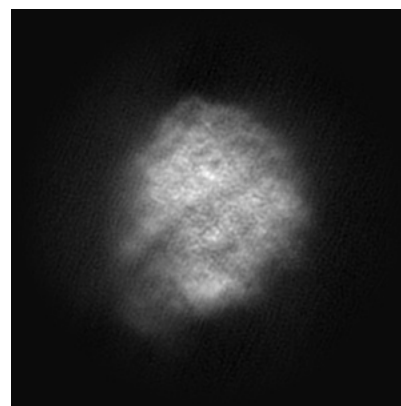
6.1.1 Primary map



X

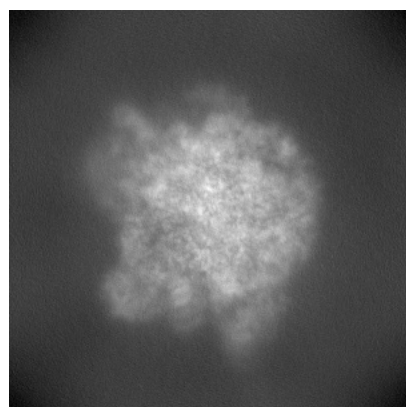


Y

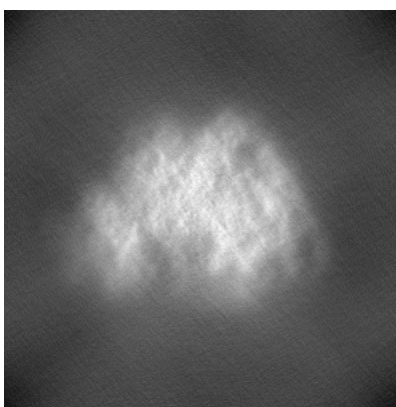


Z

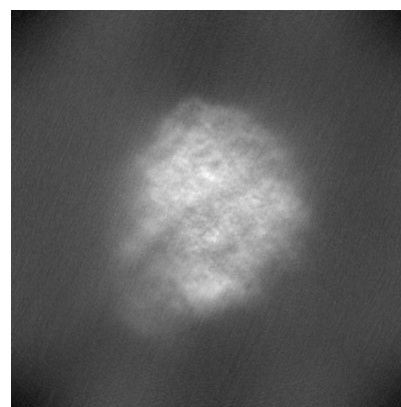
6.1.2 Raw map



X



Y

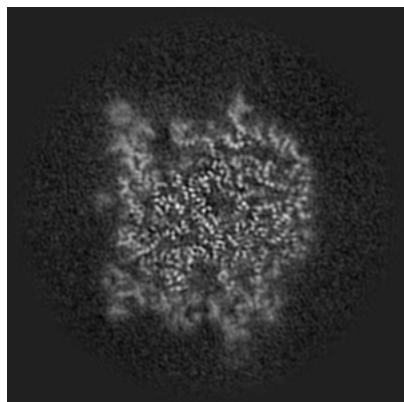


Z

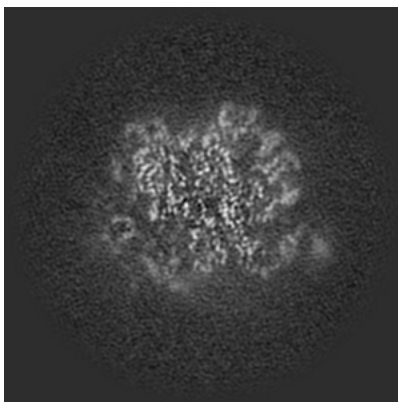
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

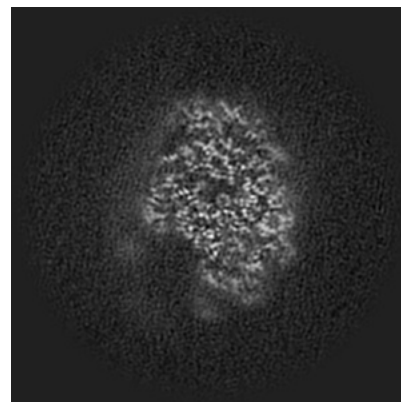
6.2.1 Primary map



X Index: 200

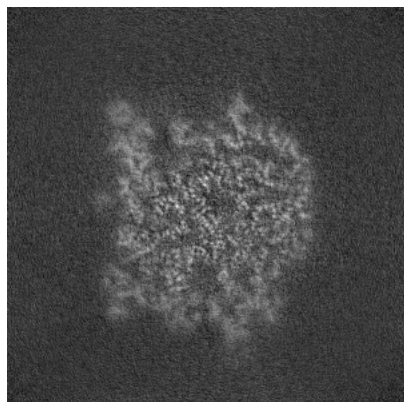


Y Index: 200

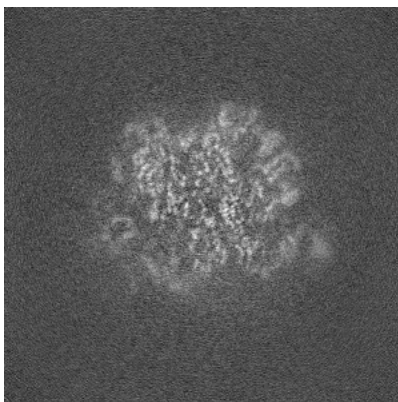


Z Index: 200

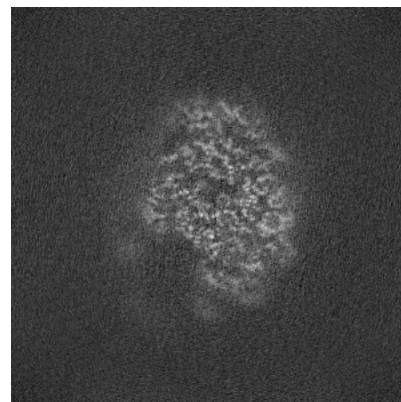
6.2.2 Raw map



X Index: 200



Y Index: 200

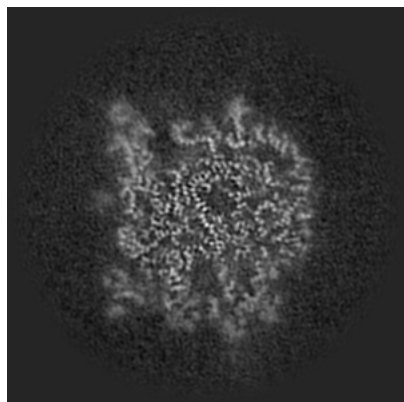


Z Index: 200

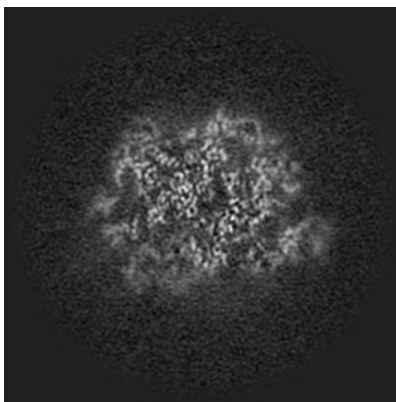
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

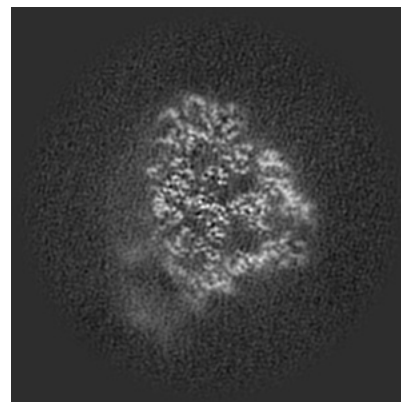
6.3.1 Primary map



X Index: 202

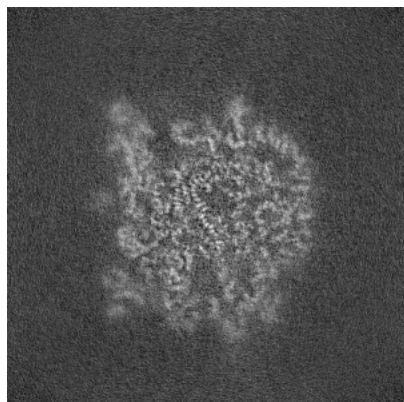


Y Index: 206

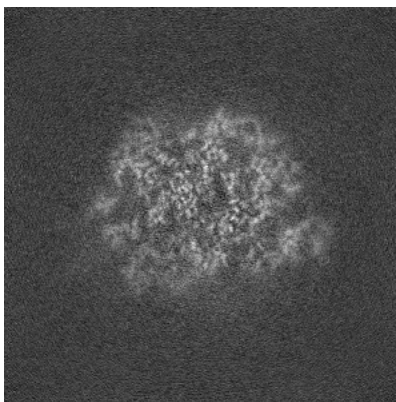


Z Index: 220

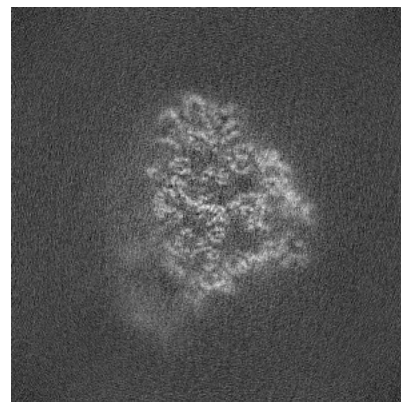
6.3.2 Raw map



X Index: 202



Y Index: 206

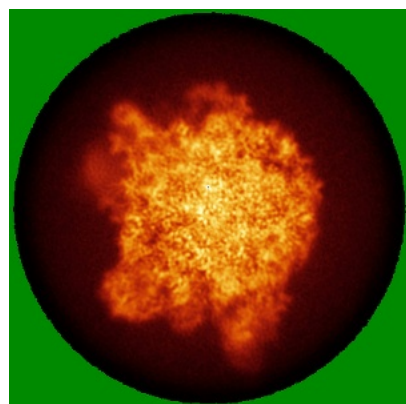


Z Index: 221

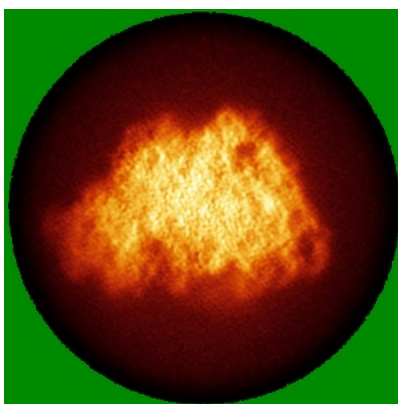
The images above show the largest variance slices of the map in three orthogonal directions.

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

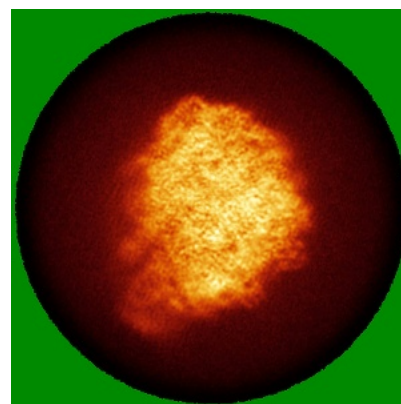
6.4.1 Primary map



X

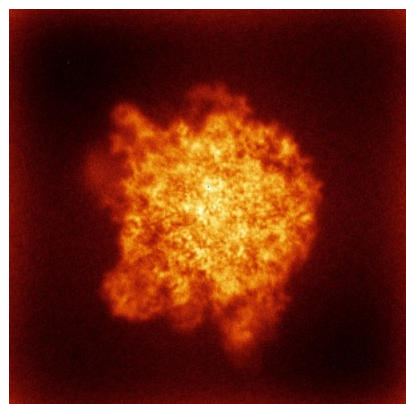


Y

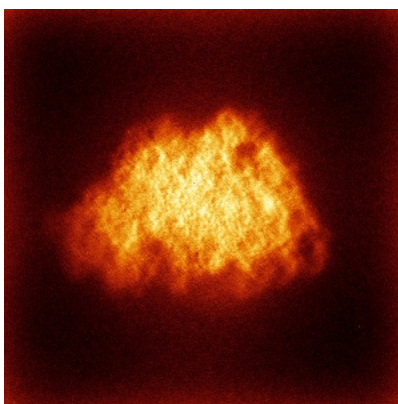


Z

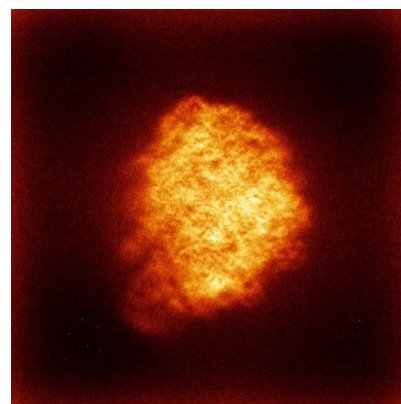
6.4.2 Raw map



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.

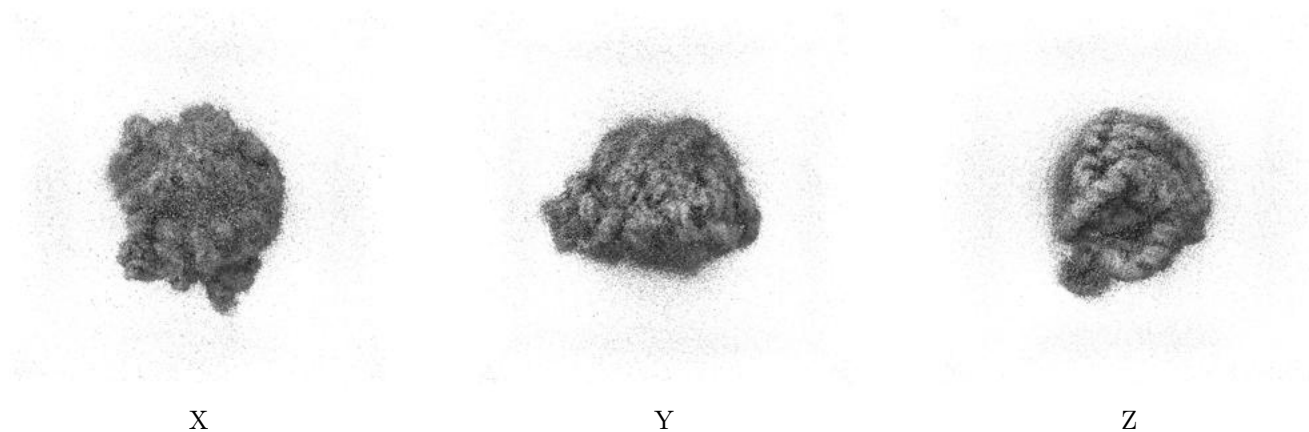
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

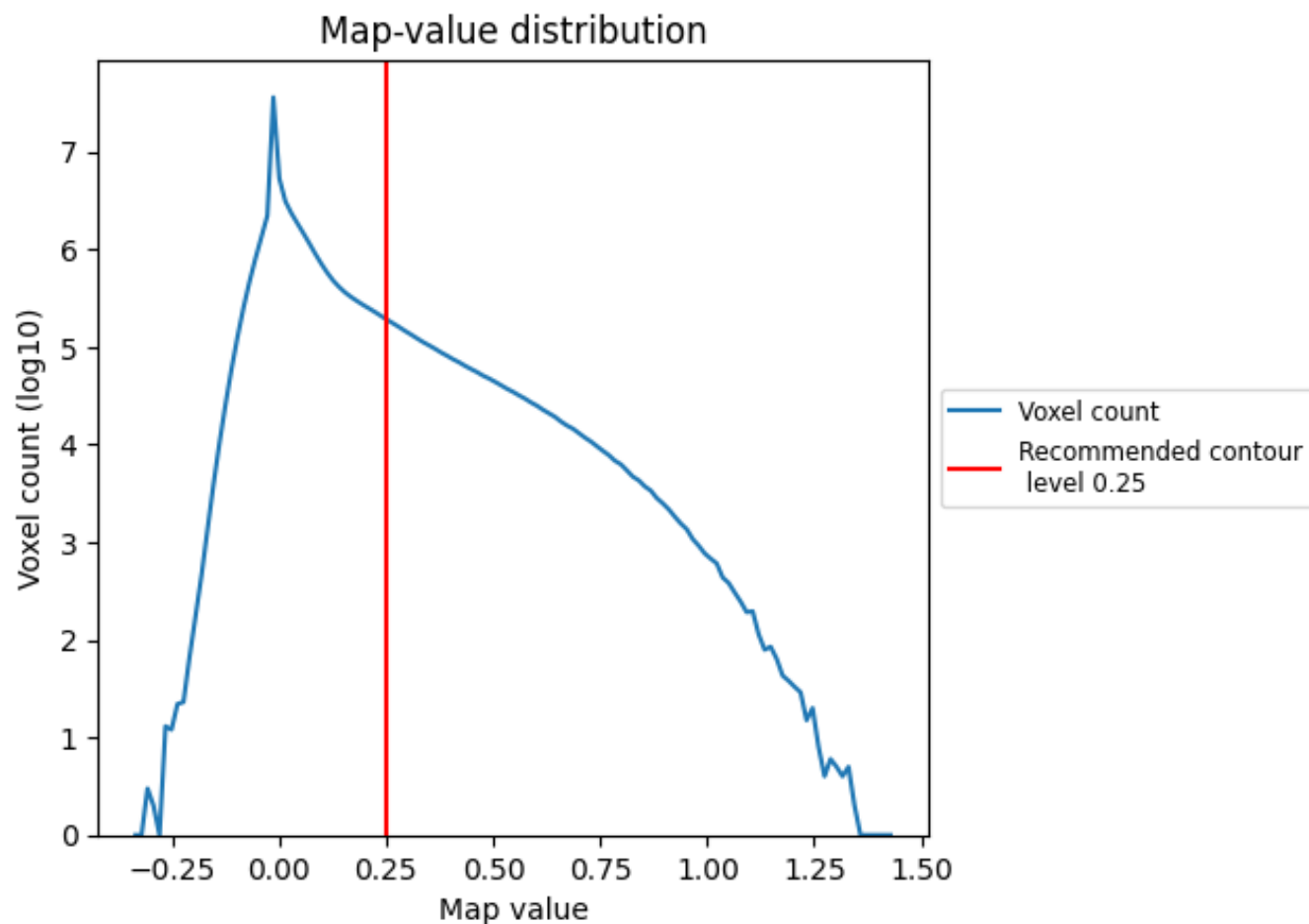
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

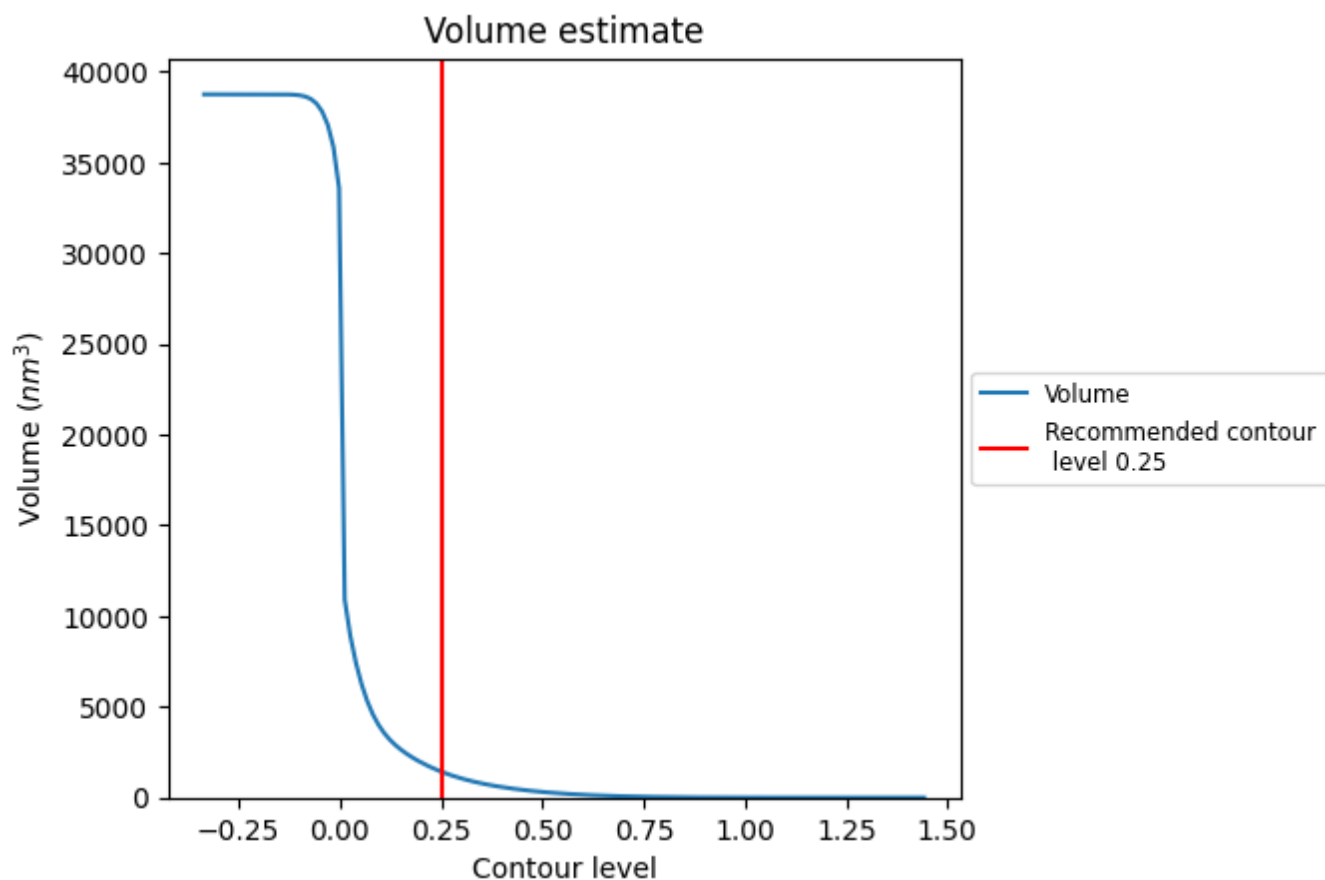
This section contains the results of statistical analysis of the map.

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.

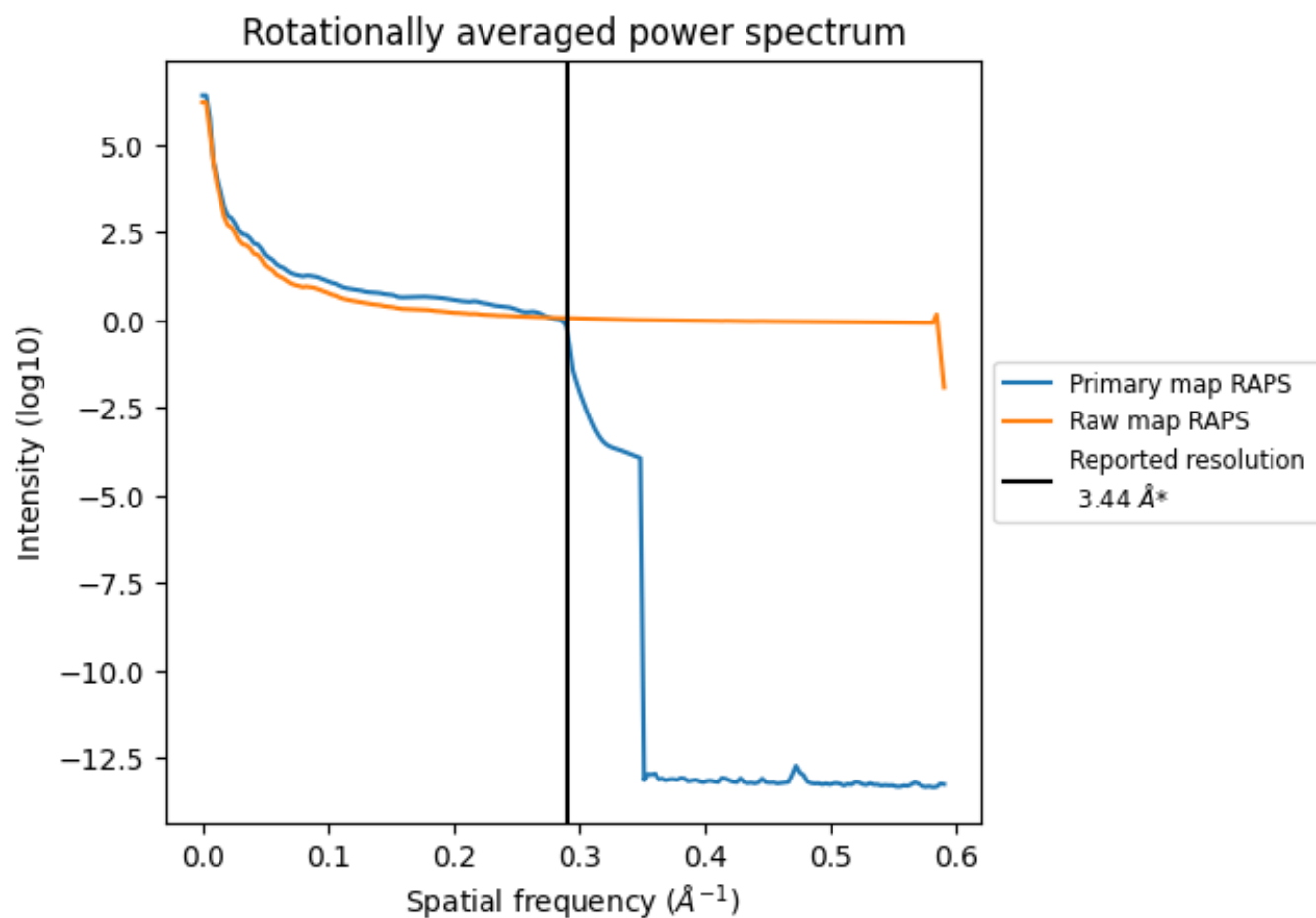
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1429 nm³; this corresponds to an approximate mass of 1291 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 ⓘ

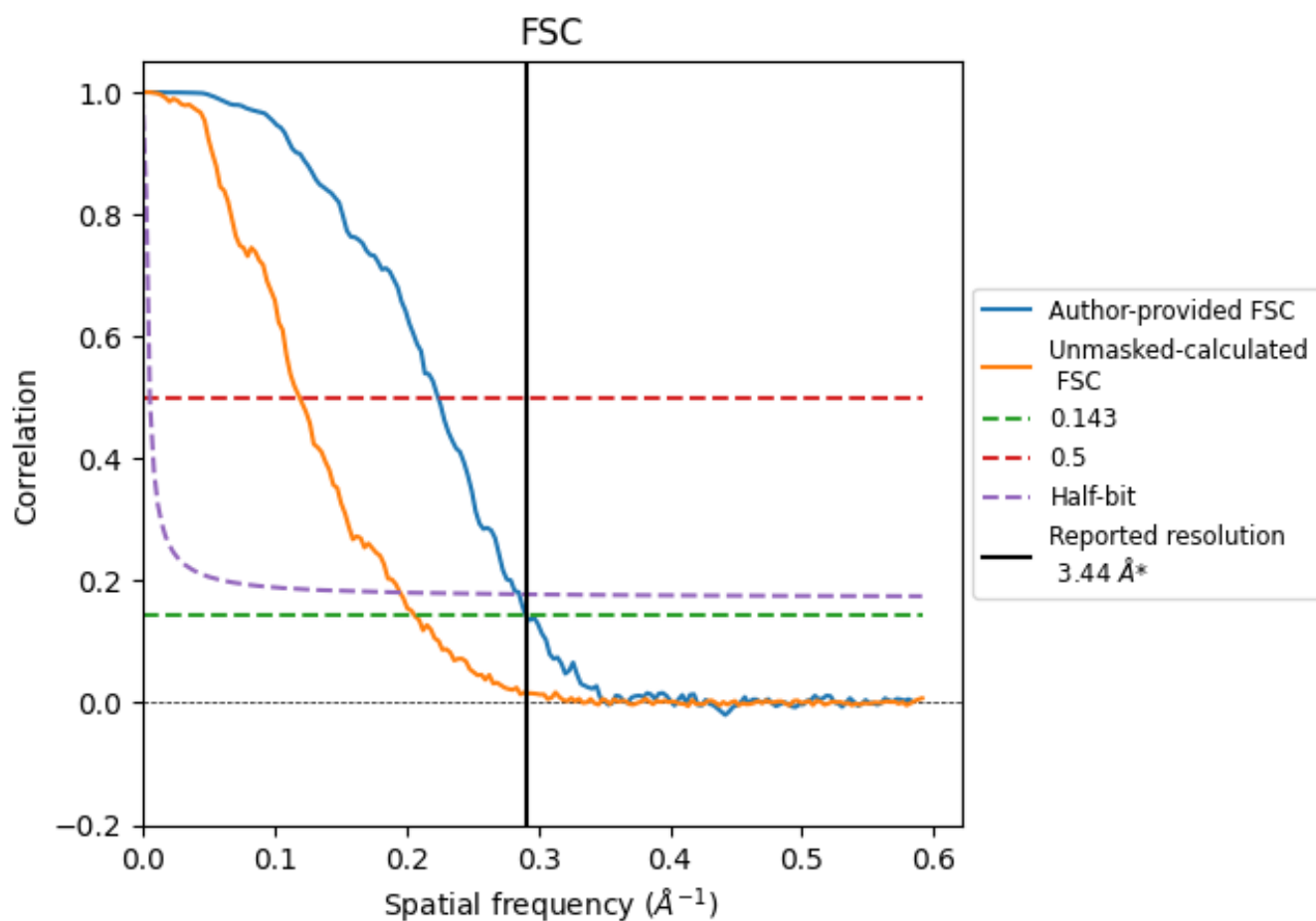


*Reported resolution corresponds to spatial frequency of 0.291 $\text{\AA}^{-1}$

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 0.291 Å⁻¹

8.2 Resolution estimates [i](#)

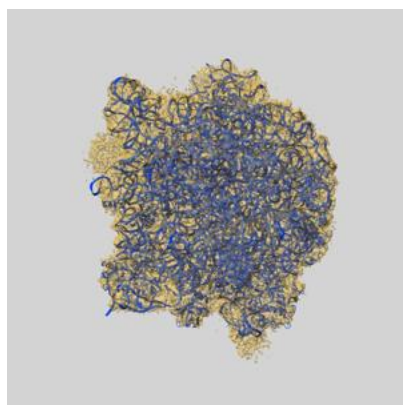
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.44	-	-
Author-provided FSC curve	3.44	4.46	3.50
Unmasked-calculated*	4.85	8.40	5.12

*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 4.85 differs from the reported value 3.44 by more than 10 %

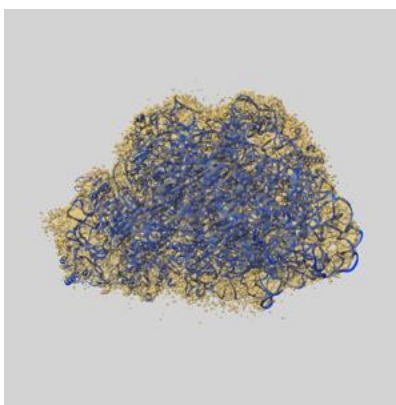
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43333 and PDB model 8VKW. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

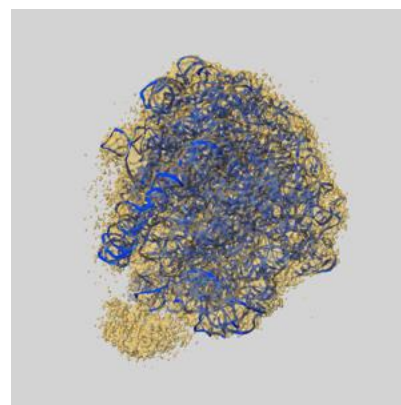
9.1 Map-model overlay [i](#)



X



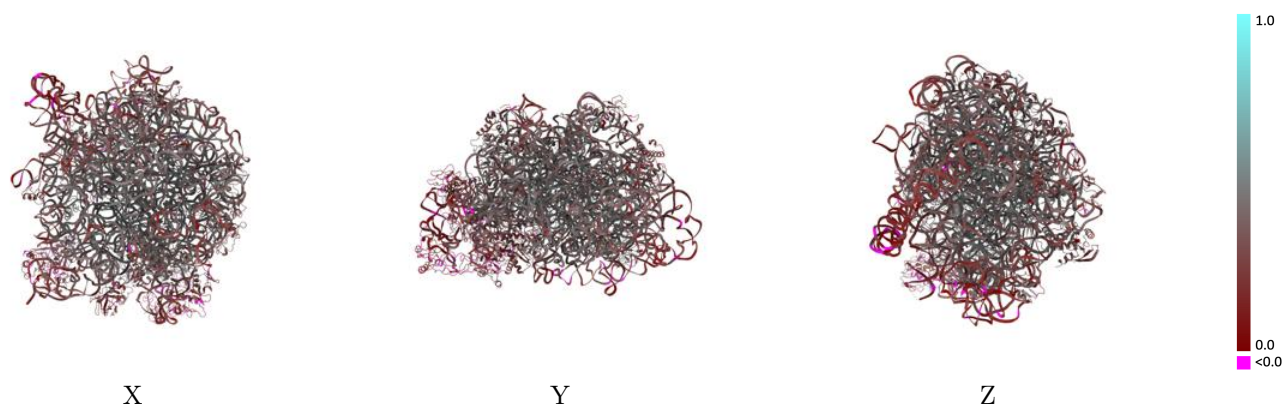
Y



Z

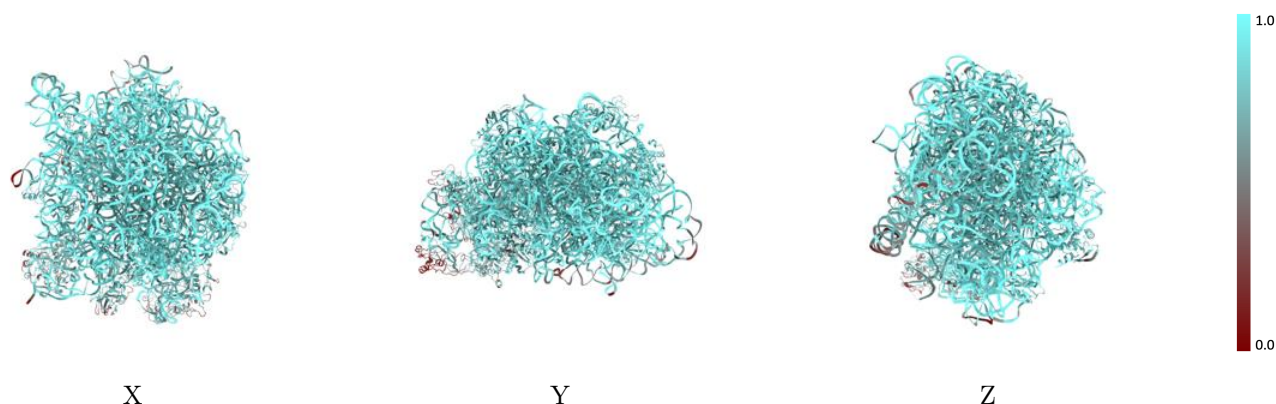
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



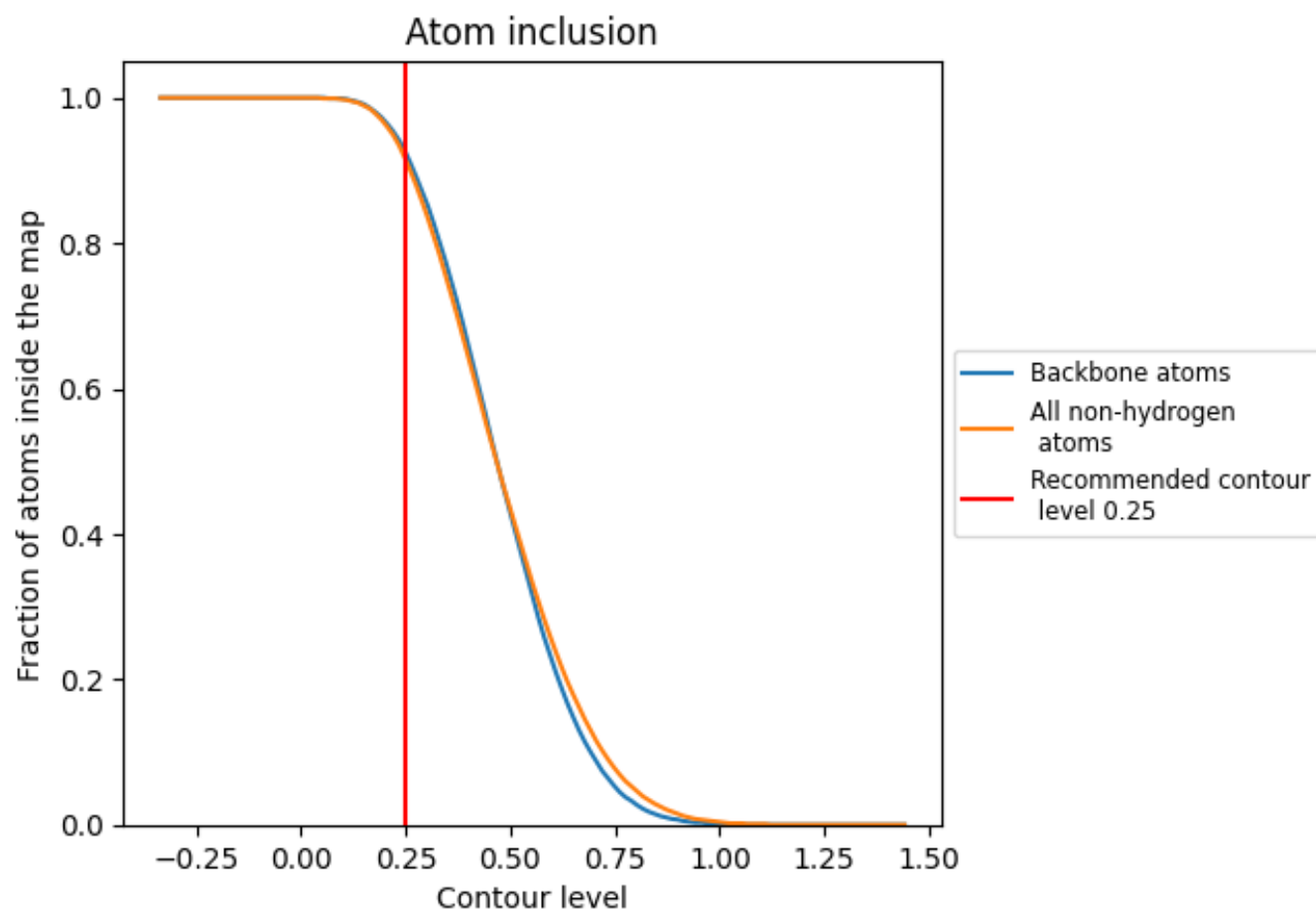
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 92% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9150	 0.3580
2	 0.9150	 0.4210
3	 0.9780	 0.4680
4	 0.7580	 0.2540
A	 0.9530	 0.3730
B	 0.9120	 0.2460
C	 0.9240	 0.4220
D	 0.9120	 0.4000
E	 0.8980	 0.3900
F	 0.6630	 0.1550
G	 0.7570	 0.2260
H	 0.7270	 0.2350
J	 0.3750	 0.1190
K	 0.9550	 0.4080
L	 0.9090	 0.3930
M	 0.9150	 0.4080
N	 0.8760	 0.3820
O	 0.9340	 0.4040
P	 0.7290	 0.1930
Q	 0.8240	 0.3410
R	 0.9620	 0.4220
S	 0.9020	 0.3900
T	 0.9480	 0.4240
U	 0.9320	 0.3740
V	 0.8950	 0.2990
W	 0.5830	 0.2260
X	 0.9030	 0.4310
Y	 0.9130	 0.4170
Z	 0.9160	 0.3110
b	 0.9350	 0.4340
c	 0.9120	 0.3980
d	 0.9690	 0.4710
e	 0.9490	 0.4660
f	 0.8990	 0.3720
g	 0.3690	 0.1650

