



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 03:09 PM UTC

PDB ID : 8VSA / pdb_00008vsa
EMDB ID : EMD-43491
Title : Endogenous trans-translation complex with tmRNA*SmpB in the P site and
alanyl-tRNA in the A site of E. coli 70S ribosome
Authors : Teran, D.; Zhang, Y.; Korostelev, A.A.
Deposited on : 2024-01-23
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

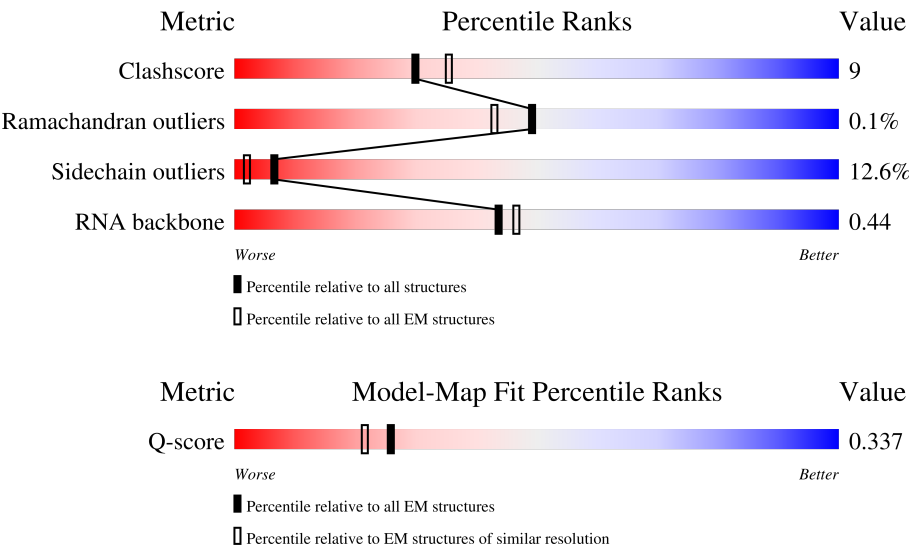
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.70 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.



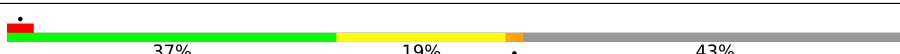
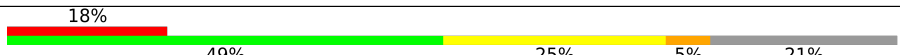
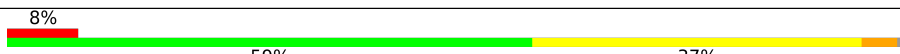
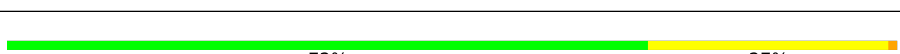
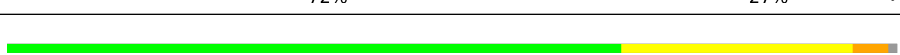
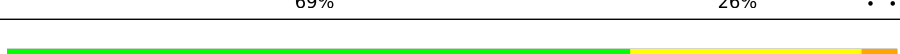
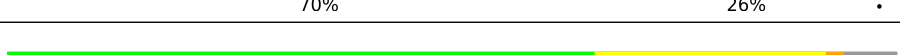
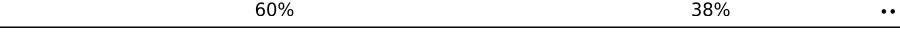
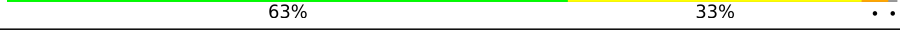
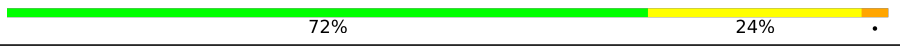
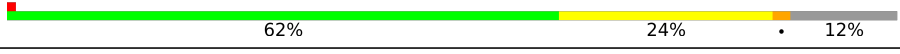
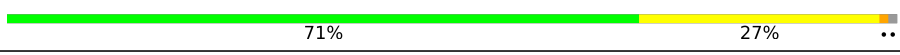
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	L02	273	69% 26% ••
2	L03	209	72% 25% •
3	L04	201	73% 25% •

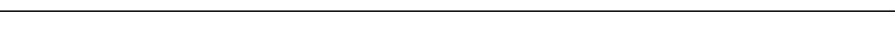
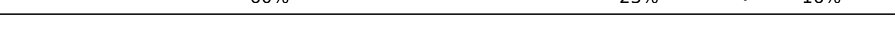
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Mol	Chain	Length	Quality of chain
4	L05	179	
5	L06	177	
6	L09	149	
7	L1	234	
8	L10	165	
9	L11	142	
10	L13	142	
11	L14	123	
12	L15	144	
13	L16	136	
14	L17	127	
15	L18	117	
16	L19	115	
17	L20	118	
18	L21	103	
19	L22	110	
20	L23	100	
21	L24	104	
22	L25	94	
23	L27	85	
24	L28	78	
25	L29	63	
26	L30	59	
27	L31	45	
28	L32	57	

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Mol	Chain	Length	Quality of chain
29	L33	55	
30	L34	46	
31	L35	65	
32	L36	38	
33	23S	2903	
34	5S	120	
35	TMRN	363	
36	16S	1539	
37	ATRN	76	
38	S02	241	
39	S03	233	
40	S04	206	
41	S05	167	
42	S06	135	
43	S07	179	
44	S08	130	
45	S09	130	
46	S10	103	
47	S11	129	
48	S12	124	
49	S13	118	
50	S14	101	
51	S15	89	
52	S16	82	
53	S17	84	

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Mol	Chain	Length	Quality of chain
54	S18	75	
55	S19	92	
56	S20	87	
57	S21	71	
58	SMPB	150	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 155832 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 L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L02	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L03	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L04	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L05	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L06	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L1	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 8 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L10	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L13	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L14	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L15	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L16	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 14 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L17	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L18	116	Total	C	N	O		0	0
			892	552	178	162			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L19	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L20	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 18 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L21	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L22	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L23	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
21	L24	102	Total	C	N	O		
			779	492	146	141	0	0

- Molecule 22 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	L25	94	Total	C	N	O	S	
			753	479	137	134	3	0

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	L27	75	Total	C	N	O	S	
			575	356	116	102	1	0

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	L28	77	Total	C	N	O	S	
			625	388	129	106	2	0

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	L29	63	Total	C	N	O	S	
			509	313	99	95	2	0

- Molecule 26 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	L30	58	Total	C	N	O	S	
			449	281	87	79	2	0

- Molecule 27 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	L31	45	Total	C	N	O	S	
			351	219	61	65	6	0

- Molecule 28 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L32	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 29 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L33	50	Total	C	N	O		0	0
			409	263	75	71			

- Molecule 30 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L34	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 31 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	L35	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 32 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	L36	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 33 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	23S	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
23S	747	C	U	variant	GB 1036415628

- Molecule 34 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	5S	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5S	120	A	U	conflict	GB 1370526515

- Molecule 35 is a RNA chain called TMRN.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	TMRN	363	Total	C	N	O	P	0	0
			7758	3465	1410	2520	363		

- Molecule 36 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	16S	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 37 is a RNA chain called A-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	ATRN	76	Total	C	N	O	P	0	0
			1621	722	289	534	76		

- Molecule 38 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	S02	225	Total	C	N	O	S	0	0
			1756	1111	315	322	8		

- Molecule 39 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	S03	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 40 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S04	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 41 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S05	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 42 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	S06	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 43 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S07	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 44 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	S08	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 45 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	S09	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 46 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S10	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S11	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 48 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S12	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 49 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S13	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 50 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S14	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 51 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S15	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 52 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S16	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 53 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S17	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 54 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	S18	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 55 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	S19	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 56 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	S20	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 57 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S21	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

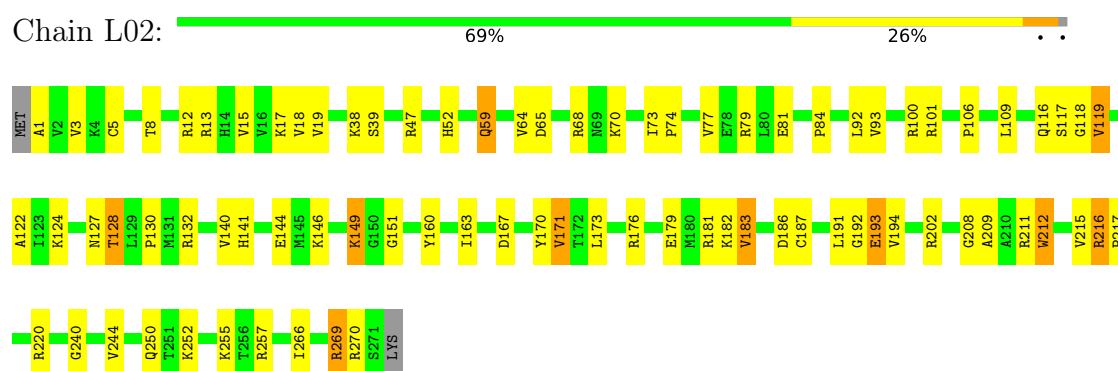
- Molecule 58 is a protein called SsrA-binding protein.

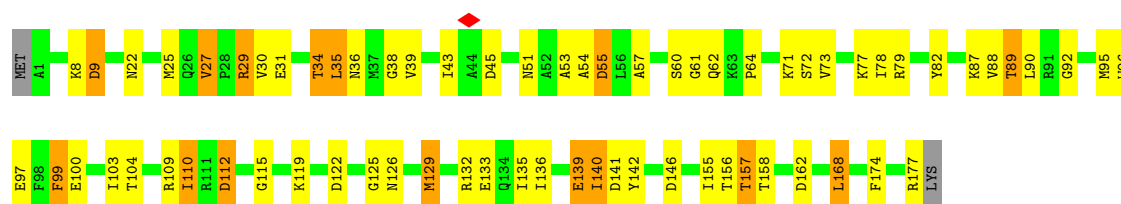
Mol	Chain	Residues	Atoms					AltConf	Trace
58	SMPB	150	Total	C	N	O	S	0	0
			1209	763	226	216	4		

3 Residue-property plots [i](#)

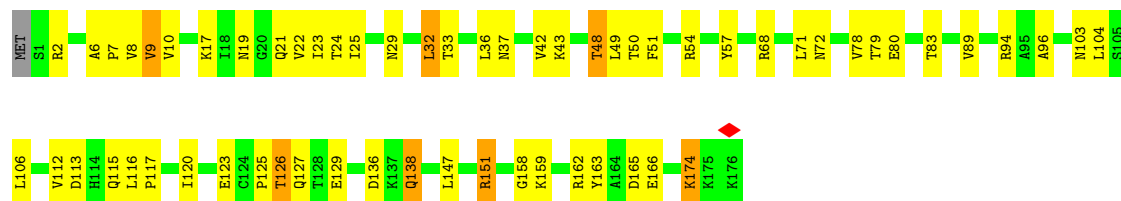
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 L2

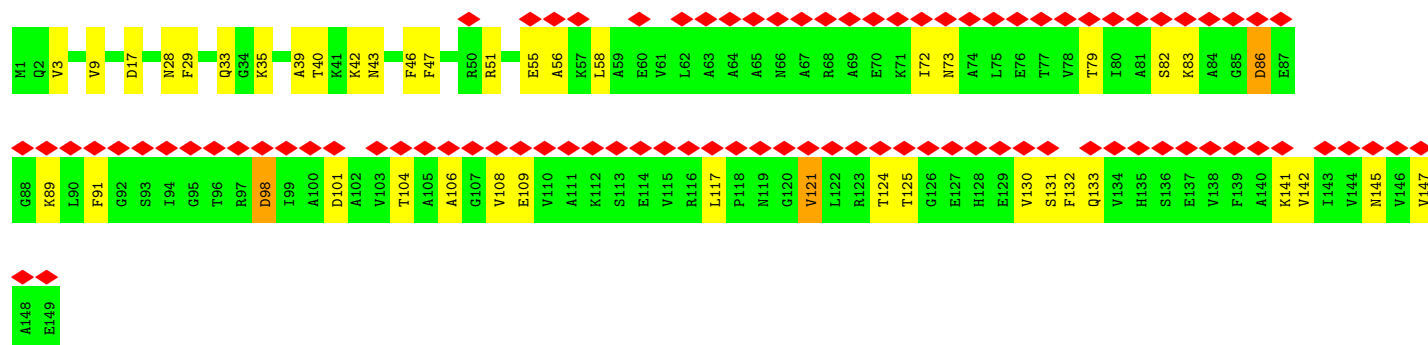
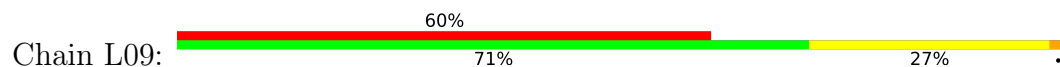




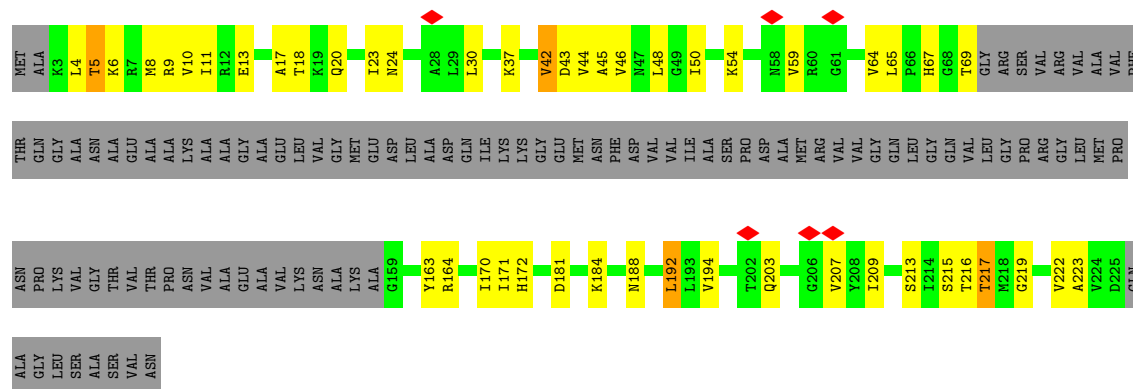
• Molecule 5: 50S ribosomal protein L6



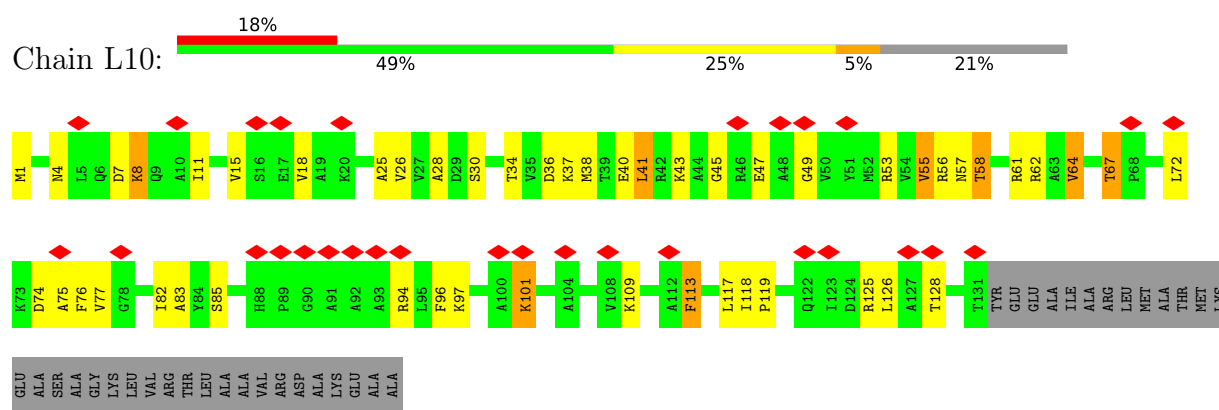
• Molecule 6: Large ribosomal subunit protein bL9



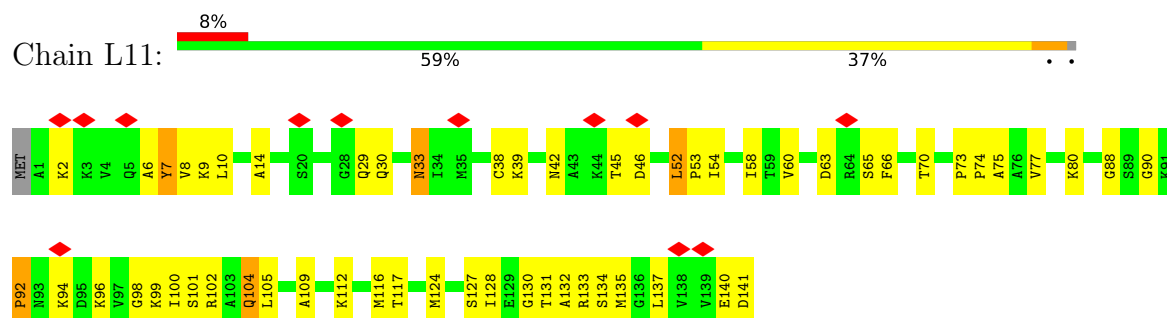
• Molecule 7: 50S ribosomal protein L1



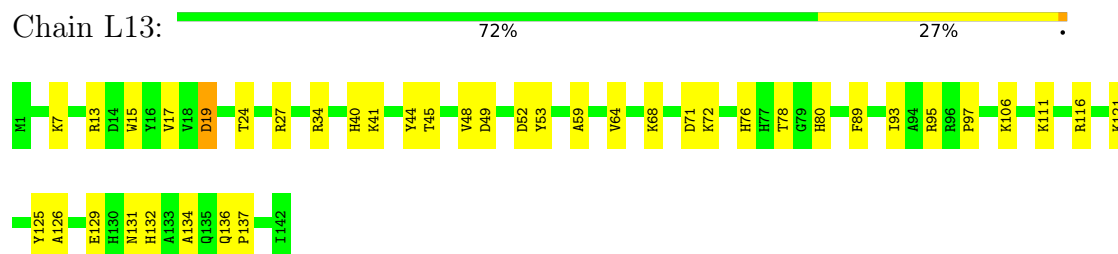
• Molecule 8: 50S ribosomal protein L10



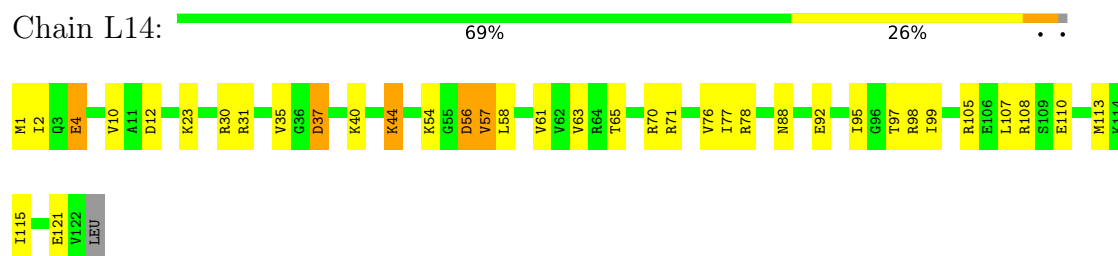
- Molecule 9: 50S ribosomal protein L11



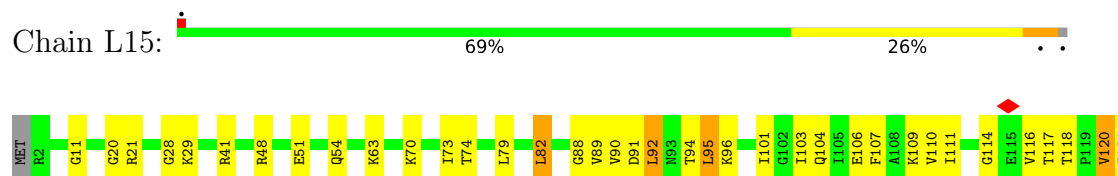
- Molecule 10: 50S ribosomal protein L13



- Molecule 11: 50S ribosomal protein L14



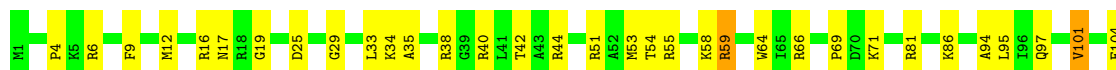
- Molecule 12: 50S ribosomal protein L15





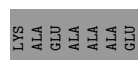
- Molecule 13: 50S ribosomal protein L16

Chain L16: 70% 26%



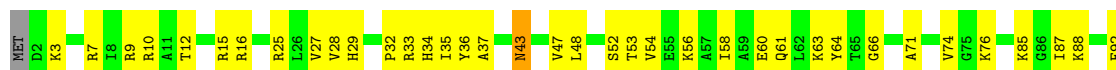
- Molecule 14: Large ribosomal subunit protein bL17

Chain L17: 66% 26% 6%



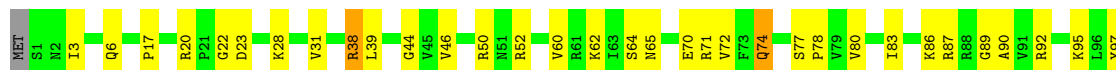
- Molecule 15: 50S ribosomal protein L18

Chain L18: 60% 38%



- Molecule 16: 50S ribosomal protein L19

Chain L19: 63% 33%

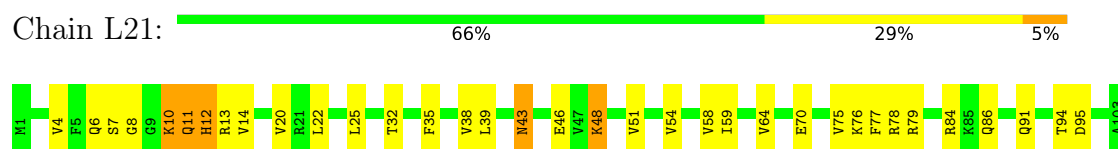


- Molecule 17: 50S ribosomal protein L20

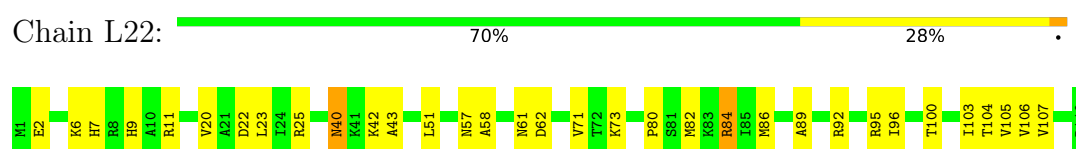
Chain L20: 71% 27%



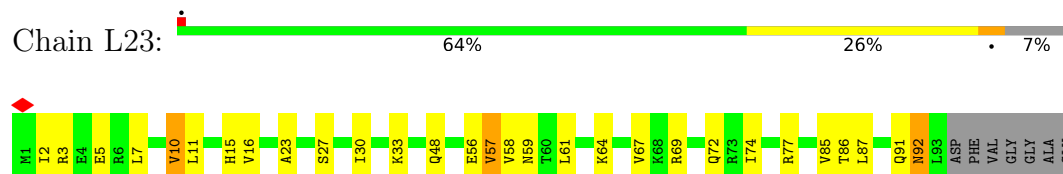
- Molecule 18: Ribosomal protein L21



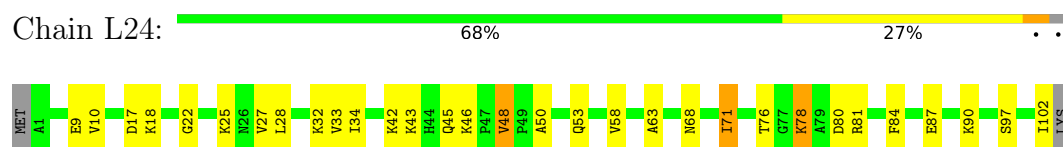
- Molecule 19: 50S ribosomal protein L22



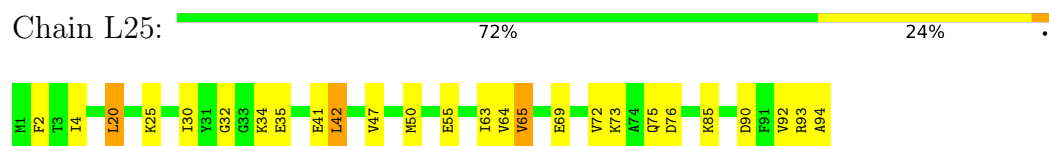
- Molecule 20: 50S ribosomal protein L23



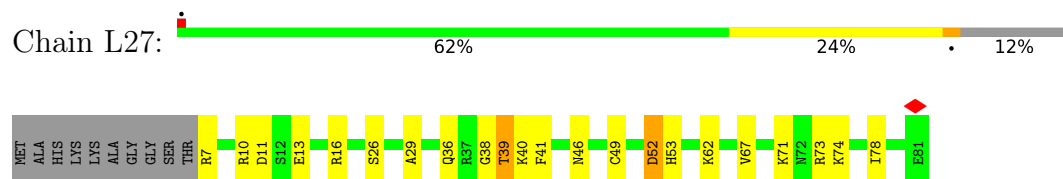
- Molecule 21: 50S ribosomal protein L24



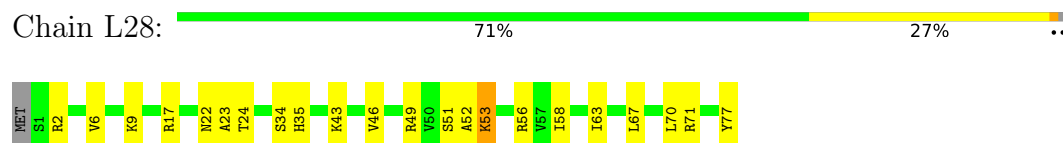
- Molecule 22: 50S ribosomal protein L25



- Molecule 23: 50S ribosomal protein L27



- Molecule 24: 50S ribosomal protein L28



- Molecule 25: 50S ribosomal protein L29

Chain L29:  70% 25% 5%



- Molecule 26: Large ribosomal subunit protein uL30

Chain L30:  64% 34% .



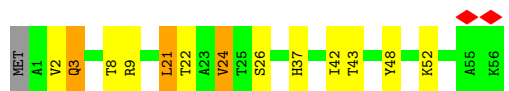
- Molecule 27: Large ribosomal subunit protein bL31

Chain L31:  53% 31% 16%



- Molecule 28: 50S ribosomal protein L32

Chain L32:  75% 18% 5% .



- Molecule 29: Large ribosomal subunit protein bL33

Chain L33:  58% 25% 7% 9%



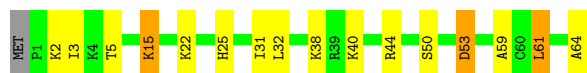
- Molecule 30: 50S ribosomal protein L34

Chain L34:  63% 33% .



- Molecule 31: 50S ribosomal protein L35

Chain L35:  74% 20% 5% .



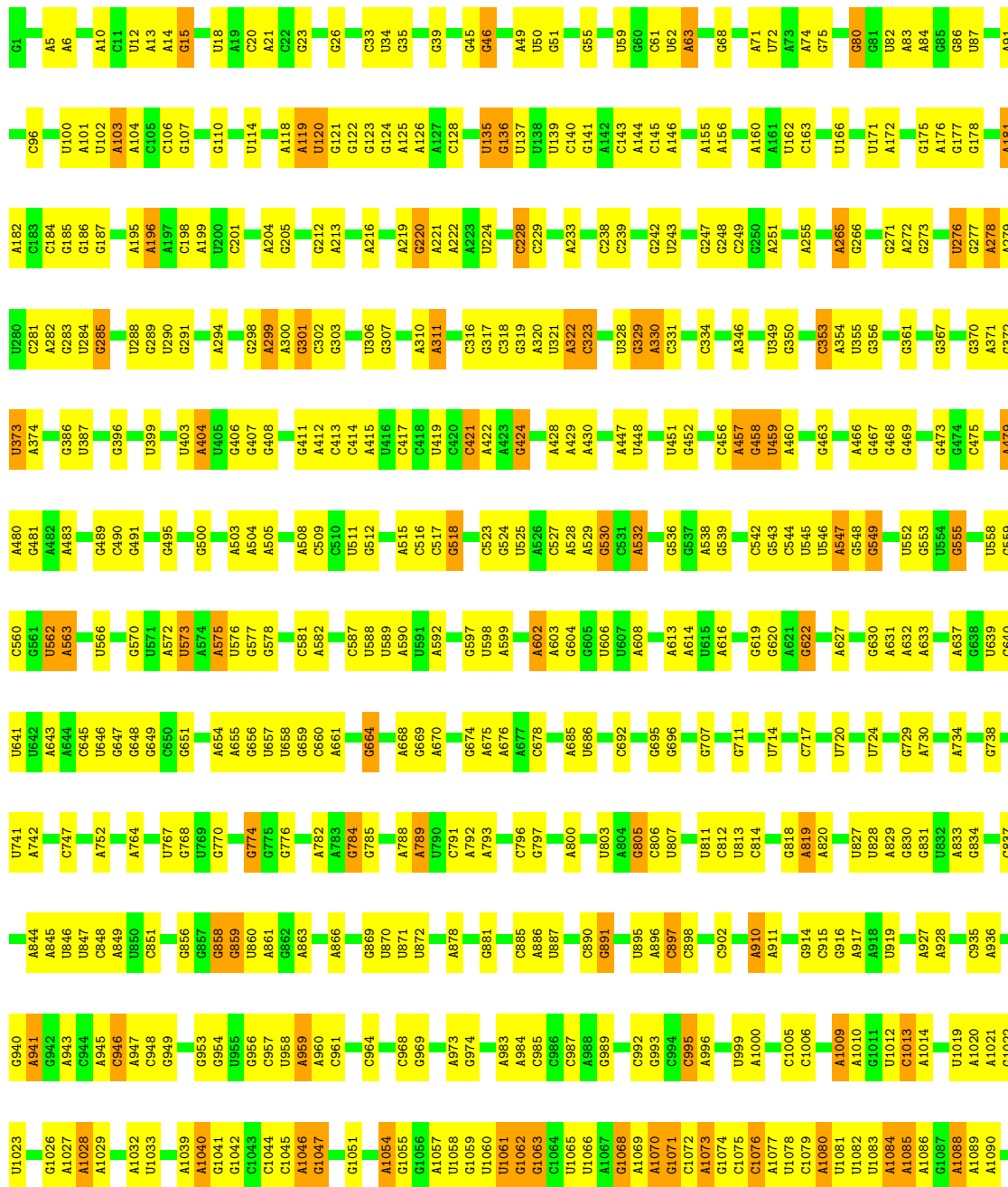
- Molecule 32: 50S ribosomal protein L36

Chain L36:  63% 34%

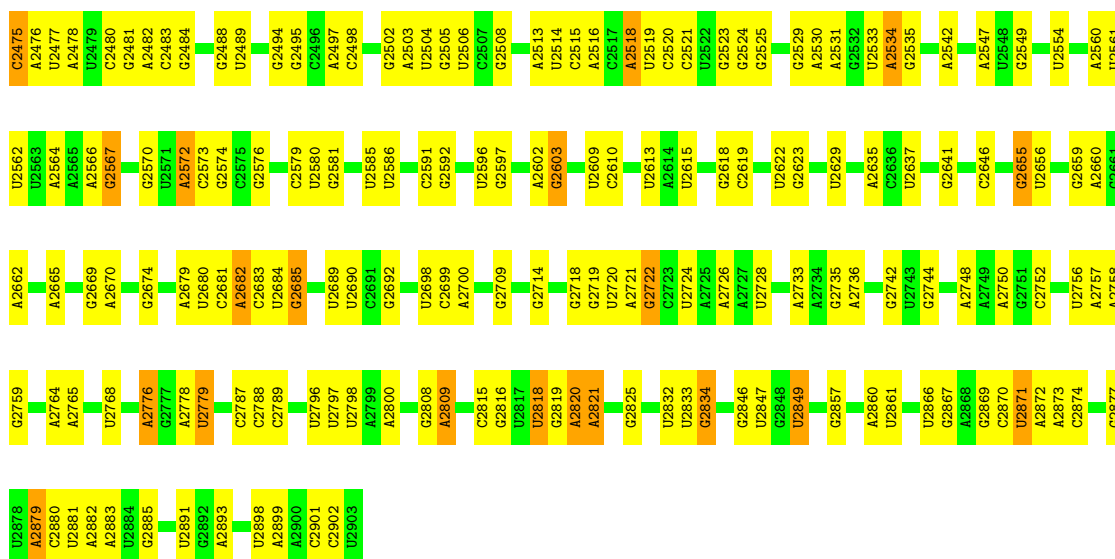


- Molecule 33: 23S ribosomal RNA

Chain 23S:  56% 38% 7%

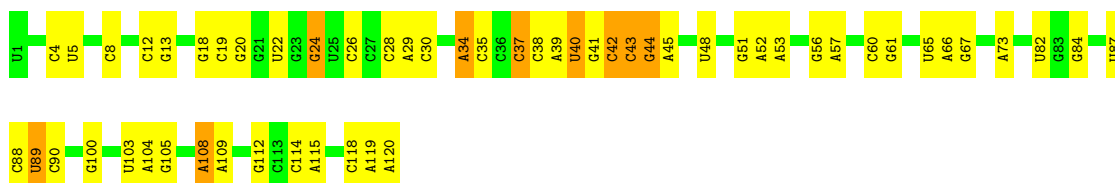


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G2382	U1094	G1182	U1294	A1386	G1478	A1571	A1688	A1787	U1883	G1972	U2075	G2145	U2220	C2301	G2382
G2383	A1095	G1186	U1294	A1387	G1482	A1578	A1669	C1788	G1884	G1980	U2076	C2146	U2221	G2302	G2383
C2385	A1096	G1187	G1296	G1388	G1483	A1579	G1674	A1791	A1889	A1982	U2077	U2147	C2221	G2303	G2385
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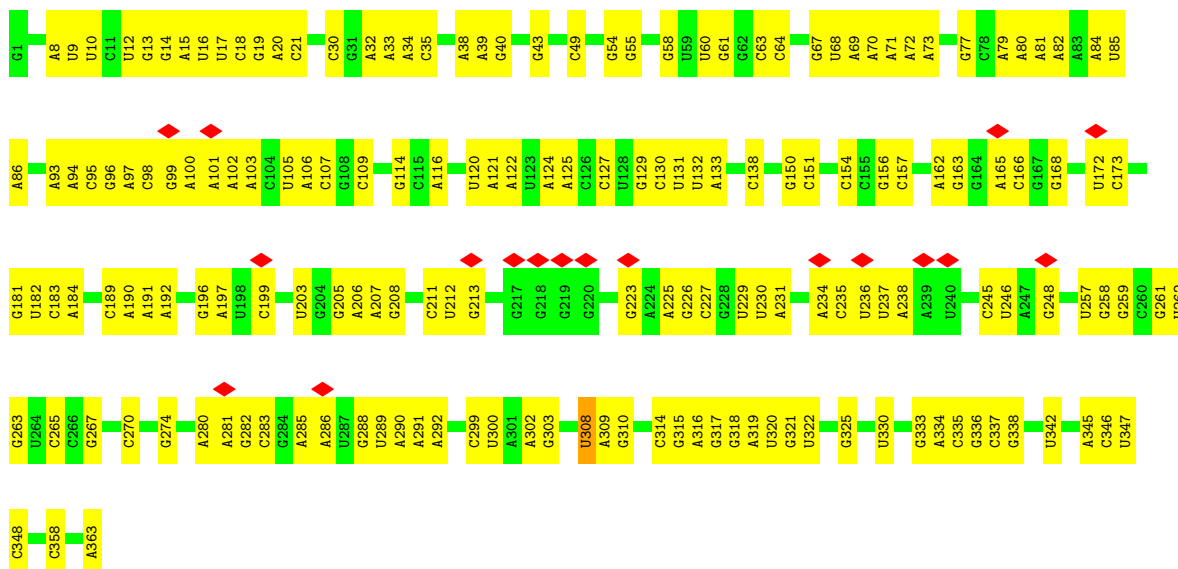
• Molecule 34: 5S ribosomal RNA

Chain 5S: 54% 38% 8%



• Molecule 35: TMRN

Chain TMRN: 5% 53% 47%



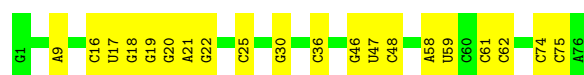
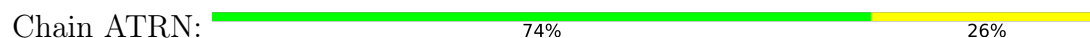
• Molecule 36: 16S ribosomal RNA

Chain 16S:  52% 41% 7%

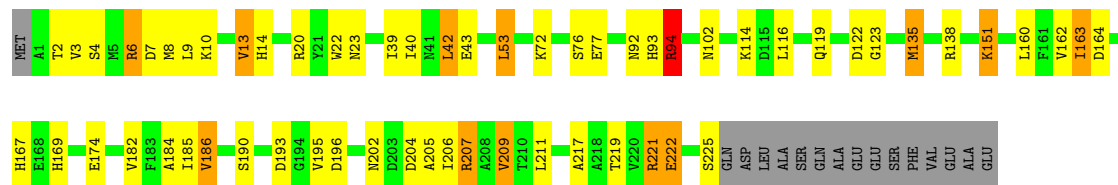
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A1157	A1161	A1065	A1162	A1241	A1242	C1168	A1243	C1244	G1245	A1246	C1247	A1248	G1249	C1250	A1259	C1260	A1261	G1262	A1263	C1264	A1265	C1266	A1190	G1267	C1268	A1269	C1277	A1190	G1278	C1279	A1204	G1280	C1281	A1210	C1290	G1291	A1294	C1295	A1296	C1297	U1300	G1301	C1306	U1307	A1308	C1311	A1314	C1315	A1316		
A1158	A1162	A1066	A1163	A1242	A1243	C1169	A1244	C1245	G1246	A1247	C1248	A1249	G1250	C1251	A1260	C1261	A1262	G1263	A1264	C1265	A1266	C1267	A1191	G1268	C1269	A1270	C1278	A1191	G1279	C1280	A1205	G1281	C1282	A1211	C1291	G1292	A1295	C1296	A1297	C1298	U1301	G1302	C1307	U1308	A1309	C1312	A1315	C1316	A1317		
A1159	A1163	A1067	A1164	A1243	A1244	C1170	A1245	C1246	G1247	A1248	C1249	A1250	G1251	C1252	A1261	C1262	A1263	G1264	A1265	C1266	A1267	C1268	A1192	G1269	C1270	A1271	C1279	A1192	G1280	C1281	A1206	G1282	C1283	A1212	C1292	G1293	A1296	C1297	A1298	C1299	U1302	G1303	C1308	U1309	A1310	C1313	A1316	C1318	A1319		
A1160	A1164	A1068	A1165	A1244	A1245	C1171	A1246	C1247	G1248	A1249	C1250	A1251	G1252	C1253	A1262	C1263	A1264	G1265	A1266	C1267	A1268	C1269	A1193	G1270	C1271	A1272	C1280	A1193	G1281	C1282	A1207	G1283	C1284	A1213	C1293	G1294	A1297	C1298	A1299	C1300	U1303	G1304	C1309	U1310	A1311	C1314	A1317	C1319	A1320		
A1161	A1165	A1069	A1166	A1245	A1246	C1172	A1247	C1248	G1249	A1250	C1251	A1252	G1253	C1254	A1263	C1264	A1265	G1266	A1267	C1268	A1269	C1270	A1194	G1271	C1272	A1273	C1281	A1194	G1282	C1283	A1208	G1284	C1285	A1214	C1294	G1295	A1298	C1299	A1300	C1301	U1304	G1305	C1310	U1311	A1312	C1315	A1318	C1320	A1321		
A1162	A1166	A1070	A1167	A1246	A1247	C1173	A1248	C1249	G1250	A1251	C1252	A1253	G1254	C1255	A1264	C1265	A1266	G1267	A1268	C1269	A1270	C1271	A1195	G1272	C1273	A1274	C1282	A1195	G1283	C1284	A1209	G1285	C1286	A1215	C1295	G1296	A1299	C1300	A1301	U1305	G1306	C1311	U1312	A1313	C1316	A1319	C1321	A1322			
A1163	A1167	A1071	A1168	A1247	A1248	C1174	A1249	C1250	G1251	A1252	C1253	A1254	G1255	C1256	A1265	C1266	A1267	G1268	A1269	C1270	A1271	C1272	A1196	G1273	C1274	A1275	C1283	A1196	G1284	C1285	A1210	G1286	C1287	A1216	C1296	G1297	A1300	C1301	U1306	G1307	C1312	U1313	A1314	C1317	A1320	C1322	A1323				
A1164	A1168	A1072	A1169	A1248	A1249	C1175	A1250	C1251	G1252	A1253	C1254	A1255	G1256	C1257	A1266	C1267	A1268	G1269	A1270	C1271	A1272	C1273	A1197	G1274	C1275	A1276	C1284	A1197	G1285	C1286	A1211	G1287	C1288	A1217	C1297	G1298	A1301	C1302	U1307	G1308	C1313	U1314	A1315	C1318	A1321	C1323	A1324				
A1165	A1169	A1073	A1170	A1249	A1250	C1176	A1251	C1252	G1253	A1254	C1255	A1256	G1257	C1258	A1267	C1268	A1269	G1270	A1271	C1272	A1273	C1274	A1198	G1275	C1276	A1277	C1285	A1198	G1286	C1287	A1212	G1288	C1289	A1218	C1298	G1299	A1302	C1303	U1308	G1309	C1314	U1315	A1316	C1319	A1322	C1324	A1325				
A1166	A1170	A1074	A1171	A1250	A1251	C1177	A1252	C1253	G1254	A1255	C1256	A1257	G1258	C1259	A1268	C1269	A1270	G1271	A1272	C1273	A1274	C1275	A1199	G1276	C1277	A1278	C1286	A1199	G1287	C1288	A1213	G1289	C1290	A1219	C1299	G1300	A1303	C1304	U1309	G1310	C1315	U1316	A1317	C1320	A1323	C1325	A1326				
A1167	A1171	A1075	A1172	A1251	A1252	C1178	A1253	C1254	G1255	A1256	C1257	A1258	G1259	C1260	A1269	C1270	A1271	G1272	A1273	C1274	A1275	C1276	A1200	G1277	C1278	A1279	C1287	A1200	G1288	C1289	A1214	G1290	C1291	A1220	C1300	A1304	C1305	U1310	G1311	C1316	U1317	A1318	C1321	A1324	C1326	A1327					
A1168	A1172	A1076	A1173	A1252	A1253	C1179	A1254	C1255	G1256	A1257	C1258	A1259	G1260	C1261	A1270	C1271	A1272	G1273	A1274	C1275	A1276	C1277	A1201	G1278	C1279	A1280	C1288	A1201	G1289	C1290	A1215	G1291	C1292	A1221	C1301	A1305	C1306	U1311	G1312	C1317	U1318	A1319	C1322	A1325	C1327	A1328					
A1169	A1173	A1077	A1174	A1253	A1254	C1180	A1255	C1256	G1257	A1258	C1259	A1260	G1261	C1262	A1271	C1272	A1273	G1274	A1275	C1276	A1277	C1278	A1202	G1279	C1280	A1281	C1289	A1202	G1290	C1291	A1216	G1292	C1293	A1222	C1302	A1306	C1307	U1312	G1313	C1318	U1319	A1320	C1323	A1326	C1328	A1329					
A1170	A1174	A1078	A1175	A1254	A1255	C1181	A1256	C1257	G1258	A1259	C1260	A1261	G1262	C1263	A1272	C1273	A1274	G1275	A1276	C1277	A1278	C1279	A1203	G1280	C1281	A1282	C1290	A1203	G1291	C1292	A1217	G1293	C1294	A1223	C1303	A1307	C1308	U1313	G1314	C1319	U1320	A1321	C1324	A1327	C1329	A1330					
A1171	A1175	A1079	A1176	A1255	A1256	C1182	A1257	C1258	G1259	A1260	C1261	A1262	G1263	C1264	A1273	C1274	A1275	G1276	A1277	C1278	A1279	C1280	A1204	G1281	C1282	A1283	C1291	A1204	G1292	C1293	A1218	G1294	C1295	A1224	C1304	A1308	C1309	U1314	G1315	C1320	U1321	A1322	C1325	A1328	C1330	A1331					
A1172	A1176	A1080	A1177	A1256	A1257	C1183	A1258	C1259	G1260	A1261	C1262	A1263	G1264	C1265	A1274	C1275	A1276	G1277	A1278	C1279	A1280	C1281	A1205																												



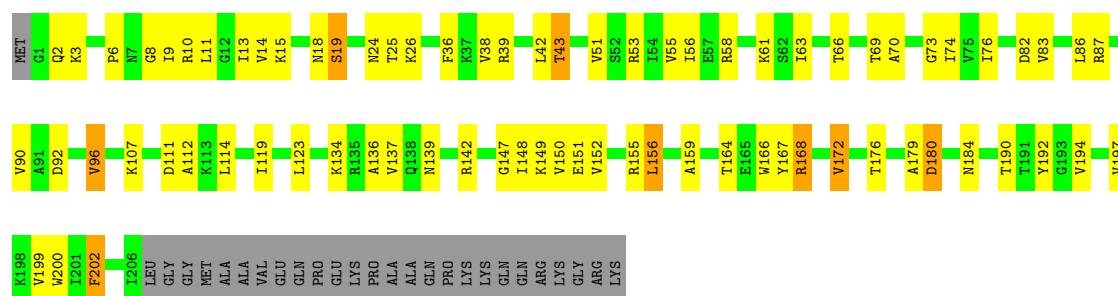
• Molecule 37: A-tRNA



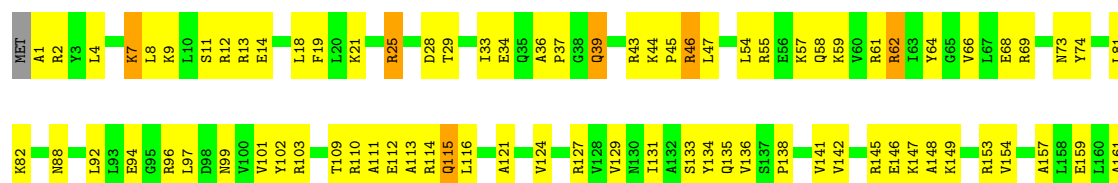
• Molecule 38: 30S ribosomal protein S2

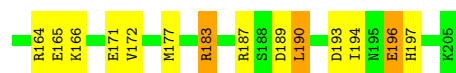


• Molecule 39: 30S ribosomal protein S3



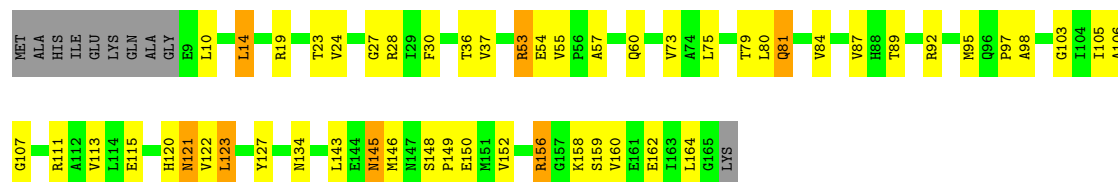
• Molecule 40: 30S ribosomal protein S4





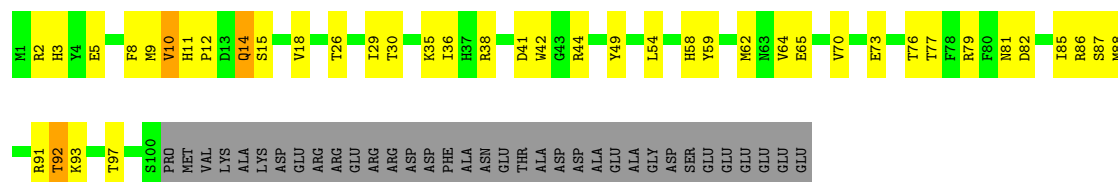
- Molecule 41: 30S ribosomal protein S5

Chain S05: 62% 28% 6%



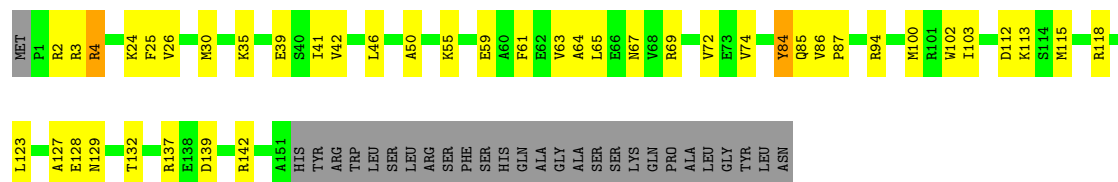
- Molecule 42: 30S ribosomal protein S6

Chain S06: 43% 29% 26%



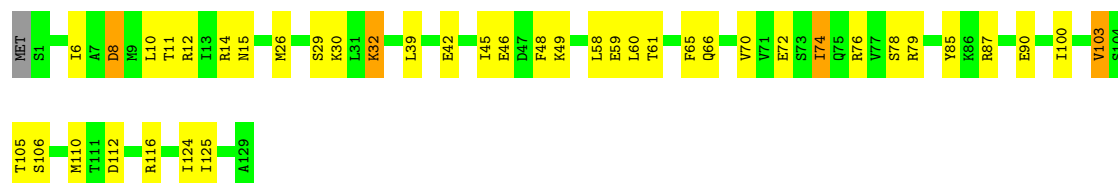
- Molecule 43: 30S ribosomal protein S7

Chain S07: 60% 23% 16%



- Molecule 44: 30S ribosomal protein S8

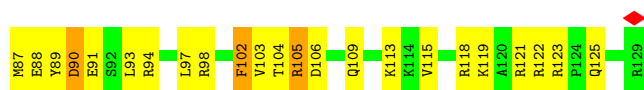
Chain S08: 68% 28% 2%



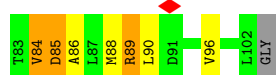
- Molecule 45: Small ribosomal subunit protein uS9

Chain S09: 54% 38% 5%





- Molecule 46: 30S ribosomal protein S10



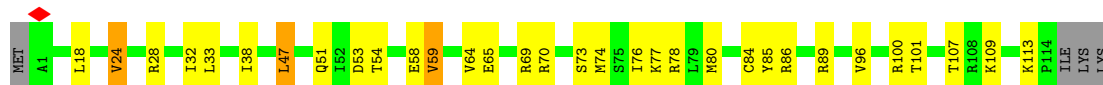
- Molecule 47: 30S ribosomal protein S11



- Molecule 48: 30S ribosomal protein S12

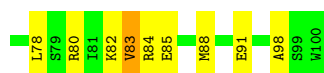


- Molecule 49: 30S ribosomal protein S13



- Molecule 50: Small ribosomal subunit protein uS14





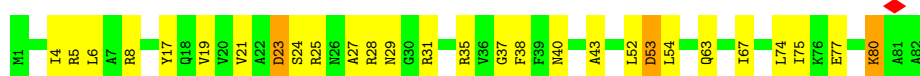
- Molecule 51: Small ribosomal subunit protein uS15

Chain S15: 75% 22% ..



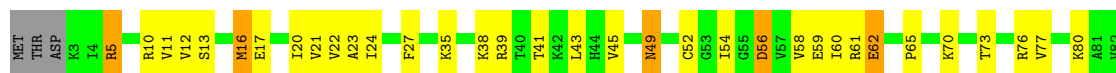
- Molecule 52: 30S ribosomal protein S16

Chain S16: 66% 30% .



- Molecule 53: Small ribosomal subunit protein uS17

Chain S17: 55% 35% 6% 5%



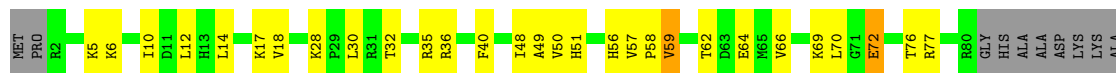
- Molecule 54: 30S ribosomal protein S18

Chain S18: 67% 16% 13%



- Molecule 55: 30S ribosomal protein S19

Chain S19: 54% 29% 14%



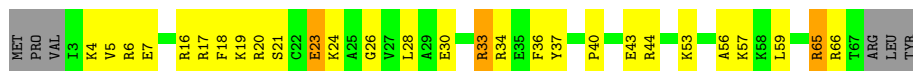
- Molecule 56: 30S ribosomal protein S20

Chain S20: 71% 24% ..



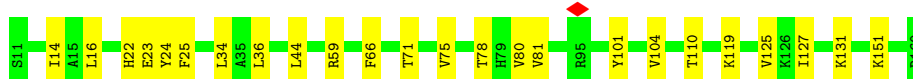
- Molecule 57: 30S ribosomal protein S21

Chain S21:  52% 35% 8%



- Molecule 58: SsrA-binding protein

Chain SMPB:  84% 16%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	5956	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 ($e^-/\text{\AA}^2$)	29.9	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1100	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	24.823	Depositor
Minimum map value	-10.783	Depositor
Average map value	0.006	Depositor
Map value standard deviation	1.735	Depositor
Recommended contour level	3	Depositor
Map size (Å)	487.2, 487.2, 487.2	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.87, 0.87, 0.87	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	L02	0.23	0/2121	0.42	0/2852
2	L03	0.21	0/1586	0.40	0/2134
3	L04	0.18	0/1571	0.37	0/2113
4	L05	0.23	0/1434	0.50	0/1926
5	L06	0.16	0/1343	0.39	0/1816
6	L09	0.17	0/1122	0.41	0/1515
7	L1	0.16	0/1033	0.41	0/1387
8	L10	0.22	0/1001	0.57	2/1350 (0.1%)
9	L11	0.22	0/1046	0.47	0/1410
10	L13	0.20	0/1152	0.35	0/1551
11	L14	0.23	0/947	0.47	0/1268
12	L15	0.21	0/1054	0.47	0/1403
13	L16	0.22	0/1093	0.47	0/1460
14	L17	0.21	0/973	0.49	0/1301
15	L18	0.18	0/902	0.46	0/1209
16	L19	0.20	0/929	0.35	0/1242
17	L20	0.18	0/960	0.31	0/1278
18	L21	0.19	0/829	0.41	0/1107
19	L22	0.20	0/864	0.38	0/1156
20	L23	0.18	0/744	0.36	0/994
21	L24	0.19	0/787	0.46	0/1051
22	L25	0.19	0/766	0.37	0/1025
23	L27	0.20	0/582	0.34	0/769
24	L28	0.21	0/635	0.36	0/848
25	L29	0.16	0/510	0.41	0/677
26	L30	0.18	0/453	0.29	0/605
27	L31	0.31	0/358	0.75	1/480 (0.2%)
28	L32	0.20	0/450	0.46	0/599
29	L33	0.16	0/416	0.33	0/554
30	L34	0.20	0/380	0.35	0/498
31	L35	0.23	0/513	0.47	0/676
32	L36	0.20	0/303	0.38	0/397
33	23S	0.23	0/69796	0.34	0/108888
34	5S	0.22	0/2872	0.37	0/4479

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	TMRN	0.19	0/8681	0.39	1/13532 (0.0%)
36	16S	0.20	0/36963	0.32	0/57662
37	ATRN	0.22	0/1810	0.36	0/2820
38	S02	0.17	0/1787	0.41	2/2408 (0.1%)
39	S03	0.17	0/1651	0.35	0/2225
40	S04	0.18	0/1665	0.47	0/2227
41	S05	0.21	0/1169	0.53	2/1573 (0.1%)
42	S06	0.21	0/835	0.51	0/1128
43	S07	0.18	0/1195	0.41	0/1602
44	S08	0.18	0/989	0.39	0/1326
45	S09	0.18	0/1034	0.49	0/1375
46	S10	0.18	0/796	0.45	0/1077
47	S11	0.19	0/885	0.44	0/1195
48	S12	0.23	0/969	0.52	0/1300
49	S13	0.18	0/892	0.49	0/1193
50	S14	0.17	0/817	0.47	0/1088
51	S15	0.17	0/722	0.45	0/964
52	S16	0.17	0/659	0.39	0/884
53	S17	0.19	0/657	0.43	0/881
54	S18	0.17	0/544	0.40	0/731
55	S19	0.18	0/652	0.40	0/877
56	S20	0.16	0/671	0.37	0/888
57	S21	0.23	0/550	0.67	0/728
58	SMPB	0.21	0/1231	0.54	2/1655 (0.1%)
All	All	0.21	0/169349	0.37	10/253357 (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
4	L05	0	1
11	L14	0	1
27	L31	0	1
41	S05	0	2
All	All	0	5

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	L10	117	LEU	CA-C-N	5.82	132.89	122.13
8	L10	117	LEU	C-N-CA	5.82	132.89	122.13
38	S02	93	HIS	CA-C-N	5.43	131.92	121.54
38	S02	93	HIS	C-N-CA	5.43	131.92	121.54
41	S05	121	ASN	CA-C-N	5.32	131.55	121.97

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	L05	61	GLY	Peptide
11	L14	92	GLU	Peptide
27	L31	1	MET	Peptide
41	S05	120	HIS	Peptide
41	S05	121	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	L02	2082	0	2157	56	0
2	L03	1565	0	1616	33	0
3	L04	1552	0	1619	28	0
4	L05	1410	0	1447	46	0
5	L06	1323	0	1374	32	0
6	L09	1111	0	1148	20	0
7	L1	1026	0	1092	25	0
8	L10	988	0	1025	26	0
9	L11	1032	0	1088	39	0
10	L13	1129	0	1162	25	0
11	L14	938	0	1012	23	0
12	L15	1045	0	1117	28	0
13	L16	1074	0	1157	25	0
14	L17	960	0	1000	25	0
15	L18	892	0	923	27	0
16	L19	917	0	965	35	0
17	L20	947	0	1022	24	0
18	L21	816	0	839	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	L22	857	0	922	19	0
20	L23	738	0	807	11	0
21	L24	779	0	834	15	0
22	L25	753	0	780	11	0
23	L27	575	0	592	16	0
24	L28	625	0	655	12	0
25	L29	509	0	543	12	0
26	L30	449	0	491	11	0
27	L31	351	0	350	17	0
28	L32	444	0	461	9	0
29	L33	409	0	440	10	0
30	L34	377	0	418	15	0
31	L35	504	0	574	14	0
32	L36	302	0	343	8	0
33	23S	62317	0	31346	690	0
34	5S	2568	0	1303	31	0
35	TMRN	7758	0	0	0	0
36	16S	33012	0	16618	460	0
37	ATRN	1621	0	0	0	0
38	S02	1756	0	1787	28	0
39	S03	1624	0	1699	39	0
40	S04	1643	0	1710	54	0
41	S05	1156	0	1199	24	0
42	S06	817	0	808	27	0
43	S07	1181	0	1240	20	0
44	S08	979	0	1034	25	0
45	S09	1022	0	1070	43	0
46	S10	786	0	828	33	0
47	S11	869	0	878	29	0
48	S12	955	0	1019	29	0
49	S13	883	0	944	17	0
50	S14	805	0	847	37	0
51	S15	714	0	737	10	0
52	S16	649	0	666	19	0
53	S17	648	0	691	22	0
54	S18	535	0	552	9	0
55	S19	637	0	665	18	0
56	S20	665	0	714	14	0
57	S21	544	0	579	22	0
58	SMPB	1209	0	0	0	0
All	All	155832	0	98907	2050	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 9.

The worst 5 of 2050 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)
36:16S:978:A:N6	36:16S:1360:A:C2	2.19	1.10
33:23S:2104:C:N4	33:23S:2185:U:H3	1.51	1.06
36:16S:372:C:N4	36:16S:389:A:H62	1.53	1.05
36:16S:978:A:C2	36:16S:1316:G:N2	2.26	1.04
33:23S:1040:A:N6	33:23S:1115:G:H1	1.56	1.04

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	L02	269/273 (98%)	243 (90%)	26 (10%)	0	100	100
2	L03	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
3	L04	199/201 (99%)	187 (94%)	11 (6%)	1 (0%)	24	56
4	L05	175/179 (98%)	152 (87%)	23 (13%)	0	100	100
5	L06	174/177 (98%)	162 (93%)	12 (7%)	0	100	100
6	L09	147/149 (99%)	129 (88%)	17 (12%)	1 (1%)	18	50
7	L1	130/234 (56%)	117 (90%)	13 (10%)	0	100	100
8	L10	129/165 (78%)	100 (78%)	28 (22%)	1 (1%)	16	48
9	L11	139/142 (98%)	118 (85%)	21 (15%)	0	100	100
10	L13	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
11	L14	120/123 (98%)	106 (88%)	14 (12%)	0	100	100
12	L15	141/144 (98%)	125 (89%)	16 (11%)	0	100	100
13	L16	134/136 (98%)	125 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	L17	118/127 (93%)	106 (90%)	12 (10%)	0	100	100
15	L18	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
16	L19	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
17	L20	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
18	L21	101/103 (98%)	89 (88%)	11 (11%)	1 (1%)	12	43
19	L22	108/110 (98%)	98 (91%)	10 (9%)	0	100	100
20	L23	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
21	L24	100/104 (96%)	84 (84%)	16 (16%)	0	100	100
22	L25	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
23	L27	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
24	L28	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
25	L29	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
26	L30	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
27	L31	43/45 (96%)	35 (81%)	8 (19%)	0	100	100
28	L32	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
29	L33	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
30	L34	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
31	L35	62/65 (95%)	55 (89%)	6 (10%)	1 (2%)	7	35
32	L36	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
38	S02	223/241 (92%)	212 (95%)	10 (4%)	1 (0%)	30	60
39	S03	204/233 (88%)	195 (96%)	9 (4%)	0	100	100
40	S04	203/206 (98%)	180 (89%)	23 (11%)	0	100	100
41	S05	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
42	S06	98/135 (73%)	81 (83%)	17 (17%)	0	100	100
43	S07	149/179 (83%)	141 (95%)	8 (5%)	0	100	100
44	S08	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
45	S09	125/130 (96%)	107 (86%)	18 (14%)	0	100	100
46	S10	96/103 (93%)	84 (88%)	12 (12%)	0	100	100
47	S11	114/129 (88%)	98 (86%)	16 (14%)	0	100	100
48	S12	121/124 (98%)	100 (83%)	21 (17%)	0	100	100
49	S13	112/118 (95%)	101 (90%)	11 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	S14	98/101 (97%)	88 (90%)	10 (10%)	0	100	100
51	S15	86/89 (97%)	73 (85%)	12 (14%)	1 (1%)	10	40
52	S16	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
53	S17	78/84 (93%)	65 (83%)	13 (17%)	0	100	100
54	S18	63/75 (84%)	60 (95%)	3 (5%)	0	100	100
55	S19	77/92 (84%)	70 (91%)	7 (9%)	0	100	100
56	S20	83/87 (95%)	80 (96%)	3 (4%)	0	100	100
57	S21	63/71 (89%)	42 (67%)	21 (33%)	0	100	100
58	SMPB	148/150 (99%)	124 (84%)	23 (16%)	1 (1%)	18	50
All	All	6110/6579 (93%)	5513 (90%)	589 (10%)	8 (0%)	49	78

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	L10	118	ILE
31	L35	31	ILE
58	SMPB	81	VAL
38	S02	94	ARG
3	L04	83	VAL

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	L02	216/218 (99%)	197 (91%)	19 (9%)	9	33
2	L03	164/164 (100%)	145 (88%)	19 (12%)	5	24
3	L04	165/165 (100%)	152 (92%)	13 (8%)	11	37
4	L05	148/150 (99%)	121 (82%)	27 (18%)	2	11
5	L06	137/138 (99%)	118 (86%)	19 (14%)	3	19
6	L09	114/114 (100%)	101 (89%)	13 (11%)	5	24
7	L1	110/181 (61%)	90 (82%)	20 (18%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	L10	100/123 (81%)	83 (83%)	17 (17%)	2	13
9	L11	109/110 (99%)	96 (88%)	13 (12%)	5	23
10	L13	116/116 (100%)	111 (96%)	5 (4%)	26	50
11	L14	103/104 (99%)	88 (85%)	15 (15%)	3	17
12	L15	102/103 (99%)	91 (89%)	11 (11%)	6	27
13	L16	109/109 (100%)	96 (88%)	13 (12%)	5	23
14	L17	100/103 (97%)	95 (95%)	5 (5%)	22	48
15	L18	86/87 (99%)	77 (90%)	9 (10%)	6	28
16	L19	99/100 (99%)	91 (92%)	8 (8%)	11	36
17	L20	89/90 (99%)	81 (91%)	8 (9%)	9	33
18	L21	84/84 (100%)	68 (81%)	16 (19%)	1	10
19	L22	93/93 (100%)	89 (96%)	4 (4%)	26	50
20	L23	80/84 (95%)	63 (79%)	17 (21%)	1	7
21	L24	83/85 (98%)	71 (86%)	12 (14%)	3	17
22	L25	78/78 (100%)	66 (85%)	12 (15%)	2	16
23	L27	57/63 (90%)	54 (95%)	3 (5%)	20	46
24	L28	67/68 (98%)	61 (91%)	6 (9%)	9	33
25	L29	55/55 (100%)	49 (89%)	6 (11%)	6	26
26	L30	48/49 (98%)	44 (92%)	4 (8%)	10	35
27	L31	42/42 (100%)	29 (69%)	13 (31%)	0	2
28	L32	47/48 (98%)	41 (87%)	6 (13%)	4	21
29	L33	45/49 (92%)	36 (80%)	9 (20%)	1	9
30	L34	38/38 (100%)	34 (90%)	4 (10%)	6	28
31	L35	51/52 (98%)	47 (92%)	4 (8%)	11	37
32	L36	34/34 (100%)	30 (88%)	4 (12%)	5	23
38	S02	186/199 (94%)	159 (86%)	27 (14%)	3	17
39	S03	170/190 (90%)	144 (85%)	26 (15%)	3	16
40	S04	172/173 (99%)	139 (81%)	33 (19%)	1	9
41	S05	119/126 (94%)	96 (81%)	23 (19%)	1	9
42	S06	87/116 (75%)	79 (91%)	8 (9%)	8	32
43	S07	124/147 (84%)	110 (89%)	14 (11%)	5	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	S08	104/105 (99%)	96 (92%)	8 (8%)	12	38
45	S09	105/107 (98%)	91 (87%)	14 (13%)	4	20
46	S10	86/90 (96%)	76 (88%)	10 (12%)	5	24
47	S11	89/99 (90%)	81 (91%)	8 (9%)	9	33
48	S12	103/104 (99%)	97 (94%)	6 (6%)	18	45
49	S13	92/96 (96%)	82 (89%)	10 (11%)	6	26
50	S14	83/84 (99%)	68 (82%)	15 (18%)	2	12
51	S15	76/77 (99%)	68 (90%)	8 (10%)	6	28
52	S16	65/65 (100%)	56 (86%)	9 (14%)	3	19
53	S17	74/78 (95%)	64 (86%)	10 (14%)	4	20
54	S18	56/65 (86%)	48 (86%)	8 (14%)	3	18
55	S19	70/79 (89%)	60 (86%)	10 (14%)	3	18
56	S20	65/66 (98%)	57 (88%)	8 (12%)	4	22
57	S21	55/61 (90%)	48 (87%)	7 (13%)	4	21
58	SMPB	125/125 (100%)	103 (82%)	22 (18%)	2	12
All	All	5075/5349 (95%)	4437 (87%)	638 (13%)	6	21

5 of 638 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	S06	5	GLU
53	S17	5	ARG
43	S07	84	TYR
41	S05	164	LEU
47	S11	75	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
7	L1	58	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
33	23S	2902/2903 (99%)	618 (21%)	14 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	5S	119/120 (99%)	29 (24%)	1 (0%)
35	TMRN	362/363 (99%)	168 (46%)	13 (3%)
36	16S	1538/1539 (99%)	321 (20%)	5 (0%)
37	ATRN	75/76 (98%)	20 (26%)	1 (1%)
All	All	4996/5001 (99%)	1156 (23%)	34 (0%)

5 of 1156 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
33	23S	10	A
33	23S	12	U
33	23S	15	G
33	23S	23	G
33	23S	34	U

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
36	16S	70	U
36	16S	890	G
36	16S	1347	G
33	23S	2655	G
33	23S	2391	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no chain breaks in this entry.

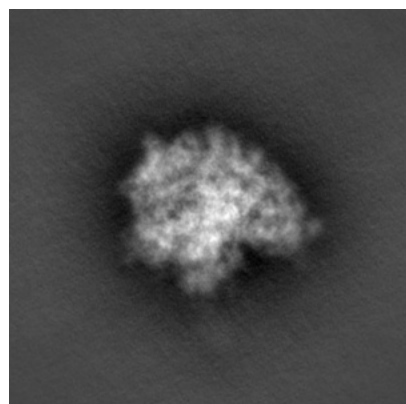
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43491. These allow visual inspection of the internal detail of the map and identification of artifacts.

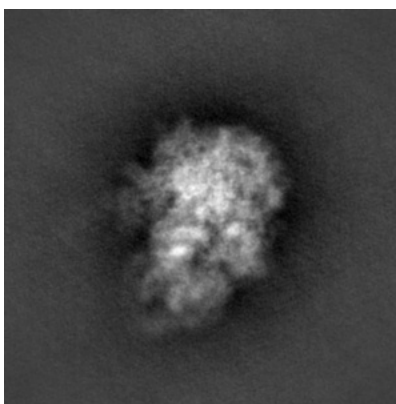
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

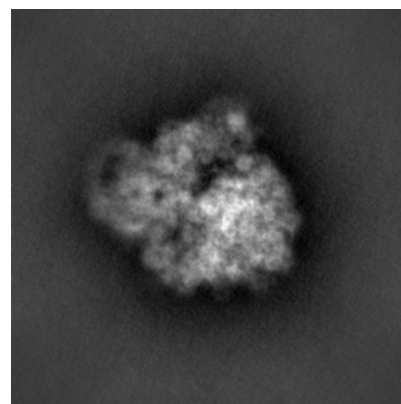
6.1.1 Primary map



X

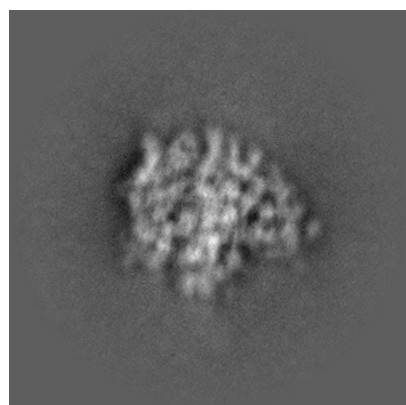


Y

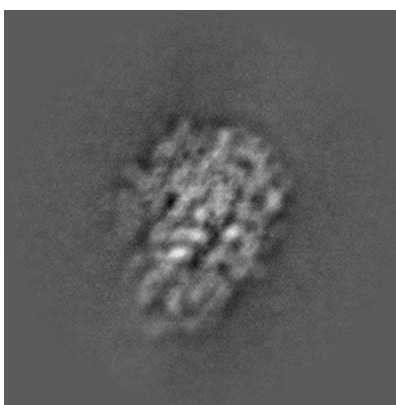


Z

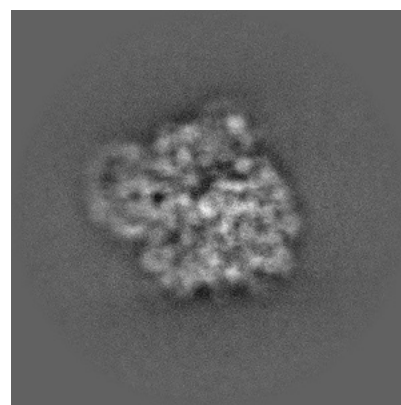
6.1.2 Raw map



X



Y

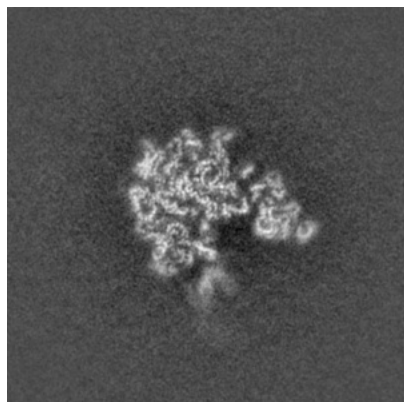


Z

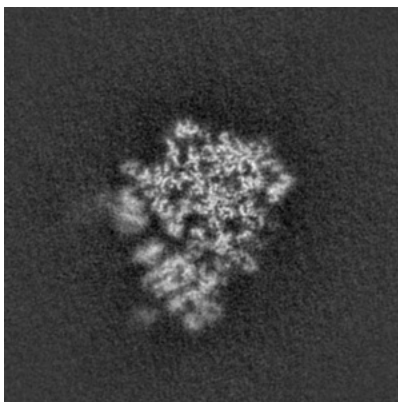
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

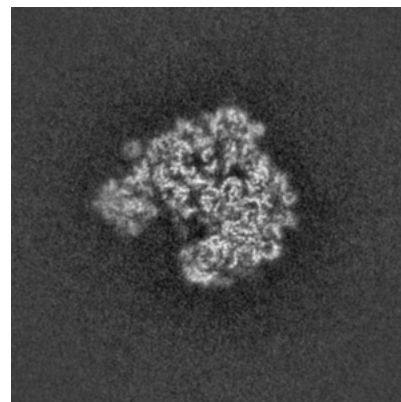
6.2.1 Primary map



X Index: 280

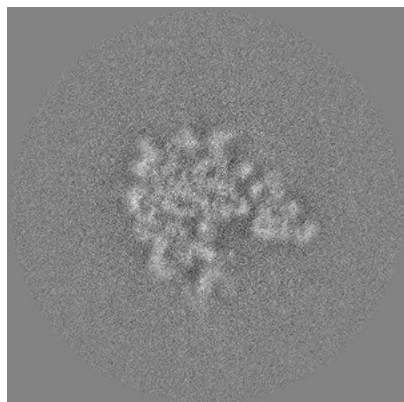


Y Index: 280

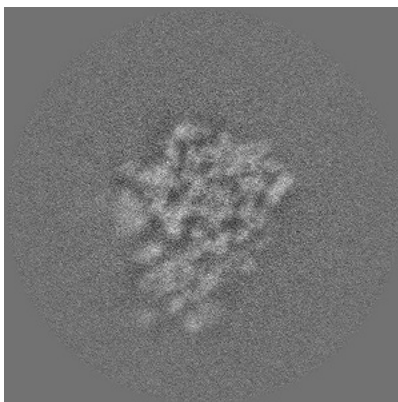


Z Index: 280

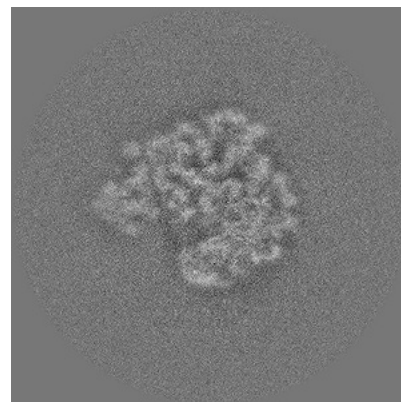
6.2.2 Raw map



X Index: 280



Y Index: 280

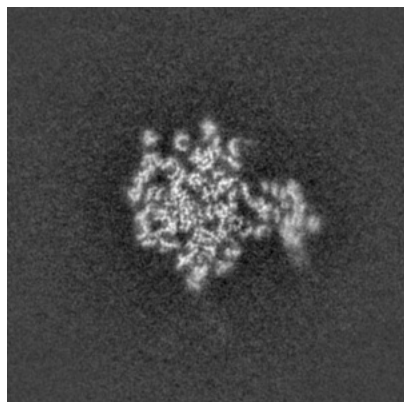


Z Index: 280

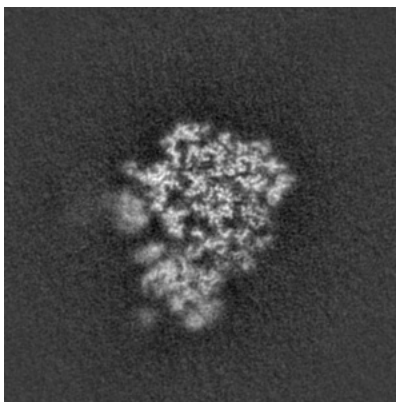
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

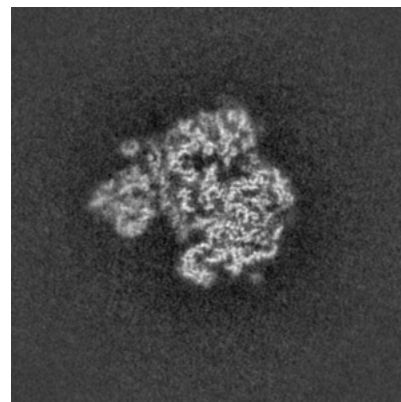
6.3.1 Primary map



X Index: 310

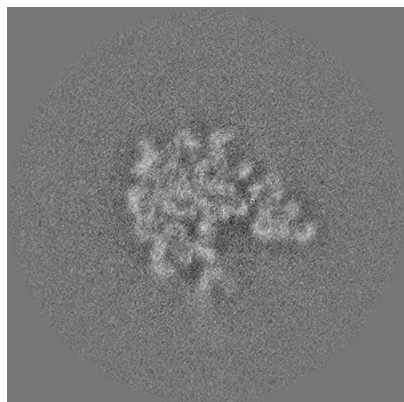


Y Index: 284

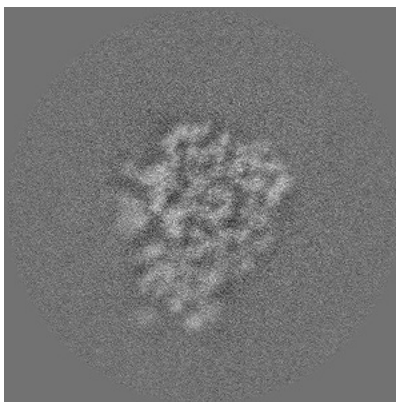


Z Index: 273

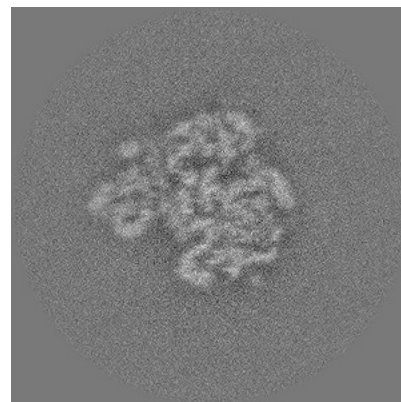
6.3.2 Raw map



X Index: 279



Y Index: 283

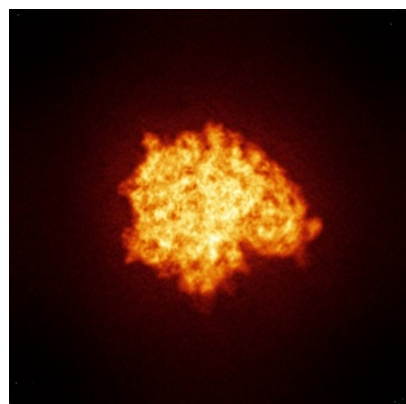


Z Index: 271

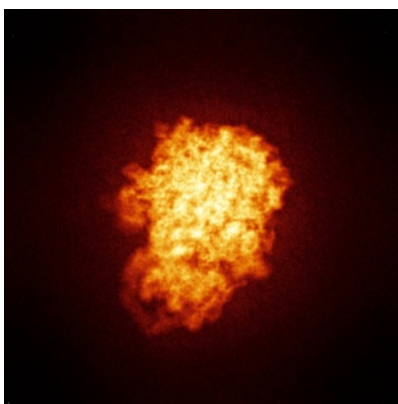
The images above show the largest variance slices of the map in three orthogonal directions.

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

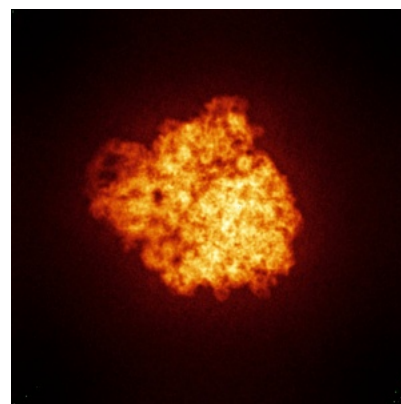
6.4.1 Primary map



X

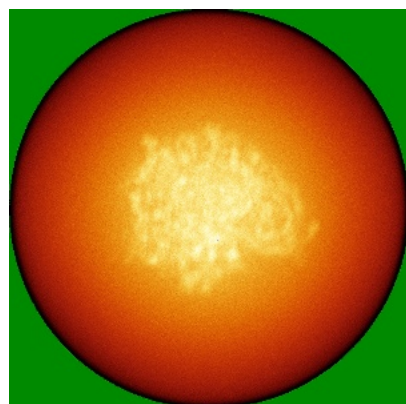


Y

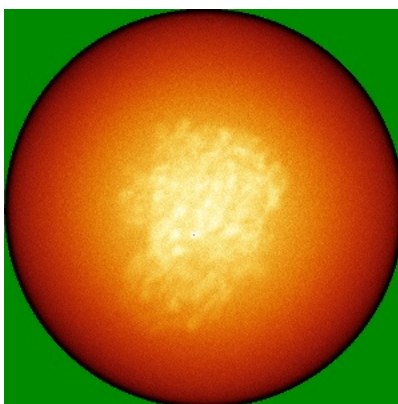


Z

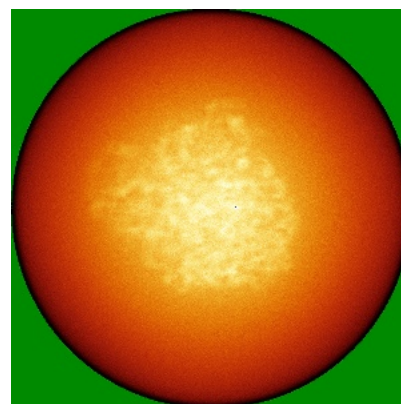
6.4.2 Raw map



X



Y

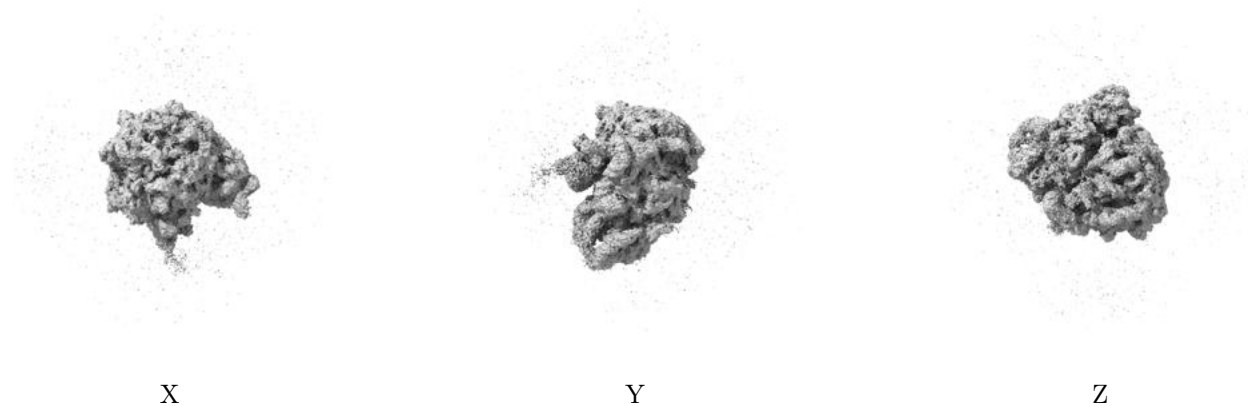


Z

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.

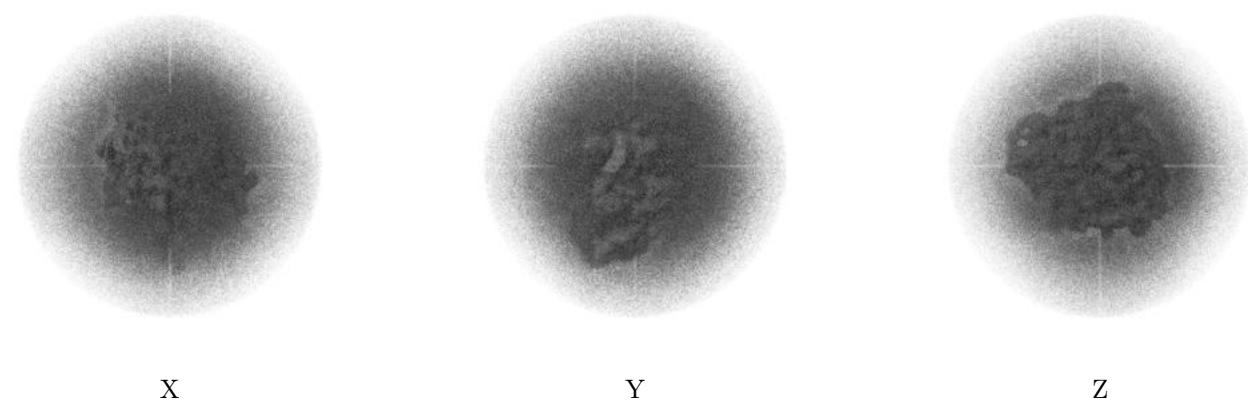
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. 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.

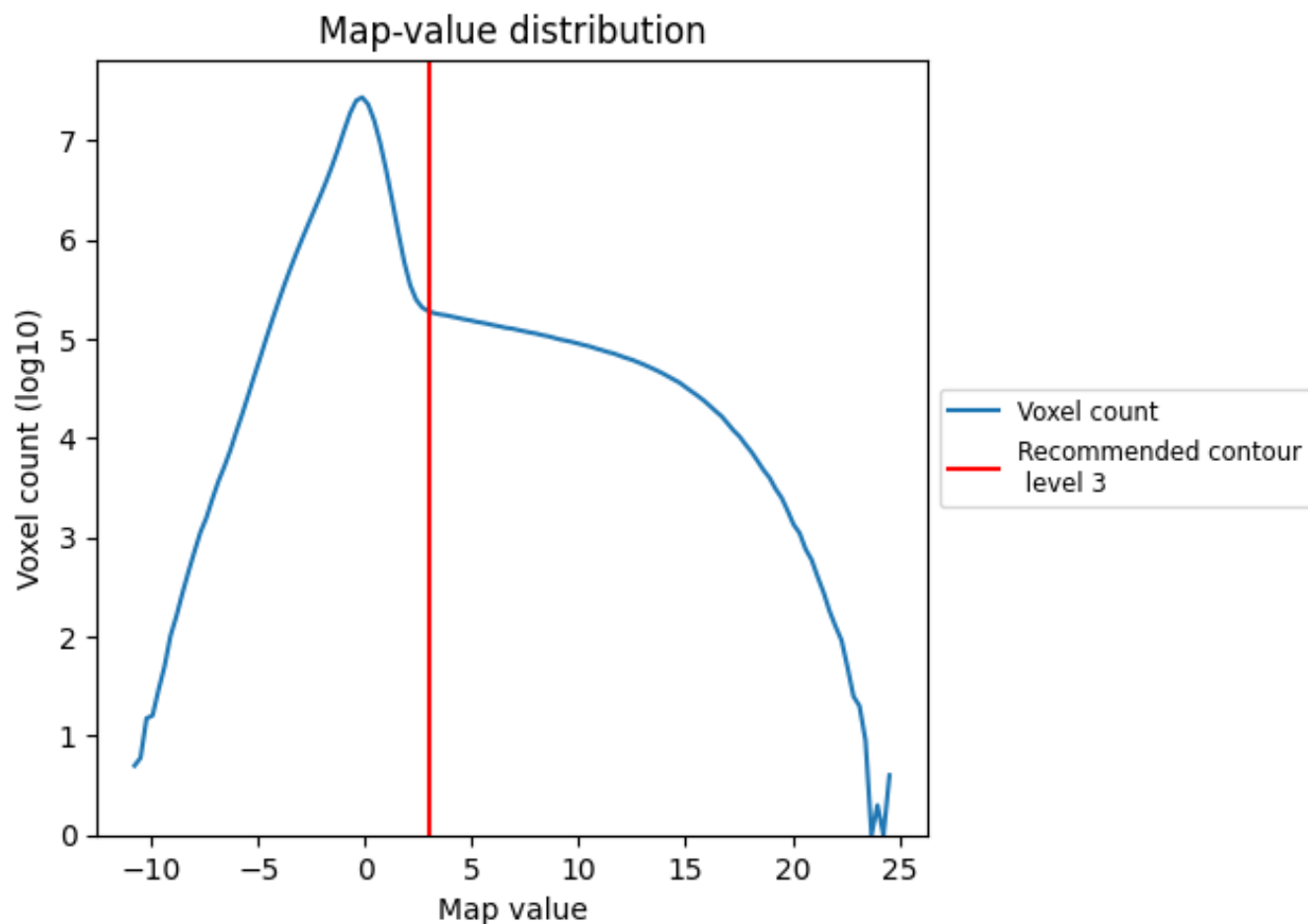
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

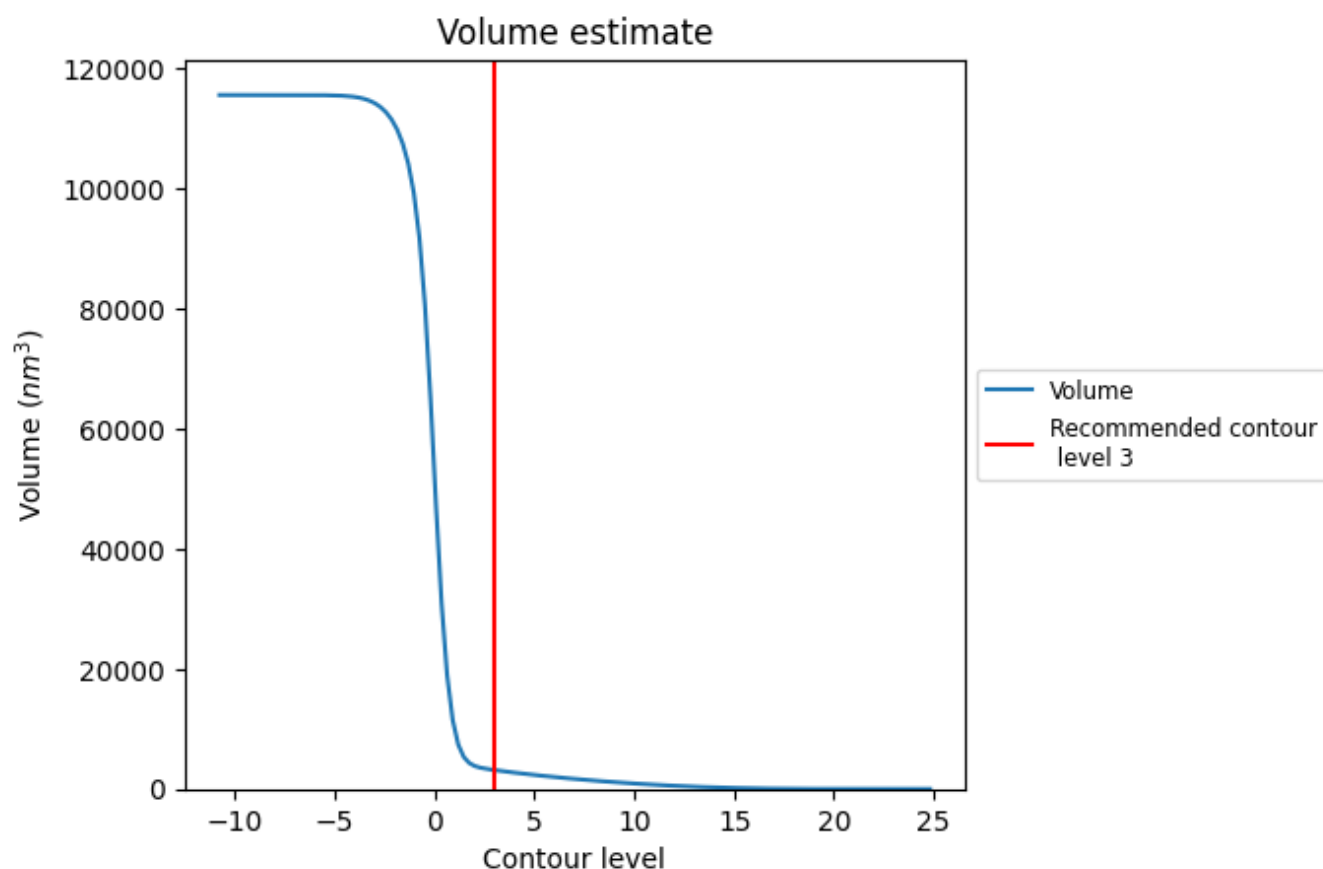
This section contains the results of statistical analysis of the map.

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.

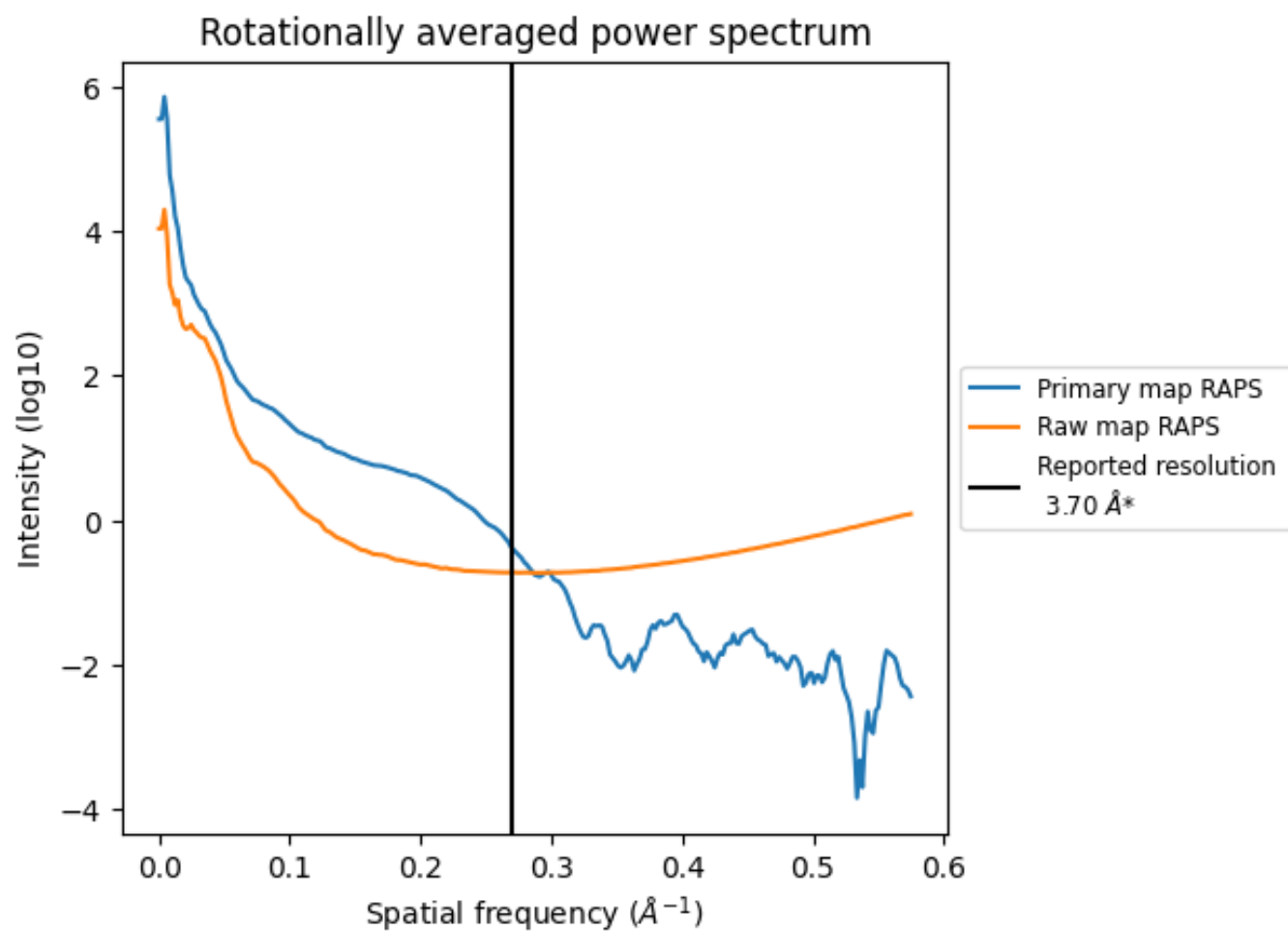
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3143 nm^3 ; this corresponds to an approximate mass of 2839 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 ⓘ

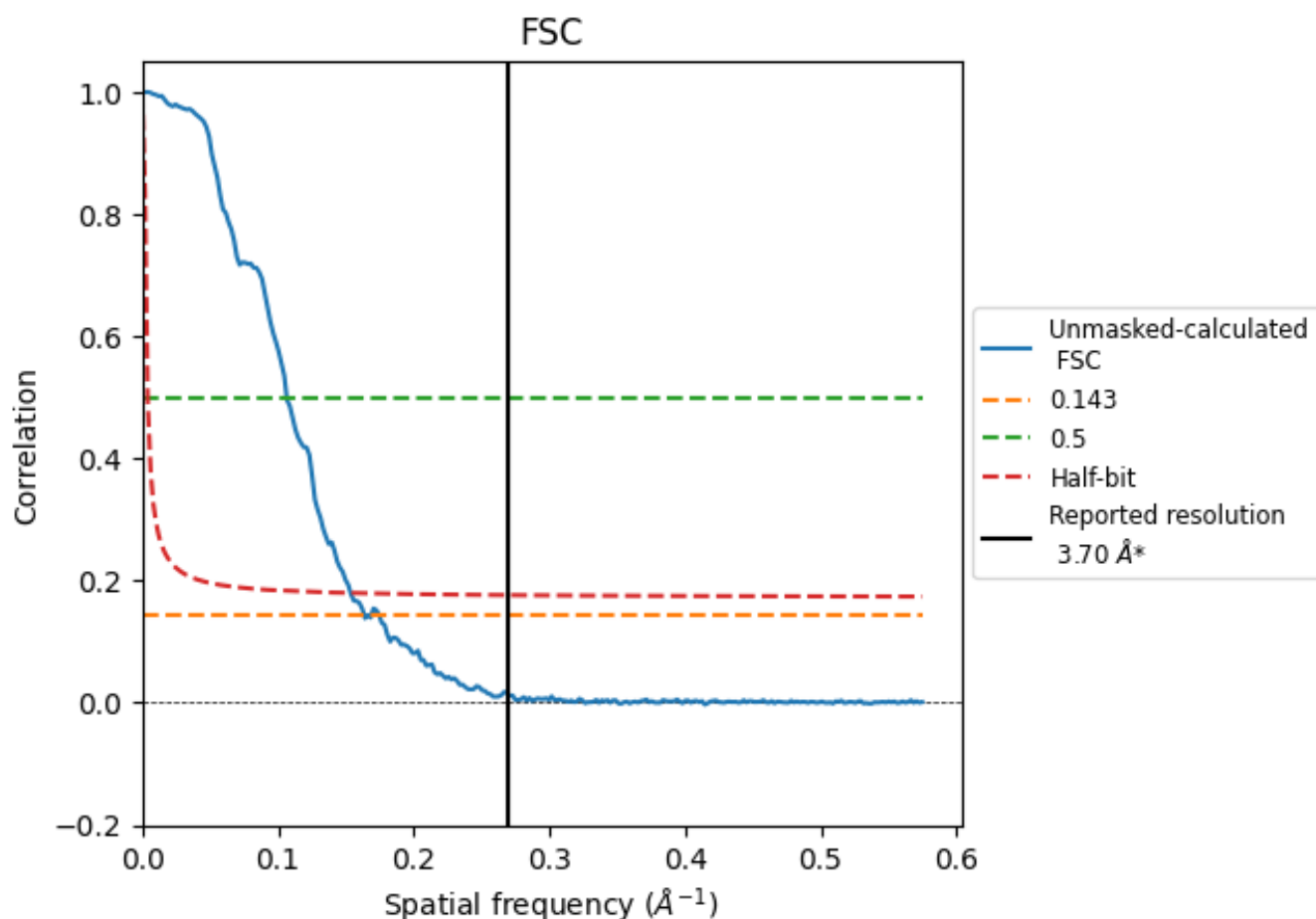


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

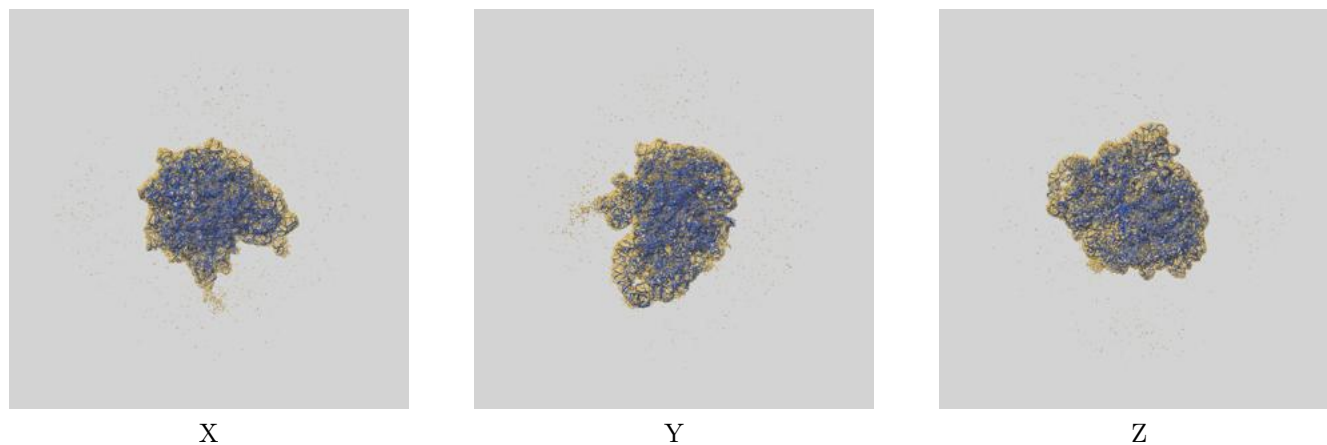
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.12	9.39	6.51

*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 6.12 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43491 and PDB model 8VSA. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



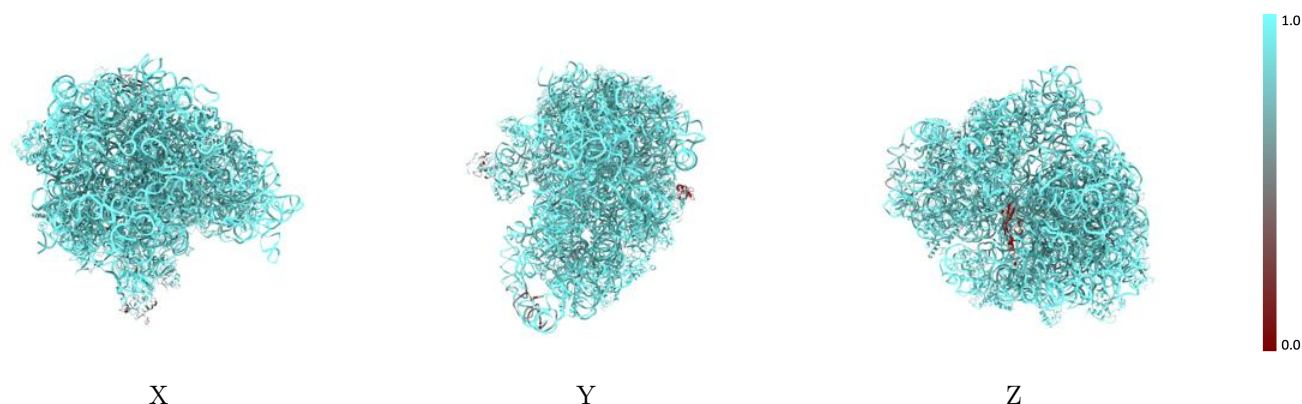
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



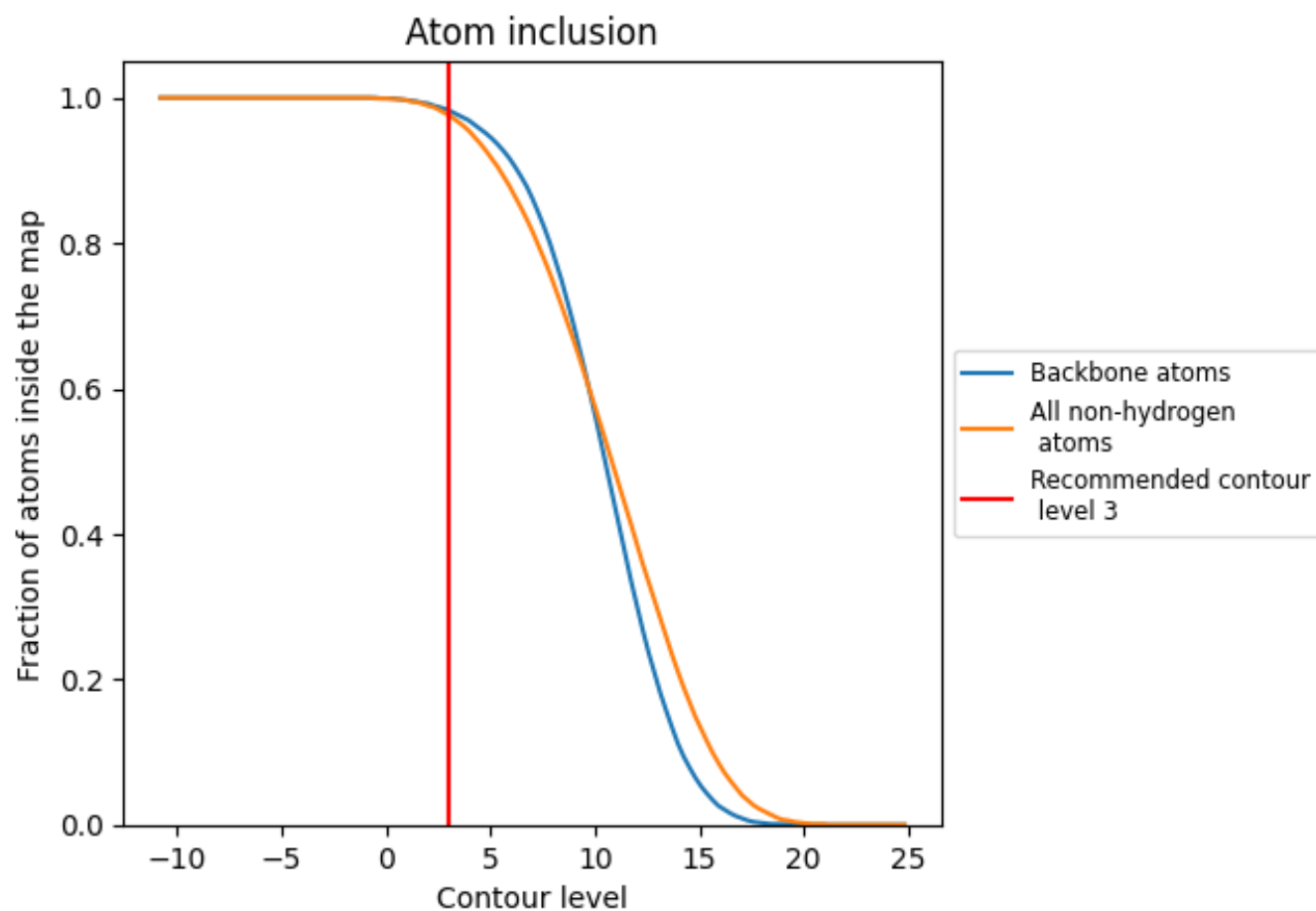
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9760	 0.3370
16S	 0.9980	 0.3320
23S	 0.9980	 0.3620
5S	 0.9980	 0.3300
ATRN	 0.9940	 0.3320
L02	 0.9710	 0.3920
L03	 0.9700	 0.3820
L04	 0.9680	 0.3500
L05	 0.9770	 0.2830
L06	 0.9710	 0.3240
L09	 0.4100	 0.2890
L1	 0.8880	 0.2150
L10	 0.7050	 0.1920
L11	 0.8460	 0.1940
L13	 0.9770	 0.3650
L14	 0.9310	 0.3940
L15	 0.9700	 0.3610
L16	 0.9600	 0.3710
L17	 0.9860	 0.3570
L18	 0.9940	 0.3270
L19	 0.9490	 0.3740
L20	 0.9750	 0.3470
L21	 0.9800	 0.3670
L22	 0.9430	 0.3630
L23	 0.9570	 0.3590
L24	 0.9640	 0.3390
L25	 0.9730	 0.3490
L27	 0.9710	 0.3670
L28	 0.9630	 0.3520
L29	 0.9640	 0.3020
L30	 0.9540	 0.3510
L31	 0.9680	 0.2220
L32	 0.9440	 0.3740
L33	 0.9800	 0.3490
L34	 0.9800	 0.3680



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Chain	Atom inclusion	Q-score
L35	 0.9880	 0.3820
L36	 0.9930	 0.3920
S02	 0.9310	 0.3190
S03	 0.9590	 0.3150
S04	 0.9740	 0.2870
S05	 0.9700	 0.3560
S06	 0.9370	 0.3290
S07	 0.9390	 0.2910
S08	 0.9600	 0.3370
S09	 0.9780	 0.2780
S10	 0.9440	 0.3130
S11	 0.9810	 0.3520
S12	 0.9350	 0.3450
S13	 0.9680	 0.2790
S14	 0.9790	 0.2980
S15	 0.9750	 0.3180
S16	 0.9860	 0.3290
S17	 0.9730	 0.3180
S18	 0.9770	 0.3310
S19	 0.9920	 0.3040
S20	 0.9740	 0.2690
S21	 0.9280	 0.3050
SMPB	 0.9220	 0.3130
TMRN	 0.9060	 0.2300