



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:10 AM UTC

PDB ID : 6BU8 / pdb_00006bu8
EMDB ID : EMD-7289
Title : 70S ribosome with S1 domains 1 and 2 (Class 1)
Authors : Loveland, A.B.; Korostelev, A.A.
Deposited on : 2017-12-08
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

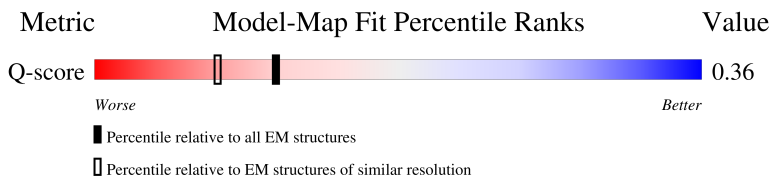
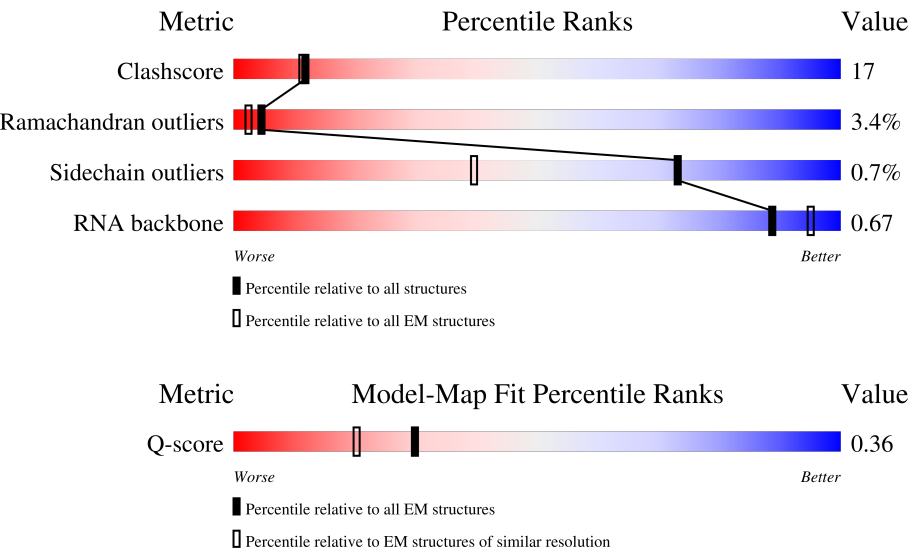
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.50 Å.

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



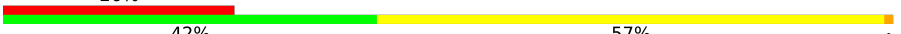
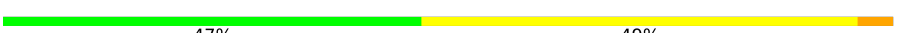
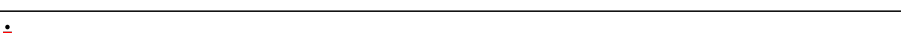
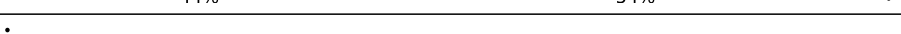
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	04	271	48% 49% .
2	05	209	56% 43%
3	06	201	48% 50% .

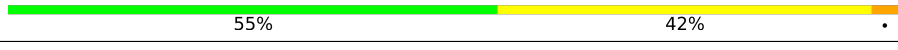
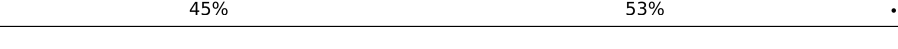
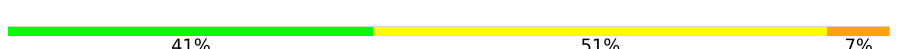
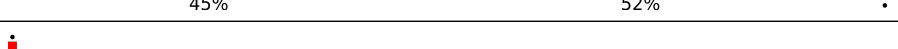
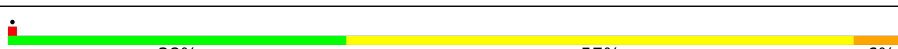
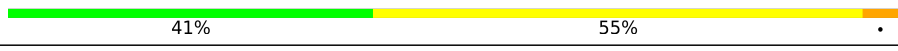
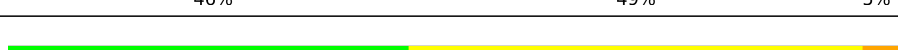
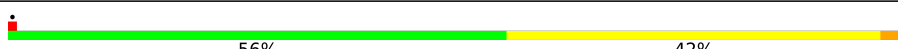
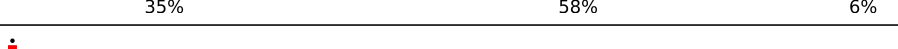
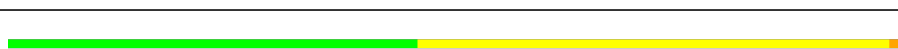
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Mol	Chain	Length	Quality of chain
4	07	177	
5	08	176	
6	09	149	
7	10	131	
8	11	141	
9	12	142	
10	13	122	
11	14	143	
12	15	136	
13	16	120	
14	17	116	
15	18	114	
16	19	117	
17	20	103	
18	21	110	
19	22	93	
20	23	102	
21	24	94	
22	25	75	
23	26	77	
24	27	63	
25	28	58	
26	29	66	
27	30	56	
28	31	50	

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Mol	Chain	Length	Quality of chain
29	32	46	
30	33	64	
31	34	38	
32	B	225	
33	C	206	
34	D	205	
35	E	157	
36	F	126	
37	G	151	
38	H	129	
39	I	127	
40	J	98	
41	K	116	
42	L	123	
43	M	114	
44	N	100	
45	O	88	
46	P	82	
47	Q	80	
48	R	65	
49	S	79	
50	T	85	
51	U	65	
52	03	223	
53	A	1539	

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Mol	Chain	Length	Quality of chain
54	01	2903	
55	02	120	
56	W	77	
56	X	77	
57	V	27	
58	Y	76	
59	Z	554	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 152151 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	04	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	05	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	06	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	07	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	08	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	10	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	12	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	13	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	14	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	15	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	16	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	17	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	18	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	19	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	20	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	21	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	22	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	23	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	24	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	25	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	26	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	27	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	28	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	29	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	30	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	31	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	32	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	33	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	34	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	C	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

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

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	E	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	F	126	Total	C	N	O	S	0	0
			1028	638	189	194	7		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	G	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

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

- Molecule 39 is a protein called 30S ribosomal protein S9.

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

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	J	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

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

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	M	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

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

- Molecule 45 is a protein called 30S ribosomal protein S15.

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

- Molecule 46 is a protein called 30S ribosomal protein S16.

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

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	R	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

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

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	U	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	03	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	01	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
01	747	C	U	SEE REMARK 999	GB 802133627

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	02	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
02	120	A	-	SEE REMARK 999	GB 1266961702

- Molecule 56 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	X	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
56	W	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	V	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

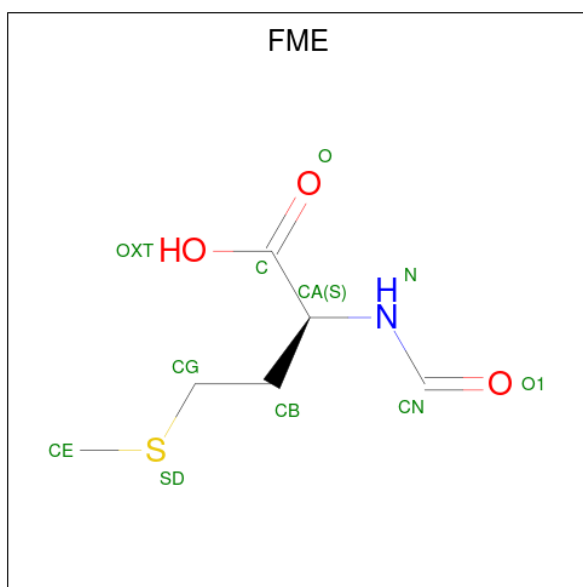
- Molecule 58 is a RNA chain called tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Y	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 59 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	Z	156	Total	C	N	O	0	0
			1204	760	209	235		

- Molecule 60 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).

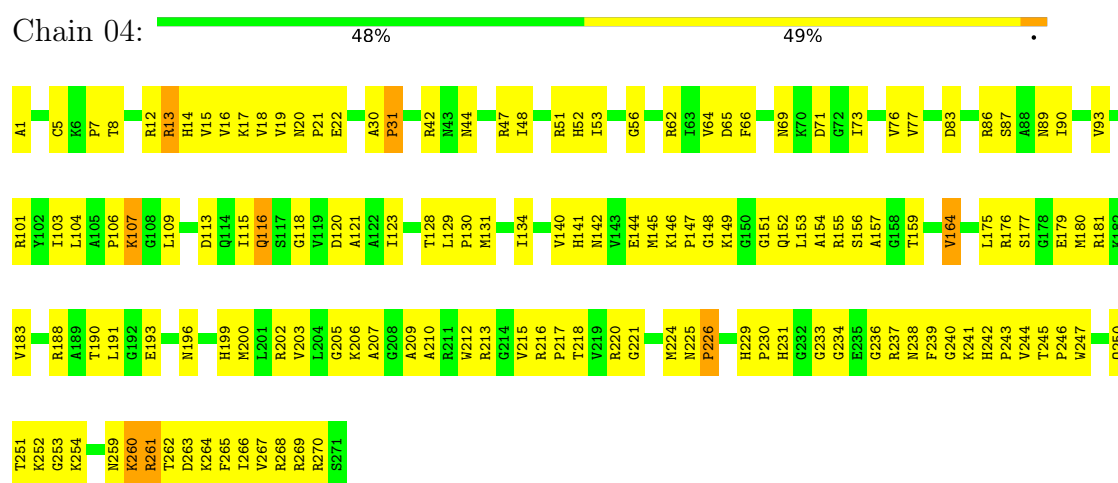


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
60	W	1	10	6	1	2	1	0

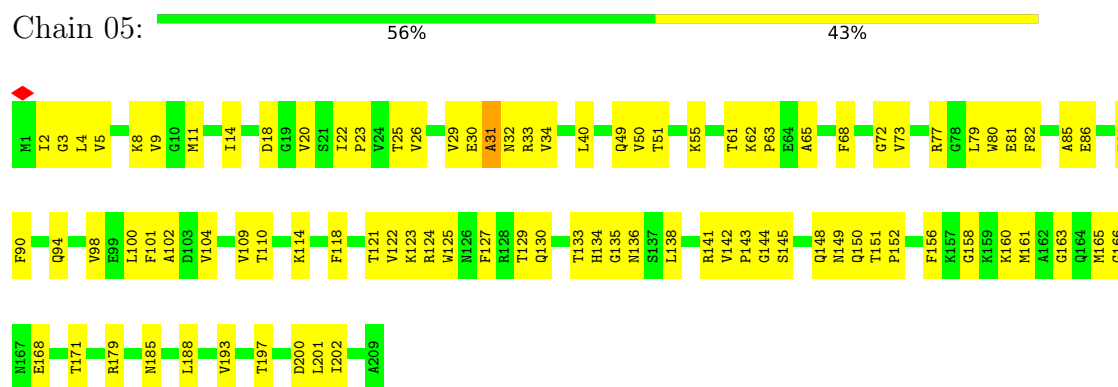
3 Residue-property plots

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

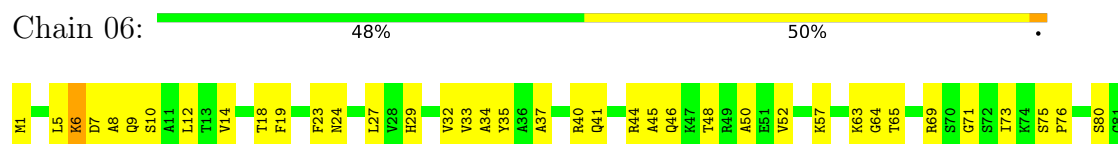
• Molecule 1: 50S ribosomal protein L2

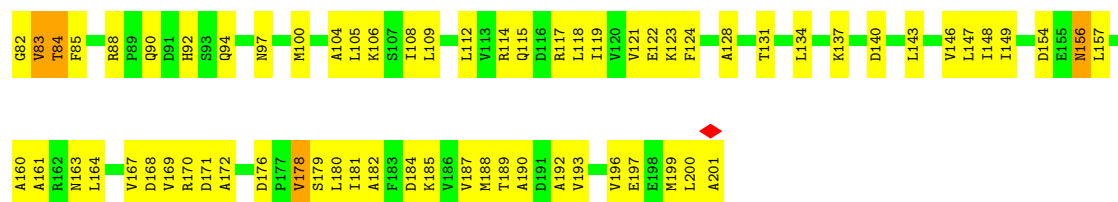


• Molecule 2: 50S ribosomal protein L3



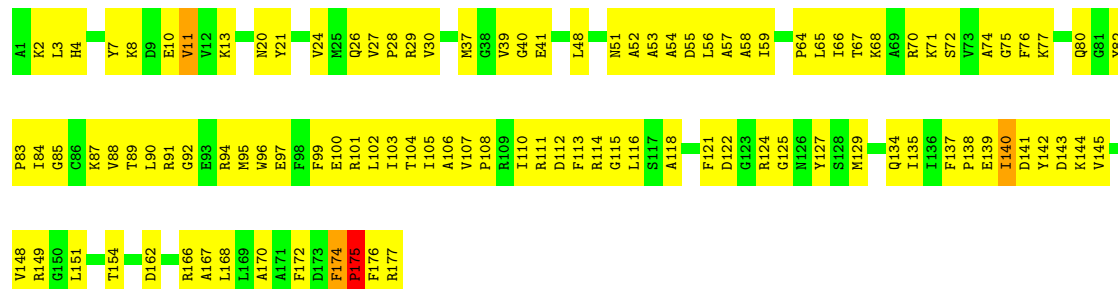
• Molecule 3: 50S ribosomal protein L4





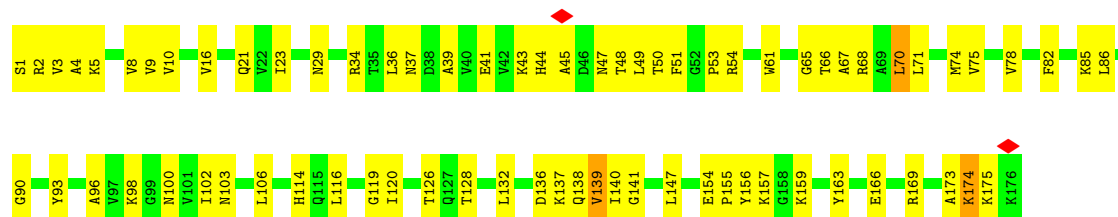
• Molecule 4: 50S ribosomal protein L5

Chain 07: 40% 58% ..



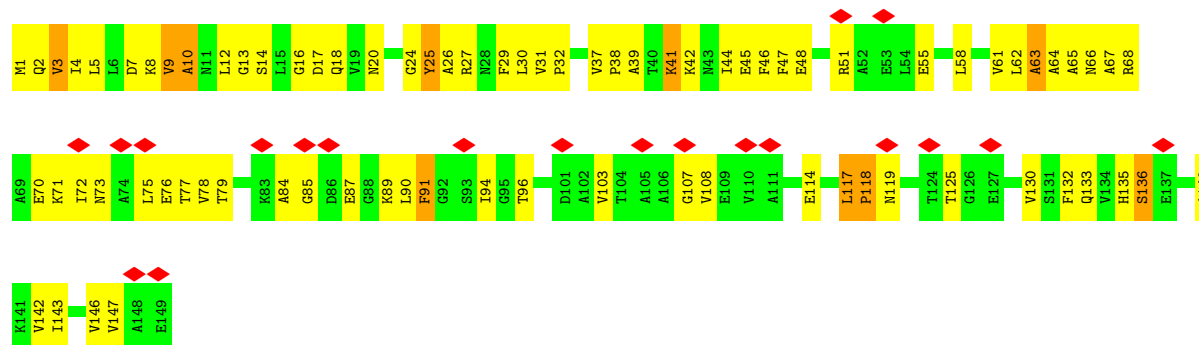
• Molecule 5: 50S ribosomal protein L6

Chain 08: 59% 40% .



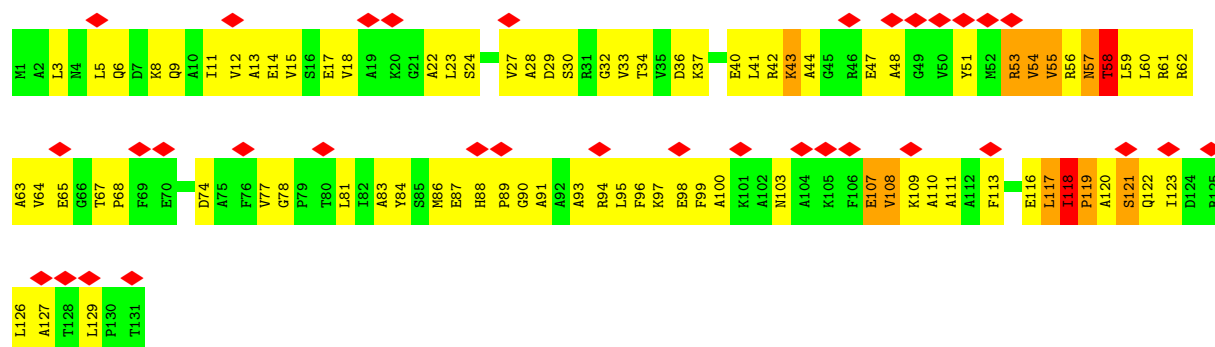
• Molecule 6: 50S ribosomal protein L9

Chain 09: 13% 46% 47% 7%

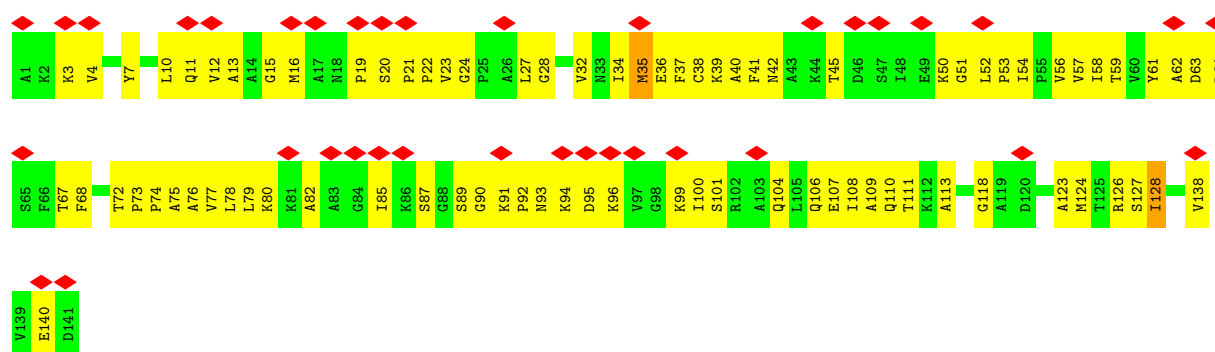
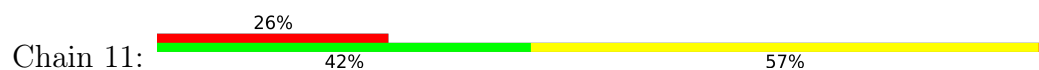


• Molecule 7: 50S ribosomal protein L10

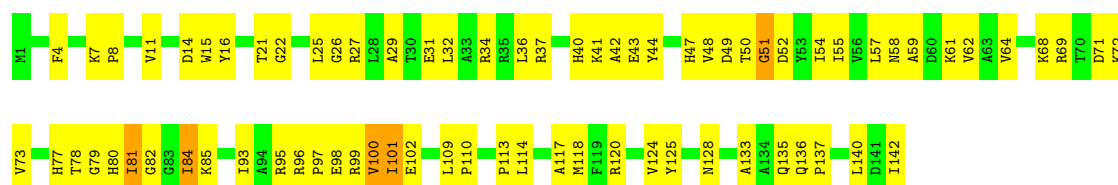
Chain 10: 26% 35% 56% 8%



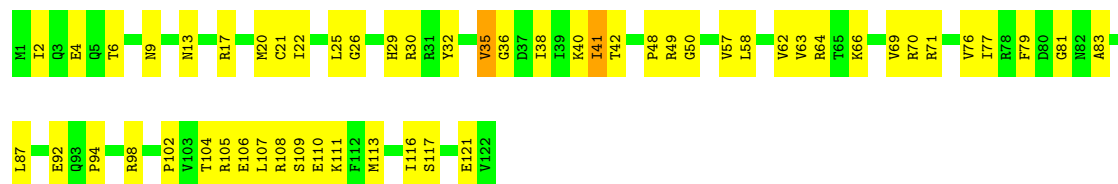
• Molecule 8: 50S ribosomal protein L11



• Molecule 9: 50S ribosomal protein L13

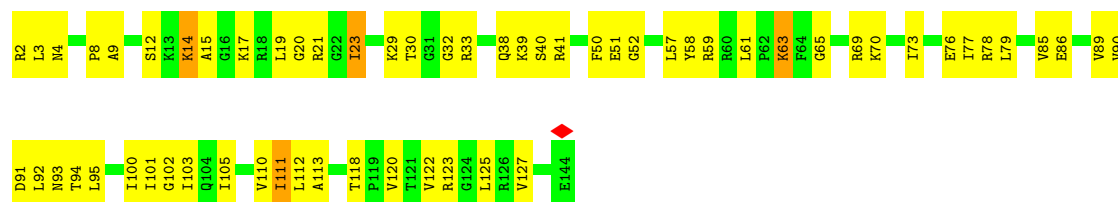


• Molecule 10: 50S ribosomal protein L14

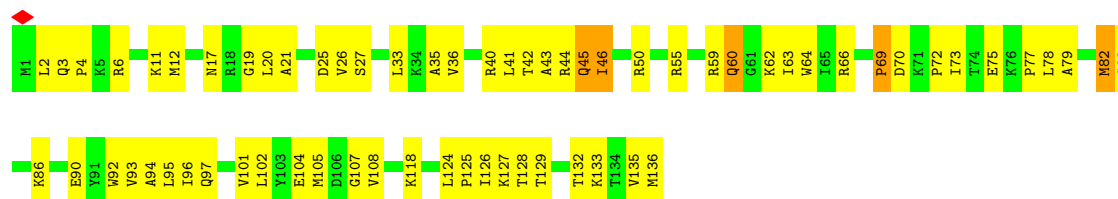


• Molecule 11: 50S ribosomal protein L15

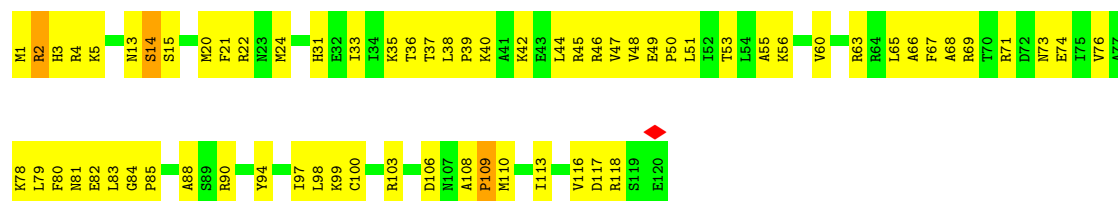




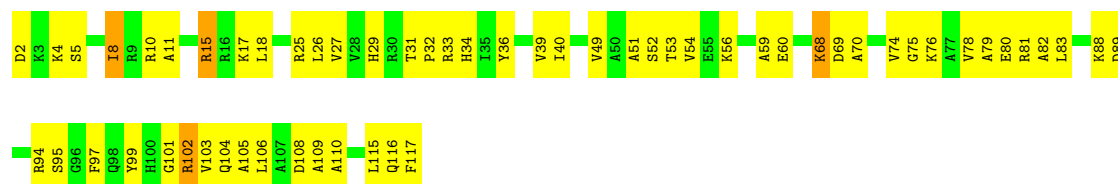
- Molecule 12: 50S ribosomal protein L16



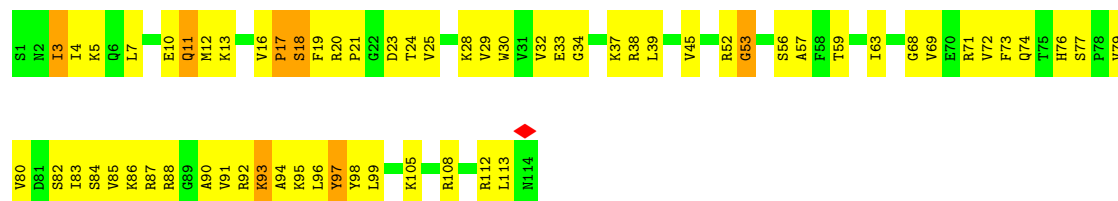
- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18



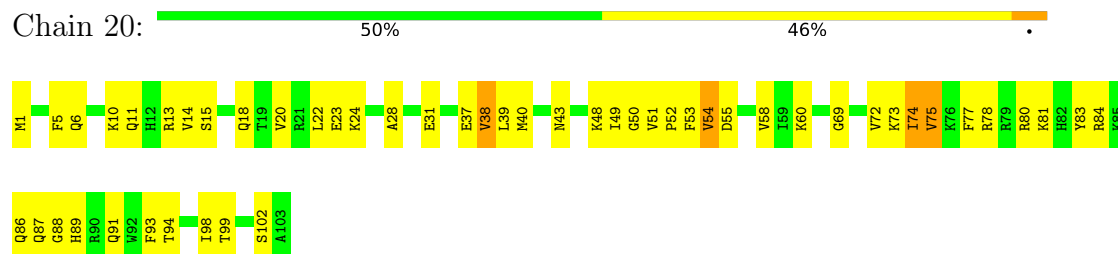
- Molecule 15: 50S ribosomal protein L19



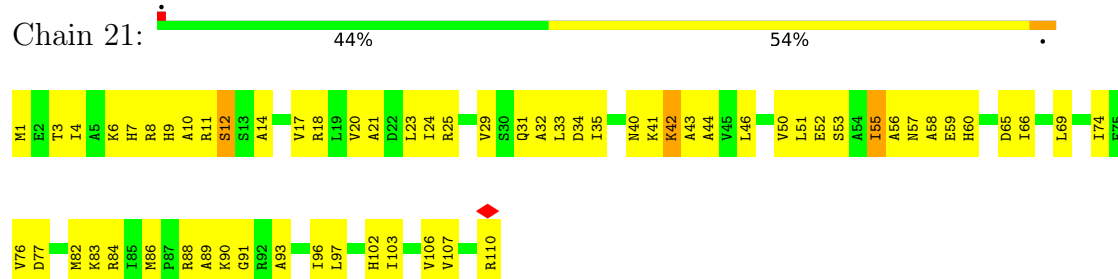
- Molecule 16: 50S ribosomal protein L20



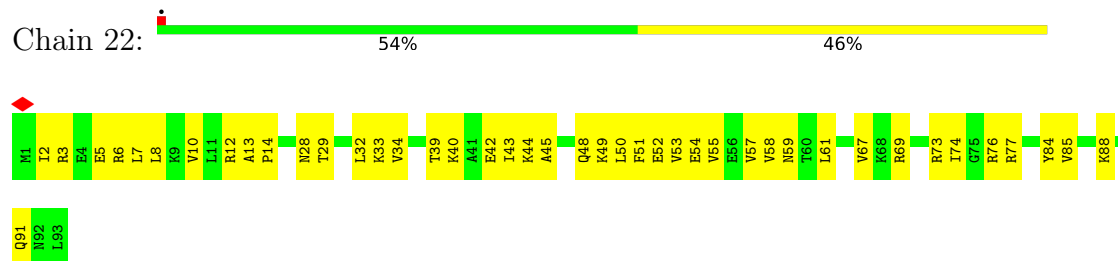
- Molecule 17: 50S ribosomal protein L21



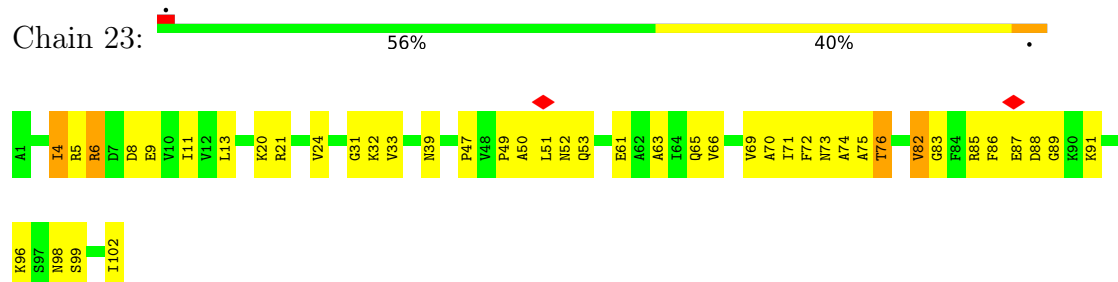
- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23



- Molecule 20: 50S ribosomal protein L24



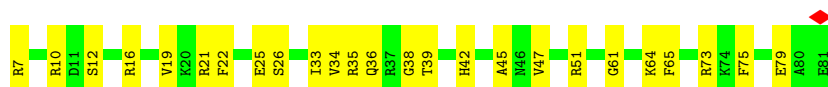
- Molecule 21: 50S ribosomal protein L25

Chain 24:  62% 37%



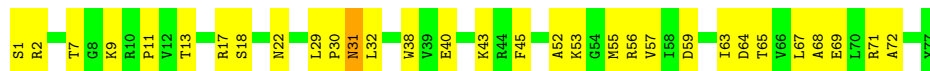
- Molecule 22: 50S ribosomal protein L27

Chain 25:  67% 33%



- Molecule 23: 50S ribosomal protein L28

Chain 26:  60% 39%



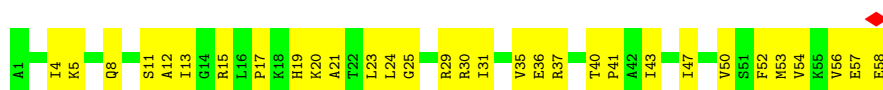
- Molecule 24: 50S ribosomal protein L29

Chain 27:  5% 51% 44% 5%



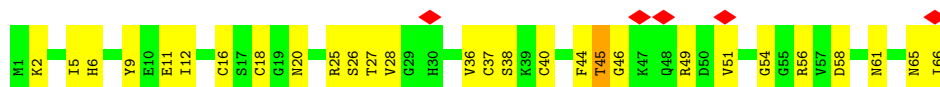
- Molecule 25: 50S ribosomal protein L30

Chain 28:  47% 53%



- Molecule 26: 50S ribosomal protein L31

Chain 29:  8% 58% 41%



- Molecule 27: 50S ribosomal protein L32

Chain 30:  36% 61%



- Molecule 28: 50S ribosomal protein L33



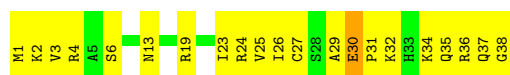
- Molecule 29: 50S ribosomal protein L34



- Molecule 30: 50S ribosomal protein L35



- Molecule 31: 50S ribosomal protein L36

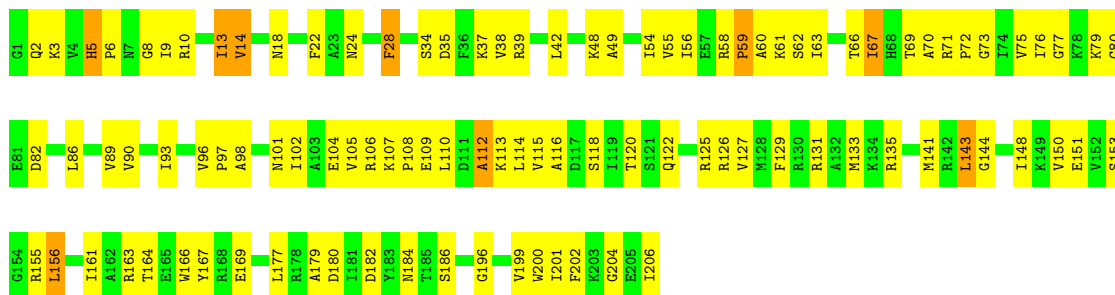


- Molecule 32: 30S ribosomal protein S2



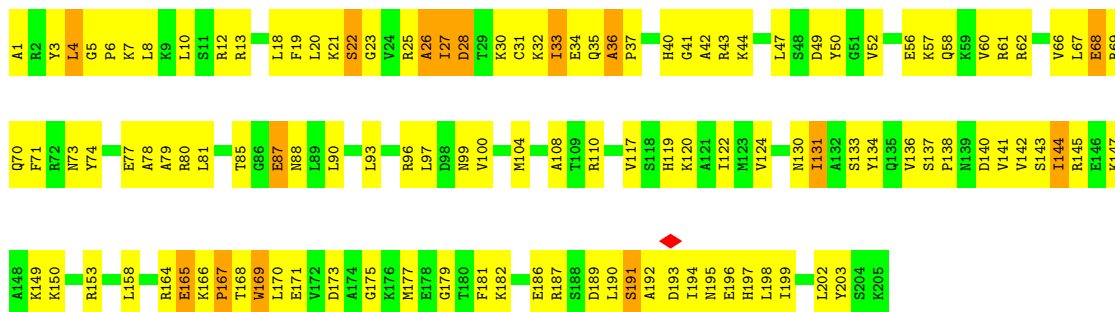
- Molecule 33: 30S ribosomal protein S3





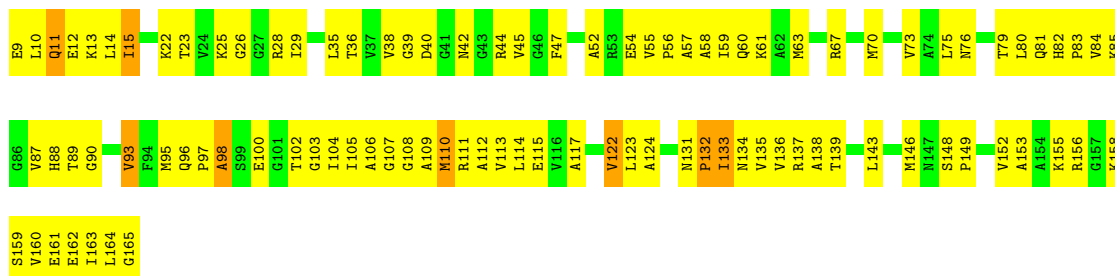
• Molecule 34: 30S ribosomal protein S4

Chain D: 41% 51% 7%



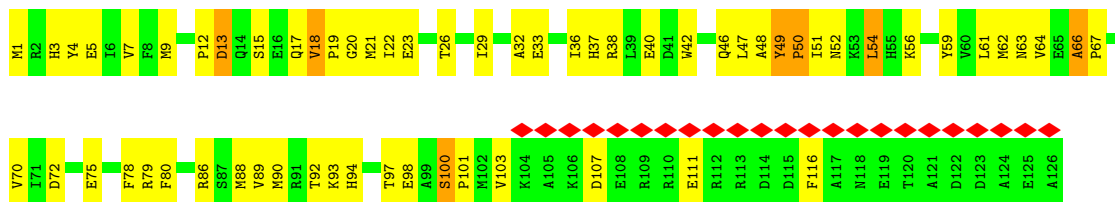
• Molecule 35: 30S ribosomal protein S5

Chain E: 38% 57% 5%



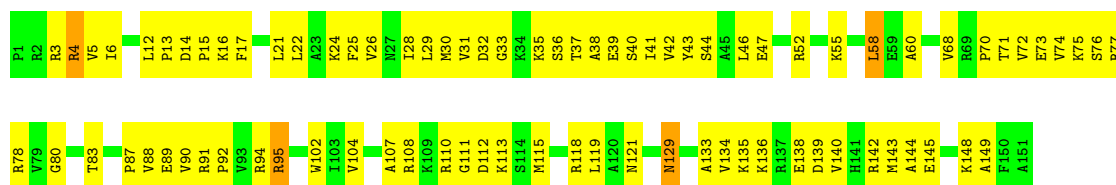
• Molecule 36: 30S ribosomal protein S6

Chain F: 18% 51% 44% 6%

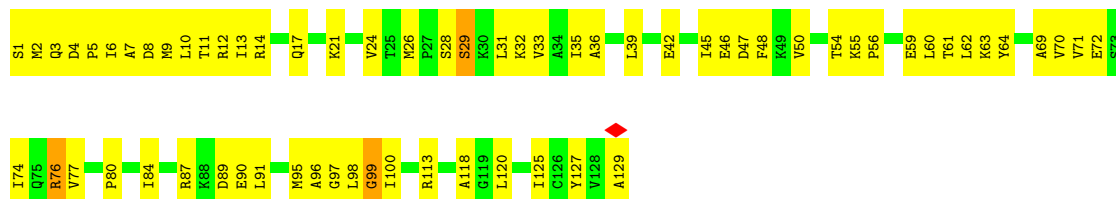


• Molecule 37: 30S ribosomal protein S7

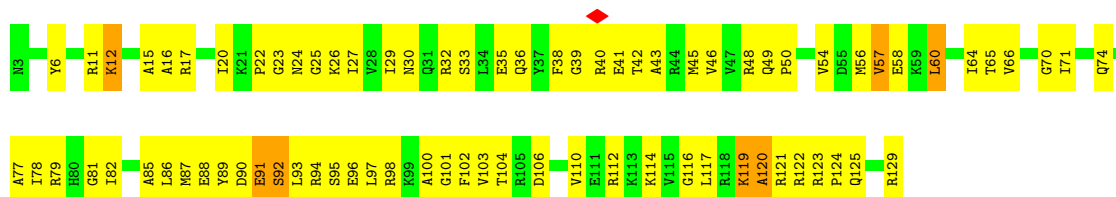
Chain G: 45% 52%



- Molecule 38: 30S ribosomal protein S8



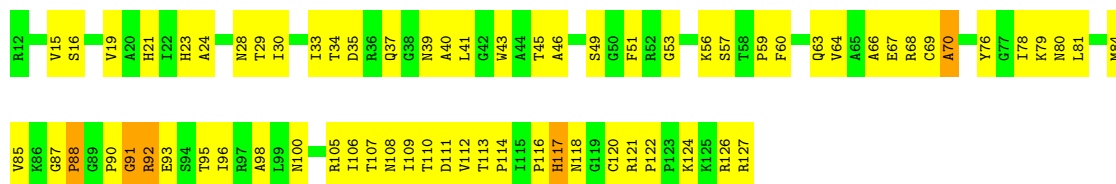
- Molecule 39: 30S ribosomal protein S9



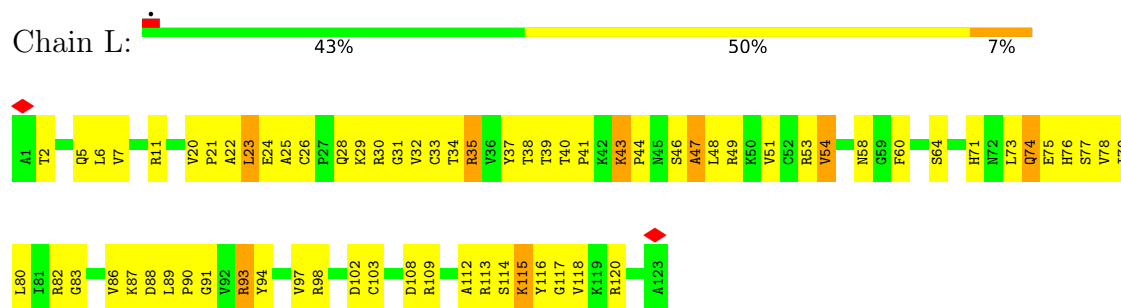
- Molecule 40: 30S ribosomal protein S10



- Molecule 41: 30S ribosomal protein S11



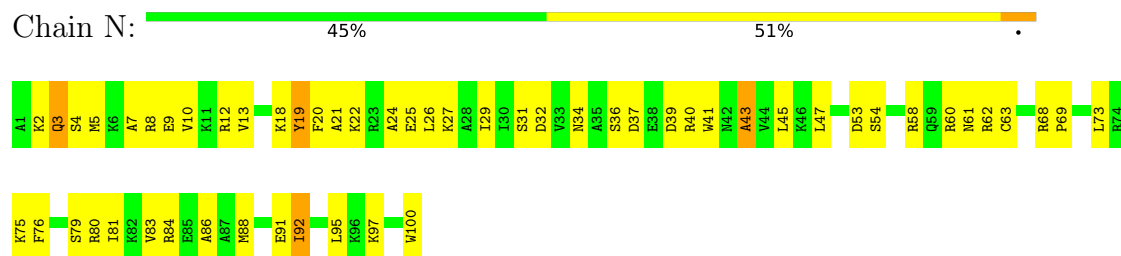
- Molecule 42: 30S ribosomal protein S12



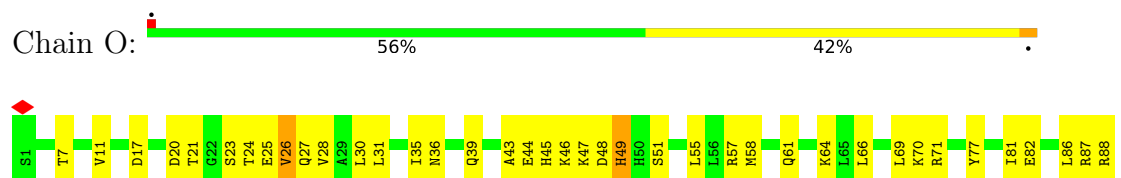
- Molecule 43: 30S ribosomal protein S13



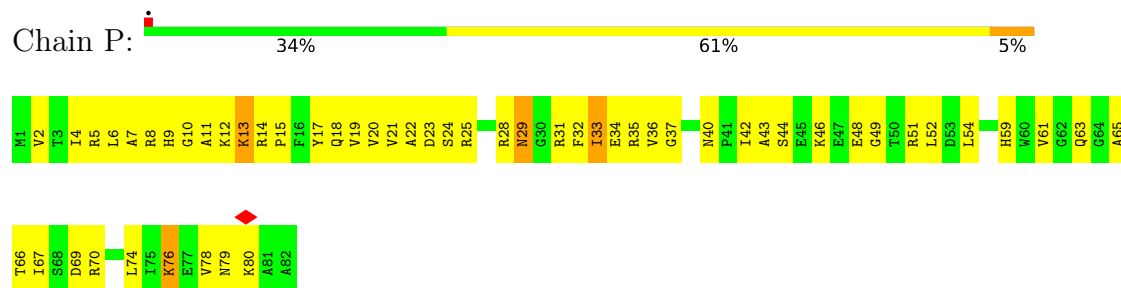
- Molecule 44: 30S ribosomal protein S14



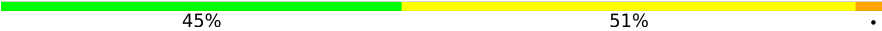
- Molecule 45: 30S ribosomal protein S15



- Molecule 46: 30S ribosomal protein S16



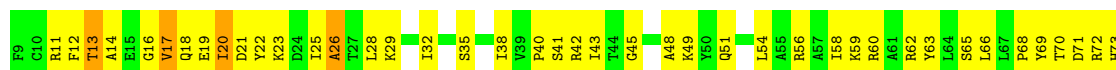
- Molecule 47: 30S ribosomal protein S17

Chain Q: 



- Molecule 48: 30S ribosomal protein S18

Chain R: 

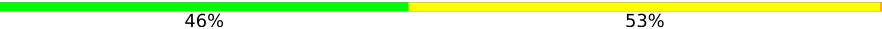


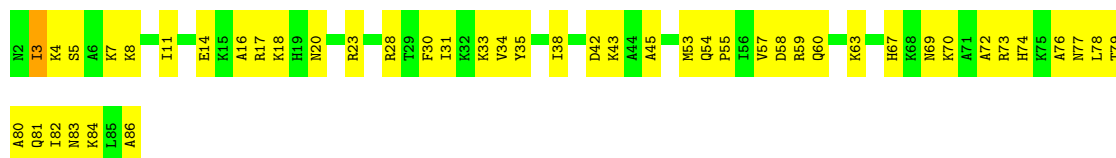
- Molecule 49: 30S ribosomal protein S19

Chain S: 



- Molecule 50: 30S ribosomal protein S20

Chain T: 



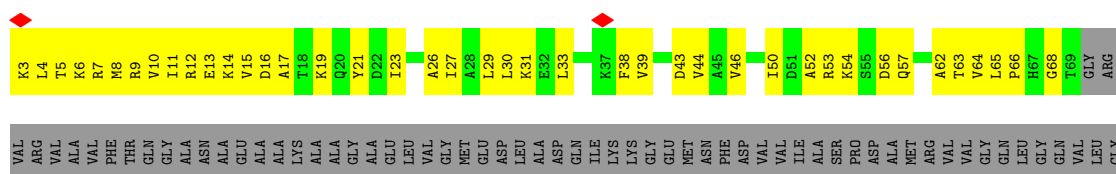
- Molecule 51: 30S ribosomal protein S21

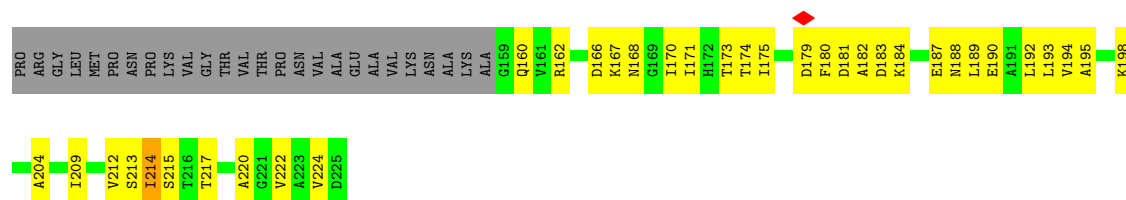
Chain U: 



- Molecule 52: 50S ribosomal protein L1

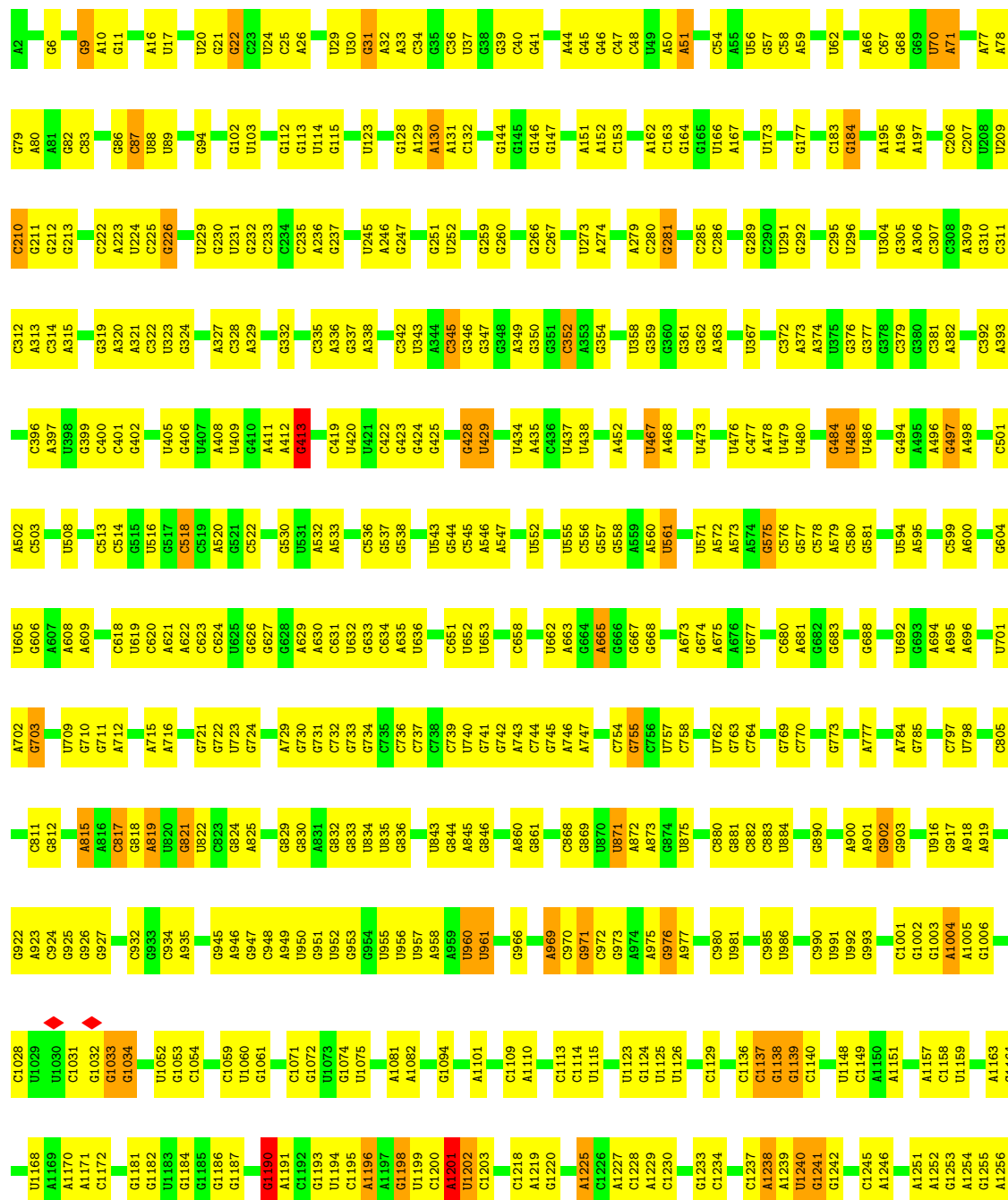
Chain 03: 





• Molecule 53: 16S ribosomal RNA

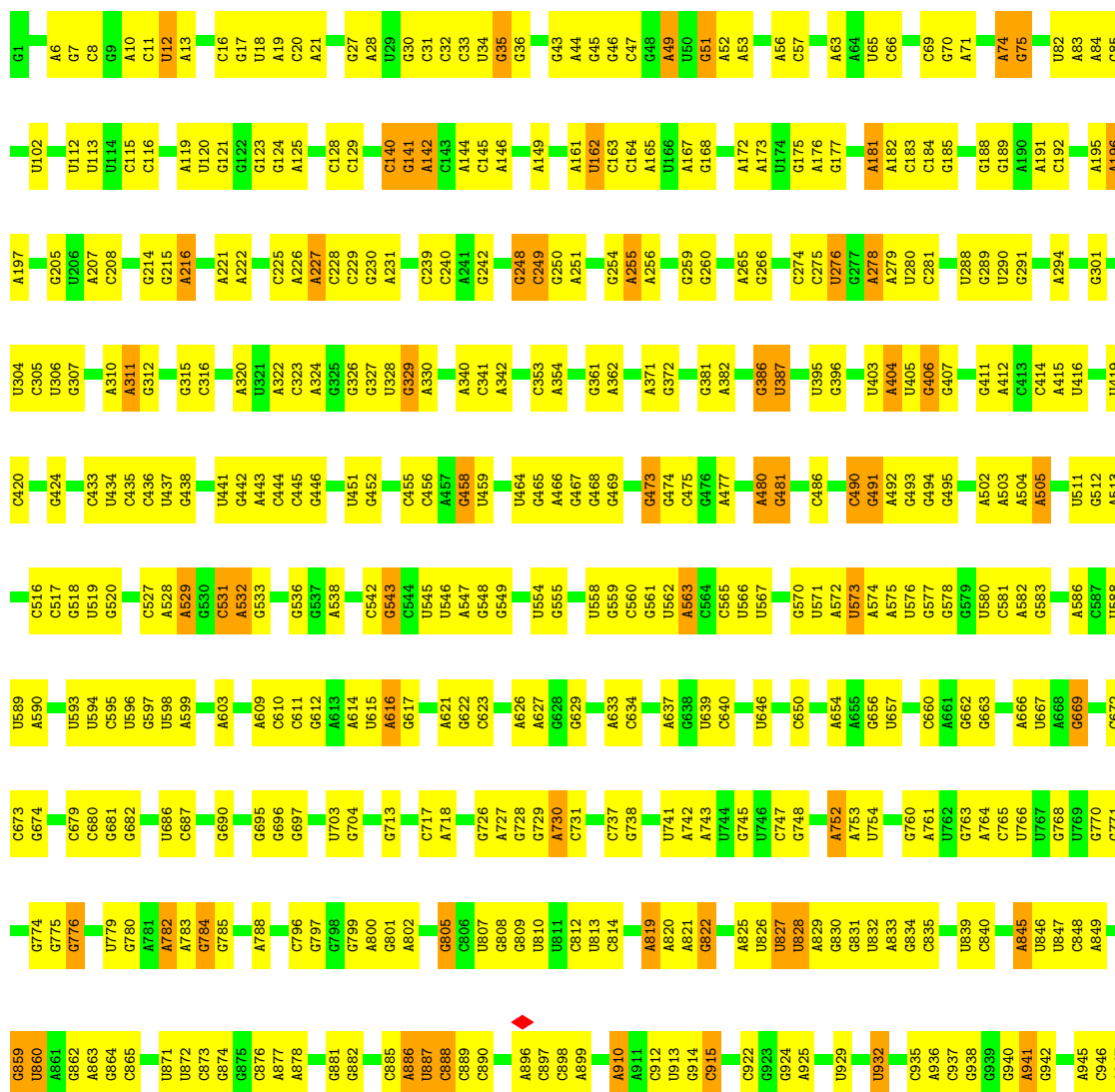
Chain A: 57% 38%



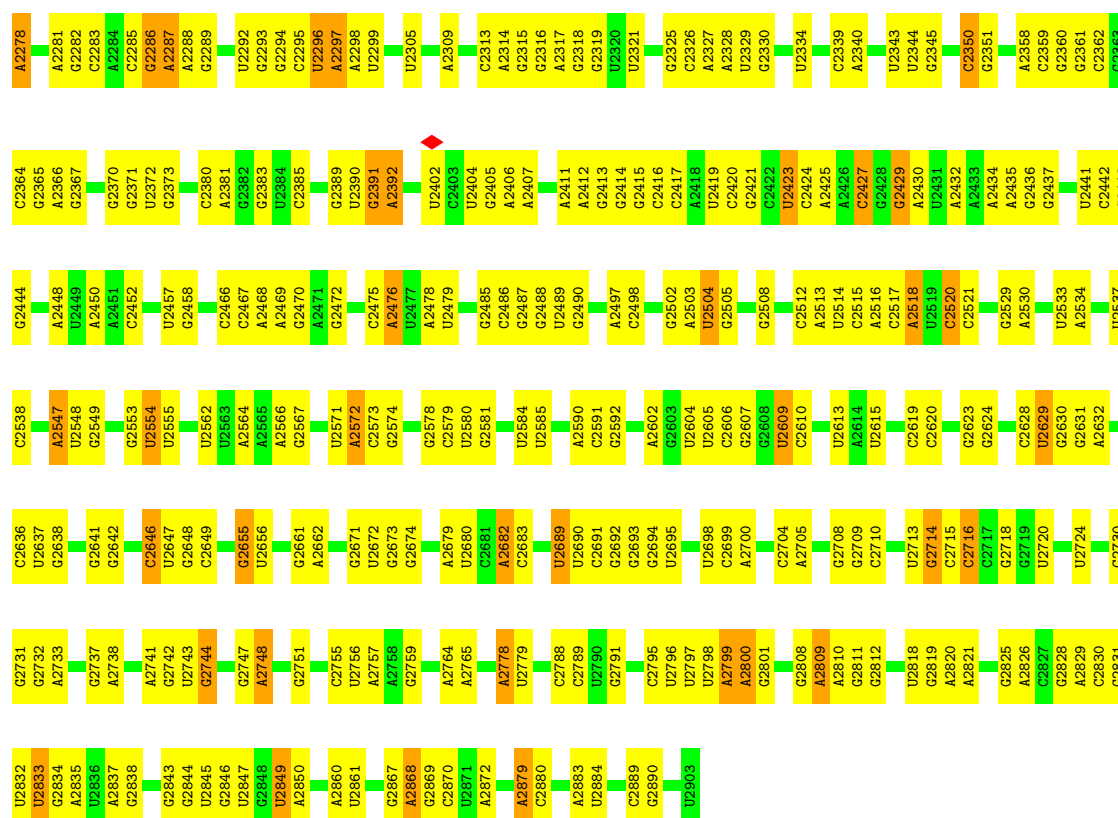


• Molecule 54: 23S ribosomal RNA

Chain 01: 54% 41% 5%



C948	C949	C950	C951	G952	G953	G954	G955	G956	C961	G962	C968	G969	G970	G971	A972	A973	G974	A975	A980	A981	G982	G983	A984	G989	C995	A996	G997	A1001	G1002	C1007	U1012	C1013	U1018	U1019	A1020	A1021	G1022	U1023	G1026	A1027	A1032	U1033	G1034	U1035	G1036	G1037	A1038	A1039		
C1045	A1046	G1047	C1053	A1054	G1055	G1056	G1059	U1060	U1061	G1062	G1063	C1064	U1065	U1066	A1067	A1070	G1071	C1075	A1076	A1077	U1078	A1080	U1083	A1084	A1085	A1088	C1092	G1093	U1097	A1098	C1101	C1102	A1103	C1104	U1105	G1106	G1110	A1111	G1112	U1113	G1122	A1128	A1129	U1130	G1131	U1132				
A1133	A1134	C1135	G1138	A1139	C1140	U1141	A1142	A1143	G1149	C1150	C1153	G1154	A1155	U1066	A1156	G1157	C1161	G1162	U1174	A1175	U1176	G1177	G1179	U1180	U1181	G1182	U1183	U1184	G1185	G1186	G1187	U1188	A1189	G1190	G1191	C1196	G1197	U1201	G1202	U1203	A1204	A1205	U1209	G1210	G1211	A1213	U1219	G1220		
G1225	G1236	G1238	C1243	C1251	G1252	A1253	G1256	C1257	U1258	G1259	A1260	A1268	A1269	C1270	G1271	A1272	U1273	A1274	A1275	C1278	G1279	G1280	A1285	A1286	A1287	G1288	G1289	C1290	C1297	G1298	G1299	A1301	A1302	U1313	G1316	G1317	U1318	C1319	C1320	A1321	U1396	U1397	U1399	A1394	A1395	A1396	U1397	U1409	G1410	U1415
G1331	G1332	C1335	A1336	G1337	G1338	U1340	U1344	U1345	A1346	A1347	C1348	A1349	C1350	C1351	U1352	A1353	A1354	G1355	G1356	C1357	G1358	G1361	C1362	G1363	C1364	A1365	A1366	A1367	G1368	G1369	C1370	G1371	U1372	A1373	G1374	A1378	U1379	A1383	A1384	C1385	C1386	A1387	G1388	U1394	A1395	A1396	U1397	U1409	G1410	U1415
G1416	C1417	G1418	A1419	A1420	G1421	G1422	G1423	G1424	G1425	G1430	A1431	G1432	A1433	A1434	G1435	C1436	C1437	U1438	A1439	U1440	G1441	U1442	C1447	G1448	G1449	G1450	C1451	C1454	U1458	G1459	U1460	C1461	G1475	U1476	G1482	A1490	G1491	C1498	G1501	A1502	U1506	C1507	A1508	A1509	G1510	A1515	G1516	U1517		
G1524	A1525	C1526	G1527	A1528	G1529	C1533	U1534	A1535	G1536	G1537	G1538	U1539	A1540	C1541	U1542	G1543	A1544	A1545	A1548	A1549	G1555	C1558	U1559	G1560	C1561	U1562	U1563	C1564	G1565	A1566	A1569	A1570	A1571	A1572	G1581	U1584	C1585	A1586	G1587	U1594	C1595	A1596	A1597	A1598	U1599	A1603	A1608	A1609		
A1610	C1611	C1612	G1613	A1614	C1615	A1616	C1625	A1626	G1627	G1628	A1637	C1638	G1642	G1643	C1644	G1645	U1647	U1648	G1651	A1652	G1653	A1654	A1655	C1656	U1657	C1658	A1664	A1665	G1666	A1668	A1669	A1672	G1673	G1674	C1675	A1676	A1678	A1679	U1680	G1681	C1686	G1687	A1697	A1698	G1699	C1704	A1705			
G1715	U1720	G1721	U1729	C1730	U1736	A1737	G1738	A1749	G1750	G1753	U1758	A1759	C1760	C1764	G1770	C1771	A1772	A1773	C1774	U1775	G1776	U1779	A1780	U1781	G1784	A1785	A1786	A1787	C1788	A1789	C1790	A1791	A1794	C1795	U1796	G1797	U1798	G1799	C1800	A1801	A1802	A1803	C1804	A1805	C1806	A1807	A1808			
A1809	A1810	G1811	U1812	G1813	C1816	A1817	U1818	A1819	U1820	U1825	G1826	U1827	G1828	C1833	C1844	G1845	U1856	G1857	A1871	A1872	G1873	U1883	G1884	A1885	A1900	A1901	G1902	G1903	C1904	G1905	G1906	G1907	A1912	A1913	C1914	U1917	U1918	A1919	G1929	U1930	U1931	A1932	C1933	G1934	A1935	A1936				
A1937	A1938	U1943	U1944	G1949	U1950	U1951	A1952	A1953	G1954	U1955	U1956	C1957	C1961	C1962	U1963	G1964	A2051	A2052	G2053	A2054	C1967	A1970	U1971	G1972	G1973	A1978	U1979	G1980	G1983	G1992	U1993	C1996	C1997	A1998	C1999	C2000	C2001	G2010	U2011	G2012	A2015	A2019	A2020	C2021	U2022	U2023	G2024	C2025	U2026	U2027
A2030	A2031	U2034	G2035	C2036	A2037	G2038	U2039	G2040	U2041	A2042	C2043	C2044	C2045	G2049	C2050	A2051	A2052	G2053	A2054	C2055	G2056	A2060	G2061	A2062	C2065	C2066	C2067	U2068	G2069	A2070	A2071	C2072	C2078	U2079	A2080	U2081	A2082	G2083	U2086	G2087	A2088	C2096	A2097	U2098	C2101	C2104	U2105	U2106	G2110	U2111
G2112	U2113	U2118	A2119	G2120	G2121	U2122	G2123	G2124	G2125	A2126	G2127	G2128	C2129	U2130	U2131	U2132	U2133	U2134	U2139	G2140	G2141	G2144	C2145	C2146	A2147	U2151	U2155	A2156	G2157	A2158	G2159	G2162	A2163	C2164	A2171	U2172	C2173	C2175	A2176	C2177	U2180	A2183	A2184	G2187	U2188	U2189	G2190	G2191	A2191	
U2194	U2195	C2196	A2197	A2198	U2203	G2204	A2205	C2208	G2209	U2210	A2211	A2212	U2213	C2214	C2215	G2216	G2224	A2225	G2230	U2231	C2232	U2236	G2237	G2238	G2239	U2240	A2241	G2242	U2243	U2244	U2245	G2246	A2247	C2248	U2249	G2250	U2257	C2258	U2262	C2263	C2264	U2265	A2266	A2267	A2268	G2269	A2270	G2271	G2276	G2277



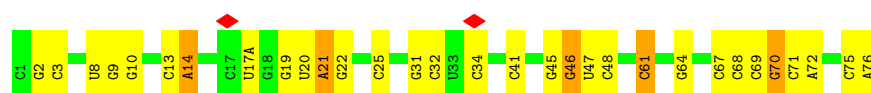
• Molecule 55: 5S ribosomal RNA

Chain 02: 55% 37% 8%



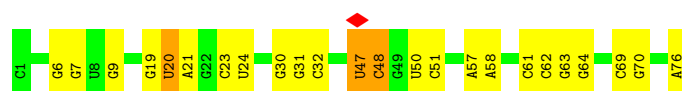
• Molecule 56: tRNA^{fMet}

Chain X: 60% 34% 6%

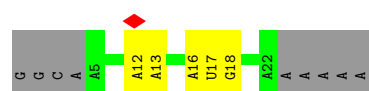


• Molecule 56: tRNA^{fMet}

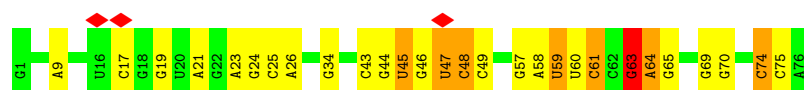
Chain W: 69% 27% 4%



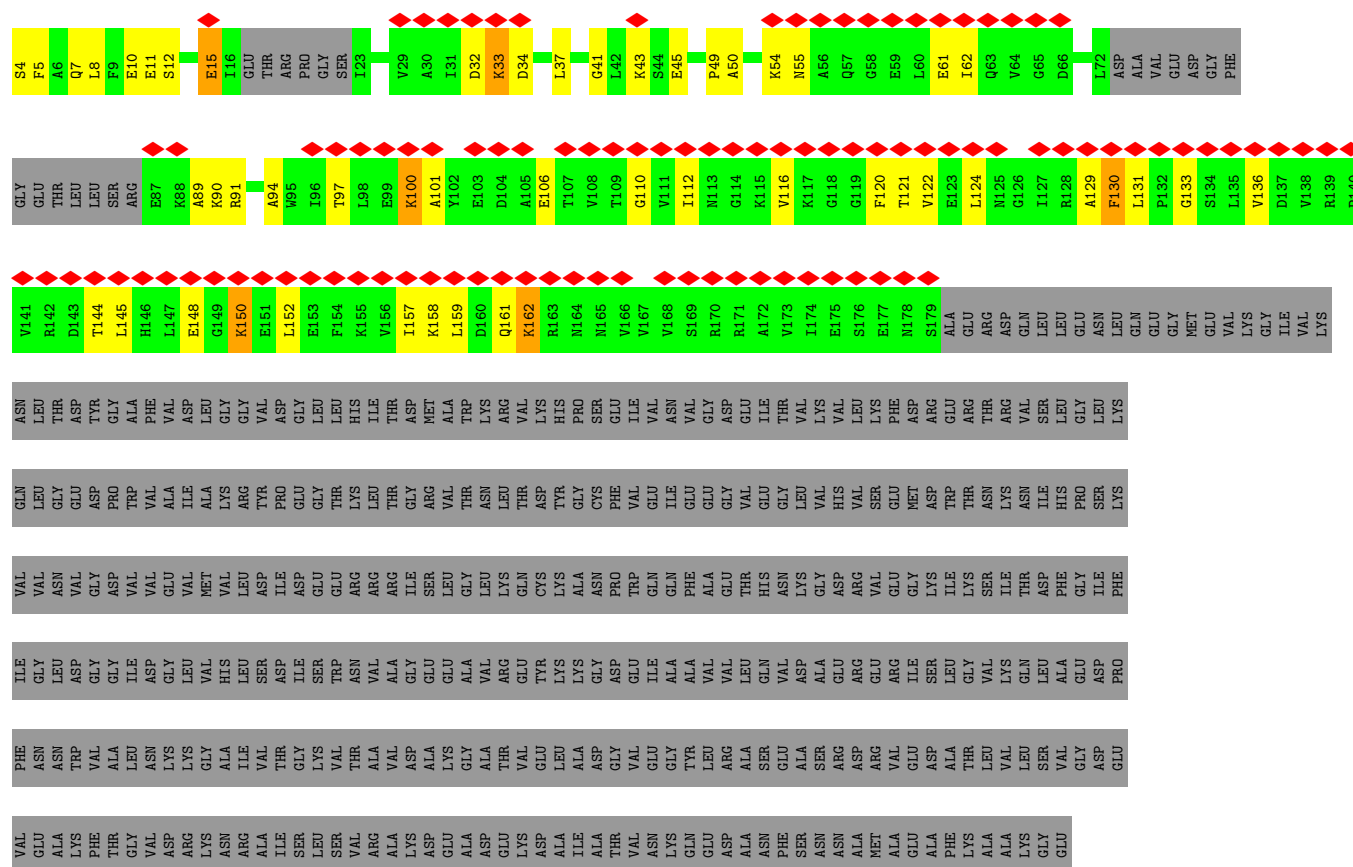
• Molecule 57: mRNA



Chain Y: 63% 26% 9%



Chain Z: 19% 19% 8% 72%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	10289	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTFFIND3 was used to determine CTF values. FREALIGN applied CTF correction.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	60976	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.062	Depositor
Minimum map value	-0.023	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.01	Depositor
Map size ($\text{\AA}$)	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: FME

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	04	0.30	0/2122	0.91	5/2852 (0.2%)
2	05	0.29	0/1586	0.81	1/2134 (0.0%)
3	06	0.29	0/1571	0.81	3/2113 (0.1%)
4	07	0.29	0/1435	0.88	2/1926 (0.1%)
5	08	0.30	0/1343	0.85	3/1816 (0.2%)
6	09	0.30	0/1122	0.90	5/1515 (0.3%)
7	10	0.33	0/1002	1.02	11/1350 (0.8%)
8	11	0.35	0/1046	0.93	1/1410 (0.1%)
9	12	0.29	0/1152	0.80	0/1551
10	13	0.28	0/948	0.89	2/1268 (0.2%)
11	14	0.29	0/1054	0.83	1/1403 (0.1%)
12	15	0.27	0/1093	0.82	3/1460 (0.2%)
13	16	0.29	0/974	0.82	0/1301
14	17	0.28	0/902	0.73	0/1209
15	18	0.28	0/929	0.81	2/1242 (0.2%)
16	19	0.29	0/960	0.82	1/1278 (0.1%)
17	20	0.28	0/829	0.87	3/1107 (0.3%)
18	21	0.28	0/864	0.84	1/1156 (0.1%)
19	22	0.27	0/745	0.78	0/994
20	23	0.27	0/788	0.77	1/1051 (0.1%)
21	24	0.28	0/766	0.81	0/1025
22	25	0.28	0/582	0.84	0/769
23	26	0.28	0/635	0.79	0/848
24	27	0.27	0/510	0.73	0/677
25	28	0.28	0/453	0.84	0/605
26	29	0.29	0/532	0.84	2/709 (0.3%)
27	30	0.28	0/450	0.82	1/599 (0.2%)
28	31	0.30	0/417	0.78	0/554
29	32	0.31	0/380	0.82	0/498
30	33	0.29	0/513	0.78	2/676 (0.3%)
31	34	0.33	0/303	0.97	2/397 (0.5%)
32	B	0.29	0/1788	0.88	2/2408 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	C	0.30	0/1652	0.88	7/2225 (0.3%)
34	D	0.28	0/1665	0.85	2/2227 (0.1%)
35	E	0.30	0/1170	0.87	3/1573 (0.2%)
36	F	0.42	0/1048	0.93	5/1413 (0.4%)
37	G	0.28	0/1196	0.90	5/1602 (0.3%)
38	H	0.29	0/989	0.88	3/1326 (0.2%)
39	I	0.29	0/1034	0.85	3/1375 (0.2%)
40	J	0.31	0/797	0.91	4/1077 (0.4%)
41	K	0.31	0/886	0.94	3/1195 (0.3%)
42	L	0.31	0/969	0.99	5/1300 (0.4%)
43	M	0.29	0/893	0.82	2/1193 (0.2%)
44	N	0.28	0/817	0.76	0/1088
45	O	0.28	0/722	0.75	1/964 (0.1%)
46	P	0.30	0/659	0.86	3/884 (0.3%)
47	Q	0.30	0/658	0.87	3/881 (0.3%)
48	R	0.32	0/545	0.85	2/731 (0.3%)
49	S	0.30	0/653	0.87	1/877 (0.1%)
50	T	0.30	0/671	0.87	2/888 (0.2%)
51	U	0.31	0/551	0.89	2/728 (0.3%)
52	03	0.30	0/1034	0.84	0/1387
53	A	0.42	0/36963	0.48	3/57662 (0.0%)
54	01	0.41	0/69796	0.49	2/108888 (0.0%)
55	02	0.42	0/2872	0.47	0/4479
56	W	0.41	0/1832	0.44	0/2855
56	X	0.41	0/1832	0.49	0/2855
57	V	0.42	0/436	0.48	0/679
58	Y	0.43	0/1812	0.49	1/2823 (0.0%)
59	Z	0.51	0/1215	0.78	1/1635 (0.1%)
All	All	0.38	0/165161	0.61	117/246711 (0.0%)

There are no bond length outliers.

The worst 5 of 117 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	08	10	VAL	N-CA-C	9.06	118.06	107.73
42	L	114	SER	N-CA-C	-8.64	101.83	111.07
37	G	5	VAL	N-CA-C	-7.70	105.06	112.29
7	10	117	LEU	N-CA-C	7.69	120.23	109.15
37	G	80	GLY	N-CA-C	-7.33	105.13	114.37

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	04	2083	0	2157	134	0
2	05	1565	0	1616	82	0
3	06	1552	0	1619	105	0
4	07	1411	0	1447	105	0
5	08	1323	0	1374	73	0
6	09	1111	0	1148	79	0
7	10	989	0	1025	85	0
8	11	1032	0	1088	87	0
9	12	1129	0	1162	83	0
10	13	939	0	1012	59	0
11	14	1045	0	1117	69	0
12	15	1074	0	1157	68	0
13	16	961	0	1000	71	0
14	17	892	0	923	53	0
15	18	917	0	965	73	0
16	19	947	0	1022	71	0
17	20	816	0	839	56	0
18	21	857	0	922	65	0
19	22	739	0	807	39	0
20	23	780	0	834	40	0
21	24	753	0	780	31	0
22	25	575	0	592	23	0
23	26	625	0	655	22	0
24	27	509	0	543	30	0
25	28	449	0	491	32	0
26	29	523	0	524	24	0
27	30	444	0	461	44	0
28	31	410	0	440	21	0
29	32	377	0	418	21	0
30	33	504	0	574	20	0
31	34	302	0	343	22	0
32	B	1757	0	1787	84	0
33	C	1625	0	1699	94	0
34	D	1643	0	1710	128	0
35	E	1157	0	1199	105	0
36	F	1028	0	1002	66	0
37	G	1182	0	1240	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	H	979	0	1034	69	0
39	I	1022	0	1070	76	0
40	J	787	0	828	63	0
41	K	870	0	878	69	0
42	L	955	0	1019	75	0
43	M	884	0	944	70	0
44	N	805	0	847	61	0
45	O	714	0	737	31	0
46	P	649	0	666	67	0
47	Q	649	0	691	47	0
48	R	536	0	552	44	0
49	S	638	0	665	35	0
50	T	665	0	714	41	0
51	U	545	0	579	65	0
52	03	1027	0	1092	68	0
53	A	33012	0	16618	510	0
54	01	62317	0	31346	1011	0
55	02	2568	0	1303	47	0
56	W	1640	0	836	12	0
56	X	1640	0	837	19	0
57	V	388	0	196	3	0
58	Y	1622	0	821	17	0
59	Z	1204	0	1221	61	0
60	W	10	0	10	0	0
All	All	152151	0	103196	4455	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 17.

The worst 5 of 4455 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)
15:18:59:THR:HG22	15:18:72:VAL:HG12	1.33	1.10
54:01:45:G:H5''	54:01:46:G:H5'	1.22	1.09
14:17:29:HIS:HB3	14:17:36:TYR:HB2	1.37	1.04
52:03:174:THR:HG21	54:01:2124:G:H4'	1.39	1.04
43:M:97:ARG:HB2	43:M:99:GLN:HE22	1.23	1.03

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	04	269/271 (99%)	225 (84%)	33 (12%)	11 (4%)	2	19
2	05	207/209 (99%)	175 (84%)	31 (15%)	1 (0%)	24	57
3	06	199/201 (99%)	164 (82%)	29 (15%)	6 (3%)	3	25
4	07	175/177 (99%)	140 (80%)	31 (18%)	4 (2%)	5	30
5	08	174/176 (99%)	155 (89%)	17 (10%)	2 (1%)	11	43
6	09	147/149 (99%)	111 (76%)	27 (18%)	9 (6%)	1	12
7	10	129/131 (98%)	98 (76%)	25 (19%)	6 (5%)	2	17
8	11	139/141 (99%)	118 (85%)	18 (13%)	3 (2%)	5	30
9	12	140/142 (99%)	122 (87%)	13 (9%)	5 (4%)	2	22
10	13	120/122 (98%)	103 (86%)	15 (12%)	2 (2%)	7	35
11	14	141/143 (99%)	120 (85%)	19 (14%)	2 (1%)	9	38
12	15	134/136 (98%)	103 (77%)	26 (19%)	5 (4%)	2	21
13	16	118/120 (98%)	83 (70%)	30 (25%)	5 (4%)	2	19
14	17	114/116 (98%)	95 (83%)	14 (12%)	5 (4%)	2	17
15	18	112/114 (98%)	89 (80%)	18 (16%)	5 (4%)	2	17
16	19	115/117 (98%)	94 (82%)	17 (15%)	4 (4%)	3	23
17	20	101/103 (98%)	86 (85%)	11 (11%)	4 (4%)	2	19
18	21	108/110 (98%)	87 (81%)	17 (16%)	4 (4%)	2	21
19	22	91/93 (98%)	78 (86%)	13 (14%)	0	100	100
20	23	100/102 (98%)	81 (81%)	15 (15%)	4 (4%)	2	19
21	24	92/94 (98%)	78 (85%)	11 (12%)	3 (3%)	3	23
22	25	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
23	26	75/77 (97%)	67 (89%)	7 (9%)	1 (1%)	9	39
24	27	61/63 (97%)	48 (79%)	10 (16%)	3 (5%)	1	16
25	28	56/58 (97%)	49 (88%)	7 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	29	64/66 (97%)	53 (83%)	9 (14%)	2 (3%)	3	25
27	30	54/56 (96%)	46 (85%)	6 (11%)	2 (4%)	2	21
28	31	48/50 (96%)	42 (88%)	6 (12%)	0	100	100
29	32	44/46 (96%)	29 (66%)	11 (25%)	4 (9%)	0	7
30	33	62/64 (97%)	50 (81%)	7 (11%)	5 (8%)	1	8
31	34	36/38 (95%)	29 (81%)	7 (19%)	0	100	100
32	B	223/225 (99%)	193 (86%)	26 (12%)	4 (2%)	6	34
33	C	204/206 (99%)	167 (82%)	29 (14%)	8 (4%)	2	20
34	D	203/205 (99%)	157 (77%)	32 (16%)	14 (7%)	1	10
35	E	155/157 (99%)	123 (79%)	24 (16%)	8 (5%)	1	14
36	F	124/126 (98%)	101 (82%)	17 (14%)	6 (5%)	2	16
37	G	149/151 (99%)	125 (84%)	21 (14%)	3 (2%)	6	32
38	H	127/129 (98%)	109 (86%)	16 (13%)	2 (2%)	7	36
39	I	125/127 (98%)	101 (81%)	16 (13%)	8 (6%)	1	11
40	J	96/98 (98%)	82 (85%)	11 (12%)	3 (3%)	3	25
41	K	114/116 (98%)	92 (81%)	19 (17%)	3 (3%)	4	27
42	L	121/123 (98%)	93 (77%)	20 (16%)	8 (7%)	1	11
43	M	112/114 (98%)	88 (79%)	20 (18%)	4 (4%)	2	22
44	N	98/100 (98%)	70 (71%)	24 (24%)	4 (4%)	2	19
45	O	86/88 (98%)	64 (74%)	20 (23%)	2 (2%)	5	30
46	P	80/82 (98%)	62 (78%)	17 (21%)	1 (1%)	9	39
47	Q	78/80 (98%)	61 (78%)	14 (18%)	3 (4%)	2	20
48	R	63/65 (97%)	50 (79%)	8 (13%)	5 (8%)	1	8
49	S	77/79 (98%)	63 (82%)	9 (12%)	5 (6%)	1	11
50	T	83/85 (98%)	74 (89%)	8 (10%)	1 (1%)	10	41
51	U	63/65 (97%)	42 (67%)	19 (30%)	2 (3%)	3	24
52	03	130/223 (58%)	114 (88%)	13 (10%)	3 (2%)	5	30
59	Z	150/554 (27%)	126 (84%)	21 (14%)	3 (2%)	6	32
All	All	6159/6758 (91%)	5040 (82%)	912 (15%)	207 (3%)	4	23

5 of 207 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	04	261	ARG
3	06	84	THR
4	07	175	PRO
6	09	10	ALA
7	10	58	THR

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	04	216/216 (100%)	216 (100%)	0	100	100
2	05	164/164 (100%)	164 (100%)	0	100	100
3	06	165/165 (100%)	165 (100%)	0	100	100
4	07	148/148 (100%)	146 (99%)	2 (1%)	59	71
5	08	137/137 (100%)	137 (100%)	0	100	100
6	09	114/114 (100%)	114 (100%)	0	100	100
7	10	100/100 (100%)	100 (100%)	0	100	100
8	11	109/109 (100%)	108 (99%)	1 (1%)	70	76
9	12	116/116 (100%)	114 (98%)	2 (2%)	53	70
10	13	103/103 (100%)	103 (100%)	0	100	100
11	14	102/102 (100%)	99 (97%)	3 (3%)	37	60
12	15	109/109 (100%)	109 (100%)	0	100	100
13	16	100/100 (100%)	100 (100%)	0	100	100
14	17	86/86 (100%)	86 (100%)	0	100	100
15	18	99/99 (100%)	98 (99%)	1 (1%)	68	75
16	19	89/89 (100%)	89 (100%)	0	100	100
17	20	84/84 (100%)	83 (99%)	1 (1%)	63	73
18	21	93/93 (100%)	93 (100%)	0	100	100
19	22	80/80 (100%)	80 (100%)	0	100	100
20	23	83/83 (100%)	81 (98%)	2 (2%)	43	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	24	78/78 (100%)	77 (99%)	1 (1%)	61	72
22	25	57/57 (100%)	57 (100%)	0	100	100
23	26	67/67 (100%)	66 (98%)	1 (2%)	57	71
24	27	55/55 (100%)	55 (100%)	0	100	100
25	28	48/48 (100%)	48 (100%)	0	100	100
26	29	59/59 (100%)	59 (100%)	0	100	100
27	30	47/47 (100%)	47 (100%)	0	100	100
28	31	45/45 (100%)	44 (98%)	1 (2%)	45	65
29	32	38/38 (100%)	38 (100%)	0	100	100
30	33	51/51 (100%)	51 (100%)	0	100	100
31	34	34/34 (100%)	34 (100%)	0	100	100
32	B	186/186 (100%)	185 (100%)	1 (0%)	81	80
33	C	170/170 (100%)	170 (100%)	0	100	100
34	D	172/172 (100%)	167 (97%)	5 (3%)	37	60
35	E	119/119 (100%)	117 (98%)	2 (2%)	53	70
36	F	108/108 (100%)	107 (99%)	1 (1%)	70	76
37	G	124/124 (100%)	124 (100%)	0	100	100
38	H	104/104 (100%)	104 (100%)	0	100	100
39	I	105/105 (100%)	104 (99%)	1 (1%)	68	75
40	J	86/86 (100%)	85 (99%)	1 (1%)	63	73
41	K	89/89 (100%)	89 (100%)	0	100	100
42	L	103/103 (100%)	103 (100%)	0	100	100
43	M	92/92 (100%)	92 (100%)	0	100	100
44	N	83/83 (100%)	82 (99%)	1 (1%)	63	73
45	O	76/76 (100%)	76 (100%)	0	100	100
46	P	65/65 (100%)	63 (97%)	2 (3%)	35	59
47	Q	74/74 (100%)	74 (100%)	0	100	100
48	R	56/56 (100%)	56 (100%)	0	100	100
49	S	70/70 (100%)	70 (100%)	0	100	100
50	T	65/65 (100%)	65 (100%)	0	100	100
51	U	55/55 (100%)	55 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	03	110/174 (63%)	109 (99%)	1 (1%)	70	76
59	Z	129/458 (28%)	123 (95%)	6 (5%)	23	49
All	All	5117/5510 (93%)	5081 (99%)	36 (1%)	73	78

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	P	33	ILE
59	Z	162	LYS
52	03	214	ILE
59	Z	130	PHE
21	24	81	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 151 such sidechains are listed below:

Mol	Chain	Res	Type
39	I	30	ASN
50	T	60	GLN
40	J	70	HIS
45	O	49	HIS
59	Z	178	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	A	1538/1539 (99%)	135 (8%)	4 (0%)
54	01	2902/2903 (99%)	345 (11%)	10 (0%)
55	02	119/120 (99%)	12 (10%)	1 (0%)
56	W	76/77 (98%)	7 (9%)	0
56	X	76/77 (98%)	15 (19%)	0
57	V	17/27 (62%)	3 (17%)	0
58	Y	75/76 (98%)	14 (18%)	1 (1%)
All	All	4803/4819 (99%)	531 (11%)	16 (0%)

5 of 531 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	A	6	G
53	A	9	G

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Mol	Chain	Res	Type
53	A	22	G
53	A	31	G
53	A	32	A

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	02	88	C
54	01	2391	G
54	01	1130	U
54	01	2326	C
54	01	1020	A

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
60	FME	W	101	56	8,9,10	0.67	0	8,9,11	1.01	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	FME	W	101	56	-	1/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	W	101	FME	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

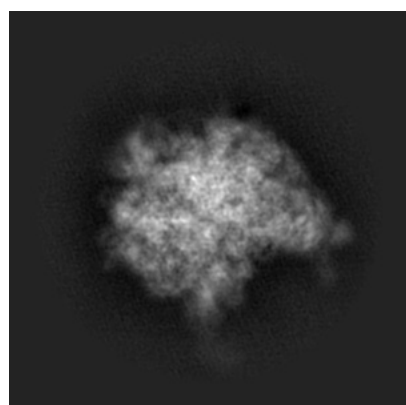
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7289. These allow visual inspection of the internal detail of the map and identification of artifacts.

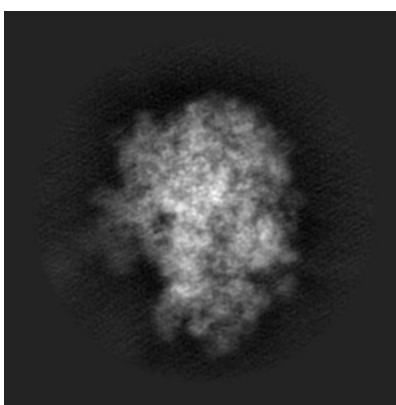
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

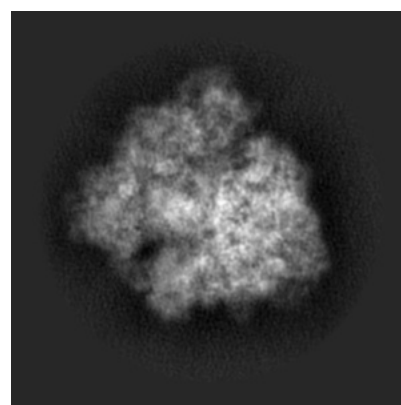
6.1.1 Primary map



X



Y

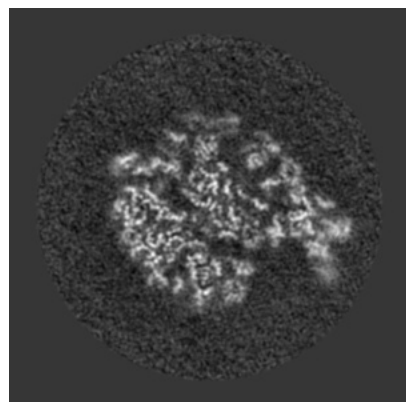


Z

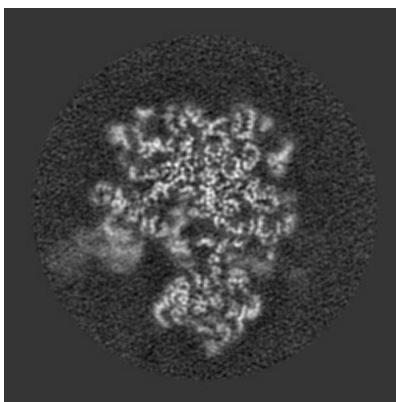
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

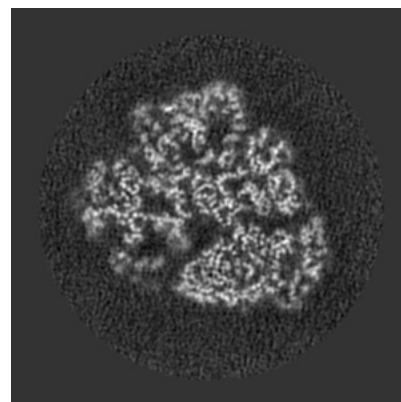
6.2.1 Primary map



X Index: 240



Y Index: 240

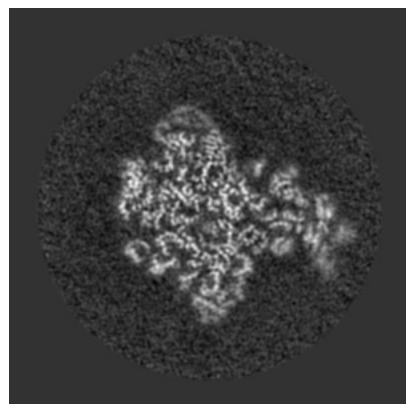


Z Index: 240

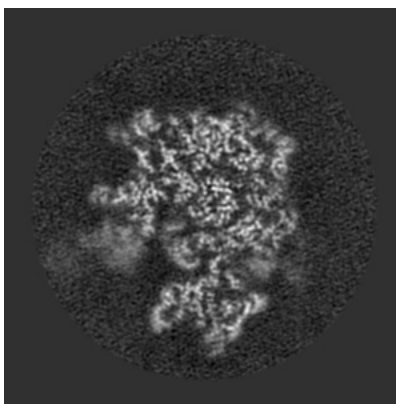
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

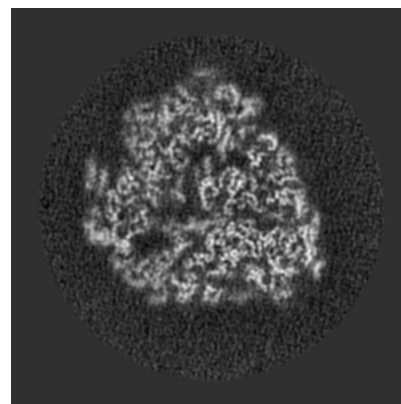
6.3.1 Primary map



X Index: 252



Y Index: 247

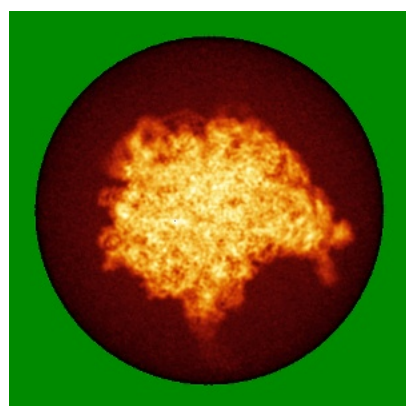


Z Index: 228

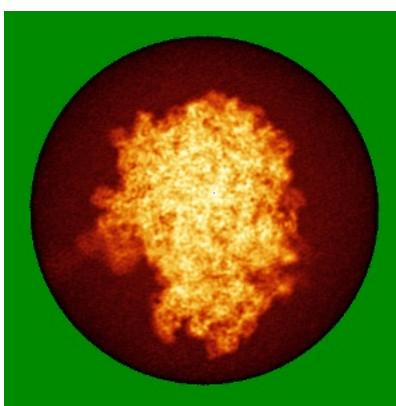
The images above show the largest variance slices of the map in three orthogonal directions.

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

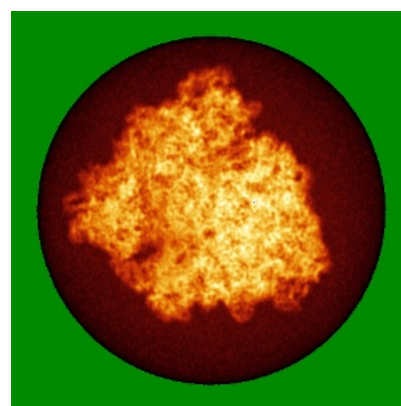
6.4.1 Primary map



X



Y

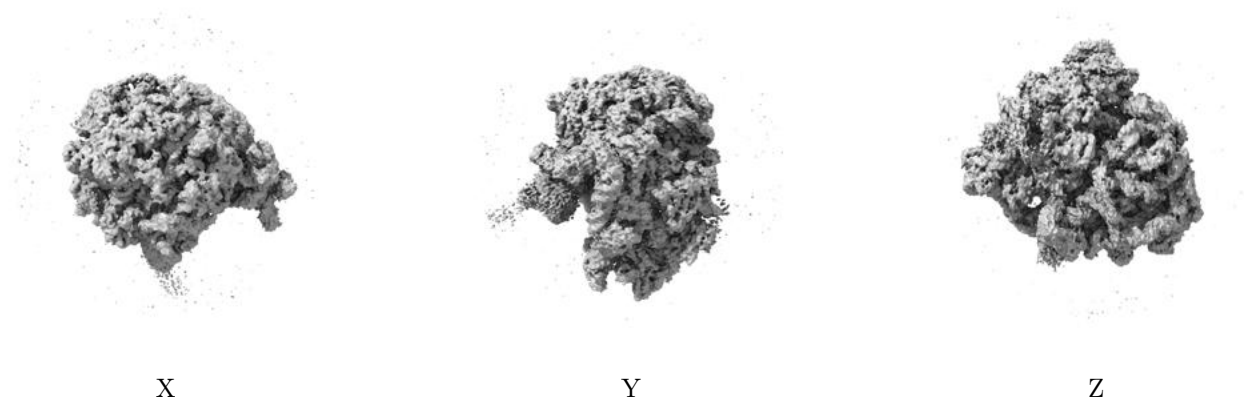


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

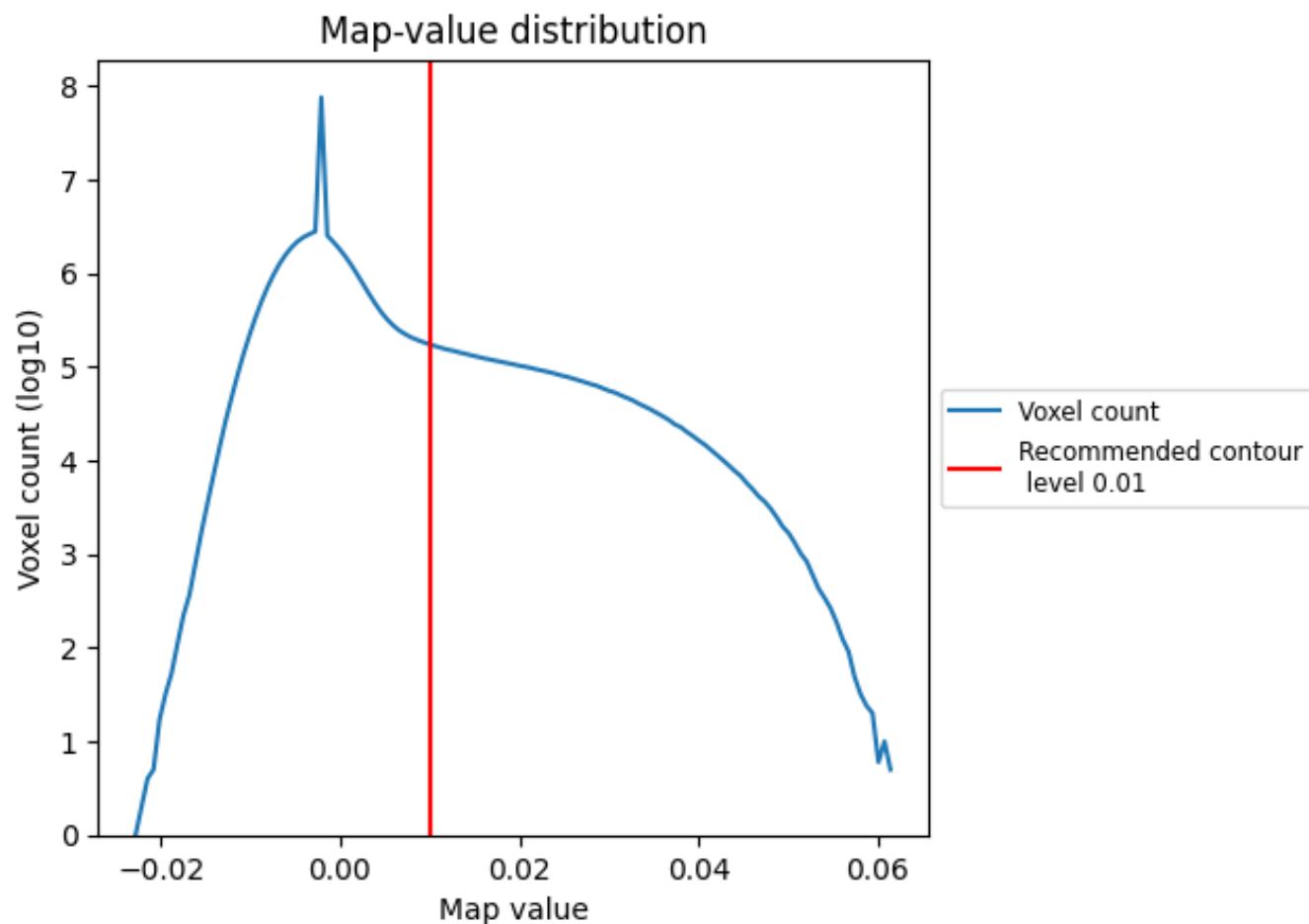
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

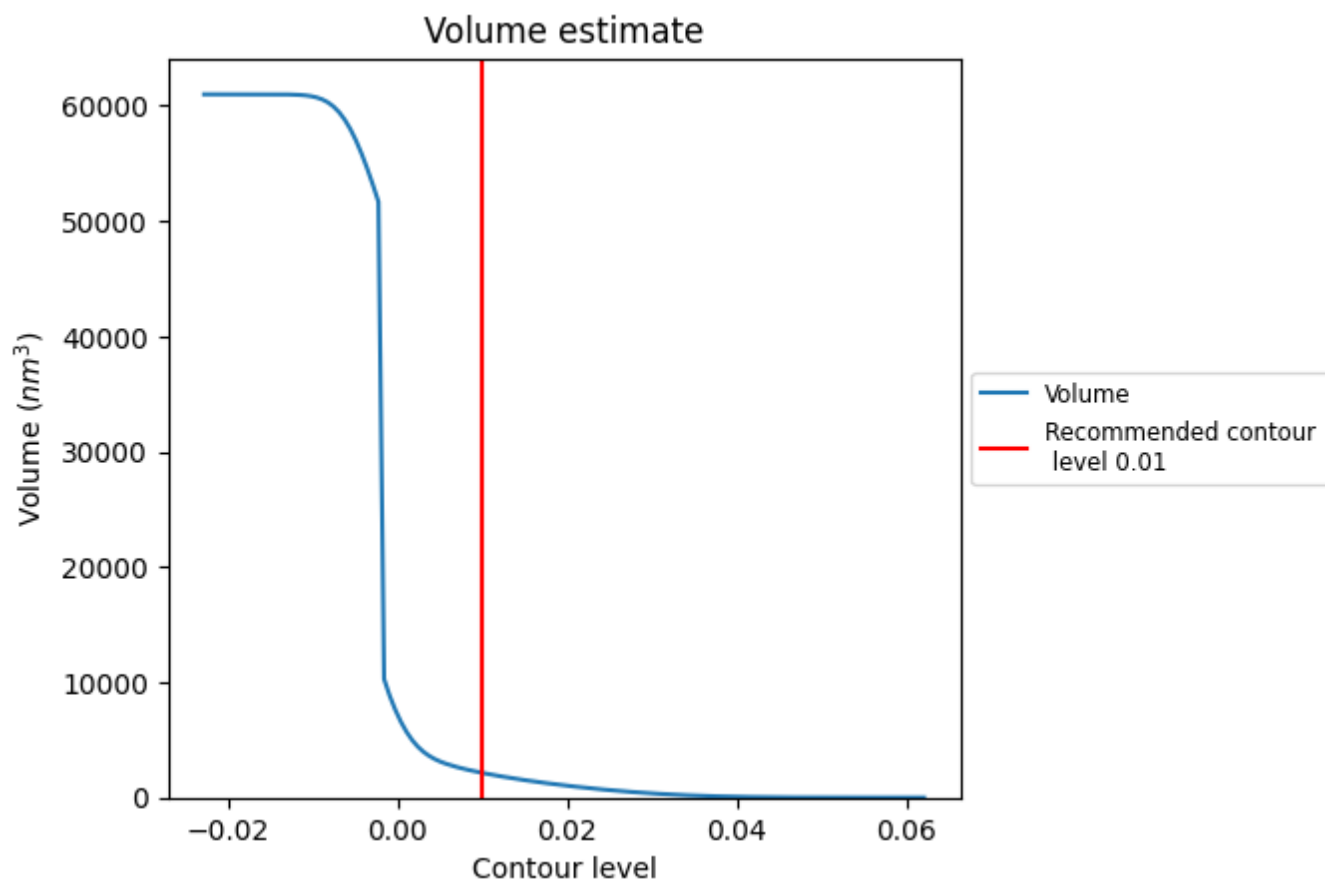
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

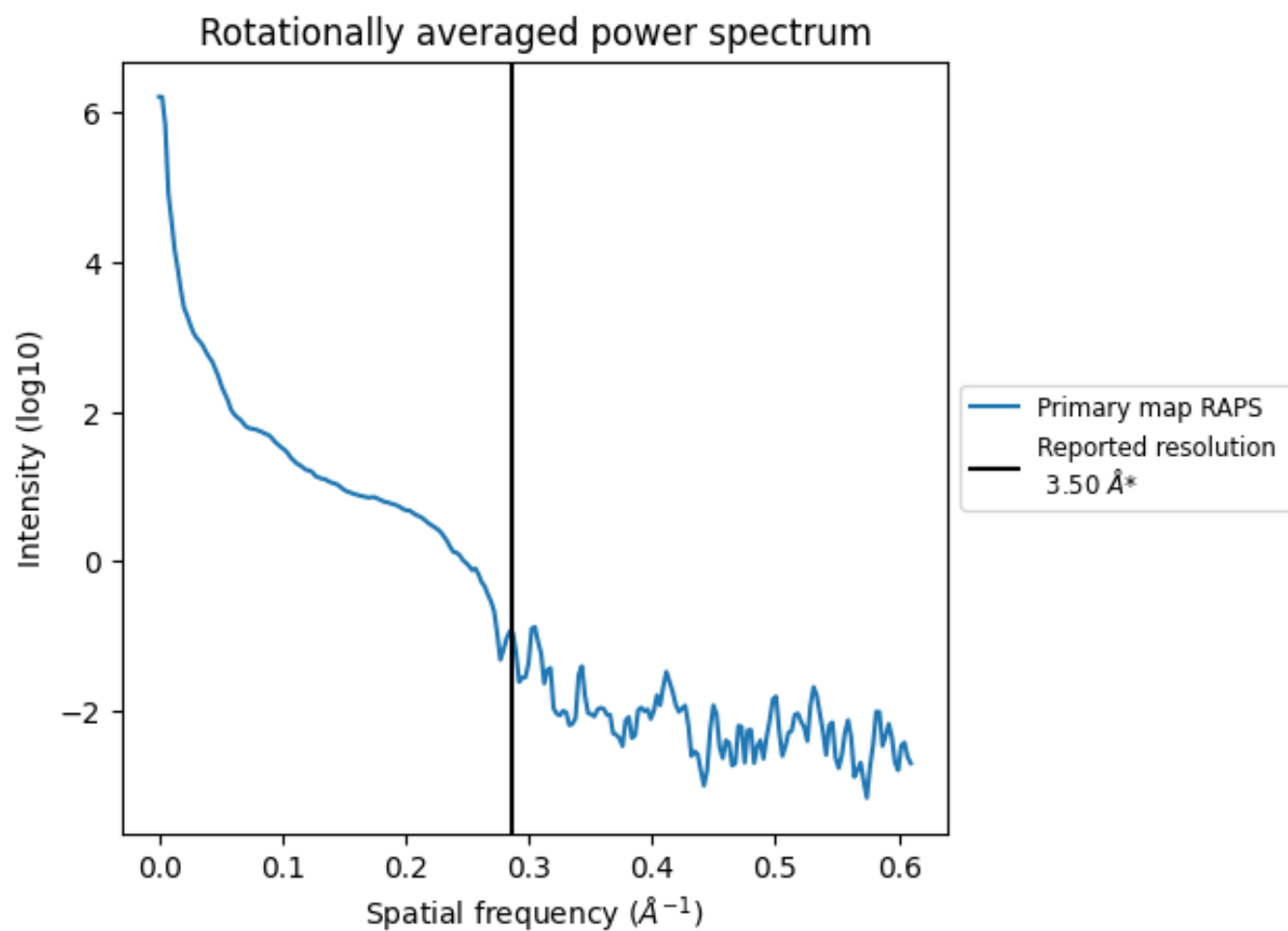
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2139 nm³; this corresponds to an approximate mass of 1932 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 0.286 Å⁻¹

8 Fourier-Shell correlation

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

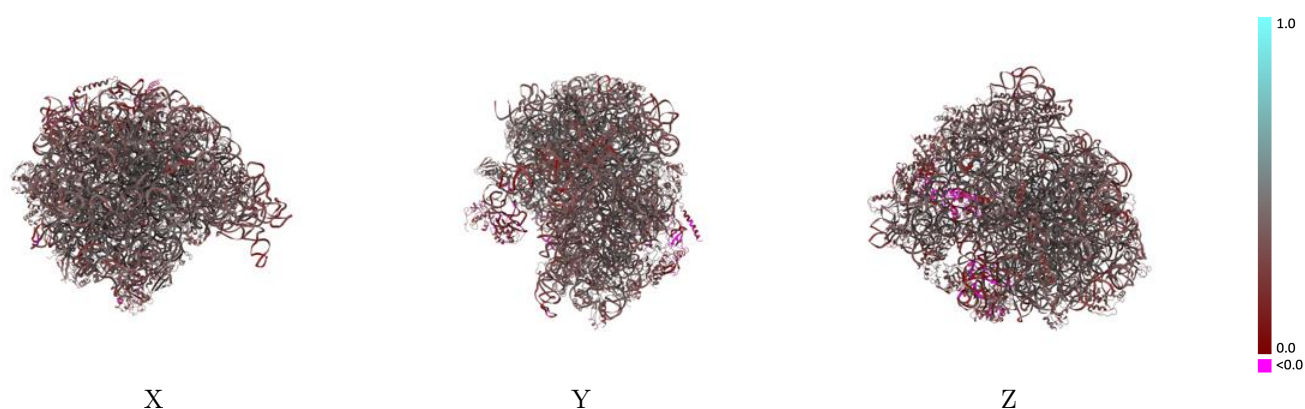
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7289 and PDB model 6BU8. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

This section was not generated.

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

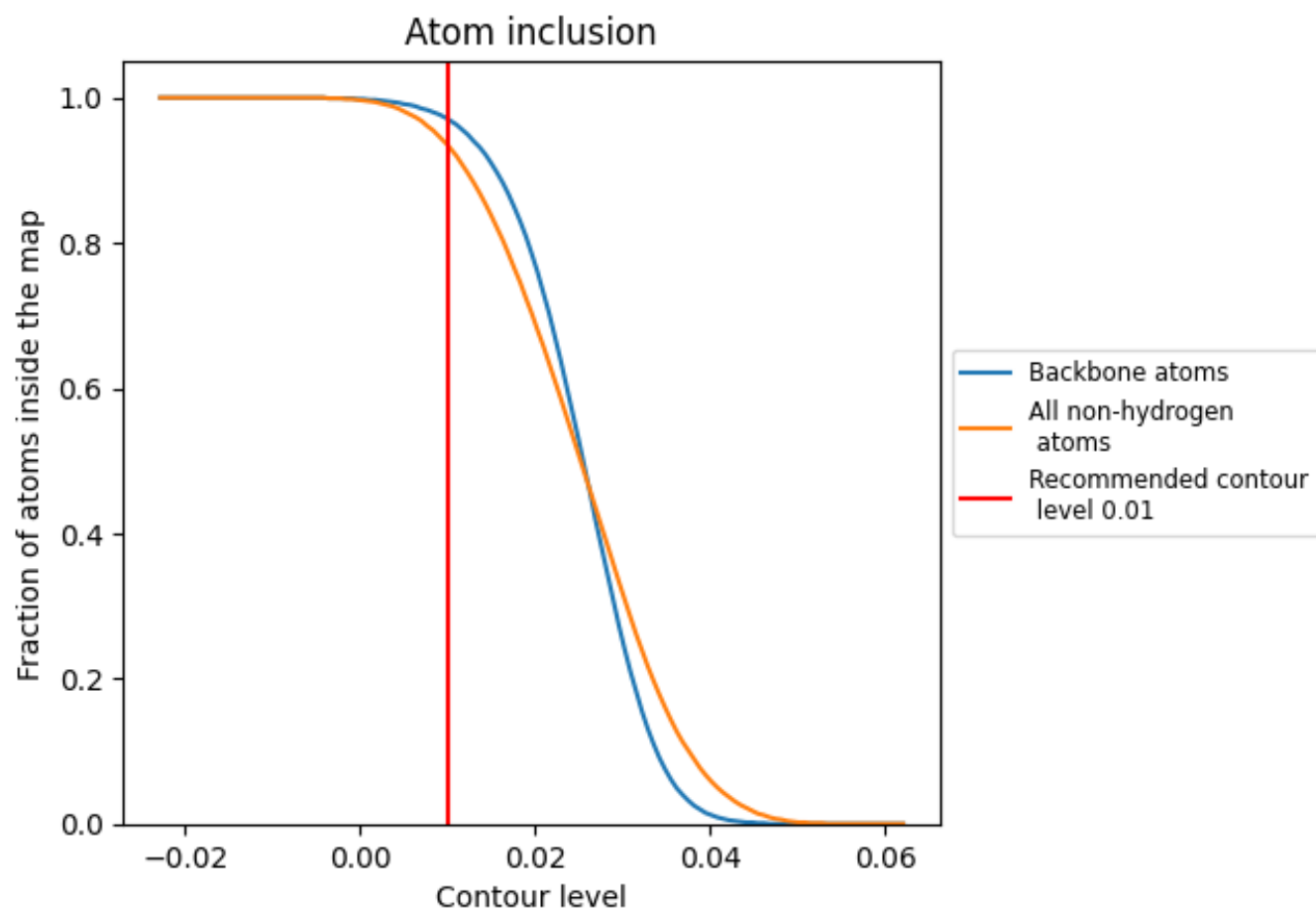


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9350	 0.3600
01	 0.9790	 0.3740
02	 0.9820	 0.3500
03	 0.8570	 0.2350
04	 0.8820	 0.4170
05	 0.8780	 0.4050
06	 0.8660	 0.3690
07	 0.8890	 0.3370
08	 0.8990	 0.3530
09	 0.7050	 0.2910
10	 0.5810	 0.1830
11	 0.6310	 0.2060
12	 0.8820	 0.3750
13	 0.8490	 0.4110
14	 0.8860	 0.3910
15	 0.8460	 0.4040
16	 0.9010	 0.3760
17	 0.9080	 0.3530
18	 0.8580	 0.3900
19	 0.8960	 0.3830
20	 0.8810	 0.3820
21	 0.8410	 0.3890
22	 0.8660	 0.3670
23	 0.9080	 0.3540
24	 0.8900	 0.3790
25	 0.9140	 0.4020
26	 0.8830	 0.3980
27	 0.8510	 0.3030
28	 0.9150	 0.3890
29	 0.8340	 0.3230
30	 0.9090	 0.3970
31	 0.8510	 0.3810
32	 0.8620	 0.4010
33	 0.8900	 0.4120
34	 0.9110	 0.4000



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Chain	Atom inclusion	Q-score
A	 0.9820	 0.3640
B	 0.8730	 0.3330
C	 0.8630	 0.3740
D	 0.8850	 0.3370
E	 0.8950	 0.3830
F	 0.7180	 0.2920
G	 0.8690	 0.3430
H	 0.8820	 0.3850
I	 0.8850	 0.3570
J	 0.8410	 0.3470
K	 0.8740	 0.3790
L	 0.8680	 0.3790
M	 0.9000	 0.3420
N	 0.8880	 0.3710
O	 0.8970	 0.3520
P	 0.9200	 0.3550
Q	 0.8770	 0.3460
R	 0.9070	 0.3730
S	 0.9160	 0.3500
T	 0.8950	 0.3300
U	 0.7740	 0.3060
V	 0.8220	 0.2680
W	 0.9350	 0.3480
X	 0.8650	 0.1800
Y	 0.9010	 0.2770
Z	 0.3090	 0.0490