



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 03:56 AM UTC

PDB ID : 5UYN / pdb_00005uyn
EMDB ID : EMD-8618
Title : 70S ribosome bound with near-cognate ternary complex not base-paired to A site codon (Structure I-nc)
Authors : Loveland, A.B.; Demo, G.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2017-02-24
Resolution : 4.00 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:

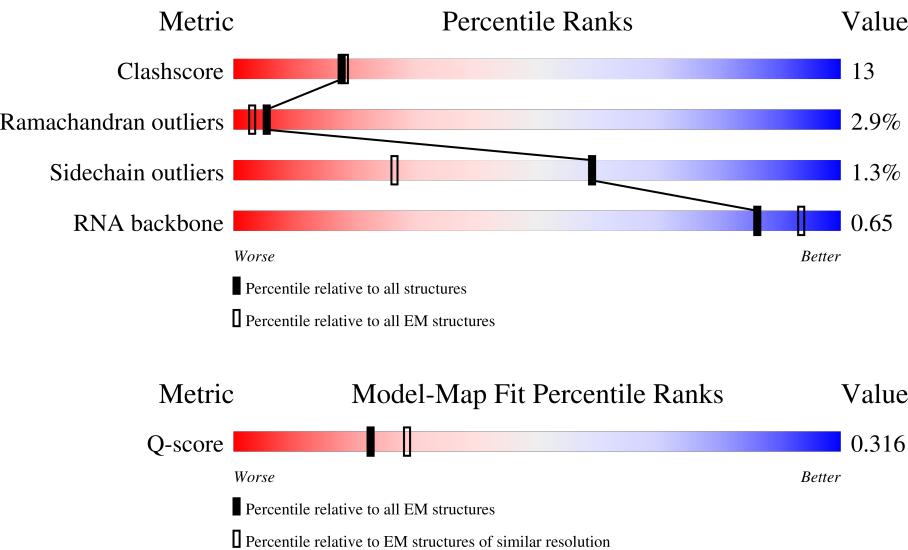
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 4.00 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	7587 (3.50 - 4.50)

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	
2	05	209	
3	06	201	

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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	

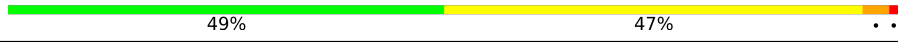
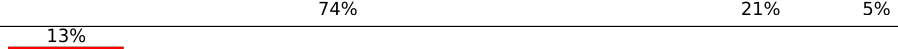
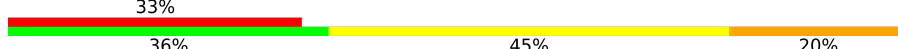
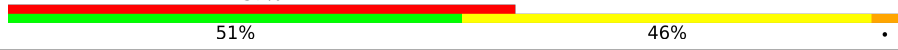
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Mol	Chain	Length	Quality of chain
29	32	46	
30	33	64	
31	34	38	
32	B	218	
33	C	206	
34	D	205	
35	E	157	
36	F	100	
37	G	151	
38	H	129	
39	I	127	
40	J	98	
41	K	116	
42	L	123	
43	M	114	
44	N	100	
45	O	88	
46	P	82	
47	Q	80	
48	R	65	
49	S	79	
50	T	85	
51	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	17	
58	Y	76	
59	Z	392	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 153717 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	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- 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	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- 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	conflict	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		

- 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	17	Total	C	N	O	P	0	0
			373	168	79	110	16		

- Molecule 58 is a RNA chain called tRNA^{Lys}.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	Y	76	Total	C	N	O	P	S	0	0
			1618	723	282	536	76	1		

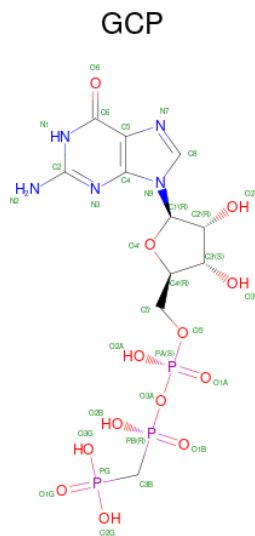
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	34	U8U	-	insertion	GB 558570689

- Molecule 59 is a protein called Elongation factor Tu 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Z	392	Total	C	N	O	S	0	0
			3029	1915	521	580	13		

- Molecule 60 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

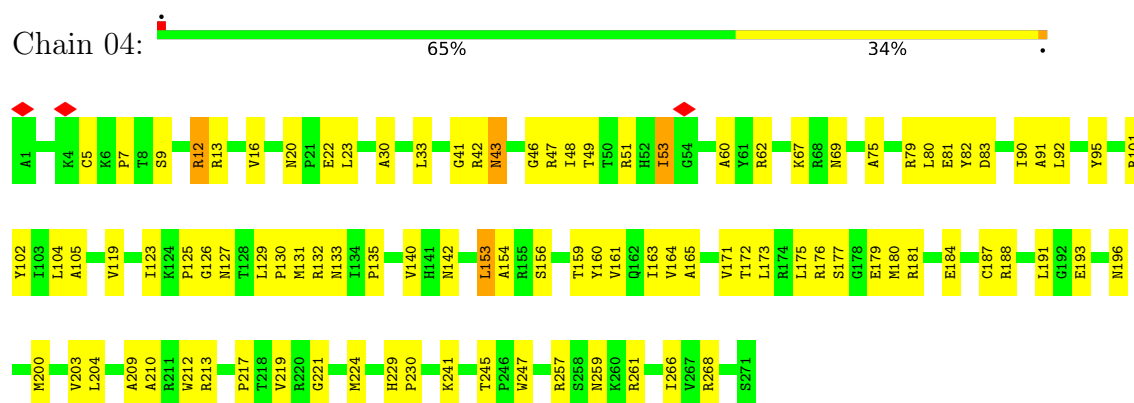


Mol	Chain	Residues	Atoms					AltConf
60	Z	1	Total	C	N	O	P	0
			32	11	5	13	3	

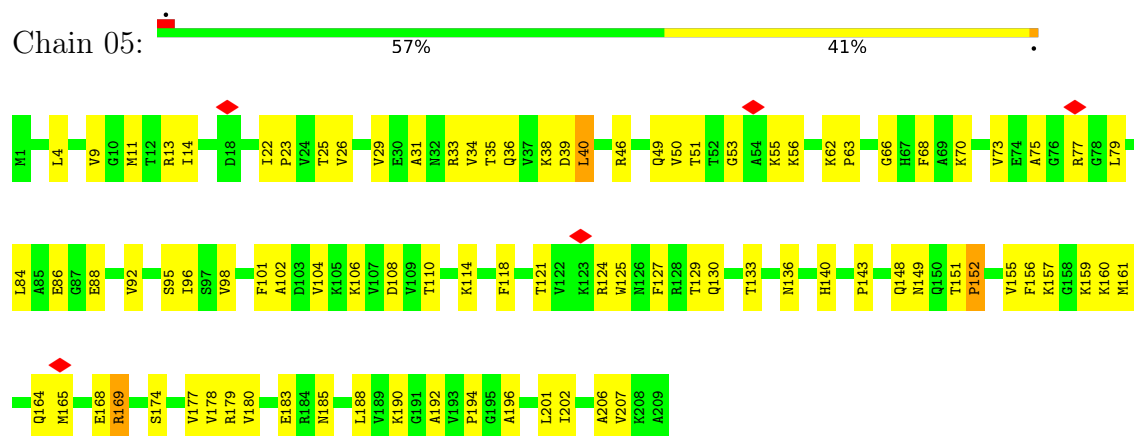
3 Residue-property plots

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.

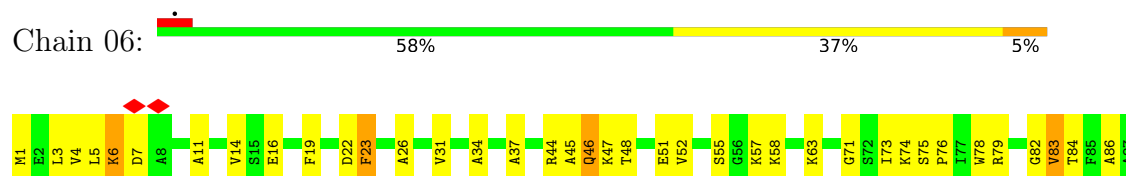
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

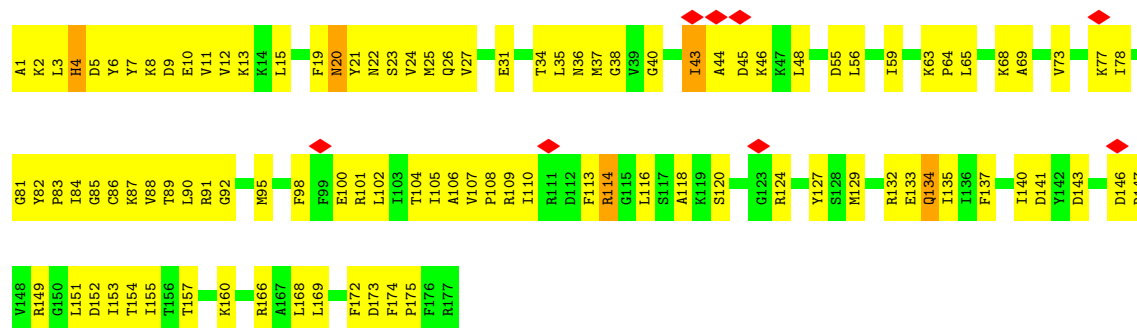


- Molecule 3: 50S ribosomal protein L4

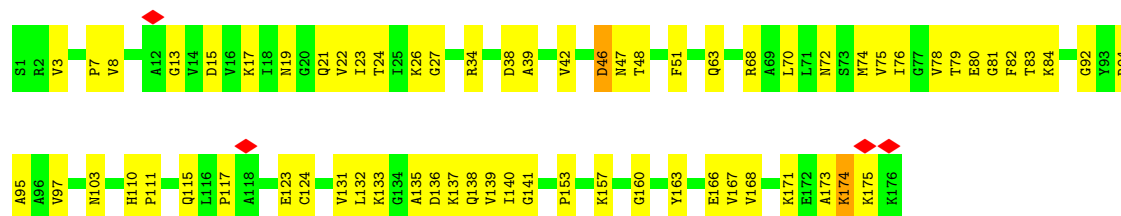




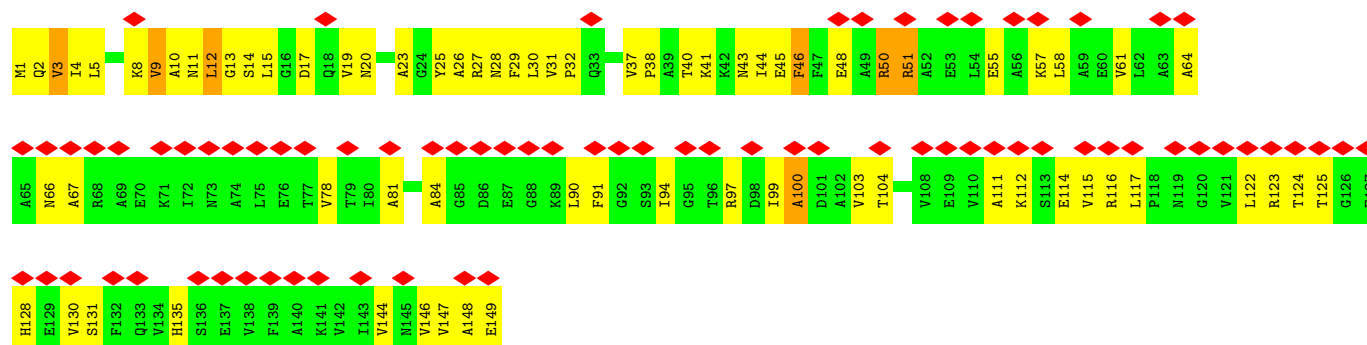
• Molecule 4: 50S ribosomal protein L5



• Molecule 5: 50S ribosomal protein L6

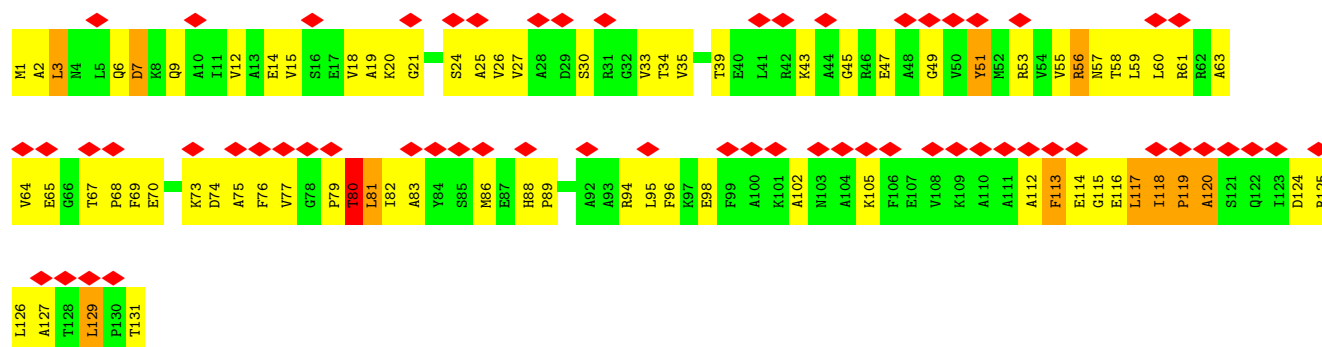


• Molecule 6: 50S ribosomal protein L9



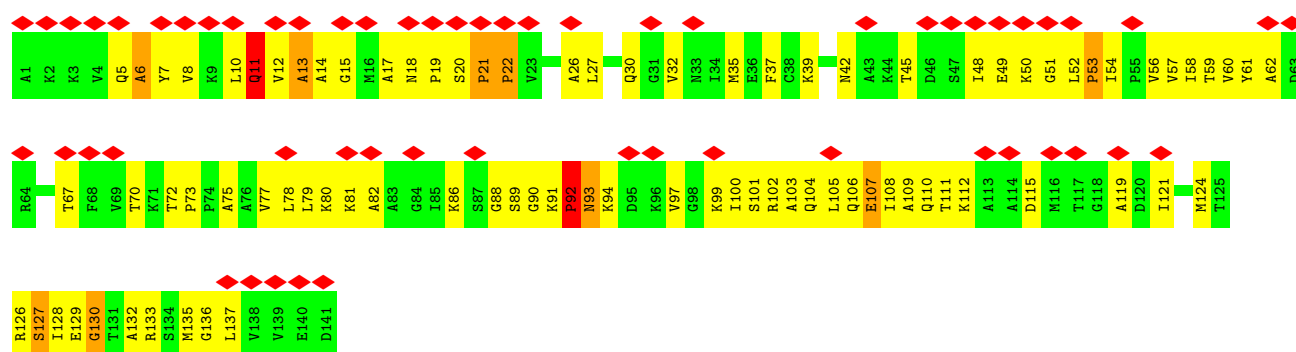
• Molecule 7: 50S ribosomal protein L10





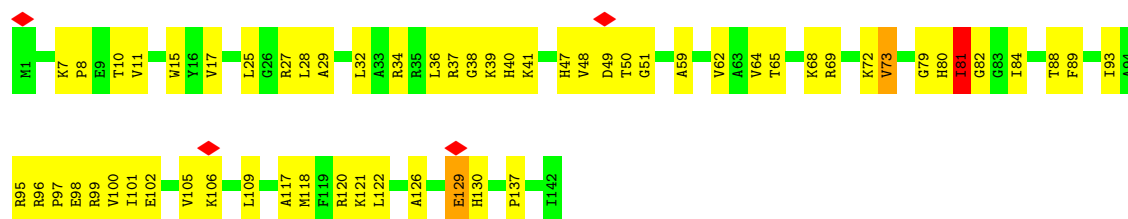
• Molecule 8: 50S ribosomal protein L11

Chain 11: 38% 54% 6%



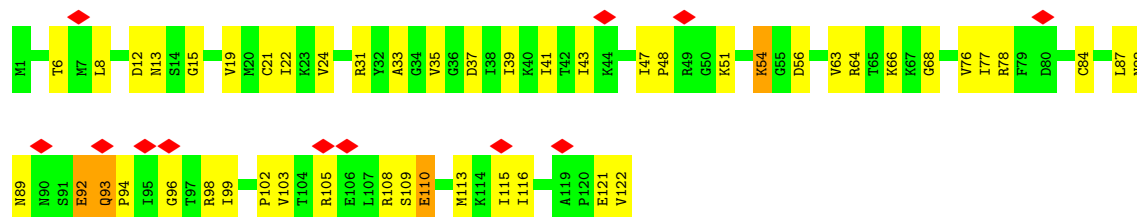
• Molecule 9: 50S ribosomal protein L13

Chain 12: 58% 39% 2%

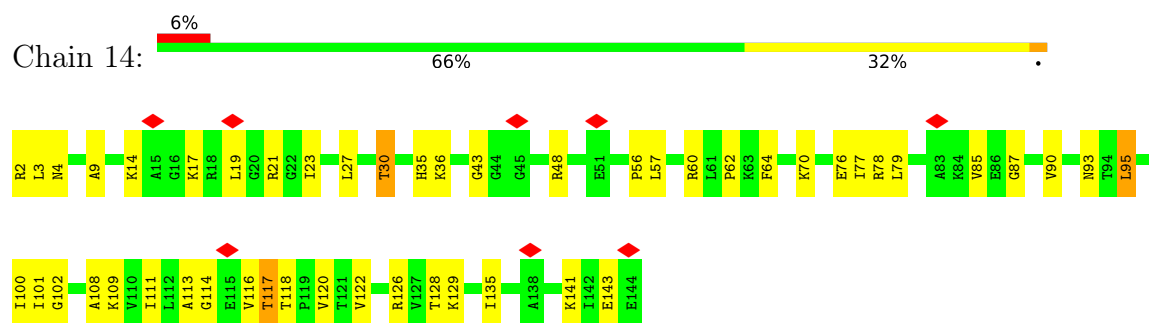


• Molecule 10: 50S ribosomal protein L14

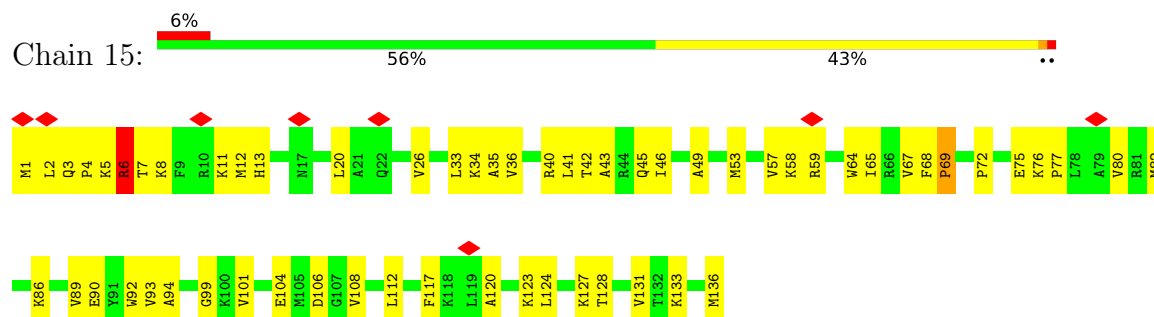
Chain 13: 60% 37% 3%



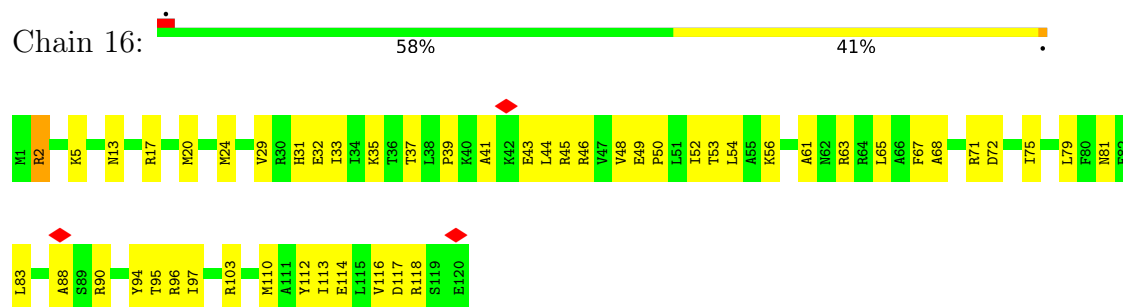
• Molecule 11: 50S ribosomal protein L15



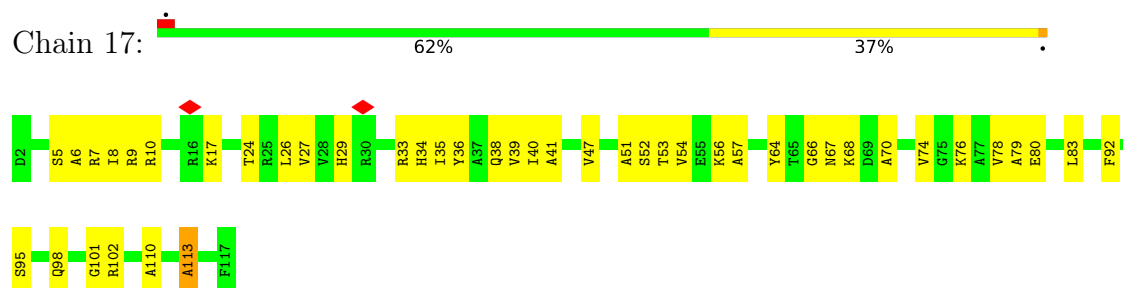
- Molecule 12: 50S ribosomal protein L16



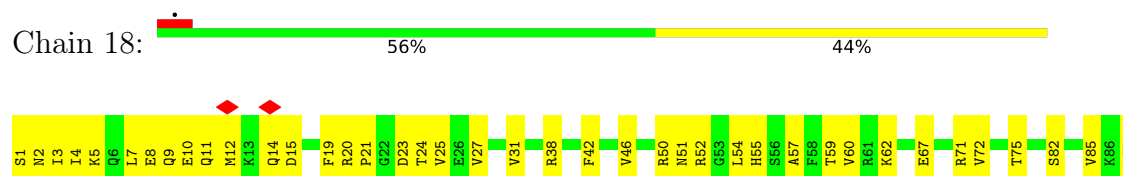
- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18



- Molecule 15: 50S ribosomal protein L19

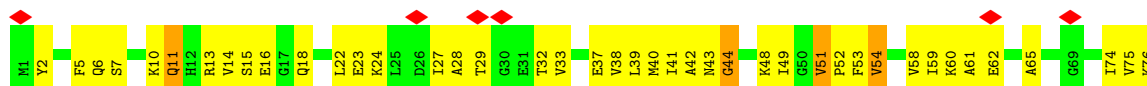




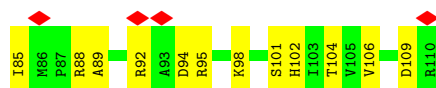
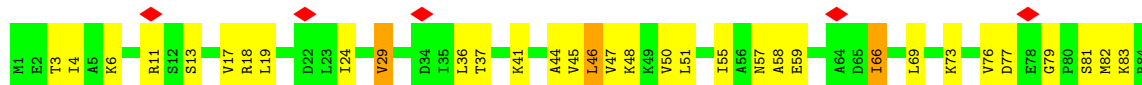
- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22

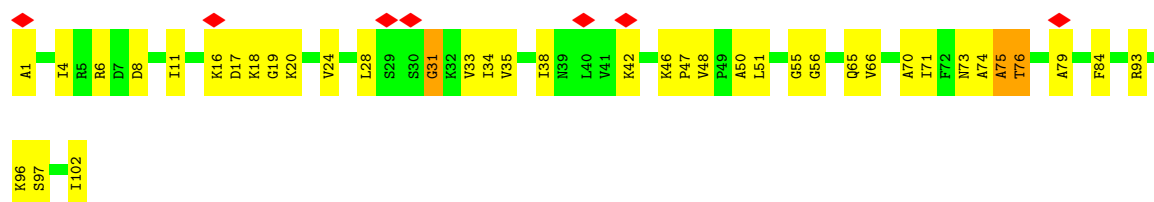


- Molecule 19: 50S ribosomal protein L23

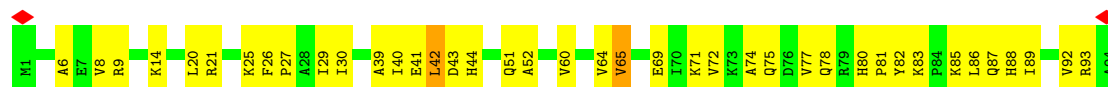


- Molecule 20: 50S ribosomal protein L24

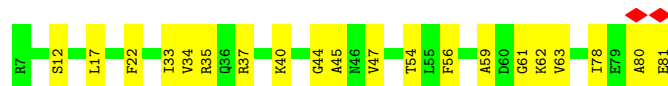
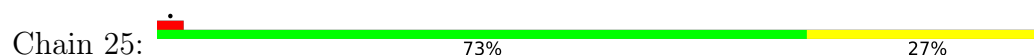




- Molecule 21: 50S ribosomal protein L25



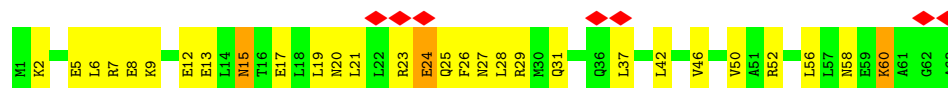
- Molecule 22: 50S ribosomal protein L27



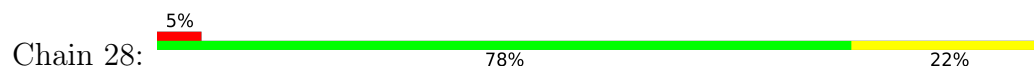
- Molecule 23: 50S ribosomal protein L28



- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30

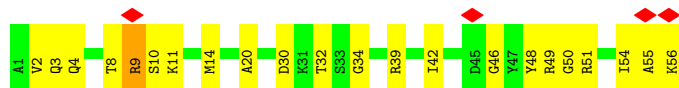


- Molecule 26: 50S ribosomal protein L31

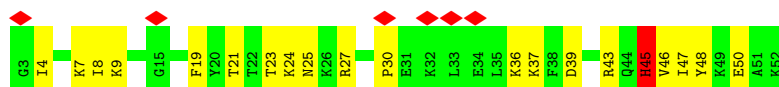




- Molecule 27: 50S ribosomal protein L32



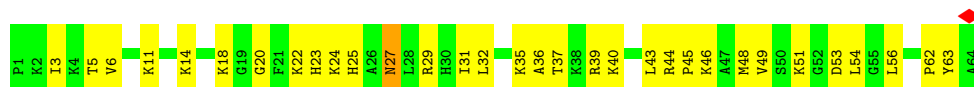
- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34



- Molecule 30: 50S ribosomal protein L35

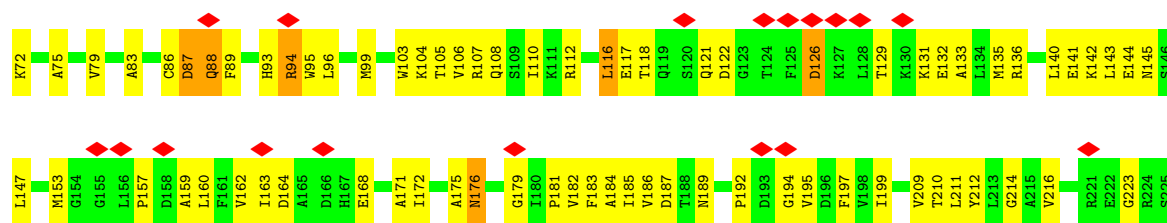


- Molecule 31: 50S ribosomal protein L36

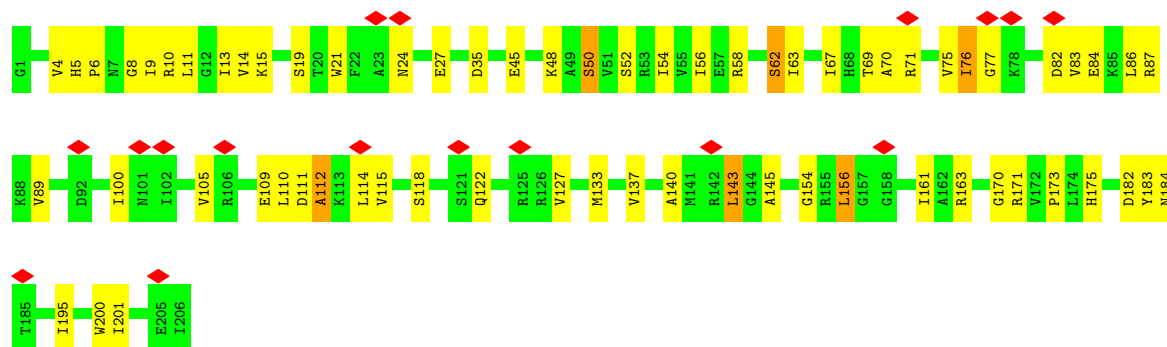


- Molecule 32: 30S ribosomal protein S2

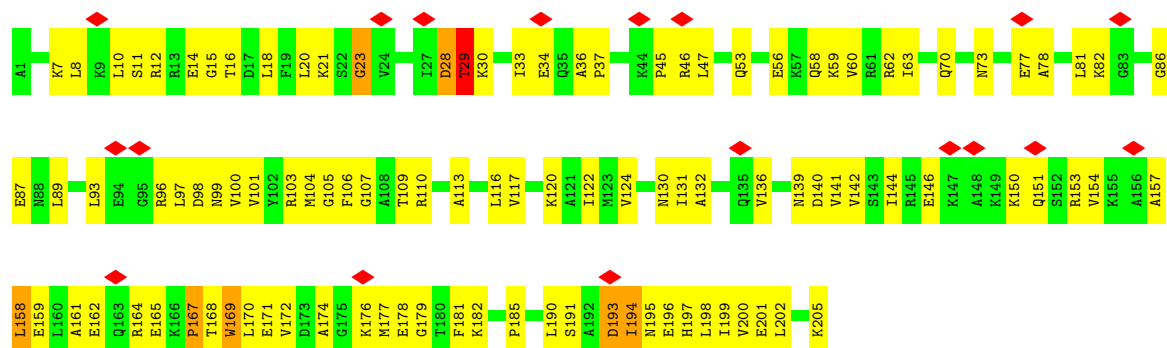




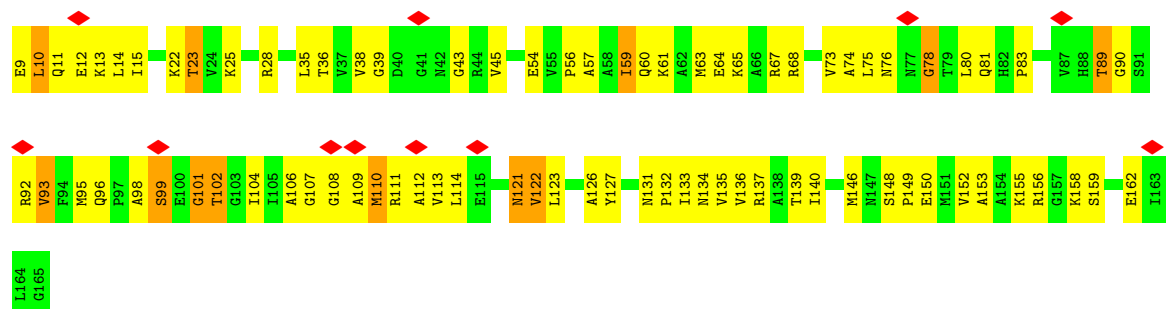
• Molecule 33: 30S ribosomal protein S3



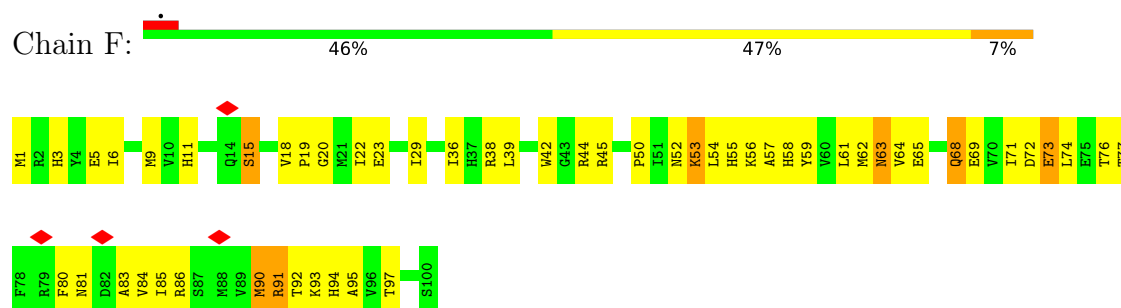
• Molecule 34: 30S ribosomal protein S4



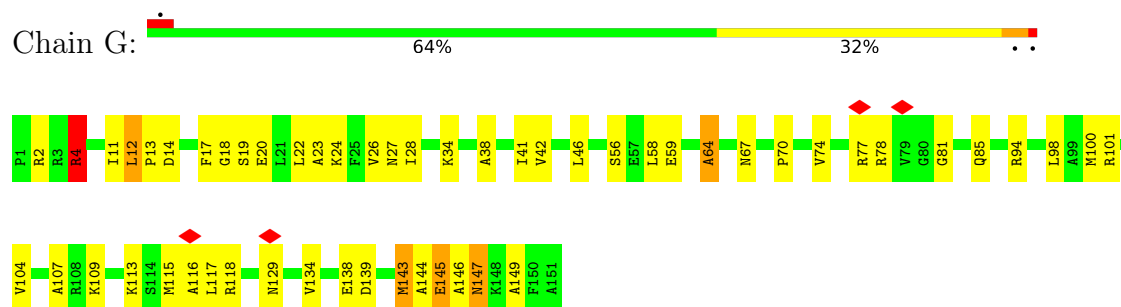
• Molecule 35: 30S ribosomal protein S5



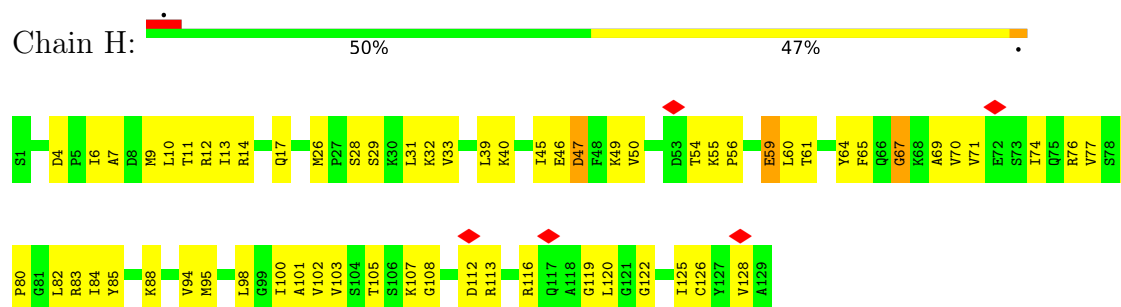
- Molecule 36: 30S ribosomal protein S6



- Molecule 37: 30S ribosomal protein S7



- Molecule 38: 30S ribosomal protein S8

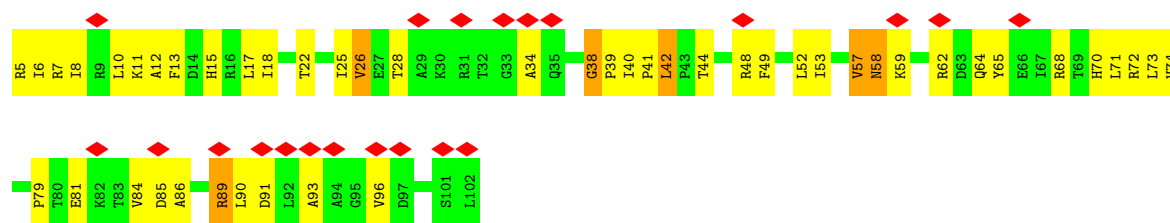


- Molecule 39: 30S ribosomal protein S9

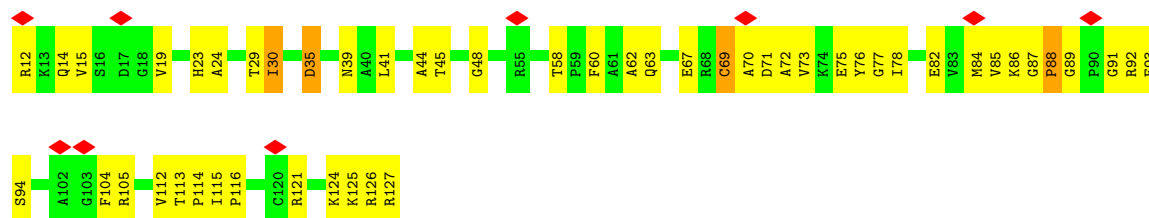


- Molecule 40: 30S ribosomal protein S10

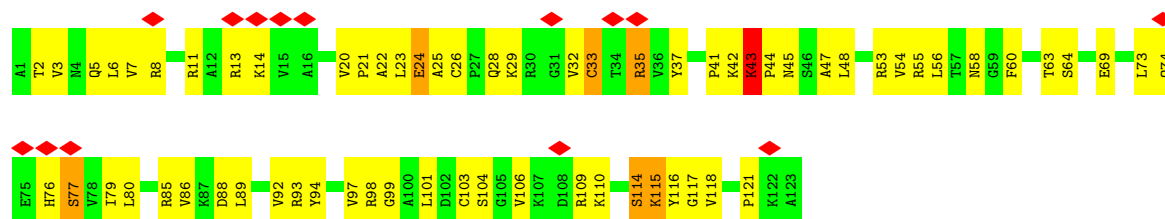




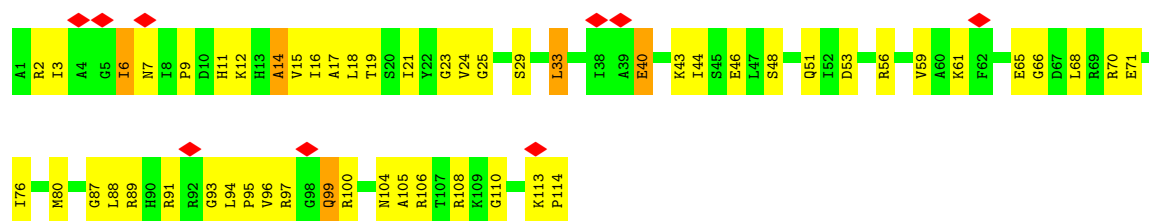
- Molecule 41: 30S ribosomal protein S11



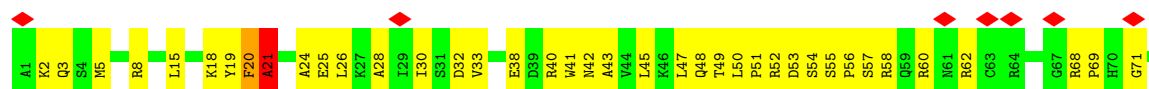
- Molecule 42: 30S ribosomal protein S12

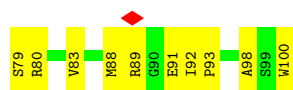


- Molecule 43: 30S ribosomal protein S13

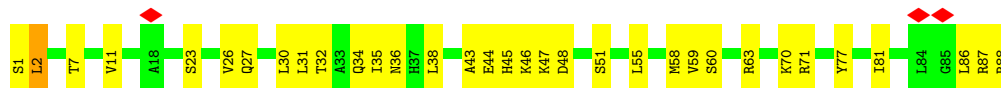


- Molecule 44: 30S ribosomal protein S14

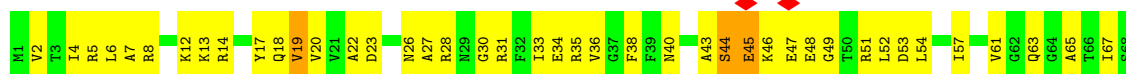




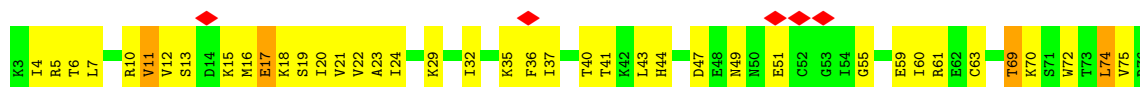
- Molecule 45: 30S ribosomal protein S15



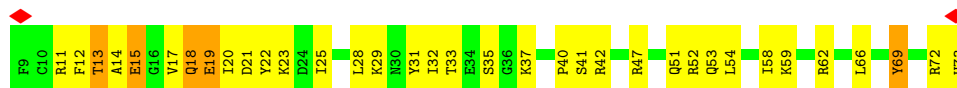
- Molecule 46: 30S ribosomal protein S16



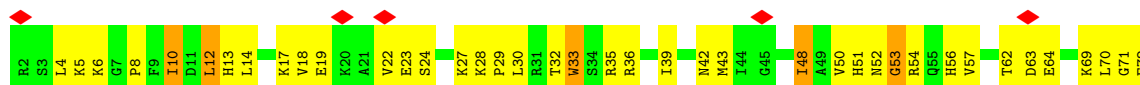
- Molecule 47: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S18

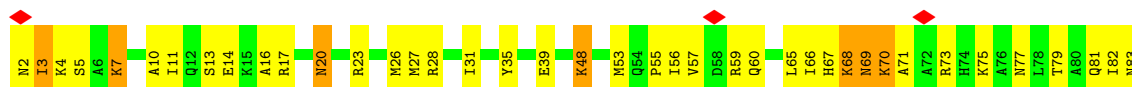


- Molecule 49: 30S ribosomal protein S19

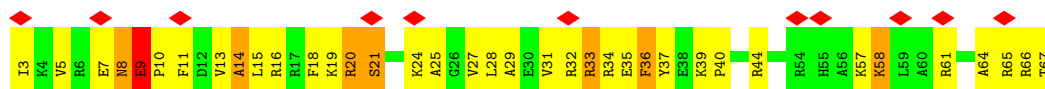
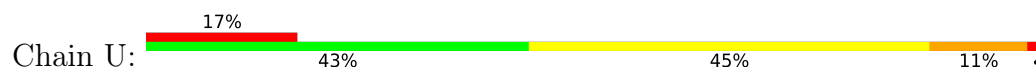




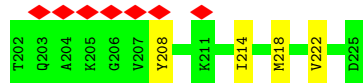
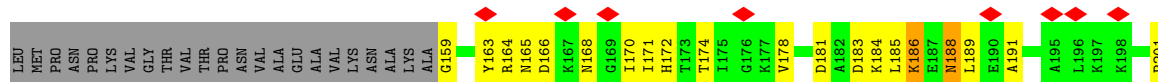
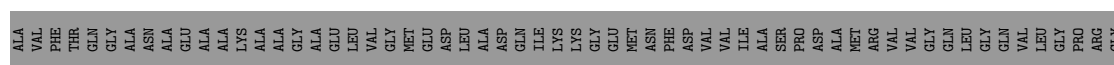
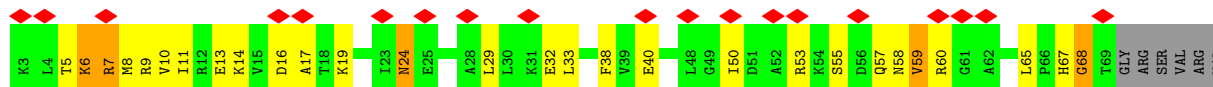
- Molecule 50: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S21

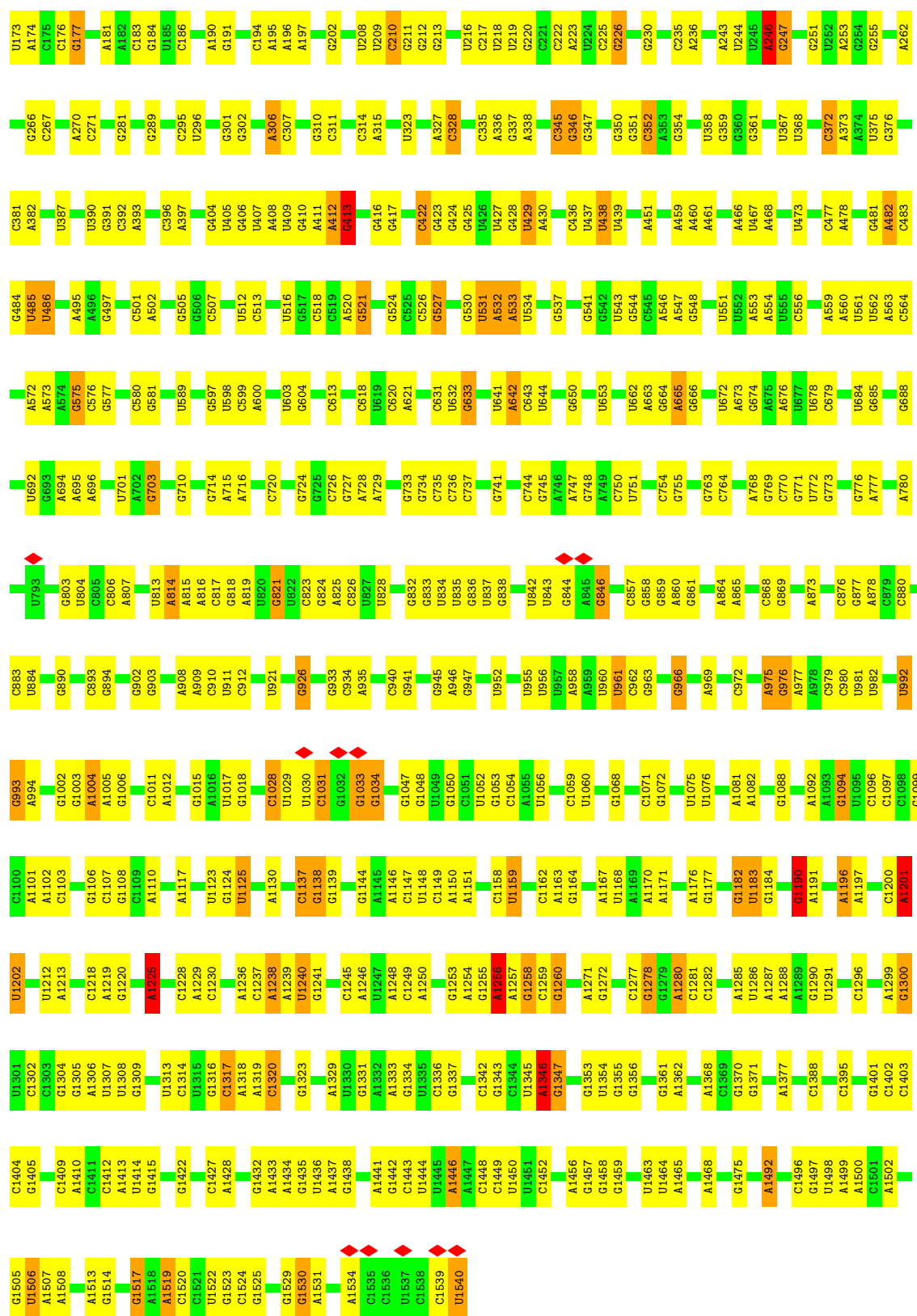


- Molecule 52: 50S ribosomal protein L1



- Molecule 53: 16S ribosomal RNA



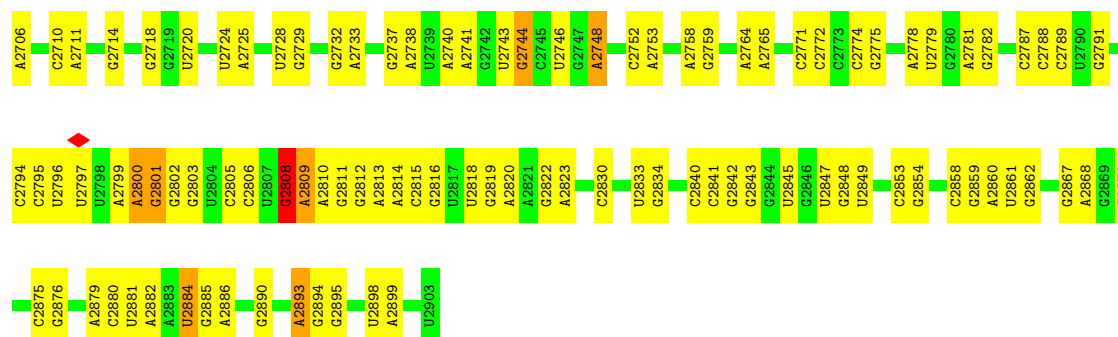


• Molecule 54: 23S ribosomal RNA

Chain 01: 56% 39% 5%

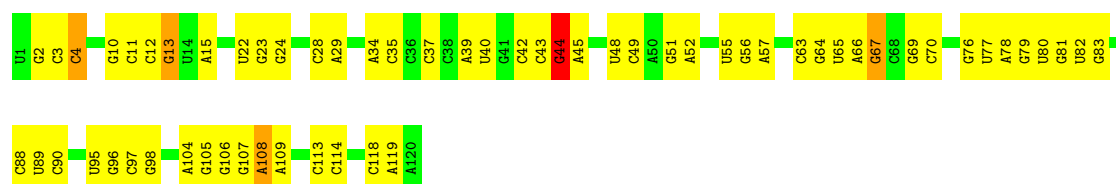
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G1271	A1169	A1168	U1082	C992	C888	G805	A722	G538	G537	U441	A324	A217	U114	G2
A1272	C1170	G1171	U1083	C993	C889	U807	C723	U639	A538	C444	G327	A218	U119	U3
C1278	A1085	A1086	A1087	C994	C890	G808	G726	C640	G539	U451	U328	A221	U120	U4
G1279	G1087	A1088	G1087	C995	G891	U810	A727	U641	A541	A454	A330	A222	G121	G7
A1287	A1089	U1176	A1088	A996	A992	U811	G728	A644	C542	C455	C331	A223	U138	C8
C1288	G1177	G1178	A1089	G997	C993	C812	A730	C645	C543	C456	C337	A226	U139	G9
G1289	G1091	A1001	G1090	A996	A996	U813	A730	U646	C544	A457	C341	A227	C140	A10
C1297	C1092	A1002	G1091	G1002	A996	C814	G740	C650	U545	G458	A342	G232	G141	C11
G1298	G1093	G1011	G1092	U1012	G907	C817	A741	G651	U546	U459	G343	G233	A142	U12
G1299	U1013	U1012	U1012	C1013	G907	G818	A742	A654	A547	A460	C353	G236	C143	C16
G1300	A1014	A1013	A1014	A910	A910	A819	A744	A655	G549	C461	A354	C237	A144	G17
A1301	U1015	U1015	U1015	A917	A917	U826	G745	A656	U552	A470	C357	C238	U150	C20
C1306	C1102	G1106	C1102	C922	C922	U827	G746	C660	G553	A471	U358	C239	U151	A21
G1309	A1103	G1107	A1020	G924	G924	U828	A747	A661	G554	A472	U359	C240	U158	U25
C1315	C1104	U1105	A1021	G925	G925	A829	G748	G662	G555	G473	G359	A241	G159	U29
U1316	G1107	G1107	U1022	A925	A925	G831	A752	G663	A563	C475	U360	G242	A160	U34
G1317	U1108	U1108	U1023	A932	A932	G833	G757	A666	A572	A479	G367	G248	U161	G35
U1318	A1111	A1111	G1026	A933	A933	G834	G760	A667	A573	G481	A368	G249	C163	G36
C1319	G1112	G1112	A1027	G940	G940	C838	A761	A668	U574	G481	U369	C254	C164	C37
A1321	U1033	U1033	A1033	A941	A941	U839	G762	G669	A575	A482	G370	G255	A165	U40
G1326	C1038	G1038	G1038	G942	G942	C840	A763	C671	A576	A483	A371	A256	U171	C41
A1327	A1039	A1039	A1039	G943	G943	A845	A764	C672	G577	C490	U372	A257	A173	G45
G1328	U1127	U1127	C1045	C946	C946	U846	G765	G674	C581	G491	U373	A258	U174	G46
C1330	A1128	A1128	A1046	A947	A947	U847	G766	A677	A582	A492	G376	C267	G175	C44
U1334	G1131	G1131	C1052	C948	C948	U852	G771	G682	U588	G493	G377	C268	A176	A49
G1335	U1132	U1132	C1053	G949	G949	G856	G772	A685	A592	G495	U387	U276	G177	U50
C1345	A1133	A1133	A1054	C950	C950	G857	G773	U686	U593	U499	G386	U277	A181	G51
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C1363	G1139	G1139	U1060	G954	G954	G862	A781	G690	C611	G506	U395	C281	G187	A64
G1364	U1141	U1141	U1061	G955	G955	A863	A782	C691	G612	A507	A404	A284	G188	U65
A1365	C1142	C1142	G1062	G956	G956	G864	A783	G696	U615	C510	U405	G295	G189	C86
C1366	U1065	U1065	C1064	G957	G957	A866	G785	A699	A616	U511	G406	G296	A190	C89
A1367	G1149	G1149	G1065	U967	U967	G869	A788	G700	G617	G512	G407	G297	C192	G70
G1368	C1150	C1150	U1066	C968	C968	U870	A792	G701	A621	G518	G411	G301	A196	A71
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G1370	G1152	G1152	G1068	U970	U970	U872	A796	U703	C623	G520	A415	G303	C198	G75
C1371	C1153	C1153	A1069	G971	G971	C873	G796	G704	A627	U521	A310	A279	A199	U200
U1372	G1154	G1154	A1070	A972	A972	G874	G797	G705	G628	A522	C420	A310	G204	A84
A1373	A1155	A1155	G1071	A973	A973	G874	G797	G706	G629	C523	G424	G312	A204	C96
C1376	U1156	U1156	C1076	A975	A975	A878	G798	G707	G630	A528	A437	G319	G205	C97
G1377	G1157	G1157	U1077	A983	A983	G879	A800	U714	A631	A529	U437	G320	A213	U102
A1378	A1162	A1162	U1078	C987	C987	C885	A802	A715	A632	G530	G438	G321	G214	U102
			C1079	A988	A988	A886	U803	C717	A633	A532	A439	A322	G215	U112

U2609	C2615	G2428	C2342	C2261	U2180	U2105	A2014	U1882	U1781				A1579	A1470	U1379
U2613	A2516	G2429	U2343	U2262	U2181	U2106	U2017	U1883	A1784				A1580	A1474	G1380
A2614	C2517	A2430	U2344	C2263	U2182	G2107		A1884					G1581	U1476	A1383
U2615	U2519	U2431	G2345	U2265	A2183	A2108	A2020	A1885	U1796				A1583		C1386
C2616	C2520	A2432	A2346	U2266	A2184	U2109	C2021	C1893	G1797				U1584	G1482	G1387
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	G2526	U2441	G2351	G2271	U2189	G2114	C2025	A1900	A1801				U1394	U1486	
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G2637	C2538	U2457	G2370	U2292	U2199	G2125	A2037	G1926	U1812				C1507	A1420	
	G2543	C2466	G2371	G2293	U2203	A2126	U2039	G1929	G1813				A1616	G1424	
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	G2553	C2475	A2376	U2302	U2210	U2131	G2048	C1941	U1825				A1515		
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	G2567	G2484	G2389	A2314	G2221	C2146	G2061	C1967	U1756				U1534	G1441	
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	G2581	C2494	U2393	G2316	C2232	U2155	C2066	G1972	A1857				U1539	G1450	
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U2689	A2586	A2497	U2402	G2324	G2239	G2158	A2070	U1991	C1763				C1454	A1453	
U2690	U2587	C2498	C2403	G2325	U2243	A2159	A2071	U1992	C1764				G1560	C1461	
C2691	G2588	U2500	A2411	G2326	U2244	C2160	C2072	G1992	U1765				C1561	C1462	
G2692	U2589	C2501	A2412	G2327	U2245	G2162	C2073	U1993	A1870				U1562	C1463	
U2693	A2590	G2502	G2413	G2328	G2246	A2163	U2074	C1997	A1871				C1563	G1464	
G2694	C2591	C2331	U2419	G2329	A2247	C2164	U2075	C1997	U1769				C1565	U1466	
U2695	G2592	U2334	G2420	G2330	G2248	A2170	C2091	G2002	A1773				A1569	A1570	
U2696	U2597	U2335	G2421	G2331	U2249	A2171	U2092	C2006	C1774				U1567	U1467	
	A2602	A2333	C2422	G2332	C2248	A2172	G2093	C2006	G1775				A1571	U1468	
U2697		G2334	U2423	G2332	U2249	A2173	A2094	C2006	A1676				U1572	A1469	
C2698		A2335	C2424	G2333	G2250	A2174	A2095	G2012	G1666						
U2699		C2336	C2425	G2334	G2251	C2174	C2104	U2013	G1667						
	G2704	U2511	U2340	G2335	U2259	C2175			G1668						
A2705		U2514	C2341	G2341	C2260	A2176									



• Molecule 55: 5S ribosomal RNA

Chain 02: 49% 47% . .



• Molecule 56: tRNA^{fMet}

Chain X: 13% 60% 32% 8%



• Molecule 56: tRNA^{fMet}

Chain W: 74% 21% 5%



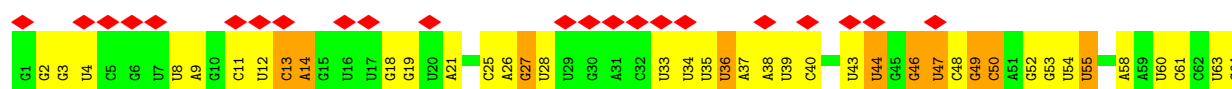
• Molecule 57: mRNA

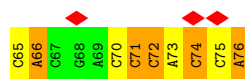
Chain V: 24% 76% 18% 6%



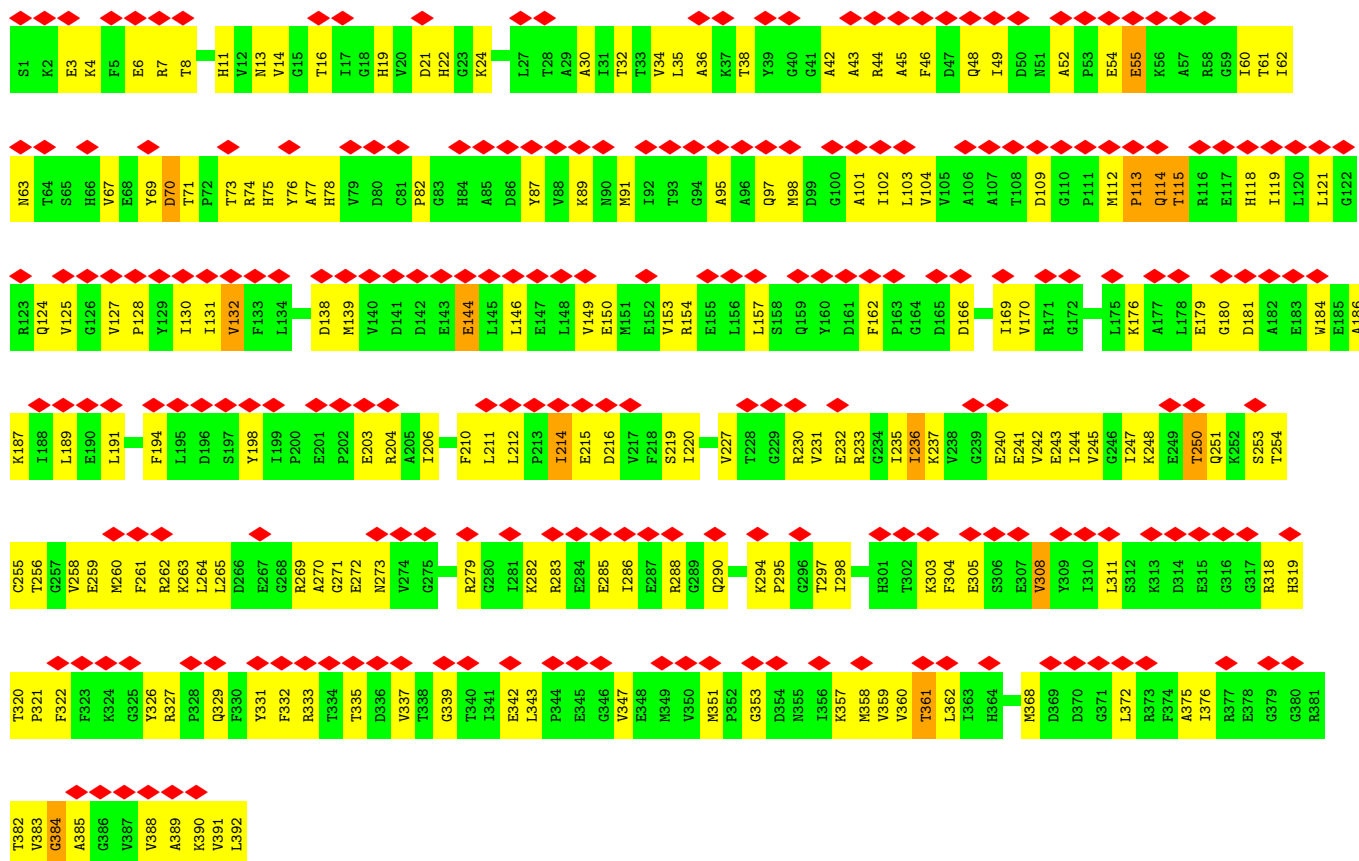
• Molecule 58: tRNA^{Lys}

Chain Y: 33% 36% 45% 20%





● Molecule 59: Elongation factor Tu 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	4629	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	12.452	Depositor
Minimum map value	-6.336	Depositor
Average map value	-0.325	Depositor
Map value standard deviation	1.041	Depositor
Recommended contour level	2.79	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: GCP, U8U

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	0.36	0/2122	0.86	5/2852 (0.2%)
2	05	0.38	0/1586	0.87	3/2134 (0.1%)
3	06	0.38	0/1571	0.97	11/2113 (0.5%)
4	07	0.38	0/1435	0.89	5/1926 (0.3%)
5	08	0.39	0/1343	0.91	1/1816 (0.1%)
6	09	0.45	0/1122	1.04	6/1515 (0.4%)
7	10	0.47	0/1002	1.05	9/1350 (0.7%)
8	11	0.49	0/1046	1.07	9/1410 (0.6%)
9	12	0.38	0/1152	0.87	4/1551 (0.3%)
10	13	0.38	0/948	0.86	2/1268 (0.2%)
11	14	0.38	0/1054	0.95	4/1403 (0.3%)
12	15	0.36	0/1093	0.83	0/1460
13	16	0.37	0/974	0.88	3/1301 (0.2%)
14	17	0.36	0/902	0.85	2/1209 (0.2%)
15	18	0.37	0/929	0.84	0/1242
16	19	0.35	0/960	0.87	0/1278
17	20	0.39	0/829	0.92	4/1107 (0.4%)
18	21	0.37	0/864	0.93	2/1156 (0.2%)
19	22	0.36	0/745	0.86	2/994 (0.2%)
20	23	0.41	0/788	0.99	4/1051 (0.4%)
21	24	0.36	0/766	0.87	3/1025 (0.3%)
22	25	0.33	0/582	0.89	2/769 (0.3%)
23	26	0.32	0/635	0.79	1/848 (0.1%)
24	27	0.32	0/510	1.00	3/677 (0.4%)
25	28	0.36	0/453	0.86	0/605
26	29	0.36	0/532	0.92	2/709 (0.3%)
27	30	0.34	0/450	0.80	1/599 (0.2%)
28	31	0.43	0/417	0.91	2/554 (0.4%)
29	32	0.35	0/380	0.83	0/498
30	33	0.34	0/513	0.84	0/676
31	34	0.37	0/303	0.84	0/397
32	B	0.40	0/1736	0.98	10/2338 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	C	0.39	0/1652	0.87	4/2225 (0.2%)
34	D	0.37	0/1665	0.98	4/2227 (0.2%)
35	E	0.40	0/1170	0.91	3/1573 (0.2%)
36	F	0.43	0/836	0.89	4/1128 (0.4%)
37	G	0.38	0/1196	0.99	3/1602 (0.2%)
38	H	0.38	0/989	0.90	1/1326 (0.1%)
39	I	0.39	0/1034	1.02	5/1375 (0.4%)
40	J	0.42	0/797	0.95	4/1077 (0.4%)
41	K	0.41	0/886	0.87	1/1195 (0.1%)
42	L	0.39	0/969	1.02	6/1300 (0.5%)
43	M	0.38	0/893	0.90	1/1193 (0.1%)
44	N	0.36	0/817	0.88	4/1088 (0.4%)
45	O	0.35	0/722	0.90	1/964 (0.1%)
46	P	0.38	0/659	0.96	2/884 (0.2%)
47	Q	0.42	0/658	0.90	3/881 (0.3%)
48	R	0.41	0/545	0.98	3/731 (0.4%)
49	S	0.42	0/653	0.88	4/877 (0.5%)
50	T	0.34	0/671	0.99	5/888 (0.6%)
51	U	0.44	0/551	1.06	7/728 (1.0%)
52	03	0.44	0/1034	1.05	8/1387 (0.6%)
53	A	0.47	0/36963	0.55	11/57662 (0.0%)
54	01	0.47	0/69796	0.55	12/108888 (0.0%)
55	02	0.49	0/2872	0.55	1/4479 (0.0%)
56	W	0.49	0/1832	0.53	0/2855
56	X	0.51	0/1832	0.58	0/2855
57	V	0.50	0/421	0.61	0/657
58	Y	0.53	0/1780	0.59	1/2767 (0.0%)
59	Z	0.46	0/3085	0.96	14/4173 (0.3%)
All	All	0.45	0/166720	0.68	212/248816 (0.1%)

There are no bond length outliers.

The worst 5 of 212 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	09	51	ARG	N-CA-C	9.59	124.23	112.54
20	23	96	LYS	N-CA-C	-9.54	96.39	110.52
50	T	69	ASN	N-CA-C	-9.22	102.16	113.41
52	03	185	LEU	N-CA-C	-8.80	101.97	112.89
34	D	46	ARG	N-CA-C	-8.75	102.04	112.89

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	86	0
2	05	1565	0	1616	72	0
3	06	1552	0	1619	71	0
4	07	1411	0	1447	84	0
5	08	1323	0	1374	46	0
6	09	1111	0	1148	60	0
7	10	989	0	1025	58	0
8	11	1032	0	1088	74	0
9	12	1129	0	1162	46	0
10	13	939	0	1012	36	0
11	14	1045	0	1117	42	0
12	15	1074	0	1157	52	0
13	16	961	0	1000	41	0
14	17	892	0	923	31	0
15	18	917	0	965	45	0
16	19	947	0	1022	47	0
17	20	816	0	839	46	0
18	21	857	0	922	33	0
19	22	739	0	807	25	0
20	23	780	0	834	30	0
21	24	753	0	780	32	0
22	25	575	0	592	14	0
23	26	625	0	655	26	0
24	27	509	0	543	22	0
25	28	449	0	491	9	0
26	29	523	0	524	15	0
27	30	444	0	461	23	0
28	31	410	0	440	12	0
29	32	377	0	418	22	0
30	33	504	0	574	29	0
31	34	302	0	343	25	0
32	B	1705	0	1732	84	0
33	C	1625	0	1699	58	0
34	D	1643	0	1710	79	0
35	E	1157	0	1199	77	0
36	F	818	0	808	43	0
37	G	1182	0	1240	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	H	979	0	1034	52	0
39	I	1022	0	1070	60	0
40	J	787	0	828	37	0
41	K	870	0	878	44	0
42	L	955	0	1019	61	0
43	M	884	0	944	50	0
44	N	805	0	847	42	0
45	O	714	0	737	28	0
46	P	649	0	666	55	0
47	Q	649	0	691	36	0
48	R	536	0	552	37	0
49	S	638	0	665	39	0
50	T	665	0	714	38	0
51	U	545	0	579	32	0
52	03	1027	0	1092	43	0
53	A	33012	0	16618	465	0
54	01	62317	0	31346	878	0
55	02	2568	0	1303	54	0
56	W	1640	0	837	11	0
56	X	1640	0	837	20	0
57	V	373	0	187	2	0
58	Y	1618	0	821	37	0
59	Z	3029	0	3043	160	0
60	Z	32	0	14	1	0
All	All	153717	0	104765	3460	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 13.

The worst 5 of 3460 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)
54:01:45:G:H5''	54:01:46:G:H5'	1.37	1.06
12:15:45:GLN:HE21	54:01:2485:G:H5''	1.26	1.00
3:06:76:PRO:HA	3:06:82:GLY:HA2	1.45	0.94
54:01:1045:C:H5'	54:01:1046:A:H5'	1.49	0.93
6:09:12:LEU:HD22	6:09:19:VAL:HG11	1.51	0.93

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%)	229 (85%)	37 (14%)	3 (1%)	11	44
2	05	207/209 (99%)	173 (84%)	30 (14%)	4 (2%)	6	34
3	06	199/201 (99%)	177 (89%)	19 (10%)	3 (2%)	8	38
4	07	175/177 (99%)	147 (84%)	26 (15%)	2 (1%)	11	44
5	08	174/176 (99%)	152 (87%)	18 (10%)	4 (2%)	5	31
6	09	147/149 (99%)	117 (80%)	22 (15%)	8 (5%)	1	18
7	10	129/131 (98%)	93 (72%)	26 (20%)	10 (8%)	1	12
8	11	139/141 (99%)	111 (80%)	19 (14%)	9 (6%)	1	15
9	12	140/142 (99%)	124 (89%)	14 (10%)	2 (1%)	9	39
10	13	120/122 (98%)	95 (79%)	20 (17%)	5 (4%)	2	21
11	14	141/143 (99%)	112 (79%)	23 (16%)	6 (4%)	2	20
12	15	134/136 (98%)	120 (90%)	10 (8%)	4 (3%)	3	26
13	16	118/120 (98%)	100 (85%)	16 (14%)	2 (2%)	7	36
14	17	114/116 (98%)	99 (87%)	13 (11%)	2 (2%)	6	34
15	18	112/114 (98%)	97 (87%)	12 (11%)	3 (3%)	4	28
16	19	115/117 (98%)	108 (94%)	6 (5%)	1 (1%)	14	48
17	20	101/103 (98%)	78 (77%)	21 (21%)	2 (2%)	6	33
18	21	108/110 (98%)	92 (85%)	15 (14%)	1 (1%)	14	48
19	22	91/93 (98%)	72 (79%)	17 (19%)	2 (2%)	5	31
20	23	100/102 (98%)	85 (85%)	11 (11%)	4 (4%)	2	21
21	24	92/94 (98%)	79 (86%)	12 (13%)	1 (1%)	11	44
22	25	73/75 (97%)	61 (84%)	12 (16%)	0	100	100
23	26	75/77 (97%)	67 (89%)	8 (11%)	0	100	100
24	27	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	7	37
25	28	56/58 (97%)	51 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	29	64/66 (97%)	44 (69%)	20 (31%)	0	100	100
27	30	54/56 (96%)	48 (89%)	6 (11%)	0	100	100
28	31	48/50 (96%)	41 (85%)	6 (12%)	1 (2%)	5	32
29	32	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
30	33	62/64 (97%)	54 (87%)	6 (10%)	2 (3%)	3	25
31	34	36/38 (95%)	28 (78%)	6 (17%)	2 (6%)	1	17
32	B	216/218 (99%)	174 (81%)	35 (16%)	7 (3%)	3	25
33	C	204/206 (99%)	186 (91%)	15 (7%)	3 (2%)	8	38
34	D	203/205 (99%)	167 (82%)	28 (14%)	8 (4%)	2	22
35	E	155/157 (99%)	123 (79%)	21 (14%)	11 (7%)	1	14
36	F	98/100 (98%)	79 (81%)	11 (11%)	8 (8%)	0	11
37	G	149/151 (99%)	124 (83%)	20 (13%)	5 (3%)	3	24
38	H	127/129 (98%)	113 (89%)	11 (9%)	3 (2%)	4	30
39	I	125/127 (98%)	93 (74%)	27 (22%)	5 (4%)	2	21
40	J	96/98 (98%)	67 (70%)	22 (23%)	7 (7%)	1	13
41	K	114/116 (98%)	89 (78%)	20 (18%)	5 (4%)	2	20
42	L	121/123 (98%)	85 (70%)	28 (23%)	8 (7%)	1	15
43	M	112/114 (98%)	93 (83%)	15 (13%)	4 (4%)	2	23
44	N	98/100 (98%)	84 (86%)	12 (12%)	2 (2%)	6	33
45	O	86/88 (98%)	77 (90%)	6 (7%)	3 (4%)	3	23
46	P	80/82 (98%)	62 (78%)	14 (18%)	4 (5%)	1	18
47	Q	78/80 (98%)	63 (81%)	13 (17%)	2 (3%)	4	29
48	R	63/65 (97%)	52 (82%)	8 (13%)	3 (5%)	2	19
49	S	77/79 (98%)	64 (83%)	11 (14%)	2 (3%)	4	29
50	T	83/85 (98%)	75 (90%)	6 (7%)	2 (2%)	4	30
51	U	63/65 (97%)	38 (60%)	21 (33%)	4 (6%)	1	15
52	03	130/223 (58%)	105 (81%)	23 (18%)	2 (2%)	8	38
59	Z	390/392 (100%)	337 (86%)	49 (13%)	4 (1%)	12	45
All	All	6366/6563 (97%)	5298 (83%)	882 (14%)	186 (3%)	5	26

5 of 186 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	06	83	VAL
3	06	184	ASP
5	08	46	ASP
5	08	174	LYS
6	09	9	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	04	216/216 (100%)	214 (99%)	2 (1%)	70	76
2	05	164/164 (100%)	162 (99%)	2 (1%)	63	73
3	06	165/165 (100%)	164 (99%)	1 (1%)	78	81
4	07	148/148 (100%)	145 (98%)	3 (2%)	48	66
5	08	137/137 (100%)	136 (99%)	1 (1%)	76	79
6	09	114/114 (100%)	113 (99%)	1 (1%)	70	76
7	10	100/100 (100%)	99 (99%)	1 (1%)	68	76
8	11	109/109 (100%)	107 (98%)	2 (2%)	51	68
9	12	116/116 (100%)	115 (99%)	1 (1%)	70	76
10	13	103/103 (100%)	102 (99%)	1 (1%)	68	76
11	14	102/102 (100%)	101 (99%)	1 (1%)	68	76
12	15	109/109 (100%)	107 (98%)	2 (2%)	51	68
13	16	100/100 (100%)	99 (99%)	1 (1%)	68	76
14	17	86/86 (100%)	86 (100%)	0	100	100
15	18	99/99 (100%)	99 (100%)	0	100	100
16	19	89/89 (100%)	89 (100%)	0	100	100
17	20	84/84 (100%)	82 (98%)	2 (2%)	43	63
18	21	93/93 (100%)	92 (99%)	1 (1%)	65	74
19	22	80/80 (100%)	79 (99%)	1 (1%)	61	72
20	23	83/83 (100%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	24	78/78 (100%)	78 (100%)	0	100	100
22	25	57/57 (100%)	57 (100%)	0	100	100
23	26	67/67 (100%)	67 (100%)	0	100	100
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	180/180 (100%)	178 (99%)	2 (1%)	65	74
33	C	170/170 (100%)	169 (99%)	1 (1%)	78	81
34	D	172/172 (100%)	167 (97%)	5 (3%)	37	58
35	E	119/119 (100%)	117 (98%)	2 (2%)	53	68
36	F	87/87 (100%)	86 (99%)	1 (1%)	65	74
37	G	124/124 (100%)	121 (98%)	3 (2%)	43	63
38	H	104/104 (100%)	103 (99%)	1 (1%)	68	76
39	I	105/105 (100%)	104 (99%)	1 (1%)	68	76
40	J	86/86 (100%)	85 (99%)	1 (1%)	63	73
41	K	89/89 (100%)	85 (96%)	4 (4%)	24	47
42	L	103/103 (100%)	103 (100%)	0	100	100
43	M	92/92 (100%)	90 (98%)	2 (2%)	45	65
44	N	83/83 (100%)	82 (99%)	1 (1%)	63	73
45	O	76/76 (100%)	74 (97%)	2 (3%)	40	61
46	P	65/65 (100%)	63 (97%)	2 (3%)	35	56
47	Q	74/74 (100%)	72 (97%)	2 (3%)	39	60
48	R	56/56 (100%)	56 (100%)	0	100	100
49	S	70/70 (100%)	68 (97%)	2 (3%)	37	58
50	T	65/65 (100%)	62 (95%)	3 (5%)	24	47
51	U	55/55 (100%)	54 (98%)	1 (2%)	51	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	03	110/174 (63%)	109 (99%)	1 (1%)	70	76
59	Z	324/325 (100%)	316 (98%)	8 (2%)	42	62
All	All	5285/5350 (99%)	5216 (99%)	69 (1%)	59	72

5 of 69 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	T	48	LYS
51	U	20	ARG
59	Z	144	GLU
32	B	23	ASN
28	31	45	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 138 such sidechains are listed below:

Mol	Chain	Res	Type
47	Q	8	GLN
49	S	55	GLN
59	Z	19	HIS
16	19	43	GLN
15	18	40	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	A	1538/1539 (99%)	150 (9%)	7 (0%)
54	01	2902/2903 (99%)	348 (11%)	12 (0%)
55	02	119/120 (99%)	11 (9%)	1 (0%)
56	W	76/77 (98%)	8 (10%)	0
56	X	76/77 (98%)	14 (18%)	0
57	V	16/17 (94%)	2 (12%)	0
58	Y	75/76 (98%)	22 (29%)	0
All	All	4802/4809 (99%)	555 (11%)	20 (0%)

5 of 555 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	31	G
53	A	32	A
53	A	39	G

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	01	1378	A
54	01	2391	G
55	02	88	C
54	01	2808	G
53	A	1347	G

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

1 non-standard protein/DNA/RNA residue 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	$\# Z > 2$
58	U8U	Y	34	58	20,24,25	1.24	2 (10%)	22,34,37	1.00	2 (9%)

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
58	U8U	Y	34	58	-	3/10/28/29	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	Y	34	U8U	C6-N1	3.84	1.44	1.38
58	Y	34	U8U	C4-C5	2.58	1.51	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	Y	34	U8U	C2'-C1'-N1	2.56	120.36	113.25
58	Y	34	U8U	C5-C6-N1	2.01	125.64	122.94

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	Y	34	U8U	N-C-C5-C4
58	Y	34	U8U	C5-C-N-CA
58	Y	34	U8U	N-C-C5-C6

There are no ring outliers.

No monomer is involved in short contacts.

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	GCP	Z	401	-	32,34,34	1.76	5 (15%)	49,54,54	2.57	15 (30%)

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	GCP	Z	401	-	-	9/19/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	Z	401	GCP	PA-O3A	-5.68	1.53	1.59
60	Z	401	GCP	PB-O3A	-4.16	1.53	1.58
60	Z	401	GCP	C1'-N9	3.16	1.56	1.47
60	Z	401	GCP	PB-O2B	-2.13	1.51	1.56
60	Z	401	GCP	C2'-C3'	2.13	1.59	1.53

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	Z	401	GCP	C1'-N9-C4	8.23	150.81	126.49
60	Z	401	GCP	C1'-N9-C8	-7.81	104.54	126.73
60	Z	401	GCP	O1G-PG-C3B	-7.37	95.29	111.37
60	Z	401	GCP	O2B-PB-O1B	3.86	122.50	109.95
60	Z	401	GCP	O5'-PA-O1A	-3.75	94.07	108.94

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	Z	401	GCP	PB-C3B-PG-O1G
60	Z	401	GCP	PB-C3B-PG-O2G
60	Z	401	GCP	PG-C3B-PB-O1B
60	Z	401	GCP	O4'-C4'-C5'-O5'
60	Z	401	GCP	C3'-C4'-C5'-O5'

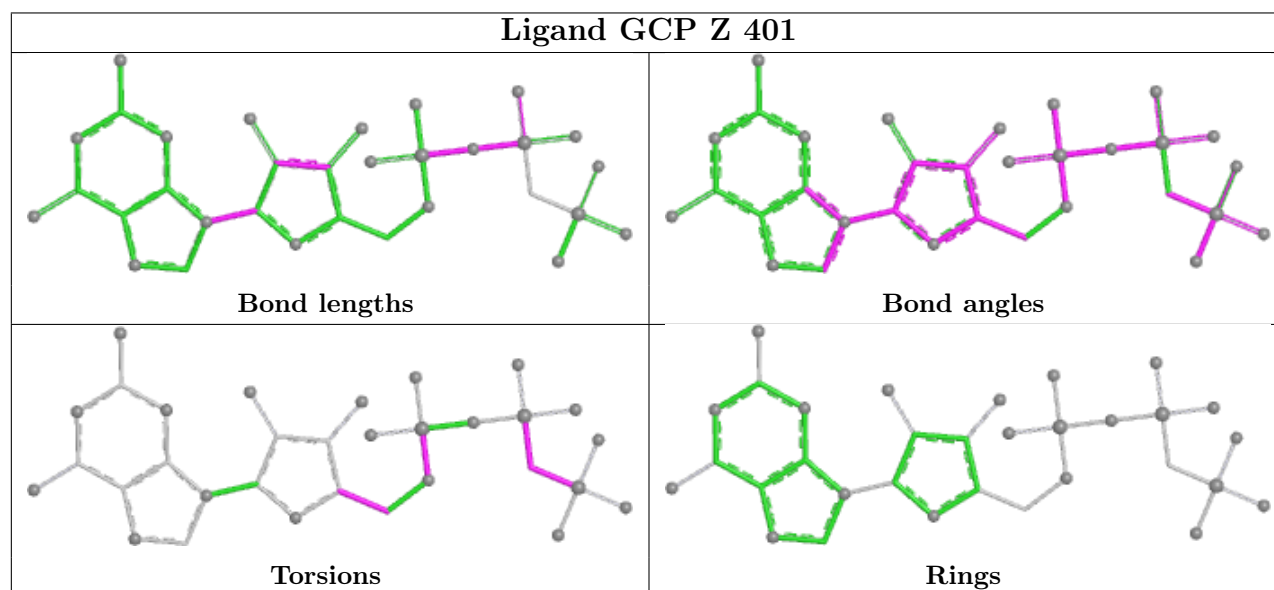
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	Z	401	GCP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

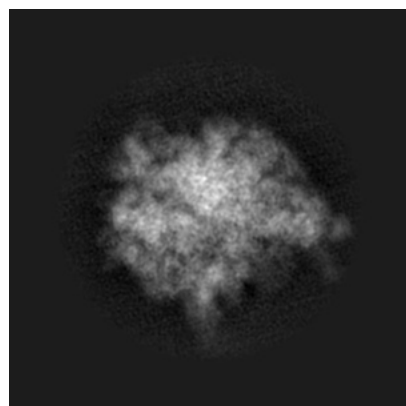
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8618. These allow visual inspection of the internal detail of the map and identification of artifacts.

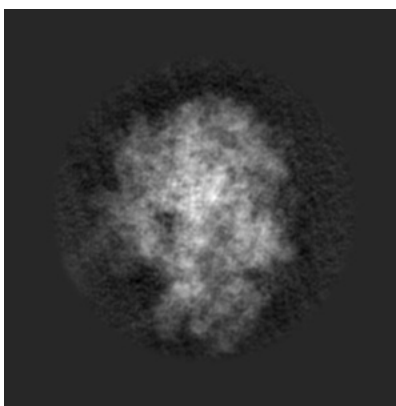
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

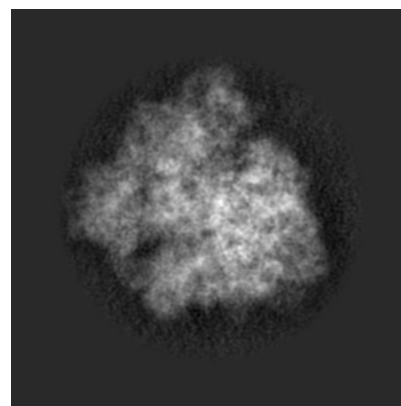
6.1.1 Primary map



X

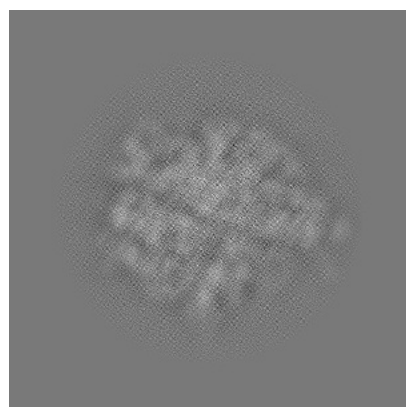


Y

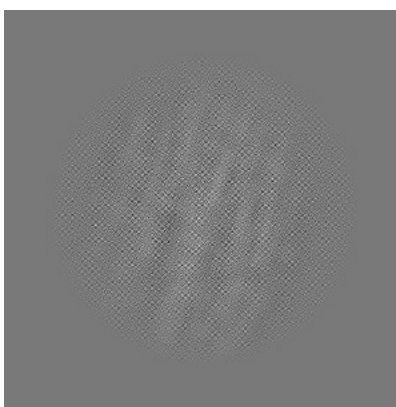


Z

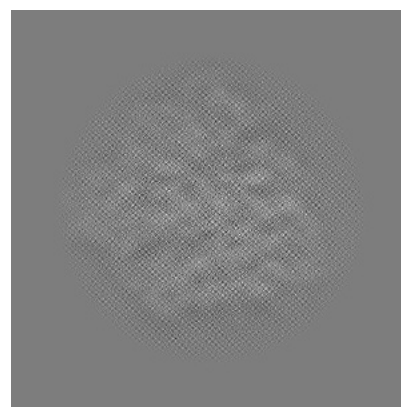
6.1.2 Raw map



X



Y

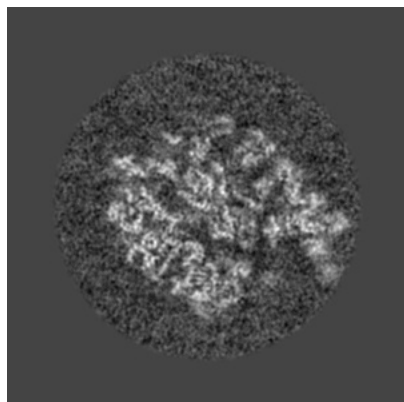


Z

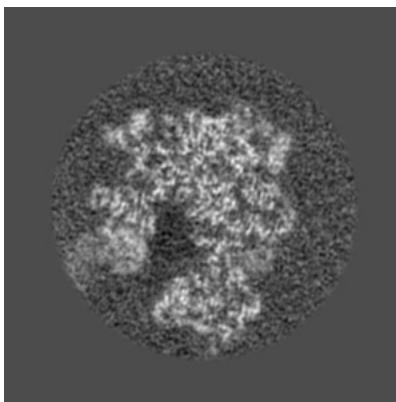
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

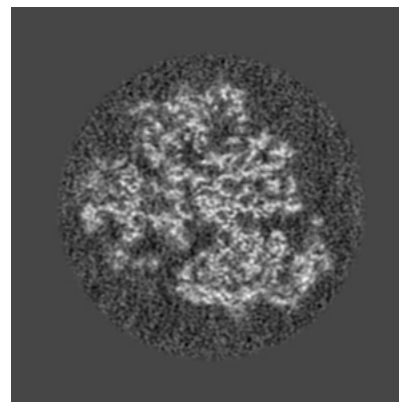
6.2.1 Primary map



X Index: 240

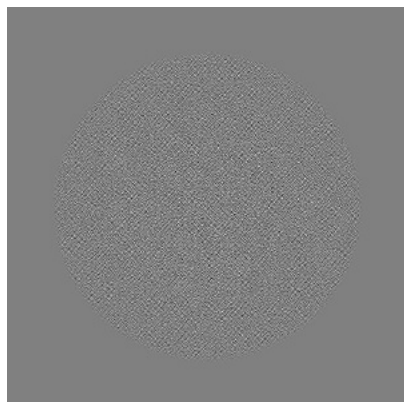


Y Index: 240

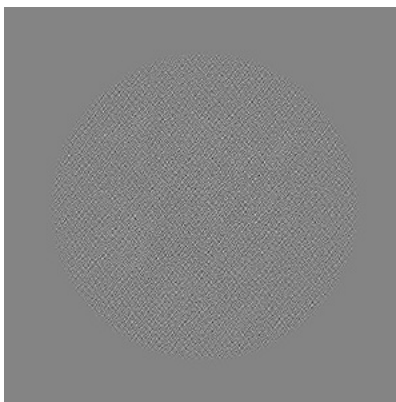


Z Index: 240

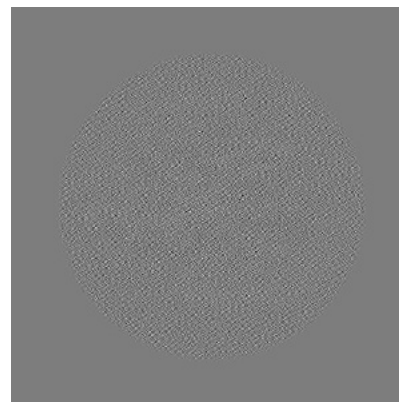
6.2.2 Raw map



X Index: 240



Y Index: 240

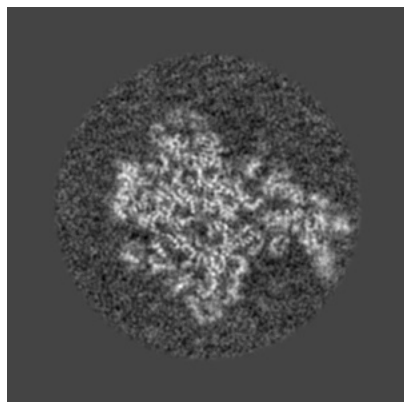


Z Index: 240

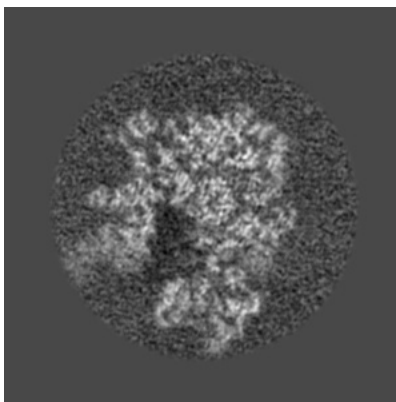
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

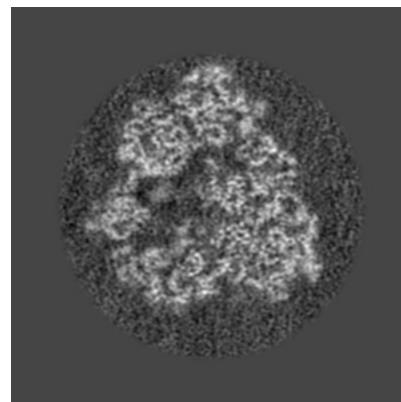
6.3.1 Primary map



X Index: 251

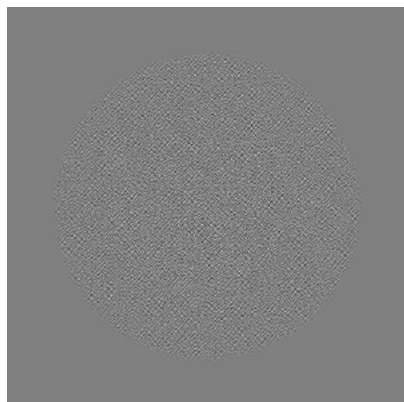


Y Index: 244

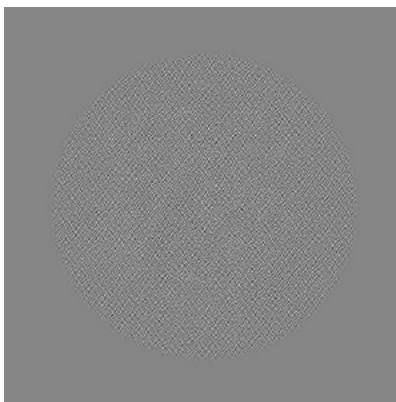


Z Index: 219

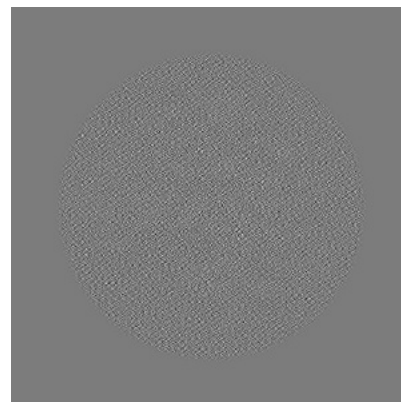
6.3.2 Raw map



X Index: 240



Y Index: 234

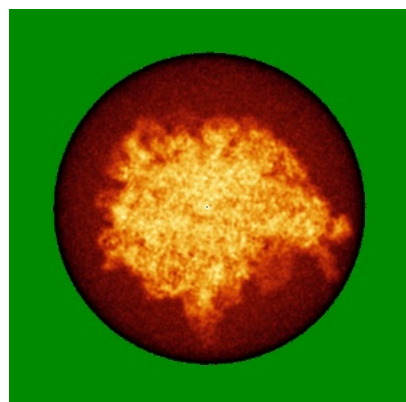


Z Index: 252

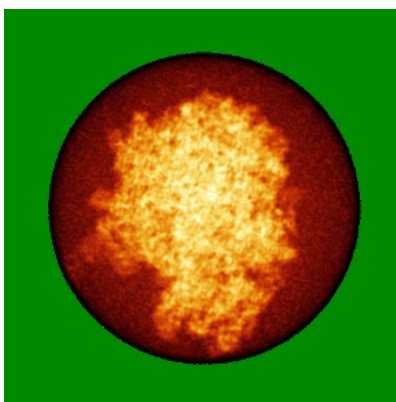
The images above show the largest variance slices of the map in three orthogonal directions.

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

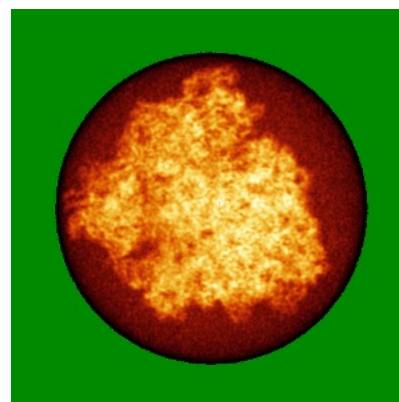
6.4.1 Primary map



X

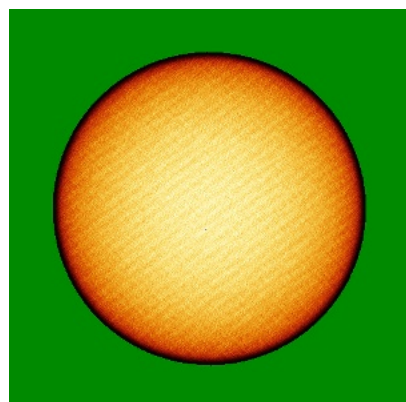


Y

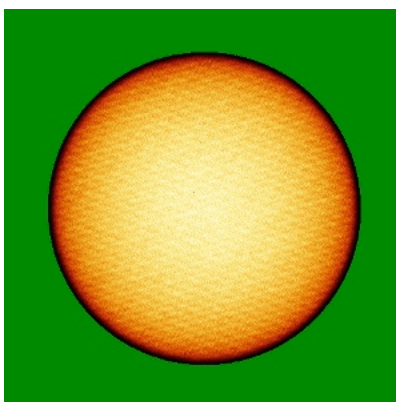


Z

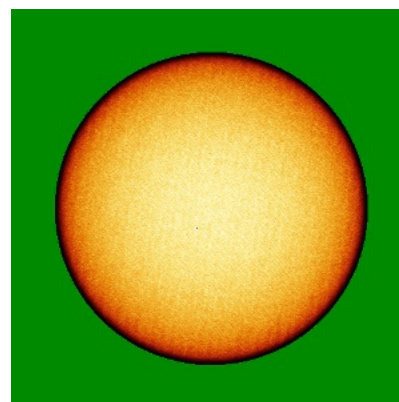
6.4.2 Raw map



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.

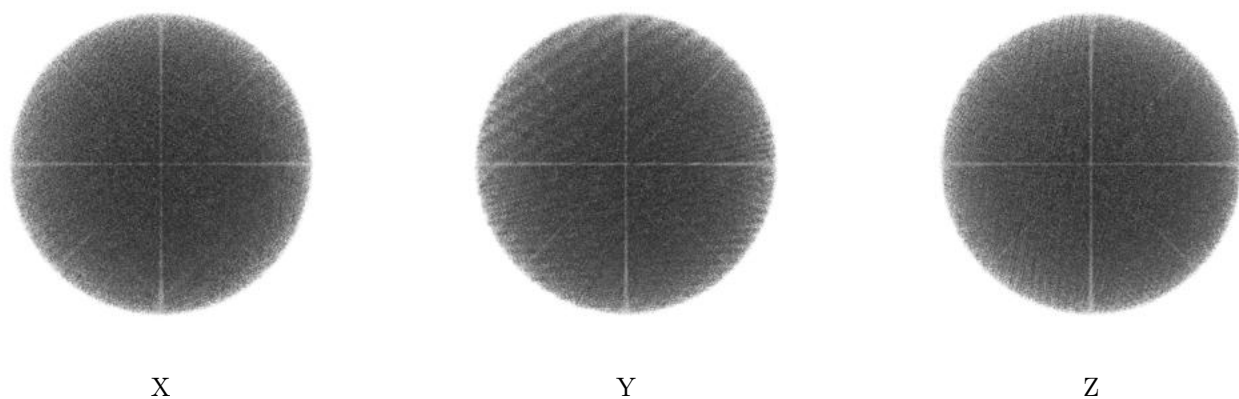
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.79. 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.

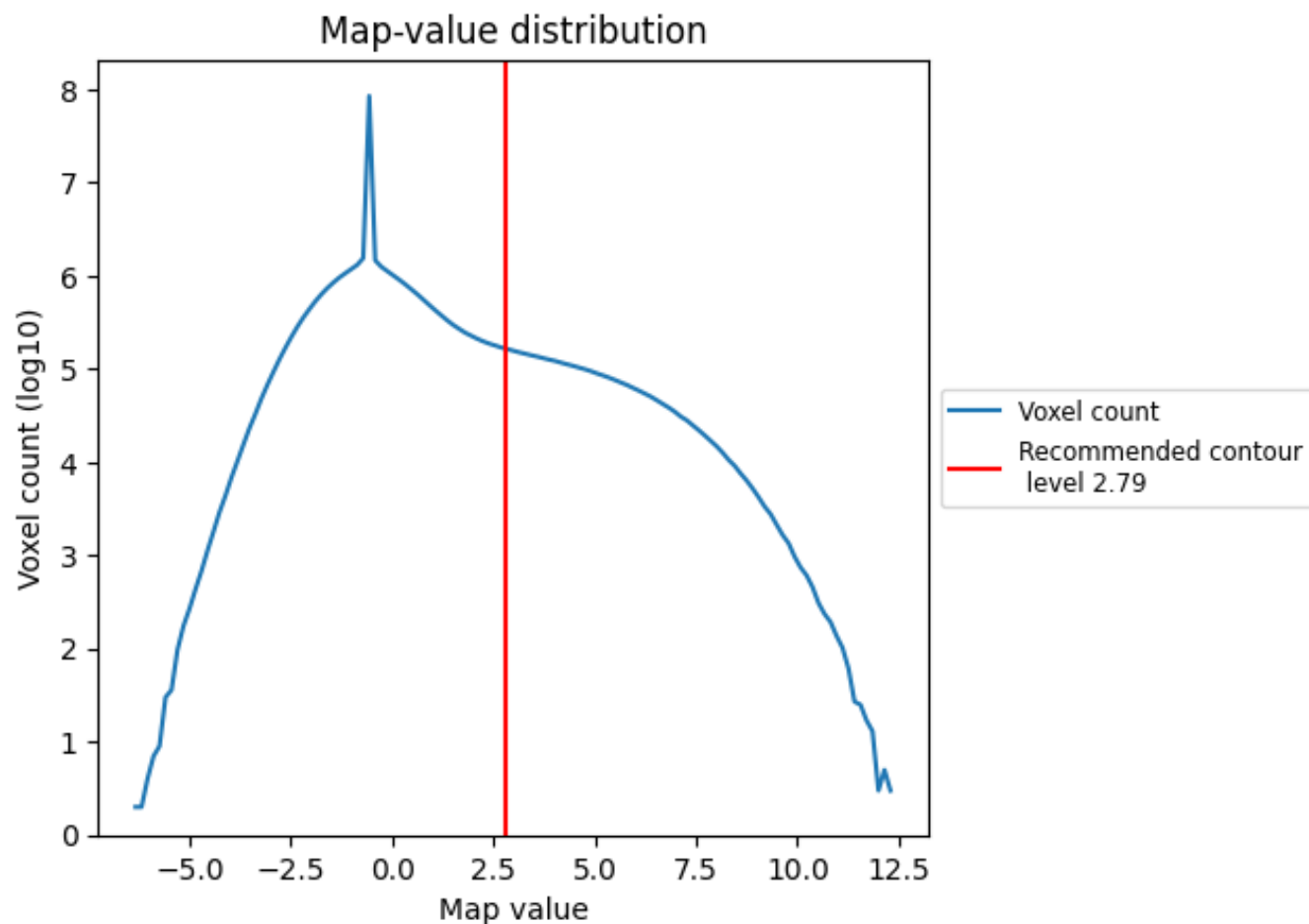
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

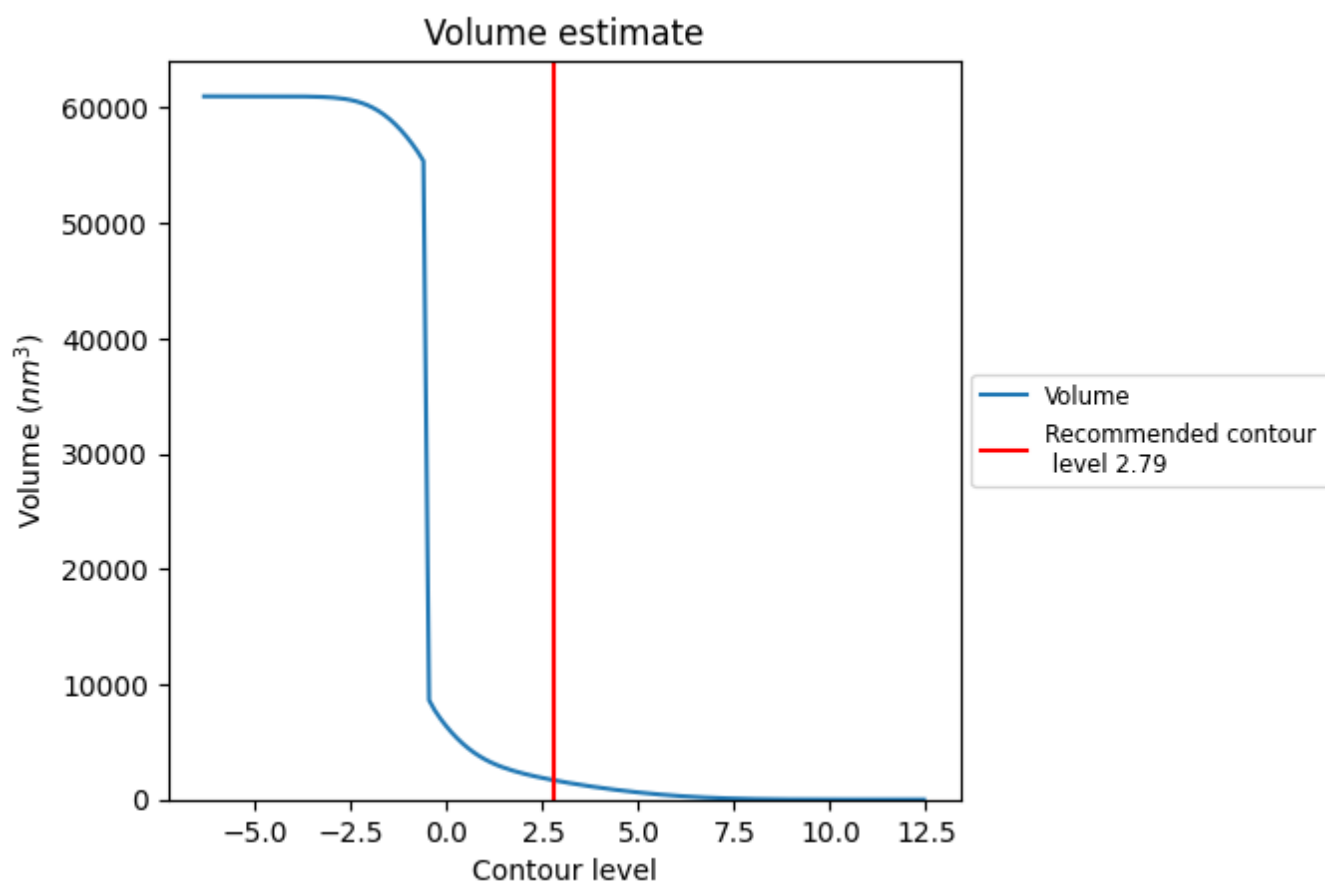
This section contains the results of statistical analysis of the map.

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.

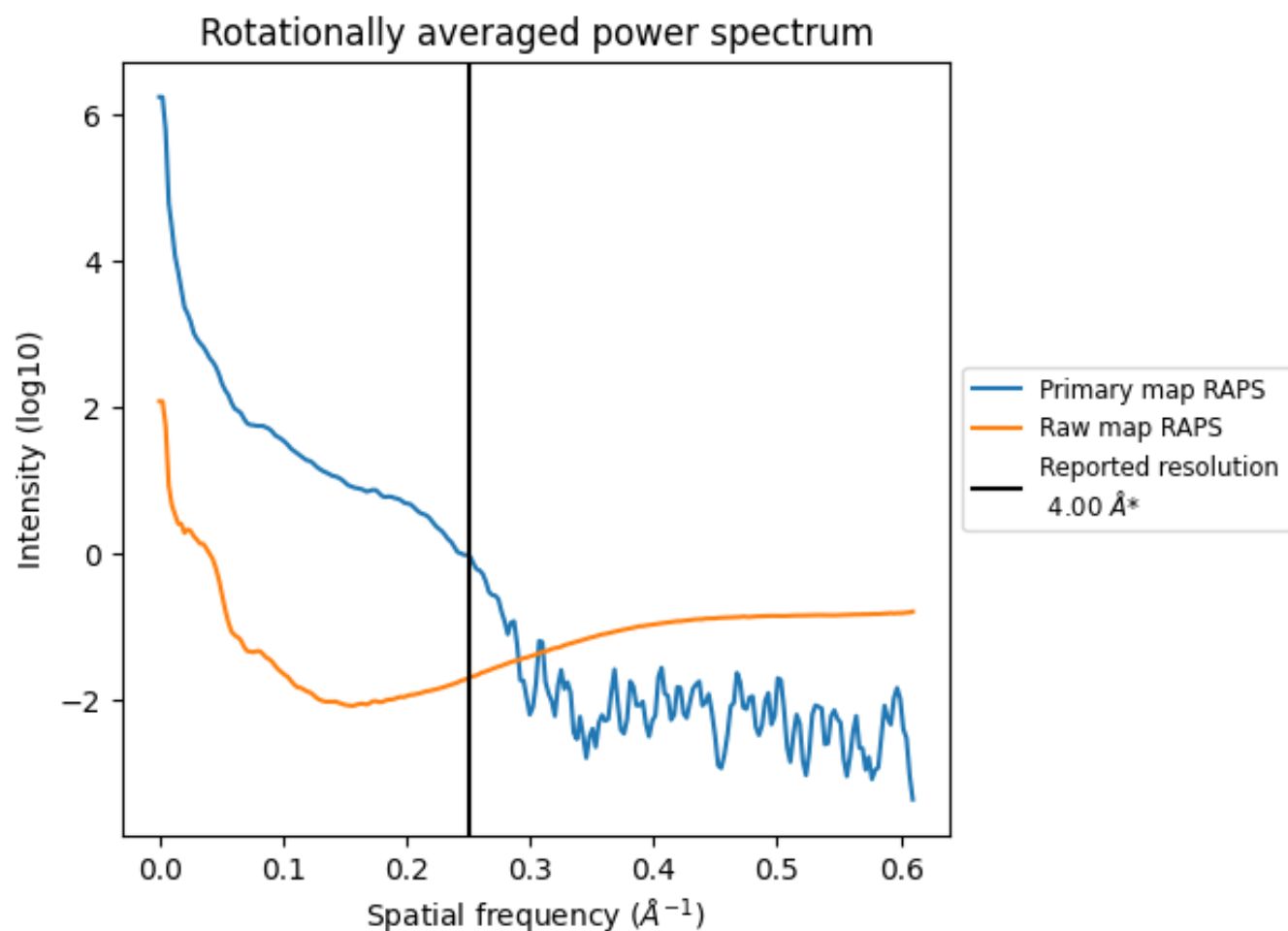
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1679 nm³; this corresponds to an approximate mass of 1517 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 ⓘ

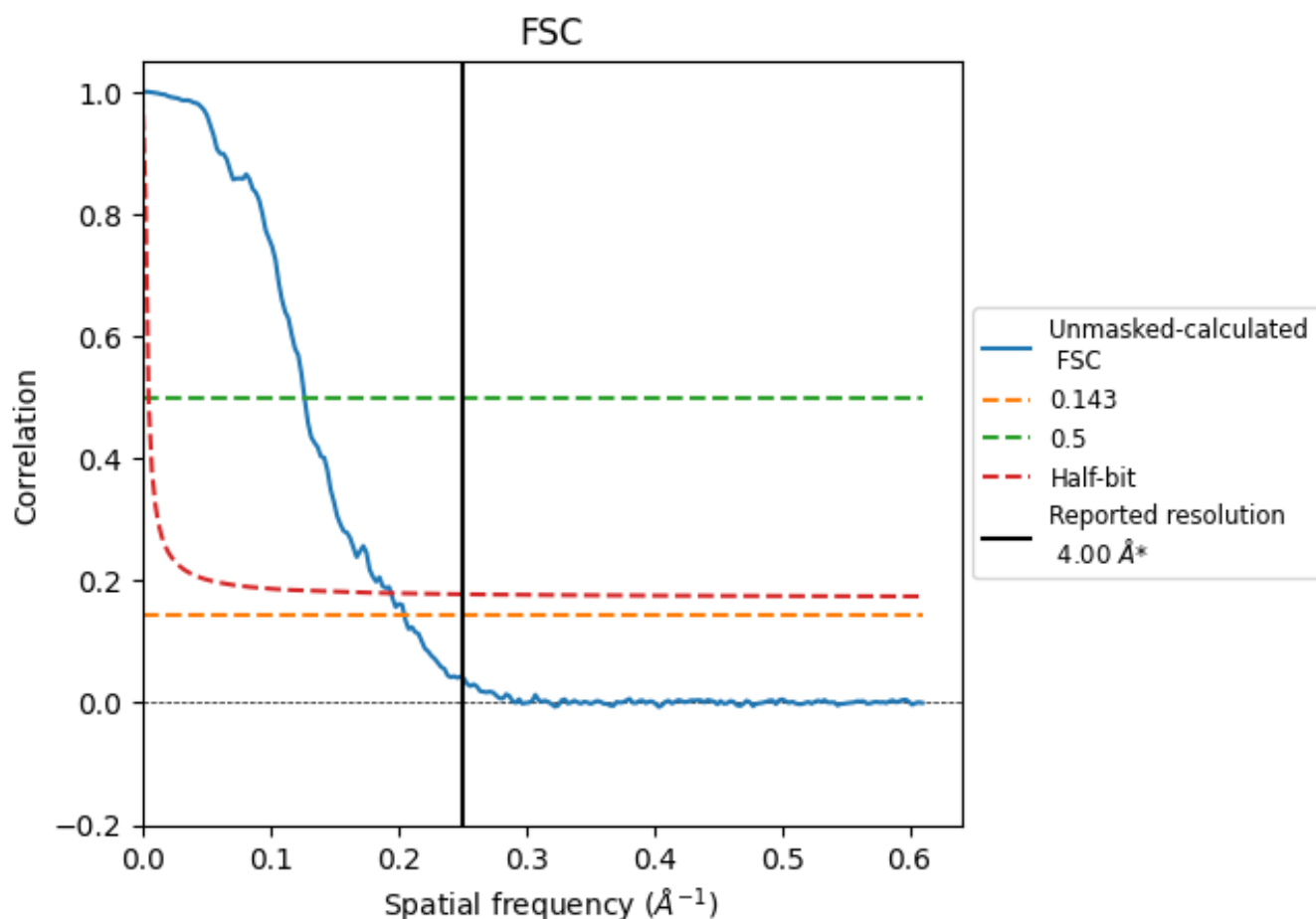


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

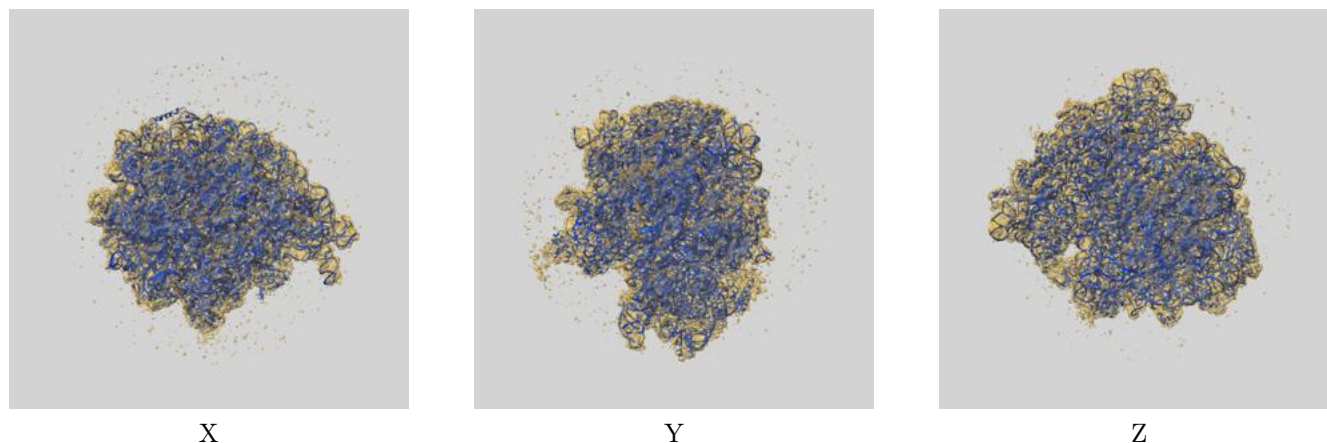
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.88	7.88	5.14

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.88 differs from the reported value 4.0 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8618 and PDB model 5UYN. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



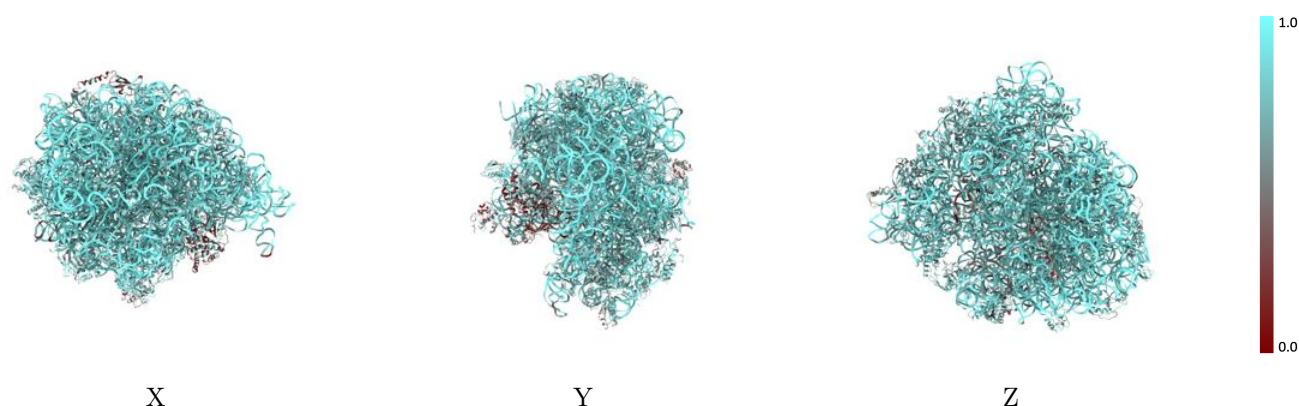
The images above show the 3D surface view of the map at the recommended contour level 2.79 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



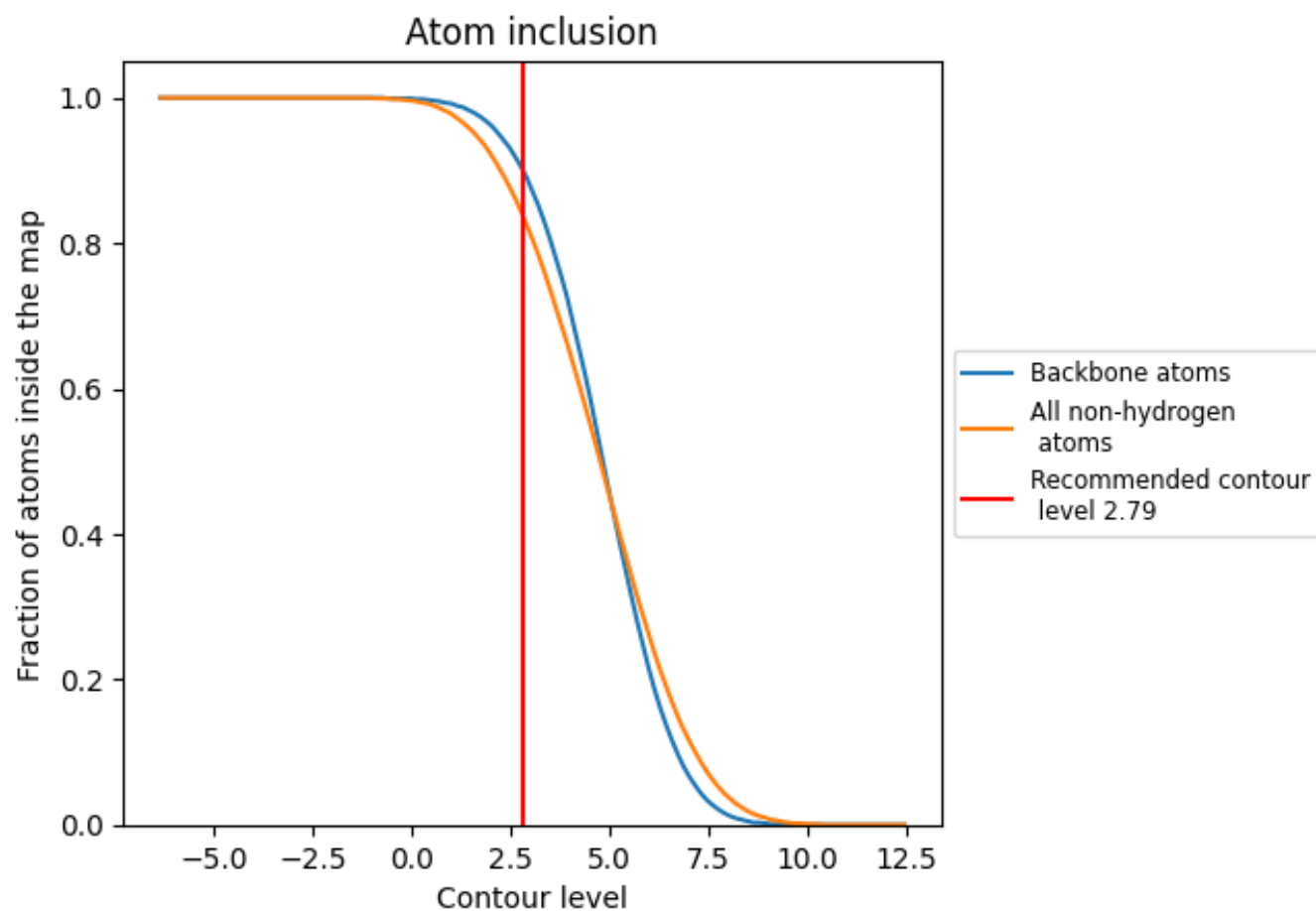
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.79).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 84% 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 (2.79) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8410	 0.3160
01	 0.9270	 0.3300
02	 0.9360	 0.3190
03	 0.5890	 0.2000
04	 0.7880	 0.3640
05	 0.7680	 0.3660
06	 0.7440	 0.3180
07	 0.7550	 0.3010
08	 0.7980	 0.3200
09	 0.4200	 0.2620
10	 0.4410	 0.1700
11	 0.5460	 0.2060
12	 0.7500	 0.3500
13	 0.6630	 0.3550
14	 0.7580	 0.3250
15	 0.6810	 0.3550
16	 0.7980	 0.3280
17	 0.7990	 0.3150
18	 0.7190	 0.3290
19	 0.7660	 0.3220
20	 0.7140	 0.3100
21	 0.7050	 0.3190
22	 0.7650	 0.3240
23	 0.7550	 0.2910
24	 0.7910	 0.3420
25	 0.7660	 0.3600
26	 0.7470	 0.3400
27	 0.7240	 0.2610
28	 0.7300	 0.3210
29	 0.7270	 0.2810
30	 0.7710	 0.3410
31	 0.6770	 0.2940
32	 0.8080	 0.3360
33	 0.7960	 0.3450
34	 0.7940	 0.3580



Continued on next page...

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Chain	Atom inclusion	Q-score
A	 0.9160	 0.3230
B	 0.6690	 0.2810
C	 0.6830	 0.3300
D	 0.7080	 0.2920
E	 0.7010	 0.3320
F	 0.7590	 0.3060
G	 0.7320	 0.2930
H	 0.7530	 0.3280
I	 0.7600	 0.2830
J	 0.5910	 0.2730
K	 0.7330	 0.3170
L	 0.7420	 0.3390
M	 0.7200	 0.2950
N	 0.7020	 0.3020
O	 0.7940	 0.3270
P	 0.8170	 0.3300
Q	 0.7160	 0.3060
R	 0.7510	 0.2930
S	 0.7600	 0.2950
T	 0.7550	 0.2940
U	 0.6330	 0.2610
V	 0.6170	 0.2090
W	 0.8310	 0.2930
X	 0.6590	 0.1740
Y	 0.5180	 0.1620
Z	 0.3720	 0.2160