



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:24 PM UTC

PDB ID : 7K55 / pdb_00007k55
EMDB ID : EMD-22674
Title : Near post-translocated +1-frameshifting(CCC-A) complex with EF-G and GDPCP (Structure III-FS)
Authors : Demo, G.; Loveland, A.B.; Svidritskiy, E.; Gamper, H.B.; Hou, Y.M.; Korostelev, A.A.
Deposited on : 2020-09-16
Resolution : 3.30 Å(reported)
Based on initial models : 5UYM, 4V9P, 4V7D, 6ENJ

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

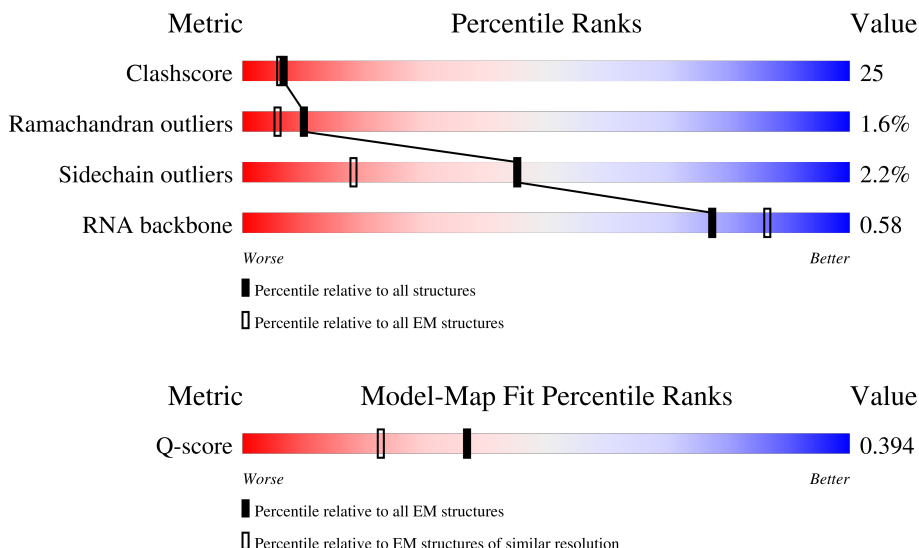
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 Å.

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



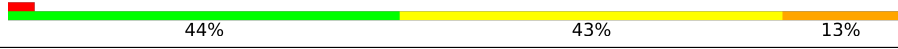
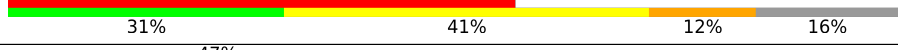
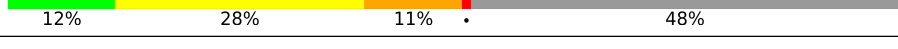
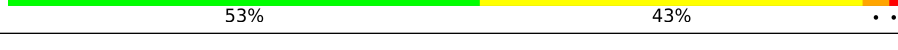
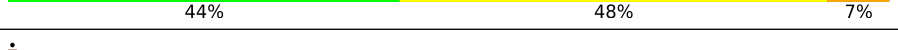
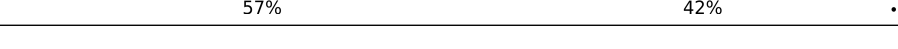
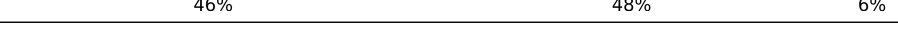
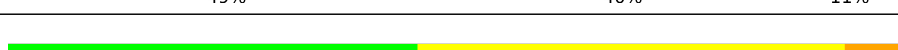
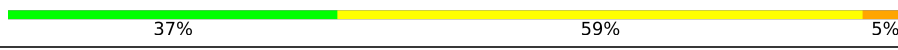
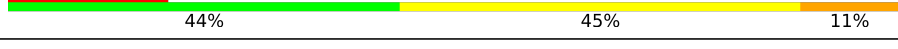
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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

Mol	Chain	Length	Quality of chain
1	b	271	
2	c	209	

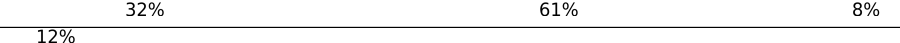
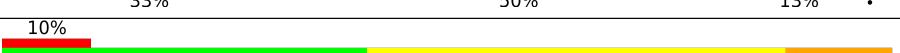
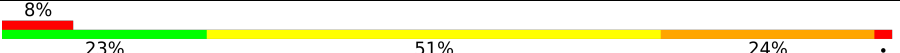
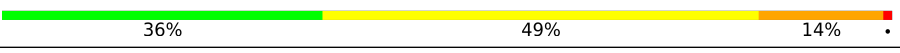
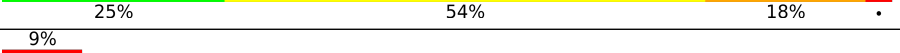
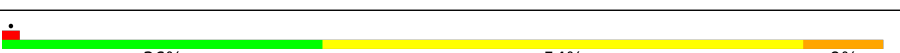
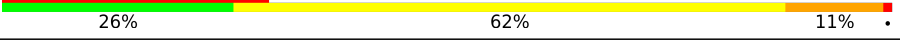
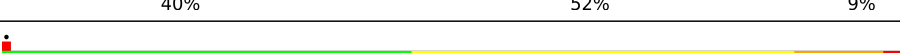
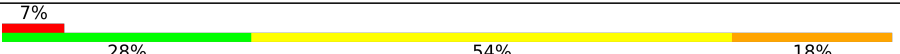
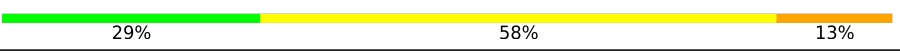
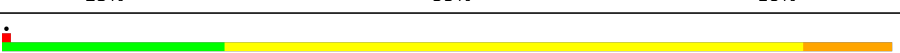
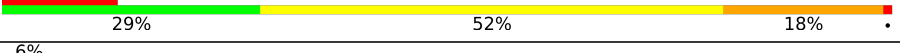
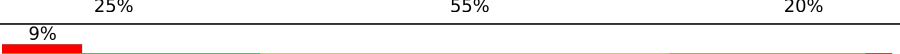
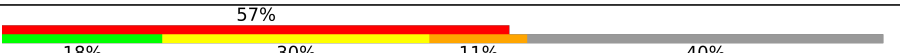
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Mol	Chain	Length	Quality of chain
3	d	201	
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	A	66	
27	B	56	

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

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Mol	Chain	Length	Quality of chain
53	3	1539	32%59%8%
54	1	2903	40%52%8%
55	2	120	45%44%10%
56	5	77	53%35%12%
57	6	77	36%40%43%14%
58	4	16	6%31%38%25%6%
59	8	711	20%25%57%14%

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 153368 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	b	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	c	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	d	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	e	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	f	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	g	125	Total	C	N	O	S	0	0
			936	590	166	179	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	84	Total	C	N	O	S	0	0
			633	397	114	118	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	74	Total	C	N	O	S	0	0
			551	358	91	99	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	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	k	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	l	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	m	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	n	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	o	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	p	114	Total	C	N	O	S	0
			917	574	179	163	1	0

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	v	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	w	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	x	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	y	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	z	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	A	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	B	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	C	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	D	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	E	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	F	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	G	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	H	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	I	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	J	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	K	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	L	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	M	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	N	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	O	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	P	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	Q	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	R	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	S	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	T	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	U	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	V	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	W	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	X	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	Y	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	Z	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	a	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	3	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	1	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
1	747	C	U	conflict	GB 802133627

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

Mol	Chain	Residues	Atoms					AltConf	Trace
55	2	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
2	120	A	-	insertion	GB 1266961702

- Molecule 56 is a RNA chain called tRNAPro.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	5	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

- Molecule 57 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 58 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	4	16	Total	C	N	O	P	0	0
			346	155	68	107	16		

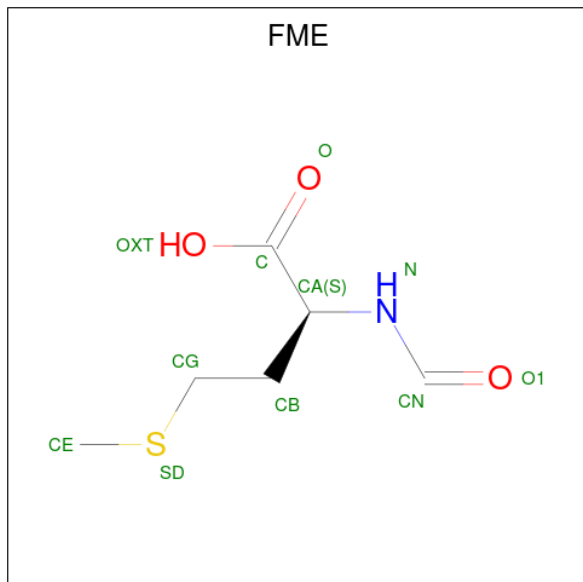
- Molecule 59 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	8	685	Total	C	N	O	S	0	0
			5312	3351	911	1025	25		

There are 8 discrepancies between the modelled and reference sequences:

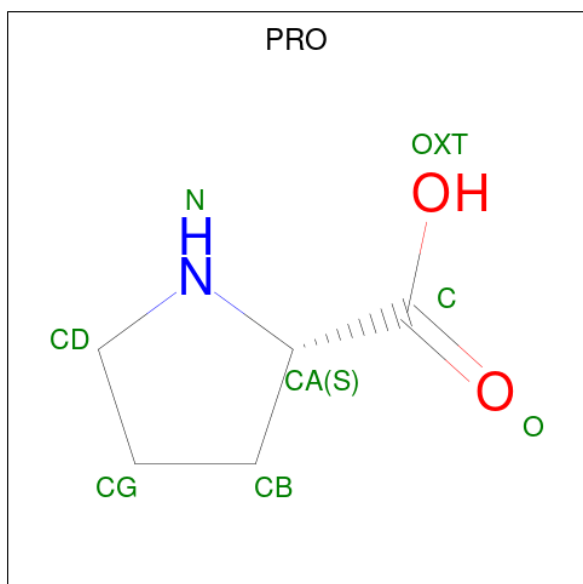
Chain	Residue	Modelled	Actual	Comment	Reference
8	705	LEU	-	expression tag	UNP U9XYS4
8	706	GLU	-	expression tag	UNP U9XYS4
8	707	HIS	-	expression tag	UNP U9XYS4
8	708	HIS	-	expression tag	UNP U9XYS4
8	709	HIS	-	expression tag	UNP U9XYS4
8	710	HIS	-	expression tag	UNP U9XYS4
8	711	HIS	-	expression tag	UNP U9XYS4
8	712	HIS	-	expression tag	UNP U9XYS4

- Molecule 60 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$) (labeled as "Ligand of Interest" by depositor).



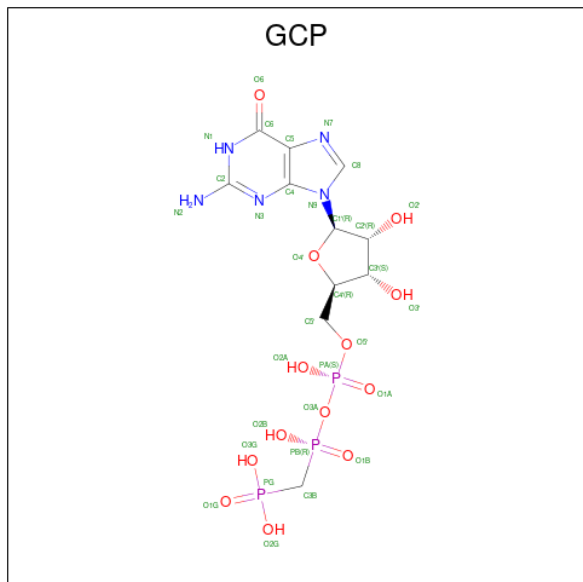
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
60	1	1	10	6	1	2	1	0

- Molecule 61 is PROLINE (CCD ID: PRO) (formula: $C_5H_9NO_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
61	5	1	7	5	1	1	0

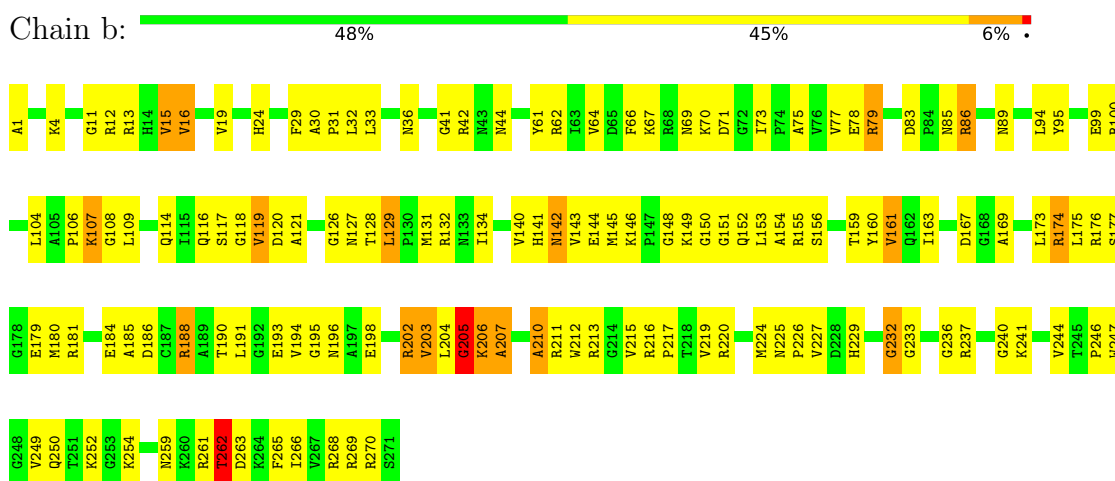
- Molecule 62 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



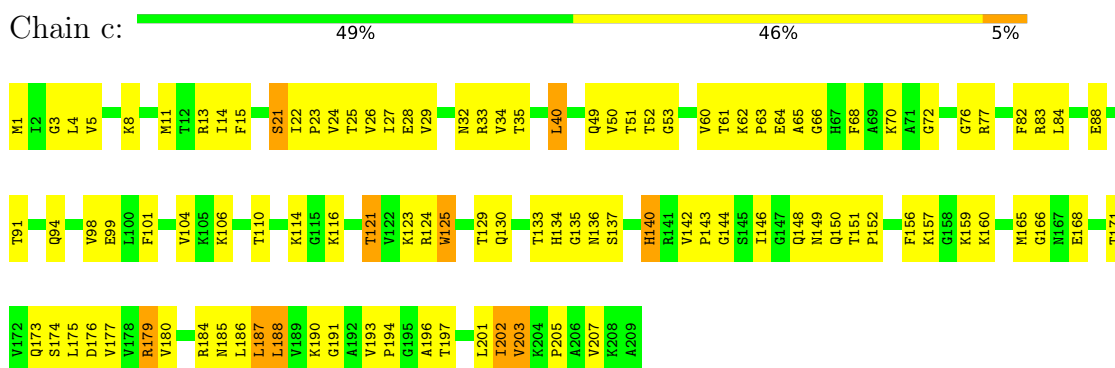
3 Residue-property plots

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.

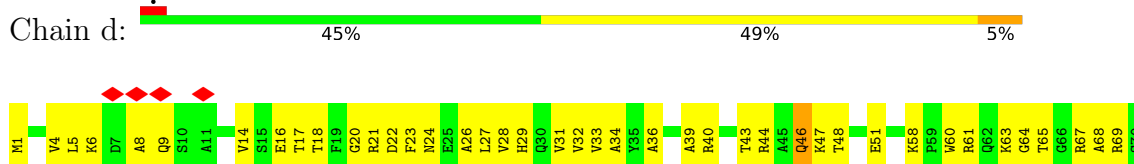
• Molecule 1: 50S ribosomal protein L2

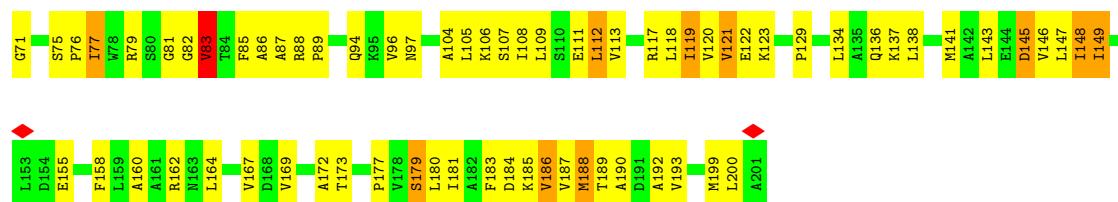


• Molecule 2: 50S ribosomal protein L3

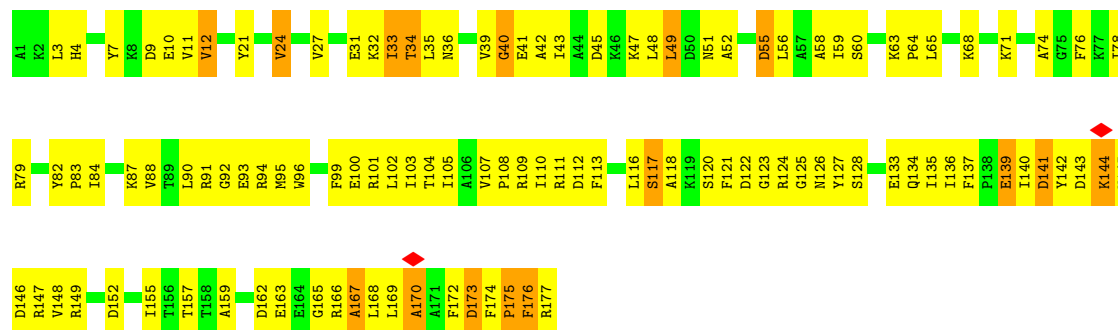


• Molecule 3: 50S ribosomal protein L4

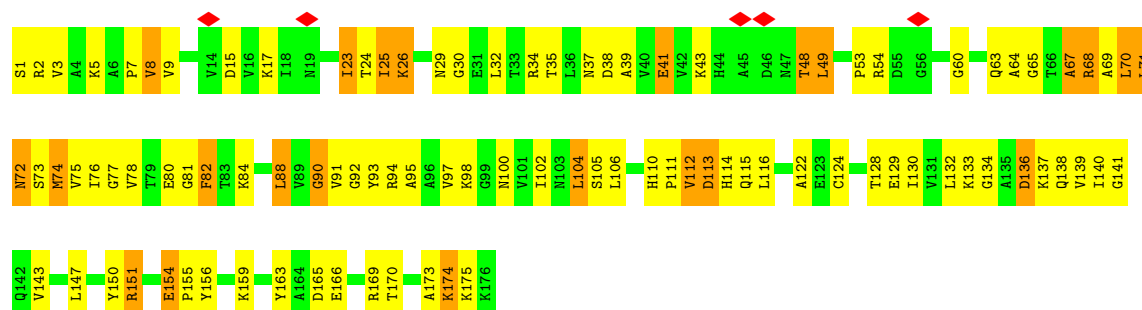




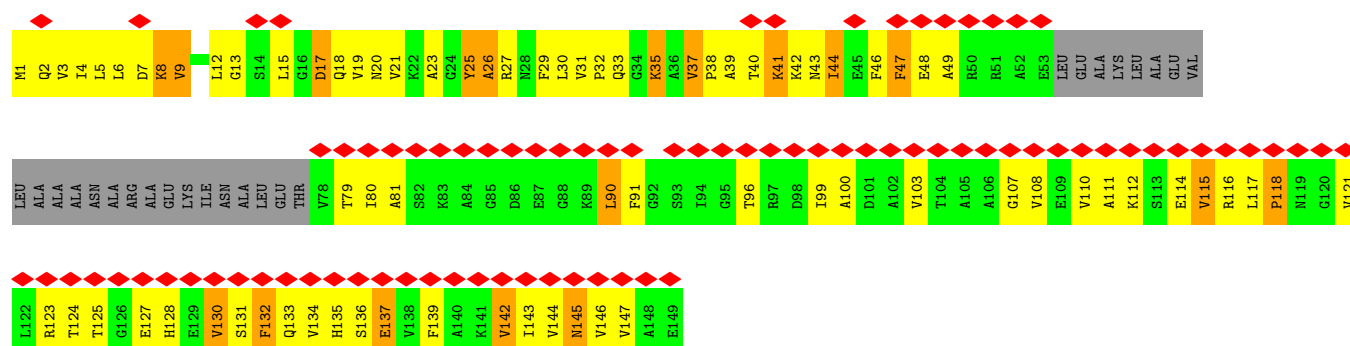
• Molecule 4: 50S ribosomal protein L5



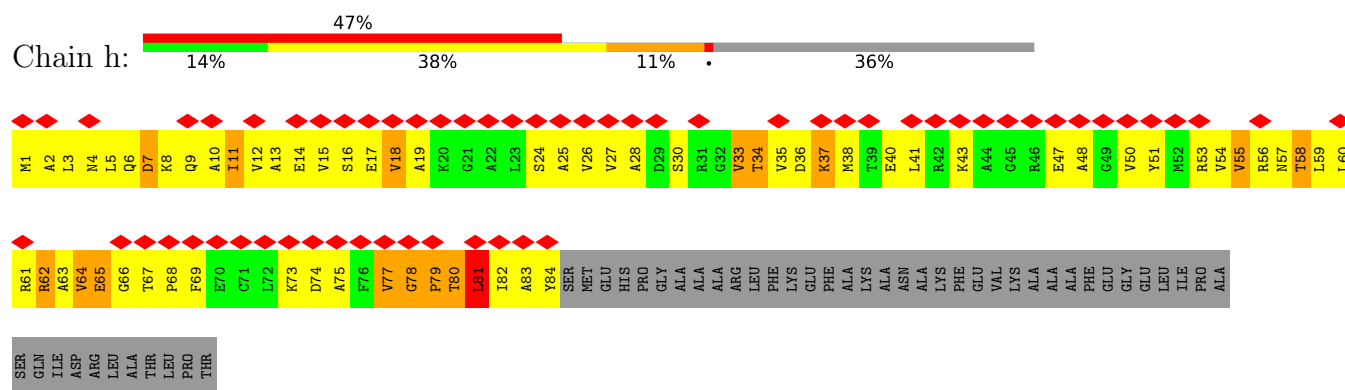
• Molecule 5: 50S ribosomal protein L6



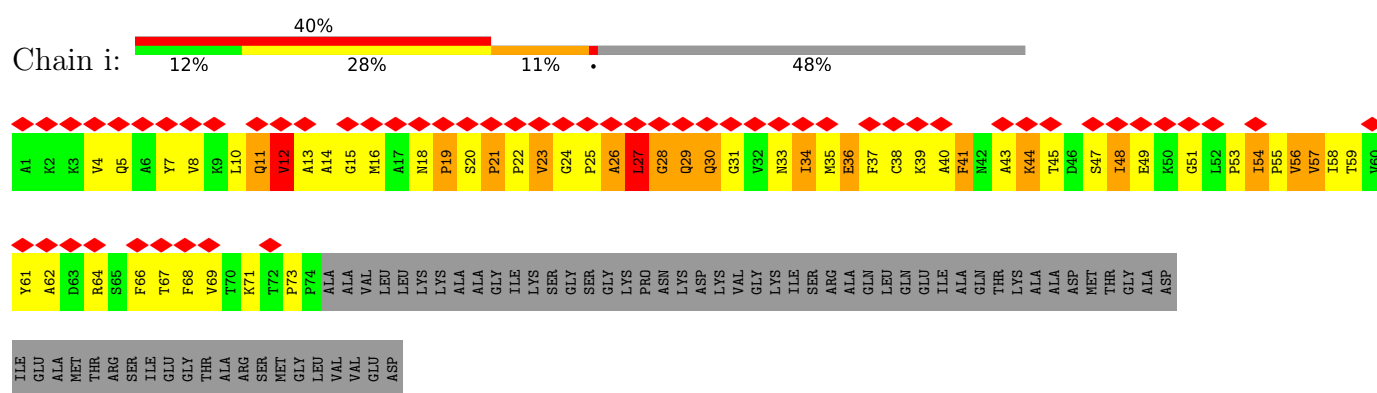
• Molecule 6: 50S ribosomal protein L9



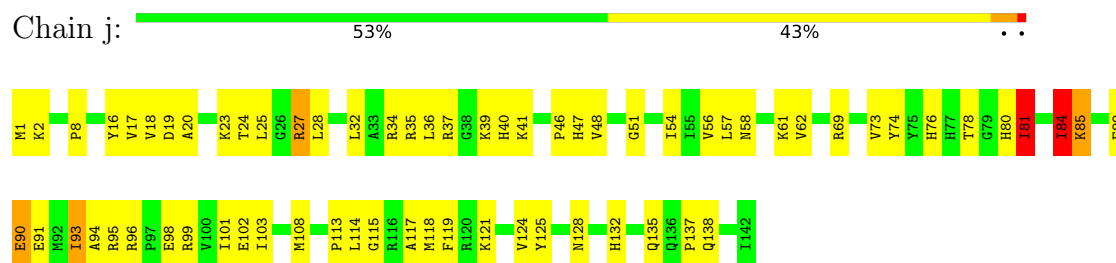
- Molecule 7: 50S ribosomal protein L10



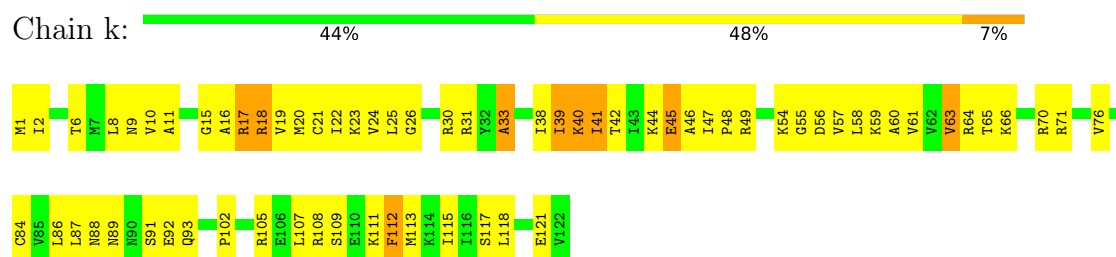
- Molecule 8: 50S ribosomal protein L11



- Molecule 9: 50S ribosomal protein L13

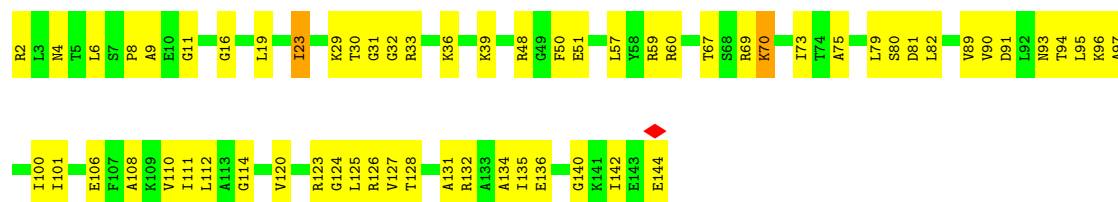


- Molecule 10: 50S ribosomal protein L14



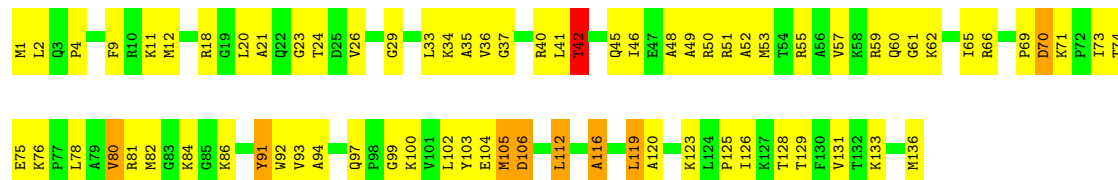
- Molecule 11: 50S ribosomal protein L15





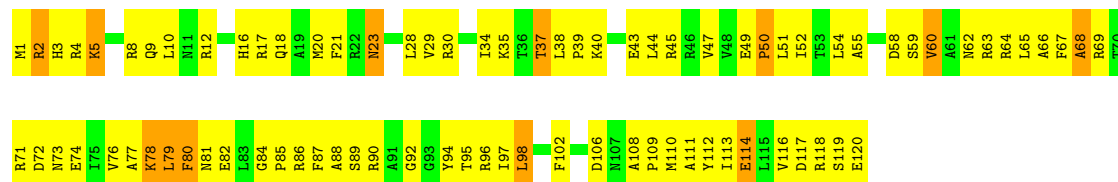
• Molecule 12: 50S ribosomal protein L16

Chain m: 46% 48% 6% .



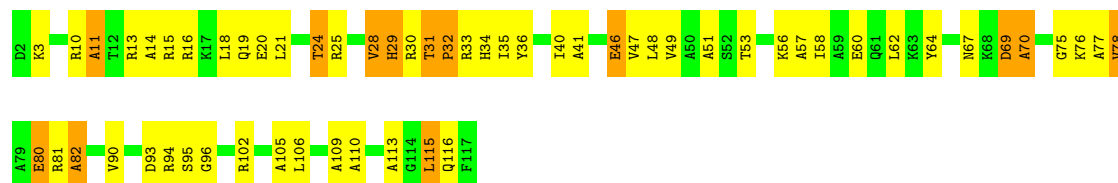
• Molecule 13: 50S ribosomal protein L17

Chain n: 31% 59% 10%



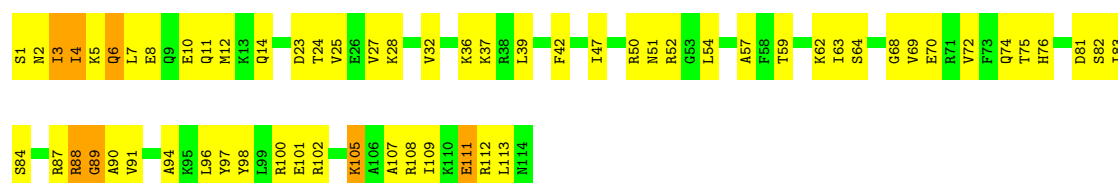
• Molecule 14: 50S ribosomal protein L18

Chain o: 49% 40% 11%



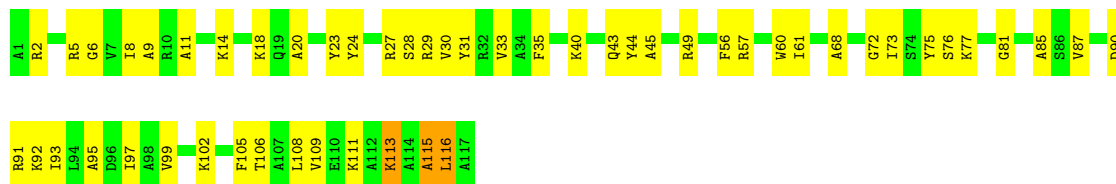
• Molecule 15: 50S ribosomal protein L19

Chain p: 46% 48% 6%



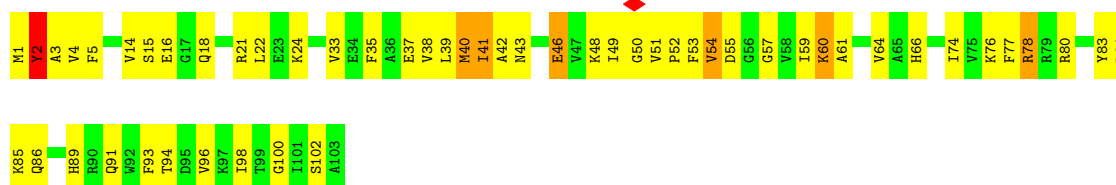
• Molecule 16: 50S ribosomal protein L20

Chain q:  56% 42% .



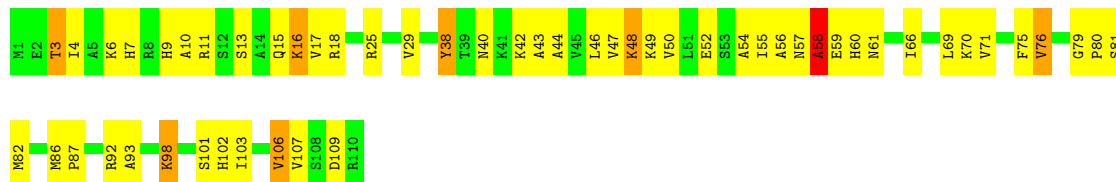
• Molecule 17: 50S ribosomal protein L21

Chain r:  49% 45% 6% .



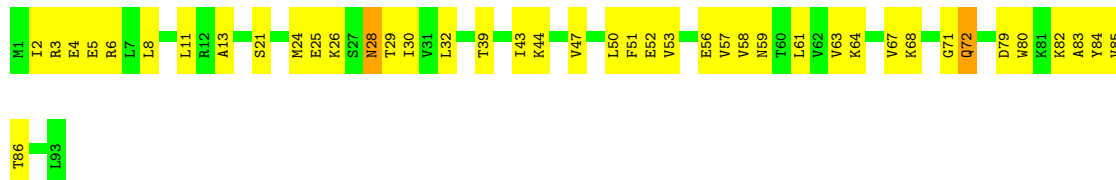
• Molecule 18: 50S ribosomal protein L22

Chain s:  51% 42% 6% .



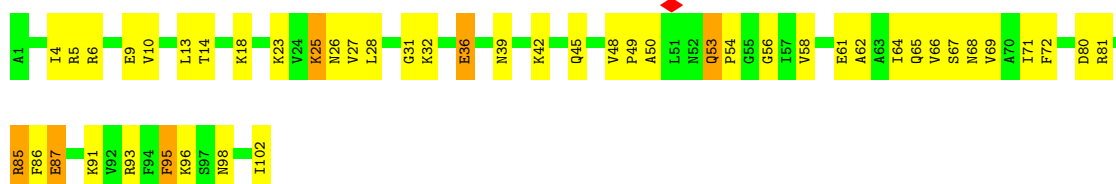
• Molecule 19: 50S ribosomal protein L23

Chain t:  55% 43% .



• Molecule 20: 50S ribosomal protein L24

Chain u:  54% 40% 6% .



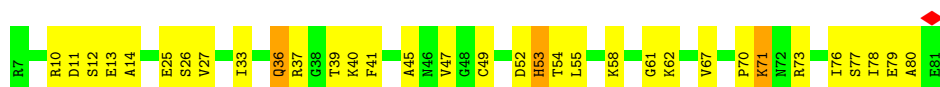
- Molecule 21: 50S ribosomal protein L25

Chain v: 

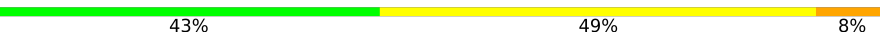


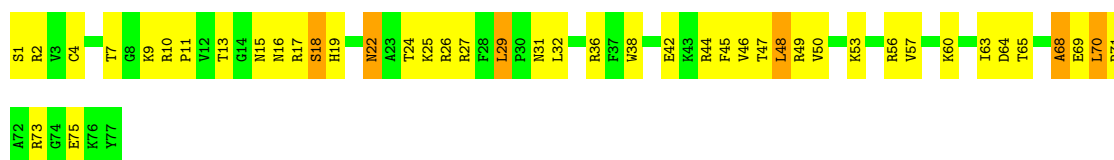
- Molecule 22: 50S ribosomal protein L27

Chain w: 

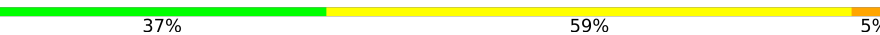


- Molecule 23: 50S ribosomal protein L28

Chain x: 

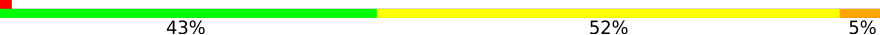


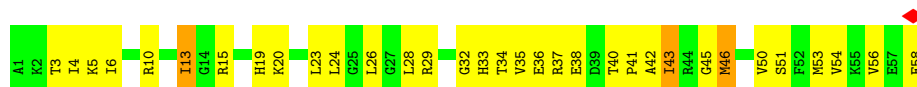
- Molecule 24: 50S ribosomal protein L29

Chain y: 



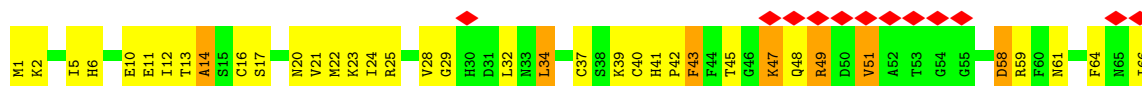
- Molecule 25: 50S ribosomal protein L30

Chain z: 



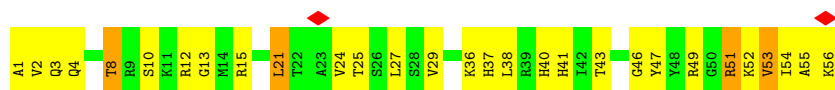
- Molecule 26: 50S ribosomal protein L31

Chain A: 



- Molecule 27: 50S ribosomal protein L32

Chain B: 



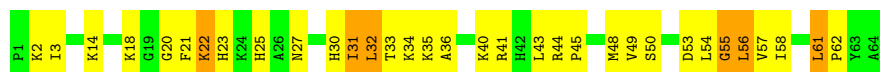
- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34



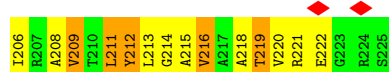
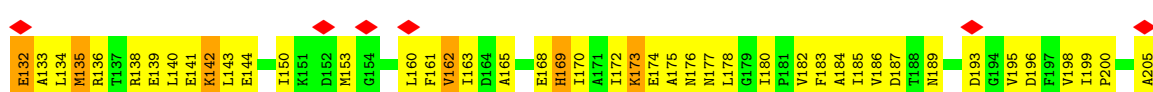
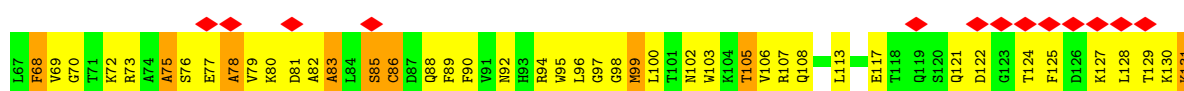
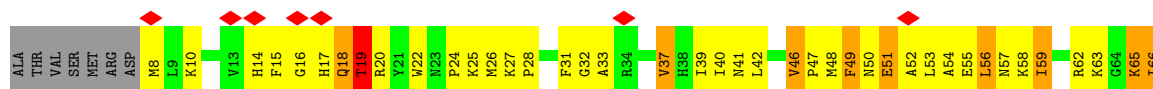
- Molecule 30: 50S ribosomal protein L35



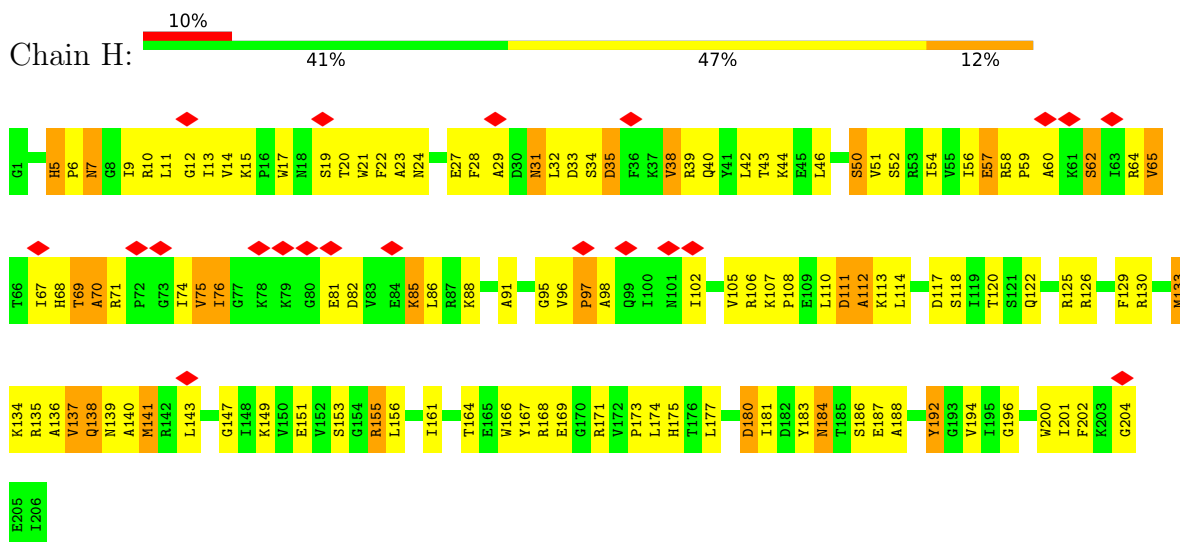
- Molecule 31: 50S ribosomal protein L36



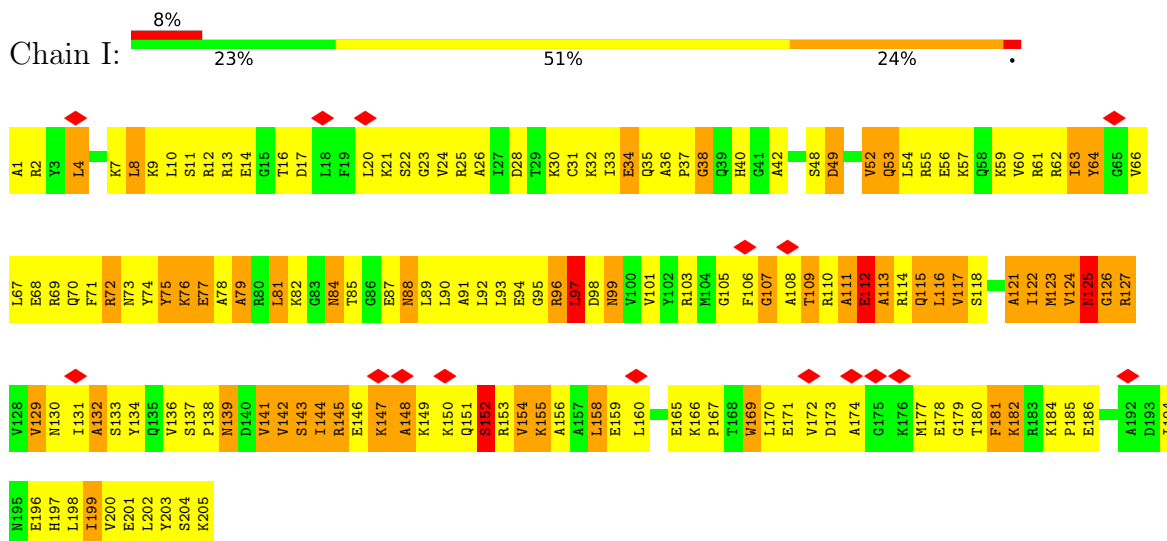
- Molecule 32: 30S ribosomal protein S2



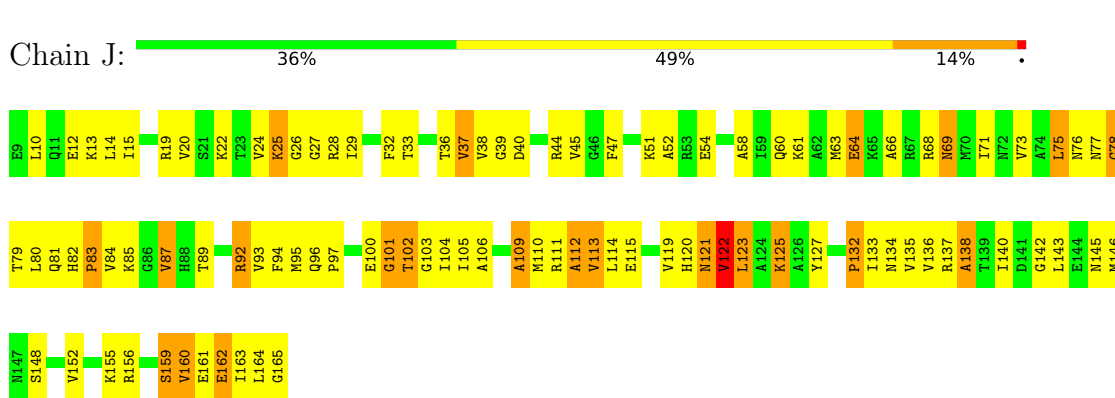
- Molecule 33: 30S ribosomal protein S3



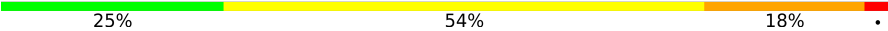
- Molecule 34: 30S ribosomal protein S4

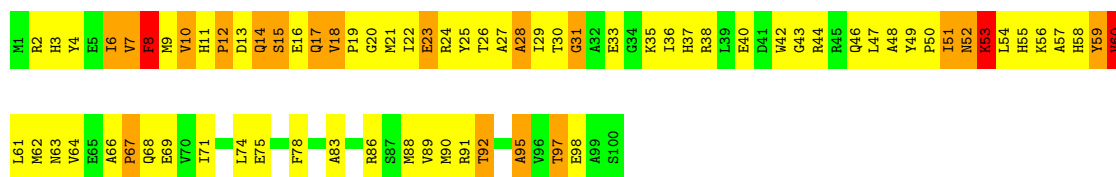


- Molecule 35: 30S ribosomal protein S5



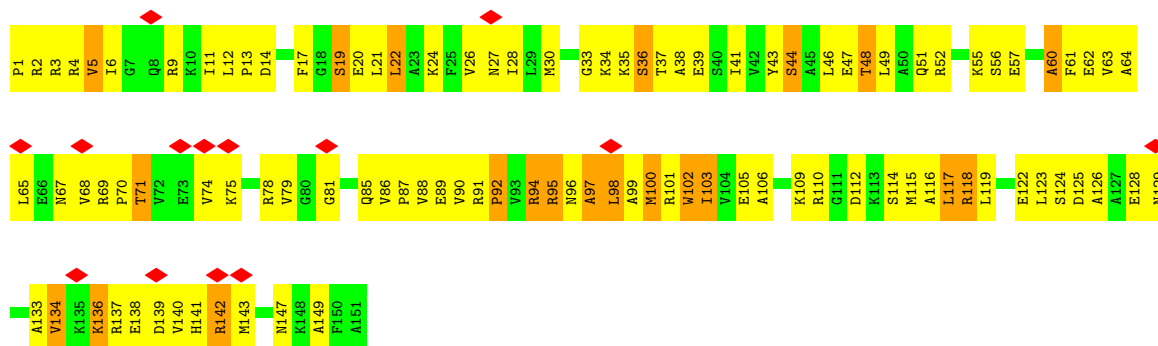
- Molecule 36: 30S ribosomal protein S6

Chain K:  25% 54% 18%



• Molecule 37: 30S ribosomal protein S7

Chain L:  9% 31% 55% 14%



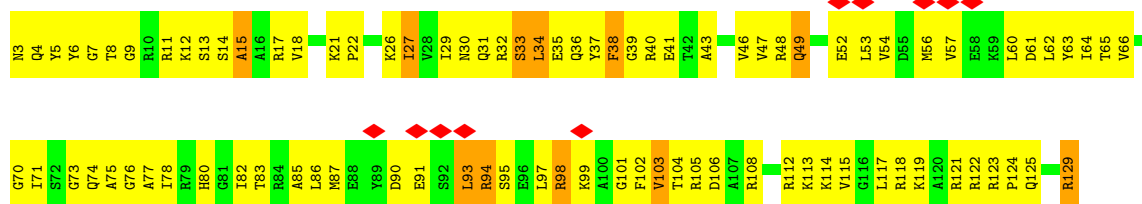
• Molecule 38: 30S ribosomal protein S8

Chain M:  36% 54% 9%



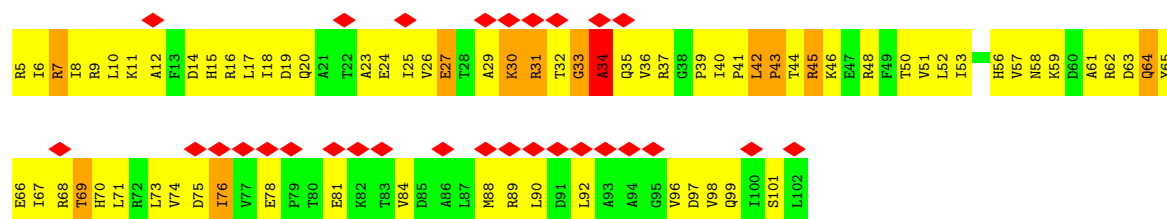
• Molecule 39: 30S ribosomal protein S9

Chain N:  8% 29% 62% 9%

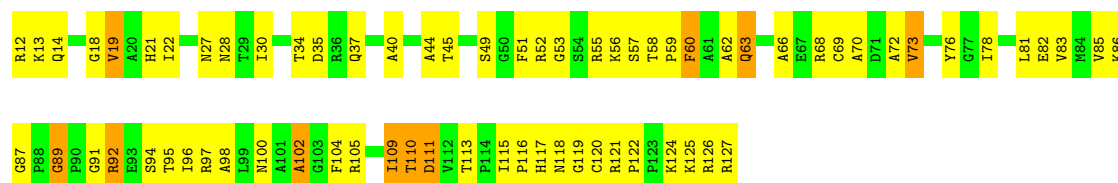


• Molecule 40: 30S ribosomal protein S10

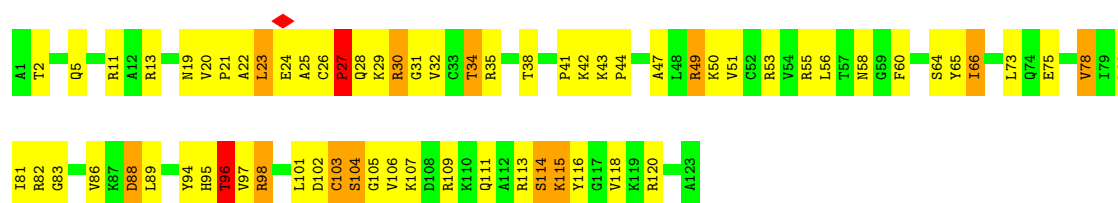
Chain O:  30% 26% 62% 11%



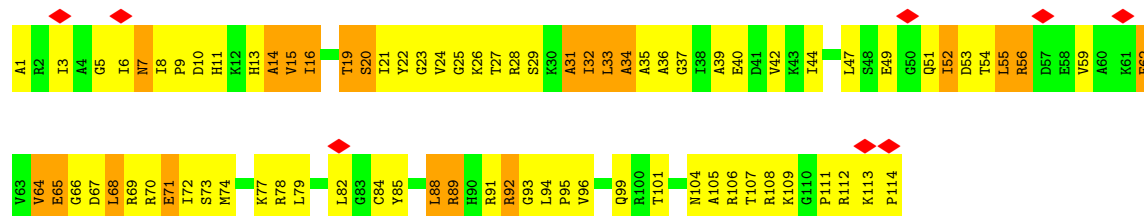
• Molecule 41: 30S ribosomal protein S11



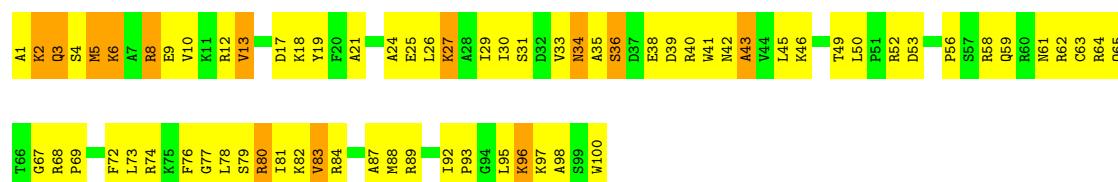
• Molecule 42: 30S ribosomal protein S12



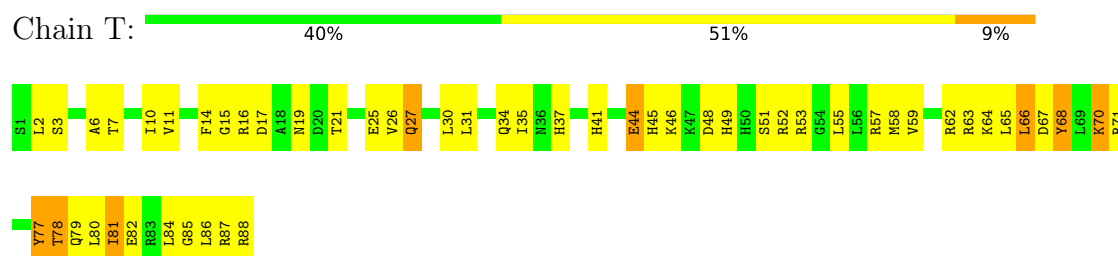
• Molecule 43: 30S ribosomal protein S13



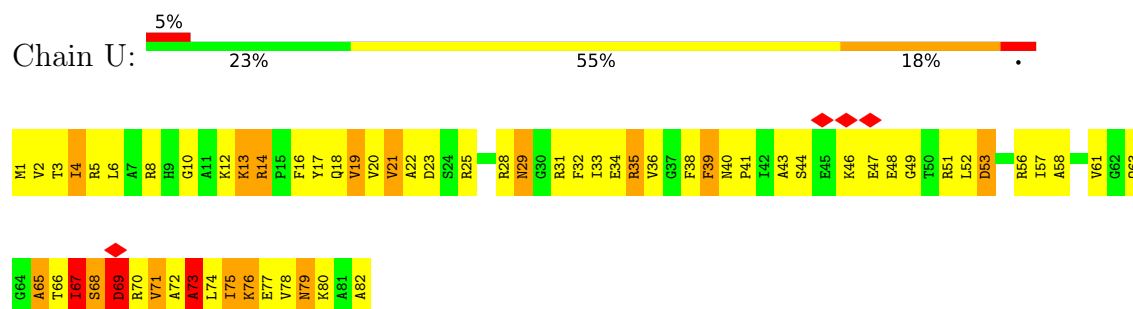
• Molecule 44: 30S ribosomal protein S14



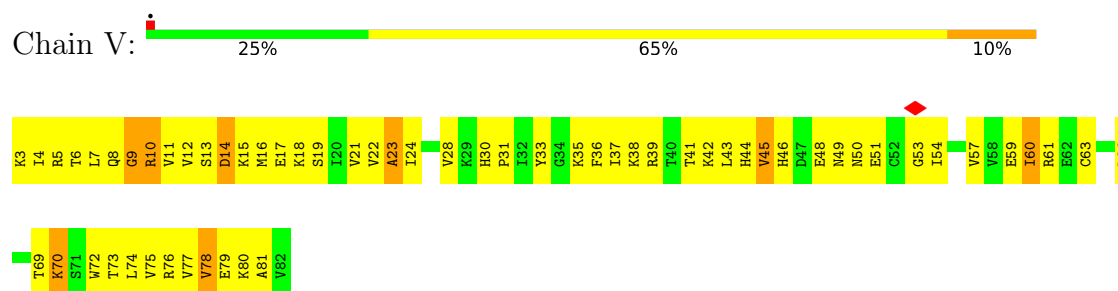
- Molecule 45: 30S ribosomal protein S15



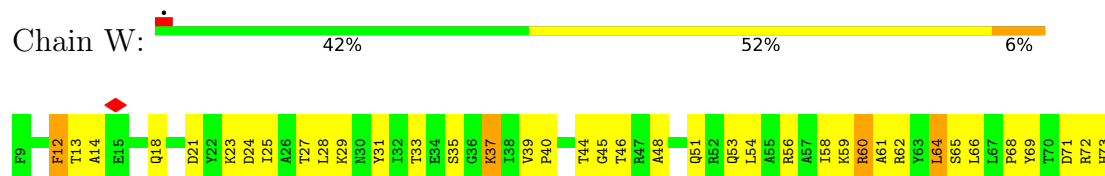
- Molecule 46: 30S ribosomal protein S16



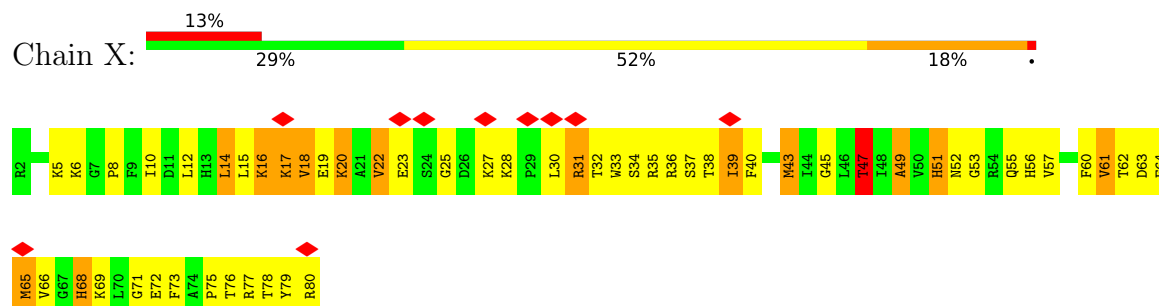
- Molecule 47: 30S ribosomal protein S17



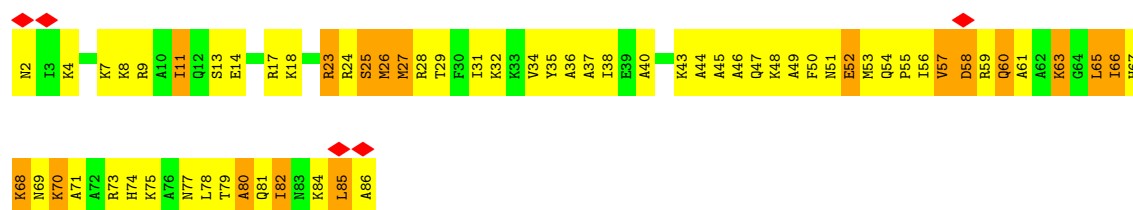
- Molecule 48: 30S ribosomal protein S18



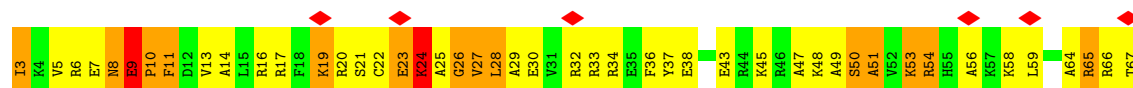
- Molecule 49: 30S ribosomal protein S19



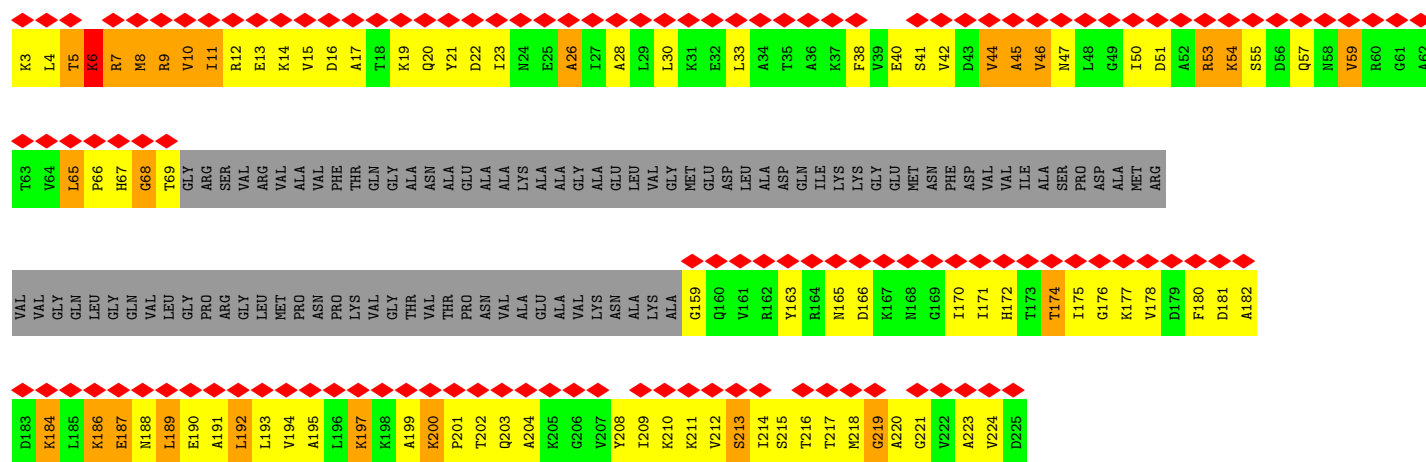
- Molecule 50: 30S ribosomal protein S20



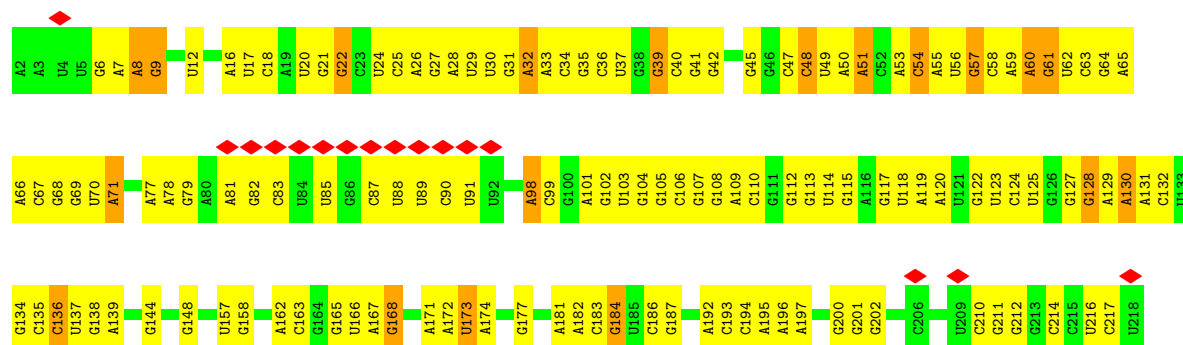
- Molecule 51: 30S ribosomal protein S21



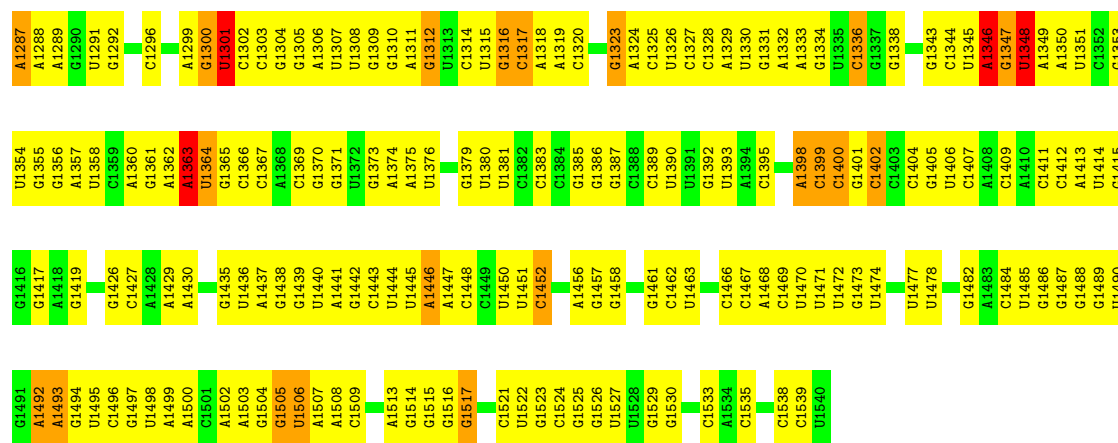
- Molecule 52: 50S ribosomal protein L1



- Molecule 53: 16S ribosomal RNA

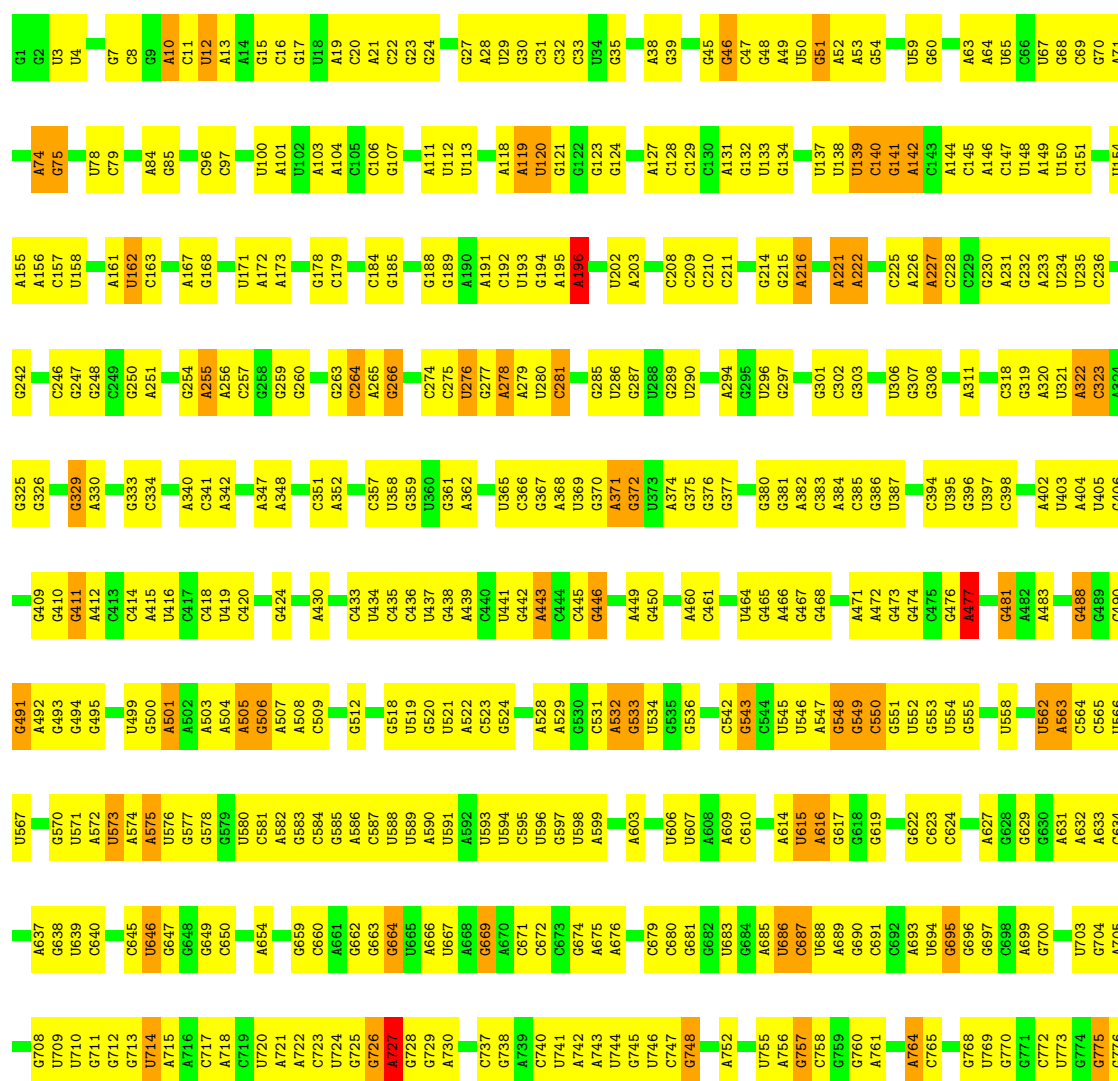


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G1216	G1217	G1144	G1059	G987	C924	C856	G785	U709	G683	A560	A495	U426	U865	U296	G220
C1218	C1219	G1145	G1060	G988	G925	C857	G786	G710	C634	U561	A496	U427	A366	G297	C221
A1219	A1218	C1146	G1061	G989	G926	G858	G787	G711	A635	U562	G497	G428	U367	A298	U224
G1220	G1221	C1147	U1062	C990	G927	G859	U789	A712	U636	A563	A498	U429	U368	G299	A223
U1221	U1222	U1148	G1063	U991	G928	A860	A790	A713	G637	C564	A430	U430	G369	A300	U224
G1223	G1224	C1149	G1064	U992	G929	G861	G791	G714	U638	U565	G500	A431	C370	G301	G227
A1225	A1226	U1150	U1065	G993	G930	G862	A792	A715	G639	G566	A502	A432	A371	G302	A228
C1227	C1228	A1151	G1066	A994	C931	U863	U793	A716	A640	U571	G505	C436	C372	A303	U229
U1229	U1230	A1152	C1067	A995	G932	A865	C795	A718	G647	A572	G506	U437	A373	U304	G230
A1231	A1232	G1153	G1068	A935	G933	A866	G796	C719	A648	A573	G507	U438	U375	G305	U231
G1233	G1234	U1154	G1069	G934	G934	G867	C797	C720	A649	A574	C507	U439	G376	C307	G232
U1235	U1236	C1155	G1070	G935	A935	C868	U798	G721	G656	G575	U508	U439	G377	C308	C233
A1237	A1238	G1156	U1071	G936	A936	G869	U799	A717	G657	C576	A509	C440	G378	A309	C234
C1239	C1240	U1157	G1072	G937	G937	U870	U801	A719	U657	A574	A510	C441	C379	G310	C235
U1241	U1242	G1158	G1073	G938	A938	U871	G802	C724	G658	C577	A511	G442	A374	U304	U233
A1243	A1244	U1159	G1074	G939	A939	U872	G803	G725	U659	A579	U512	C443	C381	G312	G237
G1245	G1246	C1159	G1075	G940	A940	U873	G804	G726	G660	C580	C513	C444	A382	A313	A238
U1247	U1248	U1160	G1076	G941	A941	G874	A807	G727	G661	C581	C514	G445	A383	C314	G240
A1249	A1250	G1161	G1077	G942	A942	U875	U808	G731	U662	G582	G515	A448	G384	A315	A243
C1251	C1252	U1162	G1078	G943	A943	G876	C808	G732	A663	G583	U516	G449	C385	G316	U244
G1253	G1254	C1163	G1079	G944	A944	U877	G809	G733	G664	G584	G517	G450	C386	U317	U245
A1255	A1256	U1164	G1080	G945	A945	U878	G810	G734	A665	G585	C518	G451	U387	A246	A246
C1257	C1258	G1165	G1081	G946	A946	G879	G811	G735	U672	G588	C522	A452	G388	G247	G247
U1259	U1260	U1166	G1082	G947	A947	C880	G812	G736	A673	U589	A523	A453	A389	A321	A250
A1261	A1262	C1167	G1083	G948	A948	G881	U813	G737	G674	U590	G524	G454	U390	G322	G251
G1263	G1264	U1168	G1084	G949	A949	G882	A814	G738	G675	U591	G525	G455	G391	U323	U252
C1265	C1266	G1169	G1085	G950	A950	U883	G815	G739	A676	G592	C526	A456	C392	G324	A253
U1267	U1268	U1170	G1086	G951	A951	G884	G816	G740	U677	U593	G527	A457	A393	A325	G256
A1269	A1270	C1170	G1087	G952	A952	G885	U817	G741	U678	A595	G528	A458	C394	G326	A257
G1271	G1272	U1171	G1088	G953	A953	G886	U818	G742	C679	A596	G529	A459	C395	A327	U258
C1273	C1274	C1172	G1089	G954	A954	U887	U820	G743	G680	U597	G530	A460	A397	G328	G257
U1275	U1276	G1173	G1090	G955	A955	G888	G821	G744	C681	U598	G531	A461	U398	A329	G259
G1277	G1278	U1174	G1091	G956	A956	U889	U822	G745	G682	U599	A532	U462	G399	G330	G260
C1279	C1280	C1175	G1092	G957	A957	G890	G823	G746	G683	C599	A533	U463	G400	G331	G261
U1281	U1282	U1176	G1093	G958	A958	G891	G824	G747	U684	G601	U534	C401	C401	A262	A262
C1283	C1284	G1177	G1094	G959	A959	G892	G825	G748	G685	A602	U535	C402	G402	A263	A263
A1285	A1286	U1178	G1095	G960	A960	U893	G826	G749	U686	U603	G536	C403	G403	C264	C264
U1287	U1288	C1179	G1096	G961	A961	G894	G827	G750	A687	G604	G537	U470	G404	G265	G265
G1289	G1290	G1180	G1097	G962	A962	G895	G828	G751	G688	U605	G538	U471	U405	G266	G266
C1291	C1292	U1181	G1098	G963	A963	G896	G829	G752	G689	G540	A539	U472	G406	C267	C267
U1293	U1294	C1182	G1099	G964	A964	U897	U830	G753	U690	A608	G541	C474	U409	U268	U268
A1295	A1296	G1183	G1100	G965	A965	G898	G831	G754	G691	G542	G541	C475	G410	C269	C269
C1297	C1298	U1184	G1101	G966	A966	U899	U832	G755	G692	C613	G542	U476	G411	A270	A270
U1299	U1300	C1185	G1102	G967	A967	G900	U833	G756	G693	C614	G543	C477	A411	C271	C271
G1301	G1302	U1186	G1103	G968	A968	G901	U834	G757	G694	G615	G544	A478	A412	G350	C272
C1303	C1304	C1187	G1104	G969	A969	U902	U835	G758	G695	C616	G545	G481	G413	G351	U273
U1305	U1306	G1188	G1105	G970	A970	G903	U836	G759	G696	A621	A546	G482	A414	C352	A274
A1307	A1308	U1189	G1106	G971	A971	G904	U837	G760	G697	A622	A547	C483	A415	A353	C280
C1309	C1310	C1190	G1107	G972	A972	U905	U838	G761	G698	C623	G548	C484	G416	C354	G281
U1311	U1312	G1191	G1108	G973	A973	U906	U839	G762	G699	C624	G549	U485	G417	C355	G282
G1313	G1314	C1192	G1109	G974	A974	U907	U840	G763	U701	C625	G550	U486	C418	A356	A282
C1315	C1316	U1193	G1110	G975	A975	U908	U841	G764	G702	G626	A553	U487	C419	G357	G283
U1317	U1318	G1194	G1111	G976	A976	U909	U842	G765	G703	G627	A554	C488	U420	G360	G284
A1319	A1320	C1195	G1112	G977	A977	U910	U843	G766	G704	G628	A555	C489	U421	G361	G285
C1321	C1322	U1196	G1113	G978	A978	U911	U844	G767	G705	G629	A556	C490	G422	G362	U294
U1323	U1324	G1197	G1114	G979	A979	U912	U845	G768	G706	A630	G557	G491	C423	G363	G294
A1325	A1326	C1198	G1115	G980	A980	U913	U846	G769	G707	C631	G558	A493	C424	A363	A363
G1327	G1328	U1199	G1116	G981	A981	U914	U847	G770	G698	G559	G559	G492	G425	G364	G295
C1329	C1330	C1199	G1117	G982	A982	U915	U848	G771	G708	G560	G560	G493	C426	G365	G296
U1331	U1332	G1200	G1118	G983	A983	U916	U849	G772	G709	G561	G561	G494	C427	G366	G297
A1333	A1334	C1201	G1119	G984	A984	U917	U850	G773	G710	G562	G562	G495	C428	G367	G298
C1335	C1336	U1202	G1120	G985	A985	U918	U851	G774	G711	G563	G563	G496	C429	G368	G299
G1337	G1338	C1203	G1121	G986	A986	U919	U852	G775	G712	G564	G564	G497	C430	G369	G300
U1339	U1340	U1204	G1122	G987	A987	U920	U853	G776	G713	G565	G565	G498	C431	G370	G301
A1341	A1342	C1205	G1123	G988	A988	U921	U854	G777	G714	G566	G566	G499	C432	G371	G302
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U1345	U1346	G1207	G1125	G990	A990	U923	U856	G779	G716	G568	G568	G501	C434	G373	G304
A1347	A1348	C1208	G1126	G991	A991	U924	U857	G780	G717	G569	G569	G502	C435	G374	G305
G1349	G1350	U1209	G1127	G992	A992	U925	U858	G781	G718	G570	G570	G503	C436	G375	G306
C1351	C1352	C1210	G1128	G993	A993	U926	U859	G782	G719	G571	G571	G504	C437	G376	G307
U1353	U1354	U1211	G1129	G994	A994	U927	U860	G783	G720	G572	G572	G505	C438	G377	G308
A1355	A1356	C1212	G1130	G995	A995	U928	U861	G784	G721	G573	G573	G506	C439	G378	G309
G1357	G1358	U1213	G1131	G996	A996	U929	U862	G785	G722	G574	G574	G507	C440	G379	G310
C1359	C1360	C1214	G1132	G997	A997	U930	U863	G786	G723	G575	G575	G508	C441	G380	G311
U1361	U1362	U1215	G1133	G998	A998	U931	U864	G787	G724	G576	G576	G509	C442	G381	G312
A1363	A1364	C1216	G1134	G999	A999	U932	U865	G788	G725	G577	G577	G510	C443	G382	G313
G1365	G1366	U1217	G1135	G1000	A1000	U933	U866	G789	G726	G578	G578	G511	C444	G383	G314
C1367	C1368	C1218	G1136	G1001	A1001	U934	U867	G790	G727	G579	G579	G512	C445	G384	G315
U1369	U1370	U1219	G1137	G1002	A1002	U935	U868	G791	G728	G580	G580	G513	C446	G385	G316
A1371	A1372	C1220	G1138	G1003	A1003	U936	U869	G792	G729	G581	G581	G514	C447	G386	G317
G1373	G1374	U1221	G1139	G1004	A1004	U937	U870	G793	G730	G582	G582	G515	C448	G387	G318
C1375	C1376	C1222	G1140	G1005	A1005	U938	U871	G794	G731	G583	G583	G516	C449	G388	G319
U1377	U1378	G1223	G1141	G1006	A1006	U939	U872	G795	G732	G584	G584	G517	C450	G389	G320
A1379	A1380	C1224	G1142	G1007	A1007	U940	U873	G796	G733	G585	G585	G518	C451	G390	G321
G1381	G1382	U1225	G1143	G1008	A1008	U941	U874	G797	G734	G586	G586	G519	C452	G391	G322
C1383	C1384	C1226	G1144	G1009	A1009	U942	U875	G798	G735	G587	G587	G520	C453	G392	G323
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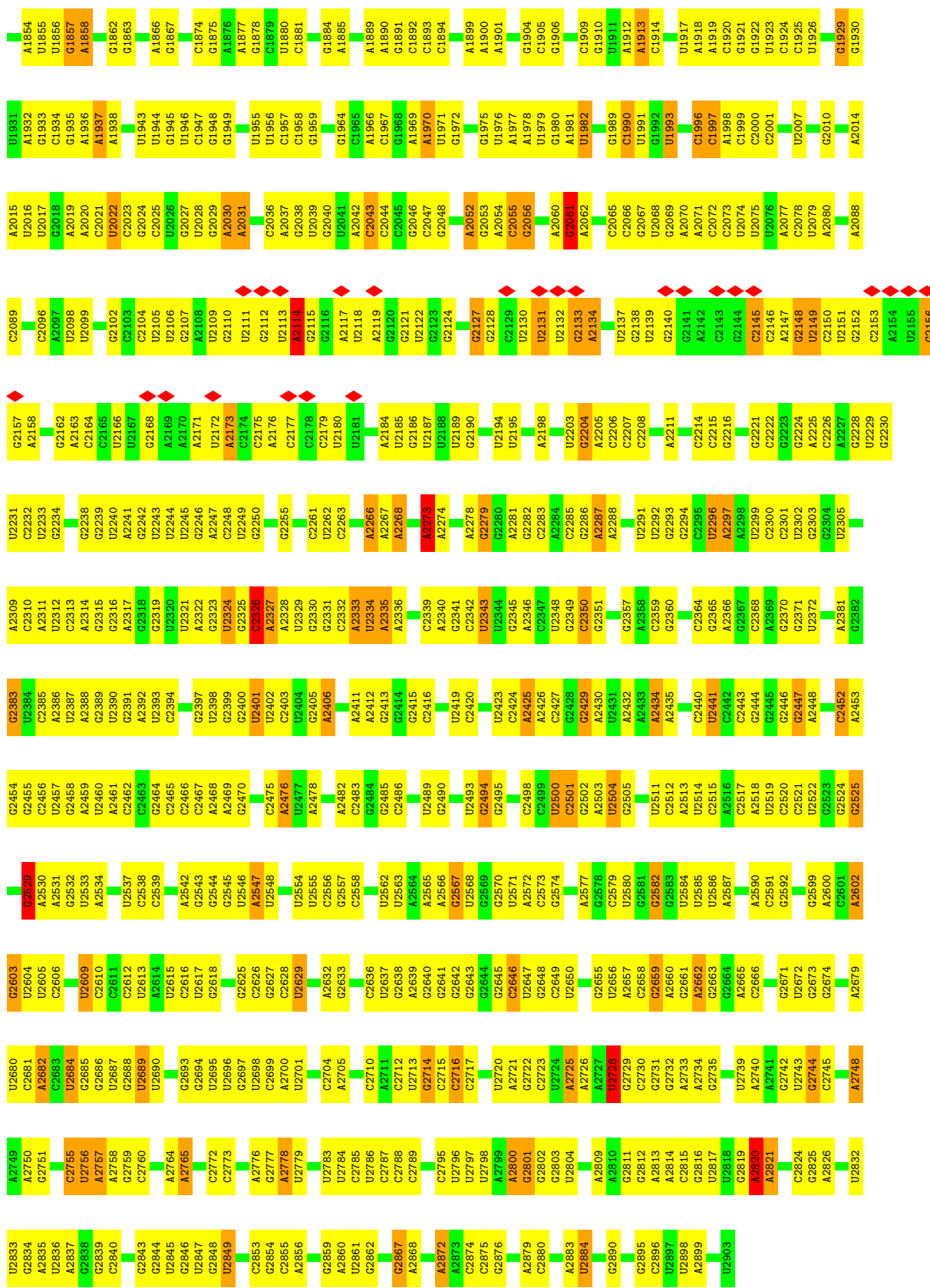


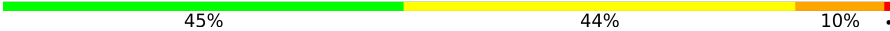
• Molecule 54: 23S ribosomal RNA

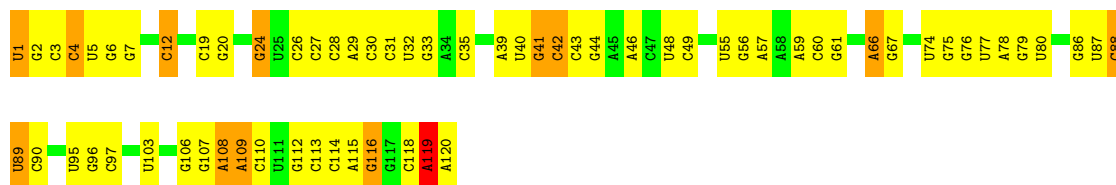
Chain 1: 40% 52% 8%



U1760	U1761	U1709	A1640	C1564	G1389	C1315	U1217	G1071	A1000	G923	U852	U779
A1784	A1785	G1710	A1641	C1565	A1393	U1316	G1218	C1072	A1001	G924	C853	G780
A1786	A1787	U1712	G1642	U1566	U1394	U1317	G1219	G1073	U1004	A925	C854	A781
A1788	A1789	U1713	G1645	U1567	A1395	U1318	G1220	G1074	C1005	G926	G855	A782
A1790	A1791	U1714	G1646	U1568	G1401	C1320	G1225	A1077	A1010	U929	G856	G783
A1792	A1793	U1715	U1647	U1569	U1402	A1322	G1236	U1078	G1011	G930	G858	G784
A1794	A1795	U1716	U1648	C1469	U1403	A1323	A1237	C1079	U1012	U931	G859	G785
A1796	A1797	U1717	U1649	A1490	C1404	C1324	G1238	U1082	C1013	U932	U860	G786
A1798	A1799	U1718	G1651	C1493	U1409	A1327	C1161	U1083	G935	G936	A861	C787
A1800	A1801	U1719	A1578	C1499	G1410	A1328	G1162	A1085	A936	A937	A863	A792
A1802	A1803	U1720	A1579	C1500	G1416	U1329	A1165	A1086	A941	G942	A864	G799
A1804	A1805	U1721	A1580	G1501	G1417	C1330	G1166	A1087	A1020	G943	C865	A800
A1806	A1807	A1722	U1581	A1502	C1418	G1331	G1167	A1088	A1021	G944	U868	U803
A1808	A1809	U1723	A1582	A1503	G1419	C1332	G1168	A1089	A1022	G945	U870	A804
A1810	A1811	G1724	A1583	A1504	A1420	U1333	G1169	A1095	G1026	G946	G871	G805
A1812	A1813	U1725	A1584	A1505	A1421	C1334	G1170	A1096	A1027	G947	U872	C806
A1814	A1815	G1726	U1585	A1506	G1422	G1335	G1171	A1097	A1028	G948	U873	U807
A1816	A1817	U1727	U1586	U1507	G1423	C1336	G1172	A1098	A1029	G949	G874	G808
A1818	A1819	C1728	A1587	C1508	G1424	G1337	G1173	A1099	G1030	G950	G875	G809
A1820	A1821	U1729	A1588	A1509	G1425	C1338	G1174	U1101	G1031	G951	C876	U810
A1822	A1823	G1730	A1589	U1510	G1426	G1339	A1175	C1102	U1032	G952	A877	U811
A1824	A1825	U1731	A1590	C1511	G1427	U1340	G1176	A1103	U1033	G953	A878	C812
A1826	A1827	G1732	A1591	G1512	C1428	C1341	G1177	C1104	G1034	G954	G879	U813
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A1830	A1831	G1734	A1593	C1514	G1430	U1343	G1179	C1106	G1036	G956	G881	C815
A1832	A1833	U1735	A1594	G1515	G1431	C1344	G1180	C1107	G1037	G957	C886	C816
A1834	A1835	G1736	A1595	G1516	G1432	C1345	U1181	C1108	G1038	G958	U887	C817
A1836	A1837	U1737	A1596	C1517	G1433	U1346	U1182	C1109	A1039	G959	A819	G818
A1838	A1839	G1738	A1597	G1518	G1434	C1347	G1183	G1110	A1040	G960	C888	A820
A1840	A1841	U1739	A1598	C1519	G1435	U1348	G1184	G1111	G1041	G961	C889	G821
A1842	A1843	G1740	A1599	G1520	G1436	C1349	G1185	G1112	C1042	G962	C890	G822
A1844	A1845	U1741	A1600	C1521	G1437	C1350	G1186	G1113	G1043	G963	G891	G823
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A1848	A1849	U1743	A1602	C1523	G1439	C1352	U1188	G1115	G1045	G971	A895	U825
A1850	A1851	G1744	A1603	G1524	G1440	U1353	G1189	G1116	A1046	A972	U896	U826
A1852	A1853	U1745	A1604	C1525	G1441	C1354	U1190	G1117	A1047	A973	A897	U827
A1854	A1855	G1746	A1605	G1526	G1442	U1355	G1191	G1118	C1048	A974	A898	U828
A1856	A1857	U1747	A1606	C1527	G1443	C1356	G1192	A1127	C1052	A975	A899	A829
A1858	A1859	G1748	A1607	G1528	G1444	U1357	G1193	G1128	C1053	A899	C903	G830
A1860	A1861	U1749	A1608	C1529	G1445	C1358	G1194	A1129	A1054	A976	G904	G831
A1862	A1863	G1750	A1609	G1530	G1446	U1359	G1195	U1130	G1055	A977	C904	G832
A1864	A1865	U1751	A1610	C1531	G1447	C1360	G1196	G1131	G1056	A978	A910	C833
A1866	A1867	G1752	A1611	G1532	G1448	U1361	G1197	G1132	G1057	A979	A911	U834
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A1870	A1871	G1754	A1613	G1534	G1450	U1363	G1199	A1134	G1059	A981	C913	G836
A1872	A1873	U1755	A1614	C1535	G1451	C1364	G1200	U1135	U1060	A982	C914	A845
A1874	A1875	G1756	A1615	G1536	G1452	U1365	G1201	C1136	U1061	A983	C915	U846
A1876	A1877	U1757	A1616	C1537	G1453	C1366	G1202	U1137	U1062	A984	C916	C848
A1878	A1879	G1758	A1617	G1538	G1454	U1367	G1203	U1138	G1063	A985	C917	A849
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A1974	A1975	G1806	A1665	A1511	G1511	U1415	G1251	U1186		A999		
A1976	A1977	U1807	A1666	A1512	G1512	U1416	G1252	U1187		A999		
A1978	A1979	G1808	A1667	A1513	G1513	U1417	G1253	U1188		A999		
A1980	A1981	U1809	A1668	A1514	G1514	U1418	G1254	U1189		A999		
A1982	A1983	G1810	A1669	A1515	G1515	U1419	G1255	U1190		A999		
A1984	A1985	U1811	A1670	A1516	G1516	U1420	G1256	U1191		A999		
A1986	A1987	G1812	A1671	C1517	G1517	U1421	G1257	U1192		A999		
A1988	A1989	U1813	A1672	G1518	G1518	U1422	G1258	U1193		A999		
A1990	A1991	G1814	A1673	A1519	G1519	U1423	G1259	U1194		A999		
A1992	A1993	U1815	A1674	A1520	G1520	U1424	G1260	U1195		A999		
A1994	A1995	G1816	A1675	A1521	G1521	U1425	G1261	U1196		A999		
A1996	A1997	U1817	A1676	A1522	G1522							



Chain 2:  45% 44% 10% .



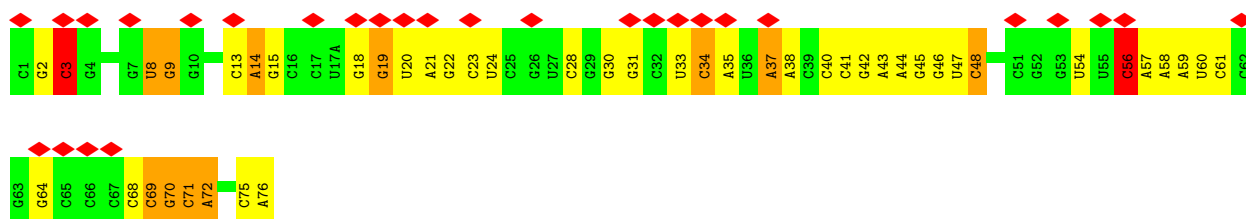
• Molecule 56: tRNAPro

Chain 5:  53% 35% 12%

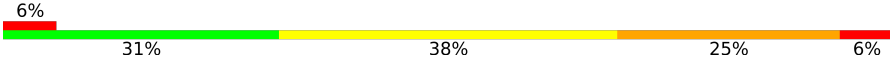


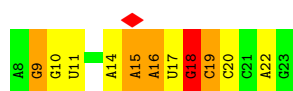
• Molecule 57: tRNAfMet

Chain 6:  36% 40% 43% 14% .

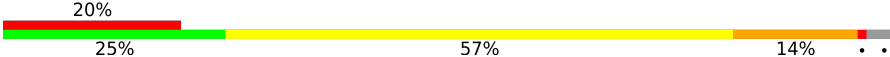


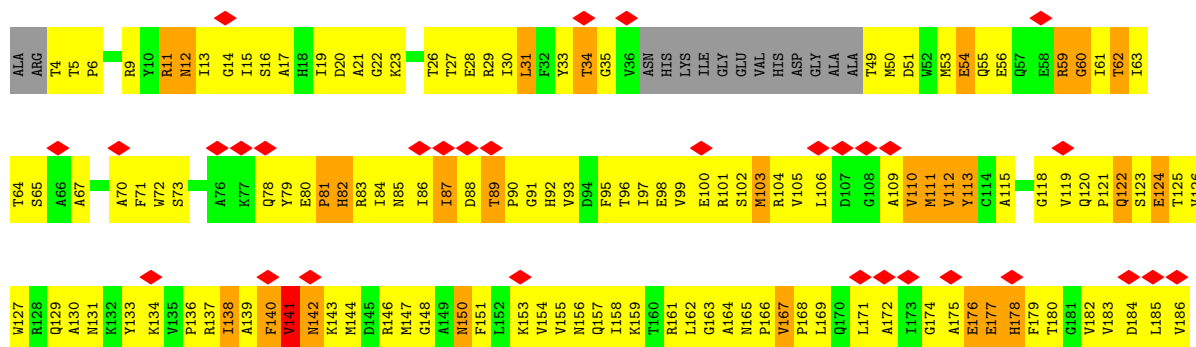
• Molecule 58: mRNA

Chain 4:  6% 31% 38% 25% 6%



• Molecule 59: Elongation factor G

Chain 8:  20% 25% 57% 14% . .



P691	S692	N693	V694	A695	O696	A697	V698	T699	E700	ALA	ARG	GLY	LYS	LEU	GLU	HIS	HIS	HIS	HIS	HIS	HIS																																							
E625	E626	N627	T628	G629	D630	V631	T632	G633	D634	L635	S636	R637	R638		I642	T643	Q644	Q645	E646	S647	E648	V649	T650	G651	V652	T653	I654	L655	S656	A657	V658	T659	A660	F661	E662	M663		Y666	A667	T668	Q669	I670	R671	S672	L673	T674	K675	G676		Y680	T681	H682	E683	F684	L685	K686	Y687	D688		
P665	L666	A667	G668	Y669	F670	V671	V672	D673	M674	G675	I676	R677	L678	H679	F680	G681	S682	Y683	H684	D685	V686	D687	S688	S689	E690	L691	A692	F693	K694	L695	A696	A697	S698	T699	A600	F601	E602	E603	G604	F605	K606	K607	A608	K609	P610	V611	L612	L613	E614	P615	L616	K617	K618	V619	E620	Q621	E622	T623	P624	
E502		H505	A506	K507	Q508	S509	G510	G511	R512	G513	Q514	Y515	G516	H517	V518	V519	I520	D521	N522	Y523	P524	L525	E526	P527	G528	S529		G533	Y534	E535	F536	T537	N538	D539	I540	K541	G542	G543	V544	I545	P546	G547	E548	Y549	I550	P551	A552	V553	D554	K555	G556	I557	Q558	E559	Q560	L561	S562	A563	G564	
A439	K440	E441	D442	P443	S444	F445	R446	V447	V448	T449	D450	E451	E452	S453	N454	Q455	T456	I457	I458	A459		G462	E463	L464	H465	L466	D467	I468	I469	V470	D471	N472	M473	K474	R475	E476	F477	N478	V479	E480	A481	N482	V483	G484	K485	P486		Y490	R491	E492	T493	I494	R495	Q496	K497	V498	T499	D500	V501	
E373	I374	K375		R378	A379	G380	R381		A384	I385	A386	G387	L388	K389	D390	V391	T392	T393	G394	D395	T396	L397	C398	D399	P400	D401	A402	P403	I404	I405	L406		E410	F411	P412	E413	P414	V415	I416	S417	I418	A419	V420	E421	P422	K423	T424	K425	A426	D427	Q428	E429	K430		A434	L435	G436	R437	L438	
A311	S312	D313	D314	E315	F316	F317	S318	A319	L320	A321	F322	K323	I324	A325	T326	D327	P328	F329	V330	G331	N332	L333	T334	F335	F336	R337	V338	Y339	S340	G341	V342		S345	G346	D347	T348	V349	L350	N351	S352	V353	K354	A355	A356	R357	E358	R359	F360	G361	R362	I363	V364	Q365	M366		N369	K370	R371	E372	
C950	A951	L952	R953	Q954	R955	V956	L957	N958	N959	E960	I961	I962	L963	A964	T965	C966	G967	S968		K971	N972	K973	G974	V975	Q976	A977	M978	L979	D980	A981	V982	I983	D984	Y985	L986	P987	S988	P989	V990	D991	V992	P993	A994	I995	N996	G997	I998	L999	D900	R901	G902	K903	D904	T905	P906	A907	E908	R909	H910	
K187	M188	K189	A190	I191	N192	H193	H194	D195	A196	D197	I198	Q199	V200		E205	D206	L207	P208	A209	D210	M211	V212	E213	L214	A215	N216	E217	V218	H219	Q220	N221	L222	I223	E224	S225	A226	A227	E228	A229	S230	E231	E232	L233	M234	E235	K236	Y237	L238	G239	G240	E241	E242	L243	T244	E245	A246	E247	I248	K249	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	6029	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47.5	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	25.366	Depositor
Minimum map value	-7.465	Depositor
Average map value	0.018	Depositor
Map value standard deviation	1.395	Depositor
Recommended contour level	3.3	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, GCP, 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	b	1.01	15/2122 (0.7%)	1.19	17/2852 (0.6%)
2	c	0.94	9/1586 (0.6%)	1.14	17/2134 (0.8%)
3	d	1.00	10/1571 (0.6%)	1.16	20/2113 (0.9%)
4	e	0.95	10/1435 (0.7%)	1.15	10/1926 (0.5%)
5	f	1.32	26/1343 (1.9%)	1.34	26/1816 (1.4%)
6	g	1.83	30/946 (3.2%)	1.58	27/1275 (2.1%)
7	h	1.72	20/638 (3.1%)	1.67	19/860 (2.2%)
8	i	2.74	29/564 (5.1%)	2.09	38/768 (4.9%)
9	j	0.96	8/1152 (0.7%)	1.12	8/1551 (0.5%)
10	k	1.00	7/948 (0.7%)	1.22	12/1268 (0.9%)
11	l	0.88	4/1054 (0.4%)	1.10	7/1403 (0.5%)
12	m	1.04	6/1093 (0.5%)	1.21	11/1460 (0.8%)
13	n	1.05	8/974 (0.8%)	1.34	16/1301 (1.2%)
14	o	1.16	11/902 (1.2%)	1.27	10/1209 (0.8%)
15	p	0.97	5/929 (0.5%)	1.12	10/1242 (0.8%)
16	q	0.94	7/960 (0.7%)	1.15	10/1278 (0.8%)
17	r	0.97	6/829 (0.7%)	1.18	8/1107 (0.7%)
18	s	1.05	9/864 (1.0%)	1.23	9/1156 (0.8%)
19	t	0.98	6/745 (0.8%)	1.04	3/994 (0.3%)
20	u	0.77	2/788 (0.3%)	0.91	4/1051 (0.4%)
21	v	0.81	2/766 (0.3%)	1.14	5/1025 (0.5%)
22	w	0.98	3/582 (0.5%)	1.15	5/769 (0.7%)
23	x	0.94	4/635 (0.6%)	1.30	14/848 (1.7%)
24	y	1.18	3/510 (0.6%)	1.20	5/677 (0.7%)
25	z	1.05	4/453 (0.9%)	1.11	6/605 (1.0%)
26	A	1.48	6/532 (1.1%)	1.28	12/709 (1.7%)
27	B	0.96	2/450 (0.4%)	1.17	2/599 (0.3%)
28	C	0.98	3/417 (0.7%)	0.97	3/554 (0.5%)
29	D	0.88	1/380 (0.3%)	1.15	3/498 (0.6%)
30	E	1.10	5/513 (1.0%)	1.21	3/676 (0.4%)
31	F	1.40	3/303 (1.0%)	1.33	7/397 (1.8%)
32	G	1.41	36/1736 (2.1%)	1.35	28/2338 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	H	1.60	33/1652 (2.0%)	1.42	38/2225 (1.7%)
34	I	1.88	46/1665 (2.8%)	1.79	68/2227 (3.1%)
35	J	1.24	15/1170 (1.3%)	1.34	20/1573 (1.3%)
36	K	2.03	20/836 (2.4%)	1.63	20/1128 (1.8%)
37	L	1.43	24/1196 (2.0%)	1.42	29/1602 (1.8%)
38	M	1.25	13/989 (1.3%)	1.29	9/1326 (0.7%)
39	N	1.05	7/1034 (0.7%)	1.26	16/1375 (1.2%)
40	O	1.56	14/797 (1.8%)	1.33	12/1077 (1.1%)
41	P	1.12	8/886 (0.9%)	1.25	10/1195 (0.8%)
42	Q	1.07	7/969 (0.7%)	1.20	9/1300 (0.7%)
43	R	1.72	19/893 (2.1%)	1.47	23/1193 (1.9%)
44	S	1.36	12/817 (1.5%)	1.28	12/1088 (1.1%)
45	T	1.31	11/722 (1.5%)	1.30	9/964 (0.9%)
46	U	1.60	15/659 (2.3%)	1.63	20/884 (2.3%)
47	V	1.03	4/658 (0.6%)	1.08	6/881 (0.7%)
48	W	1.01	4/545 (0.7%)	1.06	2/731 (0.3%)
49	X	1.60	19/653 (2.9%)	1.50	15/877 (1.7%)
50	Y	1.68	16/671 (2.4%)	1.65	22/888 (2.5%)
51	Z	1.56	15/551 (2.7%)	2.06	24/728 (3.3%)
52	a	1.42	18/1034 (1.7%)	1.51	30/1387 (2.2%)
53	3	0.56	0/36963	0.60	18/57662 (0.0%)
54	1	0.51	0/69796	0.59	32/108888 (0.0%)
55	2	0.49	0/2872	0.55	1/4479 (0.0%)
56	5	0.48	0/1840	0.57	0/2868
57	6	0.52	0/1832	0.64	4/2855 (0.1%)
58	4	0.54	0/388	0.75	2/603 (0.3%)
59	8	1.57	109/5411 (2.0%)	1.53	143/7323 (2.0%)
All	All	0.86	729/166219 (0.4%)	0.88	969/247786 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
18	s	0	1
34	I	0	1
36	K	0	1
46	U	0	1
53	3	0	20
54	1	0	59
55	2	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
56	5	0	1
57	6	0	1
58	4	0	1
59	8	0	1
All	All	0	90

The worst 5 of 729 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	K	13	ASP	C-O	24.96	1.52	1.24
59	8	312	SER	C-O	24.96	1.55	1.23
8	i	19	PRO	C-O	24.30	1.55	1.24
8	i	54	ILE	C-O	23.54	1.50	1.24
8	i	27	LEU	C-O	22.54	1.50	1.24

The worst 5 of 969 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	Z	23	GLU	CA-C-O	19.41	140.75	119.40
51	Z	23	GLU	O-C-N	-17.56	104.58	121.79
36	K	50	PRO	CA-C-N	-15.48	103.36	123.17
36	K	50	PRO	C-N-CA	-15.48	103.36	123.17
49	X	45	GLY	CA-C-O	15.06	134.01	118.95

There are no chirality outliers.

5 of 90 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
53	3	57	G	Sidechain
34	I	152	SER	Mainchain
36	K	53	LYS	Mainchain
46	U	73	ALA	Mainchain
18	s	58	ALA	Mainchain

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	b	2083	0	2157	153	0
2	c	1565	0	1616	98	0
3	d	1552	0	1619	104	0
4	e	1411	0	1447	112	0
5	f	1323	0	1374	87	0
6	g	936	0	961	58	0
7	h	633	0	666	65	0
8	i	551	0	577	57	0
9	j	1129	0	1162	61	0
10	k	939	0	1012	75	0
11	l	1045	0	1117	69	0
12	m	1074	0	1157	71	0
13	n	961	0	1000	75	0
14	o	892	0	923	47	0
15	p	917	0	965	66	0
16	q	947	0	1022	51	0
17	r	816	0	839	47	0
18	s	857	0	922	40	0
19	t	739	0	807	35	0
20	u	780	0	834	42	0
21	v	753	0	780	37	0
22	w	575	0	592	29	0
23	x	625	0	655	41	0
24	y	509	0	543	38	0
25	z	449	0	491	26	0
26	A	523	0	524	30	0
27	B	444	0	461	33	0
28	C	410	0	440	18	0
29	D	377	0	418	17	0
30	E	504	0	574	24	0
31	F	302	0	343	28	0
32	G	1705	0	1732	120	0
33	H	1625	0	1699	114	0
34	I	1643	0	1710	198	0
35	J	1157	0	1199	93	0
36	K	818	0	808	85	0
37	L	1182	0	1240	95	0
38	M	979	0	1034	90	0
39	N	1022	0	1070	102	0
40	O	787	0	828	80	0
41	P	870	0	878	75	0
42	Q	955	0	1019	100	0
43	R	884	0	944	85	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	S	805	0	847	76	0
45	T	714	0	737	43	0
46	U	649	0	666	86	0
47	V	649	0	691	81	0
48	W	536	0	552	34	0
49	X	638	0	665	58	0
50	Y	665	0	714	70	0
51	Z	545	0	579	55	0
52	a	1027	0	1092	88	0
53	3	33012	0	16618	1129	0
54	1	62317	0	31346	1557	0
55	2	2568	0	1303	70	0
56	5	1647	0	831	26	0
57	6	1640	0	837	38	0
58	4	346	0	175	19	0
59	8	5312	0	5283	508	0
60	1	10	0	10	0	0
61	5	7	0	7	0	0
62	8	32	0	14	8	0
63	8	1	0	0	0	0
All	All	153368	0	105126	6337	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 25.

The worst 5 of 6337 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)
46:U:79:ASN:HD21	46:U:82:ALA:HB3	1.06	1.14
55:2:3:C:H2'	55:2:4:C:H5''	1.27	1.12
51:Z:24:LYS:HB3	51:Z:26:GLY:H	0.95	1.11
52:a:6:LYS:O	52:a:8:MET:N	1.82	1.11
51:Z:23:GLU:O	51:Z:24:LYS:HB2	1.31	1.09

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	b	269/271 (99%)	223 (83%)	40 (15%)	6 (2%)	5	26
2	c	207/209 (99%)	179 (86%)	28 (14%)	0	100	100
3	d	199/201 (99%)	168 (84%)	30 (15%)	1 (0%)	24	55
4	e	175/177 (99%)	143 (82%)	28 (16%)	4 (2%)	5	25
5	f	174/176 (99%)	145 (83%)	27 (16%)	2 (1%)	11	39
6	g	121/149 (81%)	93 (77%)	24 (20%)	4 (3%)	3	19
7	h	82/131 (63%)	59 (72%)	18 (22%)	5 (6%)	1	9
8	i	72/141 (51%)	60 (83%)	11 (15%)	1 (1%)	9	33
9	j	140/142 (99%)	119 (85%)	20 (14%)	1 (1%)	18	49
10	k	120/122 (98%)	101 (84%)	19 (16%)	0	100	100
11	l	141/143 (99%)	124 (88%)	16 (11%)	1 (1%)	18	49
12	m	134/136 (98%)	120 (90%)	12 (9%)	2 (2%)	8	32
13	n	118/120 (98%)	98 (83%)	18 (15%)	2 (2%)	7	30
14	o	114/116 (98%)	101 (89%)	13 (11%)	0	100	100
15	p	112/114 (98%)	96 (86%)	16 (14%)	0	100	100
16	q	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
17	r	101/103 (98%)	83 (82%)	16 (16%)	2 (2%)	6	27
18	s	108/110 (98%)	93 (86%)	14 (13%)	1 (1%)	14	43
19	t	91/93 (98%)	78 (86%)	13 (14%)	0	100	100
20	u	100/102 (98%)	78 (78%)	21 (21%)	1 (1%)	12	40
21	v	92/94 (98%)	83 (90%)	8 (9%)	1 (1%)	11	39
22	w	73/75 (97%)	63 (86%)	9 (12%)	1 (1%)	9	33
23	x	75/77 (97%)	66 (88%)	9 (12%)	0	100	100
24	y	61/63 (97%)	54 (88%)	6 (10%)	1 (2%)	7	31
25	z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	A	64/66 (97%)	54 (84%)	10 (16%)	0	100	100
27	B	54/56 (96%)	42 (78%)	12 (22%)	0	100	100
28	C	48/50 (96%)	39 (81%)	9 (19%)	0	100	100
29	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
30	E	62/64 (97%)	48 (77%)	9 (14%)	5 (8%)	1	5
31	F	36/38 (95%)	29 (81%)	6 (17%)	1 (3%)	4	21
32	G	216/225 (96%)	177 (82%)	35 (16%)	4 (2%)	6	28
33	H	204/206 (99%)	183 (90%)	20 (10%)	1 (0%)	24	55
34	I	203/205 (99%)	151 (74%)	48 (24%)	4 (2%)	6	27
35	J	155/157 (99%)	122 (79%)	26 (17%)	7 (4%)	2	13
36	K	98/100 (98%)	81 (83%)	15 (15%)	2 (2%)	6	27
37	L	149/151 (99%)	124 (83%)	24 (16%)	1 (1%)	18	49
38	M	127/129 (98%)	109 (86%)	18 (14%)	0	100	100
39	N	125/127 (98%)	97 (78%)	28 (22%)	0	100	100
40	O	96/98 (98%)	75 (78%)	18 (19%)	3 (3%)	3	20
41	P	114/116 (98%)	92 (81%)	20 (18%)	2 (2%)	6	29
42	Q	121/123 (98%)	95 (78%)	24 (20%)	2 (2%)	7	30
43	R	112/114 (98%)	94 (84%)	17 (15%)	1 (1%)	14	43
44	S	98/100 (98%)	77 (79%)	20 (20%)	1 (1%)	12	40
45	T	86/88 (98%)	73 (85%)	13 (15%)	0	100	100
46	U	80/82 (98%)	53 (66%)	24 (30%)	3 (4%)	2	16
47	V	78/80 (98%)	54 (69%)	21 (27%)	3 (4%)	2	16
48	W	63/65 (97%)	49 (78%)	11 (18%)	3 (5%)	2	12
49	X	77/79 (98%)	60 (78%)	17 (22%)	0	100	100
50	Y	83/85 (98%)	73 (88%)	9 (11%)	1 (1%)	10	37
51	Z	63/65 (97%)	41 (65%)	18 (29%)	4 (6%)	1	8
52	a	130/223 (58%)	104 (80%)	19 (15%)	7 (5%)	1	10
59	8	681/711 (96%)	558 (82%)	108 (16%)	15 (2%)	5	26
All	All	6517/6889 (95%)	5386 (83%)	1025 (16%)	106 (2%)	10	31

5 of 106 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	107	LYS
3	d	83	VAL
4	e	176	PHE
7	h	80	THR
8	i	11	GLN

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	b	216/216 (100%)	210 (97%)	6 (3%)	38	62
2	c	164/164 (100%)	160 (98%)	4 (2%)	43	65
3	d	165/165 (100%)	162 (98%)	3 (2%)	51	70
4	e	148/148 (100%)	146 (99%)	2 (1%)	59	73
5	f	137/137 (100%)	134 (98%)	3 (2%)	45	66
6	g	98/114 (86%)	98 (100%)	0	100	100
7	h	66/100 (66%)	65 (98%)	1 (2%)	57	72
8	i	60/109 (55%)	57 (95%)	3 (5%)	22	50
9	j	116/116 (100%)	112 (97%)	4 (3%)	32	59
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	76
11	l	102/102 (100%)	100 (98%)	2 (2%)	48	68
12	m	109/109 (100%)	106 (97%)	3 (3%)	38	62
13	n	100/100 (100%)	96 (96%)	4 (4%)	28	56
14	o	86/86 (100%)	81 (94%)	5 (6%)	18	47
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	76
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	81 (96%)	3 (4%)	31	58
18	s	93/93 (100%)	92 (99%)	1 (1%)	65	76
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	74
20	u	83/83 (100%)	80 (96%)	3 (4%)	31	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	74
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	47 (98%)	1 (2%)	47	67
26	A	59/59 (100%)	58 (98%)	1 (2%)	53	71
27	B	47/47 (100%)	45 (96%)	2 (4%)	26	54
28	C	45/45 (100%)	45 (100%)	0	100	100
29	D	38/38 (100%)	38 (100%)	0	100	100
30	E	51/51 (100%)	50 (98%)	1 (2%)	48	68
31	F	34/34 (100%)	34 (100%)	0	100	100
32	G	180/186 (97%)	178 (99%)	2 (1%)	65	76
33	H	170/170 (100%)	166 (98%)	4 (2%)	43	65
34	I	172/172 (100%)	166 (96%)	6 (4%)	32	58
35	J	119/119 (100%)	116 (98%)	3 (2%)	42	64
36	K	87/87 (100%)	82 (94%)	5 (6%)	18	47
37	L	124/124 (100%)	124 (100%)	0	100	100
38	M	104/104 (100%)	102 (98%)	2 (2%)	50	68
39	N	105/105 (100%)	100 (95%)	5 (5%)	23	52
40	O	86/86 (100%)	84 (98%)	2 (2%)	44	66
41	P	89/89 (100%)	89 (100%)	0	100	100
42	Q	103/103 (100%)	98 (95%)	5 (5%)	22	51
43	R	92/92 (100%)	91 (99%)	1 (1%)	65	76
44	S	83/83 (100%)	82 (99%)	1 (1%)	63	75
45	T	76/76 (100%)	75 (99%)	1 (1%)	61	74
46	U	65/65 (100%)	63 (97%)	2 (3%)	35	60
47	V	74/74 (100%)	74 (100%)	0	100	100
48	W	56/56 (100%)	55 (98%)	1 (2%)	51	70
49	X	70/70 (100%)	67 (96%)	3 (4%)	26	54
50	Y	65/65 (100%)	64 (98%)	1 (2%)	57	72
51	Z	55/55 (100%)	53 (96%)	2 (4%)	31	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	a	110/174 (63%)	109 (99%)	1 (1%)	70	78
59	8	566/585 (97%)	552 (98%)	14 (2%)	42	64
All	All	5428/5616 (97%)	5311 (98%)	117 (2%)	45	66

5 of 117 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	G	169	HIS
59	8	298	ILE
36	K	6	ILE
59	8	292	VAL
50	Y	11	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 98 such sidechains are listed below:

Mol	Chain	Res	Type
34	I	130	ASN
39	N	125	GLN
35	J	69	ASN
36	K	63	ASN
43	R	99	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	3	1538/1539 (99%)	198 (12%)	5 (0%)
54	1	2902/2903 (99%)	368 (12%)	12 (0%)
55	2	119/120 (99%)	13 (10%)	2 (1%)
56	5	76/77 (98%)	12 (15%)	1 (1%)
57	6	76/77 (98%)	21 (27%)	0
58	4	15/16 (93%)	5 (33%)	0
All	All	4726/4732 (99%)	617 (13%)	20 (0%)

5 of 617 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	3	6	G
53	3	8	A
53	3	9	G

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Mol	Chain	Res	Type
53	3	22	G
53	3	32	A

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	1	2296	U
55	2	66	A
56	5	2	G
55	2	88	C
54	1	490	C

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](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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	$\# Z > 2$
62	GCP	8	801	63	32,34,34	2.09	7 (21%)	49,54,54	2.44	16 (32%)
60	FME	1	3001	61	8,9,10	0.54	0	8,9,11	0.73	0
61	PRO	5	101	60,56	6,7,8	0.52	0	7,8,10	1.20	1 (14%)

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
62	GCP	8	801	63	-	9/19/38/38	0/3/3/3
60	FME	1	3001	61	-	1/7/9/11	-
61	PRO	5	101	60,56	-	0/0/9/11	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	8	801	GCP	PA-O3A	-7.32	1.51	1.59
62	8	801	GCP	PB-O3A	-5.80	1.51	1.58
62	8	801	GCP	PB-O2B	-3.17	1.48	1.56
62	8	801	GCP	C1'-N9	2.37	1.54	1.47
62	8	801	GCP	PG-O3G	-2.26	1.49	1.55

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	8	801	GCP	C1'-N9-C4	8.09	150.38	126.49
62	8	801	GCP	C1'-N9-C8	-7.98	104.05	126.73
62	8	801	GCP	O3G-PG-O2G	4.31	120.25	107.96
62	8	801	GCP	O2G-PG-C3B	-4.29	95.99	106.40
62	8	801	GCP	O3A-PA-O1A	-4.18	98.13	110.70

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	1	3001	FME	O1-CN-N-CA
62	8	801	GCP	PB-C3B-PG-O1G
62	8	801	GCP	PB-C3B-PG-O2G
62	8	801	GCP	PG-C3B-PB-O1B
62	8	801	GCP	C5'-O5'-PA-O1A

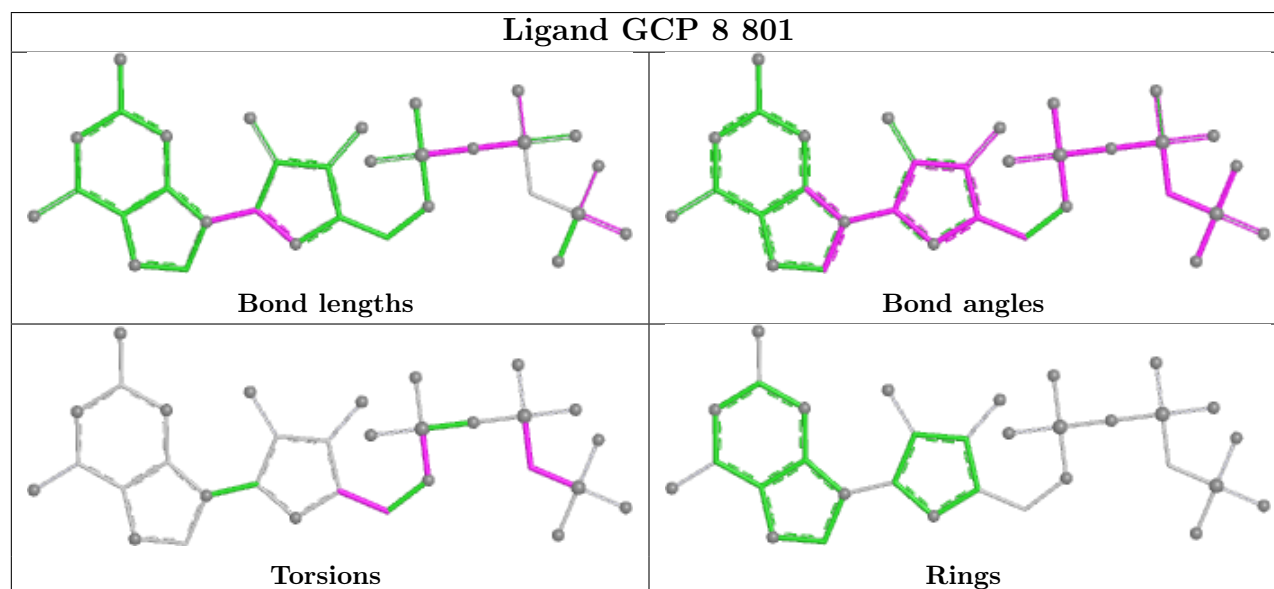
There are no ring outliers.

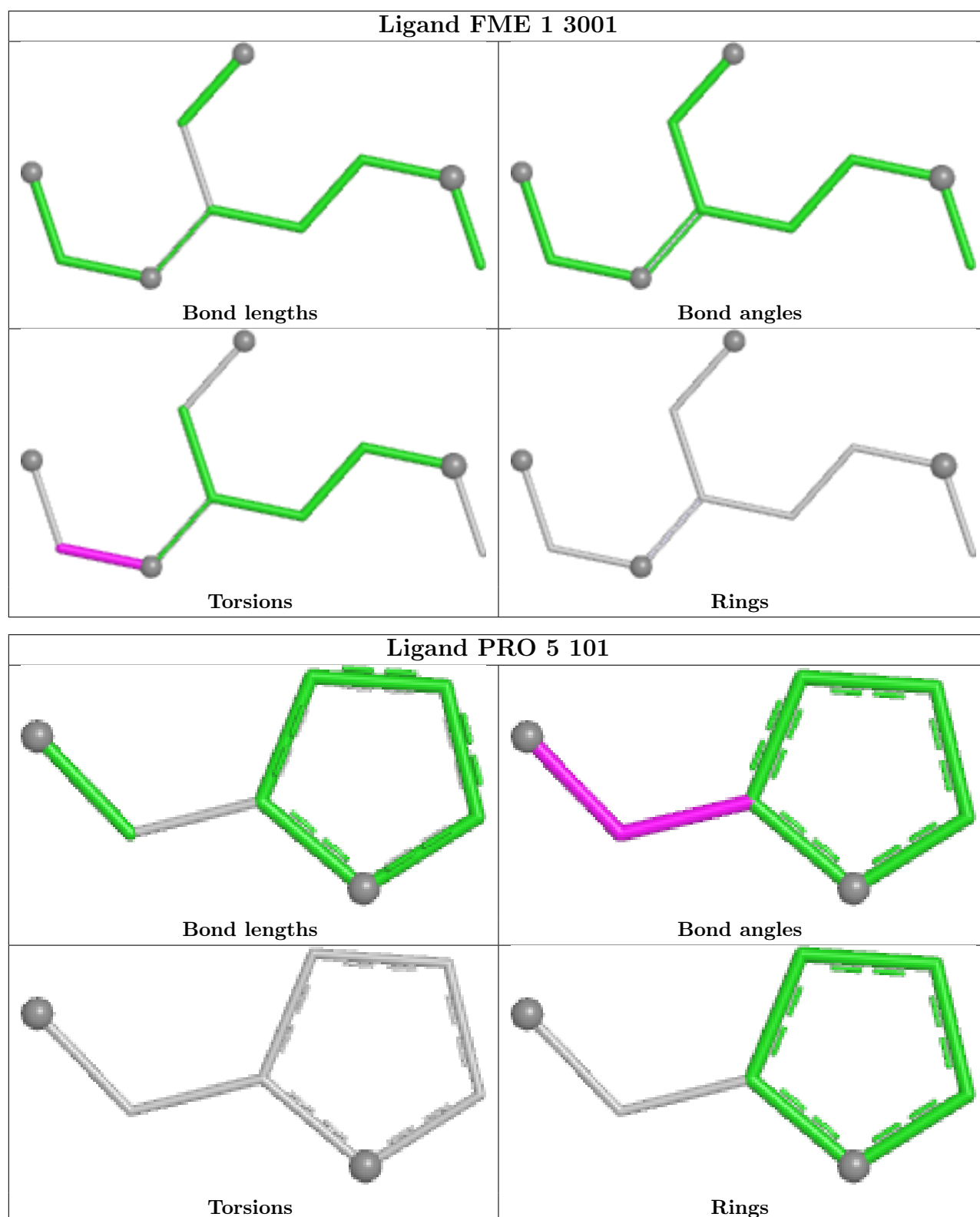
1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	8	801	GCP	8	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 ⓘ

There are no chain breaks in this entry.

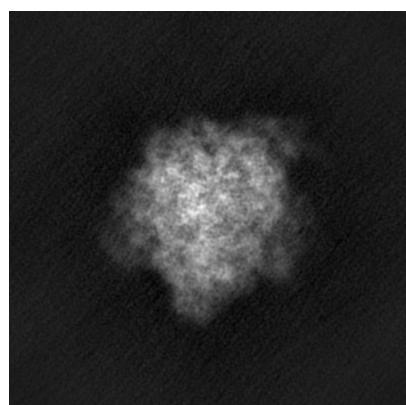
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22674. These allow visual inspection of the internal detail of the map and identification of artifacts.

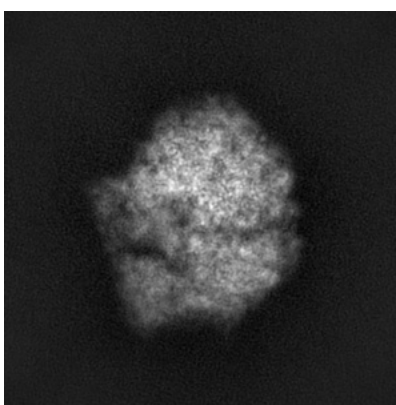
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

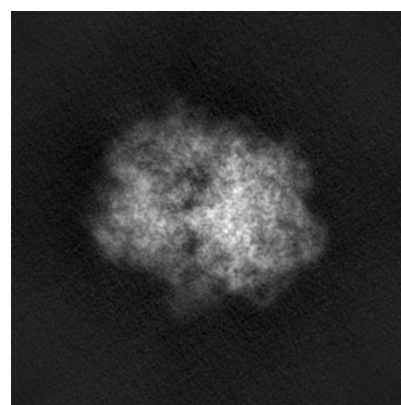
6.1.1 Primary map



X



Y

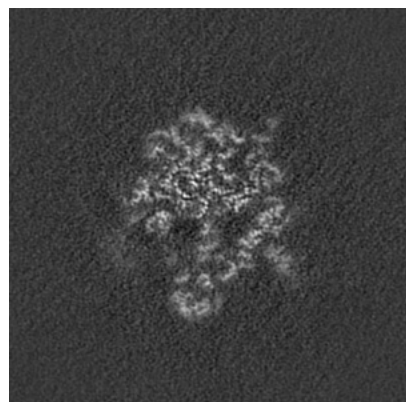


Z

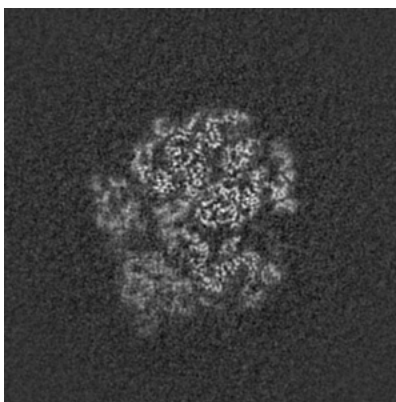
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

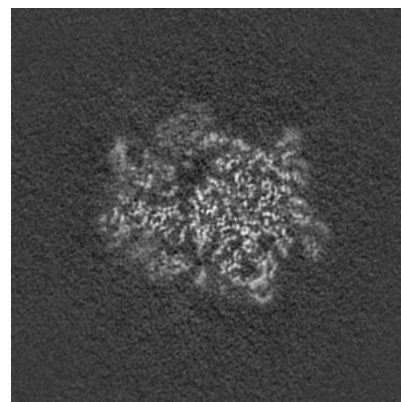
6.2.1 Primary map



X Index: 200



Y Index: 200

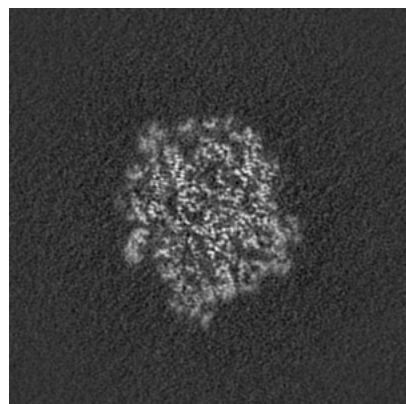


Z Index: 200

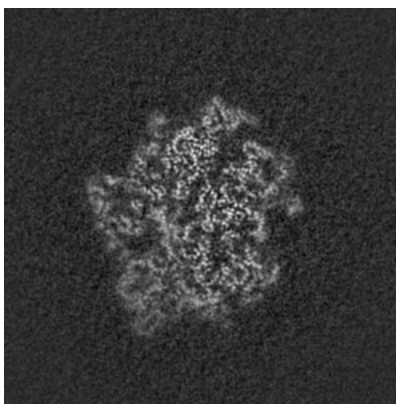
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

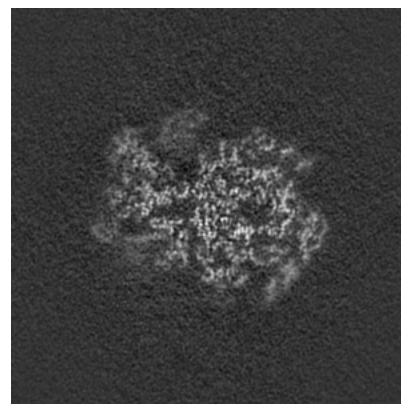
6.3.1 Primary map



X Index: 223



Y Index: 192

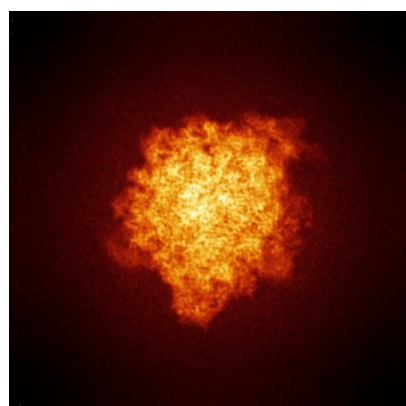


Z Index: 214

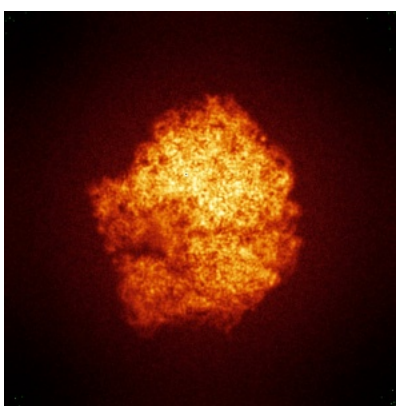
The images above show the largest variance slices of the map in three orthogonal directions.

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

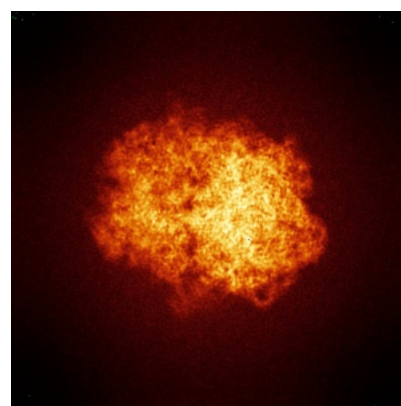
6.4.1 Primary map



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 3.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

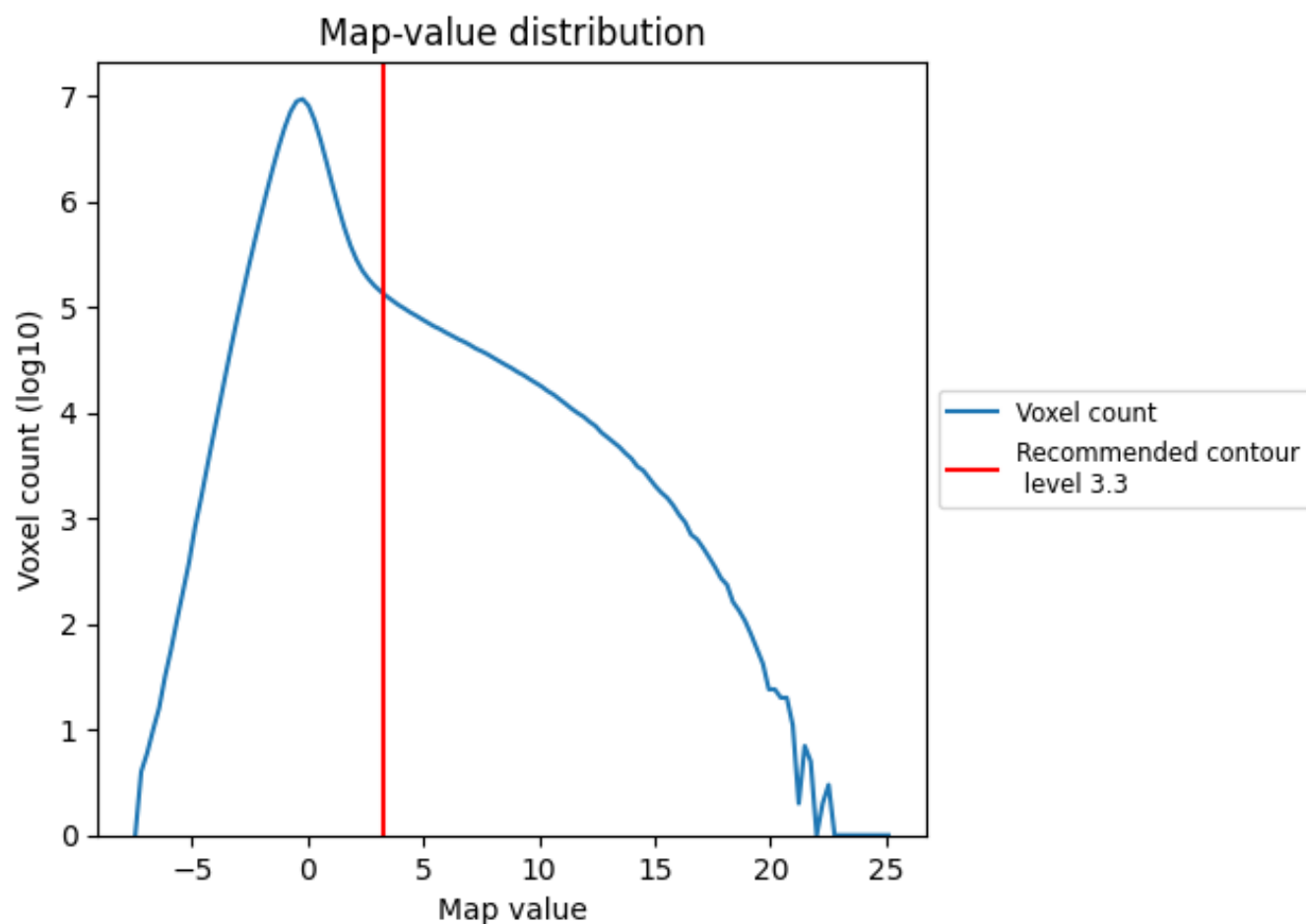
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

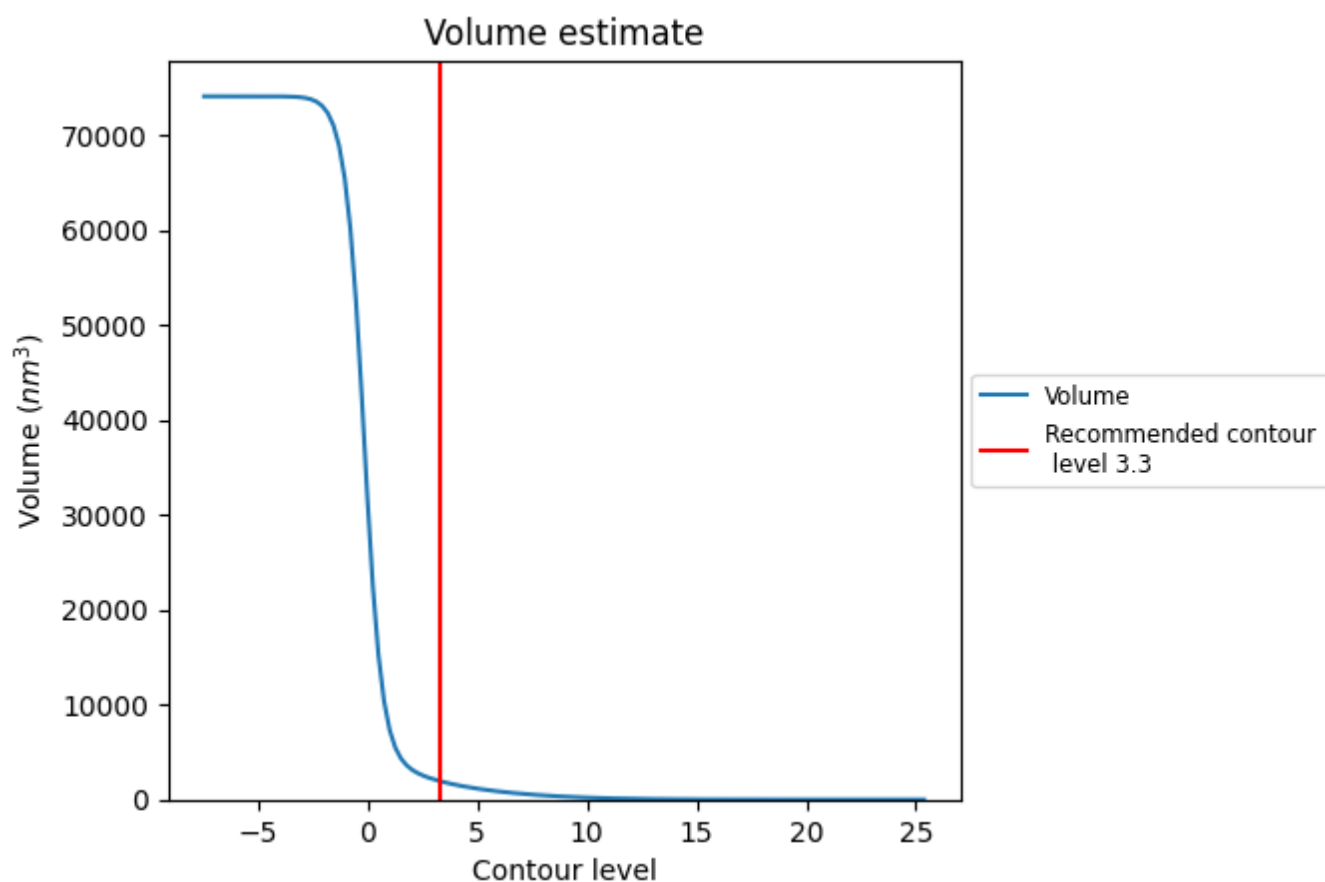
This section contains the results of statistical analysis of the map.

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.

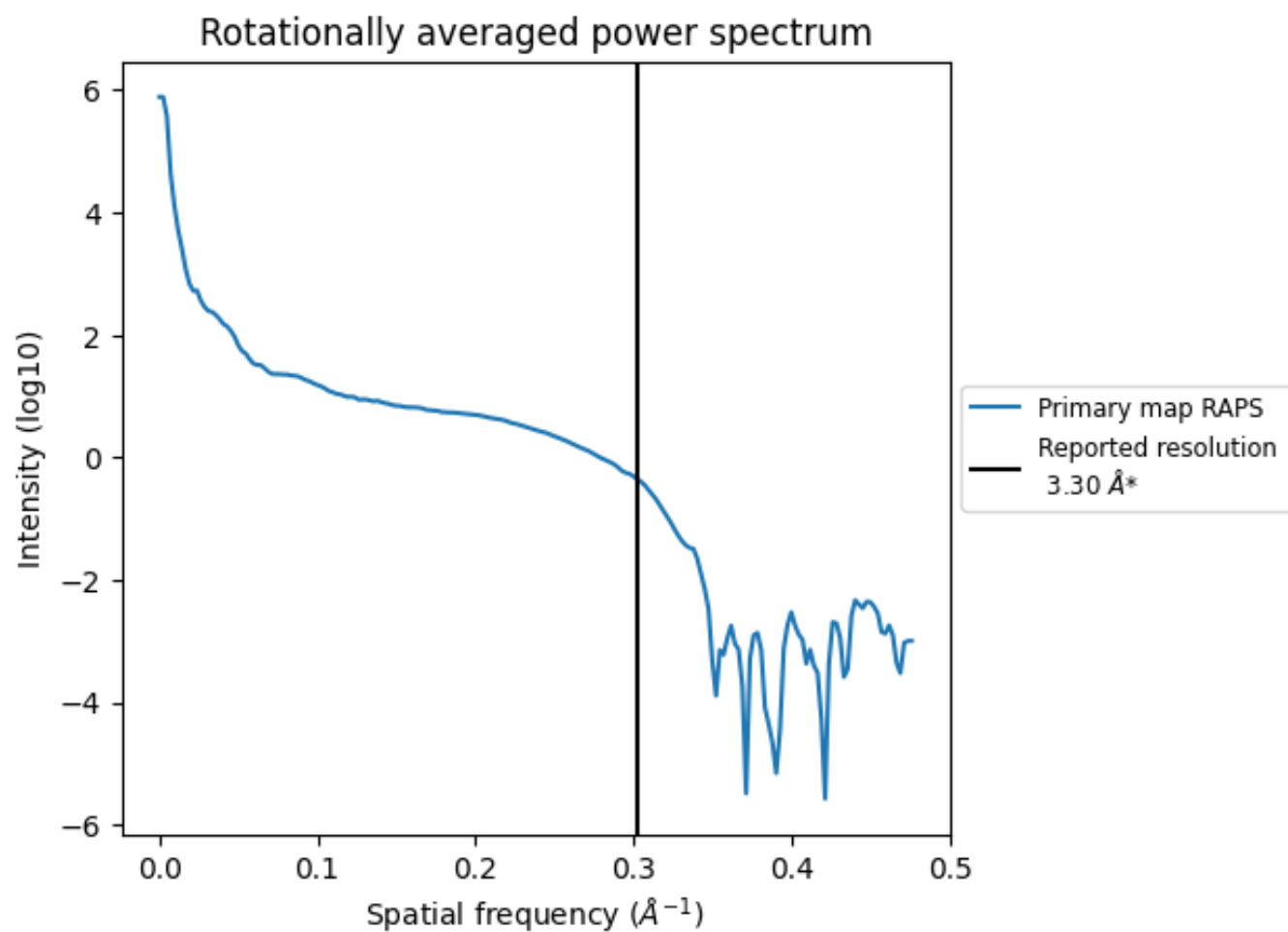
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1936 nm³; this corresponds to an approximate mass of 1749 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 0.303 Å⁻¹

8 Fourier-Shell correlation

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

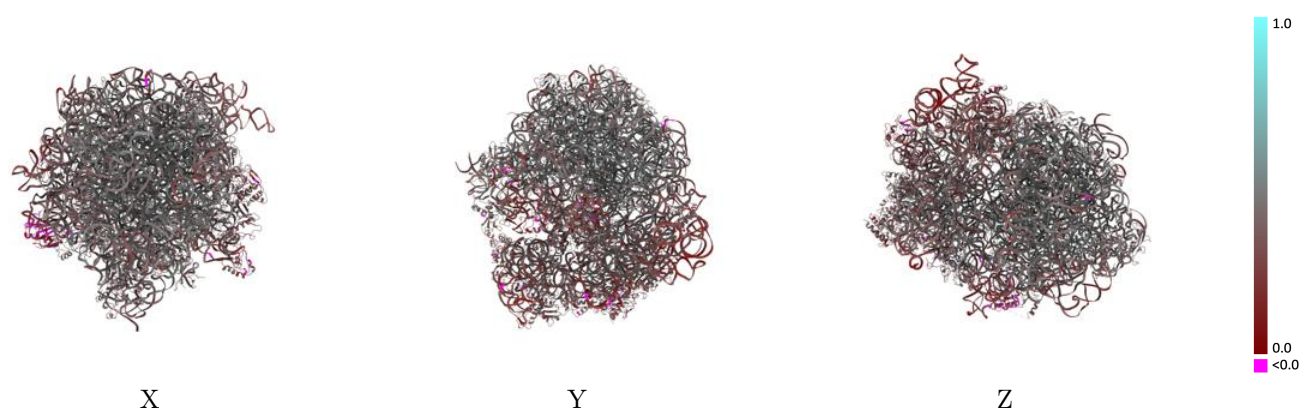
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22674 and PDB model 7K55. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)

This section was not generated.

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

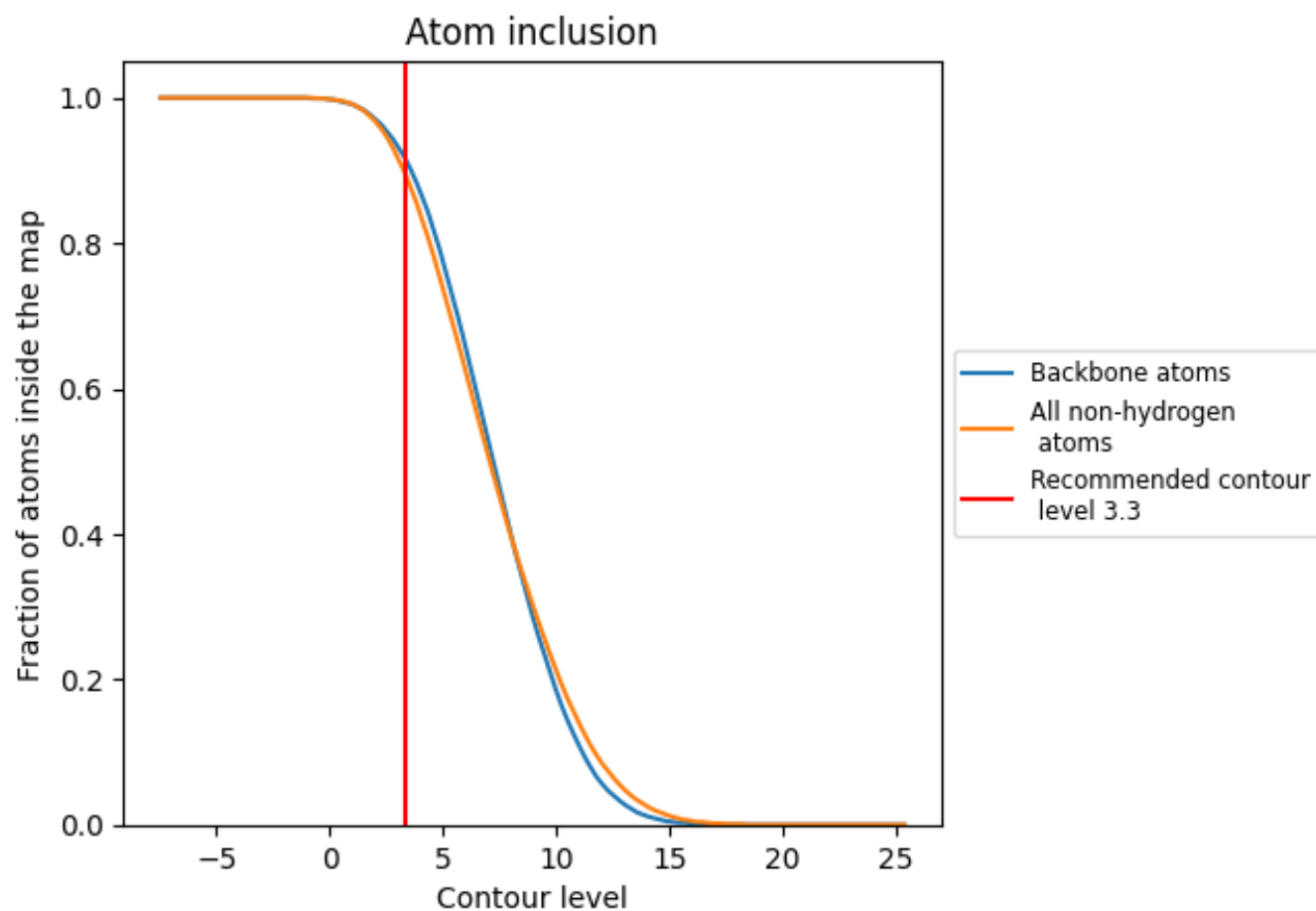


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 92% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (3.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8980	 0.3940
1	 0.9720	 0.4270
2	 0.9790	 0.4050
3	 0.9270	 0.3600
4	 0.7490	 0.2820
5	 0.9760	 0.3440
6	 0.4840	 0.1950
8	 0.6460	 0.3170
A	 0.7210	 0.3380
B	 0.8950	 0.4420
C	 0.7710	 0.4190
D	 0.9440	 0.4800
E	 0.9590	 0.4870
F	 0.8840	 0.4600
G	 0.6780	 0.3610
H	 0.7040	 0.3840
I	 0.7650	 0.2950
J	 0.8930	 0.4190
K	 0.8760	 0.3790
L	 0.7060	 0.3390
M	 0.8840	 0.4080
N	 0.7910	 0.3440
O	 0.6170	 0.3330
P	 0.9070	 0.4160
Q	 0.8780	 0.4030
R	 0.8040	 0.3370
S	 0.8440	 0.3560
T	 0.9220	 0.4050
U	 0.8500	 0.3650
V	 0.8960	 0.3680
W	 0.9220	 0.4050
X	 0.7120	 0.3320
Y	 0.8280	 0.3630
Z	 0.7280	 0.3170
a	 0.1060	 0.0370



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Chain	Atom inclusion	Q-score
b	 0.9440	 0.4720
c	 0.9230	 0.4590
d	 0.8200	 0.4300
e	 0.8930	 0.3720
f	 0.8570	 0.3950
g	 0.3050	 0.3150
h	 0.2240	 0.2420
i	 0.2430	 0.2320
j	 0.9380	 0.4560
k	 0.9120	 0.4700
l	 0.9280	 0.4580
m	 0.9230	 0.4500
n	 0.9370	 0.4490
o	 0.9150	 0.4170
p	 0.9100	 0.4580
q	 0.9390	 0.4600
r	 0.9070	 0.4550
s	 0.9020	 0.4570
t	 0.9070	 0.4480
u	 0.8850	 0.4210
v	 0.9000	 0.4260
w	 0.9210	 0.4750
x	 0.9150	 0.4440
y	 0.8830	 0.3940
z	 0.9130	 0.4430