



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:35 PM UTC

PDB ID : 7K54 / pdb_00007k54
EMDB ID : EMD-22673
Title : Mid-translocated +1-frameshifting(CCC-A) complex with EF-G and GDPCP (Structure II-FS)
Authors : Demo, G.; Loveland, A.B.; Svidritskiy, E.; Gamper, H.B.; Hou, Y.M.; Korostelev, A.A.
Deposited on : 2020-09-16
Resolution : 3.20 Å (reported)
Based on initial models : 6ENJ, 5UYM, 4V9P, 4V7D

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

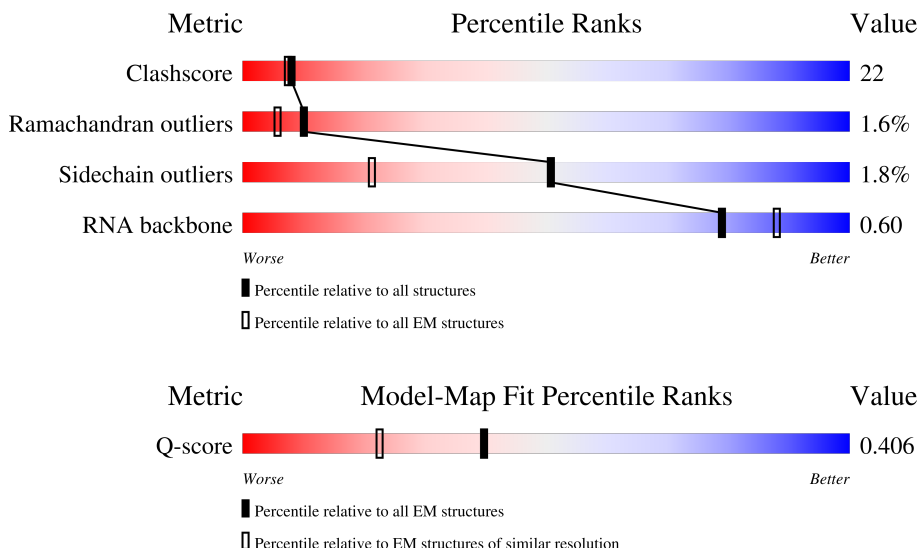
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	37%51%10%
54	1	2903	45%47%8%
55	2	120	48%42%8%
56	5	77	36%51%10%
57	6	77	48%39%13%
58	4	16	31%62%6%
59	8	711	6%35%51%9%

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		

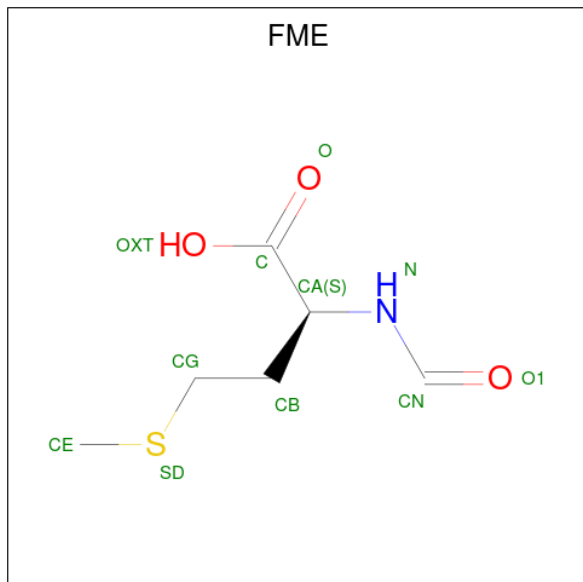
- Molecule 59 is a protein called Elongation factor G.

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:

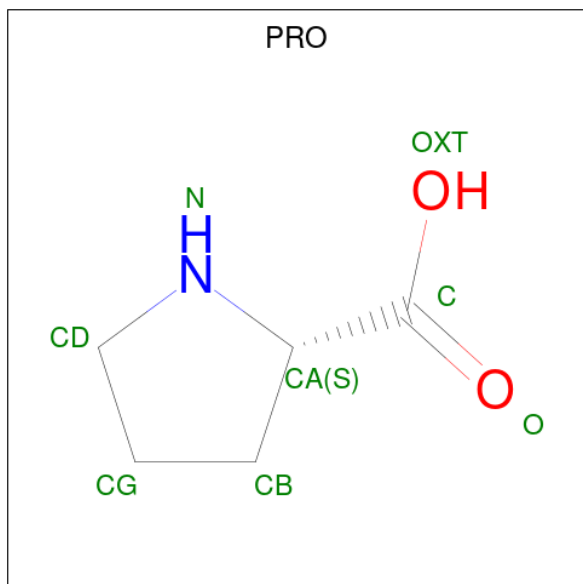
Chain	Residue	Modelled	Actual	Comment	Reference
8	705	LEU	-	expression tag	UNP U9XYS4
8	706	GLU	-	expression tag	UNP U9XYS4
8	707	HIS	-	expression tag	UNP U9XYS4
8	708	HIS	-	expression tag	UNP U9XYS4
8	709	HIS	-	expression tag	UNP U9XYS4
8	710	HIS	-	expression tag	UNP U9XYS4
8	711	HIS	-	expression tag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



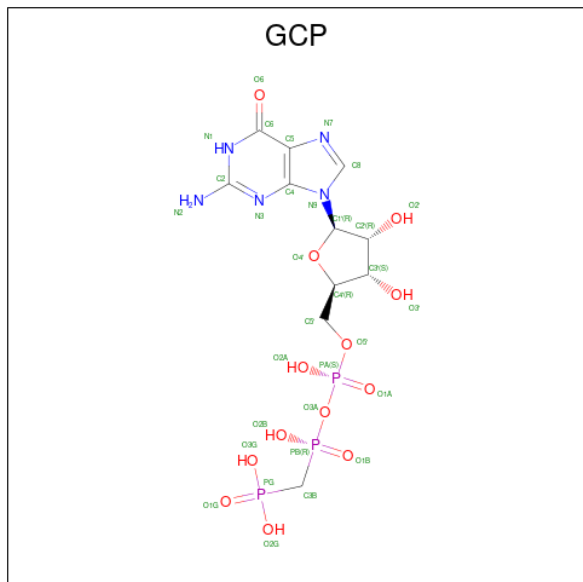
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
60	1	1	10	6	1	2	1	0

- 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).



Mol	Chain	Residues	Atoms					AltConf
62	8	1	Total	C	N	O	P	0
			32	11	5	13	3	

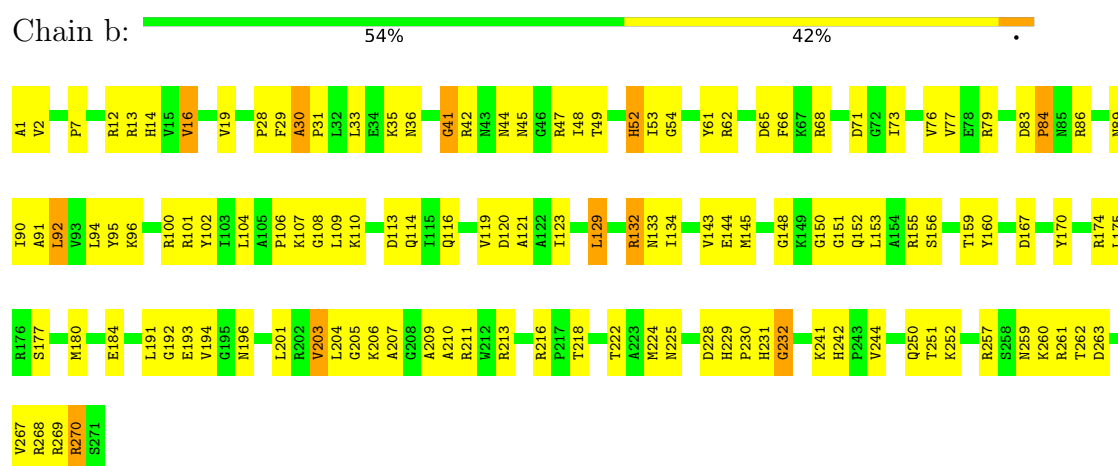
- Molecule 63 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
63	8	1	Total	Mg	0
			1	1	

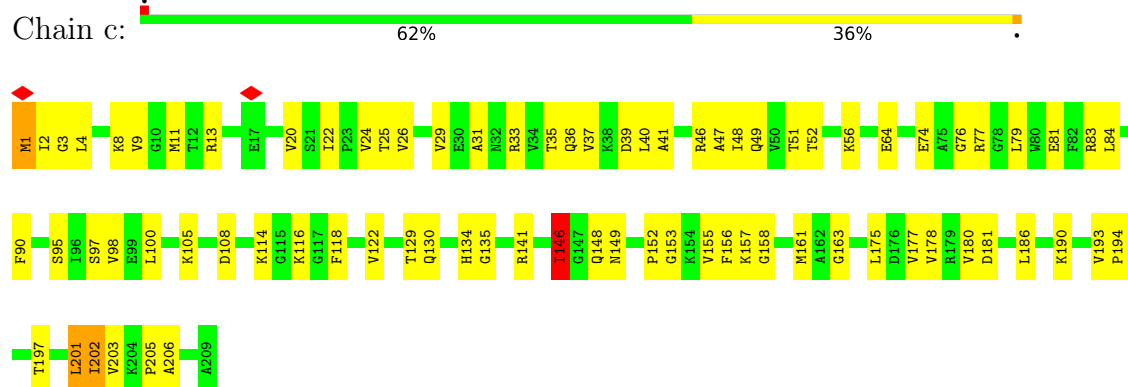
3 Residue-property plots

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

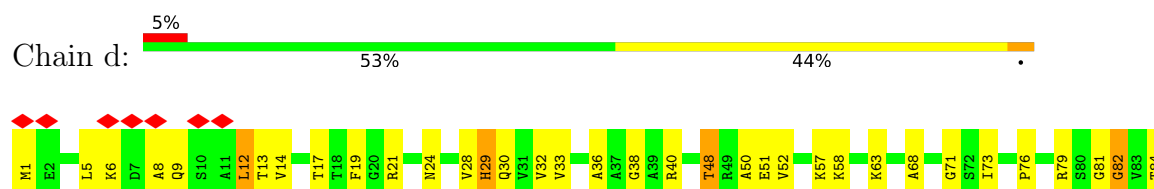
• Molecule 1: 50S ribosomal protein L2

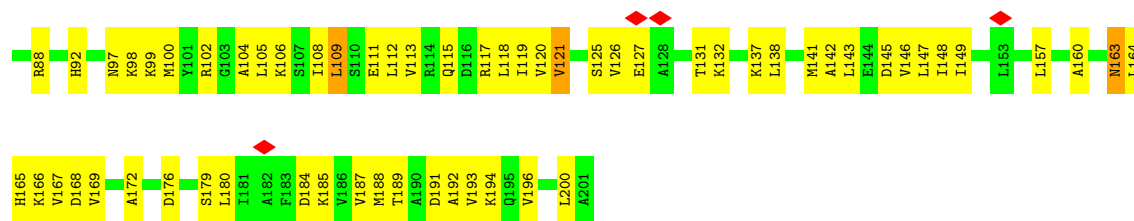


• Molecule 2: 50S ribosomal protein L3



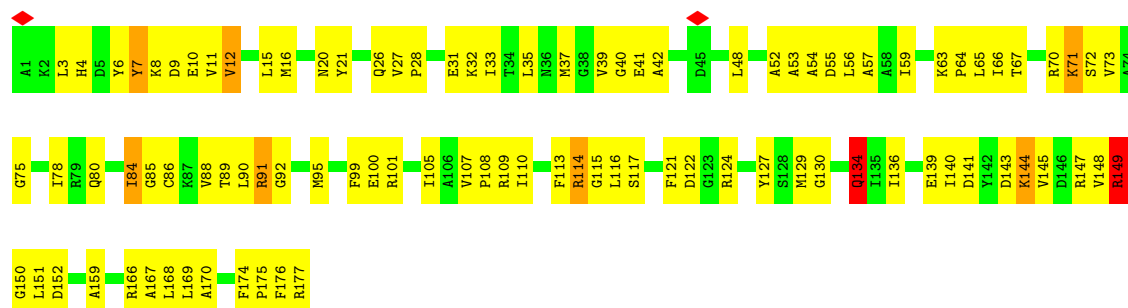
• Molecule 3: 50S ribosomal protein L4





• Molecule 4: 50S ribosomal protein L5

Chain e: 45% 50%



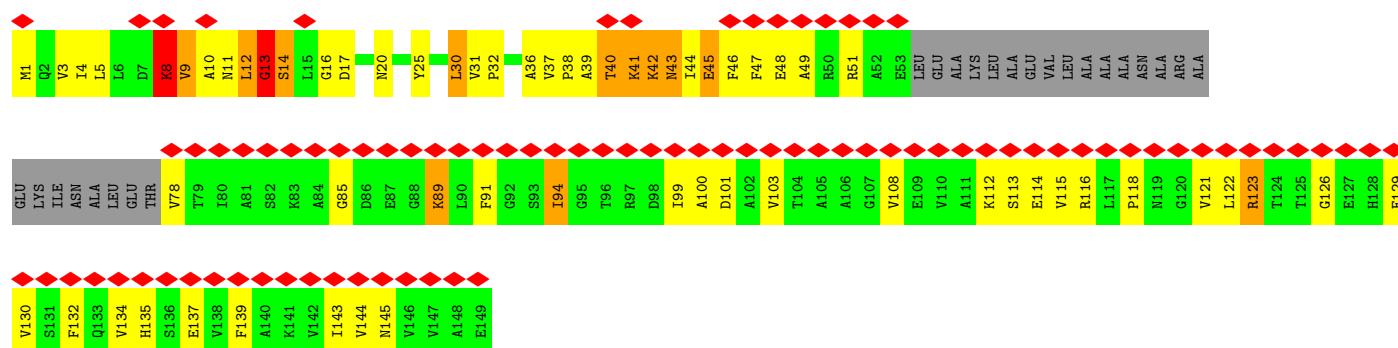
• Molecule 5: 50S ribosomal protein L6

Chain f: 48% 47% 5%

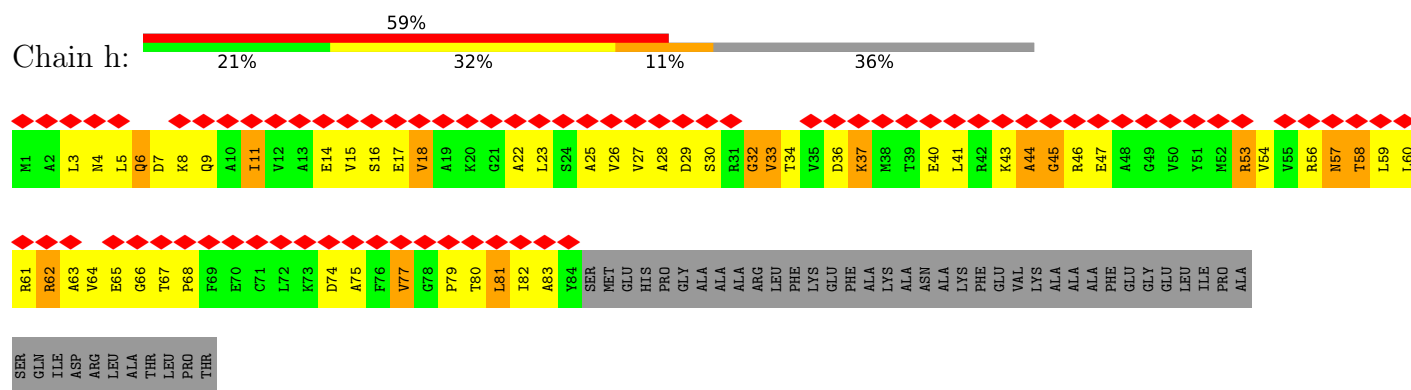


• Molecule 6: 50S ribosomal protein L9

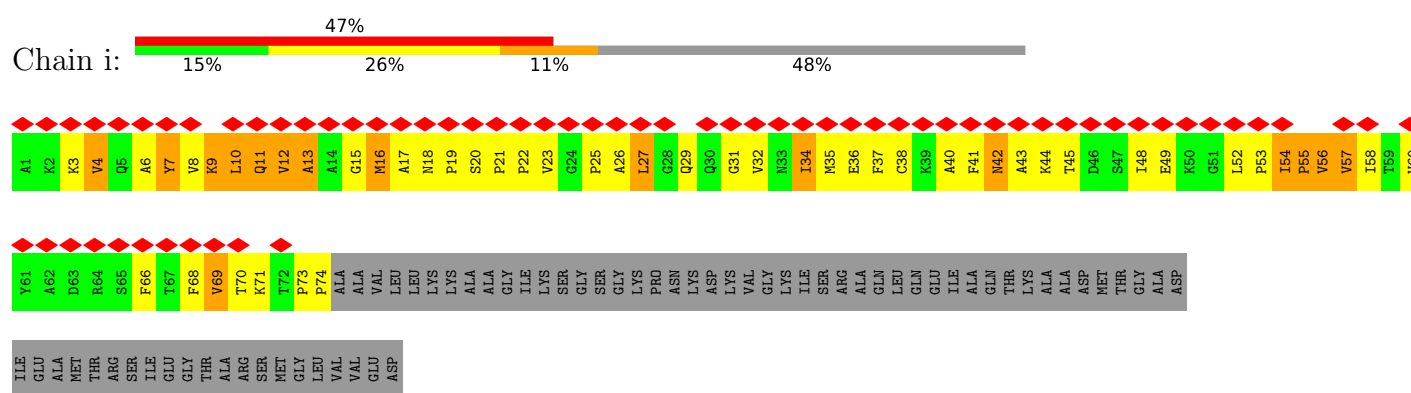
Chain g: 58% 42% 33% 8% 16%



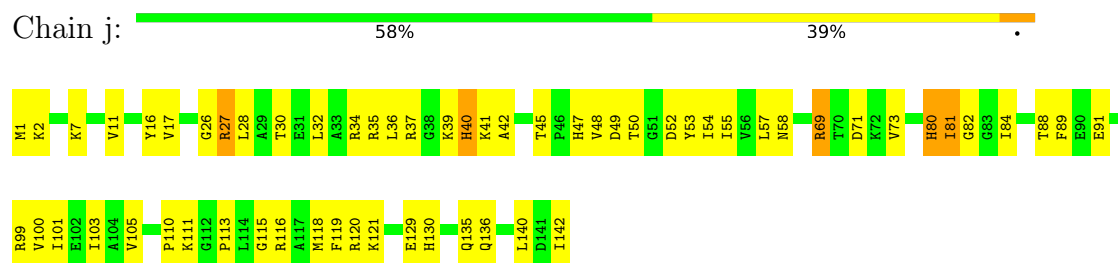
- Molecule 7: 50S ribosomal protein L10



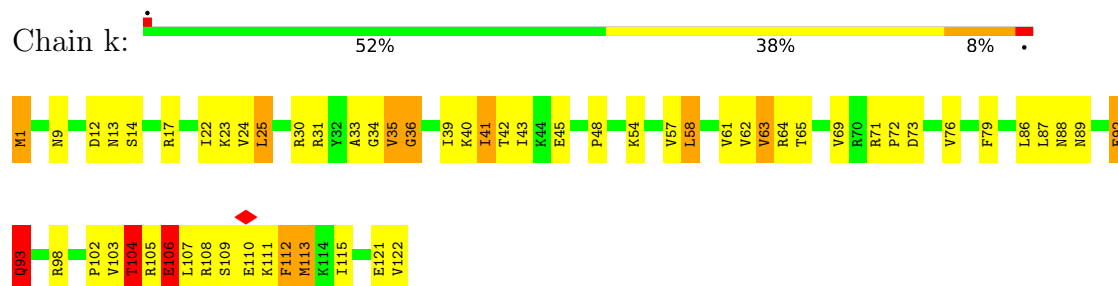
- Molecule 8: 50S ribosomal protein L11



- Molecule 9: 50S ribosomal protein L13

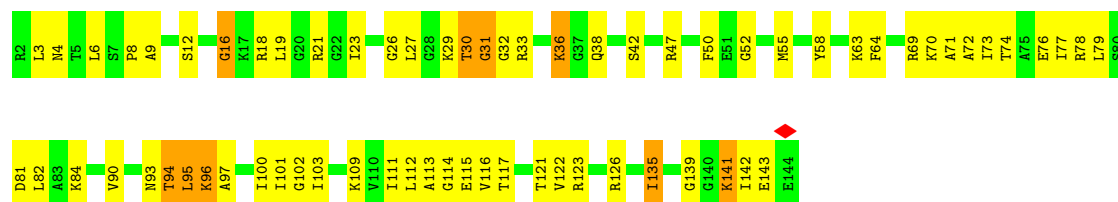


- Molecule 10: 50S ribosomal protein L14

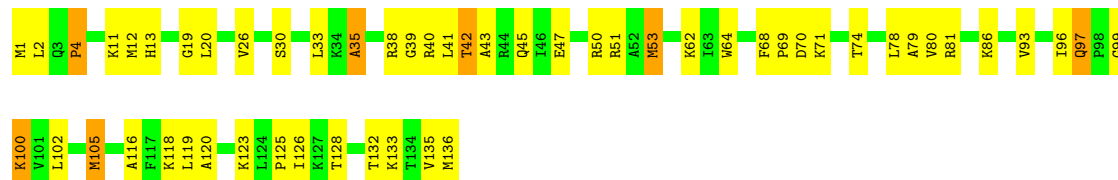


- Molecule 11: 50S ribosomal protein L15

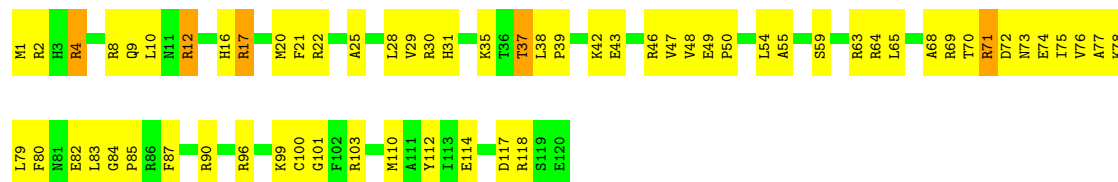




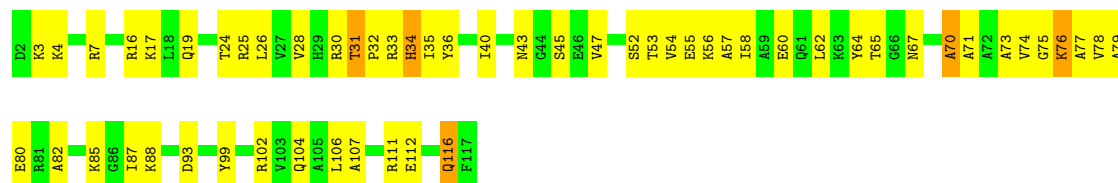
• Molecule 12: 50S ribosomal protein L16



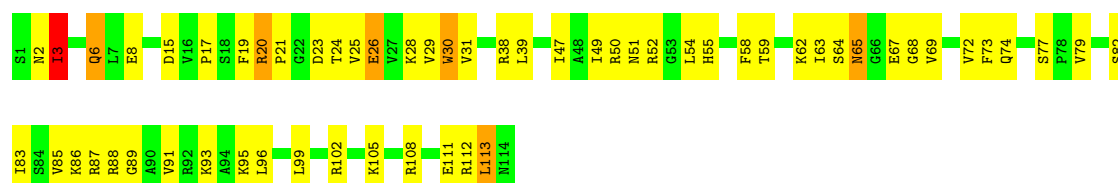
• Molecule 13: 50S ribosomal protein L17



• Molecule 14: 50S ribosomal protein L18

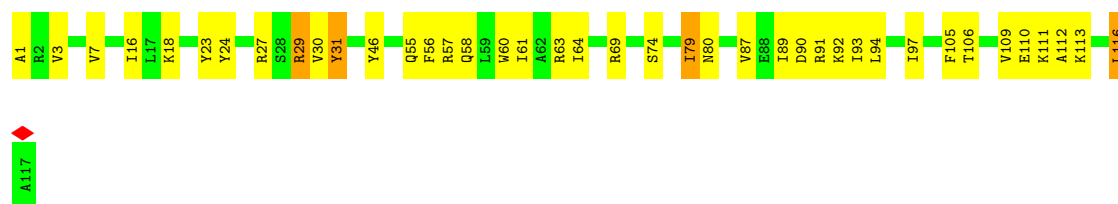


• Molecule 15: 50S ribosomal protein L19



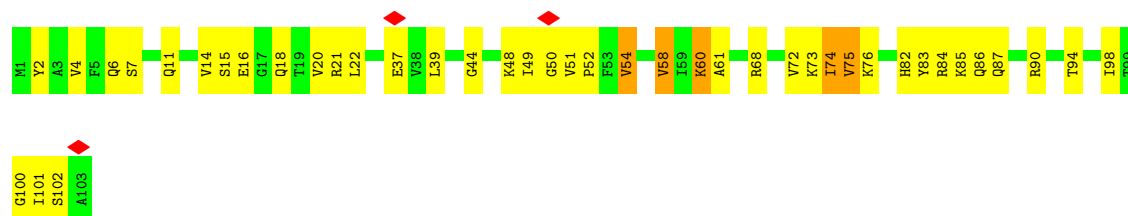
• Molecule 16: 50S ribosomal protein L20

Chain q:  66% 31%



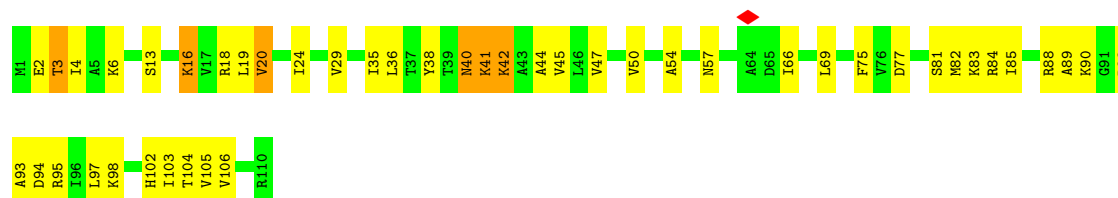
- Molecule 17: 50S ribosomal protein L21

Chain r:  59% 36% 5%



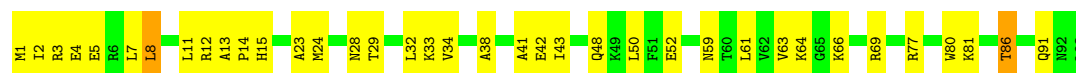
- Molecule 18: 50S ribosomal protein L22

Chain s:  58% 36% 5%



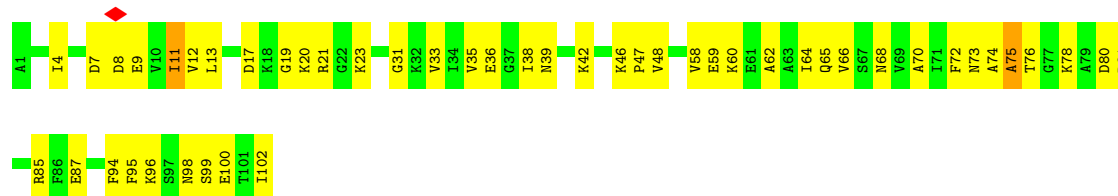
- Molecule 19: 50S ribosomal protein L23

Chain t:  60% 38%



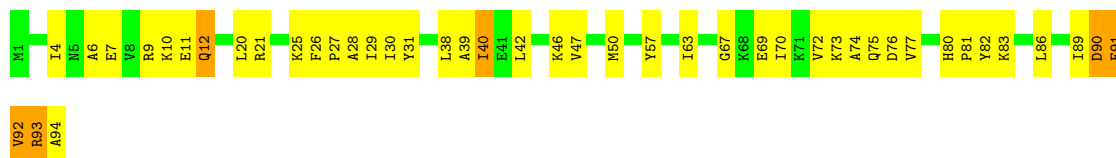
- Molecule 20: 50S ribosomal protein L24

Chain u:  53% 45%



- Molecule 21: 50S ribosomal protein L25

Chain v:  52% 41% 6%



- Molecule 22: 50S ribosomal protein L27

Chain w:  55% 45%



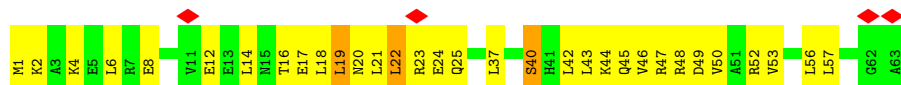
- Molecule 23: 50S ribosomal protein L28

Chain x:  55% 44%



- Molecule 24: 50S ribosomal protein L29

Chain y:  6% 49% 46% 5%



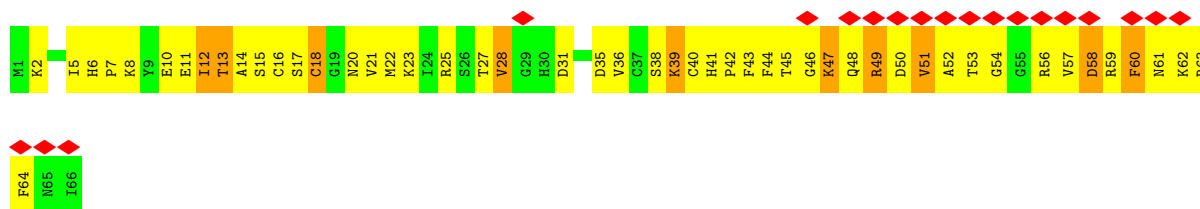
- Molecule 25: 50S ribosomal protein L30

Chain z:  5% 53% 45%



- Molecule 26: 50S ribosomal protein L31

Chain A:  29% 24% 61% 15%



- Molecule 27: 50S ribosomal protein L32

Chain B:  59% 41%



- Molecule 28: 50S ribosomal protein L33

Chain C:  6% 66% 26% 8%



- Molecule 29: 50S ribosomal protein L34

Chain D:  59% 39% 2%



- Molecule 30: 50S ribosomal protein L35

Chain E:  58% 33% 9%



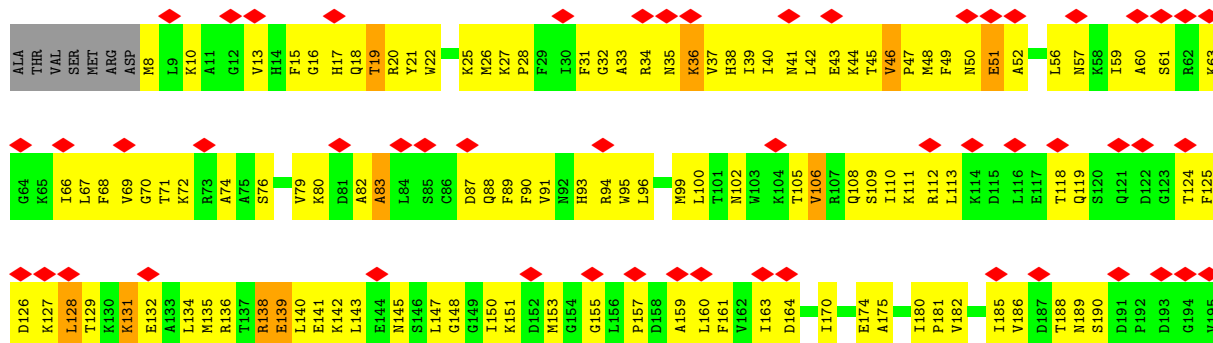
- Molecule 31: 50S ribosomal protein L36

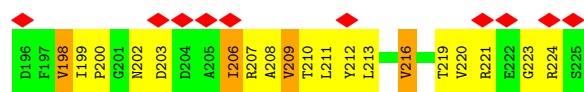
Chain F:  50% 47% 3%



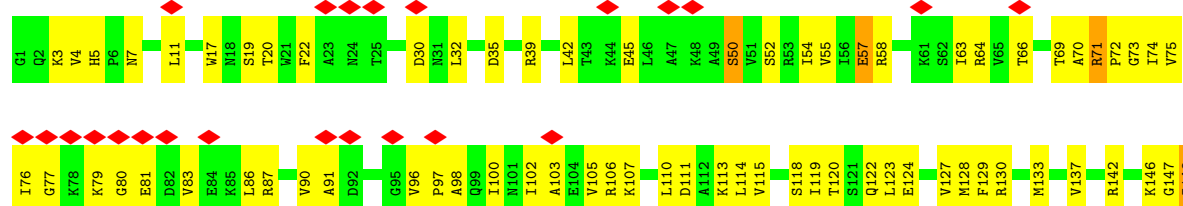
- Molecule 32: 30S ribosomal protein S2

Chain G:  28% 36% 55% 6%





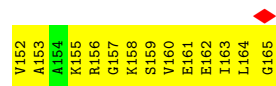
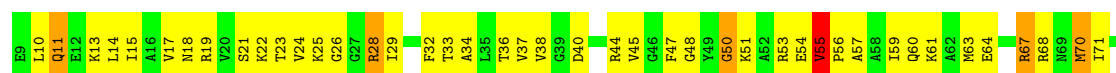
• Molecule 33: 30S ribosomal protein S3



• Molecule 34: 30S ribosomal protein S4

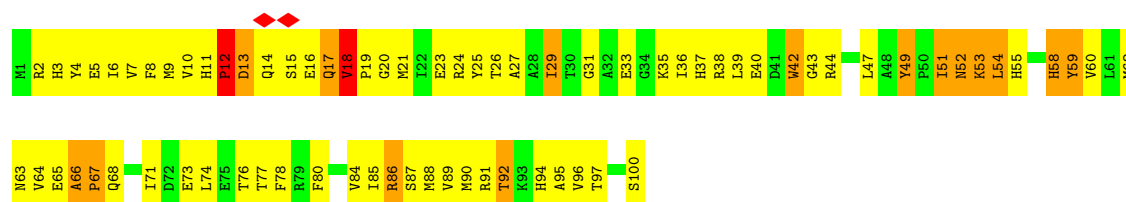


• Molecule 35: 30S ribosomal protein S5

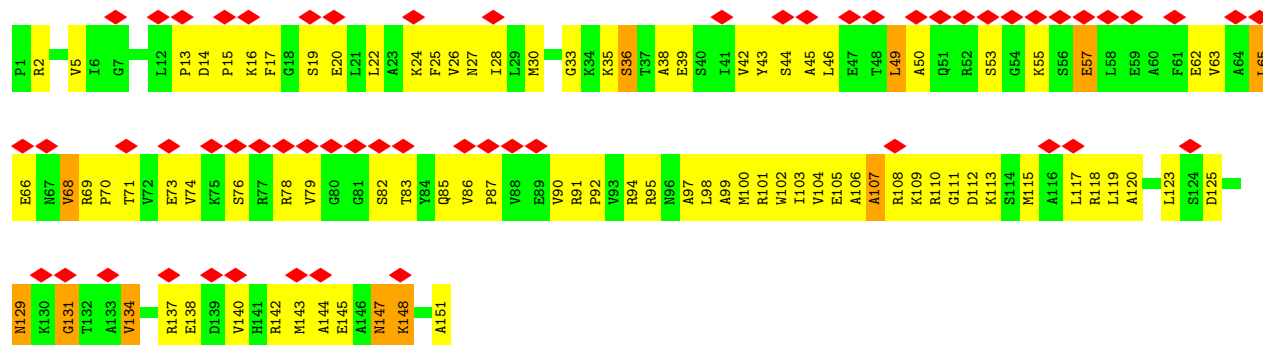


• Molecule 36: 30S ribosomal protein S6

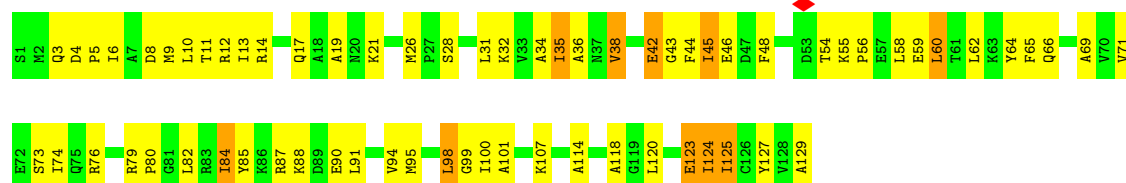




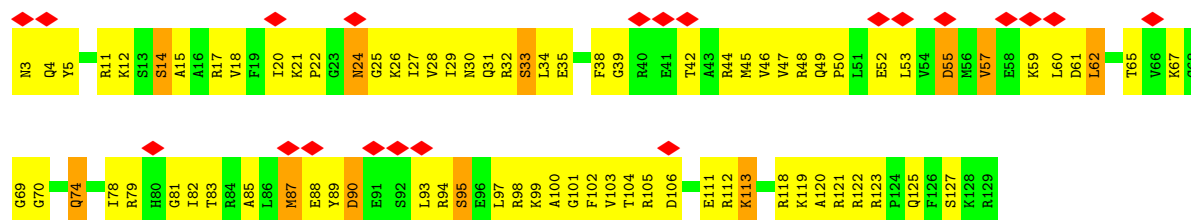
• Molecule 37: 30S ribosomal protein S7



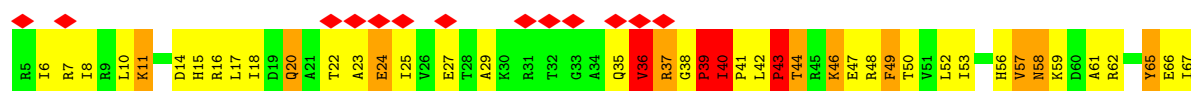
• Molecule 38: 30S ribosomal protein S8

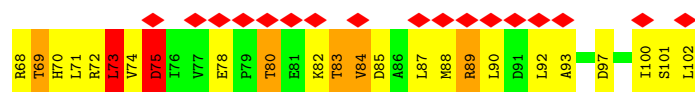


• Molecule 39: 30S ribosomal protein S9



• Molecule 40: 30S ribosomal protein S10

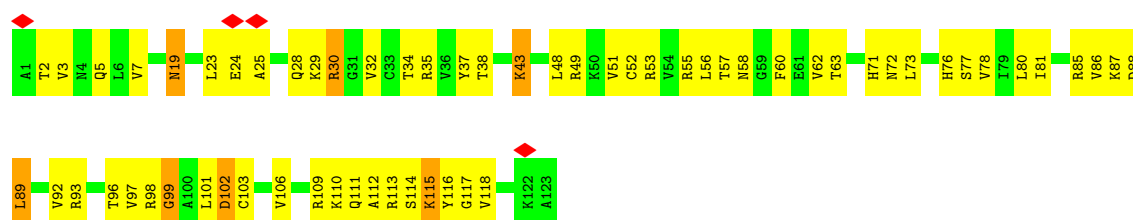




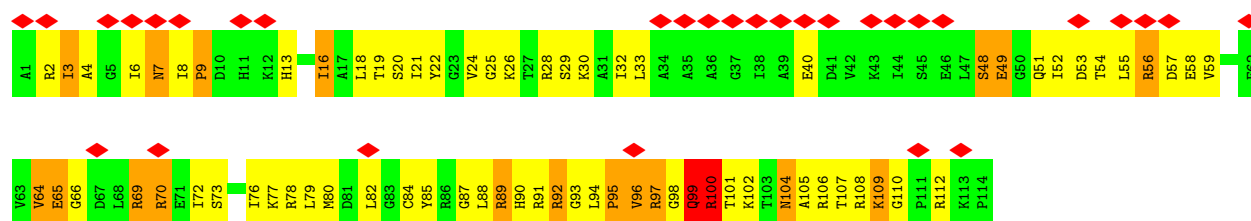
- Molecule 41: 30S ribosomal protein S11



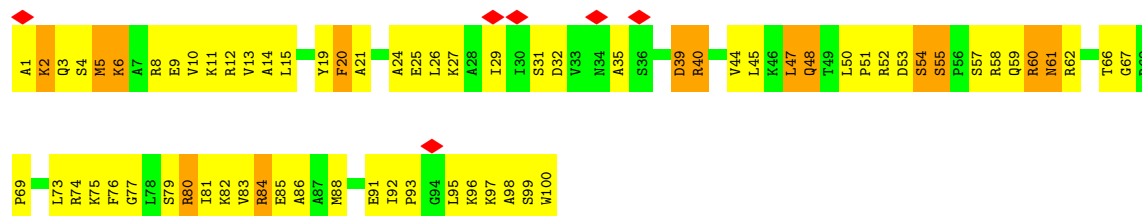
- Molecule 42: 30S ribosomal protein S12



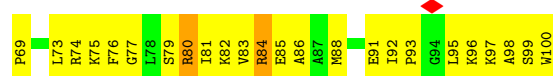
- Molecule 43: 30S ribosomal protein S13

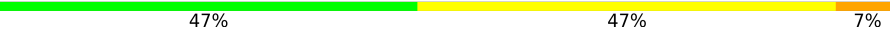


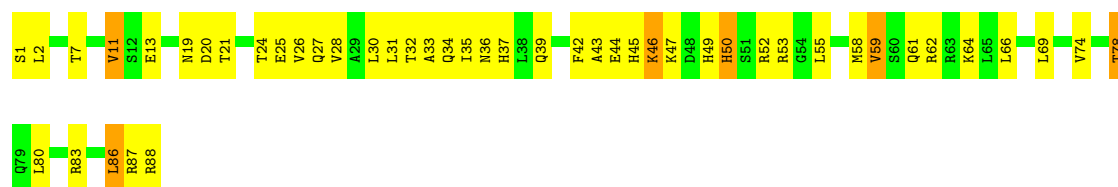
- Molecule 44: 30S ribosomal protein S14



- Molecule 45: 30S ribosomal protein S15

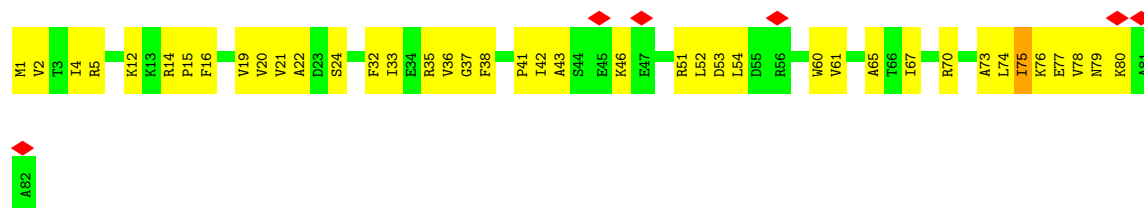


Chain T: 



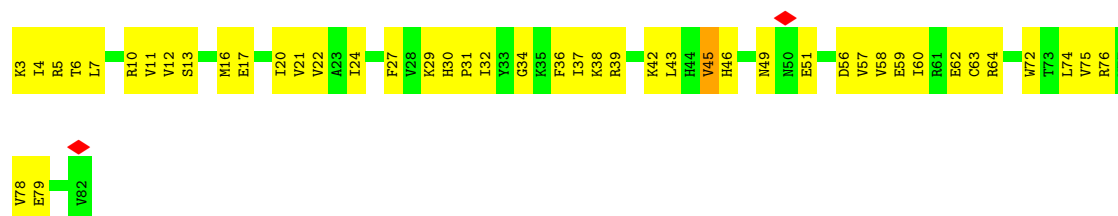
- Molecule 46: 30S ribosomal protein S16

Chain U: 



- Molecule 47: 30S ribosomal protein S17

Chain V: 



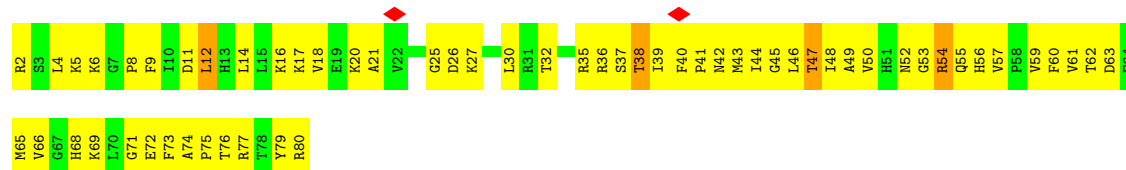
- Molecule 48: 30S ribosomal protein S18

Chain W: 



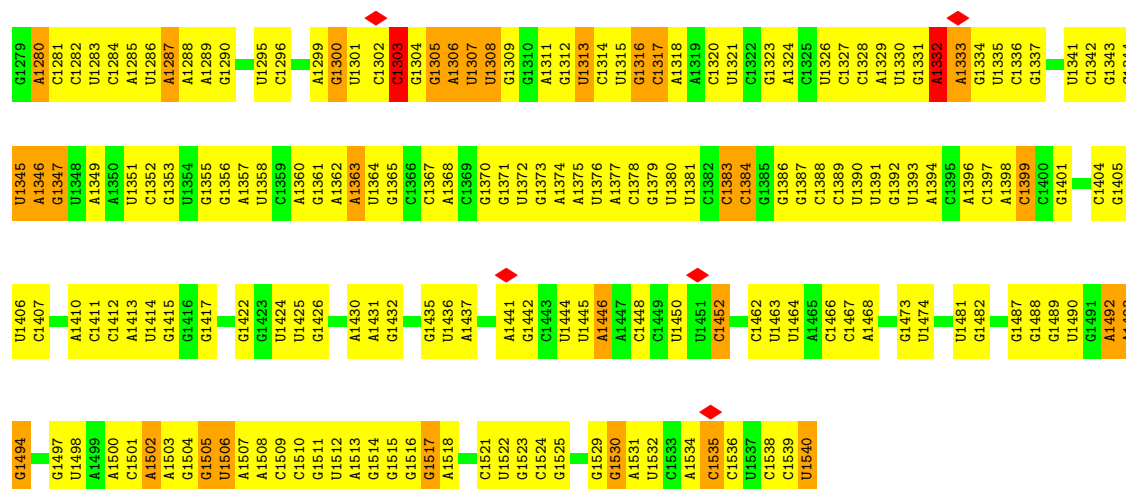
- Molecule 49: 30S ribosomal protein S19

Chain X: 

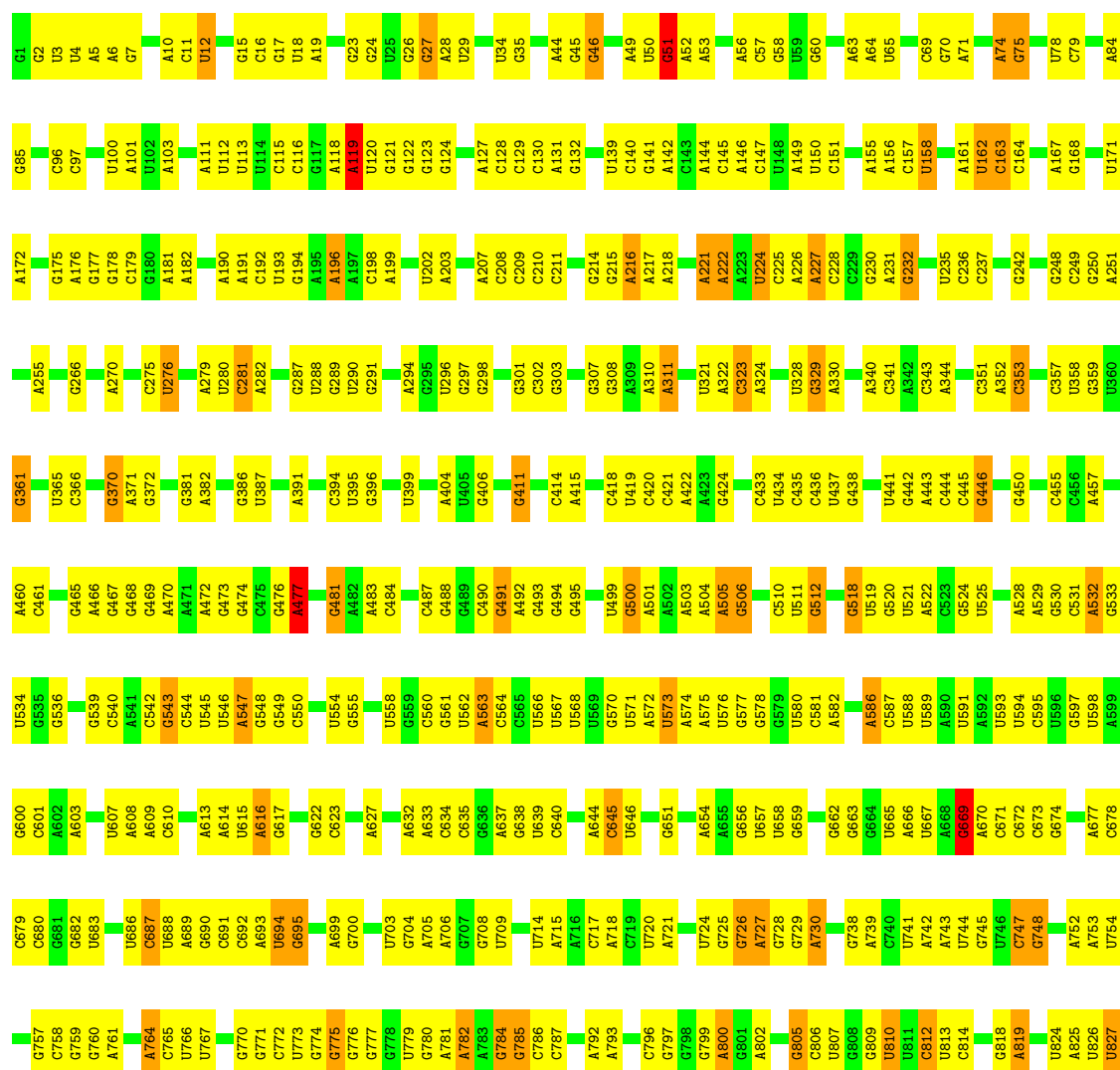


- Molecule 50: 30S ribosomal protein S20

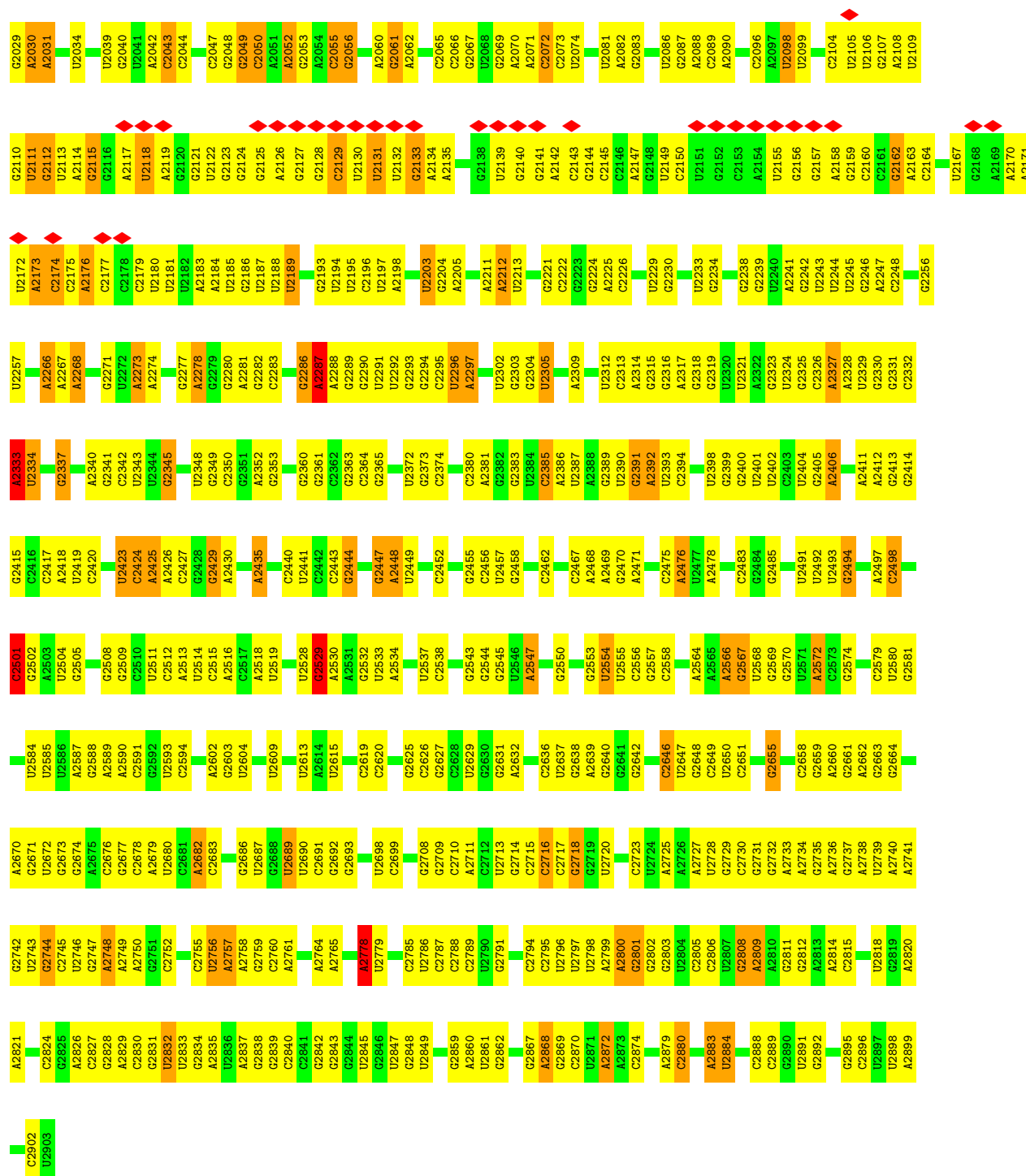




• Molecule 54: 23S ribosomal RNA

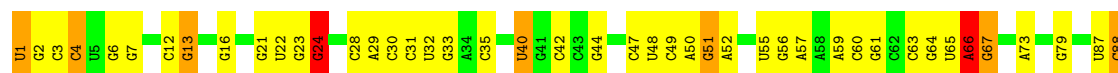


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C1774	U1775	U1776	U1777	U1778	U1779	U1780	U1781	U1782	U1783	U1784	U1785	U1786	U1787	U1788	U1789	U1790	U1791	U1792	U1793	U1794	U1795	U1796	U1797	U1798	U1799	U1800	U1801	U1802	U1803	U1804	U1805	U1806	U1807	U1808	U1809	U1810	U1811	U1812	U1813	U1814	U1815	U1816	U1817	U1818	U1819	U1820	U1821	U1822	U1823	U1824	U1825	U1826	U1827	U1828	U1829	U1830	U1831	U1832	U1833	U1834	U1835	U1836	U1837	U1838	U1839	U1840	U1841	U1842	U1843	U1844	U1845	U1846	U1847	U1848	U1849	U1850	U1851	U1852	U1853	U1854	U1855	U1856	U1857	U1858	U1859	U1860	U1861	U1862	U1863	U1864	U1865	U1866	U1867	U1868	U1869	U1870	U1871	U1872	U1873	U1874	U1875	U1876	U1877	U1878	U1879	U1880	U1881	U1882	U1883	U1884	U1885	U1886	U1887	U1888	U1889	U1890	U1891	U1892	U1893	U1894	U1895	U1896	U1897	U1898	U1899	U1900	U1901	U1902	U1903	U1904	U1905	U1906	U1907	U1908	U1909	U1910	U1911	U1912	U1913	U1914	U1915	U1916	U1917	U1918	U1919	U1920	U1921	U1922	U1923	U1924	U1925	U1926	U1927	U1928	U1929	U1930	U1931	U1932	U1933	U1934	U1935	U1936	U1937	U1938	U1939	U1940	U1941	U1942	U1943	U1944	U1945	U1946	U1947	U1948	U1949	U1950	U1951	U1952	U1953	U1954	U1955	U1956	U1957	U1958	U1959	U1960	U1961	U1962	U1963	U1964	U1965	U1966	U1967	U1968	U1969	U1970	U1971	U1972	U1973	U1974	U1975	U1976	U1977	U1978	U1979	U1980	U1981	U1982	U1983	U1984	U1985	U1986	U1987	U1988	U1989	U1990	U1991	U1992	U1993	U1994	U1995	U1996	U1997	U1998	U1999	U2000	G2001	G2002	G2003	G2004	G2005	G2006	G2007	G2008	G2009	G2010	G2011	G2012	G2013	G2014	G2015	G2016	G2017	G2018	G2019	G2020	G2021	G2022	G2023	G2024	G2025	U2026																																																																																																																																																																																																																																																															
C1522	U1523	G1524	A1525	U1526	G1527	A1528	G1529	U1530	C1531	A1532	C1533	U1534	A1535	C1536	G1537	U1538	C1539	A1540	C1541	U1542	A1543	C1544	A1545	G1546	U1547	A1548	C1549	U1550	A1551	U1552	G1553	U1554	A1555	U1556	G1557	A1558	C1559	U1560	G1561	U1562	C1563	U1564	C1565	A1566	U1567	G1568	A1569	U1570	C1571	U1572	G1573	U1574	A1575	C1576	U1577	A1578	C1579	U1580	G1581	U1582	A1583	C1584	U1585	A1586	C1587	U1588	A1589	C1590	U1591	A1592	C1593	U1594	A1595	C1596	U1597	A1598	C1599	U1600	A1601	U1602	A1603	C1604	U1605	A1606	C1607	U1608	A1609	U1610	C1611	U1612	A1613	C1614	U1615	A1616	C1617	U1618	A1619	C1620	U1621	A1622	C1623	U1624	A1625	C1626	U1627	A1628	C1629	U1630	A1631	C1632	U1633	A1634	C1635	U1636	A1637	C1638	U1639	A1640	C1641	U1642	A1643	C1644	U1645	A1646	C1647	U1648	A1649	C1650	U1651	A1652	C1653	U1654	A1655	C1656	U1657	A1658	C1659	U1660	A1661	C1662	U1663	A1664	C1665	U1666	A1667	C1668	U1669	A1670	C1671	U1672	A1673	C1674	U1675	A1676	C1677	U1678	A1679	C1680	U1681	A1682	C1683	U1684	A1685	C1686	U1687	A1688	C1689	U1690	A1691	C1692	U1693	A1694	C1695	U1696	A1697	C1698	U1699	A1700	C1701	U1702	A1703	C1704	U1705	A1706	C1707	U1708	A1709	C1710	U1711	A1712	C1713	U1714	A1715	C1716	U1717	A1718	C1719	U1720	A1721	C1722	U1723	A1724	C1725	U1726	A1727	C1728	U1729	A1729	C1730	U1731	A1732	C1733	U1734	A1735	C1736	U1737	A1738	C1739	U1740	A1741	C1742	U1743	A1744	C1745	U1746	A1747	C1748	U1749	A1750	C1751	U1752	A1753	C1754	U1755	A1756	C1757	U1758	A1759	C1760	U1761	A1762	C1763	U1764	A1765	C1766	U1767	A1768	C1769	U1770	A1771	C1772	U1773	A1774	C1775	U1776	A1777	C1778	U1779	A1780	C1781	U1782	A1783	C1784	U1785	A1786	C1787	U1788	A1789	C1790	U1791	A1792	C1793	U1794	A1795	C1796	U1797	A1798	C1799	U1800	A1801	C1802	U1803	A1804	C1805	U1806	A1807	C1808	U1809	A1809	C1810	U1811	A1812	C1813	U1814	A1815	C1816	U1817	A1818	C1819	U1820	A1821	C1822	U1823	A1824	C1825	U1826	A1827	C1828	U1829	A1830	C1831	U1832	A1833	C1834	U1835	A1836	C1837	U1838	A1839	C1840	U1841	A1842	C1843	U1844	A1845	C1846	U1847	A1848	C1849	U1850	A1851	C1852	U1853	A1854	C1855	U1856	A1857	C1858	U1859	A1860	C1861	U1862	A1863	C1864	U1865	A1866	C1867	U1868	A1869	C1870	U1871	A1872	C1873	U1874	A1875	C1876	U1877	A1878	C1879	U1880	A1881	C1882	U1883	A1884	C1885	U1886	A1887	C1888	U1889	A1890	C1891	U1892	A1893	C1894	U1895	A1896	C1897	U1898	A1899	C1900	U1901	A1902	C1903	U1904	A1905	C1906	U1907	A1908	C1909	U1910	A1911	C1912	U1913	A1914	C1915	U1916	A1917	C1918	U1919	A1920	C1921	U1922	A1923	C1924	U1925	A1926	C1927	U1928	A1929	C1930	U1931	A1932	C1933	U1934	A1935	C1936	U1937	A1938	C1939	U1940	A1941	C1942	U1943	A1944	C1945	U1946	A1947	C1948	U1949	A1950	C1951	U1952	A1953	C1954	U1955	A1956	C1957	U1958	A1959	C1960	U1961	A1962	C1963	U1964	A1965	C1966	U1967	A1968	C1969	U1969	A1970	C1971	U1972	A1973	C1974	U1975	A1976	C1977	U1978	A1979	C1980	U1981	A1982	C1983	U1984	A1985	C1986	U1987	A1988	C1989	U1990	A1991	C1992	U1993	A1994	C1995	U1996	A1997	C1998	U1999	A2000	C2001	C2002	C2003	C2004	C2005	C2006	C2007	C2008	C2009	C2010	C2011	C2012	C2013	C2014	C2015	C2016	C2017	C2018	C2019	C2020	C2021	C2022	C2023	C2024	C2025	U2026
C1150	A1151	C1152	C1153	G1154	U1155	A1156	C1157	U1158	G1159	A1160	C1161	U1162	A1163	C1164	U1165	A1166	C1167	U1168	A1169	C1170	U1171	A1172	C1173	U1174	A1175	C1176	U1177	A1178	C1179	U1180	A1181	C1182	U1183	A1184	C1185	U1186	A1187	C1188	U1189	A1190	C1191	U1192	A1193	C1194	U1195	C1196	U1197	A1198	C1199	U1200	A1201	C1202	U1203	A1204	C1205	U1206	A1207	C1208	U1209	A1210	C1211	U1212	A1213	C1214	U1215	A1216	C1217	U1218	A1219	C1220	U1221	A1222	C1223	U1224	A1225	C1226	U1227	A1228	C1229	U1230	A1231	C1232	U1233	A1234	C1235	U1236	A1237	C1238	U1239	A1240	C1241	U1242	A1243	C1244	U1245	A1246	C1247	U1248	A1249	C1250	U1251	A1252	C1253	U1254	A1255	C1256	U1257	A1258	C1259	U1260	A1261	C1262	U1263	A1264	C1265	U1266	A1267	C1268	U1269	A1270	C1271	U1272	A1273	C1274	U1275	A1276	C1277	U1278	A1279	C1280	U1281	A1282	C1283	U1284	A1285	C1286	U1287	A1288	C1289	U1290	A1291	C1292	U1293	A1294	C1295	U1296	A1297	C1298	U1299	A1300	C1301	U1302	A1303	C1304	U1305	A1306	C1307	U1308	A1309	C1310	U1311	A1312	C1313	U1314	A1315	C1316	U1317	A1318	C1319	U1320	A1321	C1322	U1323	A1324	C1325	U1326	A1327	C1328	U1329	A1330	C1331	U1332	A1333	C1334	U1335	A1336	C1337	U1338	A1339	C1340	U1341	A1342	C1343	U1344	A1345	C1346	U1347	A1348	C1349	U1350	A1351	C1352	U1353	A1354	C1355	U1356	A1357	C1358	U1359	A1360	C1361	U1362	A1363	C1364	U1365	A1366	C1367	U1368	A1369	C1370	U1371	A1372	C1373	U1374	A1375	C1376	U1377	A1378	C1379	U1380	A1381	C1382	U1383	A1384	C1385	U1386	A1387	C1388	U1389	A1390	C1391	U1392	A1393	C1394	U1395	A1396	C1397	U1398	A1399	C1400	U1401	A1402	C1403	U1404	A1405	C1406	U1407	A1408	C1409	U1410	A1411	C1412	U1413	A1414	C1415	U1416	A1417	C1418	U1419	A1420	C1421	U1422	A1423	C1424	U1425	A1426	C1427	U1428	A1429	C1430	U1431	A1432	C1433	U1434	A1435	C1436	U1437	A1438	C1439	U1440	A1441	C1442	U1443	A1444	C1445	U1446	A1447	C1448	U1449	A1450	C1451	U1452	A1453	C1454	U1455	A1456	C1457	U1458	A1459	C1460	U1461	A1462	C1463	U1464	A1465	C1466	U1467	A1468	C1469	U1470	A1471	C1472	U1473	A1474	C1475	U1476	A1477	C1478	U1479	A1480	C1481	U1482	A1483	C1484	U1485	A1486	C1487	U1488	A1489	C1490	U1491	A1492	C1493	U1494	A1495	C1496	U1497	A1498	C1499	U1500	A1501	C1502	U1503	A1504	C1505	U1506	A1507	C1508	U1509	A1510	C1511	U1512	A1513	C1514	U1515	A1516	C1517	U1518	A1519	C1520	U1521	A1522	C1523	U1524	A1525	C1526	U1527	A1528	C1529	U1530	A1531	C1532	U1533	A1534	C1535	U1536	A1537	C1538	U1539	A1540	C1541	U1542	A1543	C1544	U1545	A1546	C1547	U1548	A1549	C1550	U1551	A1552	C1553	U1554	A1555	C1556	U1557	A1558	C1559	U1560	A1561	C1562	U1563	A1564	C1565	U1566	A1567	C1568	U1569	A1570	C1571	U1572	A1573	C1574	U1575	A1576	C1577	U1578	A1579	C1580	U1581	A1582	C1583	U1584	A1585	C1586	U1587	A1588</																																																																					



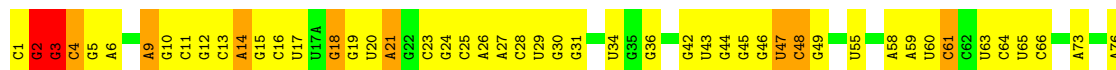
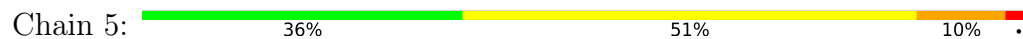
• Molecule 55: 5S ribosomal RNA

Chain 2: 48% 42% 8%

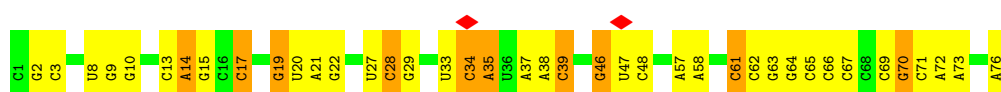




• Molecule 56: tRNA^{Pro}



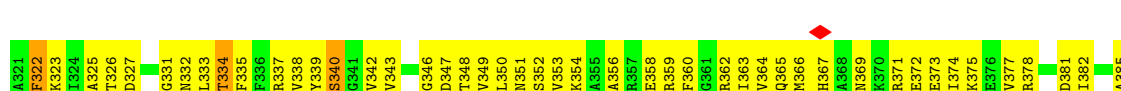
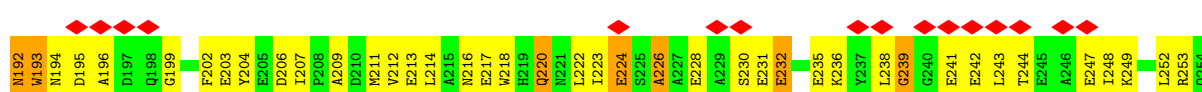
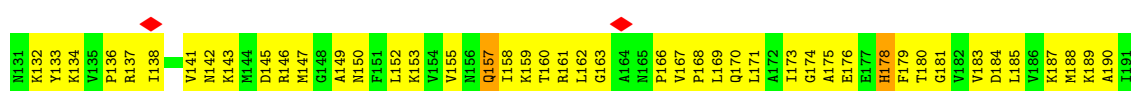
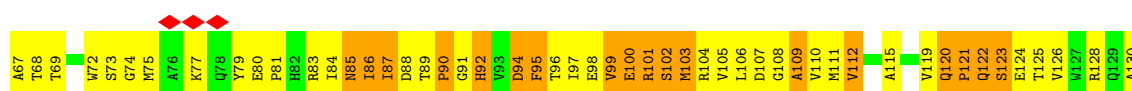
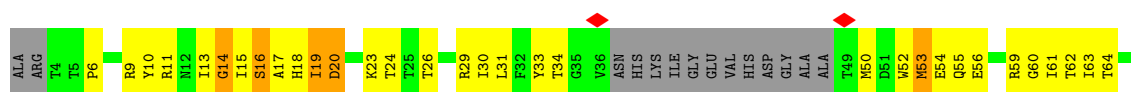
• Molecule 57: tRNA^{fMet}

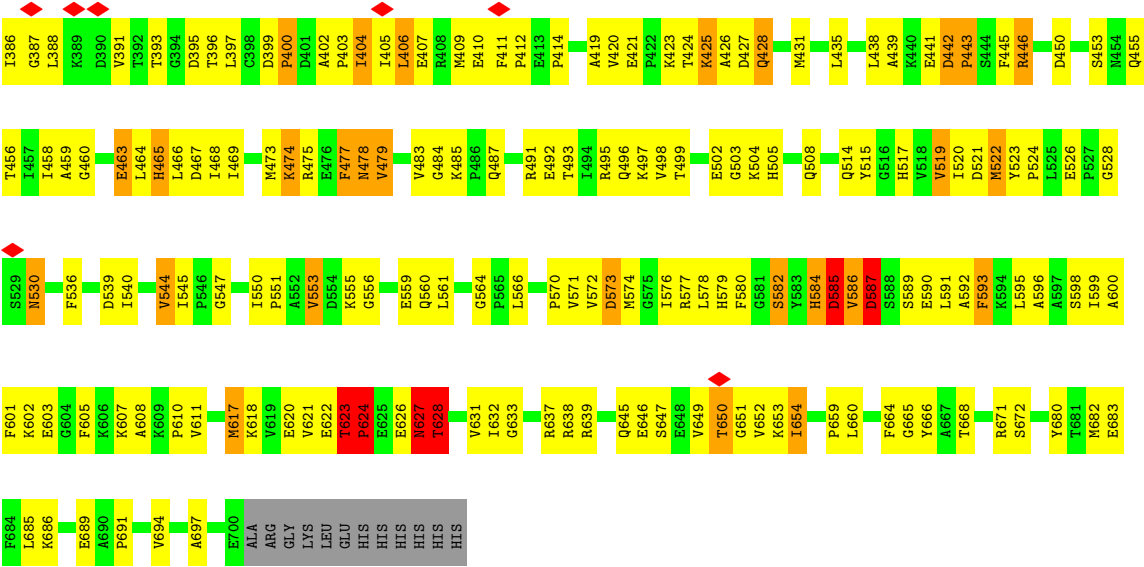


• Molecule 58: mRNA



• Molecule 59: Elongation factor G





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9059	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	23.041	Depositor
Minimum map value	-7.245	Depositor
Average map value	0.019	Depositor
Map value standard deviation	1.364	Depositor
Recommended contour level	3.7	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: GCP, MG, 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	0.86	10/2122 (0.5%)	1.10	12/2852 (0.4%)
2	c	0.82	3/1586 (0.2%)	1.04	7/2134 (0.3%)
3	d	1.02	12/1571 (0.8%)	1.08	13/2113 (0.6%)
4	e	0.90	9/1435 (0.6%)	1.10	14/1926 (0.7%)
5	f	0.85	8/1343 (0.6%)	1.03	8/1816 (0.4%)
6	g	1.89	19/946 (2.0%)	1.53	26/1275 (2.0%)
7	h	1.53	13/638 (2.0%)	1.56	16/860 (1.9%)
8	i	2.57	22/564 (3.9%)	1.89	28/768 (3.6%)
9	j	0.75	4/1152 (0.3%)	0.92	6/1551 (0.4%)
10	k	0.94	7/948 (0.7%)	1.24	12/1268 (0.9%)
11	l	0.77	4/1054 (0.4%)	1.08	6/1403 (0.4%)
12	m	0.90	8/1093 (0.7%)	1.15	10/1460 (0.7%)
13	n	0.74	1/974 (0.1%)	1.05	6/1301 (0.5%)
14	o	1.10	8/902 (0.9%)	1.11	5/1209 (0.4%)
15	p	0.71	4/929 (0.4%)	0.88	0/1242
16	q	0.76	3/960 (0.3%)	1.08	8/1278 (0.6%)
17	r	0.74	3/829 (0.4%)	1.12	9/1107 (0.8%)
18	s	1.10	9/864 (1.0%)	1.26	11/1156 (1.0%)
19	t	0.84	4/745 (0.5%)	0.95	3/994 (0.3%)
20	u	0.70	2/788 (0.3%)	0.90	3/1051 (0.3%)
21	v	0.79	3/766 (0.4%)	1.13	8/1025 (0.8%)
22	w	0.74	1/582 (0.2%)	1.01	4/769 (0.5%)
23	x	0.93	4/635 (0.6%)	1.22	5/848 (0.6%)
24	y	0.99	4/510 (0.8%)	1.08	5/677 (0.7%)
25	z	0.73	1/453 (0.2%)	0.90	0/605
26	A	1.15	8/532 (1.5%)	1.25	10/709 (1.4%)
27	B	0.57	0/450	0.83	0/599
28	C	0.81	2/417 (0.5%)	1.00	3/554 (0.5%)
29	D	0.65	0/380	0.93	1/498 (0.2%)
30	E	0.76	2/513 (0.4%)	0.93	0/676
31	F	0.85	1/303 (0.3%)	1.04	2/397 (0.5%)
32	G	1.03	12/1736 (0.7%)	1.18	14/2338 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	H	1.23	18/1652 (1.1%)	1.20	13/2225 (0.6%)
34	I	0.99	14/1665 (0.8%)	1.20	14/2227 (0.6%)
35	J	1.03	8/1170 (0.7%)	1.19	12/1573 (0.8%)
36	K	1.22	11/836 (1.3%)	1.27	9/1128 (0.8%)
37	L	1.25	13/1196 (1.1%)	1.25	17/1602 (1.1%)
38	M	0.94	5/989 (0.5%)	1.08	9/1326 (0.7%)
39	N	1.00	8/1034 (0.8%)	1.17	10/1375 (0.7%)
40	O	1.68	14/797 (1.8%)	1.41	13/1077 (1.2%)
41	P	1.09	10/886 (1.1%)	1.28	12/1195 (1.0%)
42	Q	0.78	2/969 (0.2%)	1.05	5/1300 (0.4%)
43	R	1.37	12/893 (1.3%)	1.47	15/1193 (1.3%)
44	S	1.21	10/817 (1.2%)	1.18	4/1088 (0.4%)
45	T	0.97	5/722 (0.7%)	1.19	4/964 (0.4%)
46	U	0.69	1/659 (0.2%)	0.91	1/884 (0.1%)
47	V	0.57	0/658	0.94	2/881 (0.2%)
48	W	1.26	6/545 (1.1%)	1.32	7/731 (1.0%)
49	X	1.05	5/653 (0.8%)	1.15	2/877 (0.2%)
50	Y	1.05	7/671 (1.0%)	1.12	6/888 (0.7%)
51	Z	1.02	6/551 (1.1%)	1.37	11/728 (1.5%)
52	a	2.21	33/1034 (3.2%)	1.68	37/1387 (2.7%)
53	3	0.55	0/36963	0.61	22/57662 (0.0%)
54	1	0.50	0/69796	0.57	18/108888 (0.0%)
55	2	0.48	0/2872	0.56	2/4479 (0.0%)
56	5	0.47	0/1840	0.61	1/2868 (0.0%)
57	6	0.49	0/1832	0.59	0/2855
58	4	0.72	1/388 (0.3%)	0.65	0/603
59	8	1.05	48/5411 (0.9%)	1.23	77/7323 (1.1%)
All	All	0.74	428/166219 (0.3%)	0.80	578/247786 (0.2%)

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
6	g	0	4
34	I	0	1
35	J	0	1
53	3	0	25
54	1	0	59
55	2	0	3
56	5	0	1

Continued on next page...

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Mol	Chain	#Chirality outliers	#Planarity outliers
59	8	0	2
All	All	0	96

The worst 5 of 428 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	a	59	VAL	C-O	33.06	1.59	1.24
6	g	8	LYS	C-O	-30.43	0.85	1.24
8	i	56	VAL	C-O	26.89	1.52	1.23
40	O	73	LEU	C-O	24.05	1.51	1.24
52	a	163	TYR	C-O	21.83	1.51	1.23

The worst 5 of 578 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	W	12	PHE	CA-C-O	14.32	130.50	120.19
34	I	154	VAL	CA-C-N	-13.81	100.68	120.29
34	I	154	VAL	C-N-CA	-13.81	100.68	120.29
59	8	86	ILE	N-CA-C	11.72	124.69	106.88
43	R	96	VAL	N-CA-C	11.38	124.14	113.10

There are no chirality outliers.

5 of 96 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
34	I	152	SER	Mainchain
35	J	92	ARG	Mainchain
6	g	13	GLY	Peptide,Mainchain
6	g	41	LYS	Mainchain
6	g	8	LYS	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	111	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	c	1565	0	1616	73	0
3	d	1552	0	1619	75	0
4	e	1411	0	1447	96	0
5	f	1323	0	1374	79	0
6	g	936	0	961	42	0
7	h	633	0	666	58	0
8	i	551	0	577	55	0
9	j	1129	0	1162	66	0
10	k	939	0	1012	67	0
11	l	1045	0	1117	74	0
12	m	1074	0	1157	47	0
13	n	961	0	1000	67	0
14	o	892	0	923	44	0
15	p	917	0	965	73	0
16	q	947	0	1022	40	0
17	r	816	0	839	48	0
18	s	857	0	922	36	0
19	t	739	0	807	27	0
20	u	780	0	834	45	0
21	v	753	0	780	52	0
22	w	575	0	592	43	0
23	x	625	0	655	30	0
24	y	509	0	543	25	0
25	z	449	0	491	23	0
26	A	523	0	524	47	0
27	B	444	0	461	18	0
28	C	410	0	440	15	0
29	D	377	0	418	23	0
30	E	504	0	574	35	0
31	F	302	0	343	21	0
32	G	1705	0	1732	134	0
33	H	1625	0	1699	87	0
34	I	1643	0	1710	119	0
35	J	1157	0	1199	120	0
36	K	818	0	808	75	0
37	L	1182	0	1240	74	0
38	M	979	0	1034	74	0
39	N	1022	0	1070	74	0
40	O	787	0	828	116	0
41	P	870	0	878	69	0
42	Q	955	0	1019	72	0
43	R	884	0	944	112	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	S	805	0	847	103	0
45	T	714	0	737	44	0
46	U	649	0	666	50	0
47	V	649	0	691	48	0
48	W	536	0	552	38	0
49	X	638	0	665	75	0
50	Y	665	0	714	50	0
51	Z	545	0	579	73	0
52	a	1027	0	1092	86	0
53	3	33012	0	16618	1120	0
54	1	62317	0	31346	1346	0
55	2	2568	0	1303	73	0
56	5	1647	0	831	37	0
57	6	1640	0	837	26	0
58	4	346	0	175	13	0
59	8	5312	0	5283	418	0
60	1	10	0	10	0	0
61	5	7	0	7	0	0
62	8	32	0	14	3	0
63	8	1	0	0	0	0
All	All	153368	0	105126	5696	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 22.

The worst 5 of 5696 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)
53:3:1115:U:H2'	53:3:1116:U:H5''	1.27	1.15
40:O:37:ARG:O	53:3:1123:U:H5''	1.52	1.09
54:1:1702:G:H2'	54:1:1703:G:H5''	1.29	1.08
54:1:1906:G:H2'	54:1:1907:G:H5''	1.30	1.08
56:5:13:C:H2'	56:5:14:A:H5''	1.39	1.03

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	232 (86%)	35 (13%)	2 (1%)	18	52
2	c	207/209 (99%)	187 (90%)	20 (10%)	0	100	100
3	d	199/201 (99%)	176 (88%)	22 (11%)	1 (0%)	24	59
4	e	175/177 (99%)	156 (89%)	17 (10%)	2 (1%)	11	43
5	f	174/176 (99%)	153 (88%)	19 (11%)	2 (1%)	11	43
6	g	121/149 (81%)	97 (80%)	19 (16%)	5 (4%)	2	17
7	h	82/131 (63%)	62 (76%)	16 (20%)	4 (5%)	1	13
8	i	72/141 (51%)	54 (75%)	17 (24%)	1 (1%)	9	39
9	j	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
10	k	120/122 (98%)	100 (83%)	15 (12%)	5 (4%)	2	16
11	l	141/143 (99%)	116 (82%)	23 (16%)	2 (1%)	9	39
12	m	134/136 (98%)	120 (90%)	13 (10%)	1 (1%)	18	52
13	n	118/120 (98%)	101 (86%)	16 (14%)	1 (1%)	16	50
14	o	114/116 (98%)	99 (87%)	15 (13%)	0	100	100
15	p	112/114 (98%)	98 (88%)	13 (12%)	1 (1%)	14	47
16	q	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
17	r	101/103 (98%)	82 (81%)	18 (18%)	1 (1%)	12	45
18	s	108/110 (98%)	91 (84%)	17 (16%)	0	100	100
19	t	91/93 (98%)	85 (93%)	6 (7%)	0	100	100
20	u	100/102 (98%)	82 (82%)	17 (17%)	1 (1%)	12	45
21	v	92/94 (98%)	82 (89%)	9 (10%)	1 (1%)	11	43
22	w	73/75 (97%)	64 (88%)	9 (12%)	0	100	100
23	x	75/77 (97%)	65 (87%)	10 (13%)	0	100	100
24	y	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
25	z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	A	64/66 (97%)	45 (70%)	17 (27%)	2 (3%)	3	22
27	B	54/56 (96%)	48 (89%)	6 (11%)	0	100	100
28	C	48/50 (96%)	40 (83%)	8 (17%)	0	100	100
29	D	44/46 (96%)	38 (86%)	6 (14%)	0	100	100
30	E	62/64 (97%)	50 (81%)	9 (14%)	3 (5%)	2	14
31	F	36/38 (95%)	30 (83%)	6 (17%)	0	100	100
32	G	216/225 (96%)	175 (81%)	39 (18%)	2 (1%)	14	47
33	H	204/206 (99%)	181 (89%)	22 (11%)	1 (0%)	24	59
34	I	203/205 (99%)	173 (85%)	28 (14%)	2 (1%)	12	45
35	J	155/157 (99%)	128 (83%)	20 (13%)	7 (4%)	2	15
36	K	98/100 (98%)	78 (80%)	14 (14%)	6 (6%)	1	9
37	L	149/151 (99%)	128 (86%)	20 (13%)	1 (1%)	18	52
38	M	127/129 (98%)	114 (90%)	13 (10%)	0	100	100
39	N	125/127 (98%)	93 (74%)	26 (21%)	6 (5%)	2	14
40	O	96/98 (98%)	72 (75%)	19 (20%)	5 (5%)	1	12
41	P	114/116 (98%)	96 (84%)	15 (13%)	3 (3%)	4	26
42	Q	121/123 (98%)	95 (78%)	23 (19%)	3 (2%)	4	27
43	R	112/114 (98%)	89 (80%)	19 (17%)	4 (4%)	2	19
44	S	98/100 (98%)	81 (83%)	13 (13%)	4 (4%)	2	17
45	T	86/88 (98%)	69 (80%)	16 (19%)	1 (1%)	10	42
46	U	80/82 (98%)	66 (82%)	14 (18%)	0	100	100
47	V	78/80 (98%)	59 (76%)	17 (22%)	2 (3%)	4	26
48	W	63/65 (97%)	51 (81%)	11 (18%)	1 (2%)	7	36
49	X	77/79 (98%)	58 (75%)	19 (25%)	0	100	100
50	Y	83/85 (98%)	75 (90%)	8 (10%)	0	100	100
51	Z	63/65 (97%)	35 (56%)	25 (40%)	3 (5%)	2	14
52	a	130/223 (58%)	118 (91%)	10 (8%)	2 (2%)	8	37
59	8	681/711 (96%)	561 (82%)	103 (15%)	17 (2%)	4	27
All	All	6517/6889 (95%)	5493 (84%)	919 (14%)	105 (2%)	10	36

5 of 105 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	g	14	SER
10	k	92	GLU
17	r	54	VAL
20	u	99	SER
30	E	31	ILE

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%)	212 (98%)	4 (2%)	50	73
2	c	164/164 (100%)	162 (99%)	2 (1%)	63	79
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	84
4	e	148/148 (100%)	145 (98%)	3 (2%)	48	72
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	98/114 (86%)	98 (100%)	0	100	100
7	h	66/100 (66%)	66 (100%)	0	100	100
8	i	60/109 (55%)	60 (100%)	0	100	100
9	j	116/116 (100%)	116 (100%)	0	100	100
10	k	103/103 (100%)	97 (94%)	6 (6%)	18	51
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	81
13	n	100/100 (100%)	98 (98%)	2 (2%)	48	72
14	o	86/86 (100%)	84 (98%)	2 (2%)	44	70
15	p	99/99 (100%)	96 (97%)	3 (3%)	36	66
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	78
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	71
26	A	59/59 (100%)	57 (97%)	2 (3%)	32	64
27	B	47/47 (100%)	47 (100%)	0	100	100
28	C	45/45 (100%)	44 (98%)	1 (2%)	45	71
29	D	38/38 (100%)	38 (100%)	0	100	100
30	E	51/51 (100%)	48 (94%)	3 (6%)	18	50
31	F	34/34 (100%)	33 (97%)	1 (3%)	37	67
32	G	180/186 (97%)	179 (99%)	1 (1%)	78	84
33	H	170/170 (100%)	166 (98%)	4 (2%)	43	70
34	I	172/172 (100%)	171 (99%)	1 (1%)	78	84
35	J	119/119 (100%)	113 (95%)	6 (5%)	22	55
36	K	87/87 (100%)	84 (97%)	3 (3%)	32	64
37	L	124/124 (100%)	124 (100%)	0	100	100
38	M	104/104 (100%)	103 (99%)	1 (1%)	68	80
39	N	105/105 (100%)	105 (100%)	0	100	100
40	O	86/86 (100%)	78 (91%)	8 (9%)	8	33
41	P	89/89 (100%)	85 (96%)	4 (4%)	24	58
42	Q	103/103 (100%)	101 (98%)	2 (2%)	50	73
43	R	92/92 (100%)	85 (92%)	7 (8%)	12	42
44	S	83/83 (100%)	80 (96%)	3 (4%)	31	63
45	T	76/76 (100%)	74 (97%)	2 (3%)	40	69
46	U	65/65 (100%)	64 (98%)	1 (2%)	57	76
47	V	74/74 (100%)	74 (100%)	0	100	100
48	W	56/56 (100%)	55 (98%)	1 (2%)	51	74
49	X	70/70 (100%)	69 (99%)	1 (1%)	59	77
50	Y	65/65 (100%)	64 (98%)	1 (2%)	57	76
51	Z	55/55 (100%)	54 (98%)	1 (2%)	51	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	a	110/174 (63%)	109 (99%)	1 (1%)	70	81
59	8	566/585 (97%)	550 (97%)	16 (3%)	38	68
All	All	5428/5616 (97%)	5331 (98%)	97 (2%)	51	74

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	P	30	ILE
44	S	5	MET
41	P	82	GLU
43	R	95	PRO
46	U	46	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 80 such sidechains are listed below:

Mol	Chain	Res	Type
43	R	7	ASN
50	Y	81	GLN
44	S	3	GLN
49	X	52	ASN
59	8	276	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	3	1538/1539 (99%)	214 (13%)	17 (1%)
54	1	2902/2903 (99%)	358 (12%)	15 (0%)
55	2	119/120 (99%)	12 (10%)	2 (1%)
56	5	76/77 (98%)	16 (21%)	2 (2%)
57	6	76/77 (98%)	23 (30%)	0
58	4	15/16 (93%)	3 (20%)	0
All	All	4726/4732 (99%)	626 (13%)	36 (0%)

5 of 626 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	3	6	G
53	3	9	G
53	3	22	G

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Mol	Chain	Res	Type
53	3	32	A
53	3	39	G

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	1	2333	A
56	5	3	G
54	1	2391	G
55	2	66	A
53	3	1201	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	2.56	6 (18%)	49,54,54	2.52	15 (30%)
61	PRO	5	101	56,60	6,7,8	0.57	0	7,8,10	1.23	1 (14%)
60	FME	1	3001	61	8,9,10	0.73	0	8,9,11	1.13	1 (12%)

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
61	PRO	5	101	56,60	-	0/0/9/11	0/1/1/1
60	FME	1	3001	61	-	1/7/9/11	-

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	8	801	GCP	PA-O3A	-9.79	1.48	1.59
62	8	801	GCP	PB-O3A	-8.23	1.49	1.58
62	8	801	GCP	PB-O2B	-2.93	1.49	1.56
62	8	801	GCP	PG-O2G	-2.59	1.49	1.55
62	8	801	GCP	PG-O3G	-2.52	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	8.24	150.81	126.49
62	8	801	GCP	C1'-N9-C8	-8.19	103.47	126.73
62	8	801	GCP	O3A-PA-O1A	-4.56	96.97	110.70
62	8	801	GCP	O2G-PG-C3B	-4.47	95.54	106.40
62	8	801	GCP	O3G-PG-O2G	4.28	120.16	107.96

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	PG-C3B-PB-O1B
62	8	801	GCP	C5'-O5'-PA-O1A
62	8	801	GCP	O4'-C4'-C5'-O5'

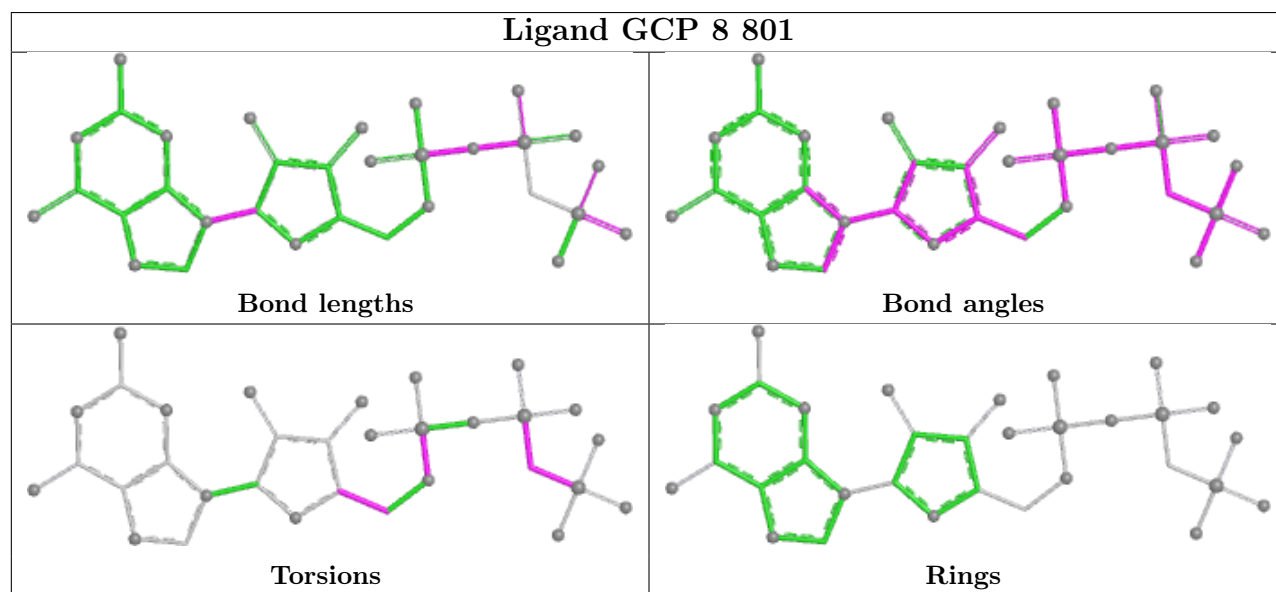
There are no ring outliers.

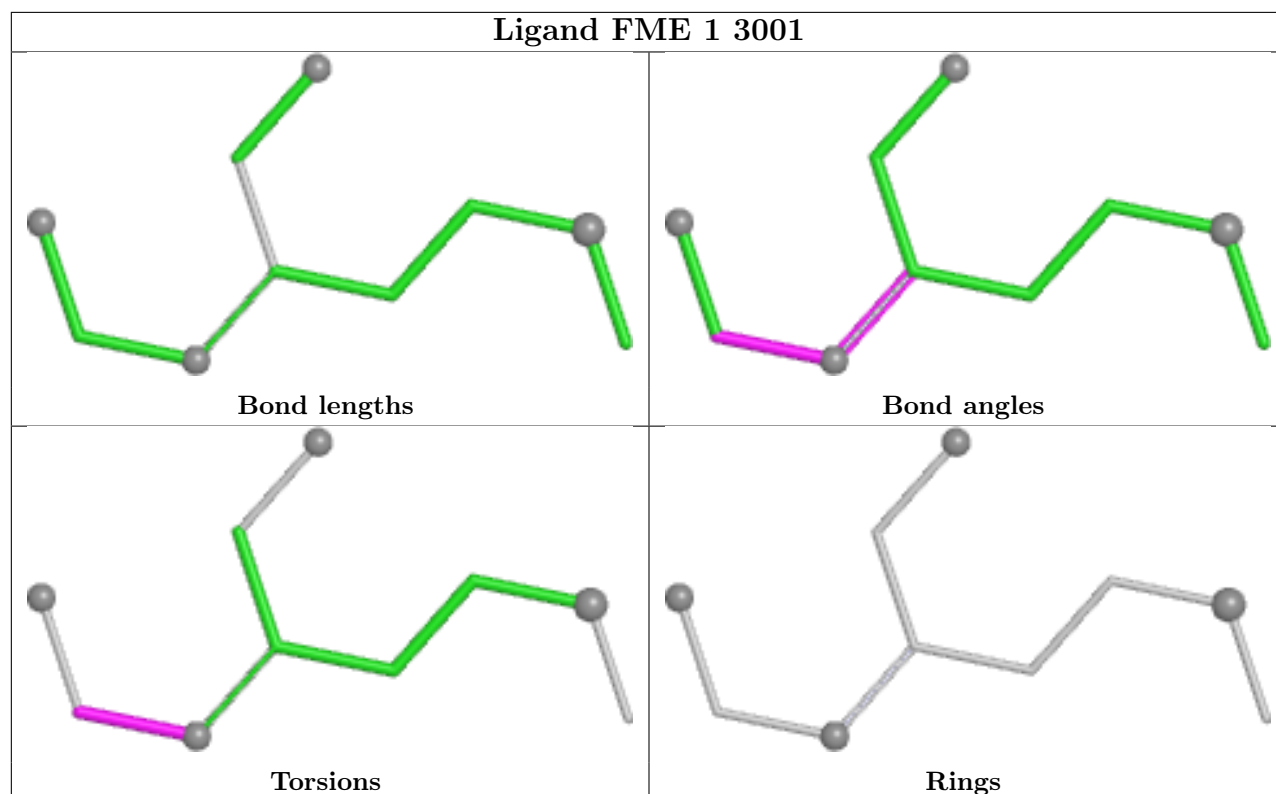
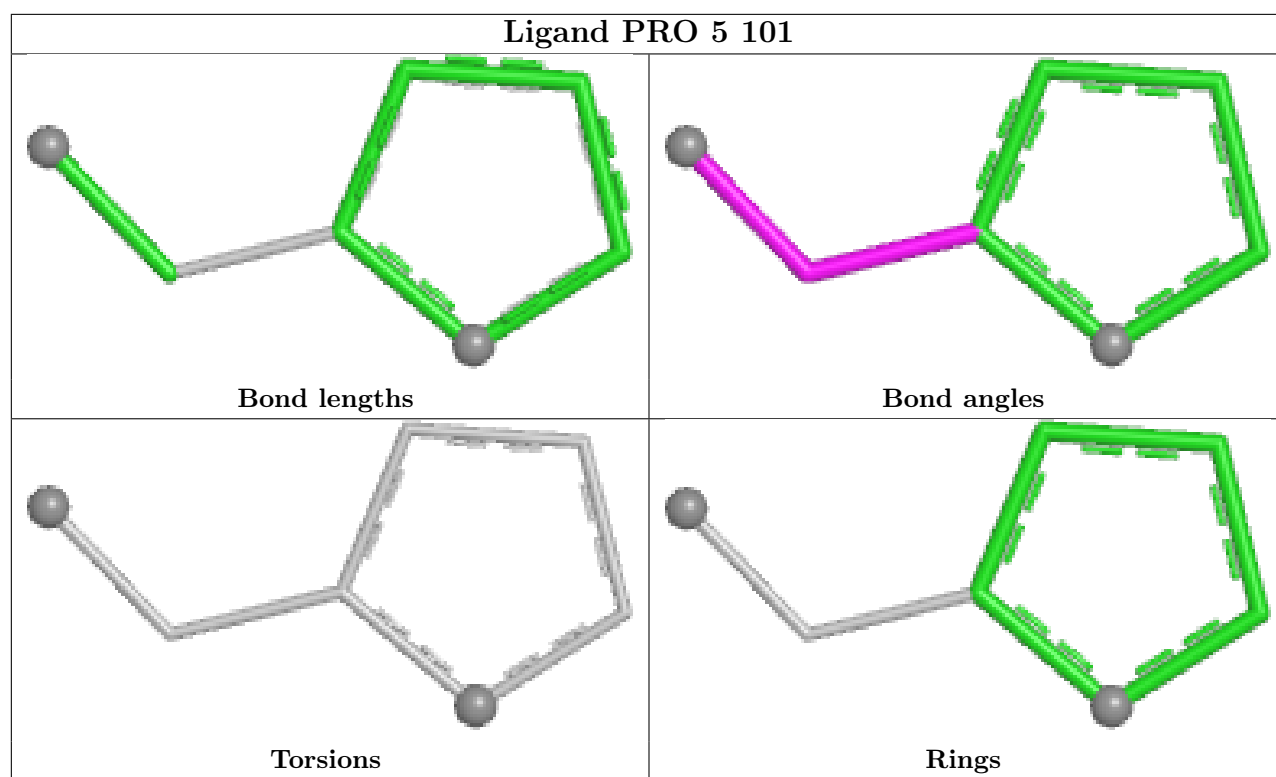
1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	8	801	GCP	3	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.

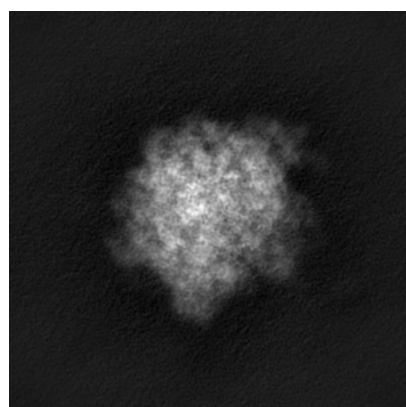
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22673. These allow visual inspection of the internal detail of the map and identification of artifacts.

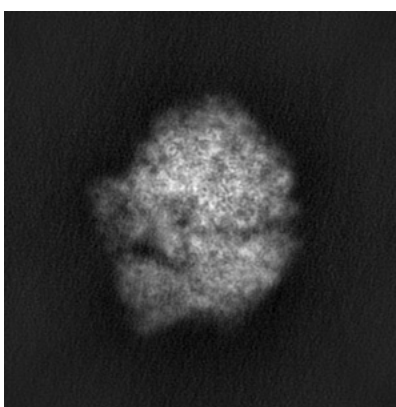
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

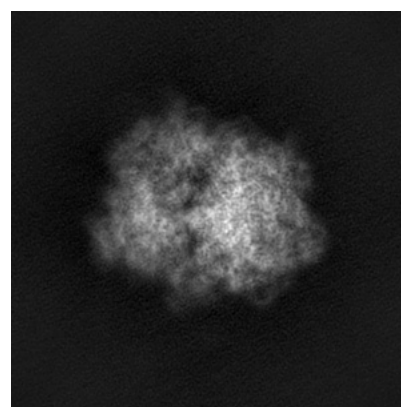
6.1.1 Primary map



X



Y

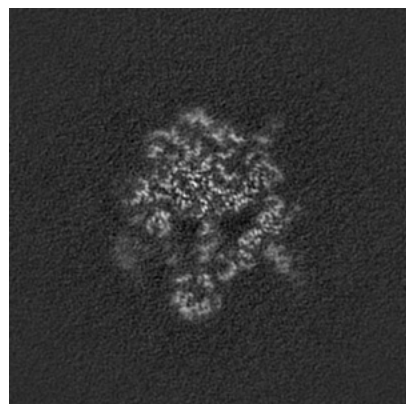


Z

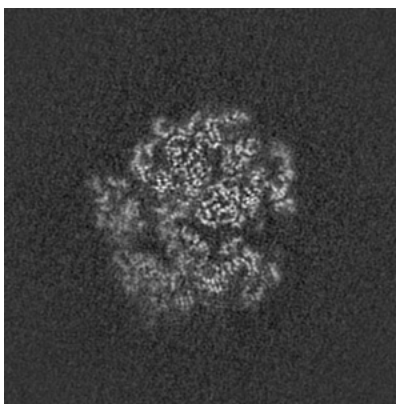
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

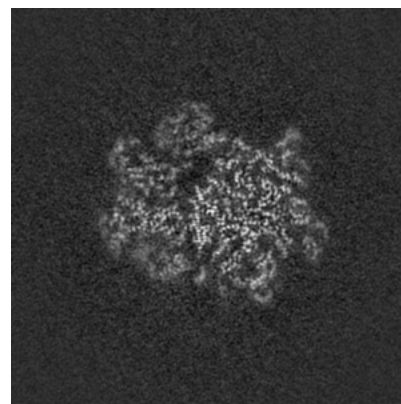
6.2.1 Primary map



X Index: 200



Y Index: 200

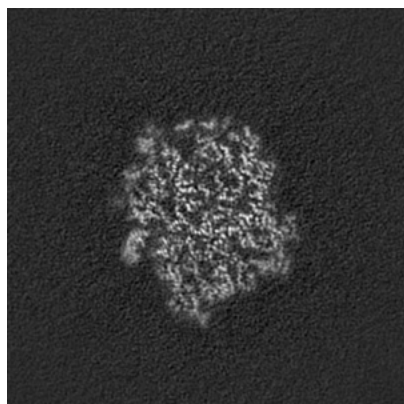


Z Index: 200

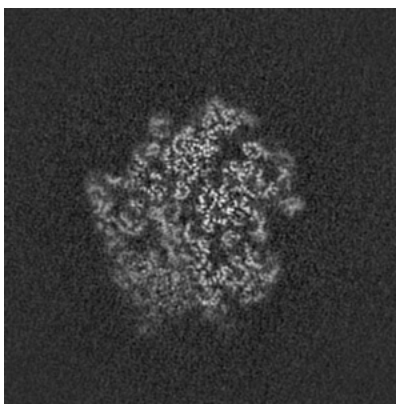
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

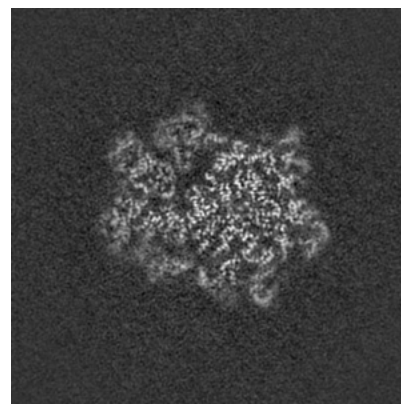
6.3.1 Primary map



X Index: 222



Y Index: 193

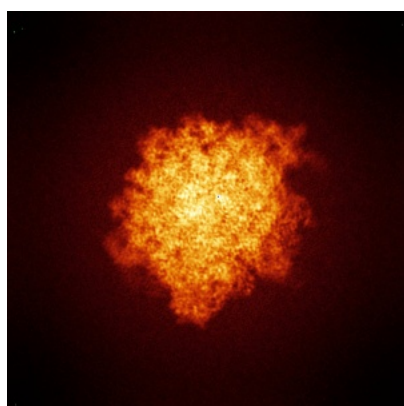


Z Index: 203

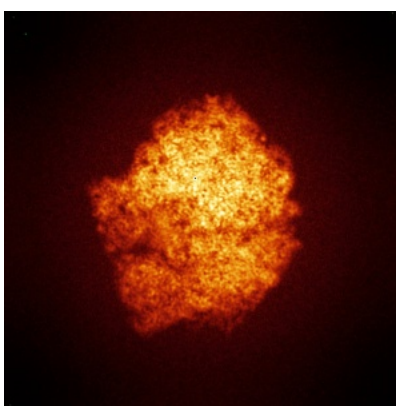
The images above show the largest variance slices of the map in three orthogonal directions.

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

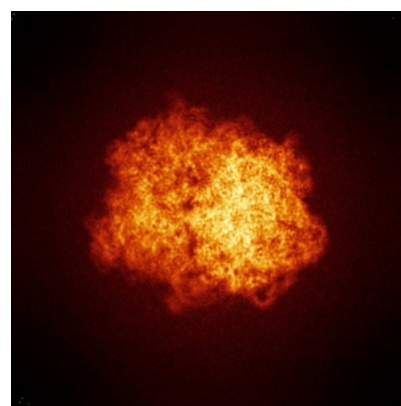
6.4.1 Primary map



X



Y

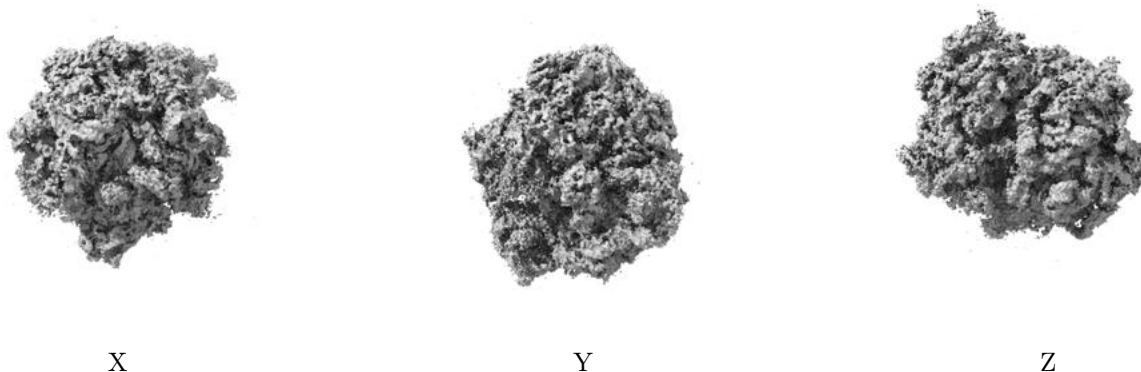


Z

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

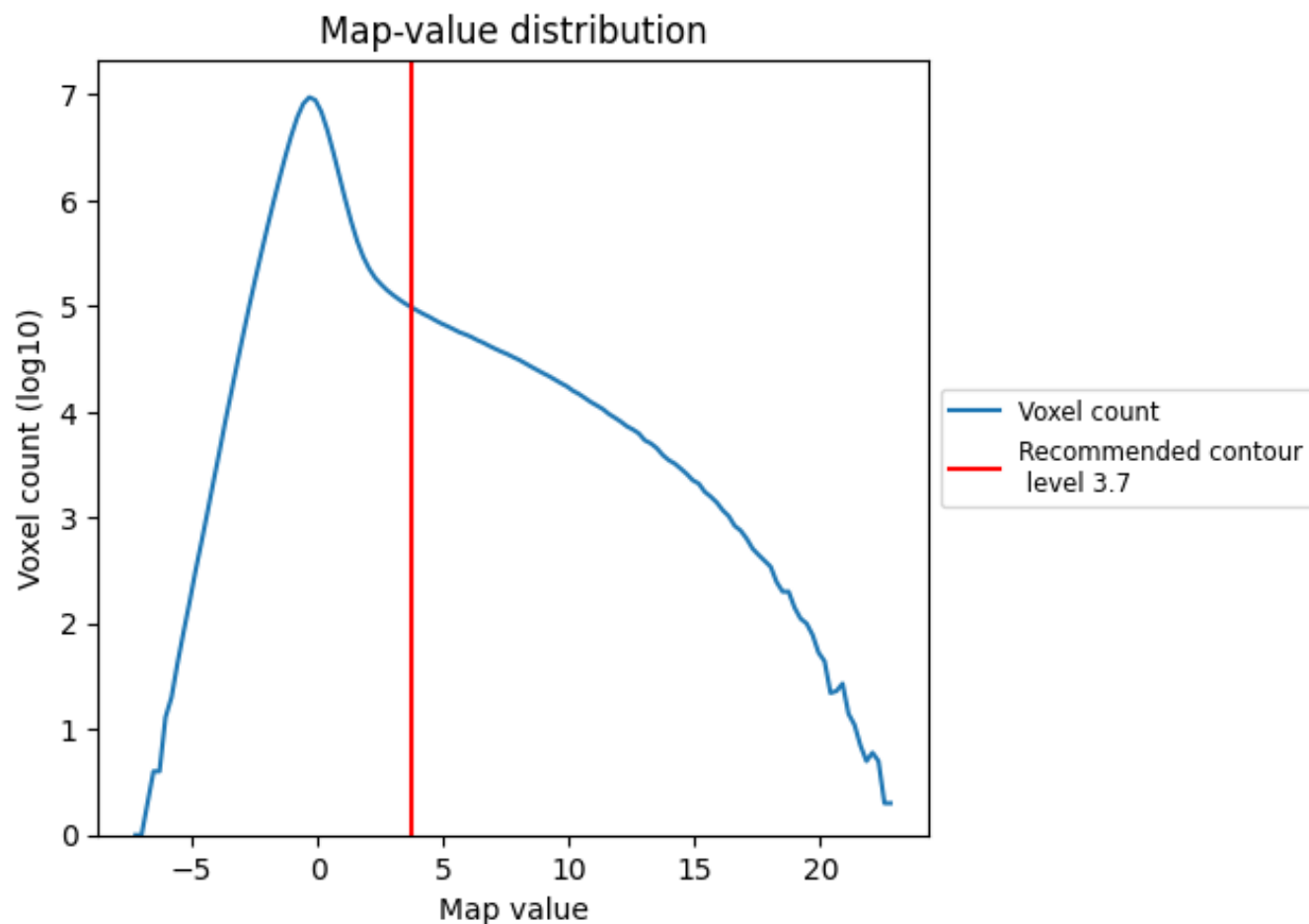
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

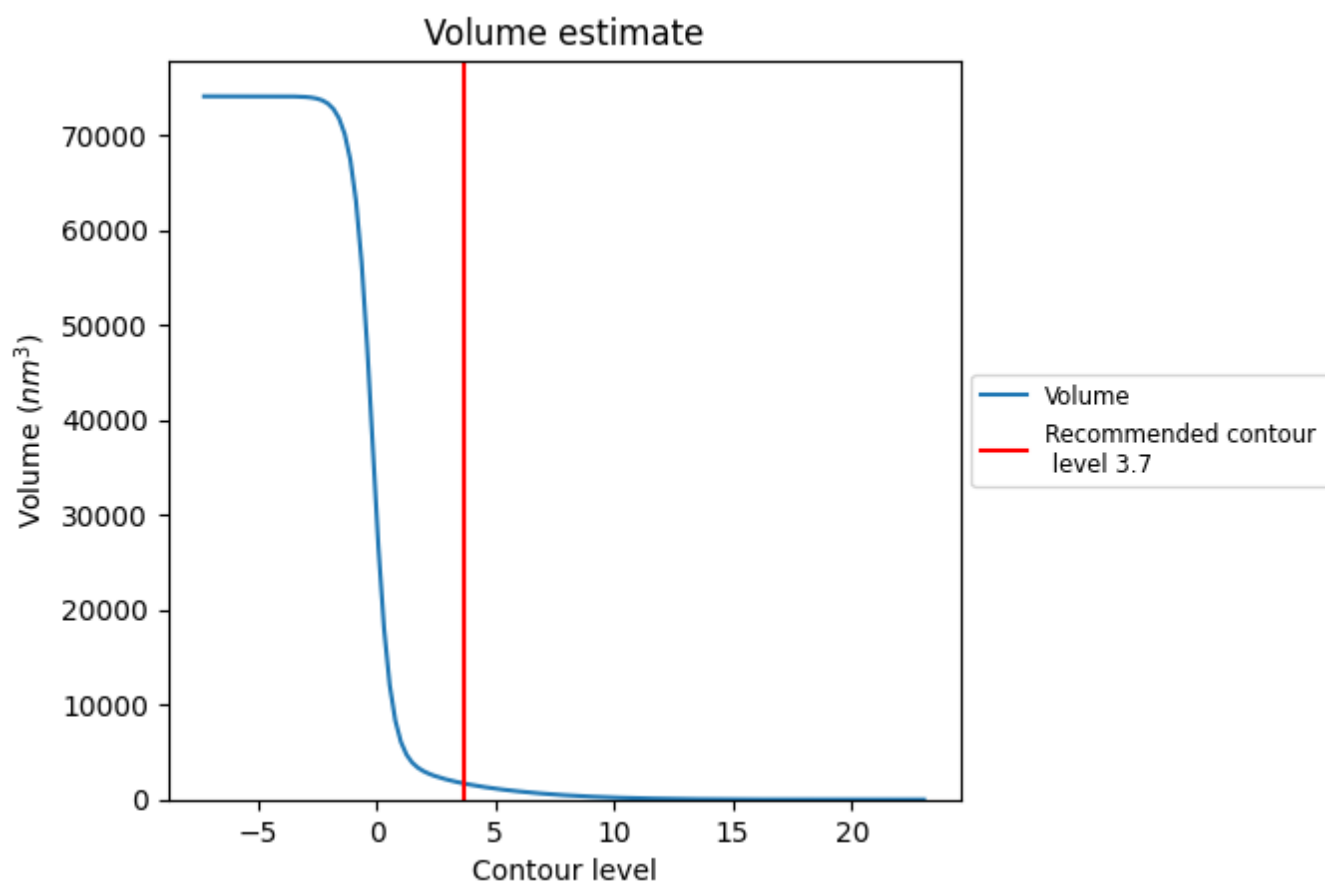
This section contains the results of statistical analysis of the map.

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.

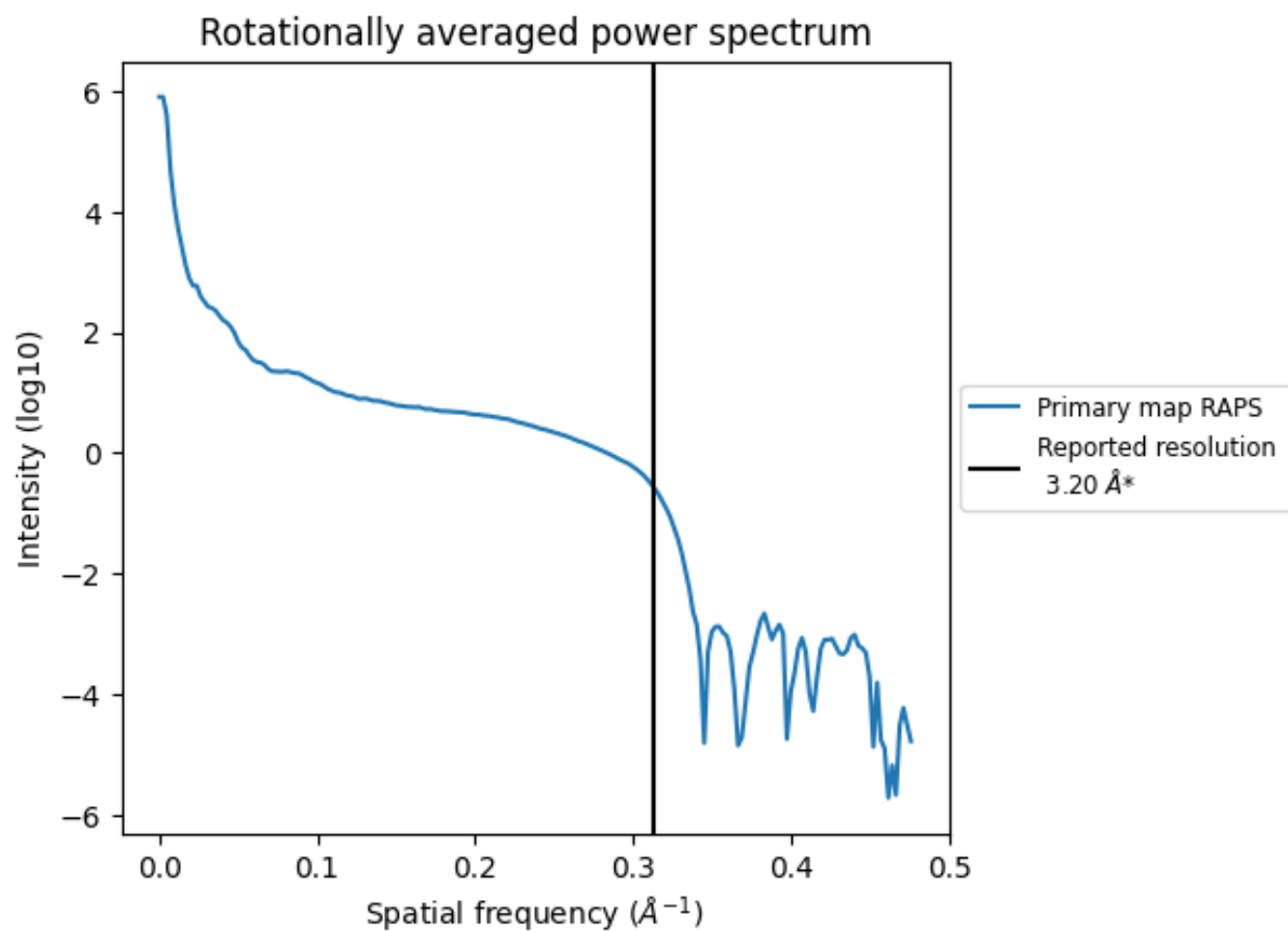
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1689 nm³; this corresponds to an approximate mass of 1525 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 0.312 Å⁻¹

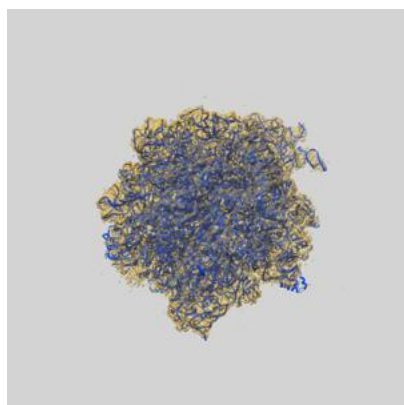
8 Fourier-Shell correlation

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

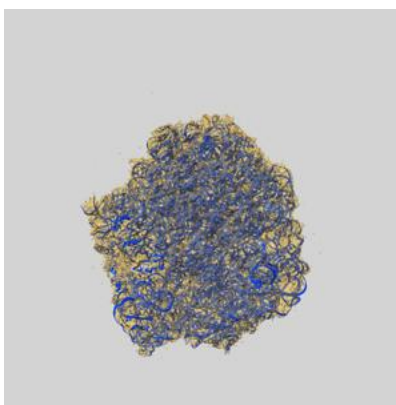
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22673 and PDB model 7K54. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

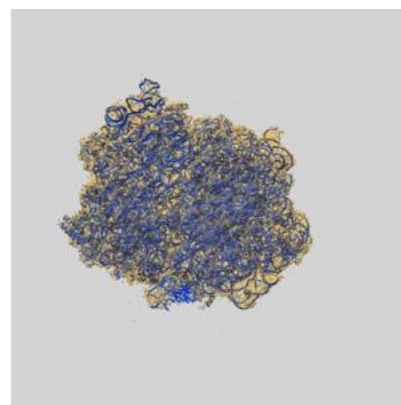
9.1 Map-model overlay [i](#)



X



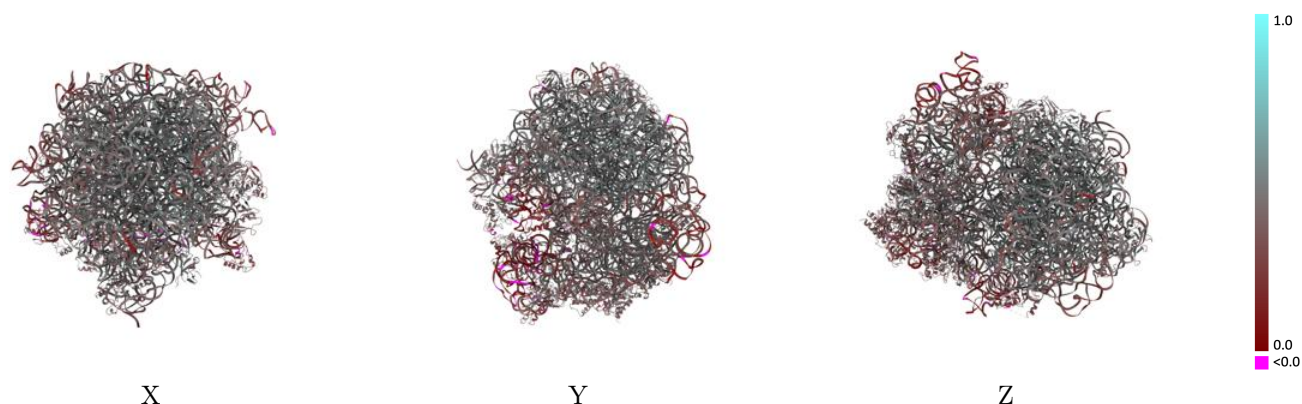
Y



Z

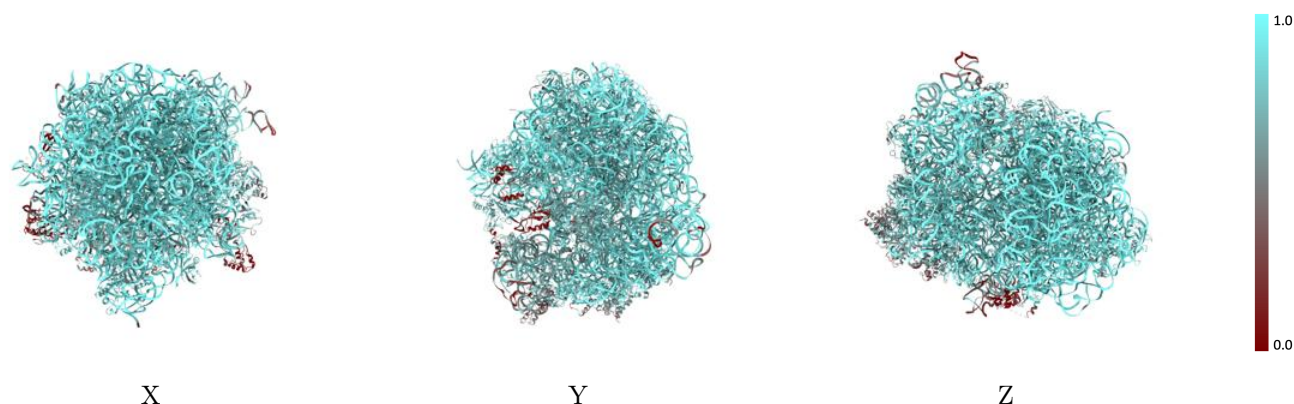
The images above show the 3D surface view of the map at the recommended contour level 3.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



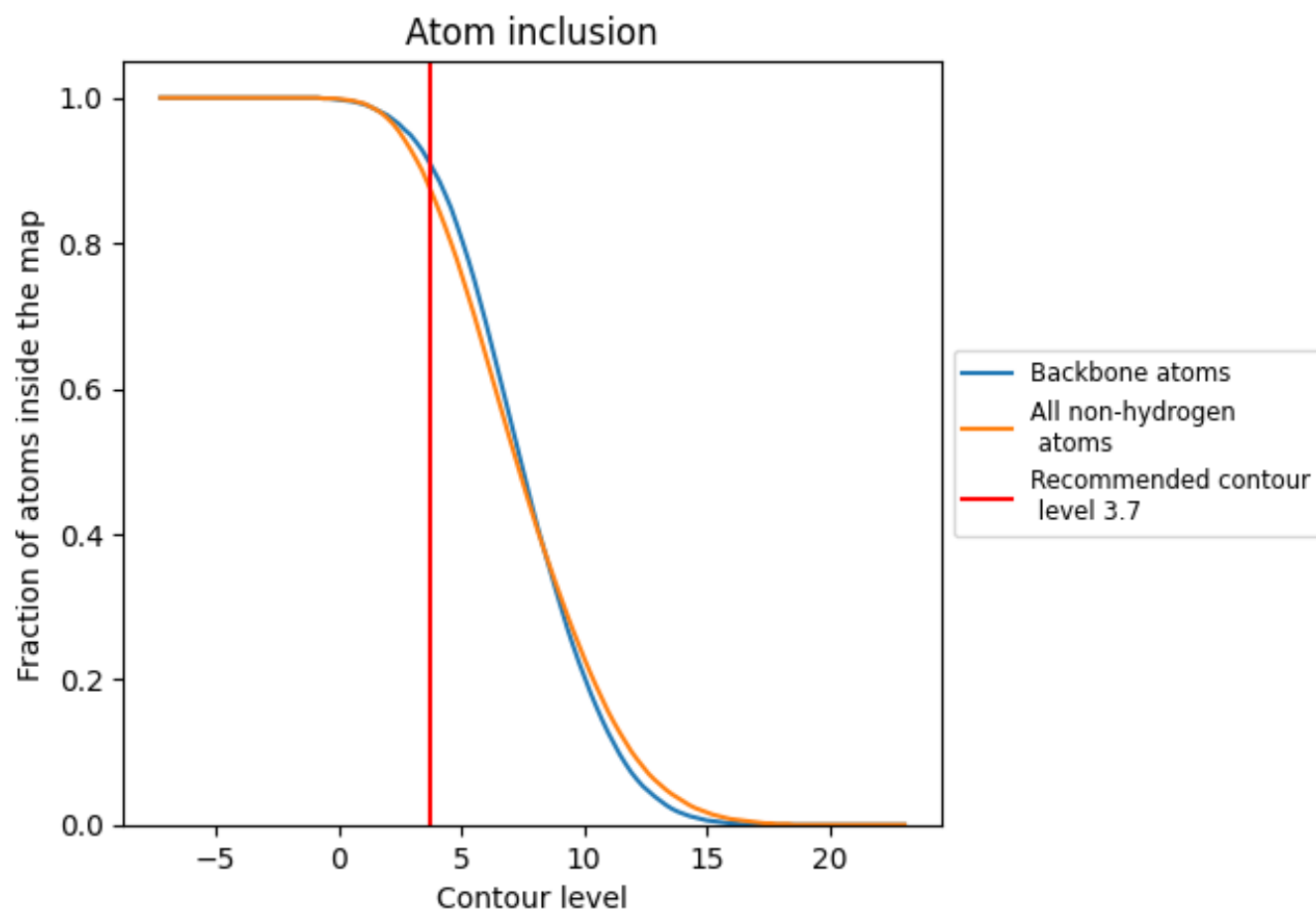
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 88% 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 (3.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8770	 0.4060
1	 0.9620	 0.4380
2	 0.9610	 0.4100
3	 0.8840	 0.3450
4	 0.7250	 0.3410
5	 0.9400	 0.3580
6	 0.9010	 0.3430
8	 0.7550	 0.3830
A	 0.5940	 0.2860
B	 0.9110	 0.4640
C	 0.7090	 0.4330
D	 0.9150	 0.4900
E	 0.9270	 0.4920
F	 0.9140	 0.4770
G	 0.5410	 0.3570
H	 0.6950	 0.4040
I	 0.7600	 0.3970
J	 0.8410	 0.4310
K	 0.8280	 0.3880
L	 0.4950	 0.3060
M	 0.8410	 0.4260
N	 0.6540	 0.3620
O	 0.5310	 0.3510
P	 0.8740	 0.4050
Q	 0.8390	 0.4580
R	 0.6050	 0.3240
S	 0.7910	 0.3810
T	 0.8510	 0.4080
U	 0.8090	 0.4220
V	 0.8640	 0.4190
W	 0.8370	 0.4010
X	 0.7640	 0.3280
Y	 0.8260	 0.3950
Z	 0.7320	 0.3320
a	 0.2020	 0.2340



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Chain	Atom inclusion	Q-score
b	 0.9190	 0.4940
c	 0.9000	 0.4780
d	 0.7920	 0.4420
e	 0.8110	 0.3850
f	 0.8220	 0.4250
g	 0.2380	 0.3080
h	 0.1120	 0.2330
i	 0.1320	 0.2020
j	 0.9000	 0.4660
k	 0.8810	 0.4820
l	 0.8850	 0.4720
m	 0.9110	 0.4820
n	 0.9130	 0.4690
o	 0.8620	 0.4220
p	 0.8820	 0.4710
q	 0.9140	 0.4790
r	 0.8530	 0.4650
s	 0.8770	 0.4680
t	 0.8490	 0.4550
u	 0.8310	 0.4200
v	 0.8480	 0.4540
w	 0.9070	 0.4890
x	 0.9030	 0.4690
y	 0.7540	 0.3880
z	 0.8740	 0.4560