



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:47 PM UTC

PDB ID : 7K51 / pdb_00007k51
EMDB ID : EMD-22670
Title : Mid-translocated non-frameshifting(CCA-A) complex with EF-G and GDPCP (Structure II)
Authors : Demo, G.; Loveland, A.B.; Svidritskiy, E.; Gamper, H.B.; Hou, Y.M.; Korostelev, A.A.
Deposited on : 2020-09-16
Resolution : 3.50 Å(reported)
Based on initial models : 4V7D, 5UYM, 6ENJ, 4V9P

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

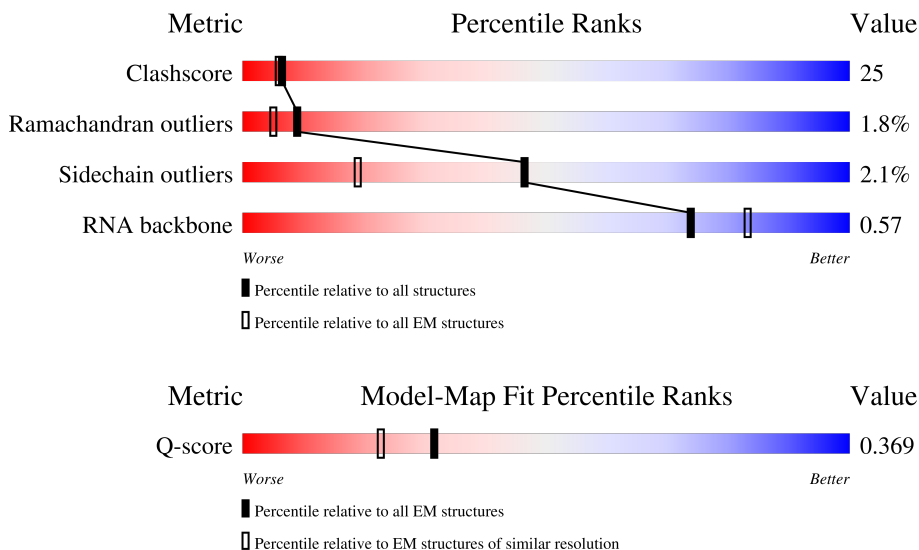
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	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	

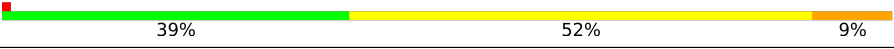
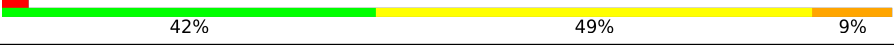
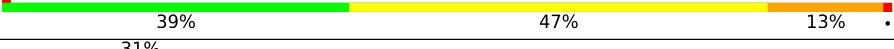
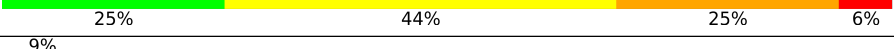
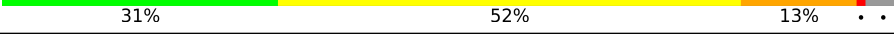
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Mol	Chain	Length	Quality of chain
28	C	50	
29	D	46	
30	E	64	
31	F	38	
32	G	225	
33	H	206	
34	I	205	
35	J	157	
36	K	100	
37	L	151	
38	M	129	
39	N	127	
40	O	98	
41	P	116	
42	Q	123	
43	R	114	
44	S	100	
45	T	88	
46	U	82	
47	V	80	
48	W	65	
49	X	79	
50	Y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

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Mol	Chain	Length	Quality of chain
53	3	1539	
54	1	2903	
55	2	120	
56	5	77	
57	6	77	
58	4	16	
59	8	711	

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 153370 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
			348	156	70	106	16		

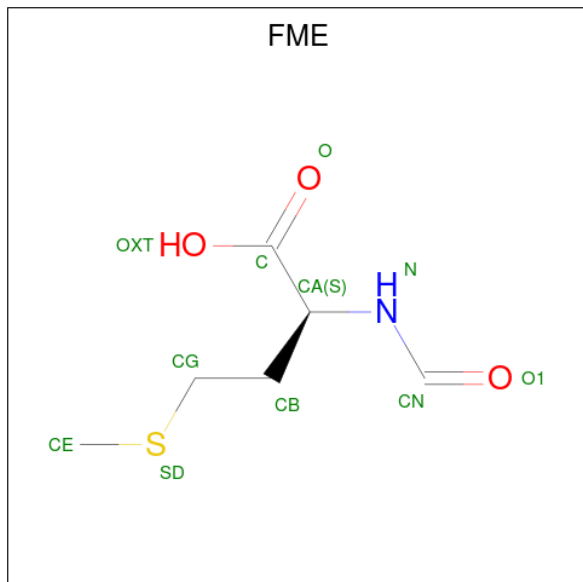
- Molecule 59 is a protein called Elongation factor G.

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:

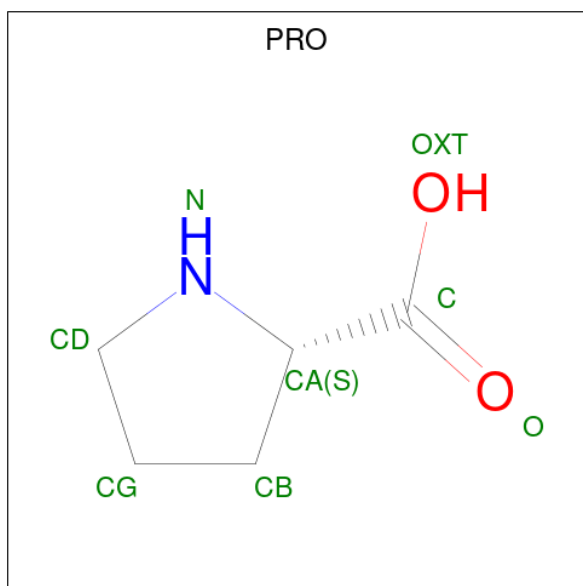
Chain	Residue	Modelled	Actual	Comment	Reference
8	705	LEU	-	expression tag	UNP H4UQ46
8	706	GLU	-	expression tag	UNP H4UQ46
8	707	HIS	-	expression tag	UNP H4UQ46
8	708	HIS	-	expression tag	UNP H4UQ46
8	709	HIS	-	expression tag	UNP H4UQ46
8	710	HIS	-	expression tag	UNP H4UQ46
8	711	HIS	-	expression tag	UNP H4UQ46
8	712	HIS	-	expression tag	UNP H4UQ46

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



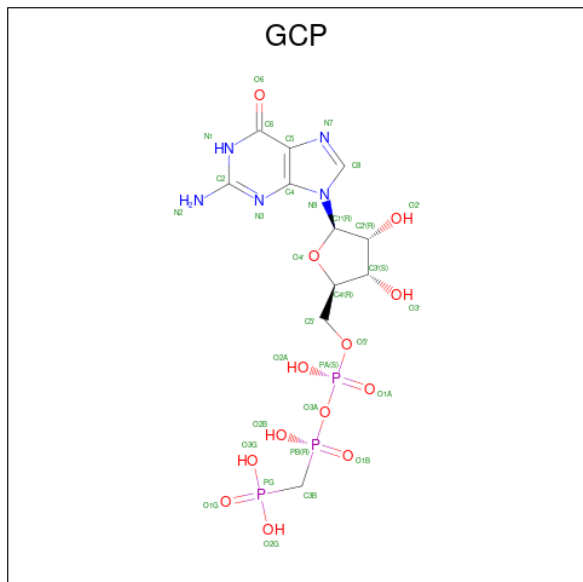
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
60	1	1	10	6	1	2	1	0

- 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

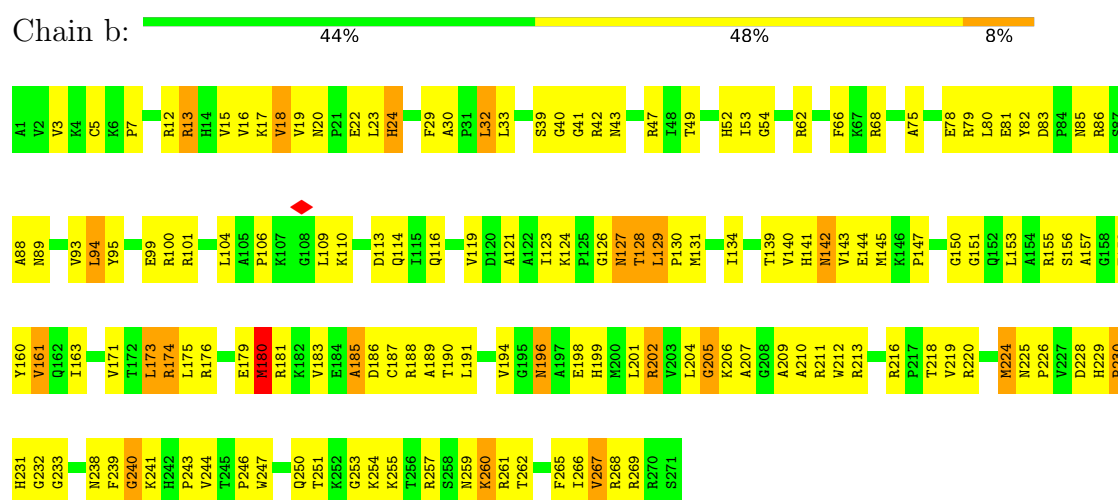
- Molecule 62 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



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.

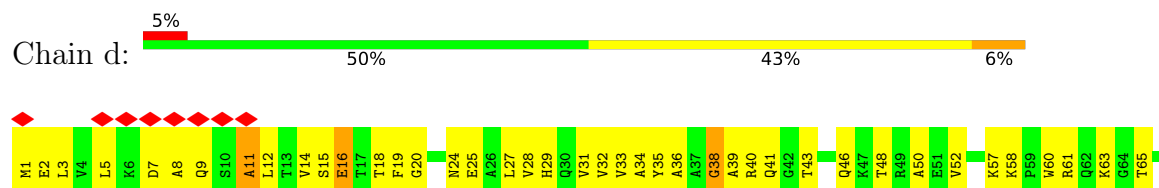
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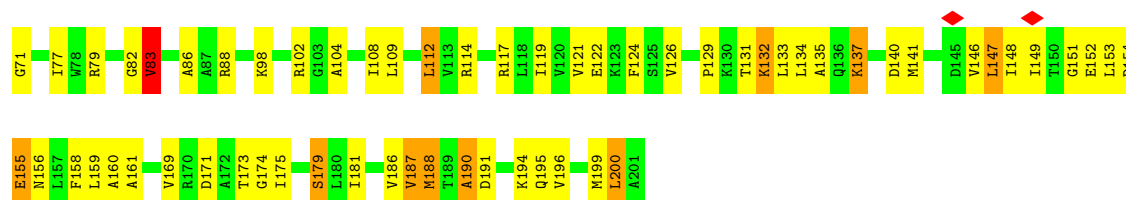


• Molecule 2: 50S ribosomal protein L3

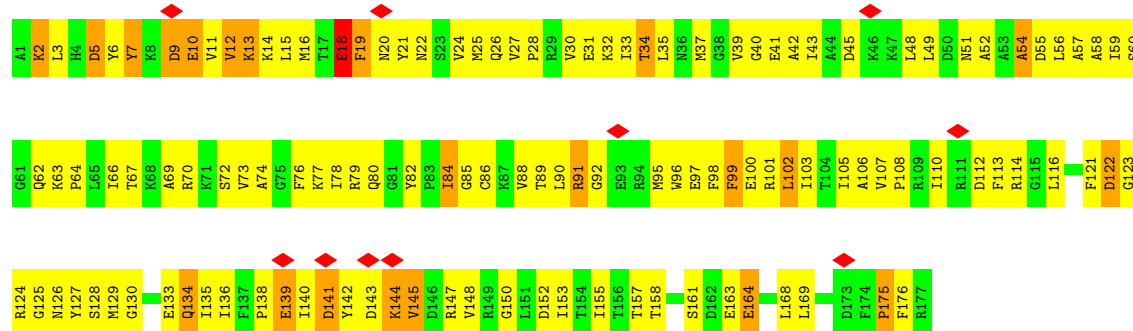


• Molecule 3: 50S ribosomal protein L4

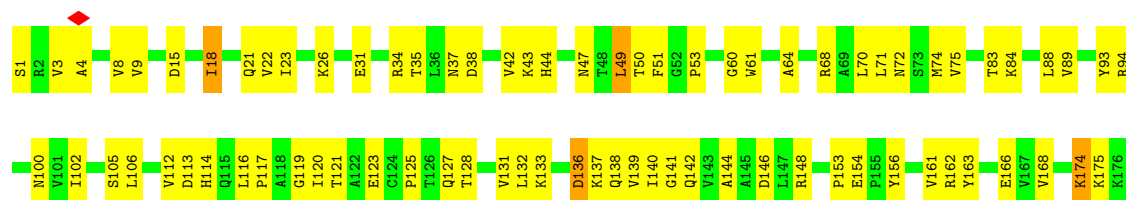




• Molecule 4: 50S ribosomal protein L5



• Molecule 5: 50S ribosomal protein L6

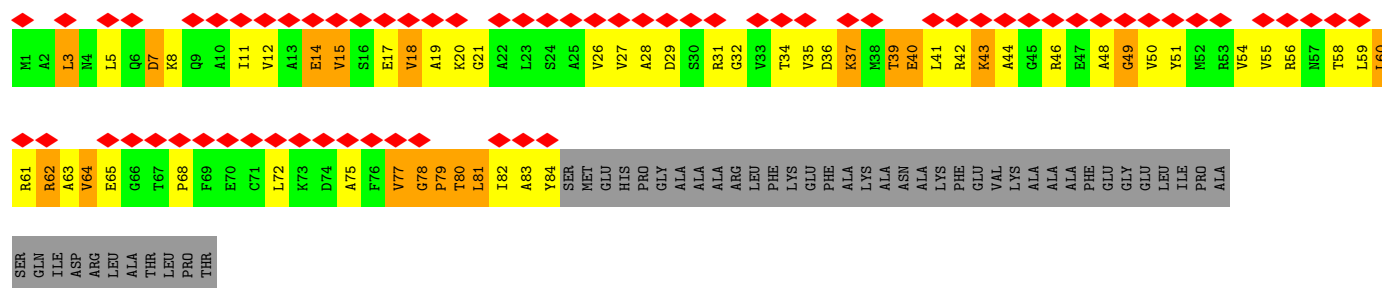


• Molecule 6: 50S ribosomal protein L9

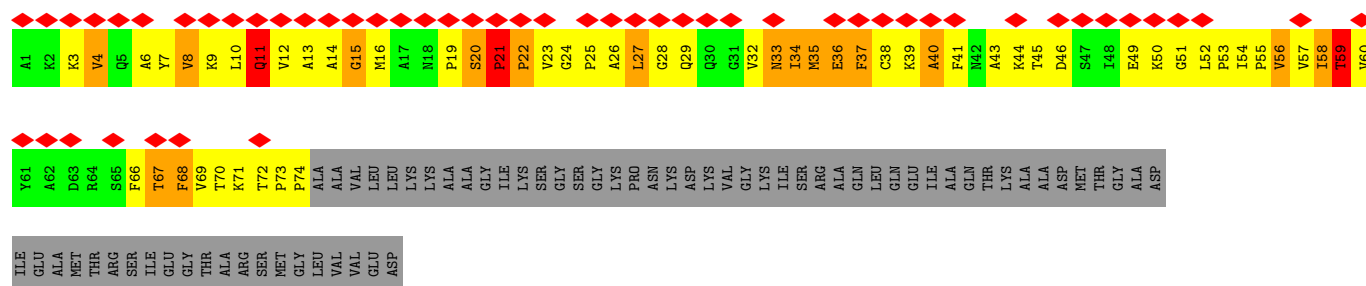
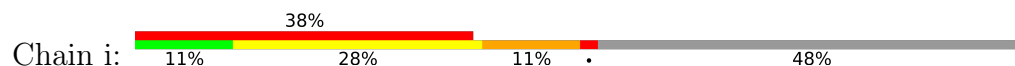


• Molecule 7: 50S ribosomal protein L10

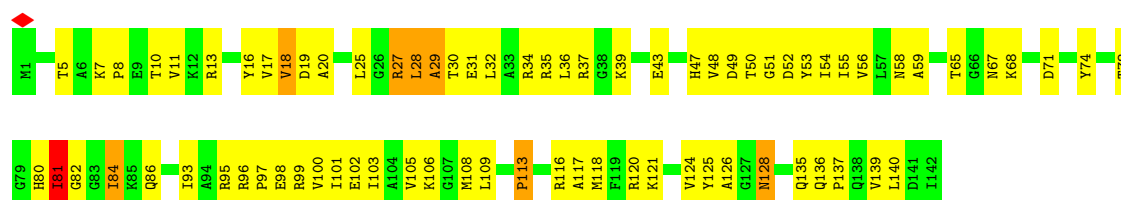




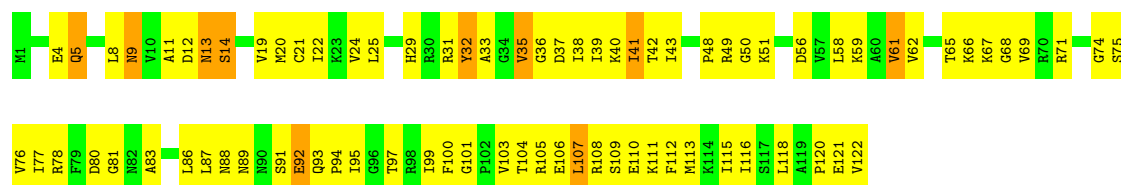
• Molecule 8: 50S ribosomal protein L11



• Molecule 9: 50S ribosomal protein L13



• Molecule 10: 50S ribosomal protein L14

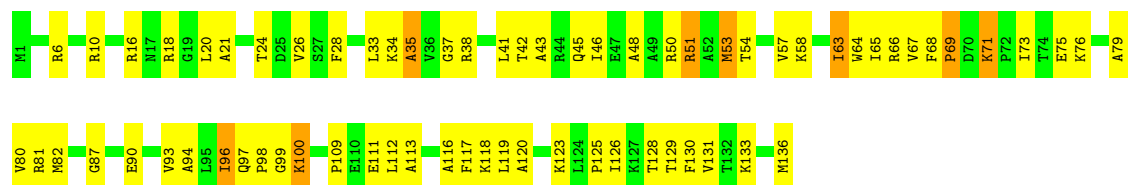


• Molecule 11: 50S ribosomal protein L15

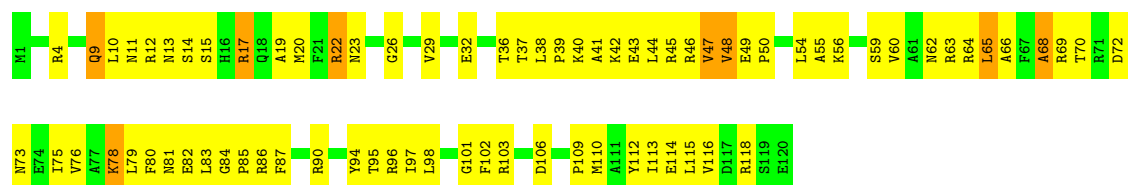




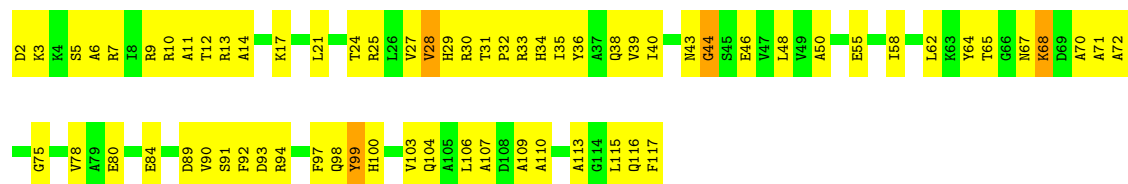
• Molecule 12: 50S ribosomal protein L16



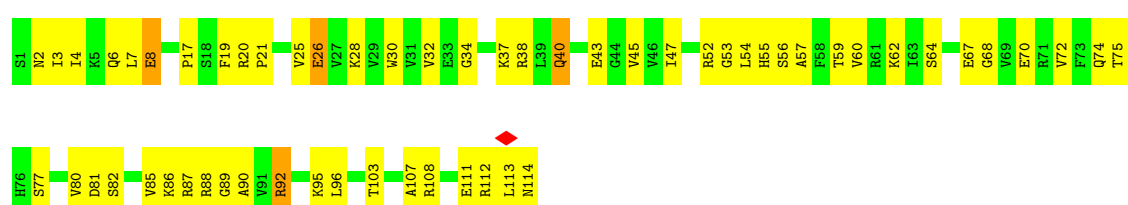
• Molecule 13: 50S ribosomal protein L17



• Molecule 14: 50S ribosomal protein L18

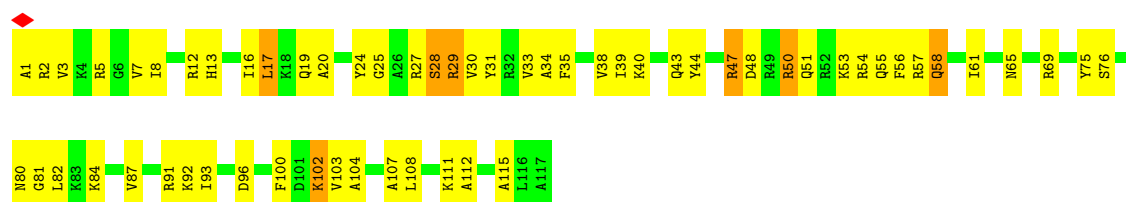


• Molecule 15: 50S ribosomal protein L19

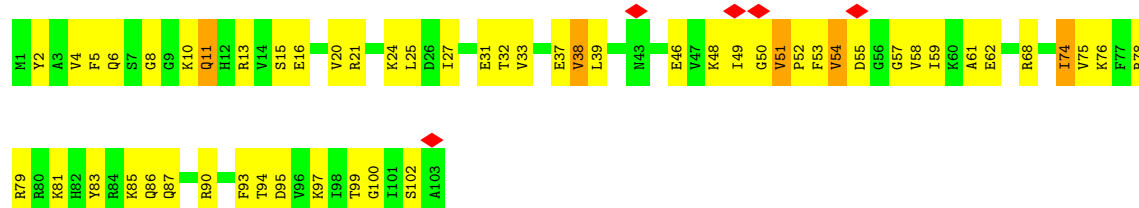


• Molecule 16: 50S ribosomal protein L20

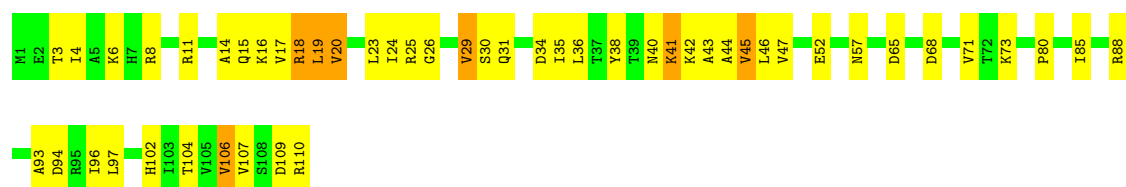




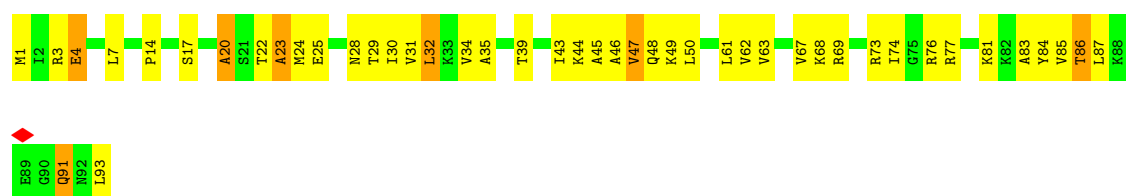
• Molecule 17: 50S ribosomal protein L21



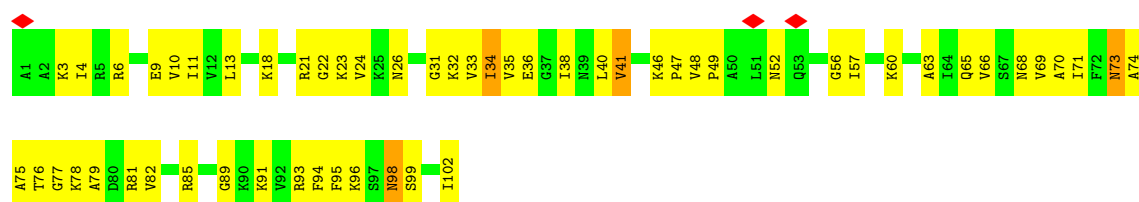
• Molecule 18: 50S ribosomal protein L22



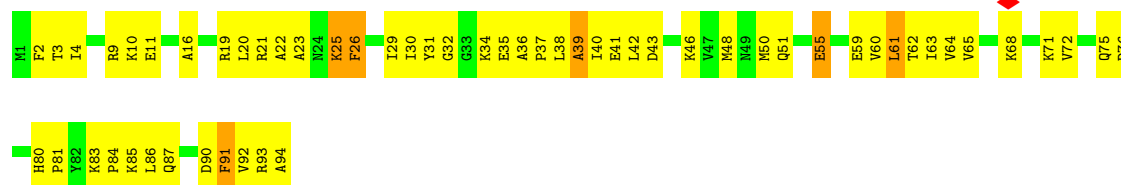
• Molecule 19: 50S ribosomal protein L23



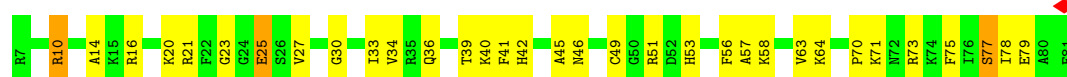
• Molecule 20: 50S ribosomal protein L24



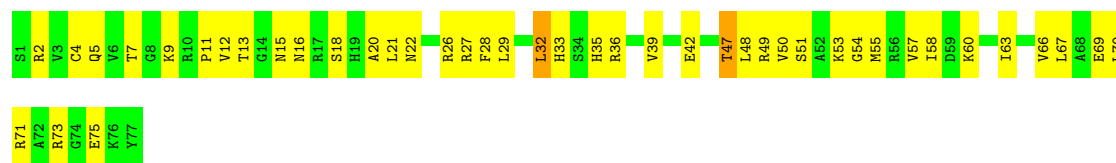
• Molecule 21: 50S ribosomal protein L25



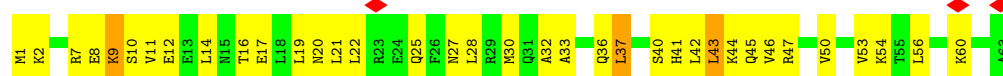
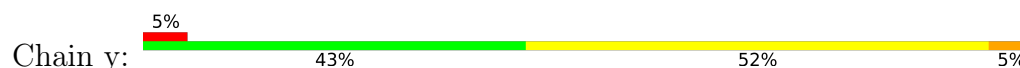
- Molecule 22: 50S ribosomal protein L27



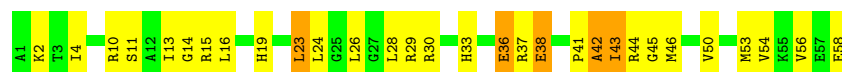
- Molecule 23: 50S ribosomal protein L28



- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30



- Molecule 26: 50S ribosomal protein L31



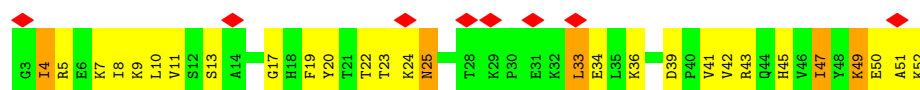
- Molecule 27: 50S ribosomal protein L32

Chain B: 



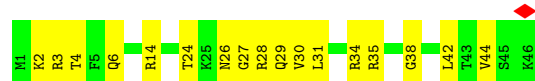
- Molecule 28: 50S ribosomal protein L33

Chain C: 



- Molecule 29: 50S ribosomal protein L34

Chain D: 



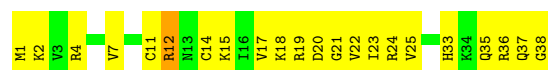
- Molecule 30: 50S ribosomal protein L35

Chain E: 



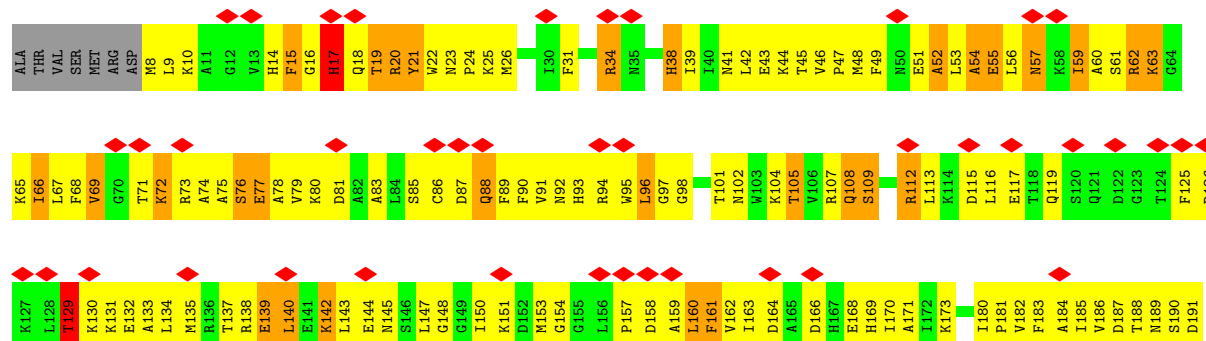
- Molecule 31: 50S ribosomal protein L36

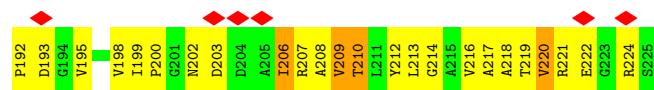
Chain F: 



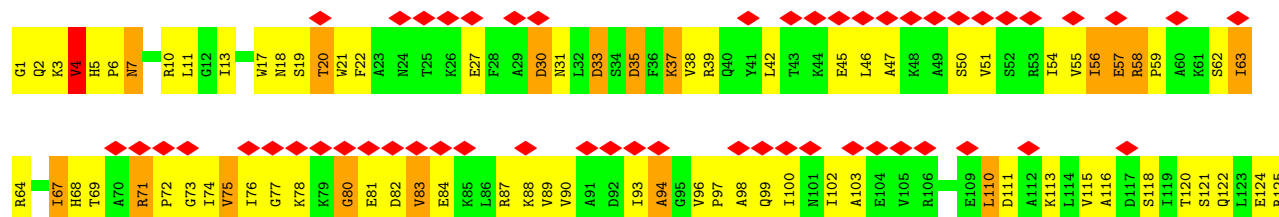
- Molecule 32: 30S ribosomal protein S2

Chain G: 

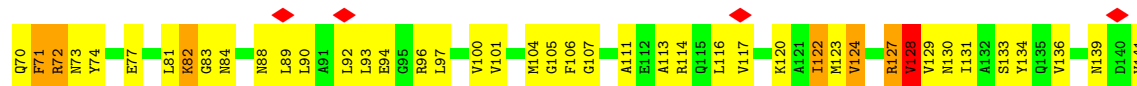




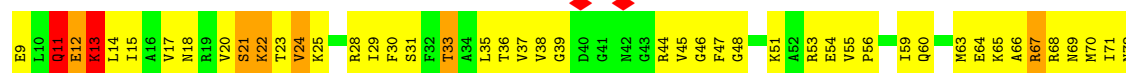
• Molecule 33: 30S ribosomal protein S3

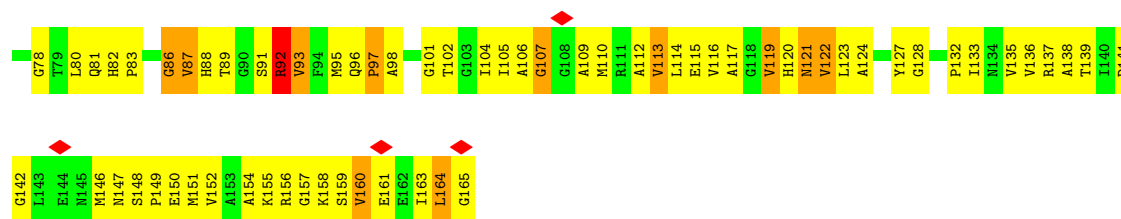


• Molecule 34: 30S ribosomal protein S4

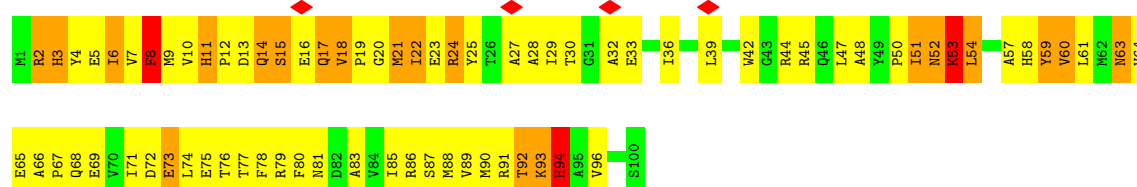


• Molecule 35: 30S ribosomal protein S5

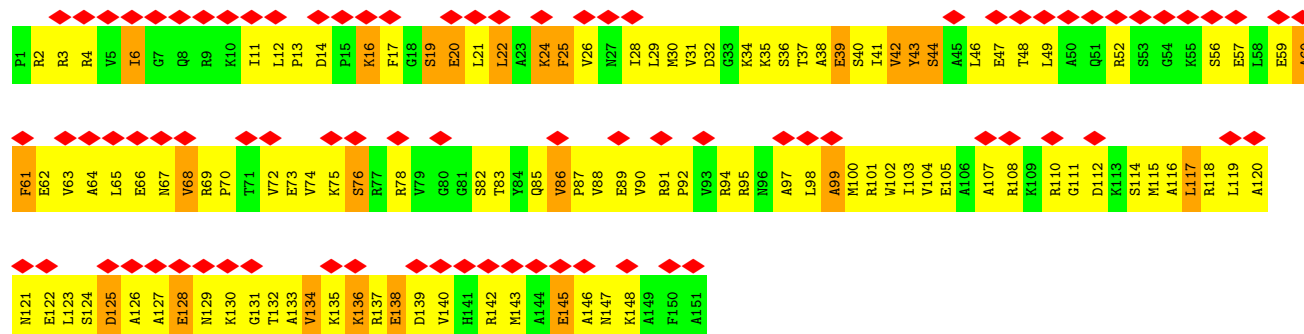




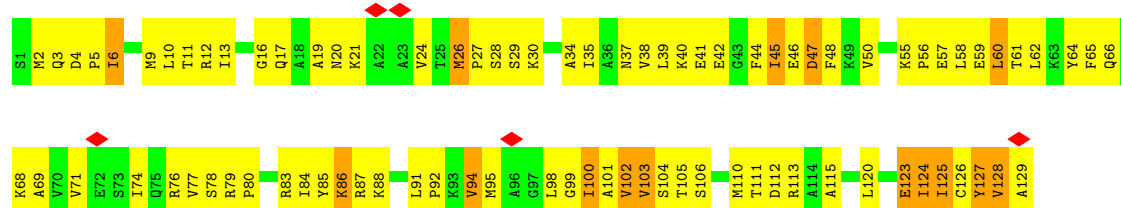
• Molecule 36: 30S ribosomal protein S6



• Molecule 37: 30S ribosomal protein S7

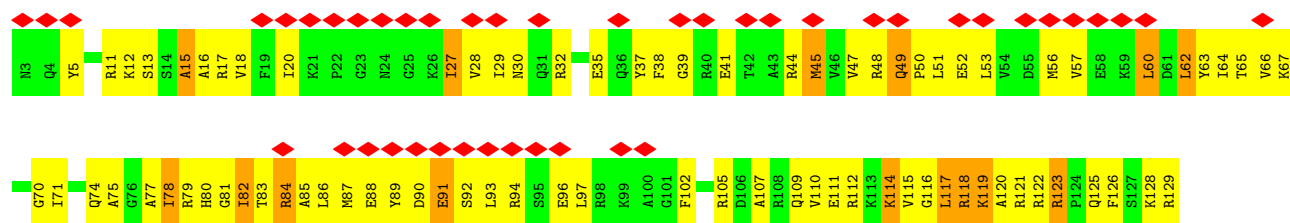


• Molecule 38: 30S ribosomal protein S8

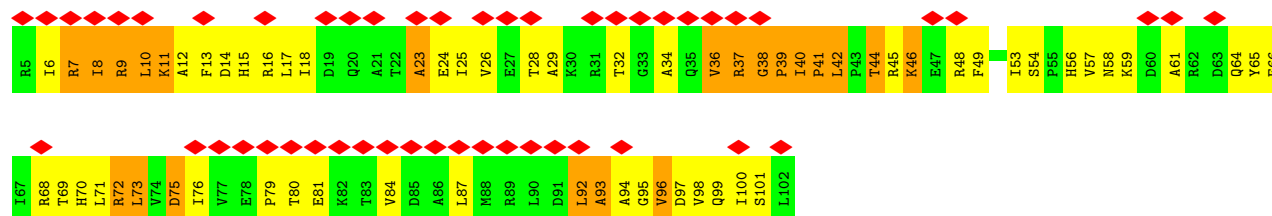


• Molecule 39: 30S ribosomal protein S9

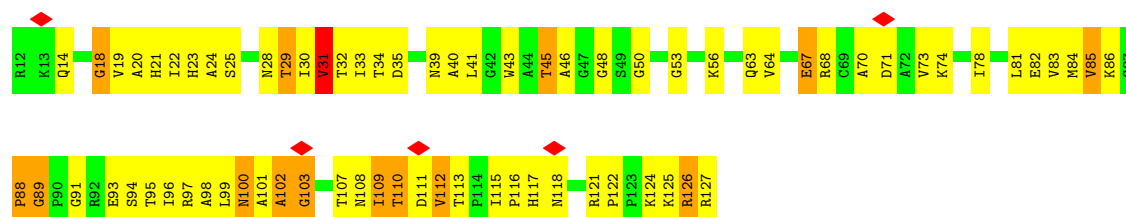




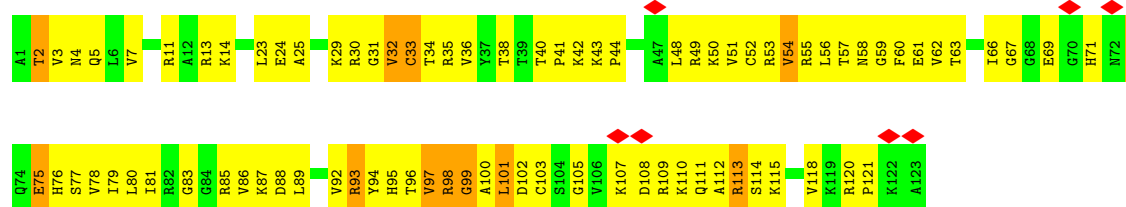
• Molecule 40: 30S ribosomal protein S10



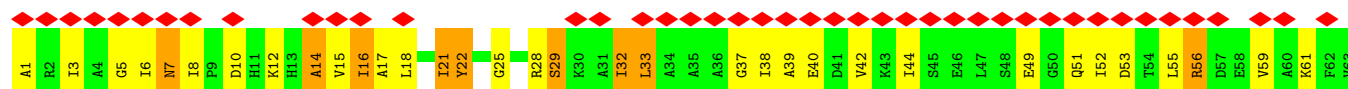
• Molecule 41: 30S ribosomal protein S11

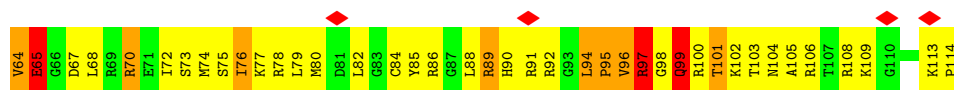


• Molecule 42: 30S ribosomal protein S12



• Molecule 43: 30S ribosomal protein S13

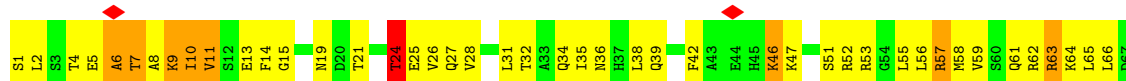




- Molecule 44: 30S ribosomal protein S14



- Molecule 45: 30S ribosomal protein S15



- Molecule 46: 30S ribosomal protein S16

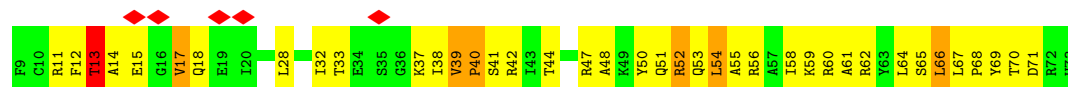
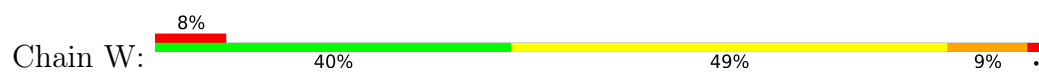


- Molecule 47: 30S ribosomal protein S17

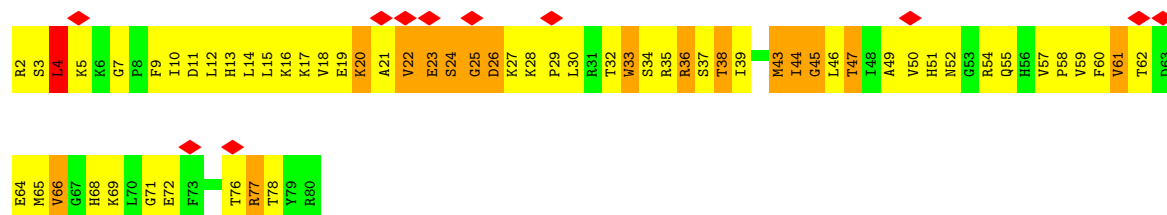


- Molecule 48: 30S ribosomal protein S18

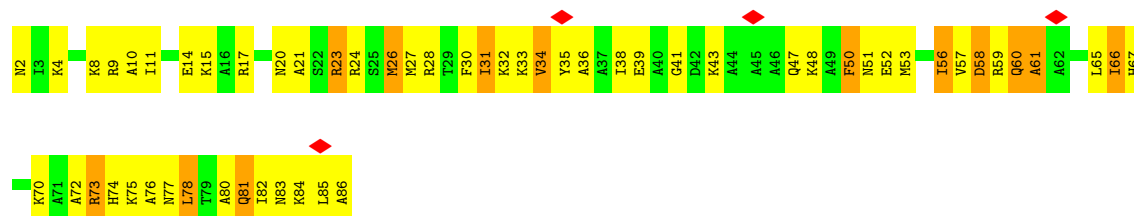




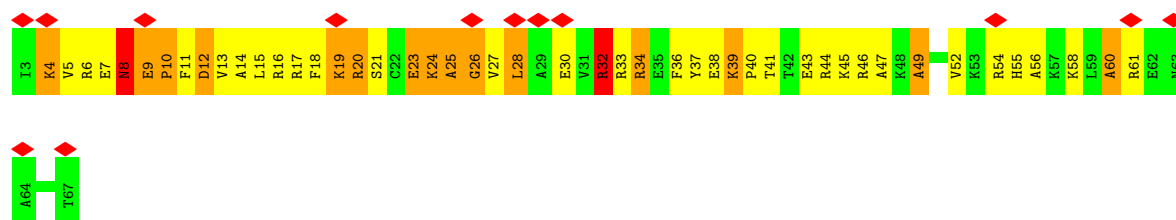
• Molecule 49: 30S ribosomal protein S19



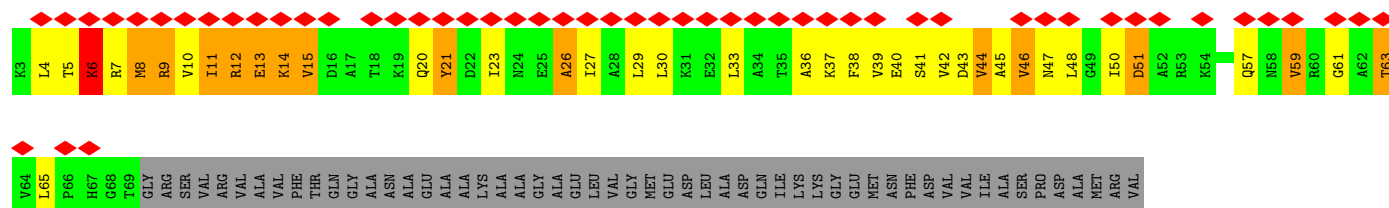
• Molecule 50: 30S ribosomal protein S20

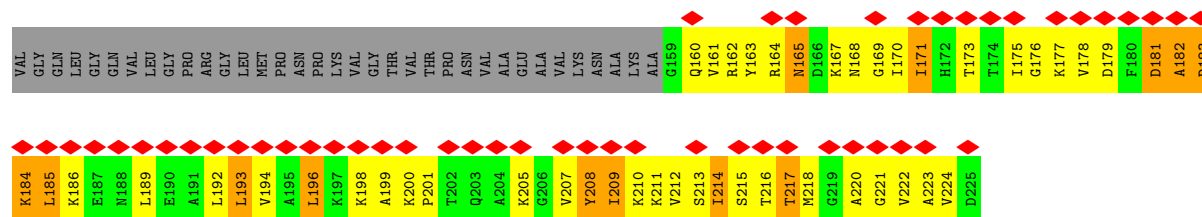


• Molecule 51: 30S ribosomal protein S21

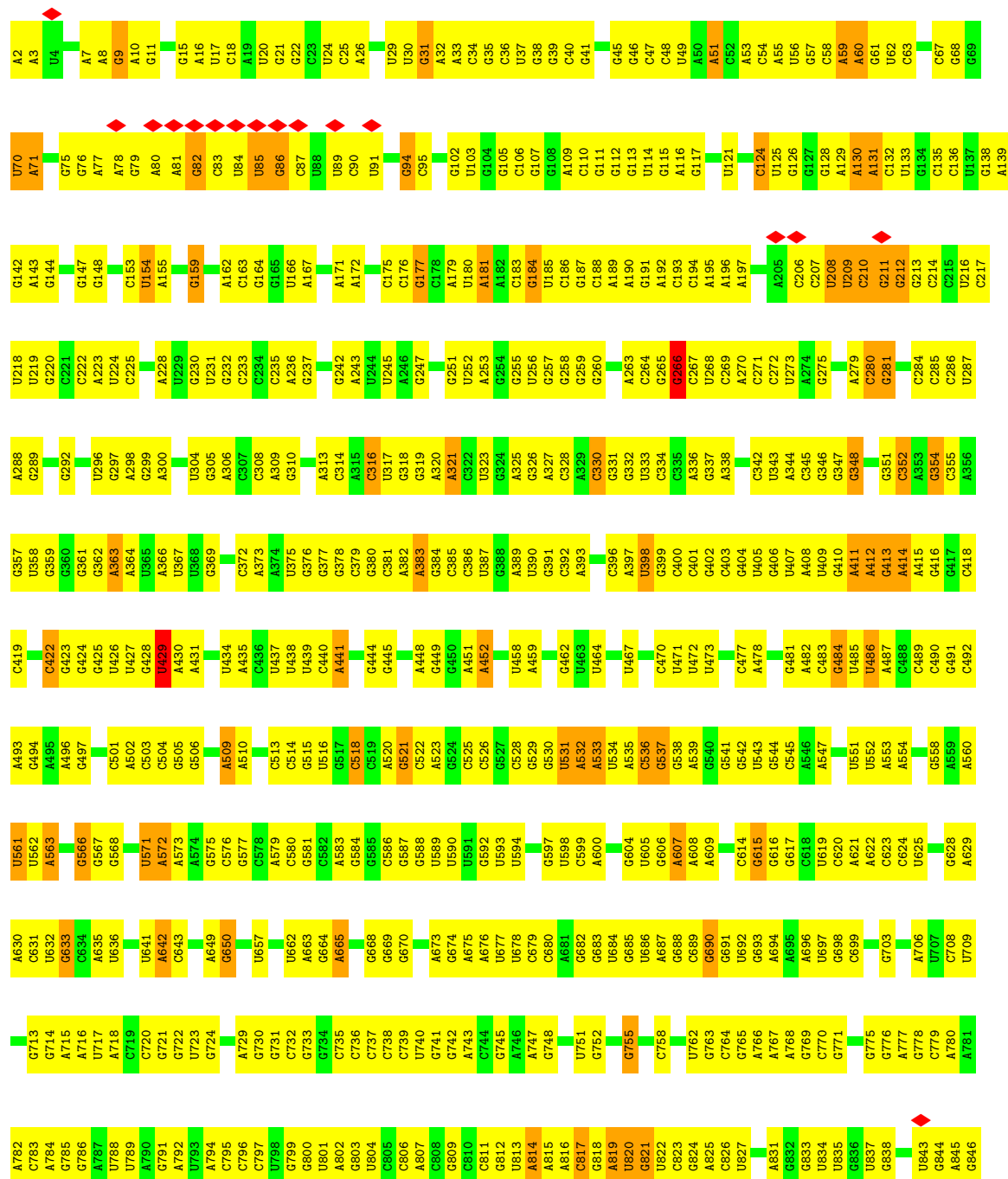


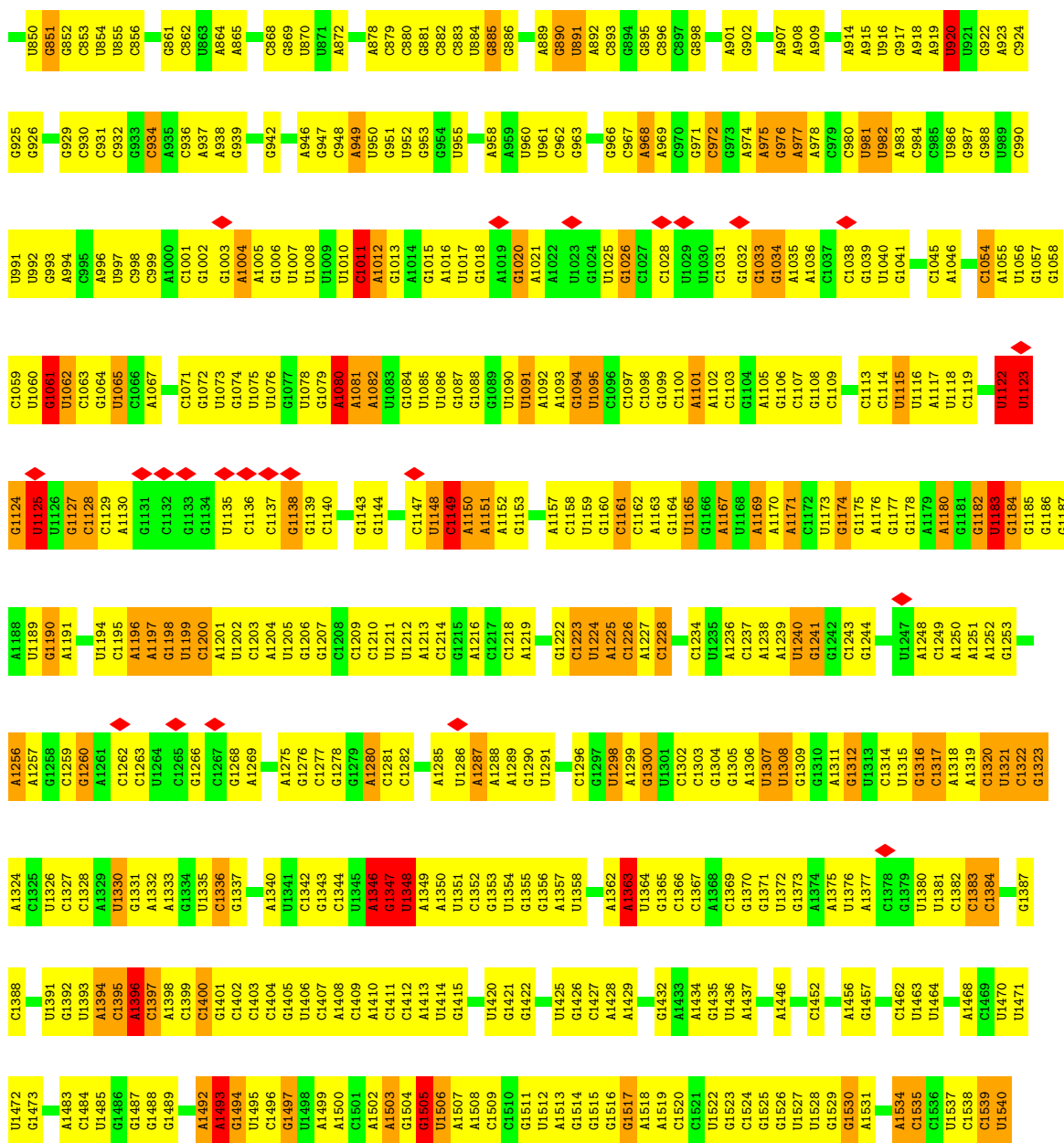
• Molecule 52: 50S ribosomal protein L1





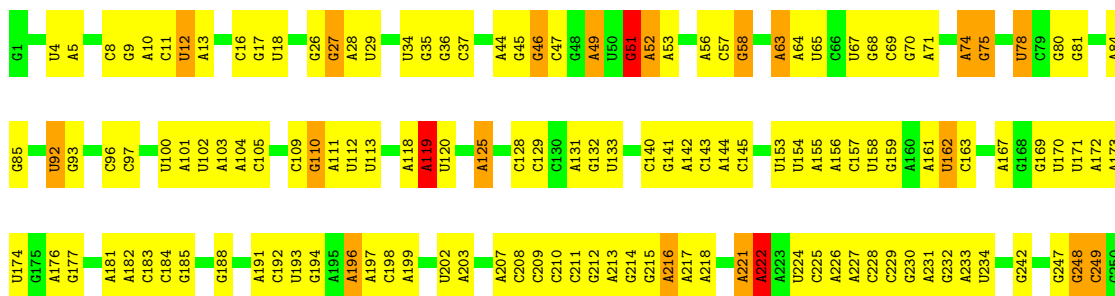
• Molecule 53: 16S ribosomal RNA





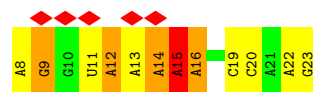
• Molecule 54: 23S ribosomal RNA

Chain 1: 41% 51% 8%

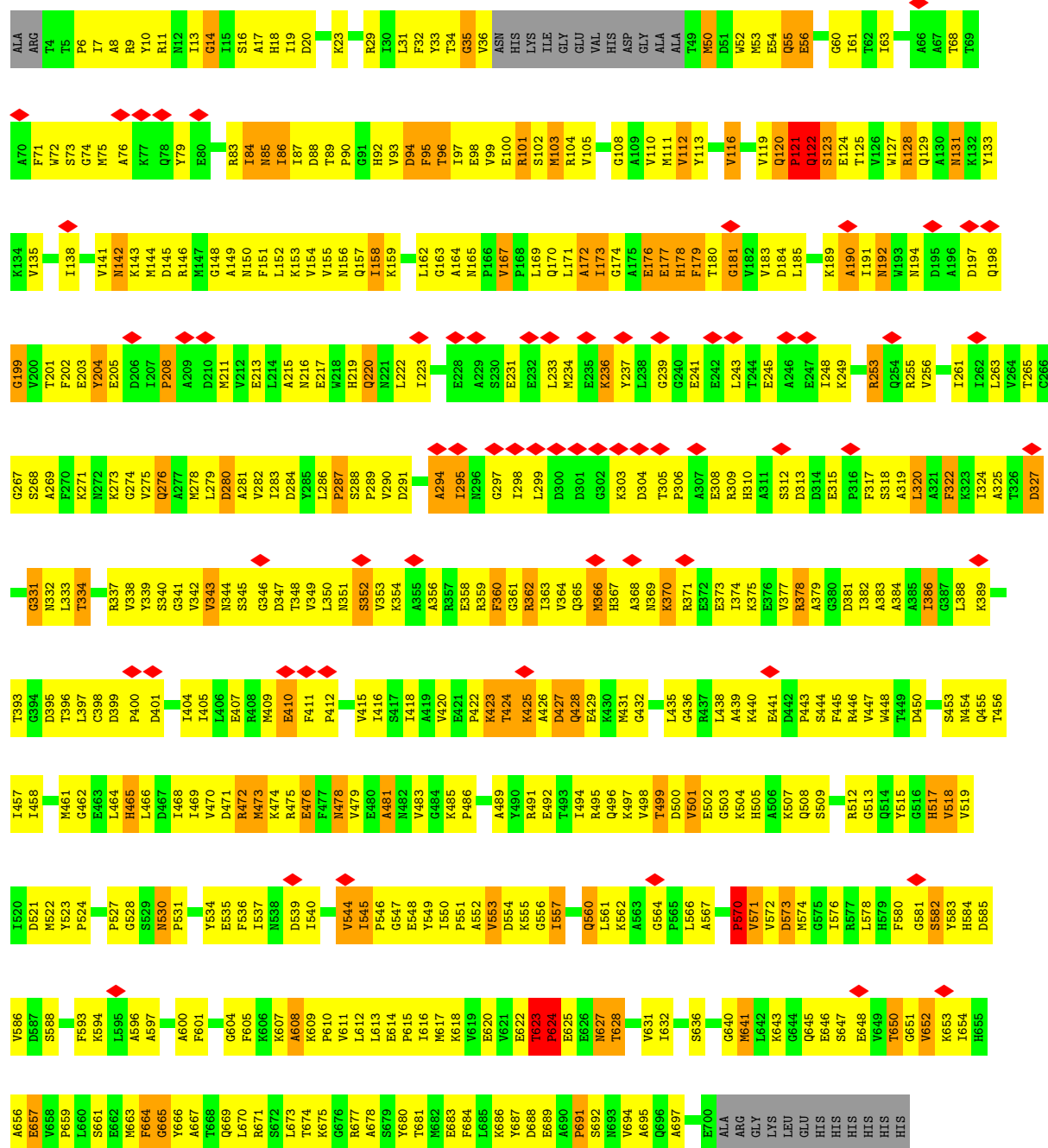




A2450	A2451	A2452	A2453	A2454	A2455	A2456	A2457	A2458	A2459	A2460	A2461	A2462	A2463	A2464		A2467	A2468	A2469	A2470	A2471	A2472	A2473	A2474	A2475	A2476	A2484	A2485	A2486	A2487	A2488	A2489	A2490	A2493	A2494	A2495	A2496	A2497	A2498	A2499	A2500	A2501	A2502	A2503	A2504	A2505		A2508		C2512	A2513	A2514	A2515	A2516	A2517	A2518	A2519	C2520	C2521							
G2379	C2380	A2381	G2382	G2383	G2384	C2385	A2386	A2387	A2388	G2389	U2390	C2391	A2392	G2393	C2394	C2395	G2396		G2400	U2401	U2402	C2403	U2404	U2405	A2406	A2407	U2408		A2411	A2412	G2413	G2414	G2415	C2416	G2417	A2418	U2419	U2423	U2424		G2427	G2428	G2429	A2430	U2431	A2432		A2435		C2440	U2441		G2442	G2443	G2444		G2447	A2448	U2449						
A2311	U2312	C2313	A2314	G2315	G2316	A2317	G2318	G2319	U2320	U2321		G2325	C2326	A2327	A2328	G2329	G2330	G2331	C2332	A2333	A2334	A2335	A2336		C2339	A2340		U2343	U2344	A2345	A2346	C2347	U2348	G2349	C2350	G2351		U2356	C2357	A2358	C2359	G2360	G2361	C2362	C2363	C2364	C2365	A2366	C2367	C2368	A2369	G2370	G2371	U2372	G2373		A2376	A2377	A2378						
U2233	G2234	G2235	U2236	G2237	G2238	G2239	U2240	A2241	G2242	U2243	U2244	U2245	G2246	A2247	U2248	U2249	G2250		G2255	A2266	A2267	A2268		G2271	U2272	A2273	A2274		G2277	A2278	G2279	G2280	A2281	G2282	C2283		G2286	A2287		G2290	U2291	U2292	G2293		U2296	A2297	A2298		G2301	U2302	G2303	G2304	U2305	C2306	G2307	U2229	G2308	A2309	G2310						
C2164	C2165	C2166	U2167	G2168	A2169	A2170	A2171	U2172	A2173	C2174	C2175	A2176	C2177	C2178	A2179	U2180	U2181	U2182	A2183	A2184	U2185	U2186	U2187	U2188	U2189	A2190	A2191		U2192	G2193	U2194	U2195	C2196	U2197	A2198		U2203	G2204		U2208	G2209	U2210	A2211	A2212	U2213	C2214		U2220	G2221	G2222	G2223	G2224	A2225	G2226	U2227	G2228	U2229	G2230	U2231	C2232					
G2096	A2097	U2098	G2099	G2100	A2101	G2102	C2103	G2104	U2105	U2106	G2107	U2108	U2109	G2110	C2111	U2112	G2113	U2114	G2115	G2116		A2117	U2118	A2119	G2120		G2124	G2125	A2126		G2127	G2128	G2129	U2130	U2131	U2132	G2133	A2134	A2135		G2140	G2141	A2142	G2143	G2144	G2145	G2146	A2147		U2151		G2152	G2153	A2154	U2155	G2156		A2158		G2162	A2163				
U1940	C1941	C1942	U1943		U1951	A1952	A1953	G1954	U1955	U1956	C1957	C1958	G1959	A1960		U1963	G1964	C1965	G2046	G2047	G2048	G2049	C2050	G2053	A2054	C2055	G2056		A2059	A2060	A2061	A2062	C2065	C2066	G2067	U2068	G2069	A2070	A2071	C2072	C2073	U2074	U2075		C2078	U2079		A2082	G2083		U2086	G2087	A2088	C2089	A2090		G2093								
A1872	G1873	U1874	G1875		G1878	G1879	U1880	C1881	U1882	U1883	G1884	A1885		G1888		G1891	C1892	C1893	C1894		U1938	A1939	A1900	A1901	G1902	G1903	G1904	C1905	G1906	G1907	C1908	C1909	G1910	U1911	A1912	A1913	C1914	U1915	A1916	U1917	A1918	A1919	C1920		U1923	C1924	G1925		U1929	U1855	G1930	U1931	A1932	G1933	C1934	G1935	A1936	A1937	A1938	U1939					
U1796	G1797	U1798	G1799	C1800	A1801	A1802	C1806	G1807	A1808	A1809	A1810	G1811		G1816	U1817	U1818	U1819	U1820	A1821	C1822	G1823	G1824	U1825	G1826	U1827	G1828	A1829	C1830	G1831	C1832	C1833	U1834		C1837	C1838		G1842	C1843	C1844	G1845	G1846	A1847		U1851	U1852	A1853	A1854	U1855	U1857	U1858	U1859	G1860	G1861		C1868	G1869									
C1728	U1729	G1730	G1731	C1732		A1735	U1736	G1737	U1738	A1739	G1740		G1743	A1744	A1745	A1746	U1747	C1748	A1749	G1750	U1751	G1752	G1753	A1754	A1755	G1756	U1757	U1758	A1759	C1760	U1683	C1684	C1685		A1689	A1690		G1695		G1702	G1703		U1709	G1710		A1713	U1714	G1715	U1716	A1717	U1718		U1719	G1720	A1614	C1615	U1616	A1617	A1618	A1619	A1620	A1637	C1638	C1639	A1640
A1549	C1550	C1551	A1552		G1555		C1558	U1559	G1560	U1561	U1562	U1563	C1564	C1565	U1567	A1568	A1569	A1570	A1571	A1572		U1576	C1577	U1578		A1583	U1584	C1585	A1586	G1587	G1588	U1589	A1590	A1591	C1592	A1593	U1594	C1595	A1596	A1597	A1598	U1599	C1600		A1603		A1608	G1609	A1610	C1611		A1614	C1615	U1616	A1617	A1618	A1619	A1620	A1637	C1638	C1639	A1640			
C1472	G1473	U1474	G1475	U1476	A1477	G1478	G1479	C1480	U1481	G1482	U1483	U1484	U1485	U1486	U1487	C1488	A1489	A1490		C1498	C1499	G1500	A1501	C1502	A1503		C1507	A1508	A1509	G1510	G1511	C1512	A1515		A1522	U1523	U1594	C1595	A1596	A1597	A1598	U1599	C1600		A1603		A1608	G1609	A1610	C1611		A1614	C1615	U1616	A1617	A1618	A1619	A1620	A1637	C1638	C1639	A1640			



• 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	3179	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	21.906	Depositor
Minimum map value	-8.364	Depositor
Average map value	0.019	Depositor
Map value standard deviation	1.404	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: FME, GCP, MG

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	0.98	19/2122 (0.9%)	1.17	17/2852 (0.6%)
2	c	0.95	9/1586 (0.6%)	1.27	17/2134 (0.8%)
3	d	1.15	16/1571 (1.0%)	1.30	30/2113 (1.4%)
4	e	1.22	18/1435 (1.3%)	1.34	25/1926 (1.3%)
5	f	1.01	9/1343 (0.7%)	1.15	13/1816 (0.7%)
6	g	1.88	24/946 (2.5%)	1.49	23/1275 (1.8%)
7	h	1.68	14/638 (2.2%)	1.61	21/860 (2.4%)
8	i	2.31	22/564 (3.9%)	2.03	29/768 (3.8%)
9	j	0.98	8/1152 (0.7%)	1.17	13/1551 (0.8%)
10	k	1.02	4/948 (0.4%)	1.29	15/1268 (1.2%)
11	l	0.74	3/1054 (0.3%)	1.08	6/1403 (0.4%)
12	m	1.14	12/1093 (1.1%)	1.26	14/1460 (1.0%)
13	n	0.93	8/974 (0.8%)	1.08	4/1301 (0.3%)
14	o	0.95	6/902 (0.7%)	1.16	9/1209 (0.7%)
15	p	0.81	5/929 (0.5%)	1.01	1/1242 (0.1%)
16	q	1.06	8/960 (0.8%)	1.21	5/1278 (0.4%)
17	r	0.69	0/829	1.02	2/1107 (0.2%)
18	s	1.18	10/864 (1.2%)	1.26	13/1156 (1.1%)
19	t	0.81	4/745 (0.5%)	1.05	3/994 (0.3%)
20	u	0.64	1/788 (0.1%)	0.96	4/1051 (0.4%)
21	v	0.91	5/766 (0.7%)	1.19	8/1025 (0.8%)
22	w	1.09	4/582 (0.7%)	1.16	4/769 (0.5%)
23	x	0.76	1/635 (0.2%)	1.01	2/848 (0.2%)
24	y	1.01	4/510 (0.8%)	1.15	2/677 (0.3%)
25	z	1.05	5/453 (1.1%)	1.00	2/605 (0.3%)
26	A	1.29	5/532 (0.9%)	1.32	8/709 (1.1%)
27	B	0.78	1/450 (0.2%)	1.08	4/599 (0.7%)
28	C	1.16	3/417 (0.7%)	1.09	3/554 (0.5%)
29	D	0.84	1/380 (0.3%)	1.15	2/498 (0.4%)
30	E	0.78	2/513 (0.4%)	0.93	2/676 (0.3%)
31	F	1.08	1/303 (0.3%)	1.00	1/397 (0.3%)
32	G	1.37	25/1736 (1.4%)	1.45	44/2338 (1.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	H	1.45	35/1652 (2.1%)	1.39	37/2225 (1.7%)
34	I	1.29	25/1665 (1.5%)	1.40	36/2227 (1.6%)
35	J	1.28	15/1170 (1.3%)	1.34	14/1573 (0.9%)
36	K	2.21	29/836 (3.5%)	1.77	31/1128 (2.7%)
37	L	1.51	24/1196 (2.0%)	1.50	32/1602 (2.0%)
38	M	1.23	15/989 (1.5%)	1.39	24/1326 (1.8%)
39	N	1.10	12/1034 (1.2%)	1.28	16/1375 (1.2%)
40	O	2.38	25/797 (3.1%)	1.78	32/1077 (3.0%)
41	P	1.35	13/886 (1.5%)	1.44	17/1195 (1.4%)
42	Q	0.87	3/969 (0.3%)	1.15	5/1300 (0.4%)
43	R	1.58	22/893 (2.5%)	1.60	17/1193 (1.4%)
44	S	1.49	18/817 (2.2%)	1.34	19/1088 (1.7%)
45	T	1.64	18/722 (2.5%)	1.44	18/964 (1.9%)
46	U	0.98	5/659 (0.8%)	1.11	5/884 (0.6%)
47	V	0.83	4/658 (0.6%)	0.97	3/881 (0.3%)
48	W	1.05	3/545 (0.6%)	1.30	10/731 (1.4%)
49	X	1.47	11/653 (1.7%)	1.66	24/877 (2.7%)
50	Y	1.49	15/671 (2.2%)	1.48	18/888 (2.0%)
51	Z	1.28	9/551 (1.6%)	1.64	17/728 (2.3%)
52	a	1.80	30/1034 (2.9%)	1.66	32/1387 (2.3%)
53	3	0.57	6/36963 (0.0%)	0.61	20/57662 (0.0%)
54	1	0.50	0/69796	0.57	16/108888 (0.0%)
55	2	0.48	0/2872	0.59	1/4479 (0.0%)
56	5	0.49	0/1840	0.63	0/2868
57	6	0.51	0/1832	0.65	2/2855 (0.1%)
58	4	0.54	0/391	0.72	3/608 (0.5%)
59	8	1.34	83/5411 (1.5%)	1.44	129/7323 (1.8%)
All	All	0.83	677/166222 (0.4%)	0.87	924/247791 (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
34	I	0	2
35	J	0	2
46	U	0	1
53	3	0	22
54	1	0	49
55	2	0	3
56	5	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
57	6	0	1
59	8	0	1
All	All	0	82

The worst 5 of 677 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	K	13	ASP	C-O	23.86	1.51	1.24
6	g	142	VAL	C-O	22.77	1.47	1.24
40	O	40	ILE	N-CA	22.43	1.74	1.46
40	O	73	LEU	C-O	21.73	1.50	1.23
40	O	39	PRO	C-N	21.67	1.57	1.33

The worst 5 of 924 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	K	13	ASP	CA-C-O	15.60	137.20	120.82
40	O	39	PRO	CA-C-O	-14.90	105.07	121.32
59	8	178	HIS	CA-C-N	-13.53	102.15	121.50
59	8	178	HIS	C-N-CA	-13.53	102.15	121.50
8	i	37	PHE	CA-C-N	-13.10	99.60	122.26

There are no chirality outliers.

5 of 82 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
34	I	152	SER	Mainchain
34	I	154	VAL	Mainchain
35	J	86	GLY	Mainchain
35	J	92	ARG	Mainchain
46	U	78	VAL	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	161	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	c	1565	0	1616	116	0
3	d	1552	0	1619	89	0
4	e	1411	0	1447	130	0
5	f	1323	0	1374	75	0
6	g	936	0	961	82	0
7	h	633	0	666	56	0
8	i	551	0	577	62	0
9	j	1129	0	1162	63	0
10	k	939	0	1012	84	0
11	l	1045	0	1117	89	0
12	m	1074	0	1157	50	0
13	n	961	0	1000	69	0
14	o	892	0	923	56	0
15	p	917	0	965	74	0
16	q	947	0	1022	64	0
17	r	816	0	839	52	0
18	s	857	0	922	37	0
19	t	739	0	807	52	0
20	u	780	0	834	55	0
21	v	753	0	780	50	0
22	w	575	0	592	33	0
23	x	625	0	655	42	0
24	y	509	0	543	26	0
25	z	449	0	491	33	0
26	A	523	0	524	57	0
27	B	444	0	461	30	0
28	C	410	0	440	24	0
29	D	377	0	418	25	0
30	E	504	0	574	43	0
31	F	302	0	343	17	0
32	G	1705	0	1732	151	0
33	H	1625	0	1699	139	0
34	I	1643	0	1710	138	0
35	J	1157	0	1199	105	0
36	K	818	0	808	67	0
37	L	1182	0	1240	121	0
38	M	979	0	1034	93	0
39	N	1022	0	1070	117	0
40	O	787	0	827	102	0
41	P	870	0	878	91	0
42	Q	955	0	1019	108	0
43	R	884	0	944	111	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	S	805	0	847	92	0
45	T	714	0	737	60	0
46	U	649	0	666	71	0
47	V	649	0	691	57	0
48	W	536	0	552	34	0
49	X	638	0	665	76	0
50	Y	665	0	714	62	0
51	Z	545	0	579	57	0
52	a	1027	0	1092	108	0
53	3	33012	0	16618	1181	0
54	1	62317	0	31346	1463	0
55	2	2568	0	1303	72	0
56	5	1647	0	831	32	0
57	6	1640	0	837	39	0
58	4	348	0	175	20	0
59	8	5312	0	5283	470	0
60	1	10	0	10	2	0
61	5	7	0	7	1	0
62	8	32	0	14	5	0
63	8	1	0	0	0	0
All	All	153370	0	105125	6522	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 6522 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)
40:O:40:ILE:N	40:O:40:ILE:CA	1.74	1.50
40:O:40:ILE:HA	53:3:1123:U:C5	1.46	1.48
40:O:40:ILE:CA	53:3:1123:U:C4	1.98	1.46
40:O:40:ILE:CA	53:3:1123:U:C5	2.08	1.35
40:O:40:ILE:HA	53:3:1123:U:C4	1.64	1.22

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%)	42 (16%)	4 (2%)	8	37
2	c	207/209 (99%)	174 (84%)	31 (15%)	2 (1%)	12	44
3	d	199/201 (99%)	165 (83%)	32 (16%)	2 (1%)	12	44
4	e	175/177 (99%)	143 (82%)	26 (15%)	6 (3%)	3	23
5	f	174/176 (99%)	150 (86%)	24 (14%)	0	100	100
6	g	121/149 (81%)	92 (76%)	26 (22%)	3 (2%)	4	28
7	h	82/131 (63%)	57 (70%)	20 (24%)	5 (6%)	1	12
8	i	72/141 (51%)	49 (68%)	18 (25%)	5 (7%)	1	10
9	j	140/142 (99%)	121 (86%)	18 (13%)	1 (1%)	18	51
10	k	120/122 (98%)	96 (80%)	22 (18%)	2 (2%)	7	35
11	l	141/143 (99%)	106 (75%)	29 (21%)	6 (4%)	2	18
12	m	134/136 (98%)	113 (84%)	19 (14%)	2 (2%)	8	37
13	n	118/120 (98%)	92 (78%)	26 (22%)	0	100	100
14	o	114/116 (98%)	98 (86%)	15 (13%)	1 (1%)	14	47
15	p	112/114 (98%)	96 (86%)	16 (14%)	0	100	100
16	q	115/117 (98%)	106 (92%)	9 (8%)	0	100	100
17	r	101/103 (98%)	84 (83%)	16 (16%)	1 (1%)	12	44
18	s	108/110 (98%)	94 (87%)	13 (12%)	1 (1%)	14	47
19	t	91/93 (98%)	79 (87%)	12 (13%)	0	100	100
20	u	100/102 (98%)	82 (82%)	18 (18%)	0	100	100
21	v	92/94 (98%)	78 (85%)	14 (15%)	0	100	100
22	w	73/75 (97%)	62 (85%)	11 (15%)	0	100	100
23	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	y	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
25	z	56/58 (97%)	48 (86%)	8 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	A	64/66 (97%)	54 (84%)	8 (12%)	2 (3%)	3	25
27	B	54/56 (96%)	46 (85%)	8 (15%)	0	100	100
28	C	48/50 (96%)	42 (88%)	6 (12%)	0	100	100
29	D	44/46 (96%)	33 (75%)	11 (25%)	0	100	100
30	E	62/64 (97%)	52 (84%)	9 (14%)	1 (2%)	7	36
31	F	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
32	G	216/225 (96%)	175 (81%)	36 (17%)	5 (2%)	5	30
33	H	204/206 (99%)	177 (87%)	26 (13%)	1 (0%)	24	57
34	I	203/205 (99%)	161 (79%)	40 (20%)	2 (1%)	12	44
35	J	155/157 (99%)	123 (79%)	24 (16%)	8 (5%)	1	14
36	K	98/100 (98%)	84 (86%)	10 (10%)	4 (4%)	2	19
37	L	149/151 (99%)	121 (81%)	28 (19%)	0	100	100
38	M	127/129 (98%)	109 (86%)	17 (13%)	1 (1%)	16	49
39	N	125/127 (98%)	97 (78%)	25 (20%)	3 (2%)	4	29
40	O	96/98 (98%)	80 (83%)	14 (15%)	2 (2%)	5	31
41	P	114/116 (98%)	84 (74%)	27 (24%)	3 (3%)	4	27
42	Q	121/123 (98%)	89 (74%)	28 (23%)	4 (3%)	3	23
43	R	112/114 (98%)	90 (80%)	20 (18%)	2 (2%)	6	34
44	S	98/100 (98%)	72 (74%)	24 (24%)	2 (2%)	6	32
45	T	86/88 (98%)	78 (91%)	6 (7%)	2 (2%)	5	30
46	U	80/82 (98%)	63 (79%)	12 (15%)	5 (6%)	1	12
47	V	78/80 (98%)	59 (76%)	18 (23%)	1 (1%)	9	39
48	W	63/65 (97%)	53 (84%)	8 (13%)	2 (3%)	3	24
49	X	77/79 (98%)	56 (73%)	18 (23%)	3 (4%)	2	20
50	Y	83/85 (98%)	75 (90%)	8 (10%)	0	100	100
51	Z	63/65 (97%)	37 (59%)	19 (30%)	7 (11%)	0	5
52	a	130/223 (58%)	104 (80%)	24 (18%)	2 (2%)	8	37
59	8	681/711 (96%)	541 (79%)	125 (18%)	15 (2%)	5	30
All	All	6517/6889 (95%)	5319 (82%)	1080 (17%)	118 (2%)	9	34

5 of 118 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	205	GLY
3	d	83	VAL
4	e	19	PHE
4	e	122	ASP
6	g	9	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	210 (97%)	6 (3%)	38	61
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	79
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	144 (97%)	4 (3%)	39	62
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	78
6	g	98/114 (86%)	97 (99%)	1 (1%)	68	75
7	h	66/100 (66%)	66 (100%)	0	100	100
8	i	60/109 (55%)	57 (95%)	3 (5%)	22	48
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	76
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	75
11	l	102/102 (100%)	97 (95%)	5 (5%)	22	48
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	76
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	73
15	p	99/99 (100%)	97 (98%)	2 (2%)	48	67
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	74
17	r	84/84 (100%)	81 (96%)	3 (4%)	31	57
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	72
20	u	83/83 (100%)	81 (98%)	2 (2%)	43	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	72
22	w	57/57 (100%)	56 (98%)	1 (2%)	51	69
23	x	67/67 (100%)	64 (96%)	3 (4%)	24	50
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	47 (98%)	1 (2%)	47	66
26	A	59/59 (100%)	59 (100%)	0	100	100
27	B	47/47 (100%)	45 (96%)	2 (4%)	26	51
28	C	45/45 (100%)	44 (98%)	1 (2%)	45	65
29	D	38/38 (100%)	38 (100%)	0	100	100
30	E	51/51 (100%)	50 (98%)	1 (2%)	48	67
31	F	34/34 (100%)	33 (97%)	1 (3%)	37	60
32	G	180/186 (97%)	176 (98%)	4 (2%)	45	65
33	H	170/170 (100%)	168 (99%)	2 (1%)	63	73
34	I	172/172 (100%)	169 (98%)	3 (2%)	53	70
35	J	119/119 (100%)	115 (97%)	4 (3%)	32	57
36	K	87/87 (100%)	84 (97%)	3 (3%)	32	57
37	L	124/124 (100%)	123 (99%)	1 (1%)	73	77
38	M	104/104 (100%)	102 (98%)	2 (2%)	50	68
39	N	105/105 (100%)	102 (97%)	3 (3%)	37	60
40	O	86/86 (100%)	84 (98%)	2 (2%)	44	64
41	P	89/89 (100%)	87 (98%)	2 (2%)	45	65
42	Q	103/103 (100%)	98 (95%)	5 (5%)	22	48
43	R	92/92 (100%)	90 (98%)	2 (2%)	45	65
44	S	83/83 (100%)	82 (99%)	1 (1%)	63	73
45	T	76/76 (100%)	74 (97%)	2 (3%)	40	62
46	U	65/65 (100%)	63 (97%)	2 (3%)	35	59
47	V	74/74 (100%)	72 (97%)	2 (3%)	39	62
48	W	56/56 (100%)	53 (95%)	3 (5%)	20	46
49	X	70/70 (100%)	68 (97%)	2 (3%)	37	60
50	Y	65/65 (100%)	65 (100%)	0	100	100
51	Z	55/55 (100%)	52 (94%)	3 (6%)	19	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
52	a	110/174 (63%)	108 (98%)	2 (2%)	51 69
59	8	566/585 (97%)	550 (97%)	16 (3%)	38 61
All	All	5428/5616 (97%)	5317 (98%)	111 (2%)	46 67

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	J	97	PRO
59	8	624	PRO
42	Q	2	THR
59	8	530	ASN
59	8	142	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
48	W	30	ASN
59	8	219	HIS
49	X	52	ASN
52	a	168	ASN
59	8	505	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	3	1538/1539 (99%)	245 (15%)	6 (0%)
54	1	2902/2903 (99%)	392 (13%)	12 (0%)
55	2	119/120 (99%)	14 (11%)	1 (0%)
56	5	76/77 (98%)	14 (18%)	1 (1%)
57	6	76/77 (98%)	17 (22%)	1 (1%)
58	4	15/16 (93%)	3 (20%)	0
All	All	4726/4732 (99%)	685 (14%)	21 (0%)

5 of 685 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	3	7	A
53	3	9	G
53	3	31	G

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

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	1	2296	U
54	1	2756	U
57	6	32	C
55	2	88	C
54	1	2391	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
60	FME	1	3001	61	8,9,10	1.13	0	8,9,11	0.87	0
62	GCP	8	801	63	32,34,34	2.20	6 (18%)	49,54,54	2.41	17 (34%)
61	PRO	5	101	56,60	6,7,8	0.46	0	7,8,10	1.31	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
60	FME	1	3001	61	-	2/7/9/11	-
62	GCP	8	801	63	-	8/19/38/38	0/3/3/3
61	PRO	5	101	56,60	-	0/0/9/11	0/1/1/1

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	-7.92	1.50	1.59
62	8	801	GCP	PB-O3A	-6.61	1.51	1.58
62	8	801	GCP	PG-O3G	-2.60	1.49	1.55
62	8	801	GCP	PB-O2B	-2.53	1.50	1.56
62	8	801	GCP	C1'-N9	2.46	1.54	1.47

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	8	801	GCP	C1'-N9-C8	-7.68	104.91	126.73
62	8	801	GCP	C1'-N9-C4	7.34	148.18	126.49
62	8	801	GCP	O3A-PA-O1A	-4.53	97.09	110.70
62	8	801	GCP	O3G-PG-O2G	4.37	120.42	107.96
62	8	801	GCP	O2G-PG-C3B	-3.83	97.11	106.40

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

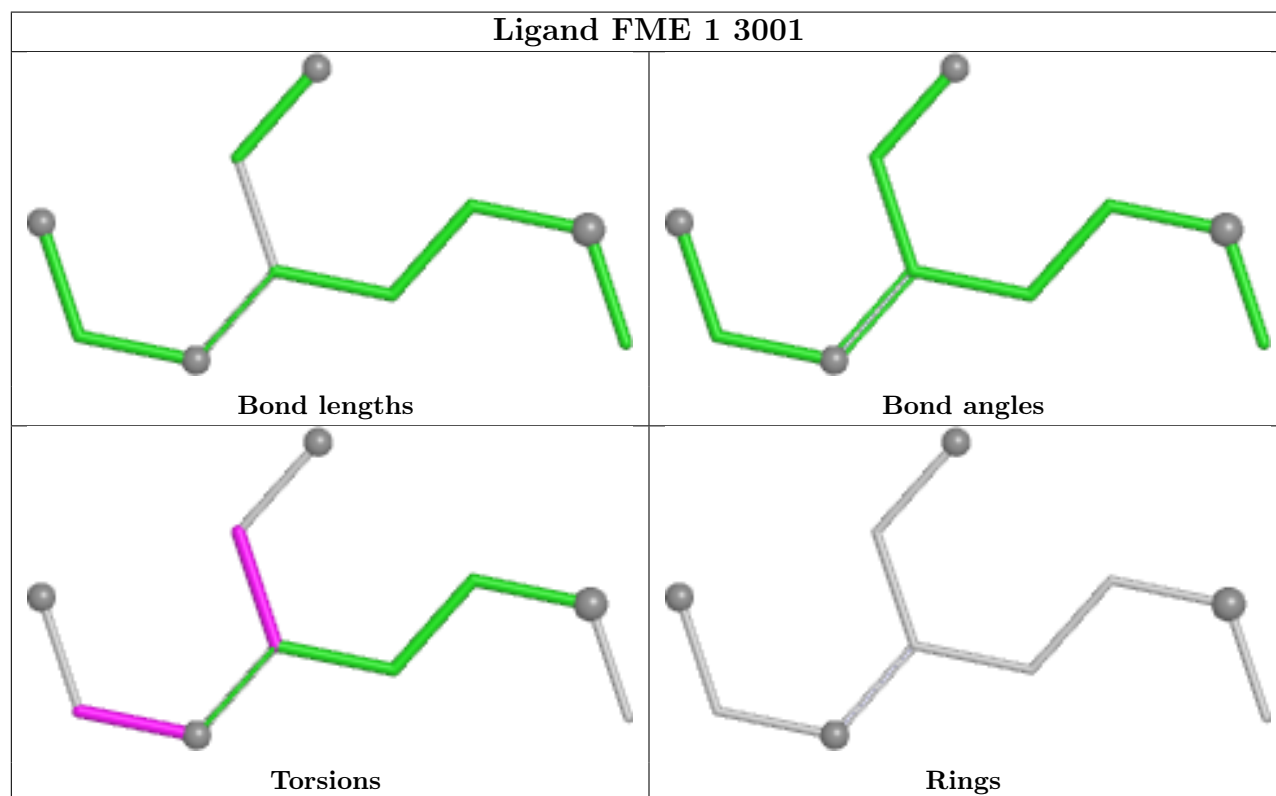
Mol	Chain	Res	Type	Atoms
60	1	3001	FME	O1-CN-N-CA
60	1	3001	FME	O-C-CA-CB
62	8	801	GCP	PB-C3B-PG-O1G
62	8	801	GCP	PB-C3B-PG-O2G
62	8	801	GCP	PG-C3B-PB-O1B

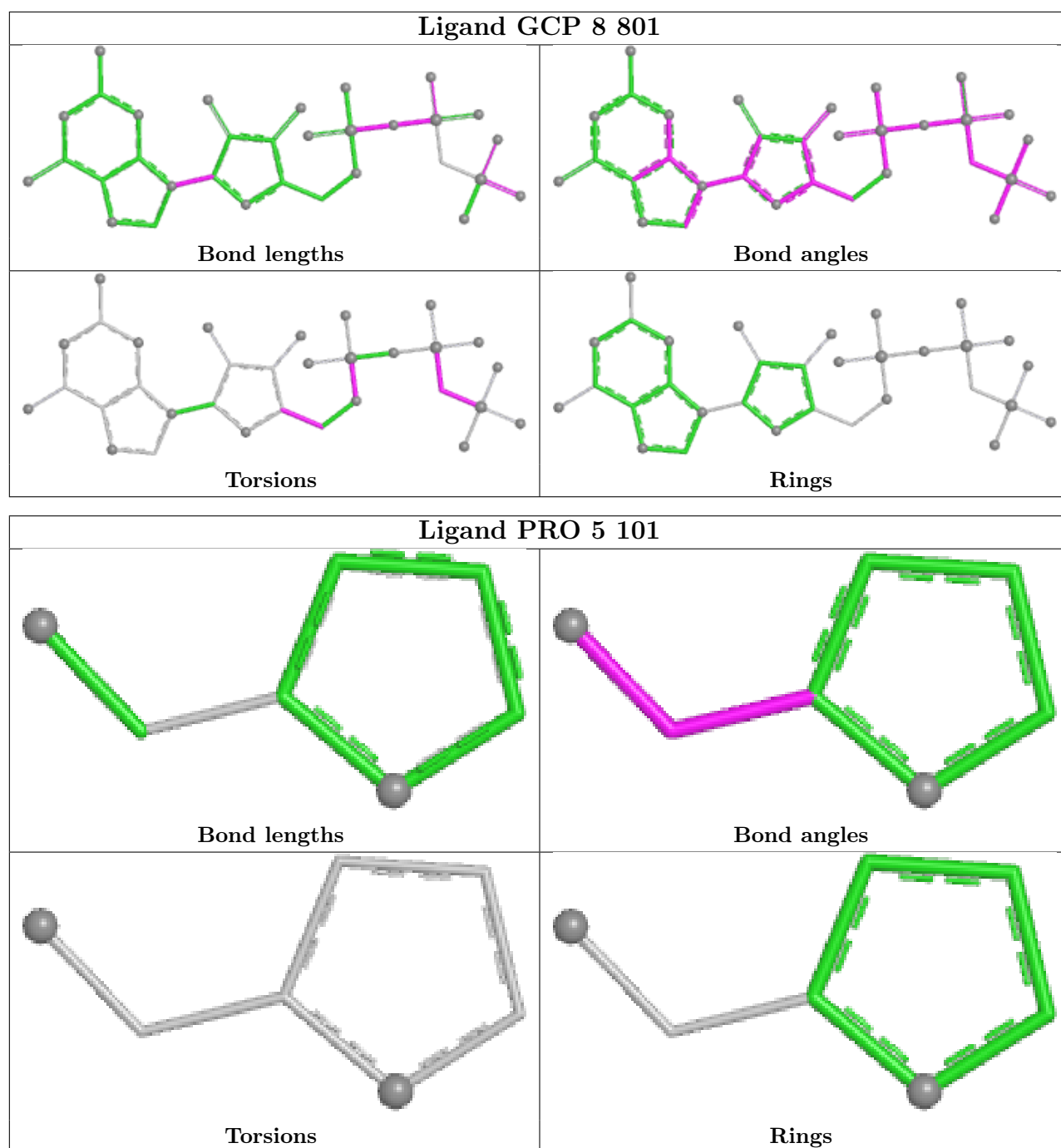
There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	1	3001	FME	2	0
62	8	801	GCP	5	0
61	5	101	PRO	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

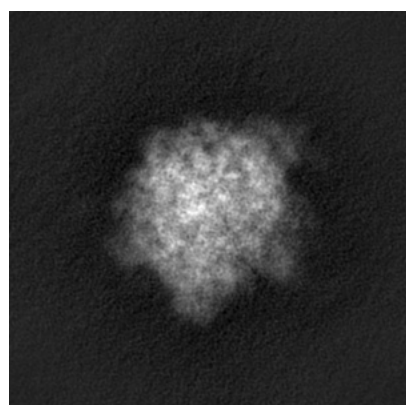
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22670. These allow visual inspection of the internal detail of the map and identification of artifacts.

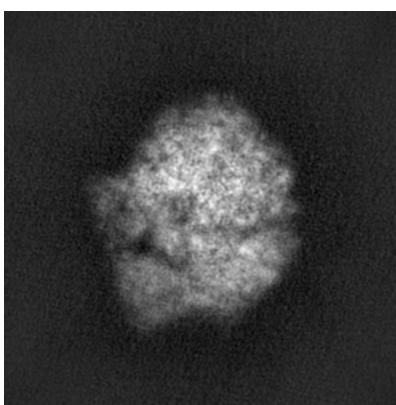
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

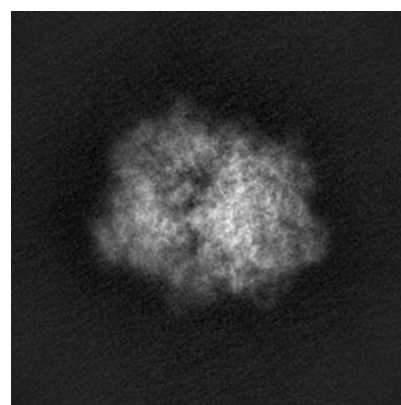
6.1.1 Primary map



X



Y

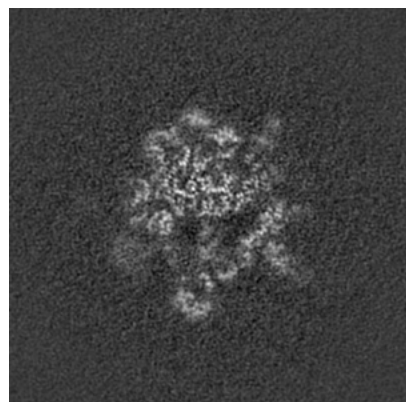


Z

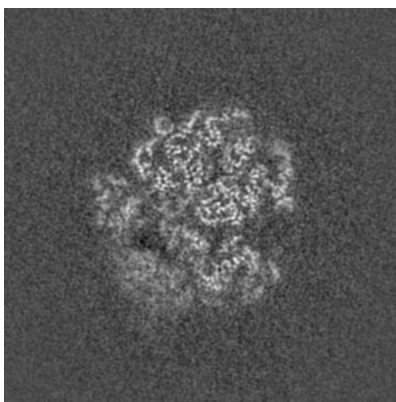
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

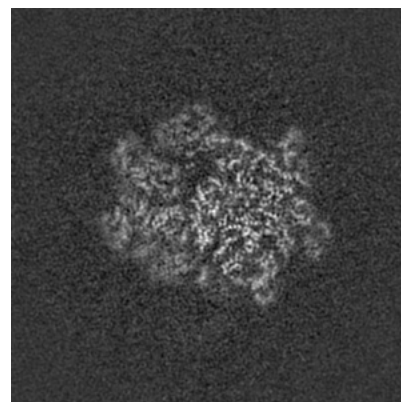
6.2.1 Primary map



X Index: 200



Y Index: 200

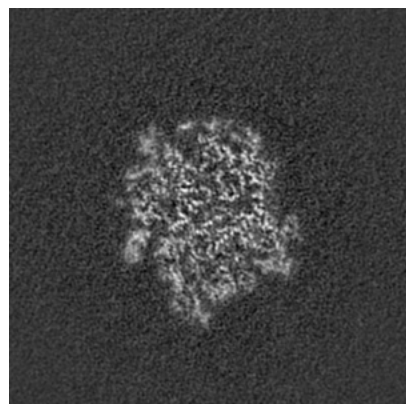


Z Index: 200

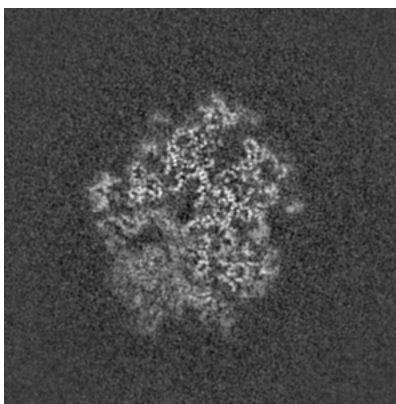
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

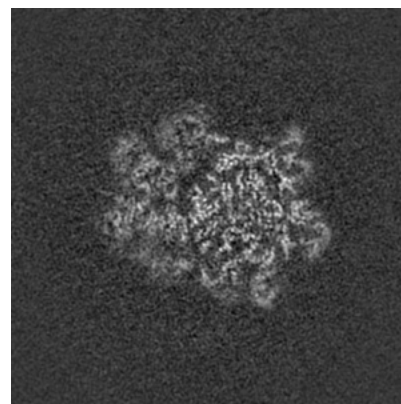
6.3.1 Primary map



X Index: 223



Y Index: 189

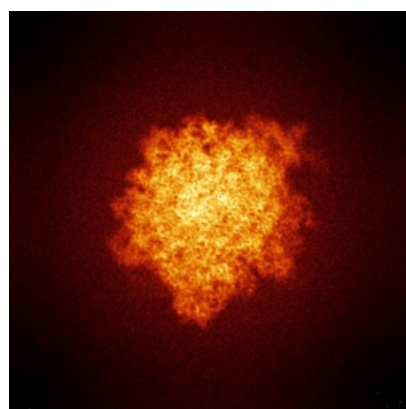


Z Index: 203

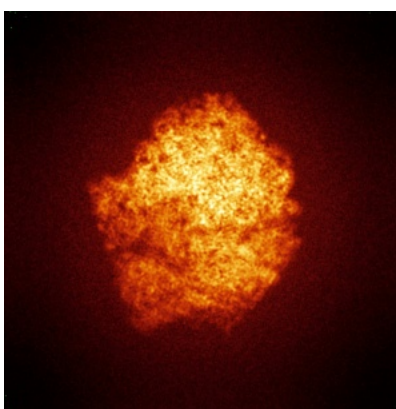
The images above show the largest variance slices of the map in three orthogonal directions.

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

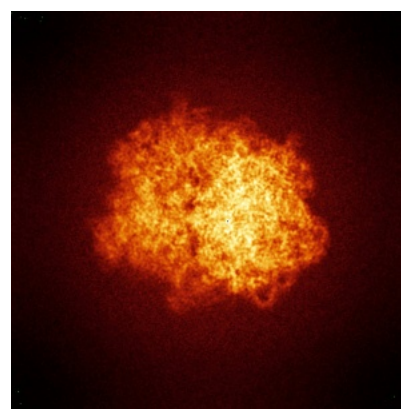
6.4.1 Primary map



X



Y

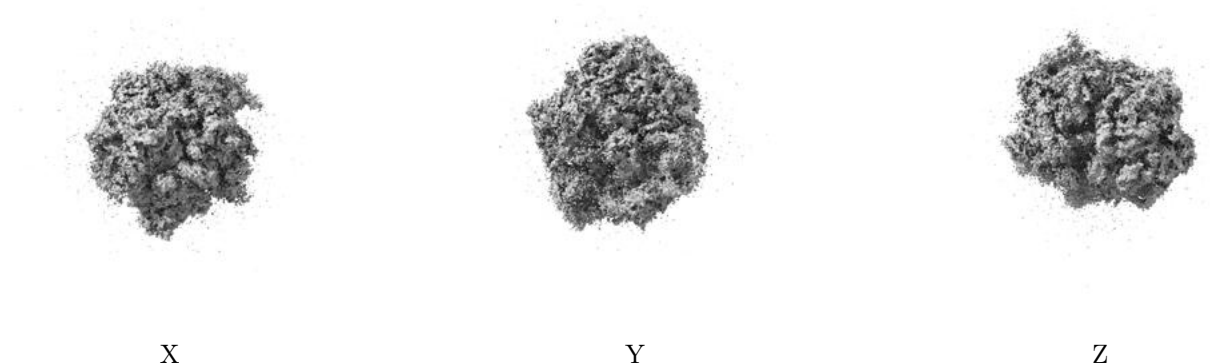


Z

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.

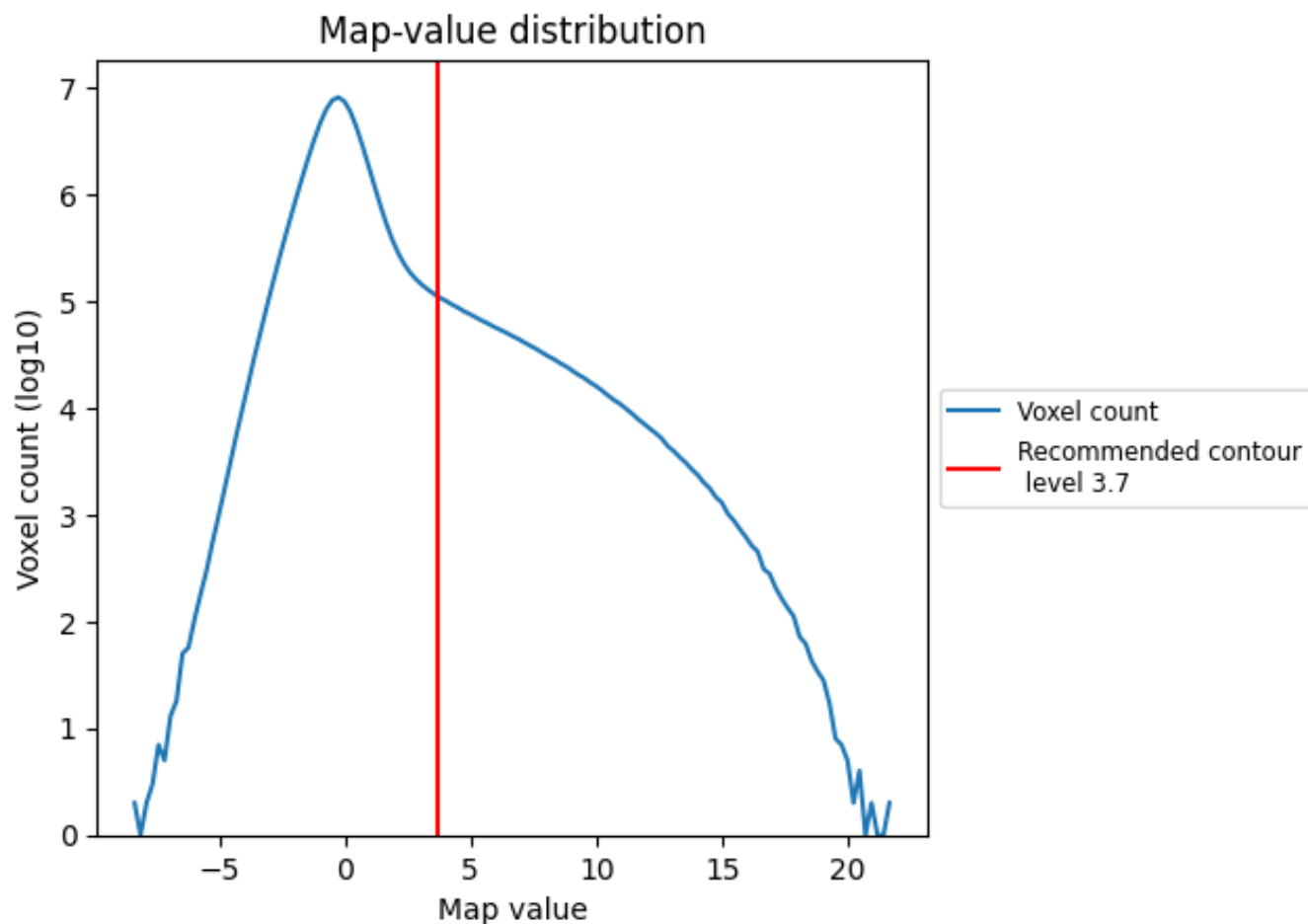
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

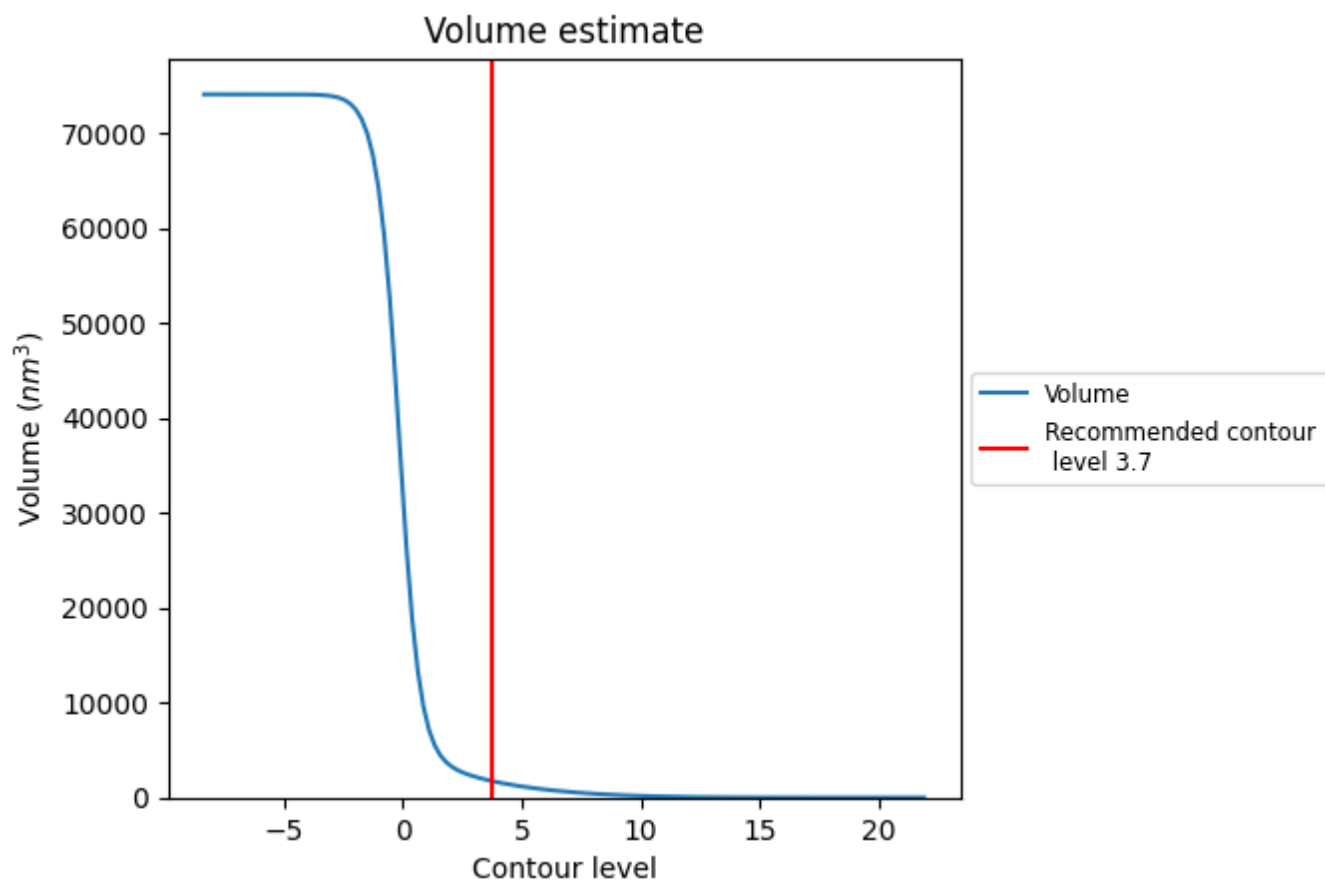
This section contains the results of statistical analysis of the map.

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.

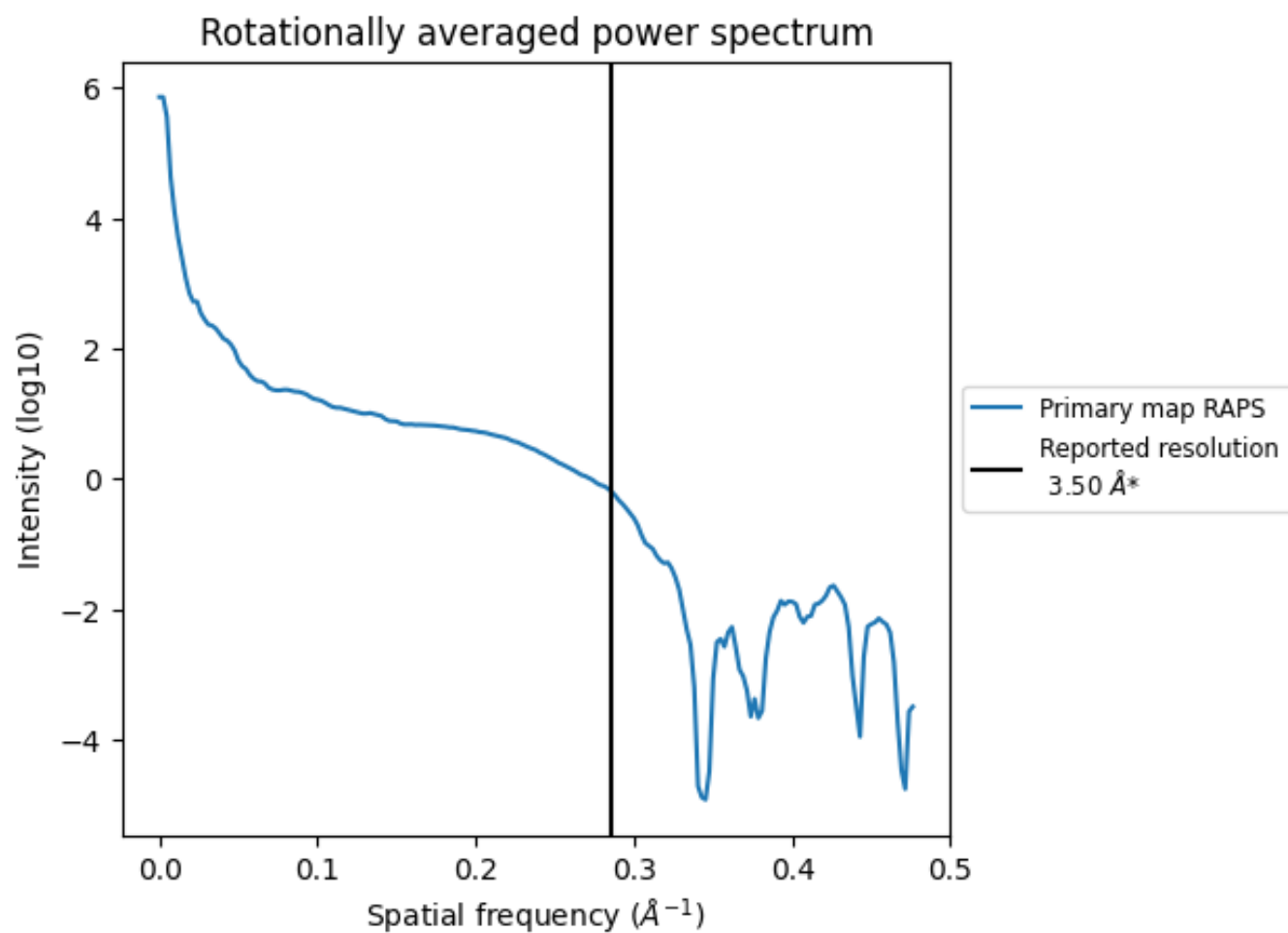
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1761 nm³; this corresponds to an approximate mass of 1590 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

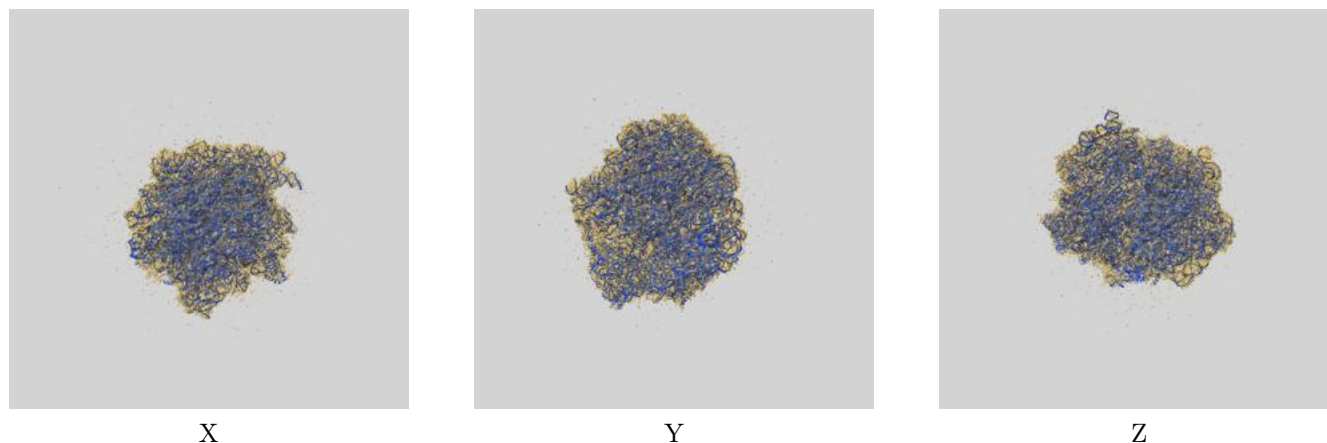
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

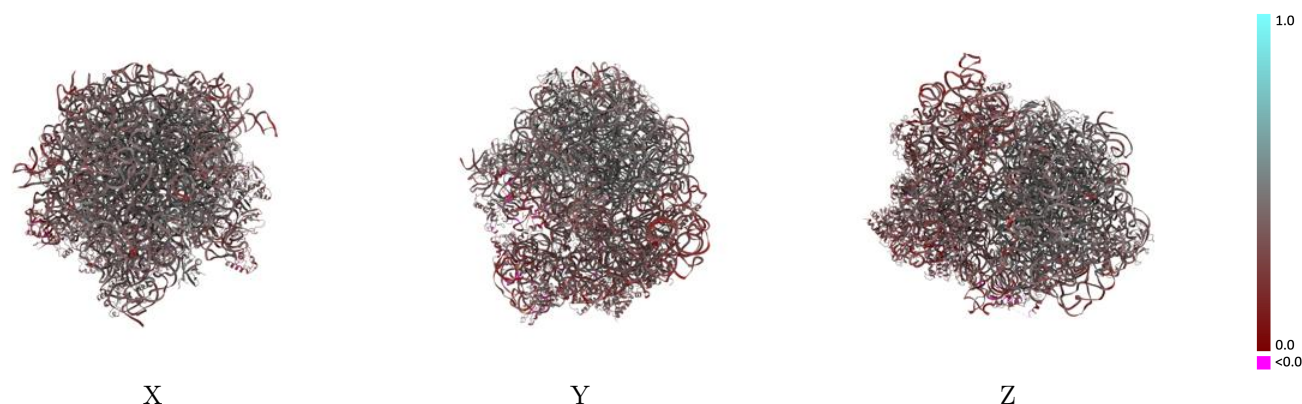
This section contains information regarding the fit between EMDB map EMD-22670 and PDB model 7K51. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



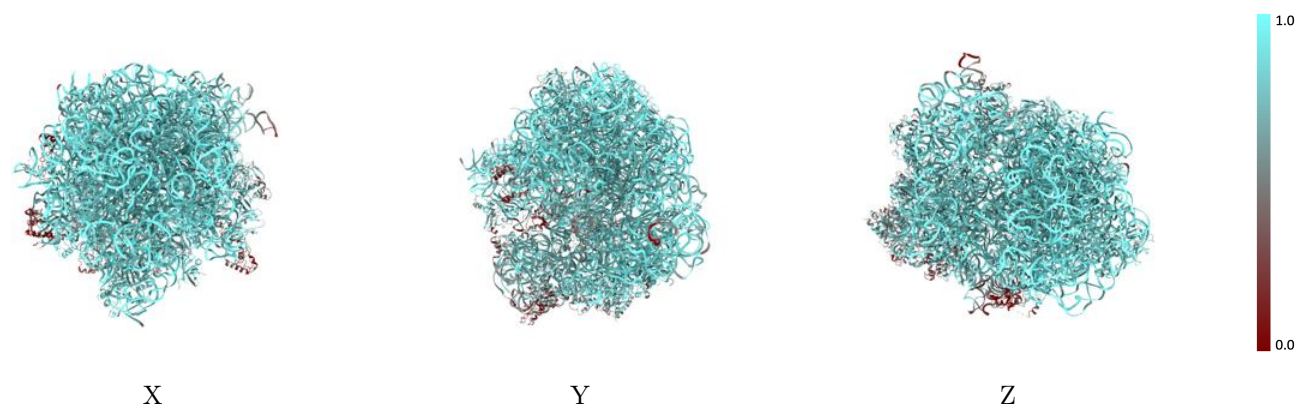
The images above show the 3D surface view of the map at the recommended contour level 3.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



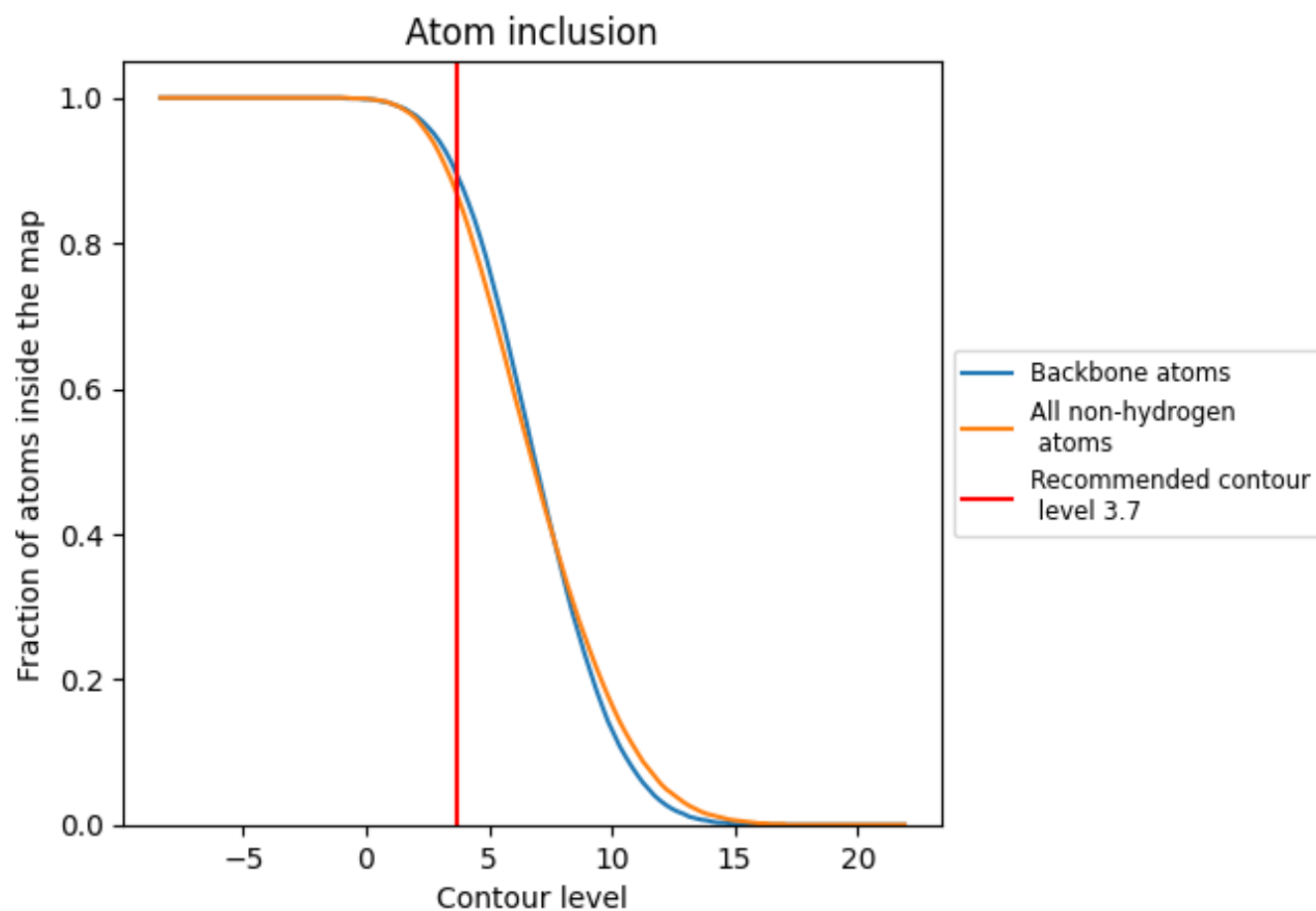
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 89% of all backbone atoms, 87% 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	 0.8670	 0.3690
1	 0.9600	 0.4030
2	 0.9510	 0.3720
3	 0.8870	 0.3140
4	 0.6520	 0.2280
5	 0.8080	 0.2890
6	 0.8420	 0.2660
8	 0.7170	 0.3480
A	 0.6130	 0.2710
B	 0.8970	 0.4310
C	 0.6320	 0.3830
D	 0.9070	 0.4600
E	 0.8720	 0.4550
F	 0.8730	 0.4570
G	 0.5820	 0.3250
H	 0.5880	 0.3240
I	 0.7540	 0.3240
J	 0.8330	 0.3820
K	 0.7840	 0.3490
L	 0.3720	 0.2830
M	 0.8290	 0.3810
N	 0.5530	 0.2890
O	 0.4070	 0.2980
P	 0.8250	 0.3530
Q	 0.8140	 0.3820
R	 0.5070	 0.2930
S	 0.7420	 0.3140
T	 0.8350	 0.3440
U	 0.8010	 0.3660
V	 0.7950	 0.3460
W	 0.8020	 0.3390
X	 0.6980	 0.3040
Y	 0.7780	 0.3160
Z	 0.6200	 0.3060
a	 0.2230	 0.2200



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Chain	Atom inclusion	Q-score
b	 0.9020	 0.4470
c	 0.8800	 0.4440
d	 0.7820	 0.4080
e	 0.7850	 0.3540
f	 0.8420	 0.3980
g	 0.2730	 0.2880
h	 0.2270	 0.2420
i	 0.2630	 0.2480
j	 0.8790	 0.4450
k	 0.8610	 0.4460
l	 0.8810	 0.4330
m	 0.8870	 0.4510
n	 0.9060	 0.4370
o	 0.8440	 0.3980
p	 0.8940	 0.4390
q	 0.8820	 0.4370
r	 0.8220	 0.4180
s	 0.8680	 0.4340
t	 0.8290	 0.4110
u	 0.8150	 0.3930
v	 0.8420	 0.4320
w	 0.8870	 0.4550
x	 0.8970	 0.4300
y	 0.7560	 0.3580
z	 0.8720	 0.4430