



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:40 AM UTC

PDB ID : 5UYL / pdb_00005uyL
EMDB ID : EMD-8616
Title : 70S ribosome bound with cognate ternary complex base-paired to A site codon (Structure II)
Authors : Loveland, A.B.; Demo, G.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2017-02-24
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

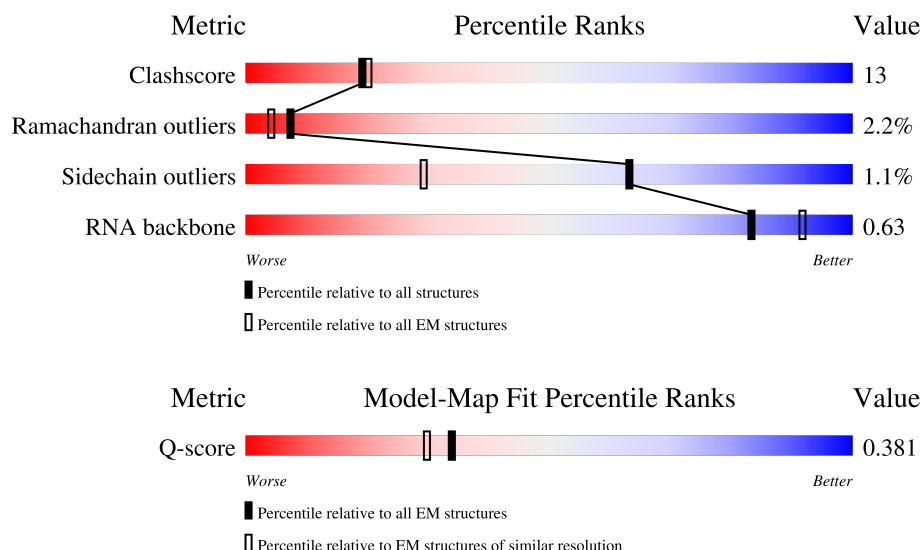
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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.



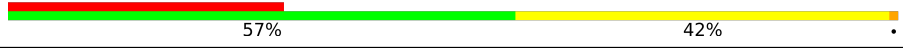
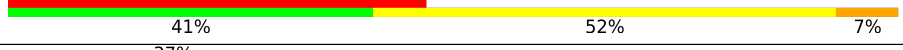
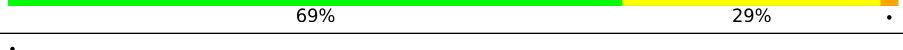
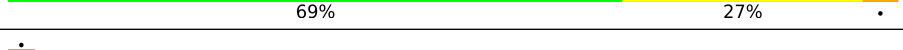
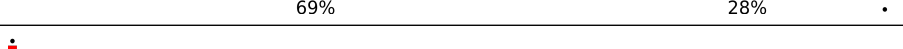
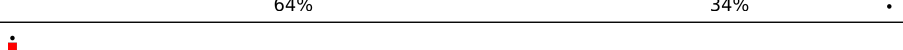
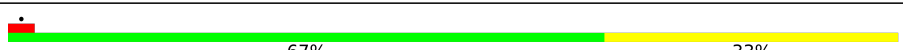
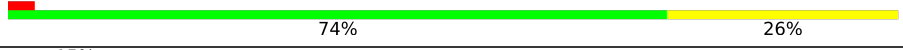
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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

Mol	Chain	Length	Quality of chain
1	04	271	
2	05	209	
3	06	201	

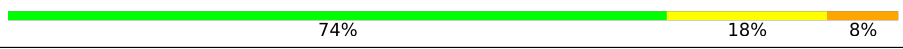
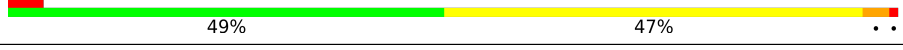
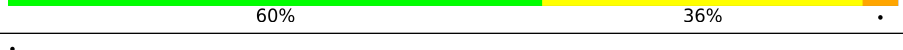
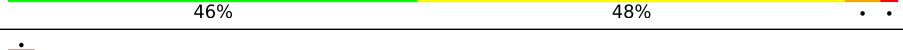
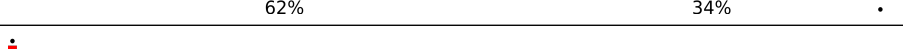
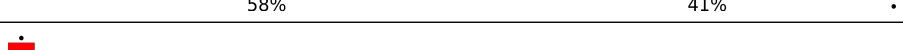
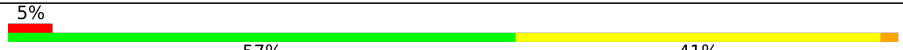
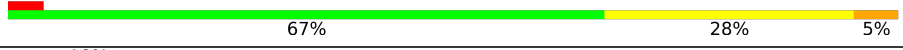
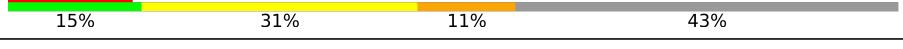
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Mol	Chain	Length	Quality of chain
4	07	177	
5	08	176	
6	09	149	
7	10	131	
8	11	141	
9	12	142	
10	13	122	
11	14	143	
12	15	136	
13	16	120	
14	17	116	
15	18	114	
16	19	117	
17	20	103	
18	21	110	
19	22	93	
20	23	102	
21	24	94	
22	25	75	
23	26	77	
24	27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

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Mol	Chain	Length	Quality of chain
29	32	46	
30	33	64	
31	34	38	
32	B	218	
33	C	206	
34	D	205	
35	E	157	
36	F	100	
37	G	151	
38	H	129	
39	I	127	
40	J	98	
41	K	116	
42	L	123	
43	M	114	
44	N	100	
45	O	88	
46	P	82	
47	Q	80	
48	R	65	
49	S	79	
50	T	85	
51	U	65	
52	03	234	
53	A	1539	

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Mol	Chain	Length	Quality of chain
54	01	2903	
55	02	120	
56	W	77	
56	X	77	
57	V	18	
58	Y	76	
59	Z	392	

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 153753 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	04	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	05	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	06	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	07	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	F	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	03	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	01	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
01	747	C	U	conflict	GB 802133627

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

Mol	Chain	Residues	Atoms					AltConf	Trace
55	02	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

- Molecule 56 is a RNA chain called tRNAfMet.

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

- Molecule 57 is a RNA chain called mRNA.

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

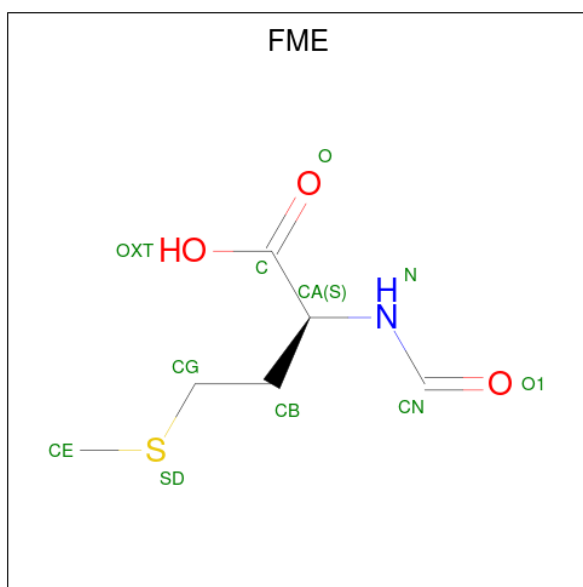
- Molecule 58 is a RNA chain called tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Y	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

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

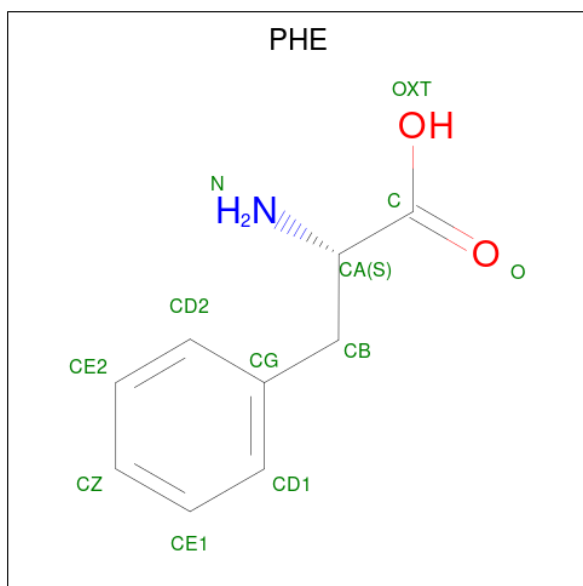
Mol	Chain	Residues	Atoms					AltConf	Trace
59	Z	392	Total	C	N	O	S	0	0
			3029	1915	521	580	13		

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



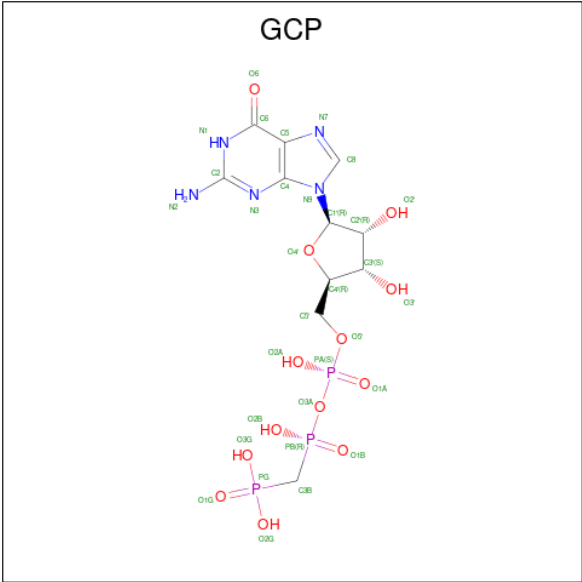
Mol	Chain	Residues	Atoms					AltConf
60	W	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 61 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



Mol	Chain	Residues	Atoms					AltConf
61	Y	1	Total	C	N	O		0
			11	9	1	1		

- Molecule 62 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

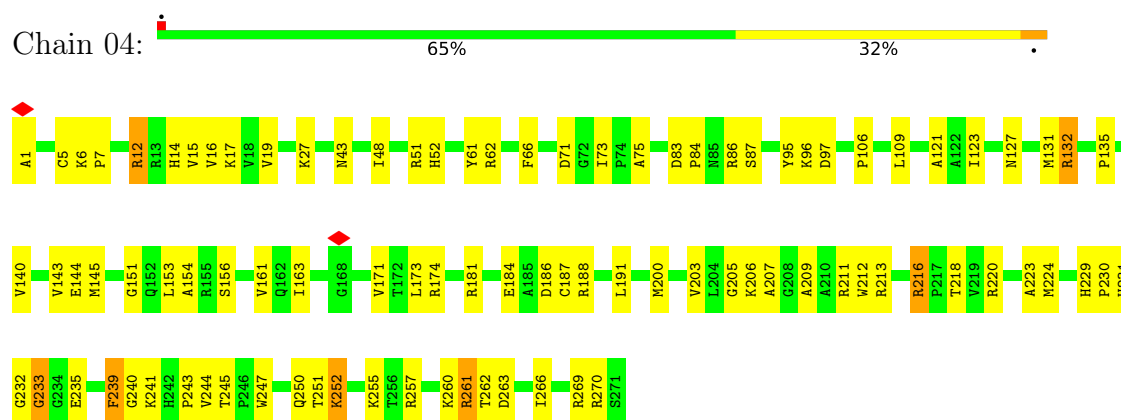


Mol	Chain	Residues	Atoms					AltConf
62	Z	1	Total	C	N	O	P	0
			32	11	5	13	3	

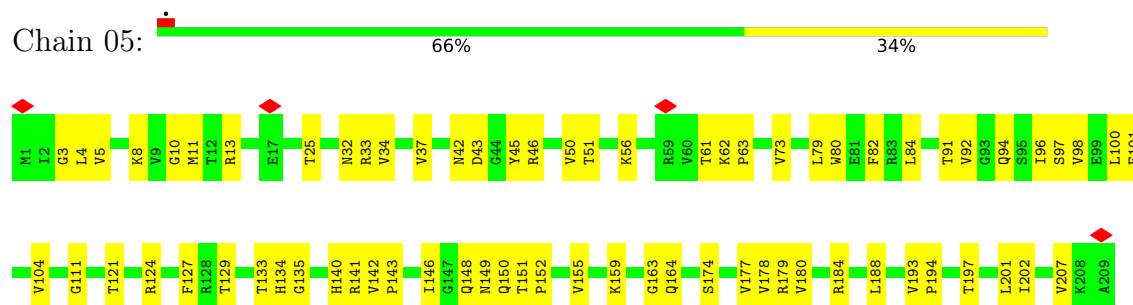
3 Residue-property plots

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

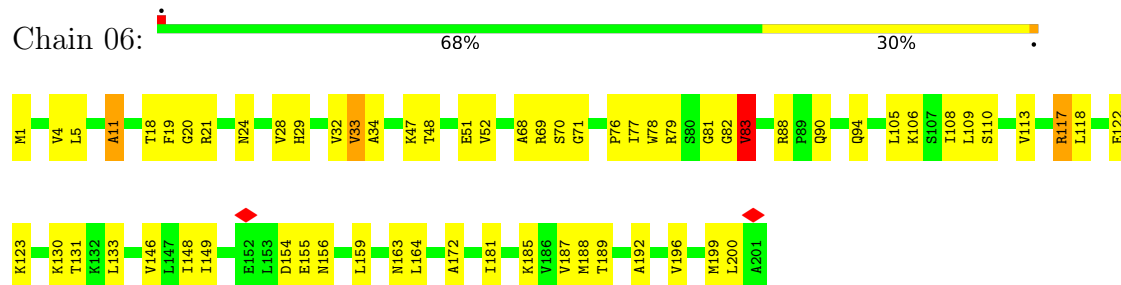
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

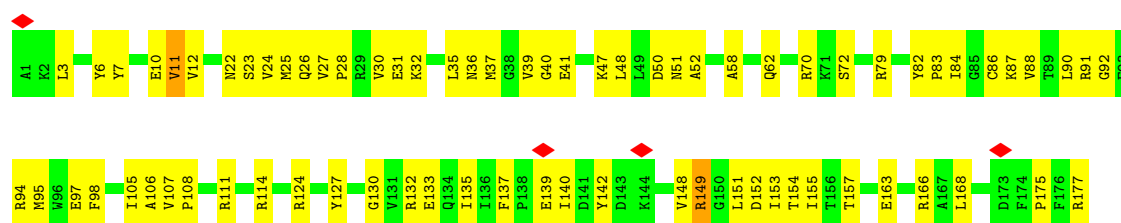


• Molecule 3: 50S ribosomal protein L4



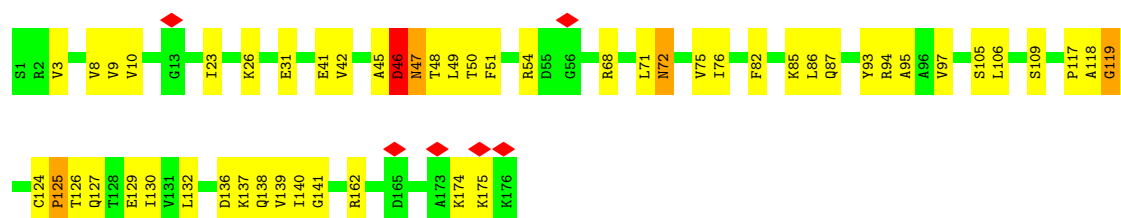
• Molecule 4: 50S ribosomal protein L5

Chain 07: 



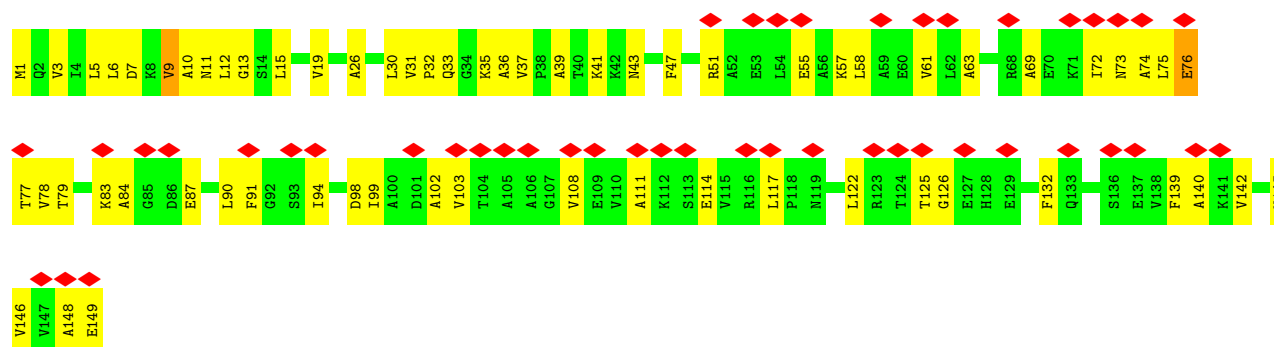
- Molecule 5: 50S ribosomal protein L6

Chain 08: 



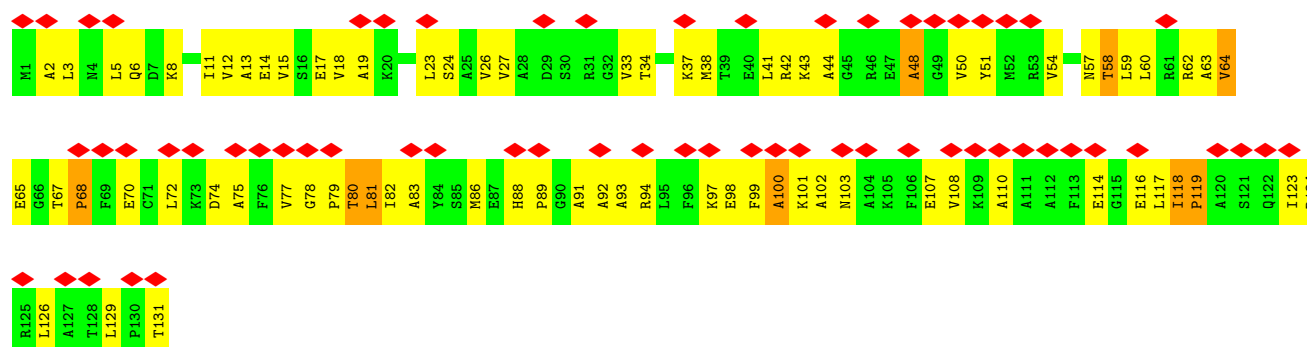
- Molecule 6: 50S ribosomal protein L9

Chain 09: 

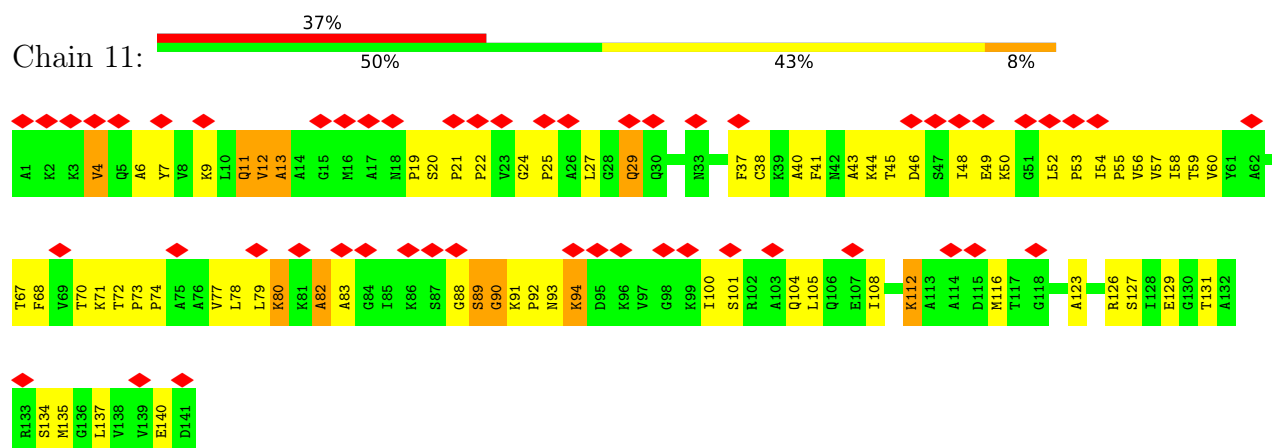


- Molecule 7: 50S ribosomal protein L10

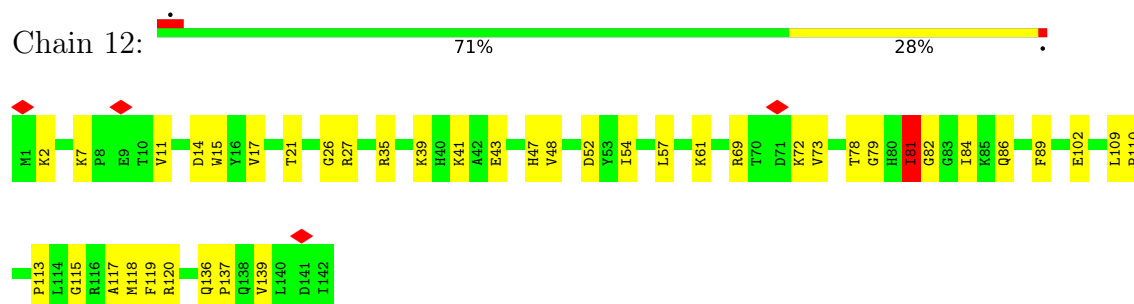
Chain 10: 



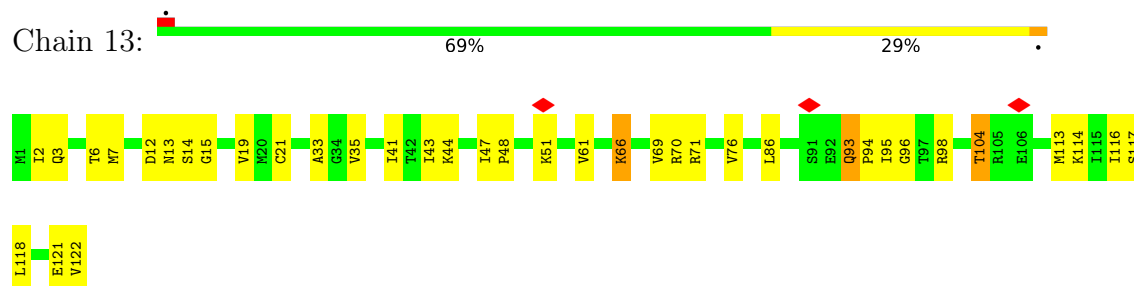
- Molecule 8: 50S ribosomal protein L11



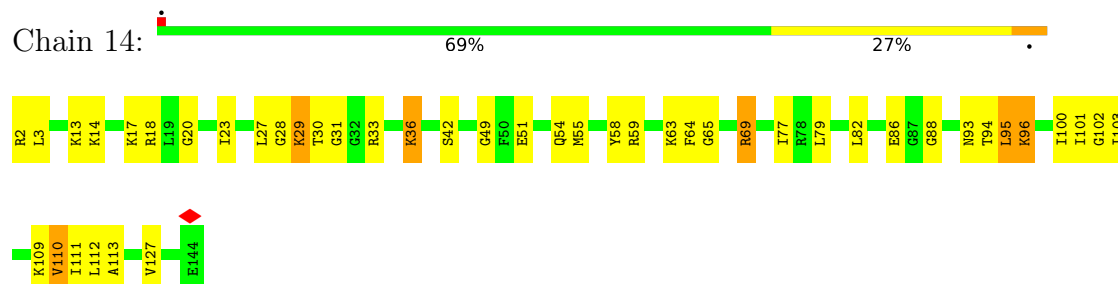
- Molecule 9: 50S ribosomal protein L13



- Molecule 10: 50S ribosomal protein L14

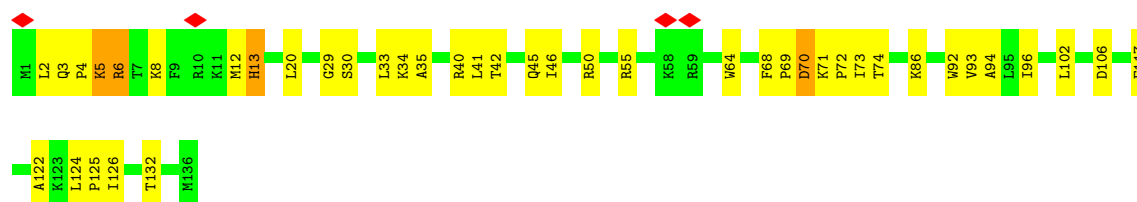


- Molecule 11: 50S ribosomal protein L15

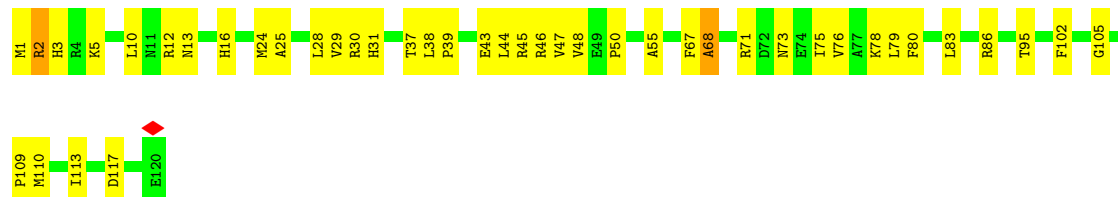


- Molecule 12: 50S ribosomal protein L16





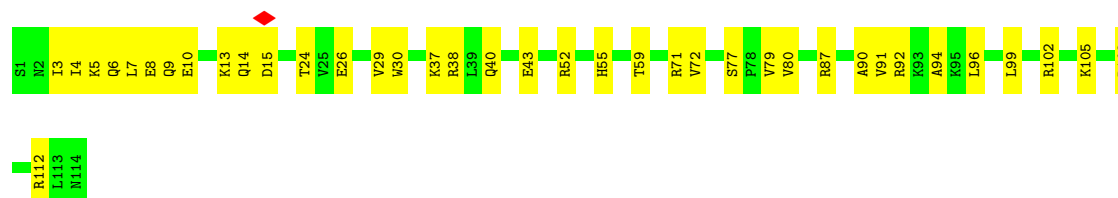
- Molecule 13: 50S ribosomal protein L17



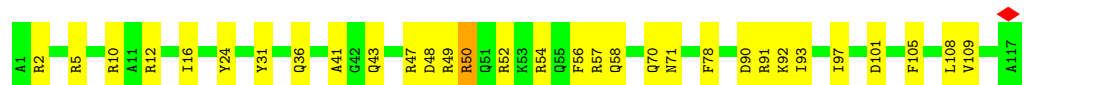
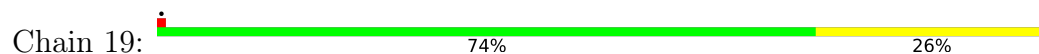
- Molecule 14: 50S ribosomal protein L18



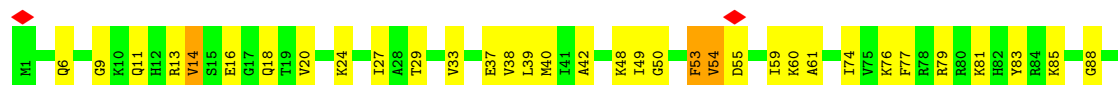
- Molecule 15: 50S ribosomal protein L19

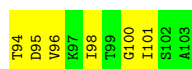


- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21





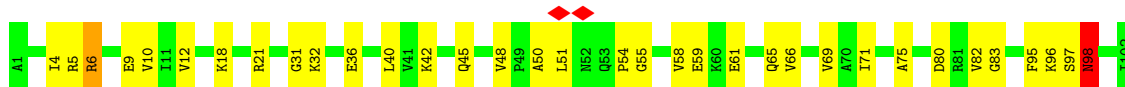
- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23



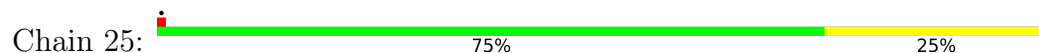
- Molecule 20: 50S ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25



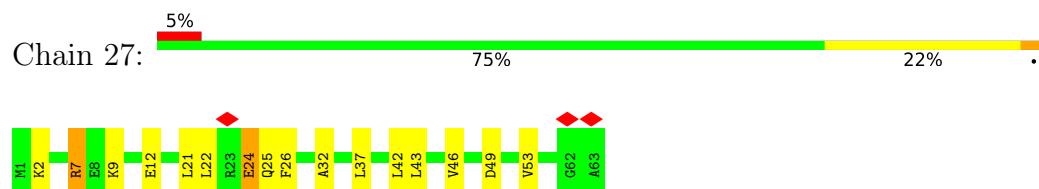
- Molecule 22: 50S ribosomal protein L27



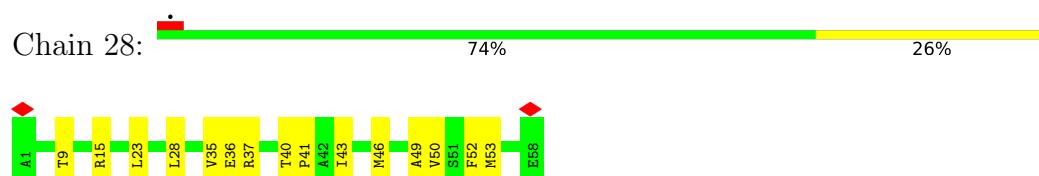
- Molecule 23: 50S ribosomal protein L28



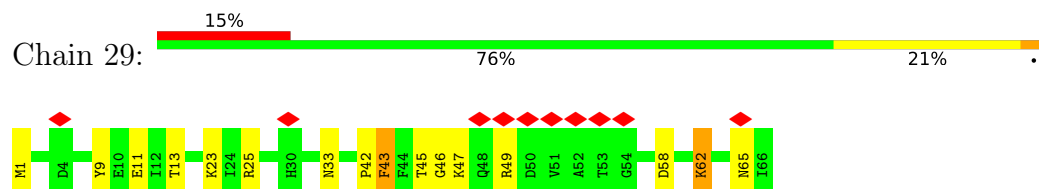
- Molecule 24: 50S ribosomal protein L29



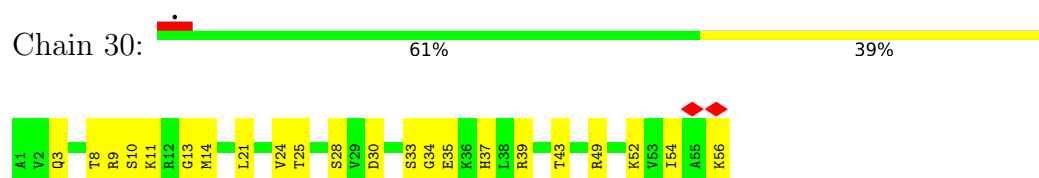
- Molecule 25: 50S ribosomal protein L30



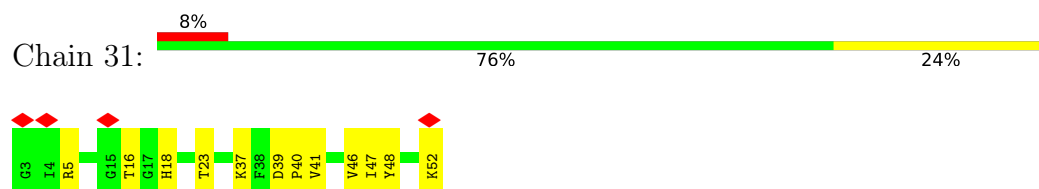
- Molecule 26: 50S ribosomal protein L31



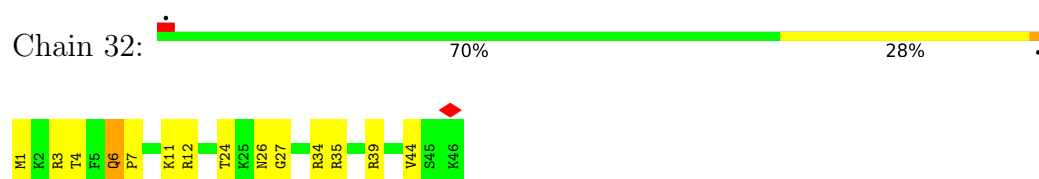
- Molecule 27: 50S ribosomal protein L32



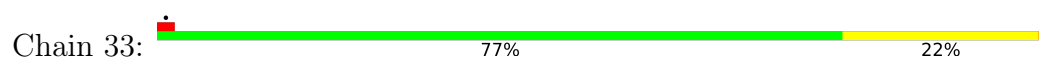
- Molecule 28: 50S ribosomal protein L33

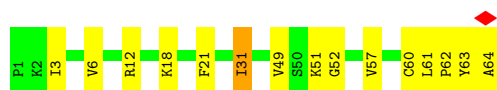


- Molecule 29: 50S ribosomal protein L34

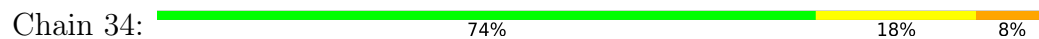


- Molecule 30: 50S ribosomal protein L35

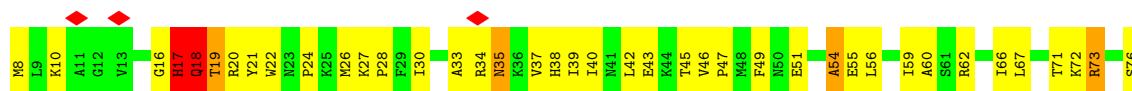




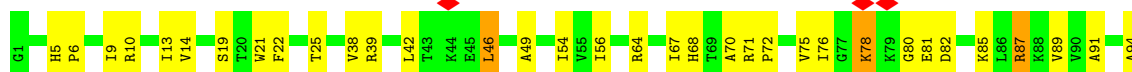
- Molecule 31: 50S ribosomal protein L36



- Molecule 32: 30S ribosomal protein S2



- Molecule 33: 30S ribosomal protein S3

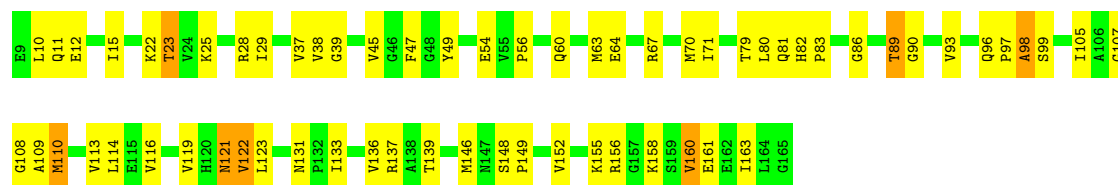


- Molecule 34: 30S ribosomal protein S4

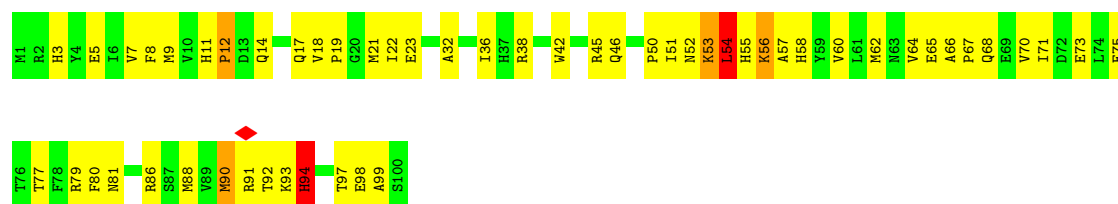




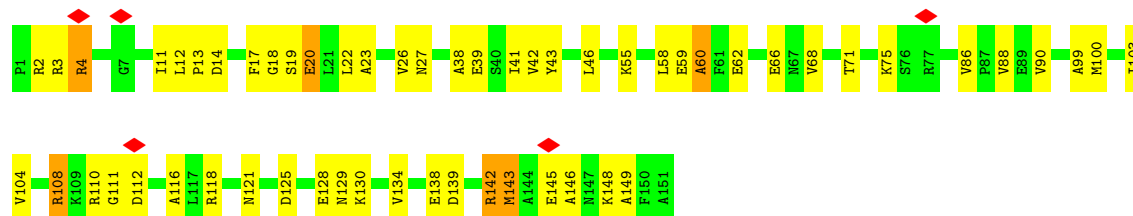
- Molecule 35: 30S ribosomal protein S5



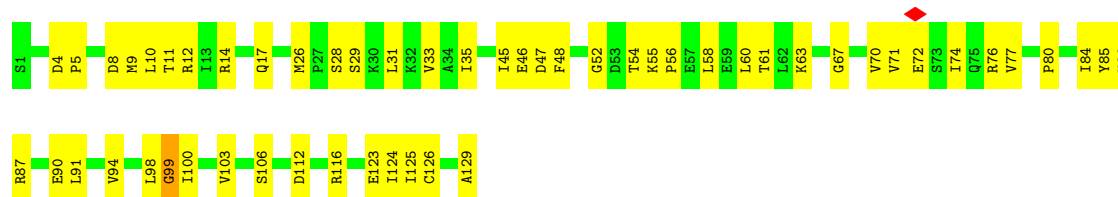
- Molecule 36: 30S ribosomal protein S6



- Molecule 37: 30S ribosomal protein S7

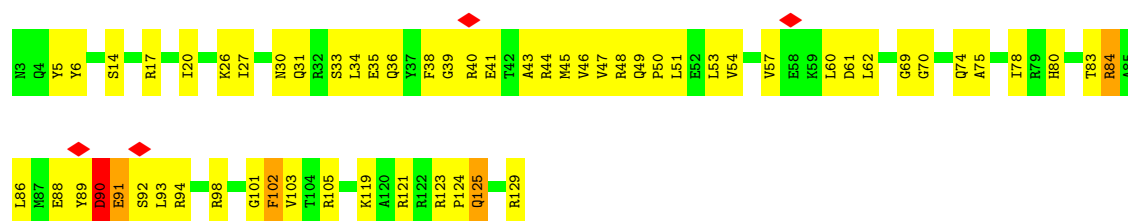


- Molecule 38: 30S ribosomal protein S8

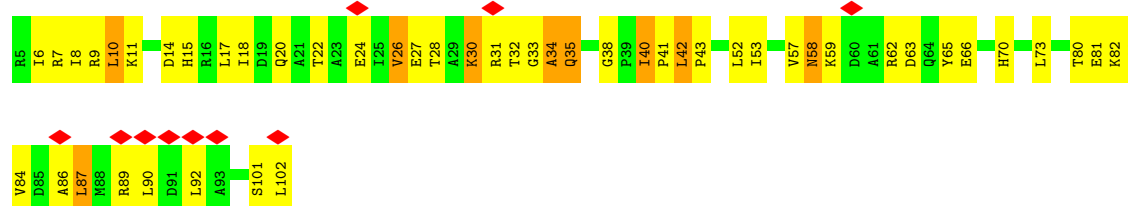


- Molecule 39: 30S ribosomal protein S9

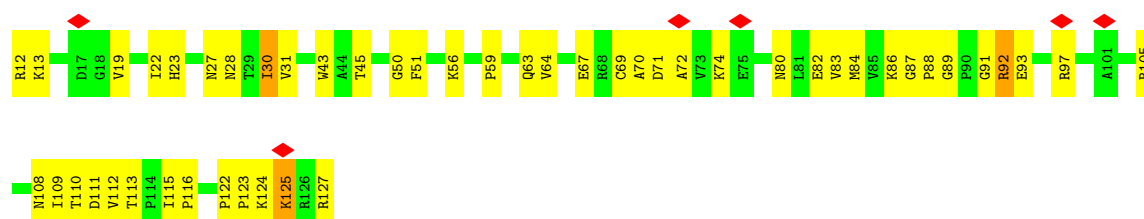




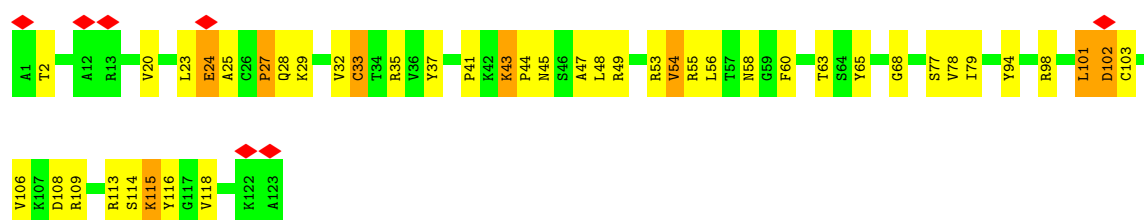
- Molecule 40: 30S ribosomal protein S10



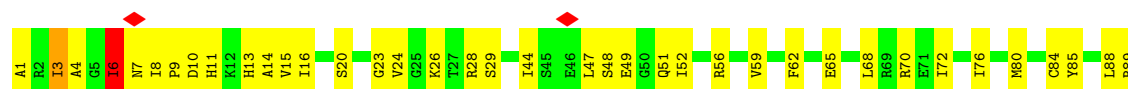
- Molecule 41: 30S ribosomal protein S11



- Molecule 42: 30S ribosomal protein S12

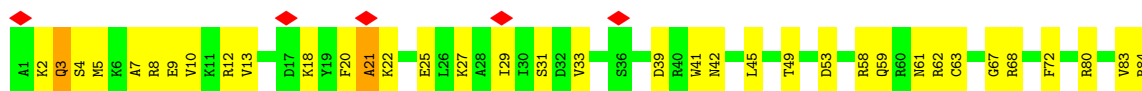


- Molecule 43: 30S ribosomal protein S13

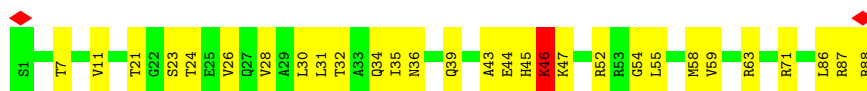




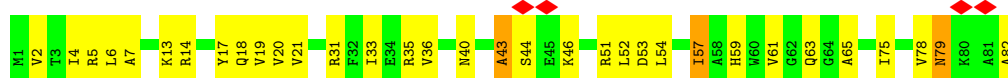
- Molecule 44: 30S ribosomal protein S14



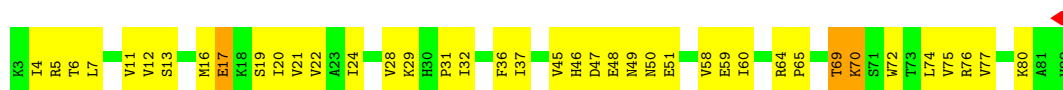
- Molecule 45: 30S ribosomal protein S15



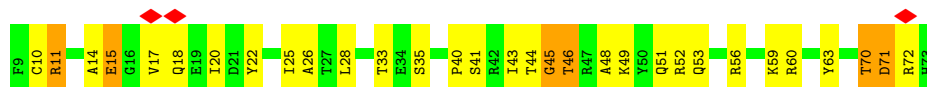
- Molecule 46: 30S ribosomal protein S16



- Molecule 47: 30S ribosomal protein S17

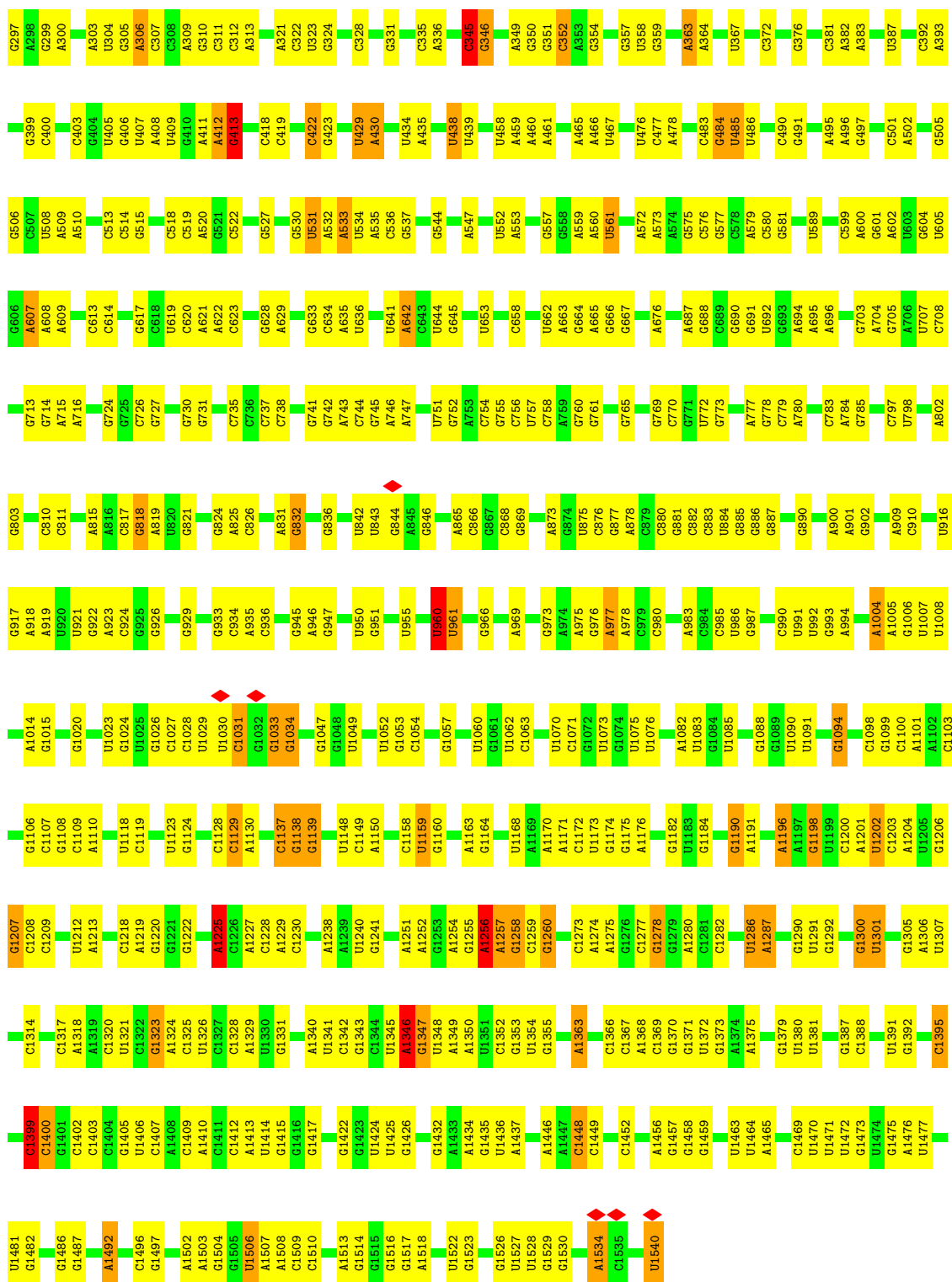


- Molecule 48: 30S ribosomal protein S18



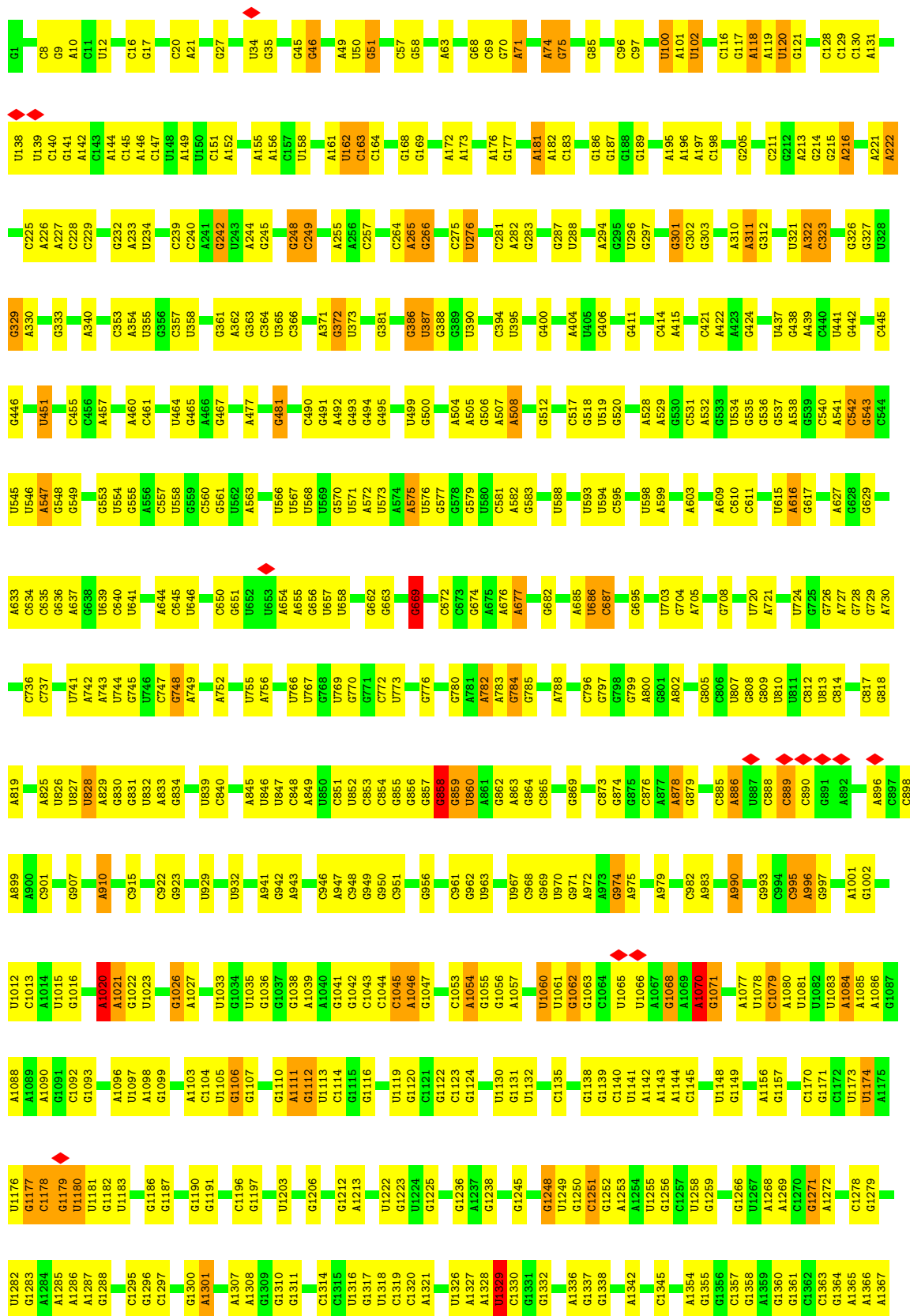
- Molecule 49: 30S ribosomal protein S19



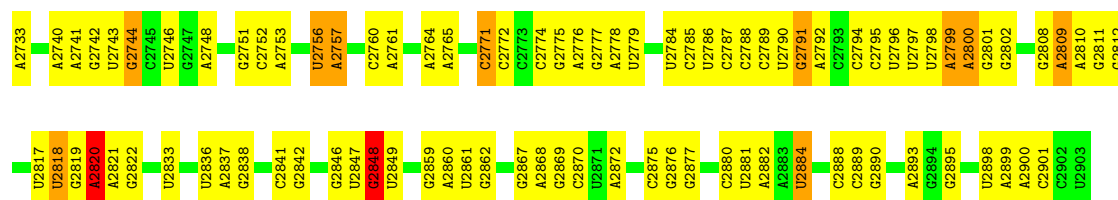


• Molecule 54: 23S ribosomal RNA



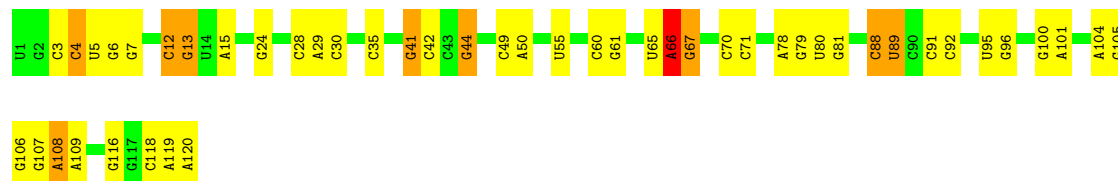


G2631	G2632	G2633	G2634	G2635	G2636	G2637	G2638	G2639	G2640	G2641	G2645	G2647	G2648	G2649	G2655	G2680	G2681	G2682	G2683	G2684	G2685	G2686	G2689	G2690	G2691	G2692	G2693	G2697	G2698	G2699	G2700	G2705	G2706	G2707	G2708	G2710	G2711	G2712	G2713	G2714	G2715	G2716	G2717	G2718	G2719	G2720	G2723	G2724	G2731	G2732																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
U2537	G2429	A2430	U2431	A2432	A2435	U2441	G2445	G2448	G2449	A2450	G2451	G2452	G2464	G2465	G2466	G2467	A2468	A2469	G2475	A2476	U2477	A2478	U2479	G2480	G2481	G2485	G2486	G2487	G2488	G2489	G2497	G2498	G2499	G2502	A2503	U2504	G2505	G2512	A2513	U2514	G2515	A2518	G2529	A2530	U2533	A2534	G2537																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
U2538	G2539	G2540	U2541	G2542	G2543	G2544	G2545	G2546	G2547	G2548	G2549	G2550	G2551	G2552	G2553	G2554	G2555	G2556	G2557	G2558	G2559	G2560	G2561	G2562	G2563	G2564	G2565	G2566	G2567	G2568	G2569	G2570	G2571	G2572	G2573	G2574	G2575	G2576	G2577	G2578	G2579	G2580	G2581	G2582	G2583	G2584	G2585	G2586	G2587	G2588	G2589	G2590	G2591	G2592	G2593	G2594	G2595	G2596	G2597	G2598	G2599	G2600	G2601	G2602	G2603	G2604	G2605	G2606	G2607	G2608	G2609	G2610	G2611	G2612	G2613	G2614	G2615	G2616	G2617	G2618	G2619	G2620	G2621	G2622	G2623	G2624	G2625	G2626	G2627	G2628	G2629	G2630	G2631	G2632	G2633	G2634	G2635	G2636	G2637	G2638	G2639	G2640	G2641	G2642	G2643	G2644	G2645	G2646	G2647	G2648	G2649	G2650	G2651	G2652	G2653	G2654	G2655	G2656	G2657	G2658	G2659	G2660	G2661	G2662	G2663	G2664	G2665	G2666	G2667	G2668	G2669	G2670	G2671	G2672	G2673	G2674	G2675	G2676	G2677	G2678	G2679	G2680	G2681	G2682	G2683	G2684	G2685	G2686	G2687	G2688	G2689	G2690	G2691	G2692	G2693	G2694	G2695	G2696	G2697	G2698	G2699	G2700	G2701	G2702	G2703	G2704	G2705	G2706	G2707	G2708	G2709	G2710	G2711	G2712	G2713	G2714	G2715	G2716	G2717	G2718	G2719	G2720	G2721	G2722	G2723	G2724	G2725	G2726	G2727	G2728	G2729	G2730	G2731	G2732	G2733	G2734	G2735	G2736	G2737	G2738	G2739	G2740	G2741	G2742	G2743	G2744	G2745	G2746	G2747	G2748	G2749	G2750	G2751	G2752	G2753	G2754	G2755	G2756	G2757	G2758	G2759	G2760	G2761	G2762	G2763	G2764	G2765	G2766	G2767	G2768	G2769	G2770	G2771	G2772	G2773	G2774	G2775	G2776	G2777	G2778	G2779	G2780	G2781	G2782	G2783	G2784	G2785	G2786	G2787	G2788	G2789	G2790	G2791	G2792	G2793	G2794	G2795	G2796	G2797	G2798	G2799	G2800	G2801	G2802	G2803	G2804	G2805	G2806	G2807	G2808	G2809	G2810	G2811	G2812	G2813	G2814	G2815	G2816	G2817	G2818	G2819	G2820	G2821	G2822	G2823	G2824	G2825	G2826	G2827	G2828	G2829	G2830	G2831	G2832	G2833	G2834	G2835	G2836	G2837	G2838	G2839	G2840	G2841	G2842	G2843	G2844	G2845	G2846	G2847	G2848	G2849	G2850	G2851	G2852	G2853	G2854	G2855	G2856	G2857	G2858	G2859	G2860	G2861	G2862	G2863	G2864	G2865	G2866	G2867	G2868	G2869	G2870	G2871	G2872	G2873	G2874	G2875	G2876	G2877	G2878	G2879	G2880	G2881	G2882	G2883	G2884	G2885	G2886	G2887	G2888	G2889	G2890	G2891	G2892	G2893	G2894	G2895	G2896	G2897	G2898	G2899	G2900	G2901	G2902	G2903	G2904	G2905	G2906	G2907	G2908	G2909	G2910	G2911	G2912	G2913	G2914	G2915	G2916	G2917	G2918	G2919	G2920	G2921	G2922	G2923	G2924	G2925	G2926	G2927	G2928	G2929	G2930	G2931	G2932	G2933	G2934	G2935	G2936	G2937	G2938	G2939	G2940	G2941	G2942	G2943	G2944	G2945	G2946	G2947	G2948	G2949	G2950	G2951	G2952	G2953	G2954	G2955	G2956	G2957	G2958	G2959	G2960	G2961	G2962	G2963	G2964	G2965	G2966	G2967	G2968	G2969	G2970	G2971	G2972	G2973	G2974	G2975	G2976	G2977	G2978	G2979	G2980	G2981	G2982	G2983	G2984	G2985	G2986	G2987	G2988	G2989	G2990	G2991	G2992	G2993	G2994	G2995	G2996	G2997	G2998	G2999	G3000	G3001	G3002	G3003	G3004	G3005	G3006	G3007	G3008	G3009	G3010	G3011	G3012	G3013	G3014	G3015	G3016	G3017	G3018	G3019	G3020	G3021	G3022	G3023	G3024	G3025	G3026	G3027	G3028	G3029	G3030	G3031	G3032	G3033	G3034	G3035	G3036	G3037	G3038	G3039	G3040	G3041	G3042	G3043	G3044	G3045	G3046	G3047	G3048	G3049	G3050	G3051	G3052	G3053	G3054	G3055	G3056	G3057	G3058	G3059	G3060	G3061	G3062	G3063	G3064	G3065	G3066	G3067	G3068	G3069	G3070	G3071	G3072	G3073	G3074	G3075	G3076	G3077	G3078	G3079	G3080	G3081	G3082	G3083	G3084	G3085	G3086	G3087	G3088	G3089	G3090	G3091	G3092	G3093	G3094	G3095	G3096	G3097	G3098	G3099	G3100	G3101	G3102	G3103	G3104	G3105	G3106	G3107	G3108	G3109	G3110	G3111	G3112	G3113	G3114	G3115	G3116	G3117	G3118	G3119	G3120	G3121	G3122	G3123	G3124	G3125	G3126	G3127	G3128	G3129	G3130	G3131	G3132	G3133	G3134	G3135	G3136	G3137	G3138	G3139	G3140	G3141	G3142	G3143	G3144	G3145	G3146	G3147	G3148	G3149	G3150	G3151	G3152	G3153	G3154	G3155	G3156	G3157	G3158	G3159	G3160	G3161	G3162	G3163	G3164	G3165	G3166	G3167	G3168	G3169	G3170	G3171	G3172	G3173	G3174	G3175	G3176	G3177	G3178	G3179	G3180	G3181	G3182	G3183	G3184	G3185	G3186	G3187	G3188	G3189	G3190	G3191	G3192	G3193	G3194	G3195	G3196	G3197	G3198	G3199	G3200	G3201	G3202	G3203	G3204	G3205	G3206	G3207	G3208	G3209	G3210	G3211	G3212	G3213	G3214	G3215	G3216	G3217	G3218	G3219	G3220	G3221	G3222	G3223	G3224	G3225	G3226	G3227	G3228	G3229	G3230	G3231	G3232	G3233	G3234	G3235	G3236	G3237	G3238	G3239	G3240	G3241	G3242	G3243	G3244	G3245	G3246	G3247	G3248	G3249	G3250	G3251	G3252	G3253	G3254	G3255	G3256	G3257	G3258	G3259	G3260	G3261	G3262	G3263	G3264	G3265	G3266	G3267	G3268	G3269	G3270	G3271	G3272	G3273	G3274	G3275	G3276	G3277	G3278	G3279	G3280	G3281	G3282	G3283	G3284	G3285	G3286	G3287	G3288	G3289	G3290	G3291	G3292	G3293	G3294	G3295	G3296	G3297	G3298	G3299	G3300	G3301	G3302	G3303	G3304	G3305	G3306	G3307	G3308	G3309	G3310	G3311	G3312	G3313	G3314	G3315	G3316	G3317	G3318	G3319	G3320	G3321	G3322	G3323	G3324	G3325	G3326	G3327	G3328	G3329	G3330	G3331	G3332	G3333	G3334	G3335	G3336	G3337	G3338	G3339	G3340	G3341	G3342	G3343	G3344	G3345	G3346	G3347	G3348	G3349	G3350	G3351	G3352	G3353	G3354	G3355	G3356	G3357	G3358	G3359	G3360	G3361	G3362	G3363	G3364	G3365	G3366	G3367	G3368	G3369	G3370	G3371	G3372	G3373	G3374	G3375	G3376	G3377	G3378	G3379	G3380	G3381	G3382	G3383	G3384	G3385	G3386	G3387	G3388	G3389	G3390	G3391	G3392	G3393	G3394	G3395	G3396	G3397	G3398	G3399	G3400	G3401	G3402	G3403	G3404	G3405	G3406	G3407	G3408	G3409	G3410	G3411	G3412	G3413	G3414	G3415	G3416	G3417	G3418	G3419	G3420	G3421	G3422	G3423	G3424	G3425	G3426	G3427	G3428	G3429	G3430	G3431	G3432	G3433	G3434	G3435	G3436	G3437	G3438	G3439	G3440	G3441	G3442	G3443	G3444	G3445	G3446	G3447	G3448	G3449	G3450	G3451	G3452	G3453	G3454	G3455	G3456	G3457	G3458	G3459	G3460	G3461	G3462	G3463	G3464	G3465	G3466	G3467	G3468	G3469	G3470	G3471	G3472	G3473	G3474	G3475	G3476	G3477	G3478	G3479	G3480	G3481	G3482	G3483	G3484	G3485	G3486	G3487	G3488	G3489	G3490	G3491	G3492	G3493	G3494	G3495	G3496	G3497	G3498	G3499	G3500	G3501	G3502	G3503	G3504	G3505	G3506	G3507	G3508	G3509	G3510	G3511	G3512	G3513	G3514	G3515	G3516	G3517	G3518	G3519	G3520	G3521	G3522	G3523	G3524	G3525	G3526	G3527	G3528	G3529	G3530	G3531	G3532	G3533	G3534	G3535	G3536	G3537	G3538	G3539	G3540	G3541	G3542	G3543	G3544	G3545	G3546	G3547	G3548	G3549	G3550	G3551	G3552	G3553	G3554	G3555	G3556	G3557	G3558	G3559	G3560	G3561	G3562	G3563	G3564	G3565	G3566	G3567	G3568	G3569	G3570	G3571	G3572	G3573	G3574	G3575	G3576	G3577	G3578	G3579	G3580	G3581	G3582	G3583	G3584	G3585	G3586	G3587	G3588	G3589	G3590	G3591	G3592	G3593	G3594	G3595	G3596	G3597	G3598	G3599	G3600	G3601	G3602	G3603	G3604	G3605	G3606	G3607	G3608	G3609	G3610	G3611	G3612	G3613	G3614	G3615	G3616	G3617	G3618	G3619	G3620	G3621	G3622	G3623	G3624	G3625	G3626	G3627	G3628	G3629	G3630	G3631	G3632	G3633	G3634	G3635	G3636	G3637	G3638	G3639	G3640	G3641	G3642	G3643	G3644	G3645	G3646	G3647	G3648	G3649	G3650	G3651	G3652	G3653	G3654	G3655	G3656	G3657	G3658	G3659	G3660	G3661	G3662	G3663	G3664	G3665	G3666	G3667	G3668	G3669	G3670	G3671	G3672	G3673	G3674	G3675	G3676	G3677	G3678	G3679	G3680	G3681	G3682	G3683	G3684	G3685	G3686	G3687	G3688	G3689	G3690	G3691	G3692	G3693	G3694	G3695	G3696	G3697	G3698	G3699	G3700	G3701	G3702	G3703	G3704	G3705	G3706	G3707	G3708	G3709	G3710	G3711	G3712	G3713	G3714	G3715	G3716	G3717	G3718	G3719	G3720	G3721	G3722	G3723	G3724	G3725	G3726	G3727	G3728	G3729	G3730	G3731	G3732	G3733	G3734	G3735	G3736	G3737	G3738	G3739	G3740	G3741	G3742	G3743	G3744	G3745	G3746	G3747	G3748	G3749	G3750	G3751	G3752	G3753	G3754	G3755	G3756	G3757	G3758	G3759	G3760	G3761	G3762	G3763	G3764	G3765	G3766	G3767	G3768	G3769	G3770	G3771	G3772	G3773	G3774	G3775	G3776	G3777	G3778	G3779	G3780	G3781	G3782	G3783	G3784	G3785	G3786	G3787	G3788	G3789	G3790	G3791	G3792	G3793	G3794	G3795	G3796	G3797	G3798	G3799	G3800	G3801	G3802	G3803	G3804	G3805	G3806	G3807	G3808	G3809	G3810	G3811	G381



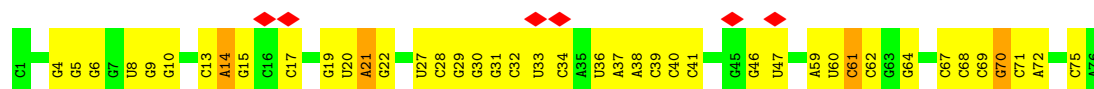
• Molecule 55: 5S ribosomal RNA

Chain 02: 60% 32% 8%



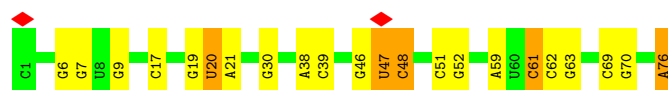
• Molecule 56: tRNA^{fMet}

Chain X: 8% 45% 49% 5%



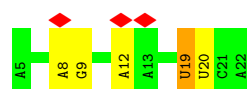
• Molecule 56: tRNA^{fMet}

Chain W: 71% 22% 6%



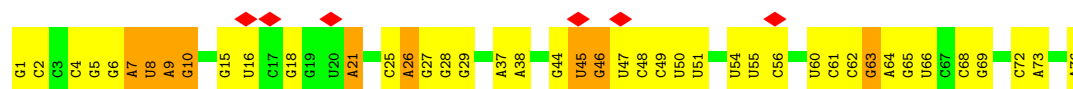
• Molecule 57: mRNA

Chain V: 17% 72% 22% 6%



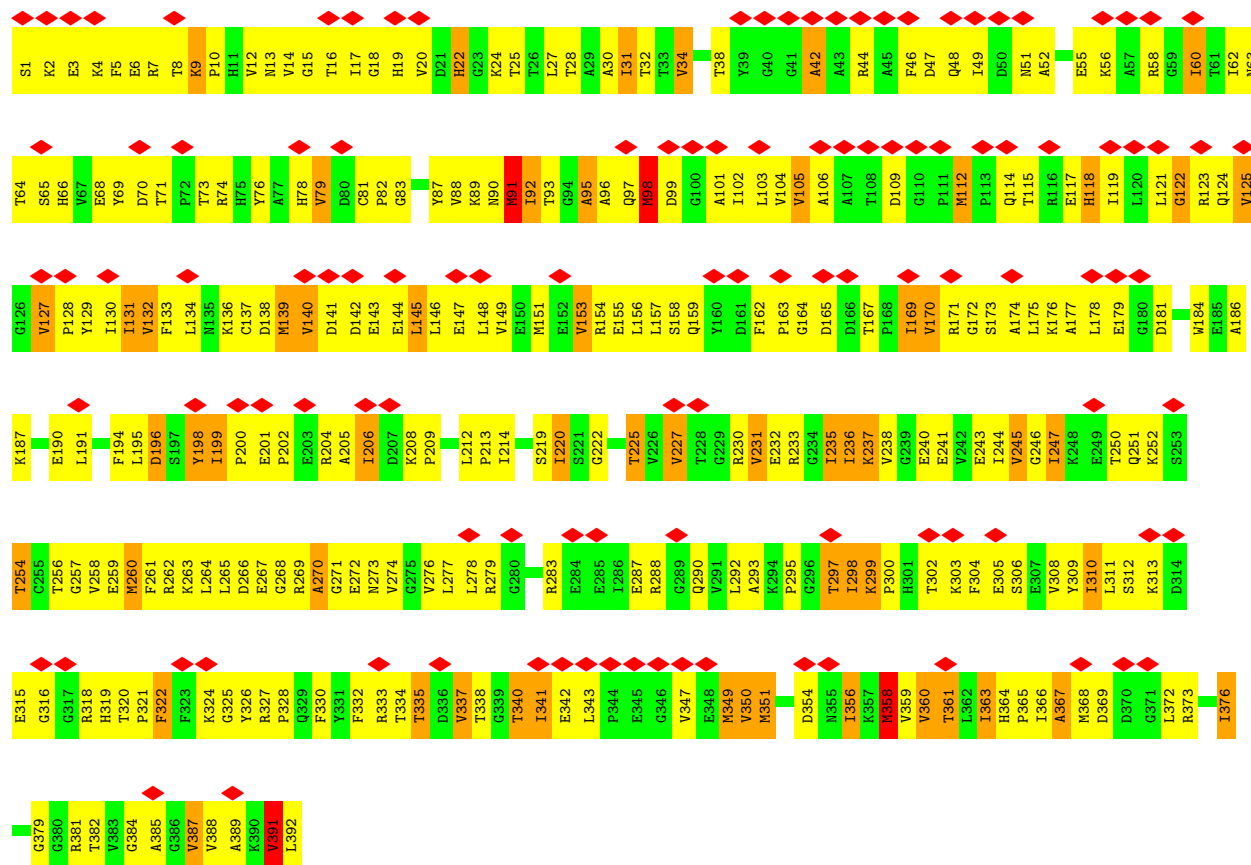
• Molecule 58: tRNA^{Phe}

Chain Y: 8% 43% 45% 12%



• Molecule 59: Elongation factor Tu 2

Chain Z: 29% 29% 55% 15%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	10431	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTFFIND3 was used to determine CTF values. FREALIGN applied CTF correction.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	60976	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	16.901	Depositor
Minimum map value	-5.858	Depositor
Average map value	-0.407	Depositor
Map value standard deviation	1.298	Depositor
Recommended contour level	3.49	Depositor
Map size (Å)	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	04	0.37	0/2122	0.92	9/2852 (0.3%)
2	05	0.37	0/1586	0.88	1/2134 (0.0%)
3	06	0.36	0/1571	0.90	6/2113 (0.3%)
4	07	0.36	0/1435	0.89	6/1926 (0.3%)
5	08	0.36	0/1343	0.87	5/1816 (0.3%)
6	09	0.43	0/1122	1.04	6/1515 (0.4%)
7	10	0.51	0/1002	1.18	9/1350 (0.7%)
8	11	0.51	0/1046	1.10	7/1410 (0.5%)
9	12	0.37	0/1152	0.88	3/1551 (0.2%)
10	13	0.35	0/948	0.92	1/1268 (0.1%)
11	14	0.36	0/1054	1.00	3/1403 (0.2%)
12	15	0.39	0/1093	0.84	2/1460 (0.1%)
13	16	0.36	0/974	0.91	3/1301 (0.2%)
14	17	0.34	0/902	0.92	3/1209 (0.2%)
15	18	0.34	0/929	0.89	3/1242 (0.2%)
16	19	0.36	0/960	0.93	4/1278 (0.3%)
17	20	0.36	0/829	0.92	3/1107 (0.3%)
18	21	0.36	0/864	0.96	2/1156 (0.2%)
19	22	0.35	0/745	0.82	0/994
20	23	0.35	0/788	0.94	2/1051 (0.2%)
21	24	0.35	0/766	0.82	2/1025 (0.2%)
22	25	0.34	0/582	0.86	0/769
23	26	0.35	0/635	0.90	1/848 (0.1%)
24	27	0.35	0/510	0.94	2/677 (0.3%)
25	28	0.36	0/453	0.83	0/605
26	29	0.41	0/532	0.92	3/709 (0.4%)
27	30	0.34	0/450	0.74	0/599
28	31	0.38	0/417	0.75	1/554 (0.2%)
29	32	0.42	0/380	0.96	3/498 (0.6%)
30	33	0.35	0/513	0.89	0/676
31	34	0.34	0/303	0.83	1/397 (0.3%)
32	B	0.45	1/1736 (0.1%)	1.06	15/2338 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	C	0.39	0/1652	0.96	6/2225 (0.3%)
34	D	0.37	0/1665	0.99	7/2227 (0.3%)
35	E	0.38	0/1170	0.96	4/1573 (0.3%)
36	F	0.40	0/836	1.06	5/1128 (0.4%)
37	G	0.36	0/1196	1.03	9/1602 (0.6%)
38	H	0.36	0/989	0.99	3/1326 (0.2%)
39	I	0.38	0/1034	1.01	6/1375 (0.4%)
40	J	0.42	0/797	1.02	4/1077 (0.4%)
41	K	0.38	0/886	0.98	4/1195 (0.3%)
42	L	0.40	0/969	1.09	8/1300 (0.6%)
43	M	0.36	0/893	0.94	0/1193
44	N	0.36	0/817	0.92	4/1088 (0.4%)
45	O	0.36	0/722	0.93	3/964 (0.3%)
46	P	0.37	0/659	0.96	4/884 (0.5%)
47	Q	0.38	0/658	0.98	3/881 (0.3%)
48	R	0.42	0/545	0.99	4/731 (0.5%)
49	S	0.39	0/653	0.91	1/877 (0.1%)
50	T	0.35	0/671	1.02	6/888 (0.7%)
51	U	0.43	0/551	1.04	5/728 (0.7%)
52	03	2.12	24/1033 (2.3%)	1.24	10/1387 (0.7%)
53	A	0.46	0/36963	0.55	16/57662 (0.0%)
54	01	0.47	0/69796	0.56	19/108888 (0.0%)
55	02	0.45	0/2872	0.58	3/4479 (0.1%)
56	W	0.47	0/1832	0.53	0/2855
56	X	0.53	0/1832	0.59	1/2855 (0.0%)
57	V	0.51	0/436	0.58	0/679
58	Y	0.53	0/1809	0.58	1/2819 (0.0%)
59	Z	2.06	62/3085 (2.0%)	1.10	15/4173 (0.4%)
All	All	0.55	87/166763 (0.1%)	0.70	257/248890 (0.1%)

The worst 5 of 87 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	Z	91	MET	SD-CE	12.16	2.10	1.79
59	Z	260	MET	SD-CE	11.22	2.07	1.79
52	03	218	MET	SD-CE	10.52	2.05	1.79
59	Z	358	MET	SD-CE	10.20	2.05	1.79
32	B	160	LEU	C-N	9.90	1.47	1.33

The worst 5 of 257 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	H	67	GLY	N-CA-C	-12.41	98.10	114.85
36	F	91	ARG	N-CA-C	10.26	123.03	110.41
7	10	117	LEU	N-CA-C	9.73	125.86	107.75
59	Z	99	ASP	N-CA-C	-9.48	100.03	111.69
8	11	12	VAL	N-CA-C	-9.46	99.52	110.21

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	04	2083	0	2157	80	0
2	05	1565	0	1616	48	0
3	06	1552	0	1619	51	0
4	07	1411	0	1447	64	0
5	08	1323	0	1374	34	0
6	09	1111	0	1148	40	0
7	10	989	0	1025	61	0
8	11	1032	0	1088	65	0
9	12	1129	0	1162	32	0
10	13	939	0	1012	29	0
11	14	1045	0	1117	35	0
12	15	1074	0	1157	40	0
13	16	961	0	1000	32	0
14	17	892	0	923	20	0
15	18	917	0	965	32	0
16	19	947	0	1022	31	0
17	20	816	0	839	31	0
18	21	857	0	922	24	0
19	22	739	0	807	21	0
20	23	780	0	834	22	0
21	24	753	0	780	30	0
22	25	575	0	592	19	0
23	26	625	0	655	21	0
24	27	509	0	543	9	0
25	28	449	0	491	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	29	523	0	524	17	0
27	30	444	0	461	22	0
28	31	410	0	440	7	0
29	32	377	0	418	13	0
30	33	504	0	574	13	0
31	34	302	0	343	9	0
32	B	1705	0	1732	93	0
33	C	1625	0	1699	51	0
34	D	1643	0	1710	51	0
35	E	1157	0	1199	51	0
36	F	818	0	808	43	0
37	G	1182	0	1240	41	0
38	H	979	0	1034	47	0
39	I	1022	0	1070	39	0
40	J	787	0	828	44	0
41	K	870	0	878	38	0
42	L	955	0	1019	26	0
43	M	884	0	944	35	0
44	N	805	0	847	36	0
45	O	714	0	737	18	0
46	P	649	0	666	26	0
47	Q	649	0	691	29	0
48	R	536	0	552	23	0
49	S	638	0	665	33	0
50	T	665	0	714	20	0
51	U	545	0	579	46	0
52	03	1026	0	1092	123	0
53	A	33012	0	16618	454	0
54	01	62317	0	31346	853	0
55	02	2568	0	1303	34	0
56	W	1640	0	836	15	0
56	X	1640	0	837	28	0
57	V	388	0	196	4	0
58	Y	1619	0	821	38	0
59	Z	3029	0	3043	303	0
60	W	10	0	10	3	0
61	Y	11	0	8	3	0
62	Z	32	0	14	0	0
All	All	153753	0	104791	3282	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

The worst 5 of 3282 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)
59:Z:112:MET:CE	59:Z:112:MET:SD	2.02	1.47
59:Z:358:MET:SD	59:Z:358:MET:CE	2.05	1.45
52:03:218:MET:CE	52:03:218:MET:SD	2.05	1.44
56:W:76:A:O3'	60:W:101:FME:C	1.63	1.43
59:Z:260:MET:CE	59:Z:260:MET:SD	2.07	1.43

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	04	269/271 (99%)	233 (87%)	33 (12%)	3 (1%)	11	43
2	05	207/209 (99%)	184 (89%)	23 (11%)	0	100	100
3	06	199/201 (99%)	175 (88%)	22 (11%)	2 (1%)	12	45
4	07	175/177 (99%)	154 (88%)	20 (11%)	1 (1%)	21	54
5	08	174/176 (99%)	155 (89%)	13 (8%)	6 (3%)	3	23
6	09	147/149 (99%)	117 (80%)	26 (18%)	4 (3%)	4	27
7	10	129/131 (98%)	97 (75%)	22 (17%)	10 (8%)	1	8
8	11	139/141 (99%)	117 (84%)	17 (12%)	5 (4%)	2	22
9	12	140/142 (99%)	132 (94%)	7 (5%)	1 (1%)	18	51
10	13	120/122 (98%)	101 (84%)	17 (14%)	2 (2%)	7	35
11	14	141/143 (99%)	112 (79%)	23 (16%)	6 (4%)	2	18
12	15	134/136 (98%)	115 (86%)	18 (13%)	1 (1%)	18	51
13	16	118/120 (98%)	102 (86%)	14 (12%)	2 (2%)	7	35
14	17	114/116 (98%)	106 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	18	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
16	19	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
17	20	101/103 (98%)	83 (82%)	16 (16%)	2 (2%)	6	32
18	21	108/110 (98%)	95 (88%)	11 (10%)	2 (2%)	6	33
19	22	91/93 (98%)	78 (86%)	13 (14%)	0	100	100
20	23	100/102 (98%)	83 (83%)	14 (14%)	3 (3%)	3	25
21	24	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
22	25	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
23	26	75/77 (97%)	66 (88%)	9 (12%)	0	100	100
24	27	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	7	36
25	28	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
26	29	64/66 (97%)	51 (80%)	13 (20%)	0	100	100
27	30	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
28	31	48/50 (96%)	45 (94%)	2 (4%)	1 (2%)	5	31
29	32	44/46 (96%)	37 (84%)	7 (16%)	0	100	100
30	33	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7	36
31	34	36/38 (95%)	29 (81%)	6 (17%)	1 (3%)	4	26
32	B	216/218 (99%)	180 (83%)	30 (14%)	6 (3%)	4	26
33	C	204/206 (99%)	187 (92%)	16 (8%)	1 (0%)	24	57
34	D	203/205 (99%)	167 (82%)	31 (15%)	5 (2%)	4	28
35	E	155/157 (99%)	133 (86%)	15 (10%)	7 (4%)	2	17
36	F	98/100 (98%)	75 (76%)	18 (18%)	5 (5%)	1	15
37	G	149/151 (99%)	129 (87%)	18 (12%)	2 (1%)	9	39
38	H	127/129 (98%)	120 (94%)	6 (5%)	1 (1%)	16	49
39	I	125/127 (98%)	98 (78%)	22 (18%)	5 (4%)	2	20
40	J	96/98 (98%)	78 (81%)	10 (10%)	8 (8%)	0	8
41	K	114/116 (98%)	92 (81%)	19 (17%)	3 (3%)	4	27
42	L	121/123 (98%)	95 (78%)	18 (15%)	8 (7%)	1	12
43	M	112/114 (98%)	95 (85%)	14 (12%)	3 (3%)	4	27
44	N	98/100 (98%)	86 (88%)	11 (11%)	1 (1%)	12	45
45	O	86/88 (98%)	74 (86%)	11 (13%)	1 (1%)	10	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	P	80/82 (98%)	69 (86%)	9 (11%)	2 (2%)	4	28
47	Q	78/80 (98%)	61 (78%)	11 (14%)	6 (8%)	1	9
48	R	63/65 (97%)	50 (79%)	7 (11%)	6 (10%)	0	6
49	S	77/79 (98%)	66 (86%)	9 (12%)	2 (3%)	4	27
50	T	83/85 (98%)	75 (90%)	7 (8%)	1 (1%)	10	41
51	U	63/65 (97%)	41 (65%)	15 (24%)	7 (11%)	0	4
52	03	130/234 (56%)	107 (82%)	22 (17%)	1 (1%)	16	49
59	Z	390/392 (100%)	329 (84%)	55 (14%)	6 (2%)	8	37
All	All	6366/6574 (97%)	5449 (86%)	776 (12%)	141 (2%)	7	30

5 of 141 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	06	83	VAL
5	08	46	ASP
5	08	47	ASN
5	08	119	GLY
6	09	9	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	04	216/216 (100%)	212 (98%)	4 (2%)	50	67
2	05	164/164 (100%)	164 (100%)	0	100	100
3	06	165/165 (100%)	164 (99%)	1 (1%)	78	79
4	07	148/148 (100%)	148 (100%)	0	100	100
5	08	137/137 (100%)	137 (100%)	0	100	100
6	09	114/114 (100%)	114 (100%)	0	100	100
7	10	100/100 (100%)	99 (99%)	1 (1%)	68	75
8	11	109/109 (100%)	107 (98%)	2 (2%)	51	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	12	116/116 (100%)	114 (98%)	2 (2%)	53	69
10	13	103/103 (100%)	101 (98%)	2 (2%)	50	67
11	14	102/102 (100%)	99 (97%)	3 (3%)	37	60
12	15	109/109 (100%)	107 (98%)	2 (2%)	51	68
13	16	100/100 (100%)	99 (99%)	1 (1%)	68	75
14	17	86/86 (100%)	86 (100%)	0	100	100
15	18	99/99 (100%)	99 (100%)	0	100	100
16	19	89/89 (100%)	89 (100%)	0	100	100
17	20	84/84 (100%)	84 (100%)	0	100	100
18	21	93/93 (100%)	92 (99%)	1 (1%)	65	74
19	22	80/80 (100%)	79 (99%)	1 (1%)	61	72
20	23	83/83 (100%)	83 (100%)	0	100	100
21	24	78/78 (100%)	78 (100%)	0	100	100
22	25	57/57 (100%)	57 (100%)	0	100	100
23	26	67/67 (100%)	67 (100%)	0	100	100
24	27	55/55 (100%)	54 (98%)	1 (2%)	51	68
25	28	48/48 (100%)	48 (100%)	0	100	100
26	29	59/59 (100%)	59 (100%)	0	100	100
27	30	47/47 (100%)	47 (100%)	0	100	100
28	31	45/45 (100%)	45 (100%)	0	100	100
29	32	38/38 (100%)	38 (100%)	0	100	100
30	33	51/51 (100%)	51 (100%)	0	100	100
31	34	34/34 (100%)	33 (97%)	1 (3%)	37	60
32	B	180/180 (100%)	178 (99%)	2 (1%)	65	74
33	C	170/170 (100%)	167 (98%)	3 (2%)	51	68
34	D	172/172 (100%)	172 (100%)	0	100	100
35	E	119/119 (100%)	119 (100%)	0	100	100
36	F	87/87 (100%)	85 (98%)	2 (2%)	44	64
37	G	124/124 (100%)	124 (100%)	0	100	100
38	H	104/104 (100%)	104 (100%)	0	100	100
39	I	105/105 (100%)	105 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	J	86/86 (100%)	84 (98%)	2 (2%)	44	64
41	K	89/89 (100%)	87 (98%)	2 (2%)	45	65
42	L	103/103 (100%)	102 (99%)	1 (1%)	68	75
43	M	92/92 (100%)	89 (97%)	3 (3%)	33	58
44	N	83/83 (100%)	83 (100%)	0	100	100
45	O	76/76 (100%)	76 (100%)	0	100	100
46	P	65/65 (100%)	64 (98%)	1 (2%)	57	70
47	Q	74/74 (100%)	74 (100%)	0	100	100
48	R	56/56 (100%)	55 (98%)	1 (2%)	51	68
49	S	70/70 (100%)	69 (99%)	1 (1%)	59	71
50	T	65/65 (100%)	65 (100%)	0	100	100
51	U	55/55 (100%)	51 (93%)	4 (7%)	13	40
52	03	110/181 (61%)	104 (94%)	6 (6%)	19	47
59	Z	324/325 (100%)	315 (97%)	9 (3%)	38	60
All	All	5285/5357 (99%)	5226 (99%)	59 (1%)	63	74

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	F	94	HIS
59	Z	237	LYS
43	M	6	ILE
59	Z	236	ILE
52	03	55	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 128 such sidechains are listed below:

Mol	Chain	Res	Type
50	T	60	GLN
52	03	160	GLN
17	20	18	GLN
17	20	6	GLN
59	Z	22	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	A	1538/1539 (99%)	162 (10%)	9 (0%)
54	01	2902/2903 (99%)	358 (12%)	16 (0%)
55	02	119/120 (99%)	11 (9%)	2 (1%)
56	W	76/77 (98%)	7 (9%)	0
56	X	76/77 (98%)	13 (17%)	0
57	V	17/18 (94%)	2 (11%)	0
58	Y	75/76 (98%)	14 (18%)	0
All	All	4803/4810 (99%)	567 (11%)	27 (0%)

5 of 567 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	A	6	G
53	A	9	G
53	A	22	G
53	A	31	G
53	A	32	A

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	01	1020	A
54	01	1130	U
54	01	2756	U
54	01	1111	A
54	01	1475	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](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
62	GCP	Z	401	-	32,34,34	2.09	12 (37%)	49,54,54	2.50	14 (28%)
61	PHE	Y	101	58	10,11,12	1.13	0	8,13,15	0.30	0
60	FME	W	101	-	8,9,10	0.77	0	8,9,11	1.26	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	Z	401	-	-	9/19/38/38	0/3/3/3
61	PHE	Y	101	58	-	1/5/6/8	0/1/1/1
60	FME	W	101	-	-	3/7/9/11	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	Z	401	GCP	PA-O3A	-5.25	1.53	1.59
62	Z	401	GCP	C1'-N9	4.34	1.59	1.47
62	Z	401	GCP	PB-O3A	-4.01	1.53	1.58
62	Z	401	GCP	C2-N2	3.06	1.41	1.34
62	Z	401	GCP	C2'-C3'	2.96	1.61	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	Z	401	GCP	C1'-N9-C4	7.76	149.41	126.49
62	Z	401	GCP	C1'-N9-C8	-7.61	105.11	126.73
62	Z	401	GCP	O1G-PG-C3B	-7.27	95.52	111.37
62	Z	401	GCP	O5'-PA-O1A	-4.06	92.84	108.94
62	Z	401	GCP	O2B-PB-O1B	3.85	122.48	109.95

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

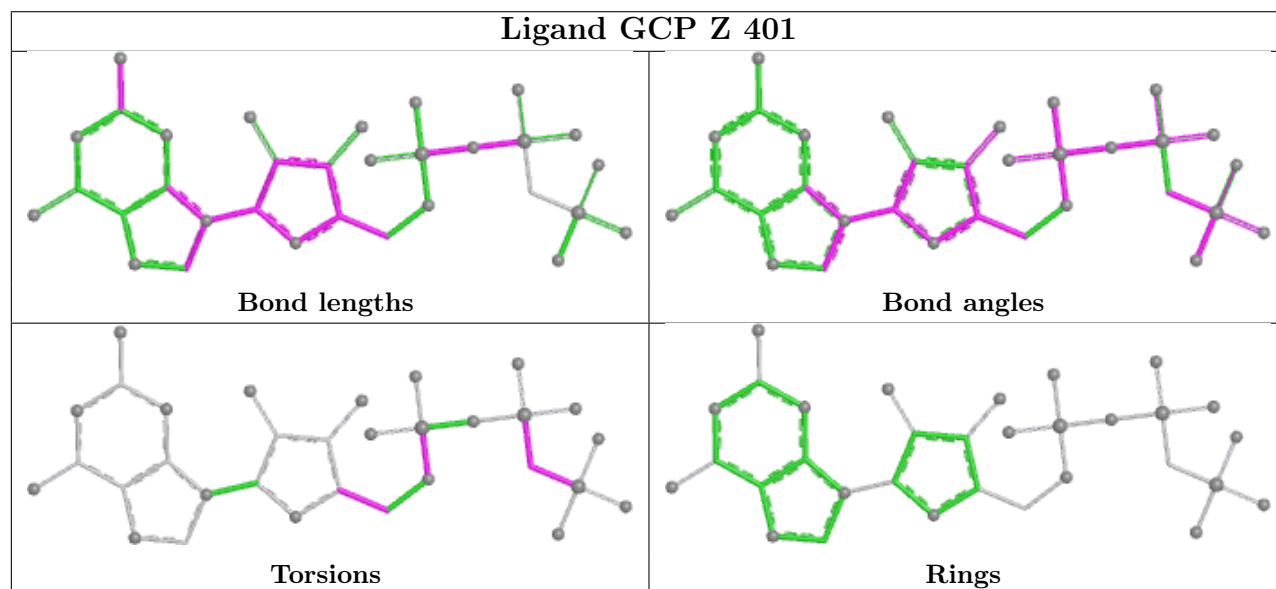
Mol	Chain	Res	Type	Atoms
60	W	101	FME	O1-CN-N-CA
60	W	101	FME	O-C-CA-CB
61	Y	101	PHE	O-C-CA-CB
62	Z	401	GCP	PB-C3B-PG-O1G
62	Z	401	GCP	PB-C3B-PG-O2G

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	Y	101	PHE	3	0
60	W	101	FME	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 [i](#)

There are no chain breaks in this entry.

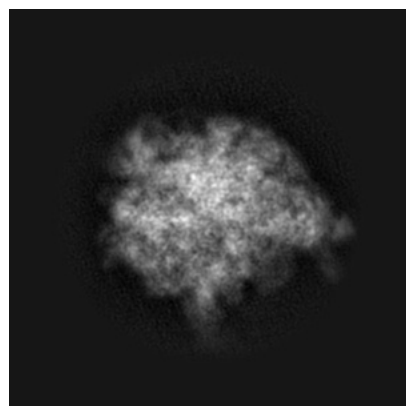
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8616. These allow visual inspection of the internal detail of the map and identification of artifacts.

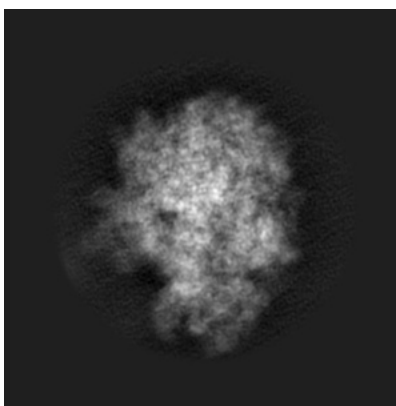
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

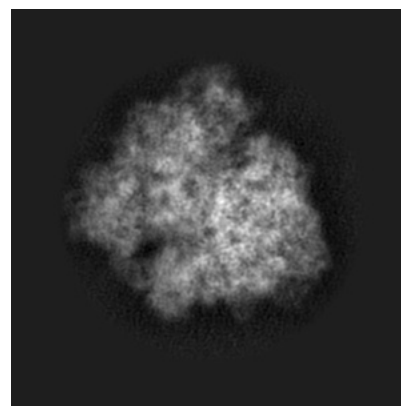
6.1.1 Primary map



X

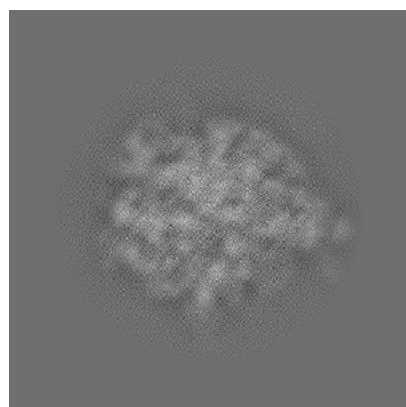


Y

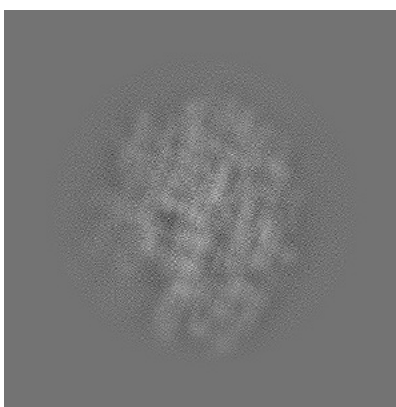


Z

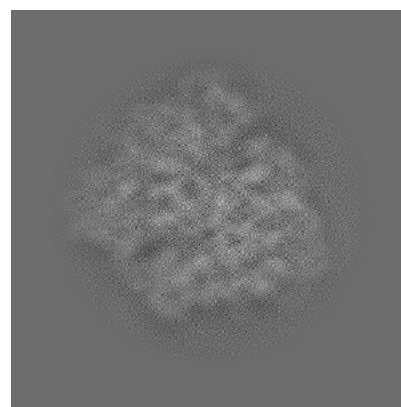
6.1.2 Raw map



X



Y

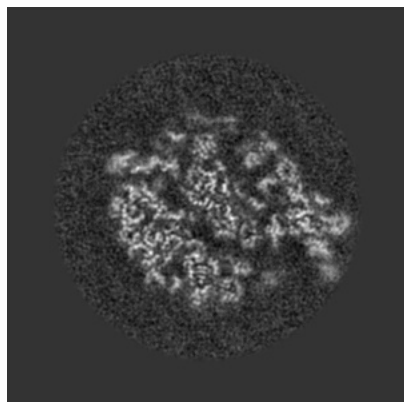


Z

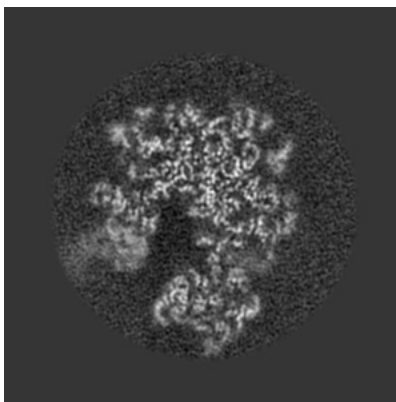
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

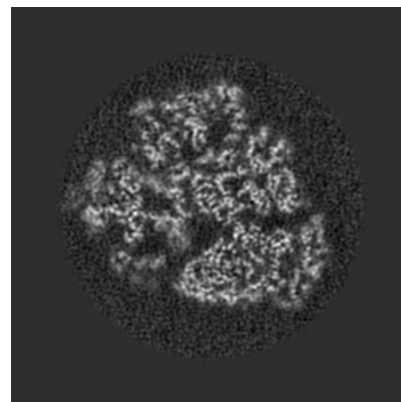
6.2.1 Primary map



X Index: 240

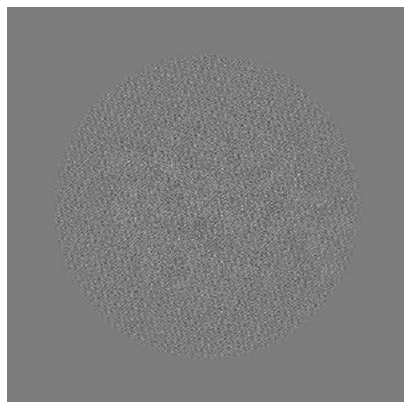


Y Index: 240

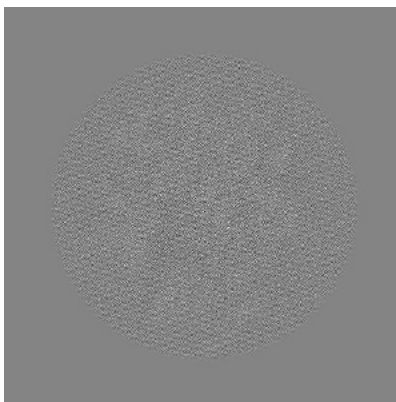


Z Index: 240

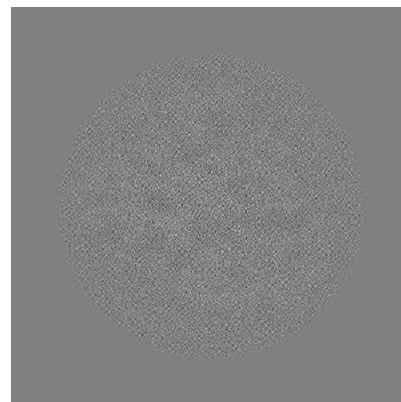
6.2.2 Raw map



X Index: 240



Y Index: 240

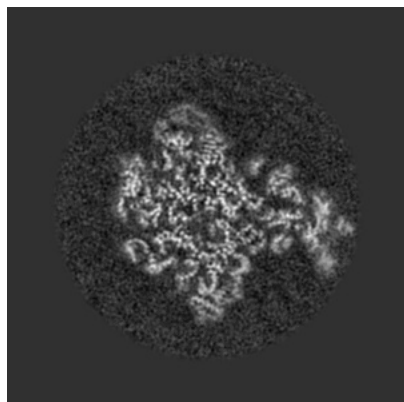


Z Index: 240

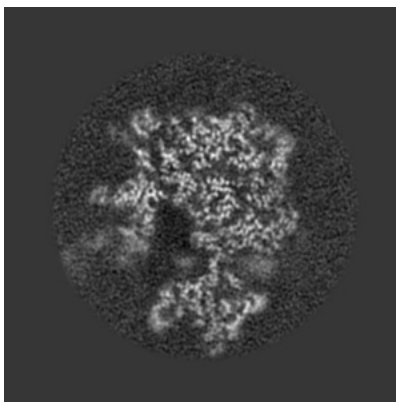
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

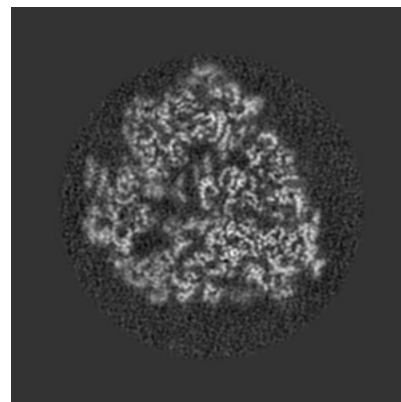
6.3.1 Primary map



X Index: 251

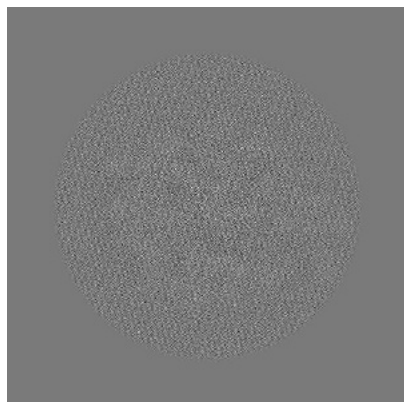


Y Index: 248

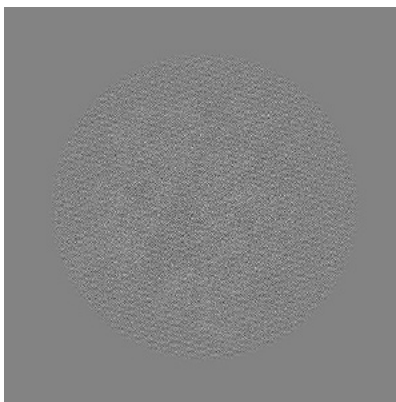


Z Index: 228

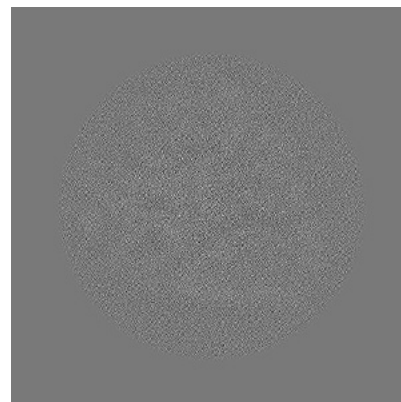
6.3.2 Raw map



X Index: 235



Y Index: 234

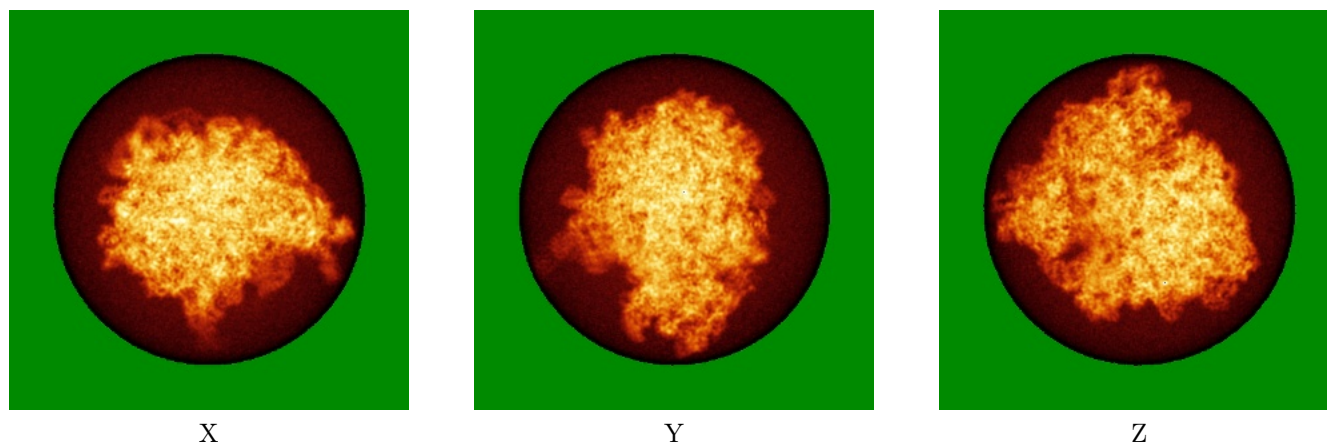


Z Index: 235

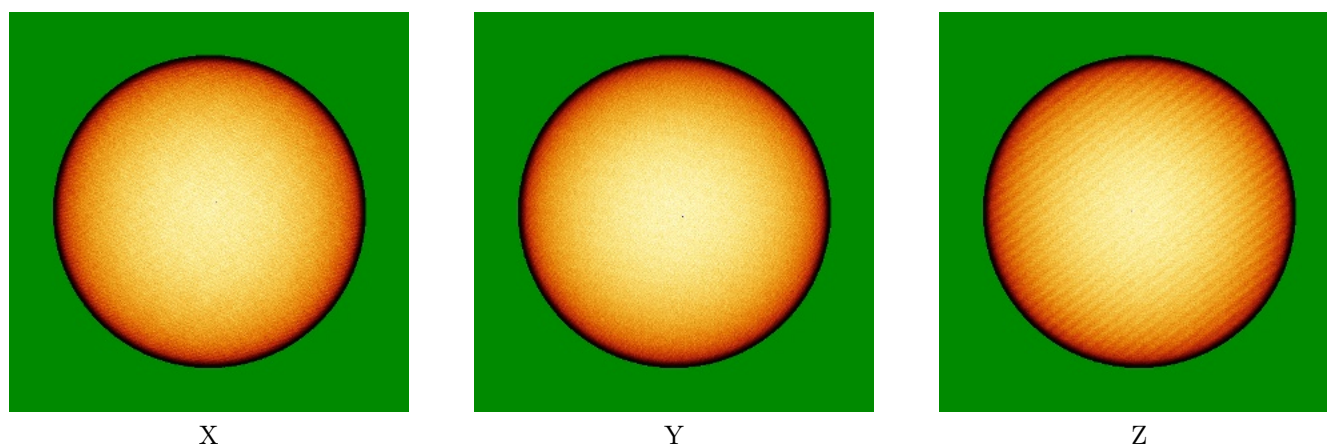
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

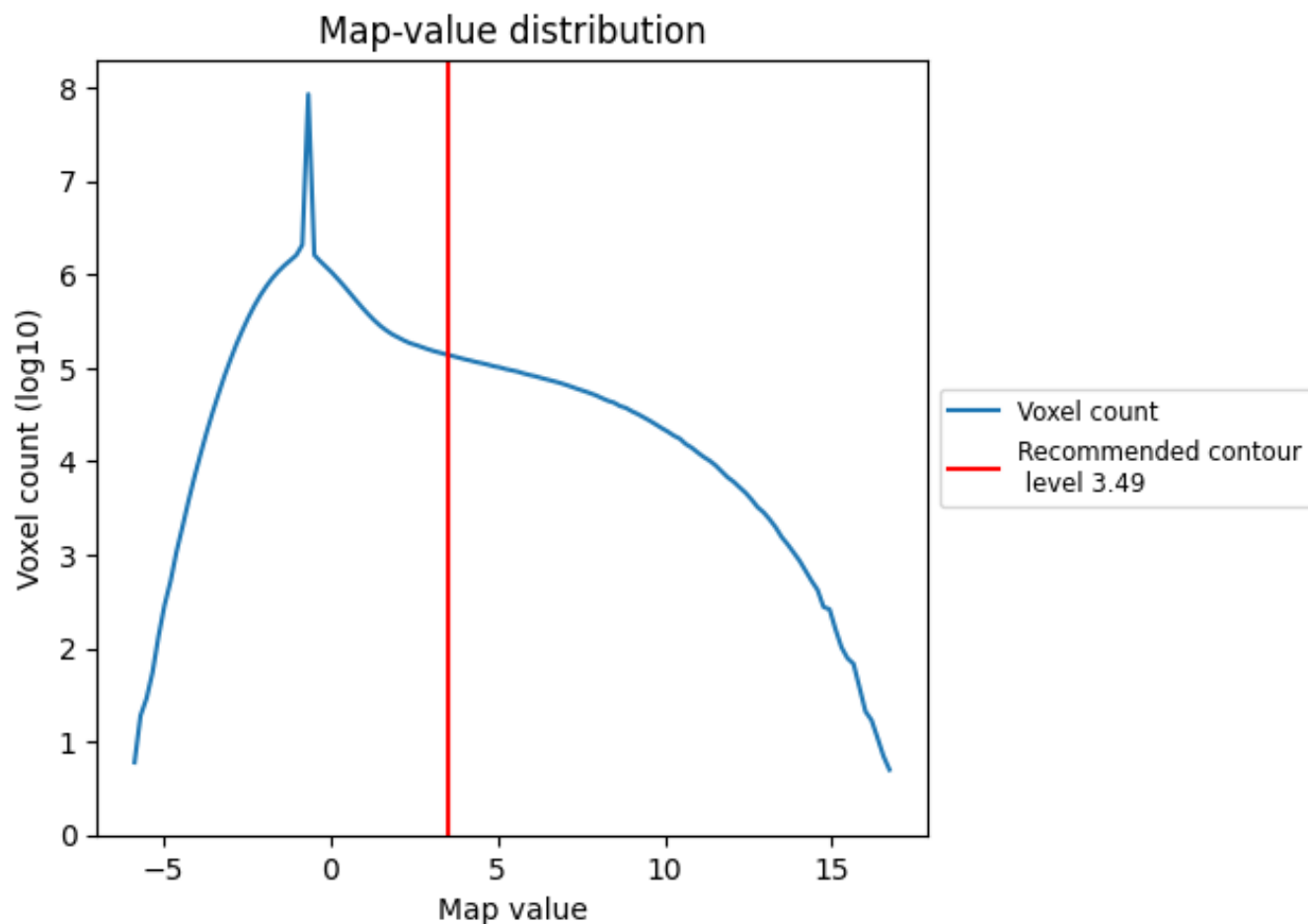
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

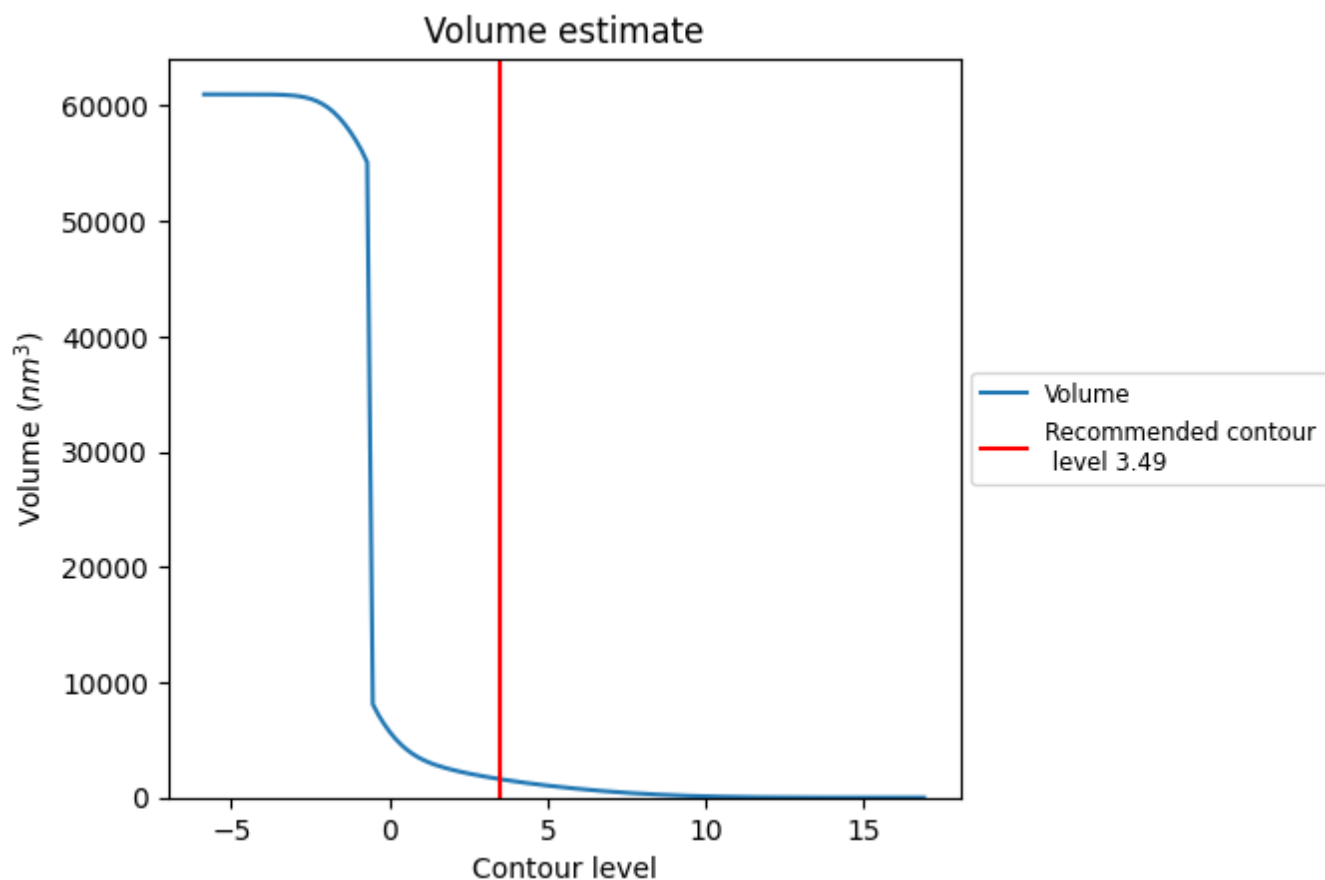
This section contains the results of statistical analysis of the map.

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.

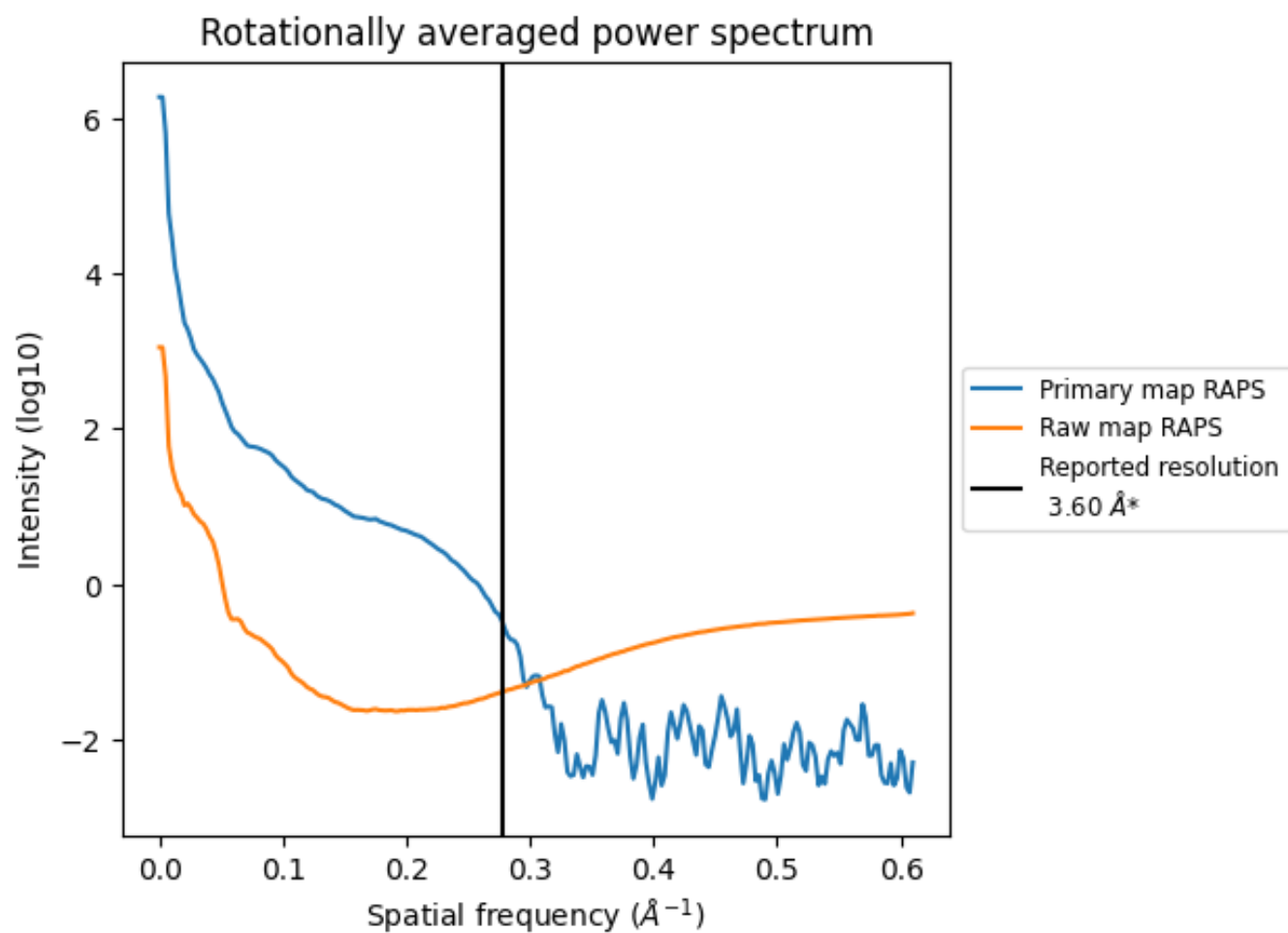
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1602 nm³; this corresponds to an approximate mass of 1447 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 ⓘ

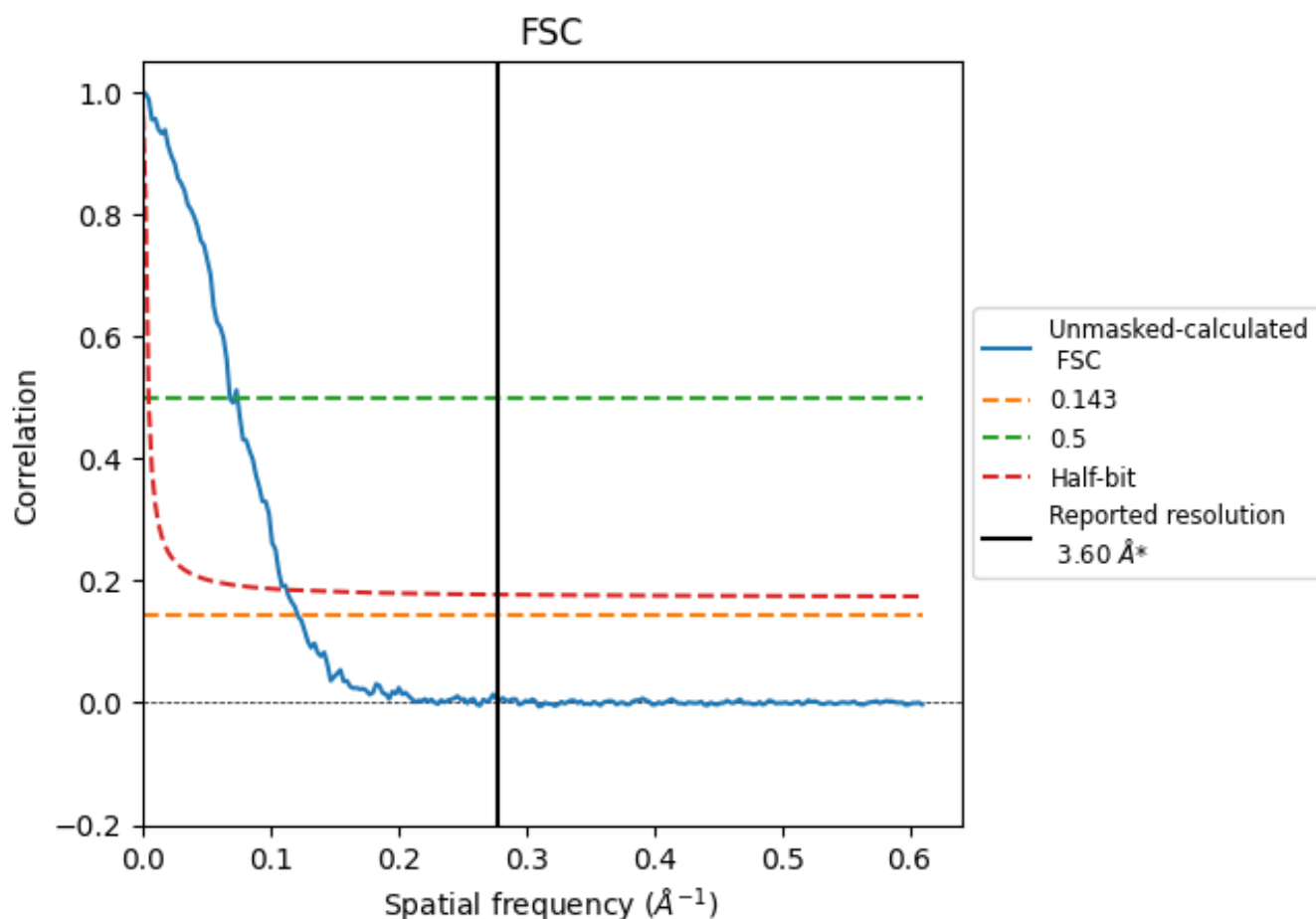


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

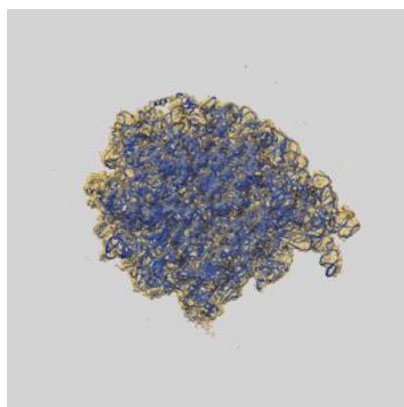
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.22	14.60	8.86

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.22 differs from the reported value 3.6 by more than 10 %

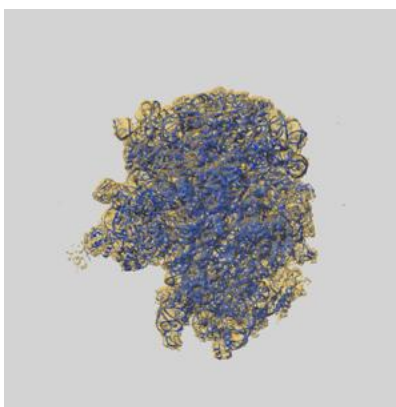
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8616 and PDB model 5UYL. Per-residue inclusion information can be found in section 3 on page 17.

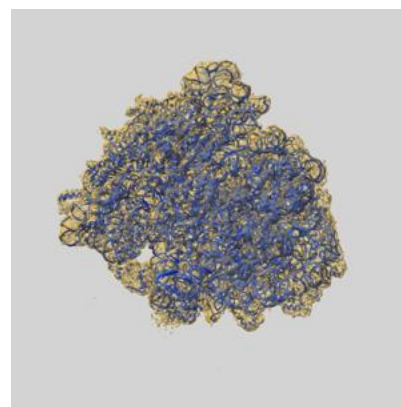
9.1 Map-model overlay [i](#)



X



Y



Z

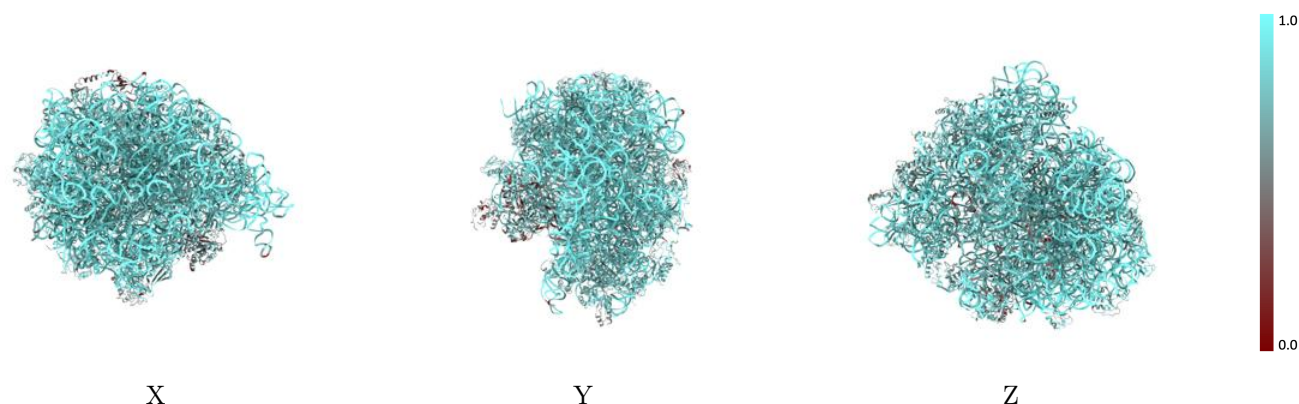
The images above show the 3D surface view of the map at the recommended contour level 3.49 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



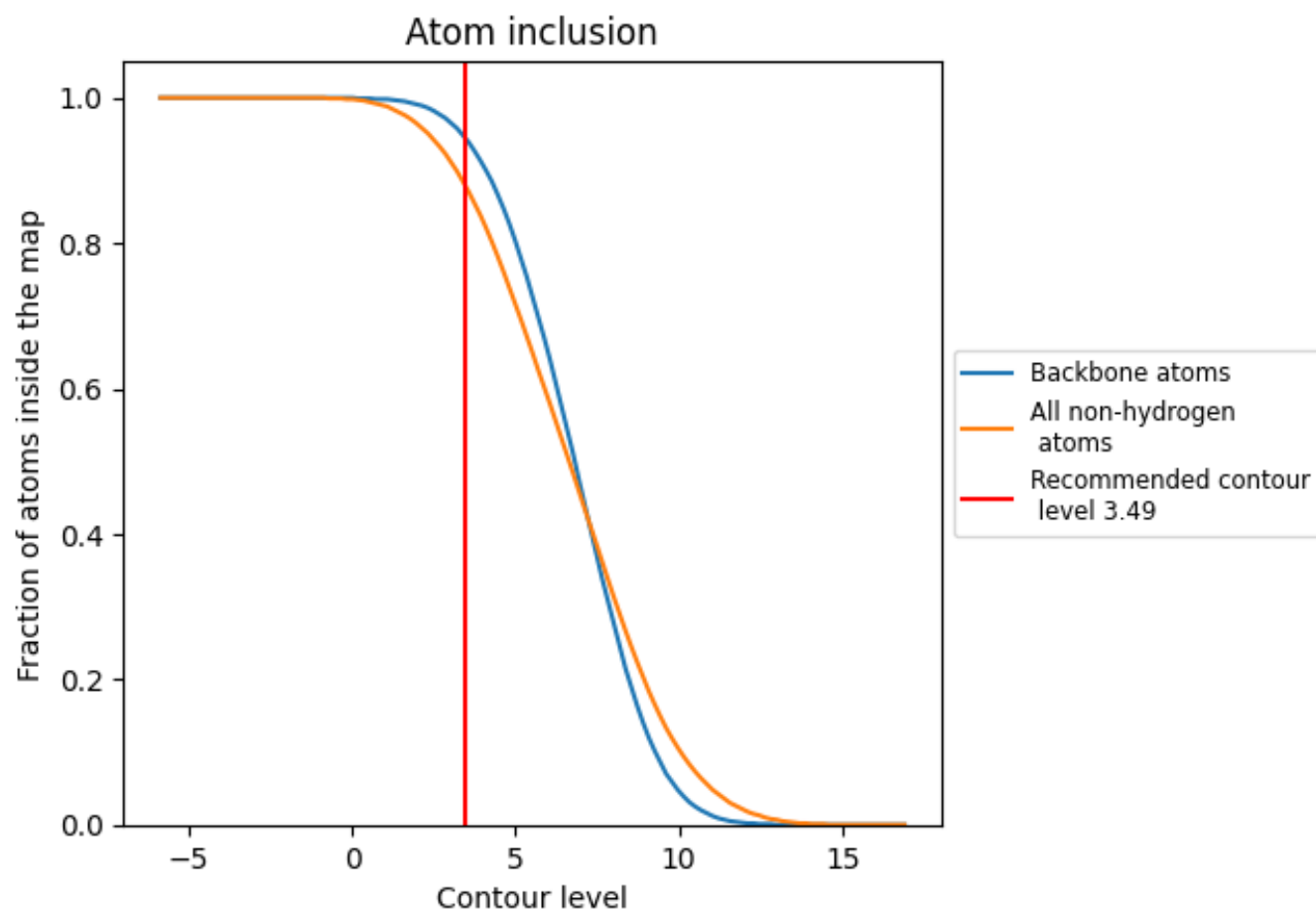
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.49).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% 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 (3.49) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8770	 0.3810
01	 0.9530	 0.4000
02	 0.9570	 0.3730
03	 0.5970	 0.2350
04	 0.8040	 0.4330
05	 0.7940	 0.4310
06	 0.7790	 0.3860
07	 0.7820	 0.3530
08	 0.7750	 0.3720
09	 0.5360	 0.3080
10	 0.4460	 0.2140
11	 0.5150	 0.2080
12	 0.7810	 0.3960
13	 0.7100	 0.4240
14	 0.7940	 0.3990
15	 0.7350	 0.4180
16	 0.8340	 0.4040
17	 0.8230	 0.3770
18	 0.7610	 0.4100
19	 0.8220	 0.4130
20	 0.7800	 0.4140
21	 0.7360	 0.3880
22	 0.7590	 0.3830
23	 0.7790	 0.3690
24	 0.7670	 0.3860
25	 0.7980	 0.4290
26	 0.7870	 0.4160
27	 0.7340	 0.3290
28	 0.8050	 0.3940
29	 0.7480	 0.3170
30	 0.7690	 0.4020
31	 0.6820	 0.3880
32	 0.7940	 0.4060
33	 0.8000	 0.4280
34	 0.7770	 0.4210



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Chain	Atom inclusion	Q-score
A	 0.9540	 0.3910
B	 0.7390	 0.3350
C	 0.7380	 0.3780
D	 0.7550	 0.3570
E	 0.7880	 0.3850
F	 0.7920	 0.3690
G	 0.7590	 0.3510
H	 0.7870	 0.3940
I	 0.7910	 0.3560
J	 0.6640	 0.3400
K	 0.7580	 0.3800
L	 0.7490	 0.4060
M	 0.7770	 0.3540
N	 0.7510	 0.3510
O	 0.7910	 0.3580
P	 0.8330	 0.3880
Q	 0.7870	 0.3860
R	 0.8040	 0.3760
S	 0.7910	 0.3700
T	 0.7780	 0.3470
U	 0.6310	 0.2810
V	 0.6570	 0.2880
W	 0.8770	 0.3650
X	 0.7320	 0.2090
Y	 0.7600	 0.2310
Z	 0.5560	 0.2740