



wwPDB EM Validation Summary Report ⓘ

Jun 21, 2026 – 06:02 am BST

PDB ID : 7ABZ / pdb_00007abz
EMDB ID : EMD-11710
Title : Structure of pre-accomodated trans-translation complex on E. coli stalled ribosome.
Authors : Guyomar, C.; D'Urso, G.; Chat, S.; Giudice, E.; Gillet, R.
Deposited on : 2020-09-09
Resolution : 3.21 Å(reported)
Based on initial model : 4YBB

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 : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

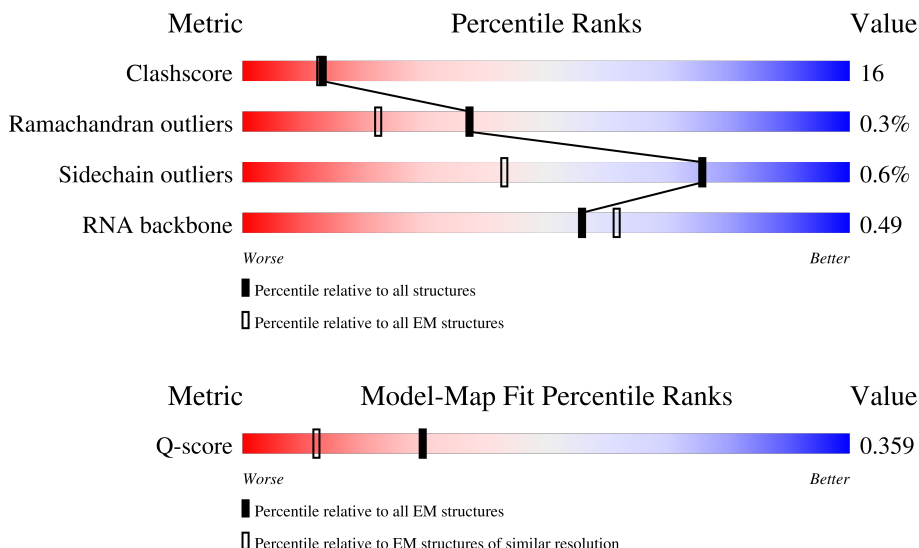
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.21 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	14613 (2.71 - 3.71)

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	1	2904	
2	2	1540	
3	3	118	

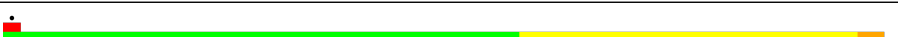
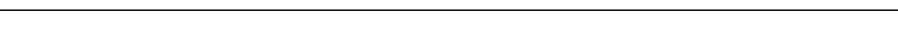
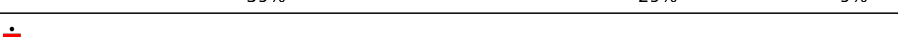
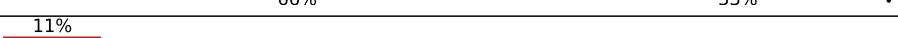
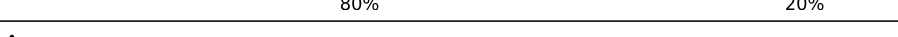
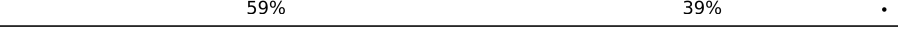
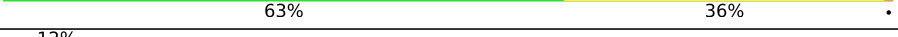
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	4	363	
5	5	146	
6	6	394	
7	7	76	
8	8	15	
9	A	80	
10	B	271	
11	C	209	
12	D	201	
13	E	177	
14	F	176	
15	G	149	
16	H	130	
17	I	142	
18	J	142	
19	K	122	
20	L	144	
21	M	136	
22	N	120	
23	O	116	
24	P	114	
25	Q	117	
26	R	103	
27	S	110	
28	T	93	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	U	102	
30	V	94	
31	X	77	
32	Y	62	
33	Z	58	
34	b	56	
35	c	50	
36	d	46	
37	e	64	
38	f	38	
39	g	224	
40	h	206	
41	i	205	
42	j	167	
43	k	100	
44	l	151	
45	m	129	
46	n	127	
47	o	98	
48	p	117	
49	q	123	
50	r	114	
51	s	100	
52	t	88	
53	u	82	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	v	80	
55	w	55	
56	x	79	
57	y	85	
58	z	56	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	PSU	7	32	-	-	X	-

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 157227 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 RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2904	Total	C	N	O	P	0	0
			62355	27825	11472	20154	2904		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1540	Total	C	N	O	P	0	0
			33048	14747	6054	10707	1540		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 4 is a RNA chain called transfer-messenger RNA (tmRNA).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	363	Total	C	N	O	P	0	0
			7760	3466	1410	2521	363		

- Molecule 5 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	146	Total	C	N	O	S	0	0
			1181	747	219	211	4		

- Molecule 6 is a protein called Elongation factor Tu 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	371	Total	C	N	O	S	0	0
			2871	1818	492	548	13		

- Molecule 7 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	76	Total	C	N	O	P	S	
			1635	735	291	532	75	2	0
									0

- Molecule 8 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	15	Total	C	N	O	P		
			327	145	60	107	15	0	0

- Molecule 9 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	80	Total	C	N	O	S		
			601	370	121	109	1	0	0

- Molecule 10 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	271	Total	C	N	O	S		
			2082	1288	423	364	7	0	0

- Molecule 11 is a protein called 50S ribosomal protein L3.

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

- Molecule 12 is a protein called 50S ribosomal protein L4.

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

- Molecule 13 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	177	Total	C	N	O	S		
			1410	899	249	256	6	0	0

- Molecule 14 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

- Molecule 15 is a protein called 50S ribosomal protein L9.

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

- Molecule 16 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	130	Total	C	N	O	S	0	0
			980	620	174	182	4		

- Molecule 17 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	66	Total	C	N	O	S	0	0
			470	289	87	91	3		

- Molecule 18 is a protein called 50S ribosomal protein L13.

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

- Molecule 19 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 20 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 21 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	136	Total	C	N	O	S	0	0
			1075	686	205	178	6		

- Molecule 22 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 23 is a protein called 50S ribosomal protein L18.

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

- Molecule 24 is a protein called 50S ribosomal protein L19.

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

- Molecule 25 is a protein called 50S ribosomal protein L20.

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

- Molecule 26 is a protein called 50S ribosomal protein L21.

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

- Molecule 27 is a protein called 50S ribosomal protein L22.

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

- Molecule 28 is a protein called 50S ribosomal protein L23.

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

- Molecule 29 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	102	Total	C	N	O	S	0	0
			780	492	146	142			

- Molecule 30 is a protein called 50S ribosomal protein L25.

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

- Molecule 31 is a protein called 50S ribosomal protein L28.

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

- Molecule 32 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 33 is a protein called 50S ribosomal protein L30.

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

- Molecule 34 is a protein called 50S ribosomal protein L32.

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

- Molecule 35 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	c	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 36 is a protein called 50S ribosomal protein L34.

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

- Molecule 37 is a protein called 50S ribosomal protein L35.

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

- Molecule 38 is a protein called 50S ribosomal protein L36.

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

- Molecule 39 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 40 is a protein called 30S ribosomal protein S3.

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

- Molecule 41 is a protein called 30S ribosomal protein S4.

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

- Molecule 42 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	152	Total	C	N	O	S	0	0
			1118	695	214	203	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	161	LYS	VAL	conflict	UNP P0A7W1

- Molecule 43 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 44 is a protein called 30S ribosomal protein S7.

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

- Molecule 45 is a protein called 30S ribosomal protein S8.

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

- Molecule 46 is a protein called 30S ribosomal protein S9.

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

- Molecule 47 is a protein called 30S ribosomal protein S10.

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

- Molecule 48 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	117	Total	C	N	O	S	0	0
			876	540	174	159	3		

- Molecule 49 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	123	Total	C	N	O	S	0	0
			956	591	196	164	5		

- Molecule 50 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 51 is a protein called 30S ribosomal protein S14.

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

- Molecule 52 is a protein called 30S ribosomal protein S15.

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

- Molecule 53 is a protein called 30S ribosomal protein S16.

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

- Molecule 54 is a protein called 30S ribosomal protein S17.

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

- Molecule 55 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	w	55	Total	C	N	O	0	0
			456	288	86	82		

- Molecule 56 is a protein called 30S ribosomal protein S19.

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

- Molecule 57 is a protein called 30S ribosomal protein S20.

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

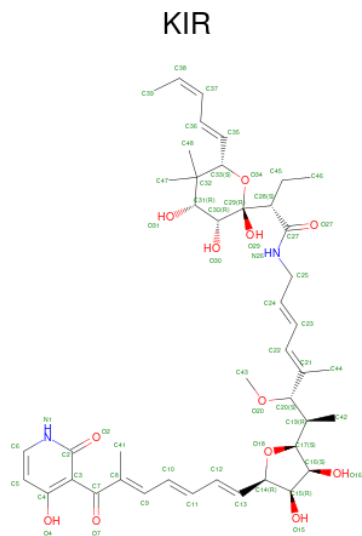
- Molecule 58 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	z	56	Total	C	N	O	S	0	0
			466	290	96	79	1		

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

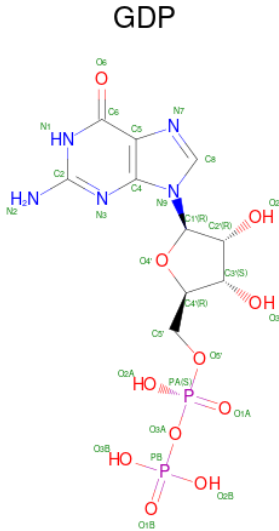
Mol	Chain	Residues	Atoms		AltConf
59	1	168	Total	Mg	0
			168	168	
59	2	18	Total	Mg	0
			18	18	
59	3	3	Total	Mg	0
			3	3	
59	B	1	Total	Mg	0
			1	1	
59	C	1	Total	Mg	0
			1	1	
59	O	1	Total	Mg	0
			1	1	

- Molecule 60 is KIRROMYCIN (CCD ID: KIR) (formula: C₄₃H₆₀N₂O₁₂).



Mol	Chain	Residues	Atoms				AltConf
60	6	1	Total	C	N	O	0
			57	43	2	12	

- Molecule 61 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
61	6	1	Total 28	C 10	N 5	O 11	P 2	0

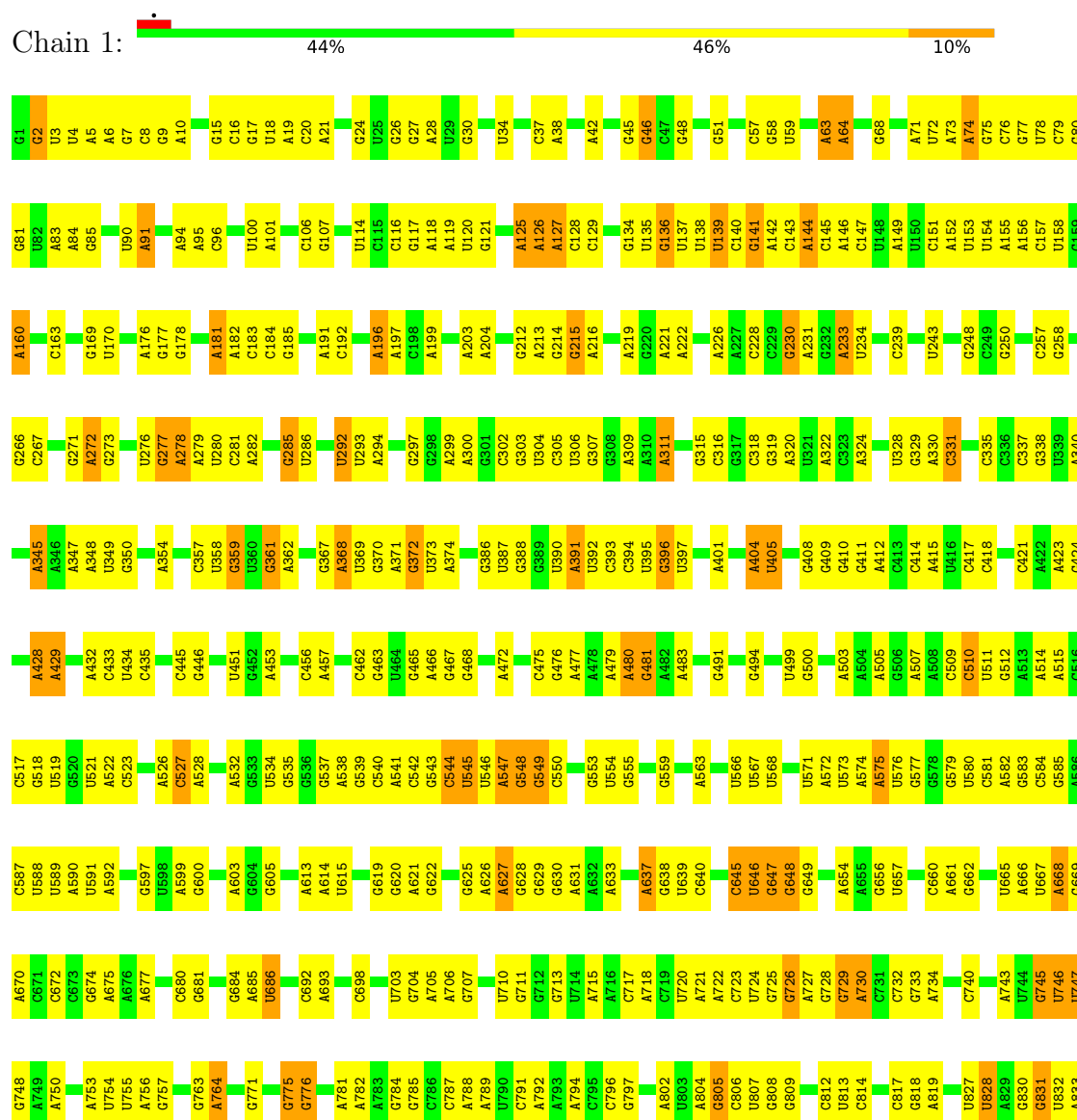
- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn).

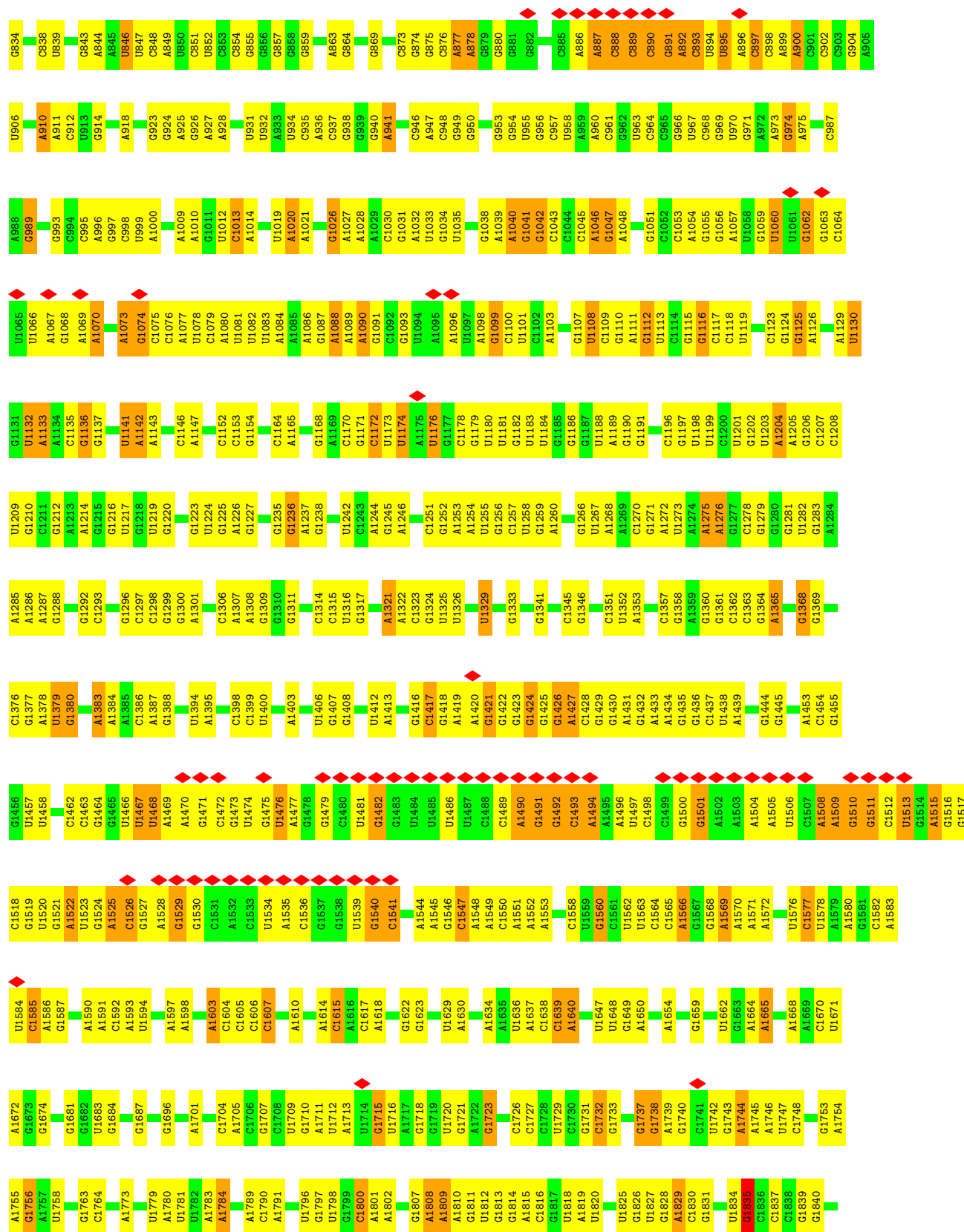
Mol	Chain	Residues	Atoms		AltConf
62	f	1	Total	Zn	0
			1	1	

3 Residue-property plots

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

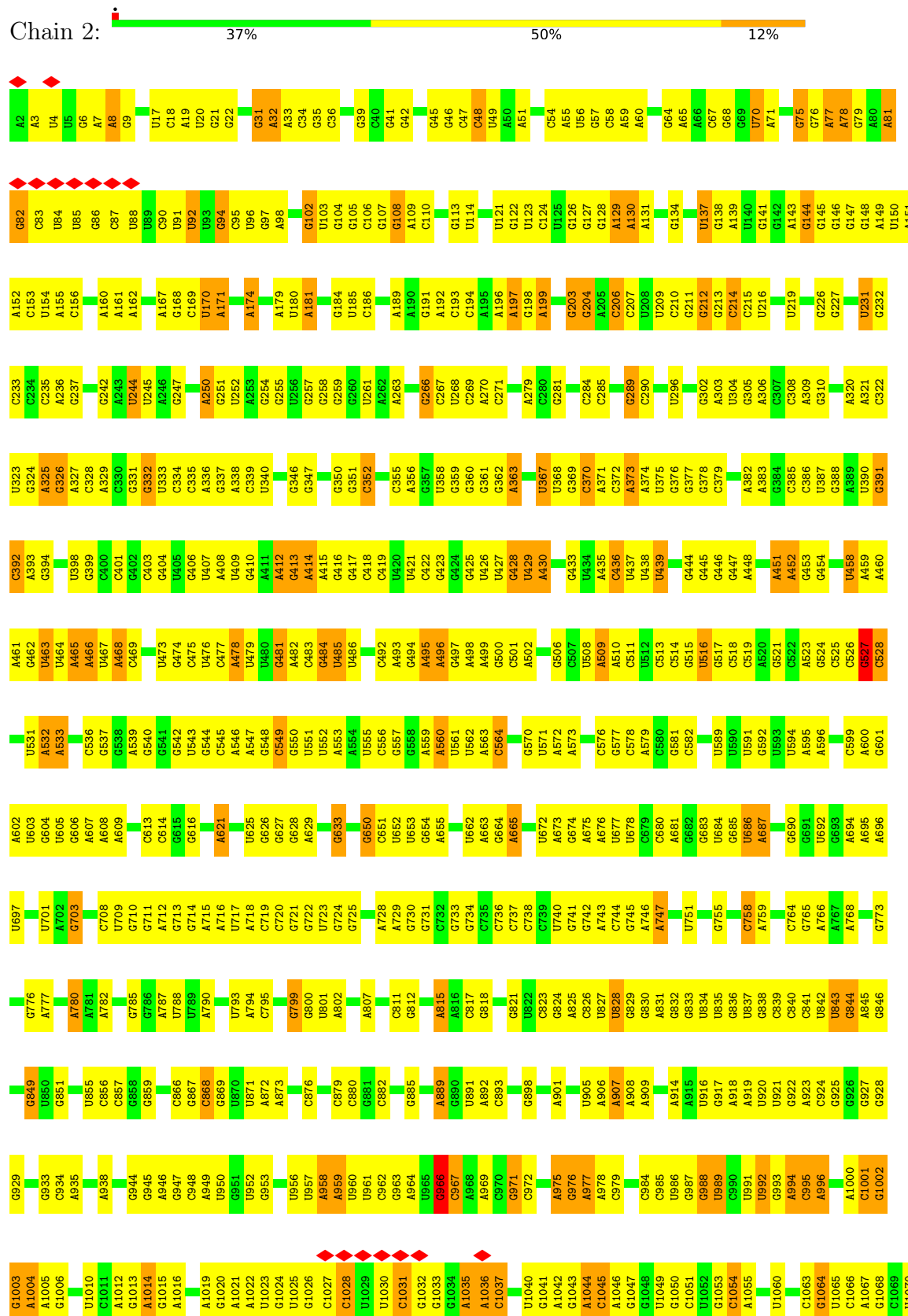
• Molecule 1: 23S ribosomal RNA

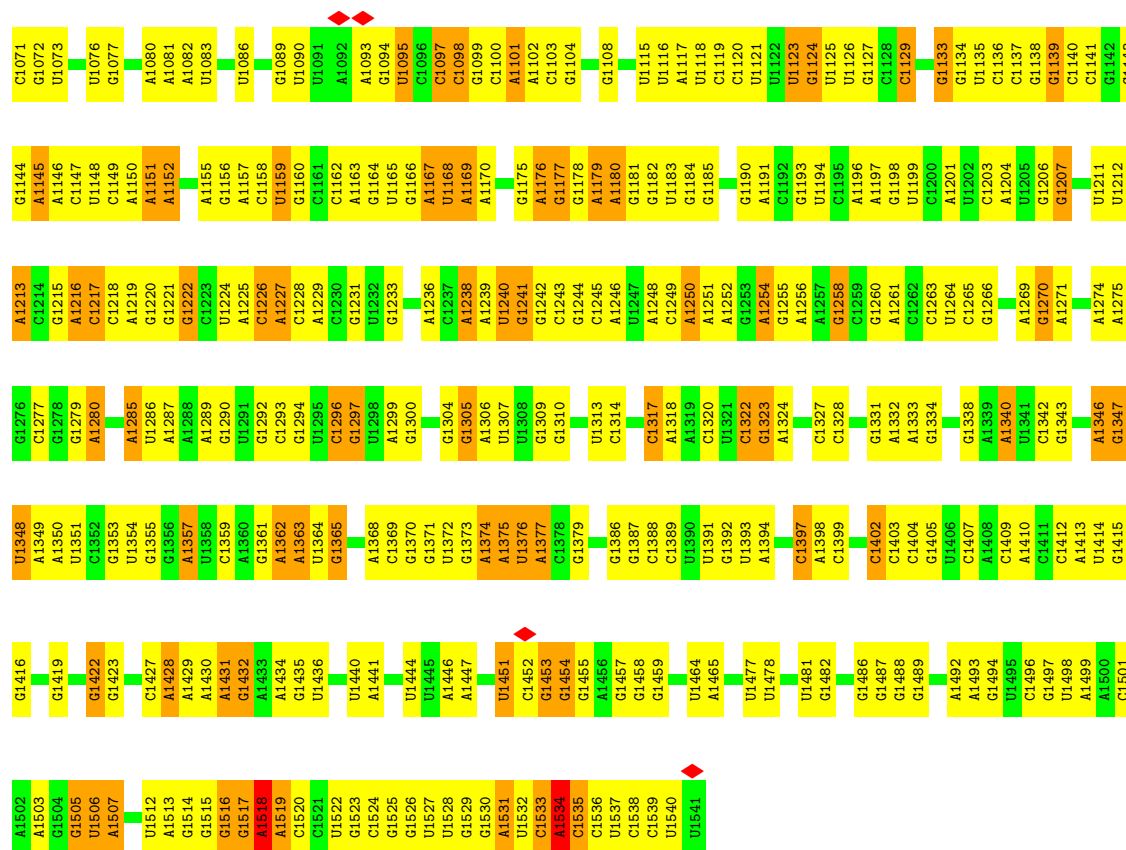




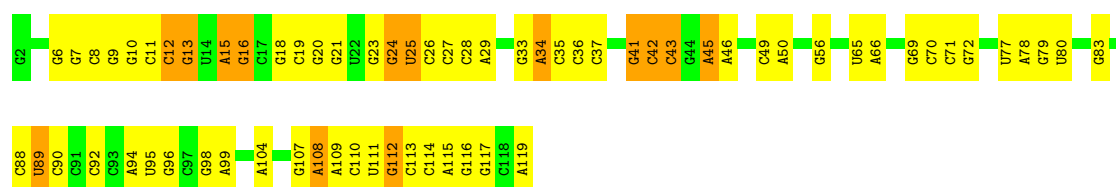
G2848	U2849	C2853	G2854	C2855	G2856	C2857	A2860	C2863	G2864	C2865	C2866	C2867	A2868	A2872	A2873	C2880	C2881	A2882	C2883	U2884	G2885	C2888	C2889	C2890	U2891	C2892	A2893	U2898	A2899	C2900	U2903	U2904	C2827	C2828	A2829	C2830	C2831	U2832	U2833	U2836	A2837	C2838	C2839	C2840	C2841	G2842	G2843	G2844	U2845	G2846	U2847					
G2697	U2698	C2699	A2700	G2701	G2702	U2707	G2708	U2709	C2710	A2711	G2714	C2715	C2716	C2717	G2718	C2719	U2720	A2721	G2722	C2723	U2724	A2725	A2726	C2727	U2728	G2729	C2730	G2731	C2732	A2733	G2737	A2738	U2739	A2740	U2743	G2744	A2748	G2751	C2752	U2753	U2754	C2755	U2756	A2757	A2765	A2766	C2841	G2842	G2843	G2844	U2845	G2846	U2847			
U2552	C2553	U2554	U2555	C2556	C2559	A2560	U2561	A2564	A2565	A2566	C2567	U2568	C2569	C2570	U2571	A2572	C2575	C2579	U2580	C2581	A2582	C2583	U2584	U2585	U2586	A2587	C2588	A2589	C2592	U2593	C2594	U2595	U2596	C2597	A2598	U2599	A2600	C2601	A2602	C2603	U2604	U2605	C2606	C2607	C2608	U2609	C2610	C2611	C2612	U2613	A2614	U2615	C2616	U2617		
A2476	U2477	A2478	U2479	C2480	C2483	C2484	C2485	C2486	C2487	C2488	C2489	U2491	C2494	C2495	A2496	C2497	C2498	C2499	U2500	C2501	A2502	C2503	U2504	C2505	U2506	C2512	C2513	U2514	C2515	A2516	C2517	C2518	C2526	C2527	U2528	U2529	A2530	C2531	C2532	G2533	C2534	U2535	A2536	C2537	C2540	C2544	A2547	U2548	C2549	C2550	C2551					
G2383	U2384	C2385	A2386	G2391	A2392	C2395	C2396	U2401	U2402	C2403	U2404	C2405	A2406	A2411	G2415	C2416	C2417	U2418	U2419	C2420	G2421	C2422	U2423	C2424	A2425	A2426	C2427	C2428	G2429	A2430	U2431	U2438	A2439	C2440	U2441	C2442	C2443	G2444	C2445	C2446	G2447	A2448	C2455	C2456	U2457	C2458	A2459	U2460	U2473	U2474	C2475					
C2310	A2311	U2312	C2313	A2314	C2315	C2316	A2317	C2318	C2319	U2320	U2321	C2322	C2323	U2324	C2325	C2326	A2327	A2328	U2329	C2330	C2331	C2332	U2333	A2334	C2335	A2336	C2339	U2343	U2344	C2345	A2346	C2347	C2348	C2349	C2350	C2351	C2357	C2361	C2362	C2363	C2364	C2365	C2370	C2371	U2372	C2373	C2374	C2375	C2376	C2377	A2378	C2379	C2380			
G2234	G2238	G2239	U2240	A2241	C2242	U2243	U2244	U2245	G2246	A2247	G2250	C2251	C2252	G2253	C2254	C2255	C2256	U2257	C2258	C2264	U2265	A2266	A2267	G2271	C2275	A2278	G2279	C2283	C2284	C2285	G2286	A2287	G2290	U2291	U2292	C2293	G2294	C2295	A2298	U2299	C2300	U2302	C2303	G2304	A2305	C2306	C2307	G2308	A2309							
U2155	G2156	C2157	A2158	C2159	C2160	C2161	C2162	A2163	C2164	U2165	U2166	U2167	A2168	C2169	A2170	U2171	U2172	A2173	C2174	C2175	C2178	A2183	A2184	U2185	C2186	U2189	C2190	A2191	U2192	C2193	U2194	U2195	A2198	U2202	C2203	G2204	C2208	G2209	U2210	A2211	A2212	C2215	G2216	G2217	A2225	U2229	G2230	U2231	C2232	U2233						
U2092	G2093	A2097	U2098	U2099	C2100	A2101	C2102	C2103	C2104	U2105	U2106	C2107	A2108	U2109	G2110	U2111	U2112	A2113	A2114	G2115	C2116	A2117	U2118	A2119	C2120	G2121	U2122	C2123	A2126	C2127	G2128	C2129	U2130	U2131	U2132	C2133	A2134	A2135	G2136	U2137	C2138	U2139	G2140	A2142	C2143	C2144	C2145	C2146	A2147	G2148	U2149	U2150	U2151	G2152	C2153	A2154
U1926	A1927	G1928	G1929	U1930	U1931	A1936	U1939	U1943	G1947	G1948	A1952	A1953	G1954	U1955	U1956	C1962	U1963	G1964	C1965	A1966	C1967	G1968	A1969	U1970	U1971	G1972	A1977	G1983	A1987	G1988	U1991	G1992	U1993	C1996	C1997	A1998	C1999	G2002	C2008	A2009	G2010	U2011	C2012	G2018	A2019	U1923	C1924	C1925								
C2021	U2022	C2023	G2024	C2025	U2026	C2027	U2028	C2029	A2030	C2031	C2032	A2033	U2034	C2035	C2036	A2037	C2038	U2039	C2040	C2043	C2047	G2048	A2052	C2055	C2056	A2059	A2060	C2061	A2062	C2063	C2064	C2065	U2068	C2069	A2070	A2071	C2072	C2073	U2074	U2075	U2076	A2077	C2078	U2079	A2080	U2081	A2082	U2086	C2087	A2090	U2091	C2091				
A1847	A1848	G1849	G1850	U1851	A1854	G1857	A1858	G1862	G1863	U1864	U1865	A1866	G1867	C1870	A1871	A1872	G1873	C1874	G1875	A1876	A1877	U1880	C1881	U1882	U1883	G1884	G1888	G1891	C1894	C1895	G1906	G1907	C1908	C1909	U1910	U1911	A1912	A1913	C1914	C1915	A1916	U1917	A1918	U1919	C1920	G1921	G1922	U1923	C1924	C1925						

● Molecule 2: 16S ribosomal RNA

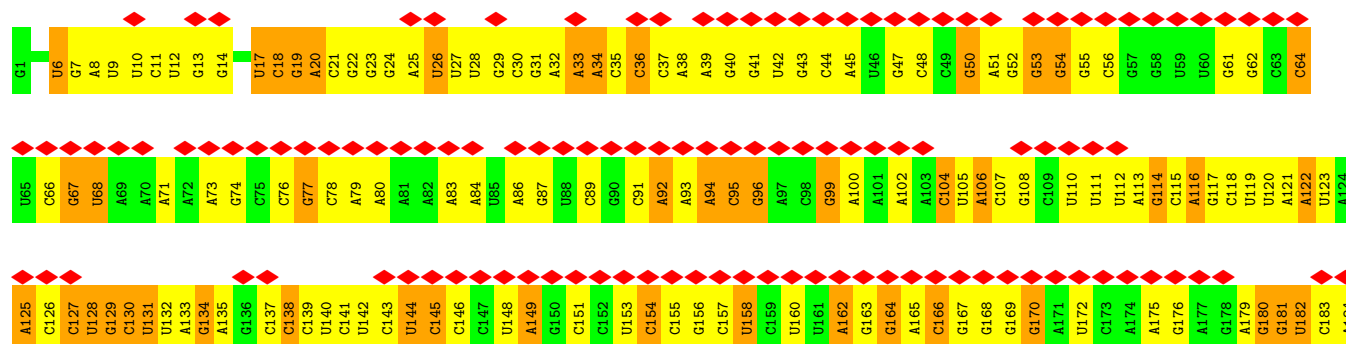




• Molecule 3: 5S ribosomal RNA



• Molecule 4: transfer-messenger RNA (tmRNA)

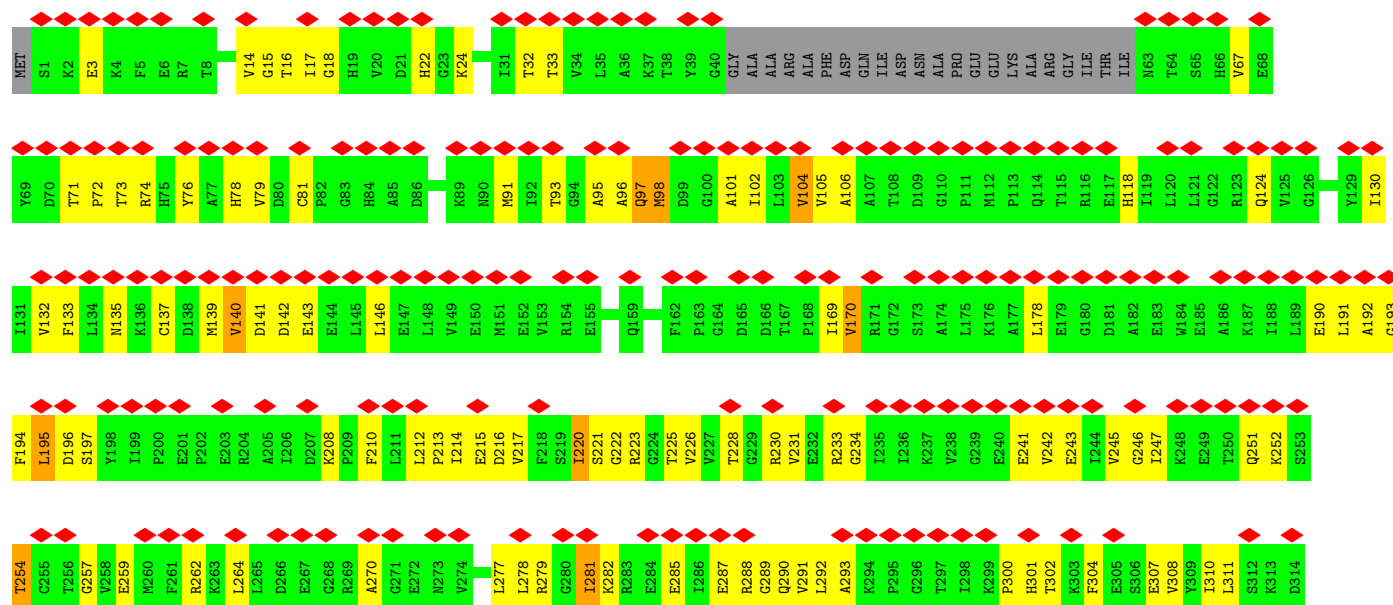


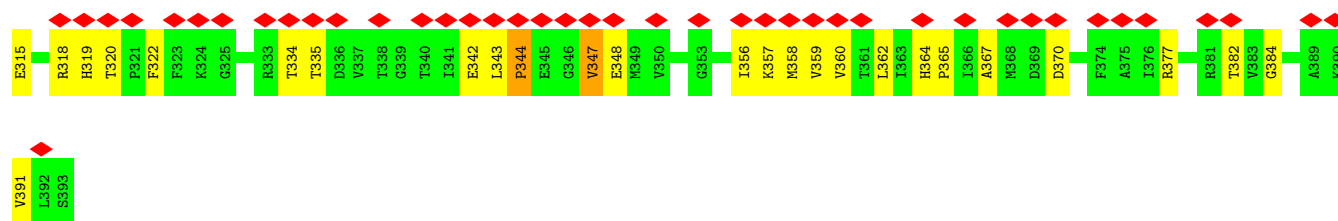


• Molecule 5: SsrA-binding protein

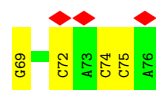


• Molecule 6: Elongation factor Tu 2

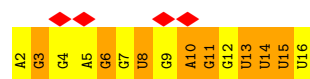




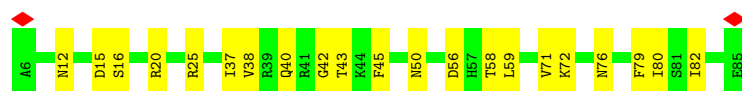
- Molecule 7: tRNA-Phe



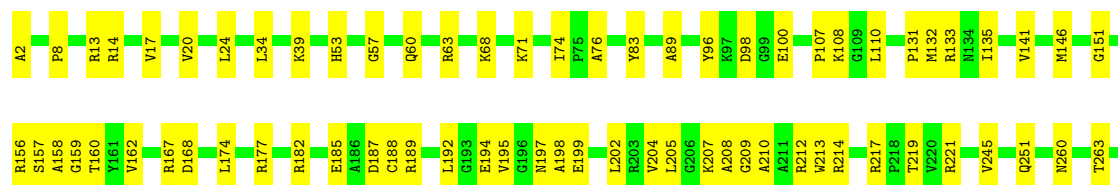
- Molecule 8: mRNA



- Molecule 9: 50S ribosomal protein L27

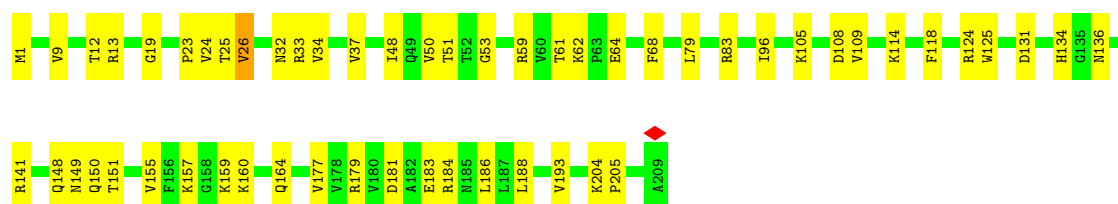


- Molecule 10: 50S ribosomal protein L2



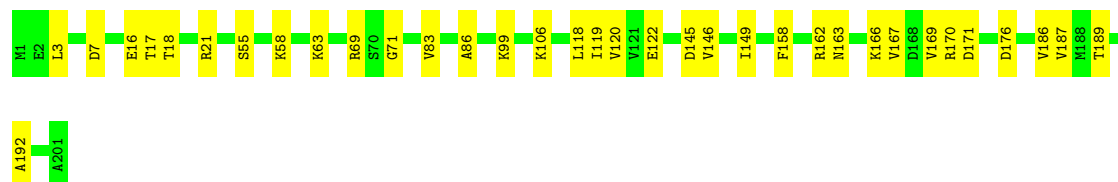
- Molecule 11: 50S ribosomal protein L3





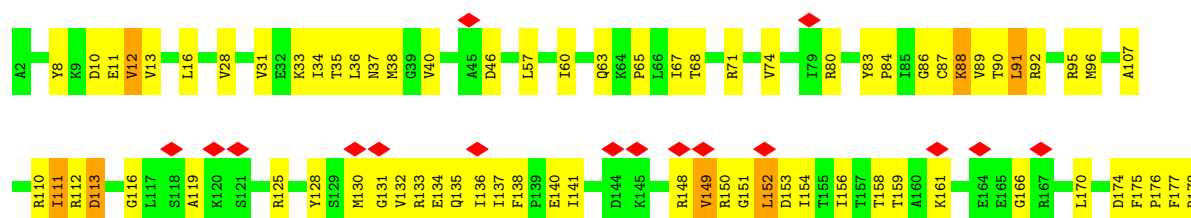
• Molecule 12: 50S ribosomal protein L4

Chain D: 83% 17%



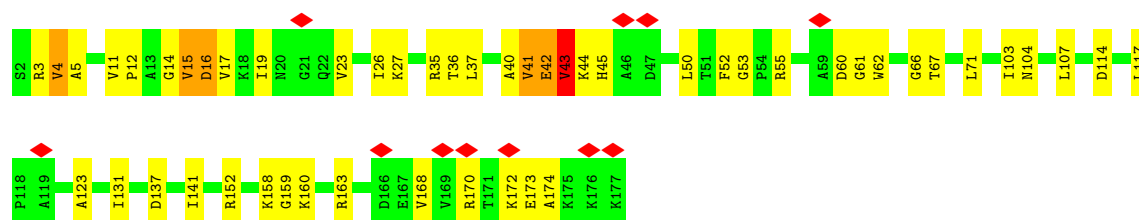
• Molecule 13: 50S ribosomal protein L5

Chain E: 9% 58% 38%



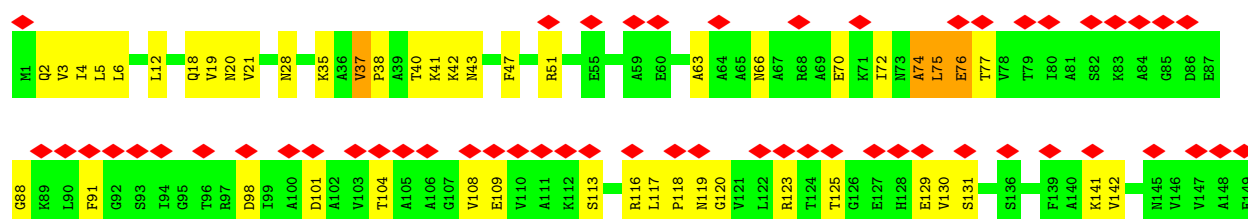
• Molecule 14: 50S ribosomal protein L6

Chain F: 6% 71% 26%

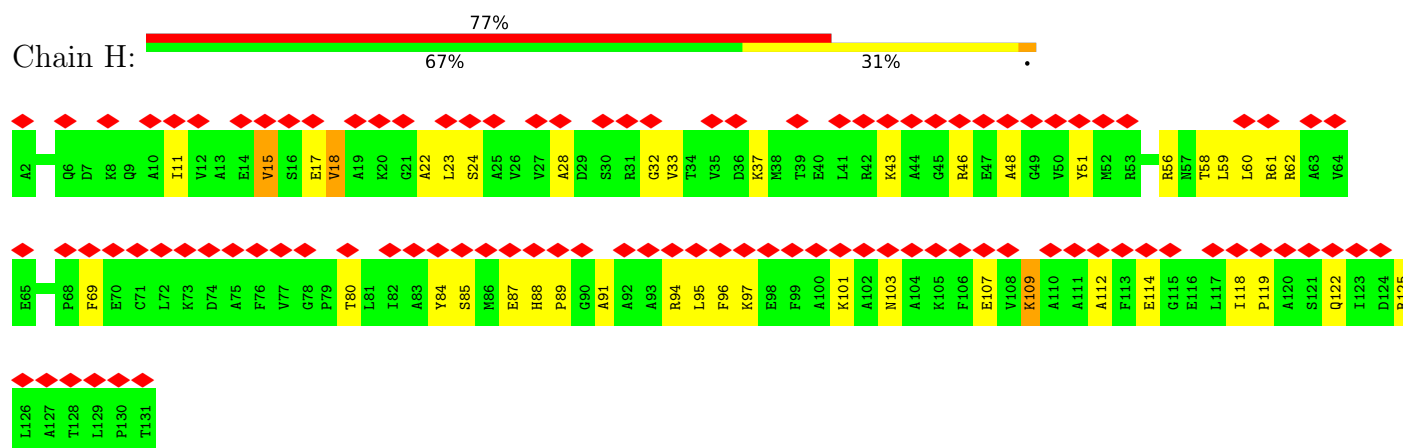


• Molecule 15: 50S ribosomal protein L9

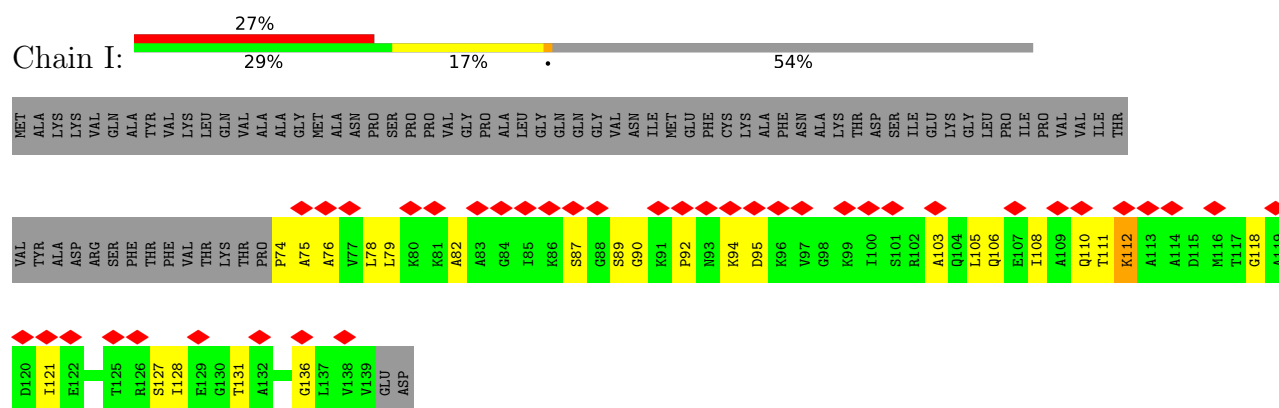
Chain G: 37% 68% 30%



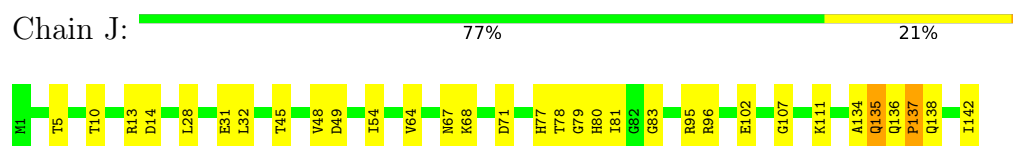
- Molecule 16: 50S ribosomal protein L10



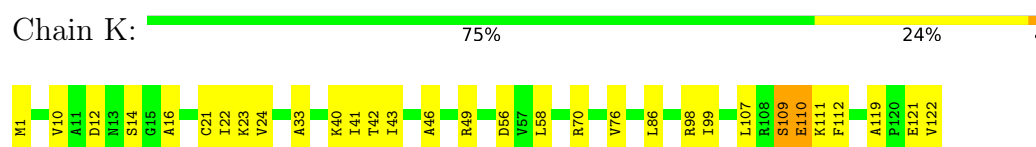
- Molecule 17: 50S ribosomal protein L11



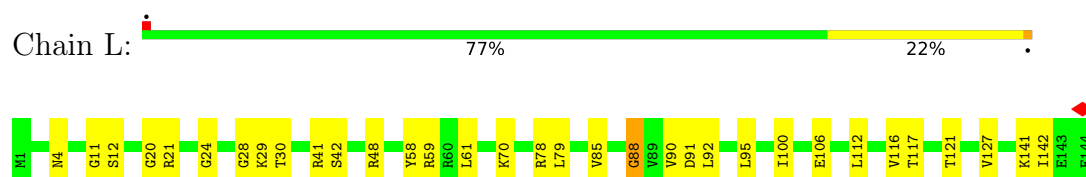
- Molecule 18: 50S ribosomal protein L13



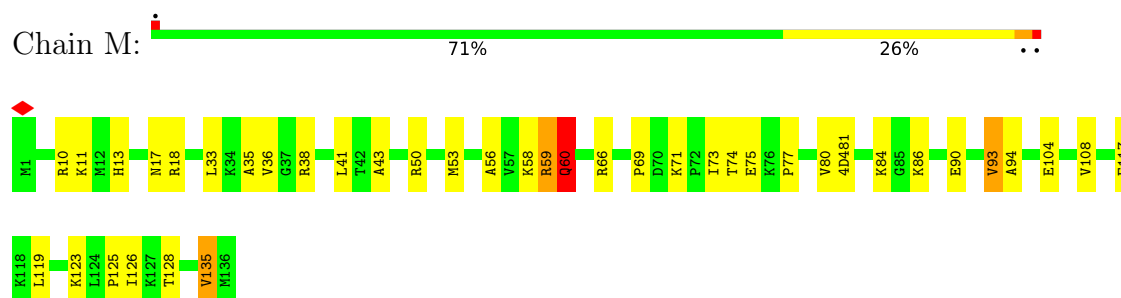
- Molecule 19: 50S ribosomal protein L14



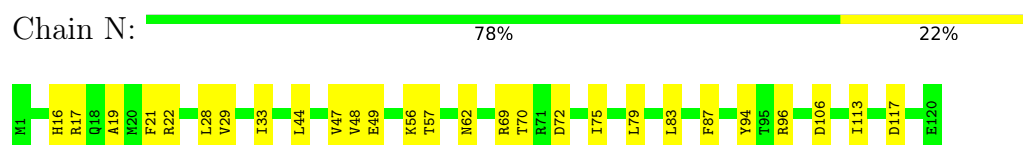
- Molecule 20: 50S ribosomal protein L15



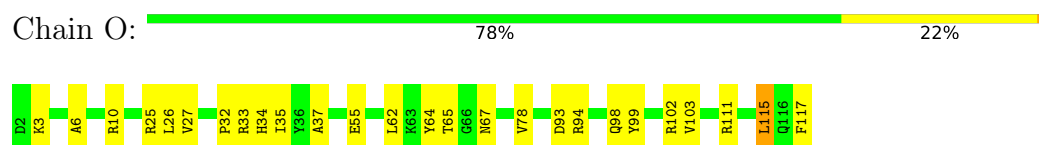
- Molecule 21: 50S ribosomal protein L16



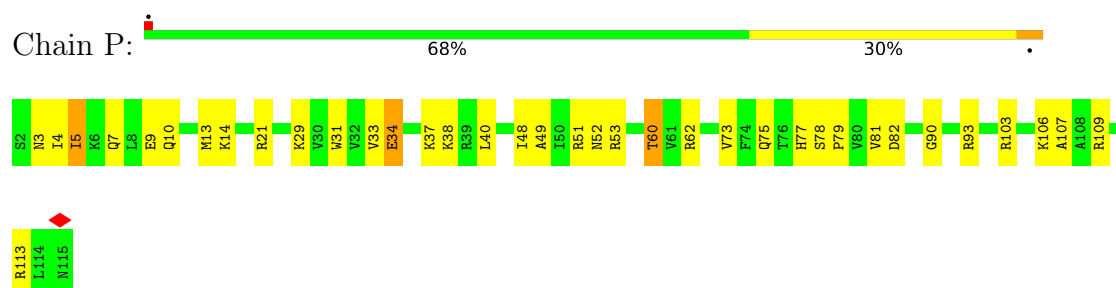
- Molecule 22: 50S ribosomal protein L17



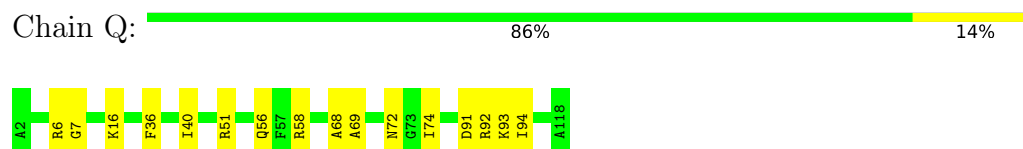
- Molecule 23: 50S ribosomal protein L18



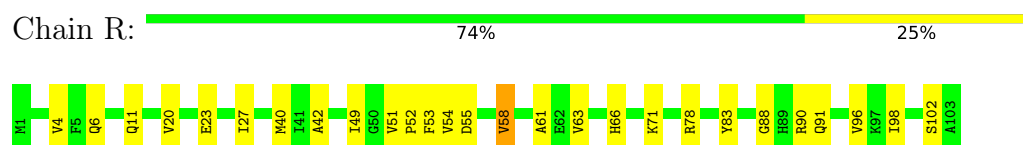
- Molecule 24: 50S ribosomal protein L19



- Molecule 25: 50S ribosomal protein L20



- Molecule 26: 50S ribosomal protein L21



- Molecule 27: 50S ribosomal protein L22

Chain S:  75% 25%



- Molecule 28: 50S ribosomal protein L23

Chain T:  85% 15%



- Molecule 29: 50S ribosomal protein L24

Chain U:  71% 27%



- Molecule 30: 50S ribosomal protein L25

Chain V:  65% 35%



- Molecule 31: 50S ribosomal protein L28

Chain X:  69% 30%



- Molecule 32: 50S ribosomal protein L29

Chain Y:  84% 16%



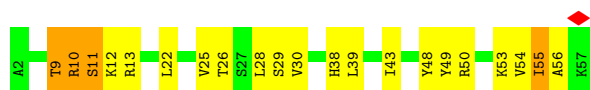
- Molecule 33: 50S ribosomal protein L30

Chain Z:  72% 28%



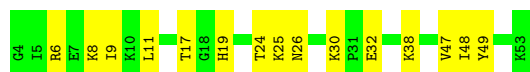
- Molecule 34: 50S ribosomal protein L32

Chain b:  62% 30% 7%



- Molecule 35: 50S ribosomal protein L33

Chain c:  70% 30%



- Molecule 36: 50S ribosomal protein L34

Chain d:  83% 15% .



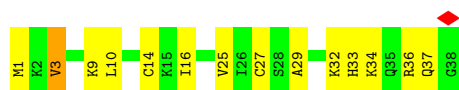
- Molecule 37: 50S ribosomal protein L35

Chain e:  73% 23% .



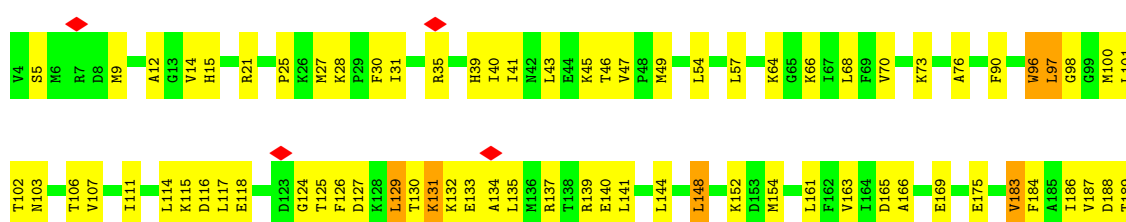
- Molecule 38: 50S ribosomal protein L36

Chain f:  63% 34% .



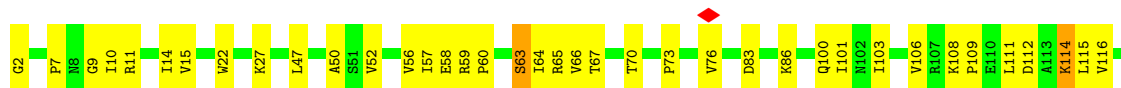
- Molecule 39: 30S ribosomal protein S2

Chain g:  58% 38% .

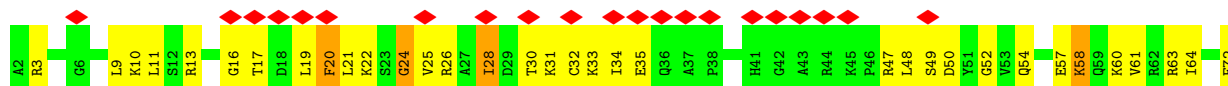




- Molecule 40: 30S ribosomal protein S3



- Molecule 41: 30S ribosomal protein S4



- Molecule 42: 30S ribosomal protein S5

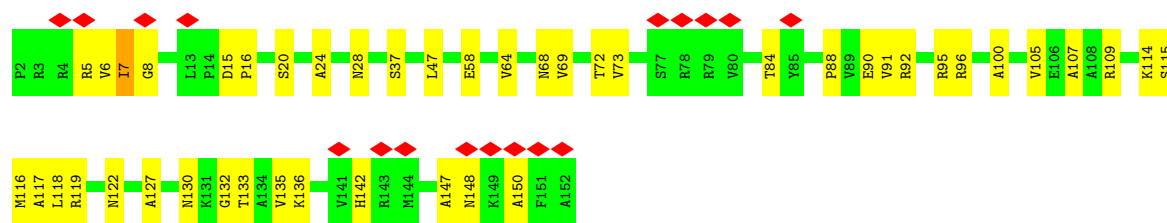


- Molecule 43: 30S ribosomal protein S6



- Molecule 44: 30S ribosomal protein S7





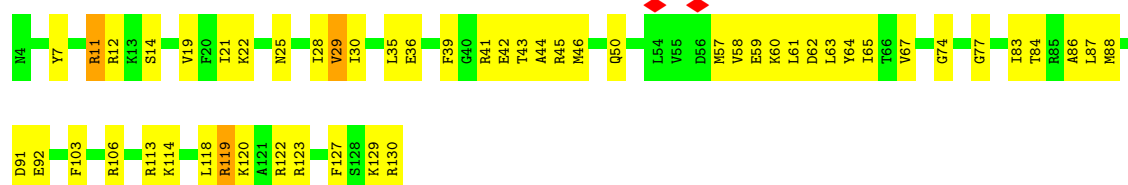
• Molecule 45: 30S ribosomal protein S8

Chain m: 80% 20%



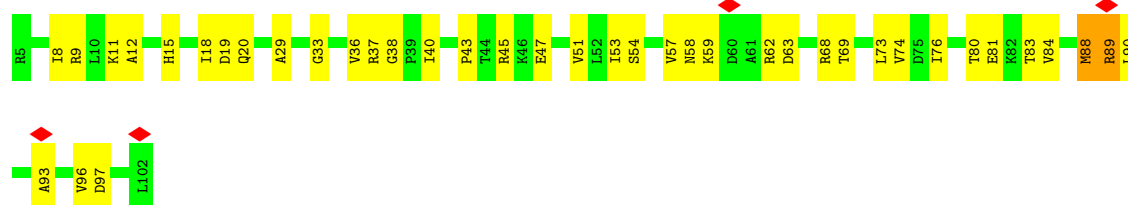
• Molecule 46: 30S ribosomal protein S9

Chain n: 59% 39%



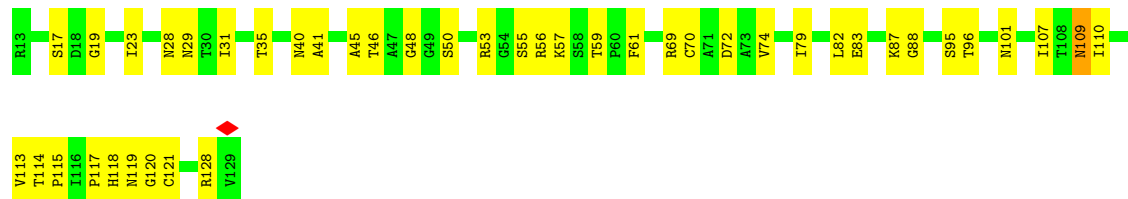
• Molecule 47: 30S ribosomal protein S10

Chain o: 59% 39%



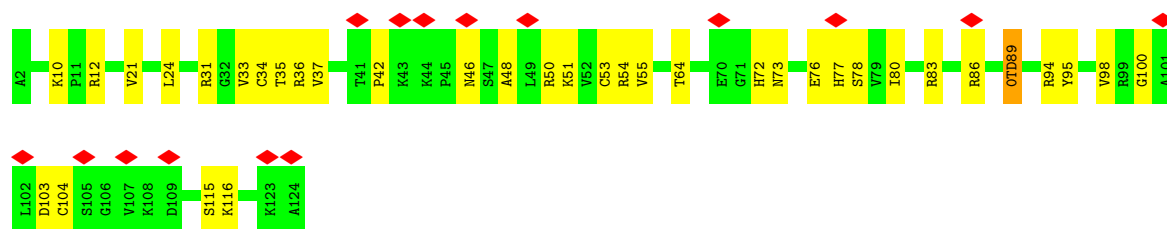
• Molecule 48: 30S ribosomal protein S11

Chain p: 63% 36%

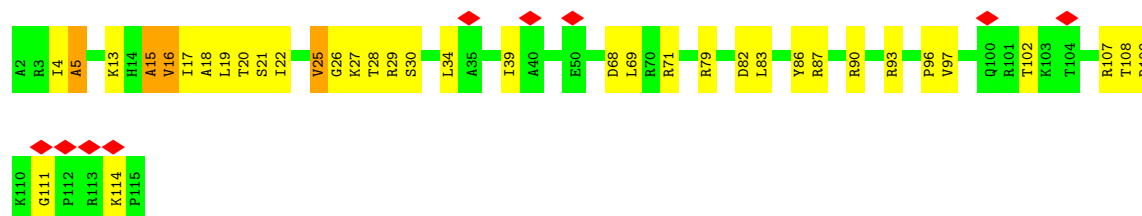


• Molecule 49: 30S ribosomal protein S12

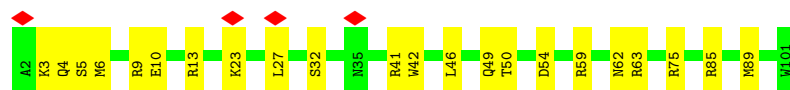
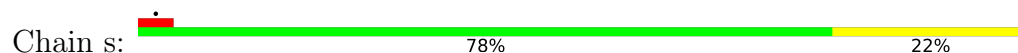
Chain q: 12% 71% 28%



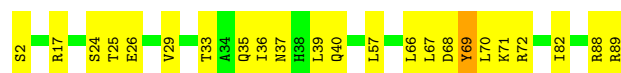
- Molecule 50: 30S ribosomal protein S13



- Molecule 51: 30S ribosomal protein S14



- Molecule 52: 30S ribosomal protein S15



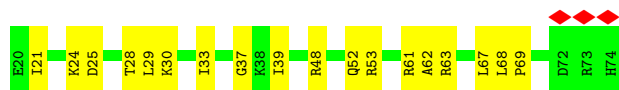
- Molecule 53: 30S ribosomal protein S16



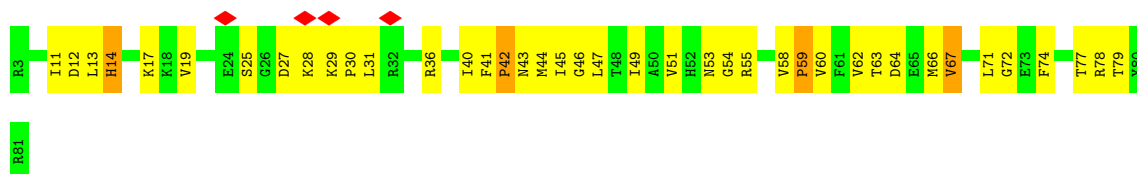
- Molecule 54: 30S ribosomal protein S17



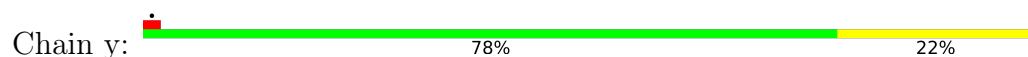
- Molecule 55: 30S ribosomal protein S18



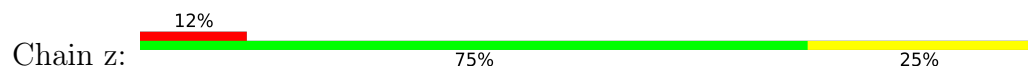
- Molecule 56: 30S ribosomal protein S19



- Molecule 57: 30S ribosomal protein S20



- Molecule 58: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18452	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	-1000	Depositor
Maximum defocus (nm)	-3000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	19.820	Depositor
Minimum map value	-6.531	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	446.784, 446.784, 446.784	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.074, 1.074, 1.074	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, OMC, 3TD, UR3, PSU, OMU, MA6, 5MU, 2MG, 6MZ, 3AU, KIR, 4OC, 5MC, 4SU, OMG, MG, 4D4, G7M, MIA, 0TD, 1MG, 2MA, ZN

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	1	0.09	1/69307 (0.0%)	0.25	12/108118 (0.0%)
2	2	0.10	1/36722 (0.0%)	0.22	1/57280 (0.0%)
3	3	0.08	0/2828	0.22	0/4410
4	4	0.10	0/8616	0.27	0/13430
5	5	0.34	2/1203 (0.2%)	0.77	8/1616 (0.5%)
6	6	0.33	3/2924 (0.1%)	0.75	19/3955 (0.5%)
7	7	0.49	6/1624 (0.4%)	0.30	0/2527
8	8	0.17	0/366	0.45	0/570
9	A	0.14	0/608	0.48	0/804
10	B	0.17	0/2121	0.53	3/2852 (0.1%)
11	C	0.15	0/1586	0.42	0/2134
12	D	0.14	0/1571	0.49	2/2113 (0.1%)
13	E	0.35	1/1434 (0.1%)	0.88	7/1926 (0.4%)
14	F	0.23	0/1342	0.80	9/1816 (0.5%)
15	G	0.41	3/1122 (0.3%)	0.77	5/1515 (0.3%)
16	H	0.18	0/993	0.70	4/1340 (0.3%)
17	I	0.14	0/471	0.62	2/627 (0.3%)
18	J	0.42	1/1152 (0.1%)	0.55	3/1551 (0.2%)
19	K	0.28	1/947 (0.1%)	0.62	5/1268 (0.4%)
20	L	0.17	0/1062	0.55	1/1413 (0.1%)
21	M	0.18	0/1081	0.52	2/1443 (0.1%)
22	N	0.16	0/973	0.49	0/1301
23	O	0.14	0/902	0.43	0/1209
24	P	0.17	0/929	0.68	4/1242 (0.3%)
25	Q	0.20	0/960	0.56	2/1278 (0.2%)
26	R	0.22	0/829	0.55	2/1107 (0.2%)
27	S	0.16	0/864	0.58	3/1156 (0.3%)
28	T	0.13	0/745	0.43	0/994
29	U	0.49	2/788 (0.3%)	0.76	4/1051 (0.4%)
30	V	0.14	0/766	0.39	0/1025
31	X	0.31	1/635 (0.2%)	0.72	4/848 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.10	0/502	0.34	0/667
33	Z	0.13	0/453	0.46	0/605
34	b	0.83	4/450 (0.9%)	0.81	1/599 (0.2%)
35	c	0.15	0/416	0.54	0/554
36	d	0.16	0/380	0.55	0/498
37	e	0.44	1/513 (0.2%)	0.84	3/676 (0.4%)
38	f	0.14	0/303	0.45	0/397
39	g	0.23	0/1784	0.77	9/2403 (0.4%)
40	h	0.15	0/1652	0.51	3/2225 (0.1%)
41	i	0.30	1/1665 (0.1%)	0.85	14/2227 (0.6%)
42	j	0.34	1/1131 (0.1%)	0.81	7/1520 (0.5%)
43	k	0.18	0/835	0.61	2/1128 (0.2%)
44	l	0.26	0/1196	0.72	5/1602 (0.3%)
45	m	0.15	0/989	0.42	0/1326
46	n	0.25	0/1034	0.91	10/1375 (0.7%)
47	o	0.26	1/797 (0.1%)	0.62	3/1077 (0.3%)
48	p	0.21	0/892	0.59	2/1205 (0.2%)
49	q	0.17	0/959	0.54	0/1286
50	r	0.18	0/892	0.75	7/1193 (0.6%)
51	s	0.14	0/817	0.41	0/1088
52	t	0.14	0/722	0.57	2/964 (0.2%)
53	u	0.15	0/659	0.56	1/884 (0.1%)
54	v	0.21	0/658	0.80	6/881 (0.7%)
55	w	0.14	0/463	0.47	0/621
56	x	0.71	2/653 (0.3%)	0.96	6/877 (0.7%)
57	y	0.15	0/671	0.46	0/888
58	z	0.14	0/473	0.37	0/627
All	All	0.17	32/169430 (0.0%)	0.39	183/253312 (0.1%)

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	x	59	PRO	N-CD	14.93	1.68	1.47
18	J	137	PRO	N-CD	-13.52	1.28	1.47
29	U	50	PRO	N-CD	10.82	1.62	1.47
34	b	10	ARG	C-O	-9.88	1.11	1.24
6	6	72	PRO	N-CD	9.36	1.60	1.47

The worst 5 of 183 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2439	A	C3'-C2'-O2'	-20.98	83.12	114.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2439	A	C1'-C2'-O2'	-16.93	86.40	111.80
13	E	174	ASP	CA-C-N	14.36	139.91	120.67
13	E	174	ASP	C-N-CA	14.36	139.91	120.67
1	1	2439	A	C2'-C3'-O3'	-14.08	88.38	109.50

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	1	62355	0	31381	1249	0
2	2	33048	0	16654	807	0
3	3	2529	0	1281	53	0
4	4	7760	0	3921	150	0
5	5	1181	0	1198	107	0
6	6	2871	0	2888	214	0
7	7	1635	0	844	60	0
8	8	327	0	161	18	0
9	A	601	0	615	15	0
10	B	2082	0	2154	90	0
11	C	1565	0	1616	48	0
12	D	1552	0	1619	26	0
13	E	1410	0	1444	116	0
14	F	1322	0	1371	45	0
15	G	1111	0	1148	71	0
16	H	980	0	1013	74	0
17	I	470	0	508	24	0
18	J	1129	0	1162	31	0
19	K	938	0	1012	27	0
20	L	1053	0	1129	30	0
21	M	1075	0	1154	32	0
22	N	960	0	1000	31	0
23	O	892	0	923	20	0
24	P	917	0	962	44	0
25	Q	947	0	1019	20	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	R	816	0	837	38	0
27	S	857	0	922	30	0
28	T	739	0	807	25	0
29	U	780	0	831	32	0
30	V	753	0	780	23	0
31	X	625	0	652	20	0
32	Y	501	0	531	9	0
33	Z	449	0	488	10	0
34	b	444	0	458	39	0
35	c	409	0	440	14	0
36	d	377	0	418	9	0
37	e	504	0	572	17	0
38	f	302	0	340	10	0
39	g	1753	0	1779	128	0
40	h	1625	0	1696	69	0
41	i	1643	0	1706	122	0
42	j	1118	0	1162	76	0
43	k	817	0	808	50	0
44	l	1182	0	1238	61	0
45	m	979	0	1031	35	0
46	n	1022	0	1070	76	0
47	o	787	0	828	36	0
48	p	876	0	887	36	0
49	q	956	0	1015	66	0
50	r	883	0	941	40	0
51	s	805	0	844	29	0
52	t	714	0	734	30	0
53	u	649	0	666	21	0
54	v	649	0	691	30	0
55	w	456	0	478	18	0
56	x	638	0	665	79	0
57	y	665	0	714	21	0
58	z	466	0	491	16	0
59	1	168	0	0	0	0
59	2	18	0	0	0	0
59	3	3	0	0	0	0
59	B	1	0	0	0	0
59	C	1	0	0	0	0
59	O	1	0	0	0	0
60	6	57	0	59	3	0
61	6	28	0	12	0	0
62	f	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	157227	0	105768	4191	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 16.

The worst 5 of 4191 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)
6:6:191:LEU:HA	6:6:194:PHE:CE2	1.24	1.66
16:H:59:LEU:HD23	16:H:62:ARG:CG	1.16	1.60
52:t:25:THR:HG21	52:t:70:LEU:CD1	1.26	1.58
43:k:3:HIS:CE1	43:k:95:ALA:H	1.22	1.58
39:g:129:LEU:HD21	39:g:135:LEU:CD1	1.11	1.57

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	
5	5	144/146 (99%)	127 (88%)	17 (12%)	0	100	100
6	6	367/394 (93%)	343 (94%)	24 (6%)	0	100	100
9	A	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
10	B	269/271 (99%)	257 (96%)	12 (4%)	0	100	100
11	C	207/209 (99%)	200 (97%)	7 (3%)	0	100	100
12	D	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
13	E	175/177 (99%)	149 (85%)	23 (13%)	3 (2%)	7	33
14	F	174/176 (99%)	161 (92%)	11 (6%)	2 (1%)	11	42
15	G	147/149 (99%)	133 (90%)	14 (10%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	H	128/130 (98%)	105 (82%)	23 (18%)	0	100	100
17	I	64/142 (45%)	55 (86%)	8 (12%)	1 (2%)	7	35
18	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
19	K	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
20	L	142/144 (99%)	131 (92%)	11 (8%)	0	100	100
21	M	133/136 (98%)	127 (96%)	5 (4%)	1 (1%)	16	48
22	N	118/120 (98%)	111 (94%)	7 (6%)	0	100	100
23	O	114/116 (98%)	113 (99%)	1 (1%)	0	100	100
24	P	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
25	Q	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
26	R	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
27	S	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
28	T	91/93 (98%)	86 (94%)	5 (6%)	0	100	100
29	U	100/102 (98%)	88 (88%)	10 (10%)	2 (2%)	6	30
30	V	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
31	X	75/77 (97%)	75 (100%)	0	0	100	100
32	Y	60/62 (97%)	55 (92%)	5 (8%)	0	100	100
33	Z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
34	b	54/56 (96%)	47 (87%)	5 (9%)	2 (4%)	2	17
35	c	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
36	d	44/46 (96%)	42 (96%)	1 (2%)	1 (2%)	5	27
37	e	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
38	f	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
39	g	222/224 (99%)	201 (90%)	20 (9%)	1 (0%)	24	58
40	h	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
41	i	203/205 (99%)	185 (91%)	17 (8%)	1 (0%)	24	58
42	j	150/167 (90%)	129 (86%)	20 (13%)	1 (1%)	18	52
43	k	98/100 (98%)	89 (91%)	9 (9%)	0	100	100
44	l	149/151 (99%)	143 (96%)	5 (3%)	1 (1%)	18	52
45	m	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
46	n	125/127 (98%)	114 (91%)	11 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	o	96/98 (98%)	87 (91%)	9 (9%)	0	100	100
48	p	115/117 (98%)	98 (85%)	17 (15%)	0	100	100
49	q	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
50	r	112/114 (98%)	100 (89%)	12 (11%)	0	100	100
51	s	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
52	t	86/88 (98%)	83 (96%)	3 (4%)	0	100	100
53	u	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
54	v	78/80 (98%)	75 (96%)	3 (4%)	0	100	100
55	w	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
56	x	77/79 (98%)	68 (88%)	9 (12%)	0	100	100
57	y	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
58	z	54/56 (96%)	54 (100%)	0	0	100	100
All	All	6203/6425 (96%)	5787 (93%)	400 (6%)	16 (0%)	37	67

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	F	42	GLU
42	j	103	THR
21	M	60	GLN
29	U	99	ASN
34	b	11	SER

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	
5	5	122/122 (100%)	122 (100%)	0	100	100
6	6	310/327 (95%)	310 (100%)	0	100	100
9	A	59/59 (100%)	59 (100%)	0	100	100
10	B	216/216 (100%)	215 (100%)	1 (0%)	81	84

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	C	164/164 (100%)	163 (99%)	1 (1%)	78	83
12	D	165/165 (100%)	165 (100%)	0	100	100
13	E	148/148 (100%)	143 (97%)	5 (3%)	32	62
14	F	137/137 (100%)	135 (98%)	2 (2%)	57	74
15	G	114/114 (100%)	113 (99%)	1 (1%)	70	79
16	H	99/99 (100%)	98 (99%)	1 (1%)	68	78
17	I	48/110 (44%)	48 (100%)	0	100	100
18	J	116/116 (100%)	116 (100%)	0	100	100
19	K	103/103 (100%)	103 (100%)	0	100	100
20	L	103/103 (100%)	102 (99%)	1 (1%)	68	78
21	M	108/108 (100%)	106 (98%)	2 (2%)	50	71
22	N	100/100 (100%)	100 (100%)	0	100	100
23	O	86/86 (100%)	85 (99%)	1 (1%)	63	77
24	P	99/99 (100%)	99 (100%)	0	100	100
25	Q	89/89 (100%)	89 (100%)	0	100	100
26	R	84/84 (100%)	83 (99%)	1 (1%)	63	77
27	S	93/93 (100%)	93 (100%)	0	100	100
28	T	80/80 (100%)	80 (100%)	0	100	100
29	U	83/83 (100%)	83 (100%)	0	100	100
30	V	78/78 (100%)	76 (97%)	2 (3%)	40	66
31	X	67/67 (100%)	67 (100%)	0	100	100
32	Y	54/54 (100%)	54 (100%)	0	100	100
33	Z	48/48 (100%)	48 (100%)	0	100	100
34	b	47/47 (100%)	46 (98%)	1 (2%)	47	69
35	c	45/45 (100%)	45 (100%)	0	100	100
36	d	38/38 (100%)	38 (100%)	0	100	100
37	e	51/51 (100%)	51 (100%)	0	100	100
38	f	34/34 (100%)	33 (97%)	1 (3%)	37	64
39	g	186/186 (100%)	185 (100%)	1 (0%)	81	84
40	h	170/170 (100%)	168 (99%)	2 (1%)	63	77
41	i	172/172 (100%)	170 (99%)	2 (1%)	63	77

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	j	114/126 (90%)	113 (99%)	1 (1%)	70	79
43	k	87/87 (100%)	85 (98%)	2 (2%)	44	68
44	l	124/124 (100%)	124 (100%)	0	100	100
45	m	104/104 (100%)	104 (100%)	0	100	100
46	n	105/105 (100%)	105 (100%)	0	100	100
47	o	86/86 (100%)	86 (100%)	0	100	100
48	p	90/90 (100%)	90 (100%)	0	100	100
49	q	102/102 (100%)	102 (100%)	0	100	100
50	r	92/92 (100%)	92 (100%)	0	100	100
51	s	83/83 (100%)	83 (100%)	0	100	100
52	t	76/76 (100%)	76 (100%)	0	100	100
53	u	65/65 (100%)	65 (100%)	0	100	100
54	v	74/74 (100%)	74 (100%)	0	100	100
55	w	48/48 (100%)	48 (100%)	0	100	100
56	x	70/70 (100%)	67 (96%)	3 (4%)	26	57
57	y	65/65 (100%)	65 (100%)	0	100	100
58	z	48/48 (100%)	46 (96%)	2 (4%)	26	58
All	All	5149/5240 (98%)	5116 (99%)	33 (1%)	76	83

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	x	25	SER
56	x	27	ASP
58	z	28	VAL
21	M	93	VAL
20	L	116	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
32	Y	20	ASN
41	i	85	ASN
52	t	62	GLN
32	Y	45	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
40	h	140	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2903/2904 (99%)	560 (19%)	24 (0%)
2	2	1539/1540 (99%)	337 (21%)	14 (0%)
3	3	117/118 (99%)	22 (18%)	3 (2%)
4	4	362/363 (99%)	175 (48%)	10 (2%)
7	7	75/76 (98%)	16 (21%)	3 (4%)
8	8	14/15 (93%)	10 (71%)	1 (7%)
All	All	5010/5016 (99%)	1120 (22%)	55 (1%)

5 of 1120 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	G
1	1	10	A
1	1	15	G
1	1	27	G
1	1	28	A

5 of 55 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	391	G
2	2	1346	A
8	8	14	U
4	4	334	A
2	2	429	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

46 non-standard protein/DNA/RNA residues 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
1	PSU	1	746	1,59	18,21,22	1.07	1 (5%)	22,30,33	1.71	5 (22%)
21	4D4	M	81	21	9,11,12	2.03	2 (22%)	8,13,15	1.86	3 (37%)
1	6MZ	1	2030	1	22,25,26	2.71	3 (13%)	30,36,39	2.38	11 (36%)
1	PSU	1	2457	1	18,21,22	1.04	1 (5%)	22,30,33	1.73	4 (18%)
2	MA6	2	1518	2	23,26,27	1.75	4 (17%)	34,38,41	3.94	14 (41%)
1	2MG	1	2445	1	23,26,27	3.04	8 (34%)	32,38,41	2.76	12 (37%)
2	MA6	2	1519	2	23,26,27	1.76	4 (17%)	34,38,41	3.97	14 (41%)
1	2MG	1	1835	1	23,26,27	3.09	7 (30%)	32,38,41	2.85	12 (37%)
1	PSU	1	1917	1	18,21,22	1.14	2 (11%)	22,30,33	1.84	5 (22%)
2	4OC	2	1402	2	20,23,24	3.21	8 (40%)	26,32,35	0.88	1 (3%)
1	1MG	1	745	1	22,26,27	2.65	5 (22%)	33,39,42	1.76	8 (24%)
2	UR3	2	1498	2	19,22,23	3.01	8 (42%)	26,32,35	1.29	2 (7%)
1	5MU	1	1939	1	19,22,23	5.27	5 (26%)	28,32,35	3.60	9 (32%)
1	PSU	1	955	1	18,21,22	1.10	1 (5%)	22,30,33	1.74	4 (18%)
1	2MA	1	2503	1,59	22,25,26	3.88	7 (31%)	33,37,40	3.58	11 (33%)
2	2MG	2	1516	2	23,26,27	3.05	8 (34%)	32,38,41	2.74	13 (40%)
7	PSU	7	55	7	18,21,22	1.10	1 (5%)	22,30,33	1.74	4 (18%)
49	0TD	q	89	49	7,9,10	1.47	0	6,11,13	2.02	2 (33%)
1	G7M	1	2069	1	23,26,27	2.63	8 (34%)	35,39,42	2.44	10 (28%)
7	G7M	7	46	7	23,26,27	4.08	11 (47%)	35,39,42	1.69	7 (20%)
2	PSU	2	516	2	18,21,22	1.08	1 (5%)	22,30,33	1.75	4 (18%)
7	PSU	7	32	7	18,21,22	1.10	1 (5%)	22,30,33	1.69	5 (22%)
1	5MU	1	747	1	19,22,23	5.26	5 (26%)	28,32,35	3.60	9 (32%)
1	5MC	1	1962	1	18,22,23	3.74	7 (38%)	26,32,35	1.04	2 (7%)
2	5MC	2	967	2	18,22,23	3.75	7 (38%)	26,32,35	0.98	1 (3%)
2	5MC	2	1407	2	18,22,23	3.76	7 (38%)	26,32,35	0.99	2 (7%)
7	5MU	7	54	7	19,22,23	5.19	5 (26%)	28,32,35	3.51	9 (32%)
2	G7M	2	527	2	23,26,27	2.66	8 (34%)	35,39,42	2.42	10 (28%)
1	PSU	1	2504	1	18,21,22	1.09	1 (5%)	22,30,33	1.76	4 (18%)
1	OMU	1	2552	1	19,22,23	2.99	8 (42%)	26,31,34	1.70	5 (19%)
4	PSU	4	347	4	18,21,22	1.10	1 (5%)	22,30,33	1.82	5 (22%)
7	4SU	7	8	7	18,21,22	3.83	7 (38%)	26,30,33	2.23	4 (15%)
1	6MZ	1	1618	1	22,25,26	2.72	3 (13%)	30,36,39	2.33	11 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	2MG	2	966	2	23,26,27	3.08	8 (34%)	32,38,41	2.82	12 (37%)
4	PSU	4	342	4	18,21,22	1.12	1 (5%)	22,30,33	1.76	4 (18%)
1	PSU	1	2580	1	18,21,22	1.05	1 (5%)	22,30,33	1.86	5 (22%)
1	3TD	1	1915	1	18,22,23	4.22	6 (33%)	22,32,35	1.65	3 (13%)
4	5MU	4	341	4	19,22,23	5.27	5 (26%)	28,32,35	3.52	9 (32%)
7	PSU	7	39	7	18,21,22	1.10	1 (5%)	22,30,33	1.73	4 (18%)
1	PSU	1	2605	1	18,21,22	1.11	1 (5%)	22,30,33	1.75	4 (18%)
7	MIA	7	37	7	28,31,32	2.55	4 (14%)	40,44,47	5.72	18 (45%)
1	PSU	1	1911	1	18,21,22	1.08	1 (5%)	22,30,33	1.76	4 (18%)
7	3AU	7	47	7	24,28,29	2.40	8 (33%)	33,40,43	1.23	2 (6%)
1	OMG	1	2251	1,7	23,26,27	2.67	6 (26%)	33,38,41	3.30	9 (27%)
1	OMC	1	2498	1,59	19,22,23	3.40	8 (42%)	26,31,34	0.75	0
2	2MG	2	1207	2	23,26,27	3.07	8 (34%)	32,38,41	2.75	12 (37%)

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
1	PSU	1	746	1,59	-	2/7/25/26	0/2/2/2
21	4D4	M	81	21	-	4/11/12/14	-
1	6MZ	1	2030	1	-	4/9/27/28	0/3/3/3
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	2/11/29/30	0/3/3/3
1	2MG	1	2445	1	-	3/9/27/28	0/3/3/3
2	MA6	2	1519	2	-	2/11/29/30	0/3/3/3
1	2MG	1	1835	1	-	0/9/27/28	0/3/3/3
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
2	4OC	2	1402	2	-	0/9/29/30	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
2	UR3	2	1498	2	-	2/7/25/26	0/2/2/2
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	2MA	1	2503	1,59	-	3/7/25/26	0/3/3/3
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
7	PSU	7	55	7	-	0/7/25/26	0/2/2/2
49	0TD	q	89	49	-	5/7/12/14	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	G7M	1	2069	1	-	1/7/25/26	0/3/3/3
7	G7M	7	46	7	-	2/7/25/26	0/3/3/3
2	PSU	2	516	2	-	0/7/25/26	0/2/2/2
7	PSU	7	32	7	-	0/7/25/26	0/2/2/2
1	5MU	1	747	1	-	1/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
7	5MU	7	54	7	-	0/7/25/26	0/2/2/2
2	G7M	2	527	2	-	2/7/25/26	0/3/3/3
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	0/9/27/28	0/2/2/2
4	PSU	4	347	4	-	0/7/25/26	0/2/2/2
7	4SU	7	8	7	-	1/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	2/9/27/28	0/3/3/3
2	2MG	2	966	2	-	2/9/27/28	0/3/3/3
4	PSU	4	342	4	-	2/7/25/26	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	3TD	1	1915	1	-	4/7/25/26	0/2/2/2
4	5MU	4	341	4	-	2/7/25/26	0/2/2/2
7	PSU	7	39	7	-	0/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
7	MIA	7	37	7	-	2/15/33/34	0/3/3/3
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
7	3AU	7	47	7	-	1/16/34/35	0/2/2/2
1	OMG	1	2251	1,7	-	3/9/27/28	0/3/3/3
1	OMC	1	2498	1,59	-	2/9/27/28	0/2/2/2
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3

The worst 5 of 213 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	4	341	5MU	C6-N1	12.75	1.59	1.38
1	1	1939	5MU	C6-N1	12.71	1.59	1.38
1	1	747	5MU	C6-N1	12.70	1.59	1.38
7	7	54	5MU	C6-N1	12.64	1.59	1.38
1	1	1915	3TD	C6-C5	12.36	1.49	1.35

The worst 5 of 308 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	7	37	MIA	N6-C6-N1	-23.59	88.40	118.50
7	7	37	MIA	C5-C6-N6	17.52	151.33	121.76
2	2	1519	MA6	N1-C6-N6	-15.07	100.61	117.08
2	2	1518	MA6	N1-C6-N6	-14.93	100.76	117.08
1	1	2503	2MA	C1'-N9-C8	-12.94	97.93	127.14

There are no chirality outliers.

5 of 56 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
21	M	81	4D4	C-CA-CB-OB
21	M	81	4D4	C-CA-CB-CG
21	M	81	4D4	N-CA-CB-OB
21	M	81	4D4	N-CA-CB-CG
49	q	89	0TD	CG-CB-SB-CSB

There are no ring outliers.

27 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	746	PSU	1	0
1	1	2030	6MZ	2	0
1	1	2457	PSU	2	0
2	2	1518	MA6	3	0
2	2	1519	MA6	2	0
1	1	1835	2MG	1	0
1	1	1917	PSU	1	0
2	2	1402	4OC	1	0
1	1	745	1MG	1	0
2	2	1516	2MG	3	0
49	q	89	0TD	3	0
7	7	46	G7M	1	0
2	2	516	PSU	1	0
7	7	32	PSU	7	0
2	2	967	5MC	1	0
2	2	527	G7M	1	0
1	1	2504	PSU	1	0
1	1	2552	OMU	1	0
2	2	966	2MG	1	0
4	4	342	PSU	1	0
1	1	2580	PSU	1	0
1	1	1915	3TD	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	7	37	MIA	4	0
1	1	1911	PSU	1	0
7	7	47	3AU	1	0
1	1	2251	OMG	1	0
2	2	1207	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 195 ligands modelled in this entry, 193 are monoatomic - leaving 2 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	KIR	6	401	-	57,59,59	0.95	3 (5%)	63,84,84	1.01	2 (3%)
61	GDP	6	402	-	28,30,30	1.14	3 (10%)	44,47,47	1.84	8 (18%)

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	KIR	6	401	-	-	22/53/98/98	0/3/3/3
61	GDP	6	402	-	-	1/16/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	6	401	KIR	C37-C36	-4.13	1.32	1.44
60	6	401	KIR	C23-C22	-3.55	1.32	1.43

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	6	402	GDP	C5-C4	3.13	1.47	1.38
61	6	402	GDP	C6-N1	-2.47	1.34	1.38
60	6	401	KIR	C8-C7	-2.45	1.42	1.48

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	6	402	GDP	C5-C4-N3	-6.15	118.49	128.46
61	6	402	GDP	C2-N3-C4	4.94	121.11	112.30
61	6	402	GDP	N9-C4-N3	4.55	135.08	125.94
60	6	401	KIR	C11-C10-C9	3.73	131.10	123.47
61	6	402	GDP	PA-O3A-PB	-3.49	120.84	132.83

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

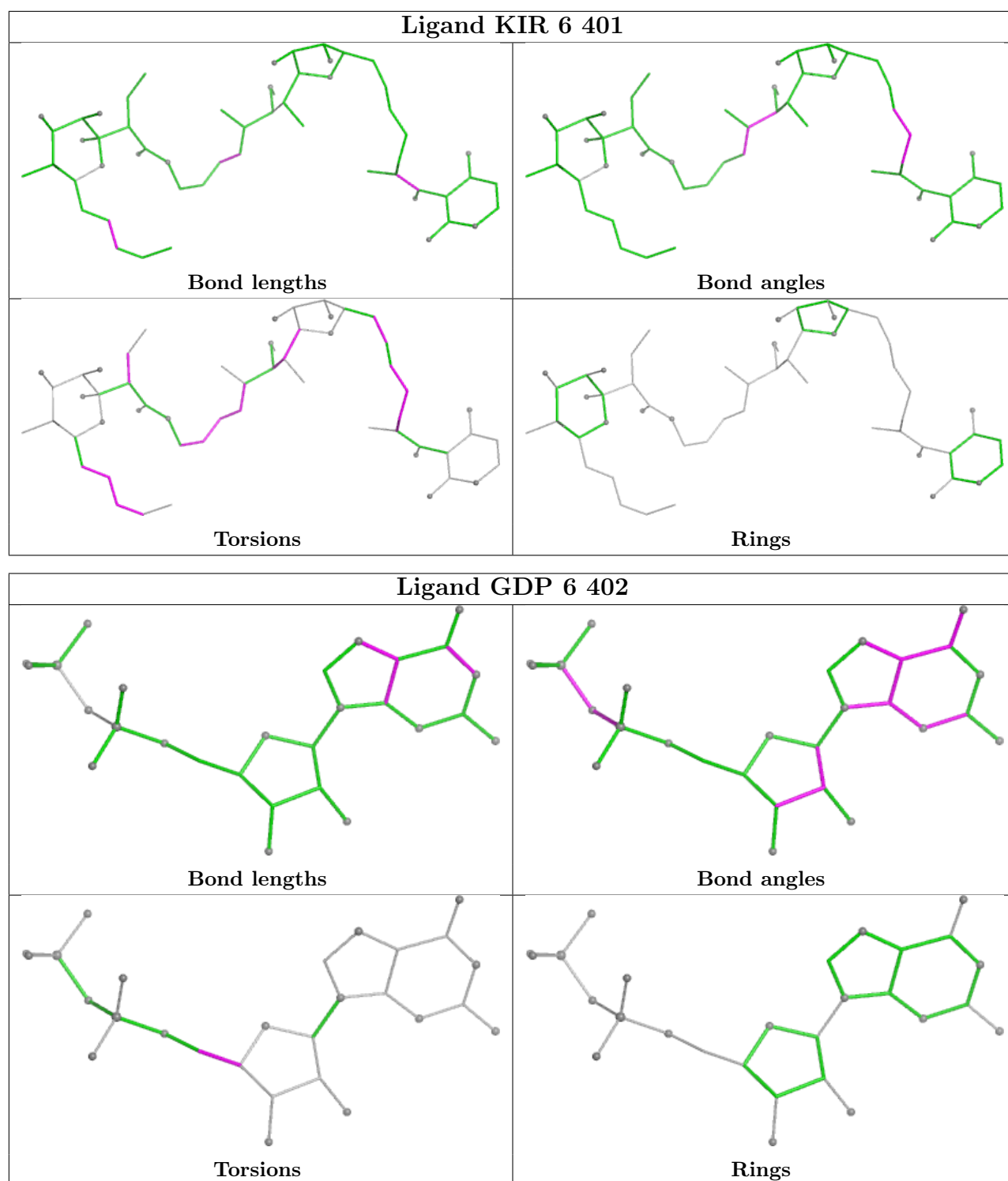
Mol	Chain	Res	Type	Atoms
60	6	401	KIR	C17-C19-C20-O20
60	6	401	KIR	C20-C21-C22-C23
60	6	401	KIR	C44-C21-C22-C23
60	6	401	KIR	C22-C23-C24-C25
60	6	401	KIR	C9-C10-C11-C12

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	6	401	KIR	3	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

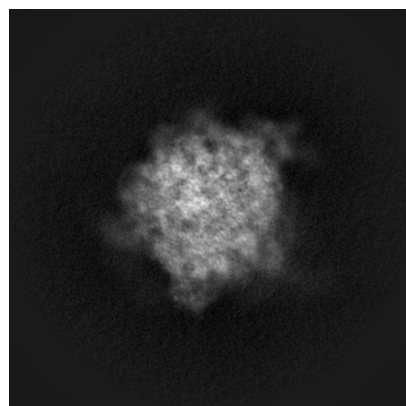
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11710. These allow visual inspection of the internal detail of the map and identification of artifacts.

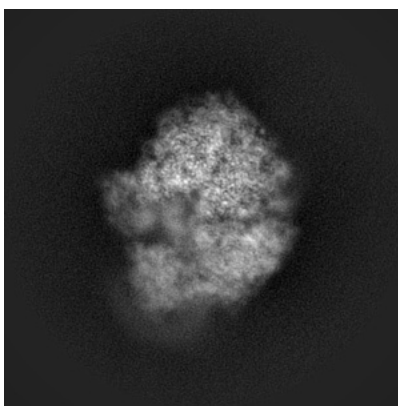
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

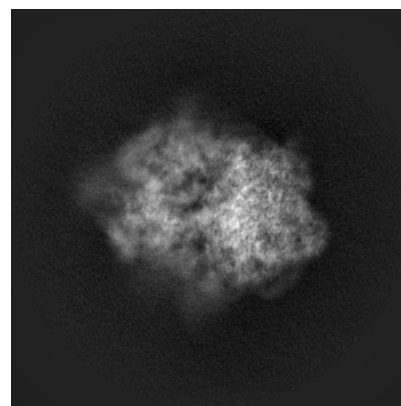
6.1.1 Primary map



X

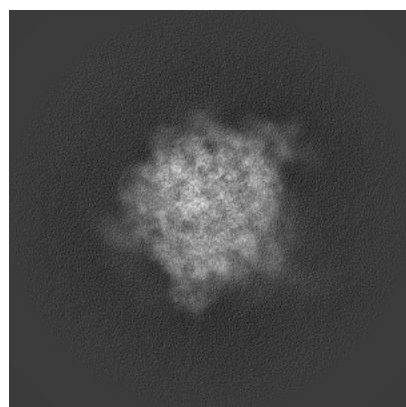


Y

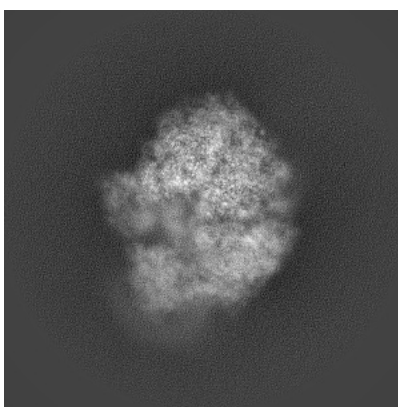


Z

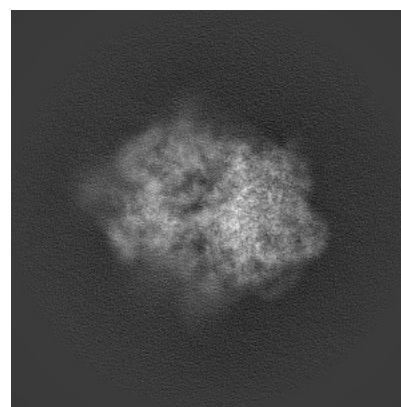
6.1.2 Raw map



X



Y

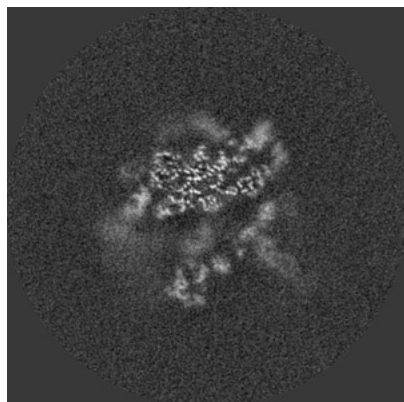


Z

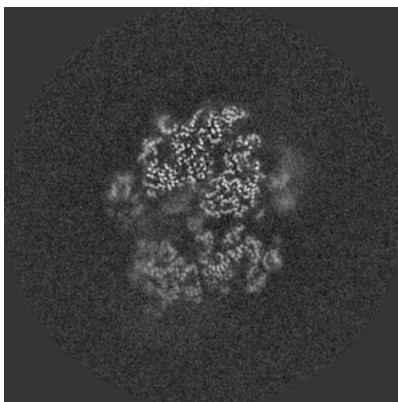
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

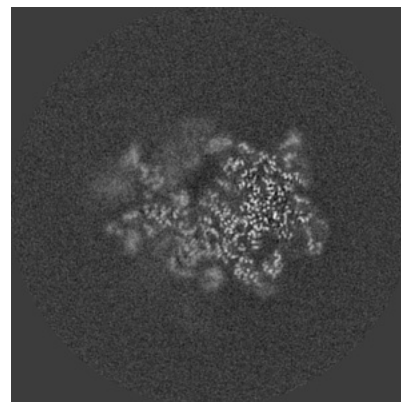
6.2.1 Primary map



X Index: 208

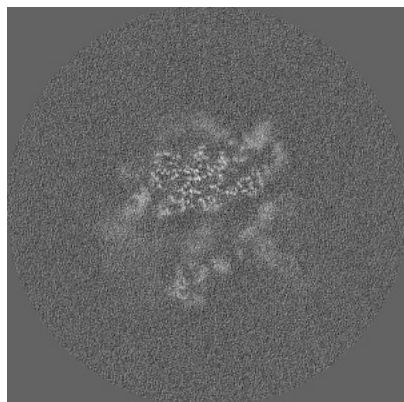


Y Index: 208

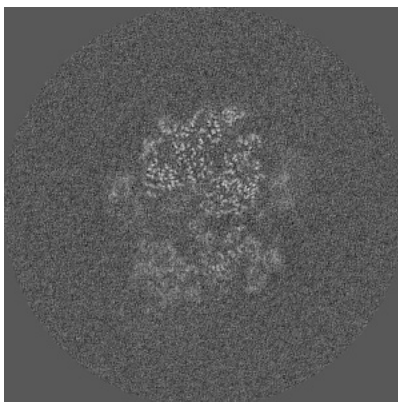


Z Index: 208

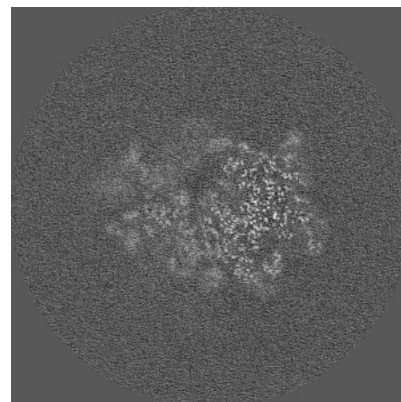
6.2.2 Raw map



X Index: 208



Y Index: 208

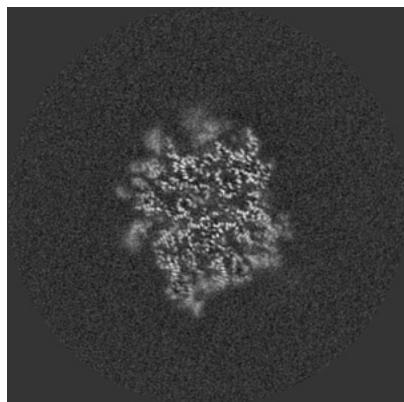


Z Index: 208

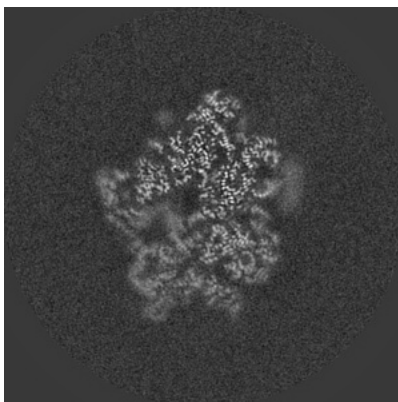
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

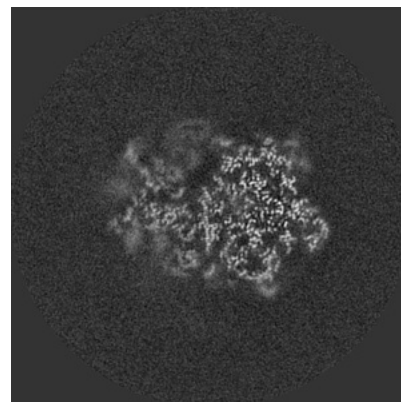
6.3.1 Primary map



X Index: 236

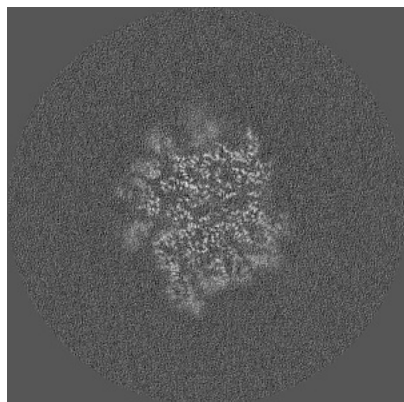


Y Index: 194

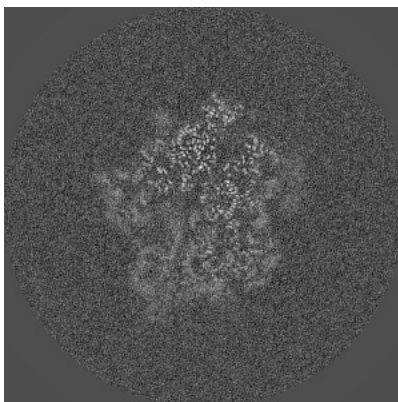


Z Index: 213

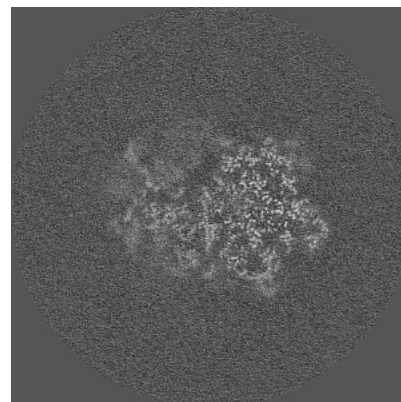
6.3.2 Raw map



X Index: 235



Y Index: 199

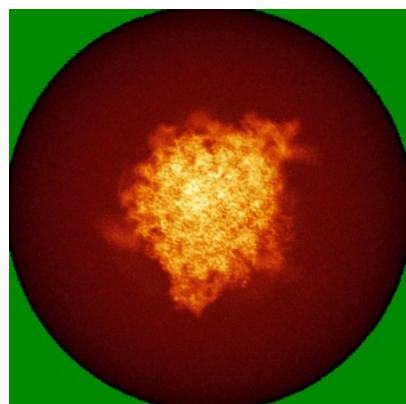


Z Index: 213

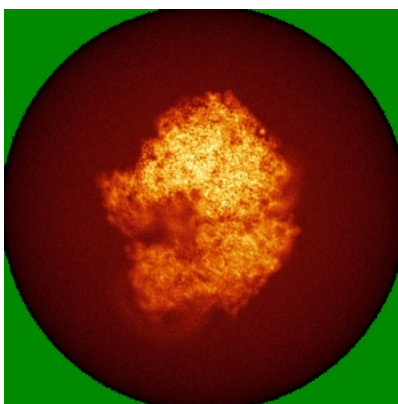
The images above show the largest variance slices of the map in three orthogonal directions.

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

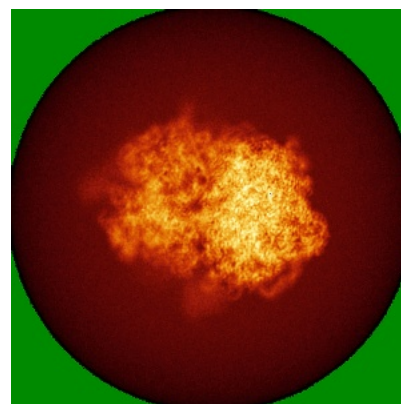
6.4.1 Primary map



X

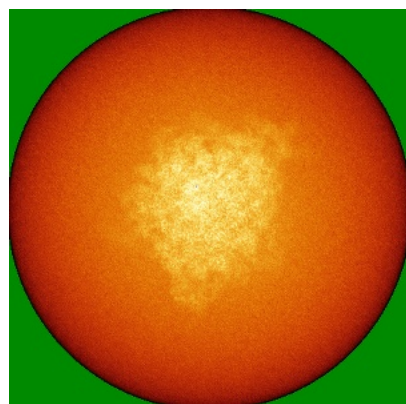


Y

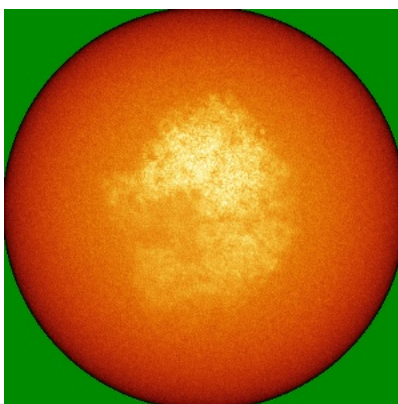


Z

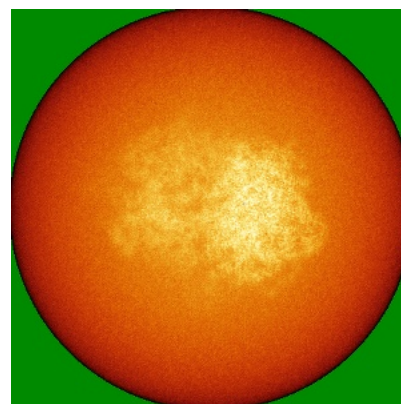
6.4.2 Raw map



X



Y

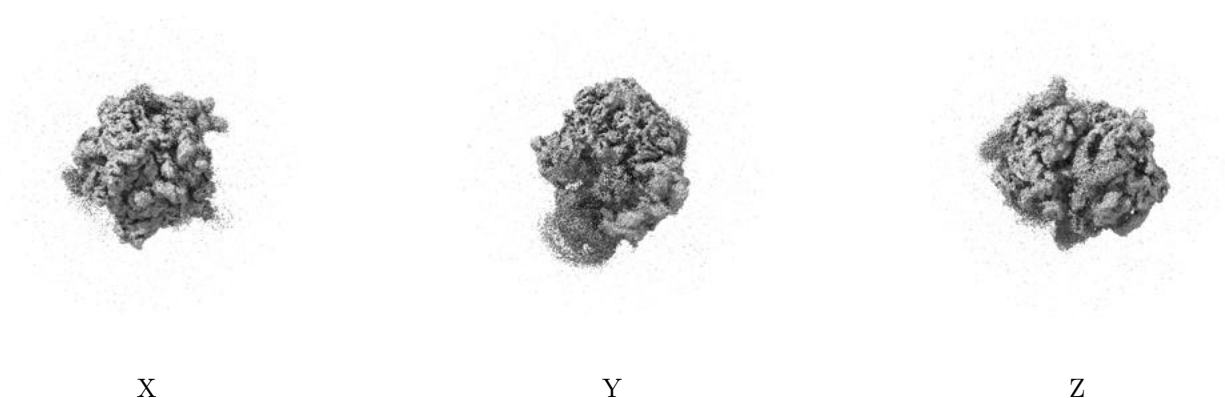


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

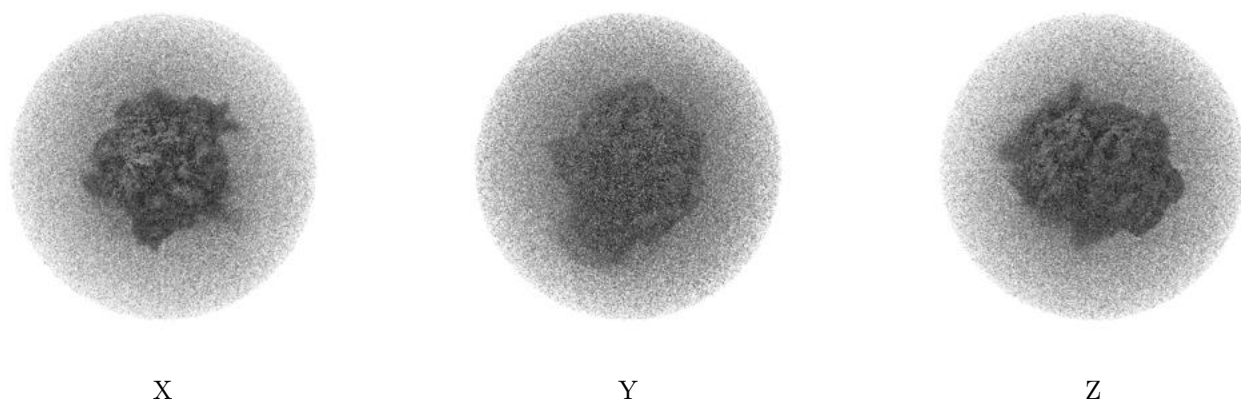
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

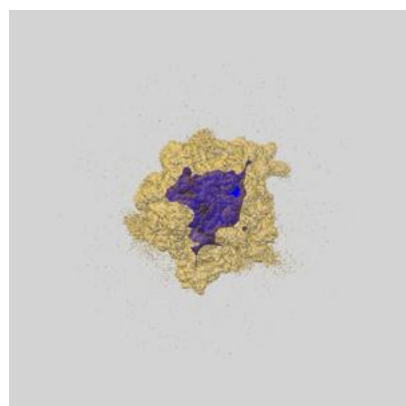
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

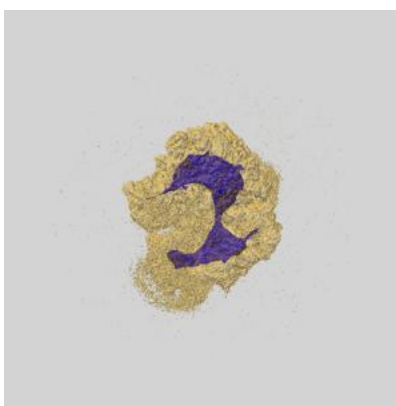
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

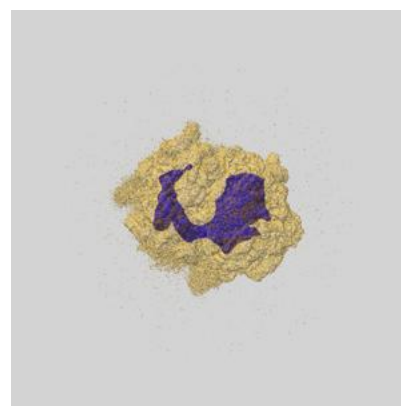
6.6.1 emd_11710_msk_1.map [i](#)



X



Y

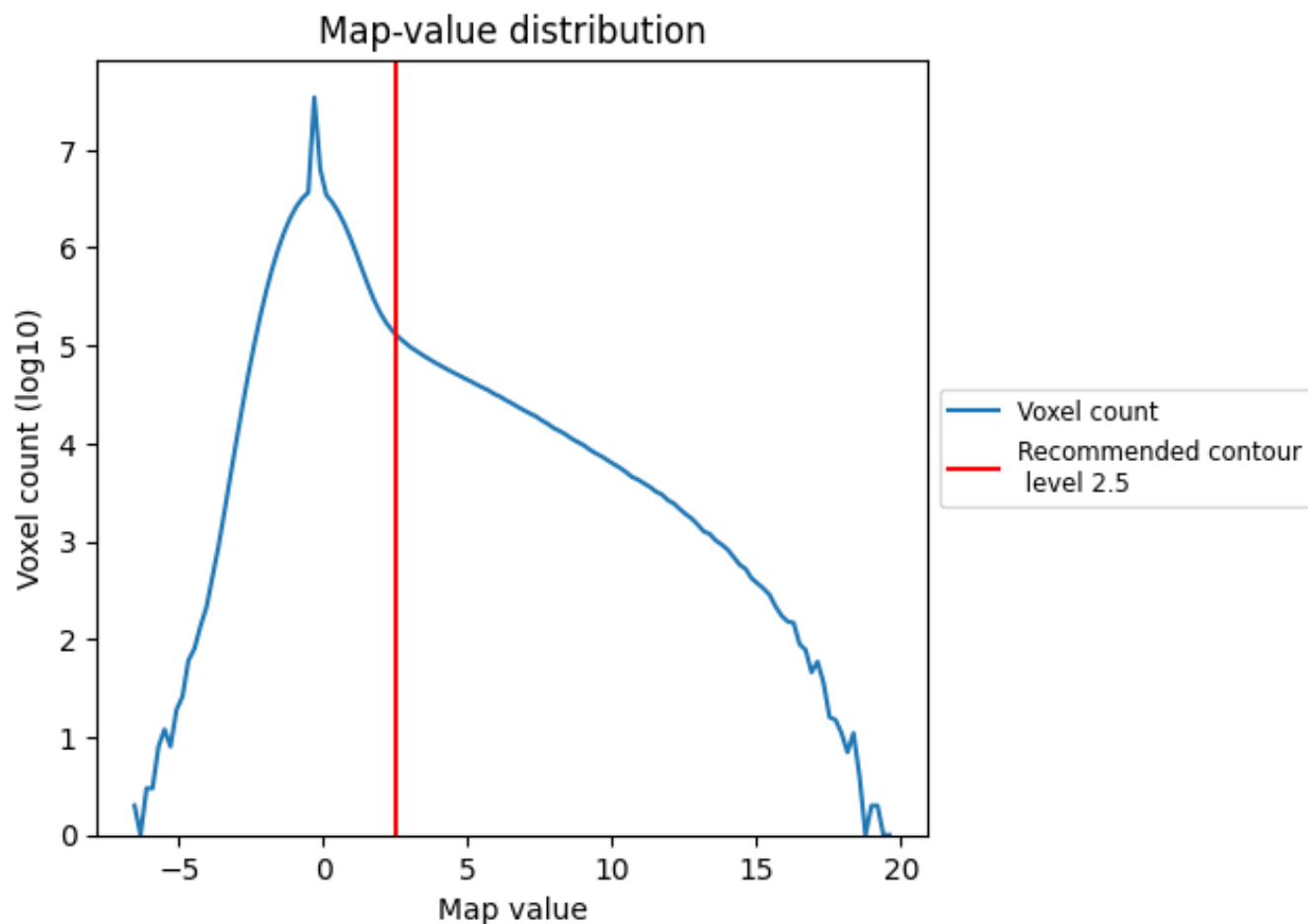


Z

7 Map analysis [i](#)

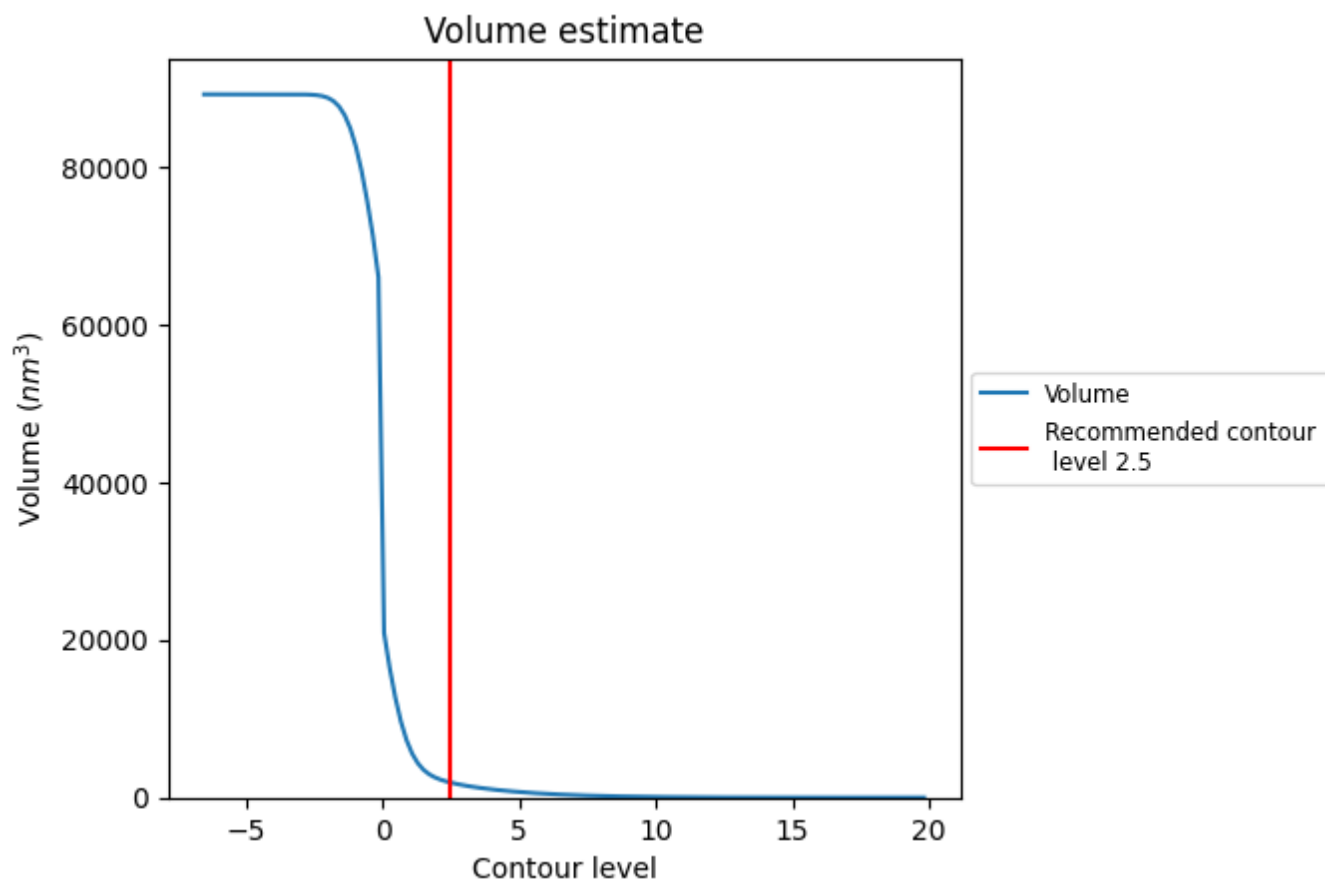
This section contains the results of statistical analysis of the map.

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.

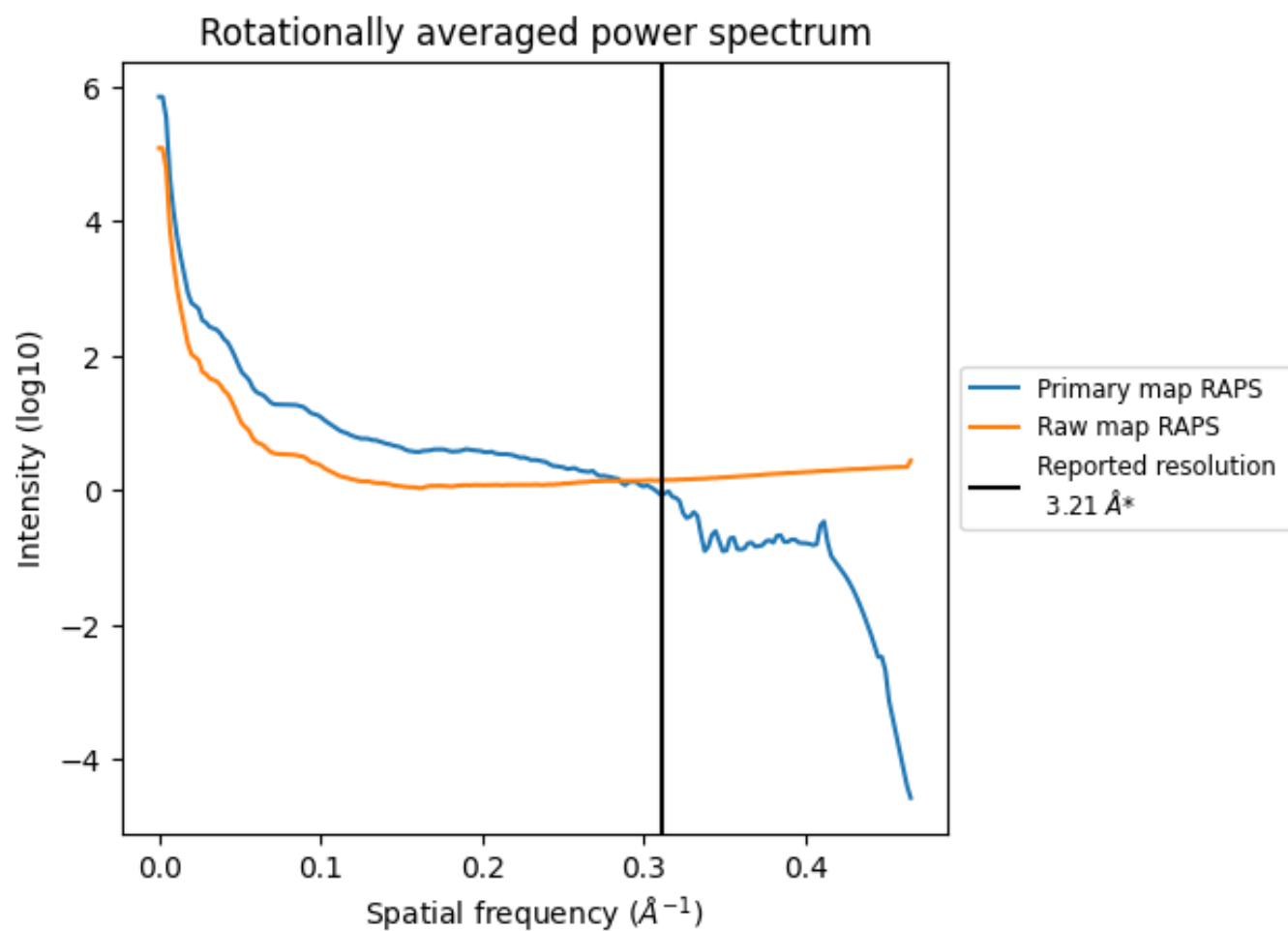
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1895 nm³; this corresponds to an approximate mass of 1712 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

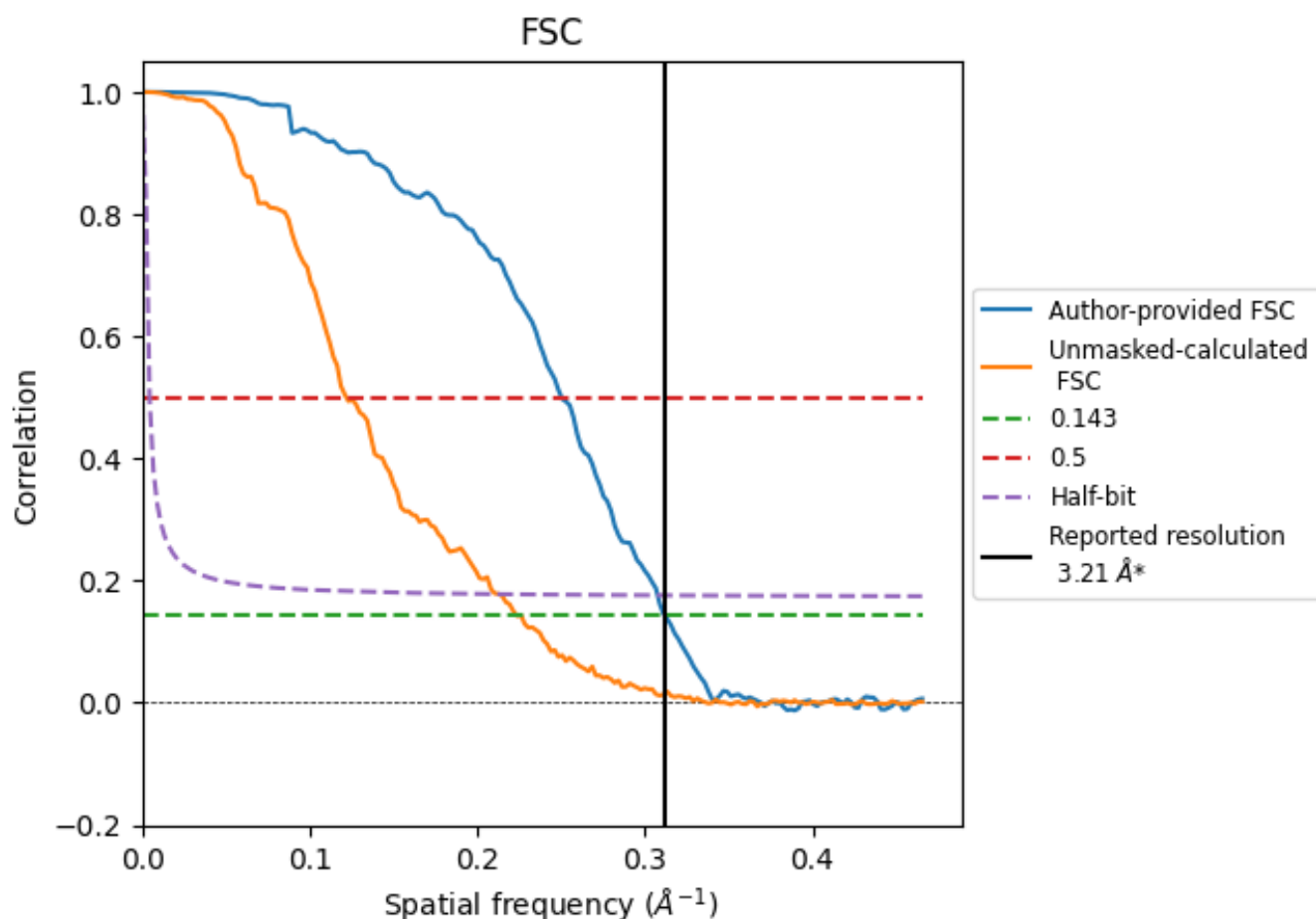


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

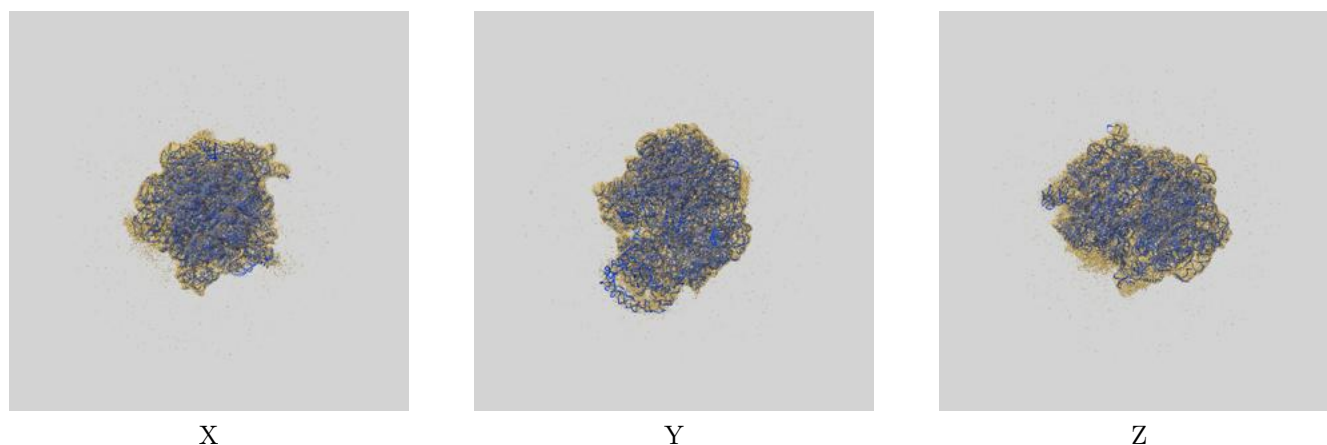
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.21	-	-
Author-provided FSC curve	3.21	4.00	3.25
Unmasked-calculated*	4.47	8.21	4.70

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.47 differs from the reported value 3.21 by more than 10 %

9 Map-model fit [i](#)

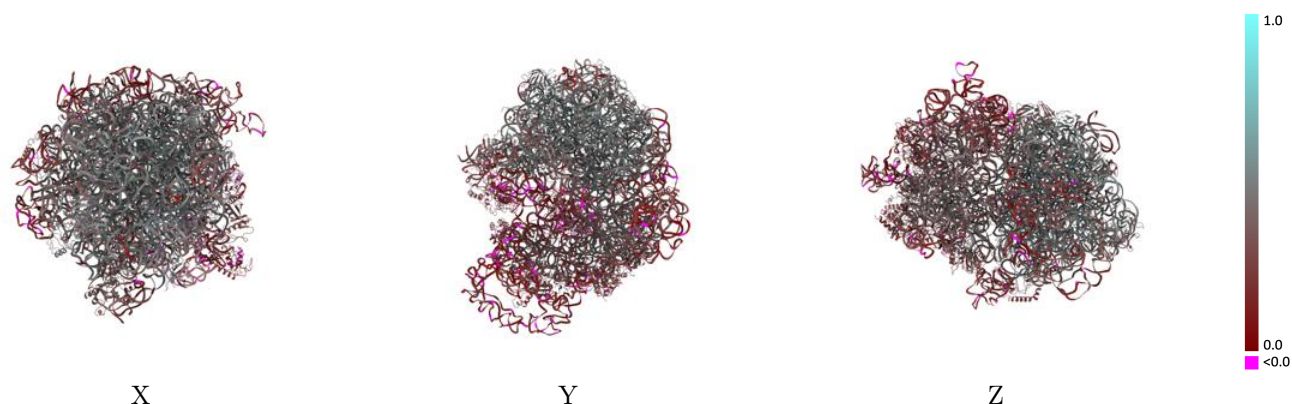
This section contains information regarding the fit between EMDB map EMD-11710 and PDB model 7ABZ. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



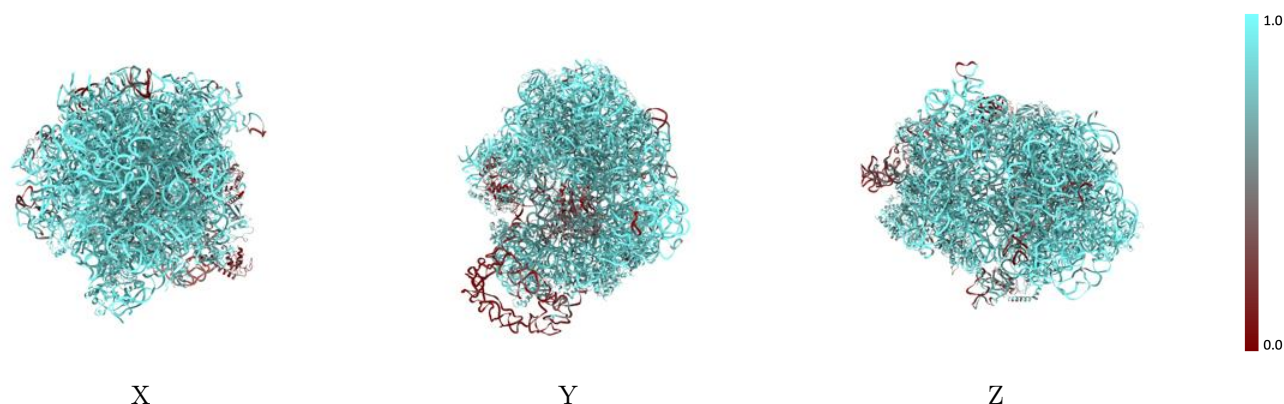
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



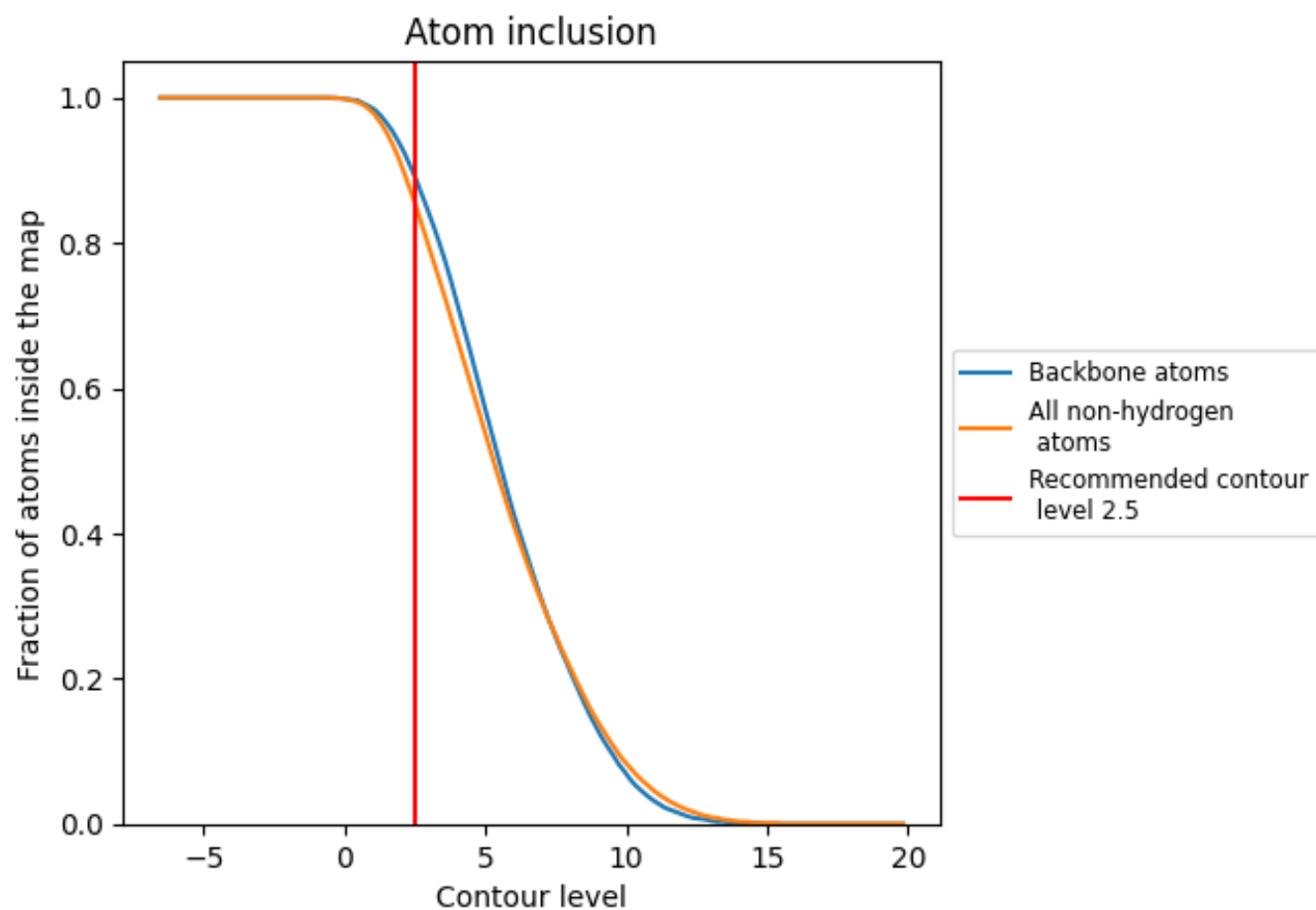
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.5).

9.4 Atom inclusion ⓘ



At the recommended contour level, 89% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8550	 0.3590
1	 0.9320	 0.4120
2	 0.9490	 0.3250
3	 0.9780	 0.3560
4	 0.2840	 0.1290
5	 0.4340	 0.1850
6	 0.3330	 0.2090
7	 0.6880	 0.1980
8	 0.6420	 0.1550
A	 0.8840	 0.4690
B	 0.9180	 0.4830
C	 0.9080	 0.4870
D	 0.9000	 0.4620
E	 0.7550	 0.2140
F	 0.7370	 0.3160
G	 0.5450	 0.2720
H	 0.2320	 0.1770
I	 0.3430	 0.1790
J	 0.9280	 0.4840
K	 0.8760	 0.4660
L	 0.9030	 0.4760
M	 0.8840	 0.4680
N	 0.9180	 0.4750
O	 0.9040	 0.3780
P	 0.8720	 0.4560
Q	 0.9260	 0.4920
R	 0.9060	 0.4780
S	 0.8890	 0.4670
T	 0.8930	 0.4460
U	 0.9090	 0.4360
V	 0.8830	 0.4260
X	 0.8920	 0.4420
Y	 0.8510	 0.3830
Z	 0.9020	 0.4770
b	 0.9040	 0.4680



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
c	 0.9030	 0.4520
d	 0.9180	 0.5090
e	 0.9060	 0.5070
f	 0.8160	 0.4060
g	 0.7820	 0.2890
h	 0.8310	 0.3320
i	 0.7490	 0.2570
j	 0.8690	 0.3970
k	 0.8420	 0.3170
l	 0.7070	 0.2120
m	 0.8780	 0.3910
n	 0.8210	 0.2320
o	 0.7940	 0.2700
p	 0.8500	 0.3360
q	 0.7540	 0.3250
r	 0.7600	 0.2110
s	 0.8130	 0.2840
t	 0.8750	 0.3510
u	 0.8520	 0.3320
v	 0.8750	 0.3700
w	 0.8380	 0.3370
x	 0.7810	 0.2120
y	 0.8030	 0.2710
z	 0.6650	 0.3150