



## wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 04:50 am GMT

PDB ID : 7PAI  
EMDB ID : EMD-13273  
Title : 70S ribosome with P-site tRNA in Mycoplasma pneumoniae cells  
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.  
Deposited on : 2021-07-30  
Resolution : 6.70 Å(reported)  
Based on initial models : 7OOD, 7OOC, 4V7C

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

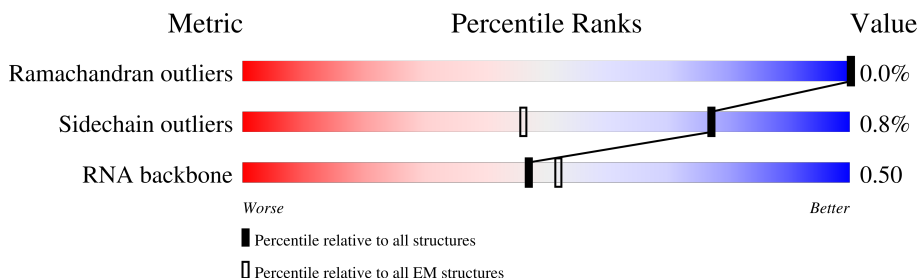
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 6.70 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	0	48	<div> <div>98%</div> </div>
2	1	59	<div> <div>98%</div> </div>
3	2	37	<div> <div>5%</div> <div>100%</div> </div>
4	A	294	<div> <div>12%</div> <div>81%</div> <div>18%</div> </div>
5	B	273	<div> <div>13%</div> <div>79%</div> <div>21%</div> </div>
6	C	205	<div> <div>17%</div> <div>99%</div> </div>
7	D	219	<div> <div>7%</div> <div>69%</div> <div>30%</div> </div>
8	E	215	<div> <div>14%</div> <div>77%</div> <div>22%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	F	155	
10	G	142	
11	H	132	
12	I	108	
13	J	121	
14	K	139	
15	L	124	
16	M	61	
17	N	86	
18	O	94	
19	P	85	
20	Q	104	
21	R	87	
22	S	87	
23	T	60	
24	a	287	
25	b	287	
26	c	212	
27	d	180	
28	e	184	
29	f	149	
30	g	161	
31	h	137	
32	i	146	
33	j	122	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	k	151	
35	l	139	
36	m	124	
37	n	116	
38	o	119	
39	p	127	
40	q	100	
41	r	159	
42	s	237	
43	t	111	
44	u	104	
45	v	65	
46	w	111	
47	x	97	
48	y	57	
49	z	53	
50	3	2907	
51	4	108	
52	5	1520	
53	7	76	

## 2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 144502 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 L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	240	Total	C	N	O	S	0	0
			1921	1226	334	352	9		

- Molecule 5 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	215	Total	C	N	O	S	0	0
			1698	1073	313	307	5		

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	203	Total	C	N	O	S	0	0
			1660	1051	314	290	5		

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	153	Total	C	N	O	S	0	0
			1173	742	226	202	3		

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	167	Total	C	N	O	S	0	0
			1362	857	240	263	2		

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	154	Total	C	N	O	S	0	0
			1246	785	239	216	6		

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	141	Total	C	N	O	S	0	0
			1110	723	193	192	2		

- Molecule 11 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	128	Total	C	N	O	S	0	0
			1028	655	191	181	1		

- Molecule 12 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	101	Total	C	N	O	S	0	0
			809	523	142	143	1		

- Molecule 13 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	114	Total	C	N	O	S	0	0
			829	514	153	156	6		

- Molecule 14 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

- Molecule 15 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	118	Total	C	N	O		0	0
			951	594	191	166			

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	83	Total	C	N	O		0	0
			673	428	125	120			

- Molecule 18 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	80	Total	C	N	O	S	0	0
			646	414	119	111	2		

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	83	Total	C	N	O		0	0
			675	425	135	115			

- Molecule 20 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 22 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	77	Total	C	N	O		0	0
			629	383	135	111			

- Molecule 23 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 28 is a protein called 50S ribosomal protein L6.



Mol	Chain	Residues	Atoms				AltConf	Trace
28	e	176	Total	C	N	O	0	0
			1396	899	247	250		

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	f	145	Total	C	N	O	S	0
			1160	746	204	207	3	0

- Molecule 30 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	g	126	Total	C	N	O	S	0
			960	612	167	178	3	0

- Molecule 31 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	h	128	Total	C	N	O	S	0
			959	616	160	177	6	0

- Molecule 32 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	i	144	Total	C	N	O	S	0
			1164	737	213	209	5	0

- Molecule 33 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	j	122	Total	C	N	O	S	0
			944	595	178	167	4	0

- Molecule 34 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	k	148	Total	C	N	O	0	0
			1153	731	226	196		

- Molecule 35 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 36 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 37 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 38 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 39 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	114	Total	C	N	O	S	0	0
			947	603	188	154	2		

- Molecule 40 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 41 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 42 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 43 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 45 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	w	100	Total	C	N	O	0	0
			818	517	153	148		

- Molecule 47 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 49 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 50 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 51 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

- Molecule 53 is a RNA chain called tRNA-Phe.

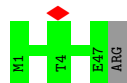
Mol	Chain	Residues	Atoms					AltConf	Trace
53	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

### 3 Residue-property plots [i](#)

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 L34

Chain 0:  98%



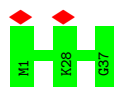
- Molecule 2: 50S ribosomal protein L35

Chain 1:  98%




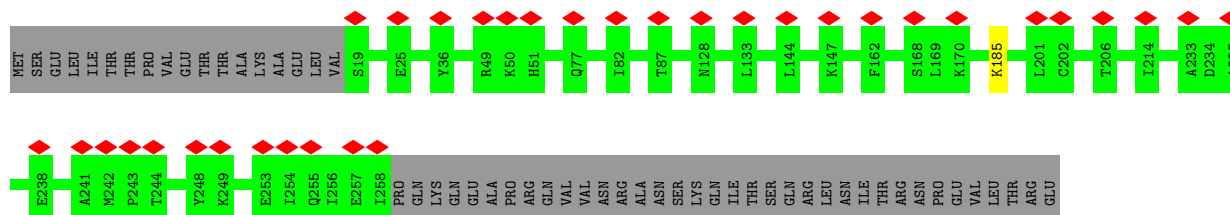
- Molecule 3: 50S ribosomal protein L36

Chain 2:  5% 100%




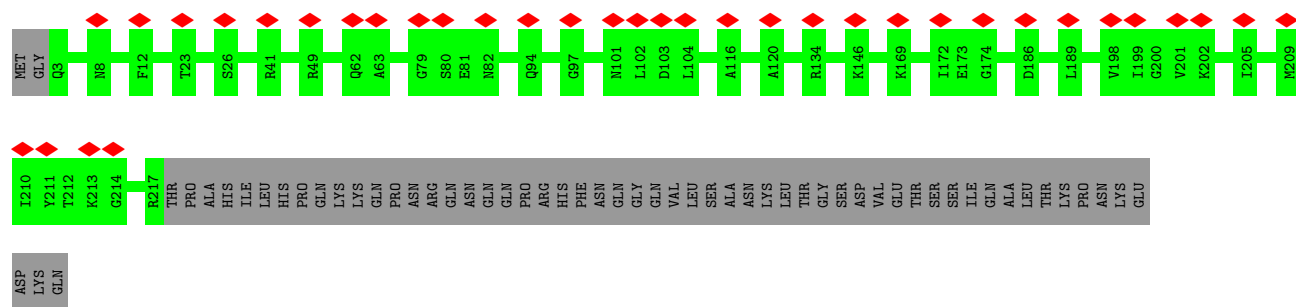
- Molecule 4: 30S ribosomal protein S2

Chain A:  12% 81% 18%

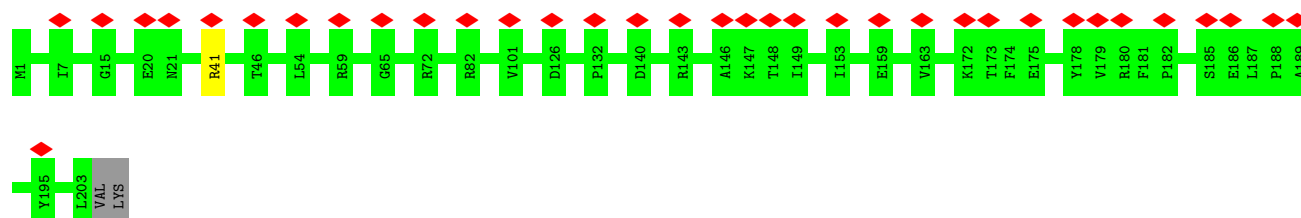


- Molecule 5: 30S ribosomal protein S3

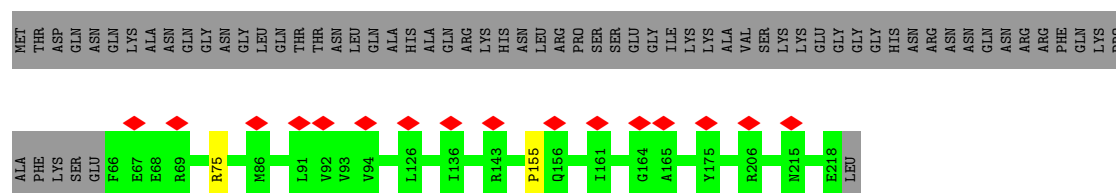
Chain B:  13% 79% 21%



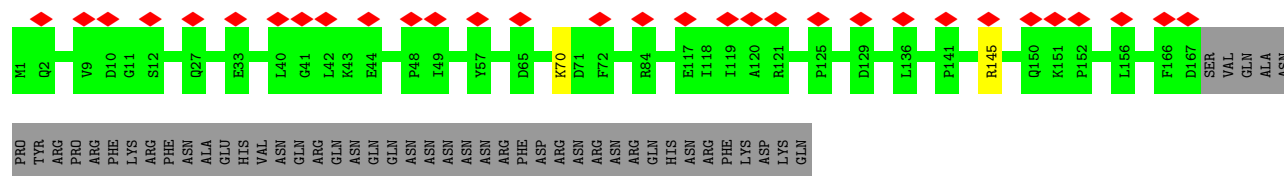
- Molecule 6: 30S ribosomal protein S4



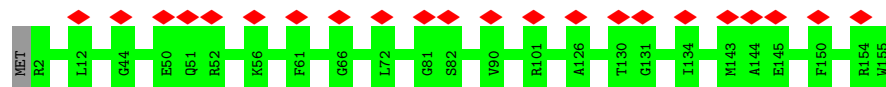
- Molecule 7: 30S ribosomal protein S5



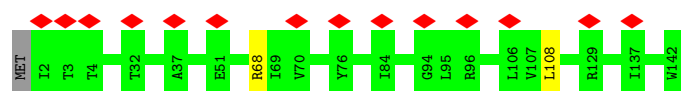
- Molecule 8: 30S ribosomal protein S6



- Molecule 9: 30S ribosomal protein S7



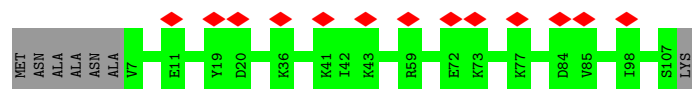
- Molecule 10: 30S ribosomal protein S8



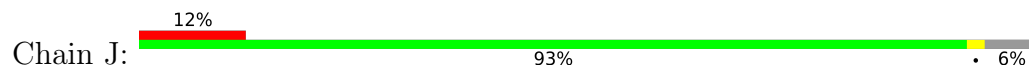
- Molecule 11: 30S ribosomal protein S9



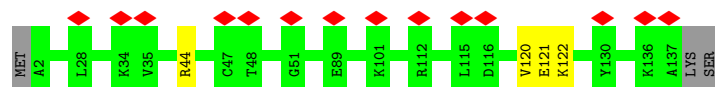
- Molecule 12: 30S ribosomal protein S10



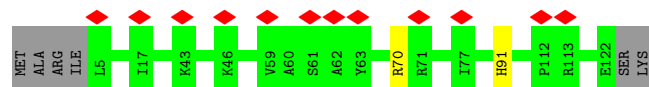
- Molecule 13: 30S ribosomal protein S11



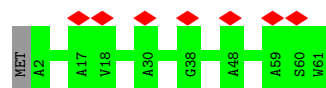
- Molecule 14: 30S ribosomal protein S12



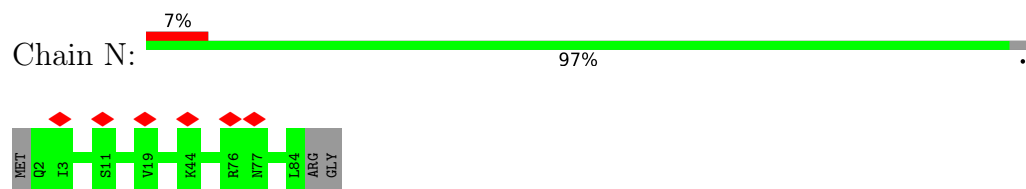
- Molecule 15: 30S ribosomal protein S13



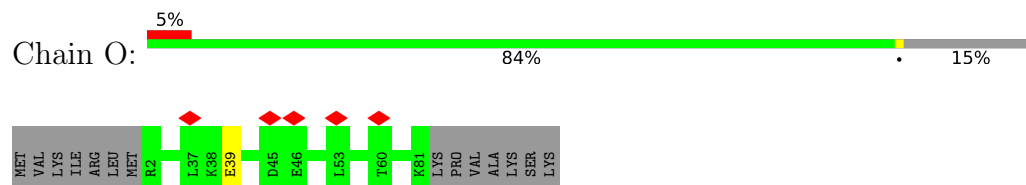
- Molecule 16: 30S ribosomal protein S14 type Z



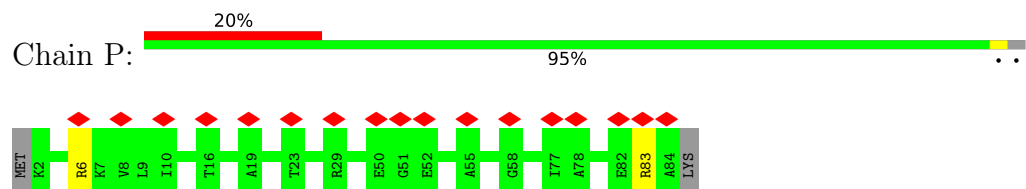
- Molecule 17: 30S ribosomal protein S15



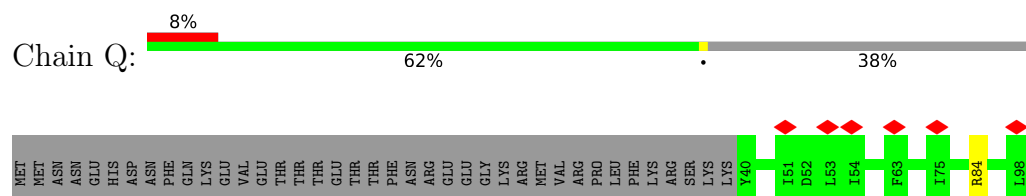
- Molecule 18: 30S ribosomal protein S16



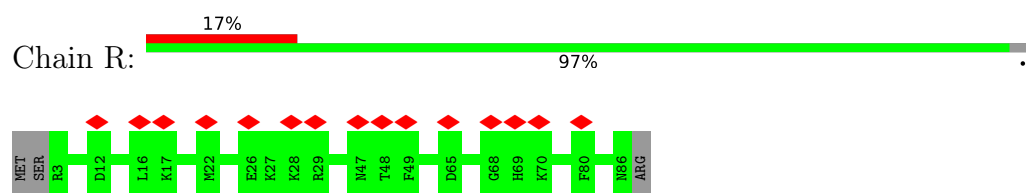
- Molecule 19: 30S ribosomal protein S17



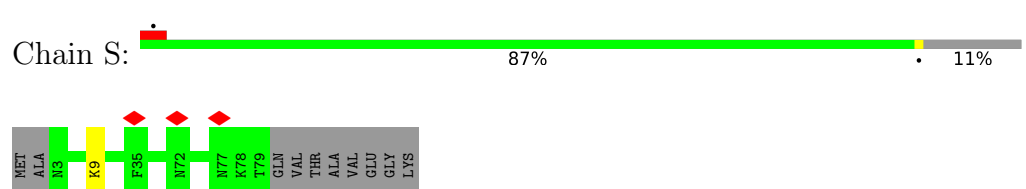
- Molecule 20: 30S ribosomal protein S18



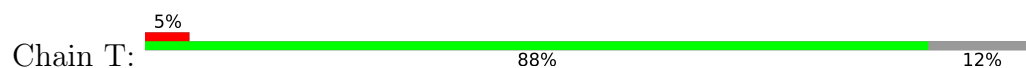
- Molecule 21: 30S ribosomal protein S19



- Molecule 22: 30S ribosomal protein S20

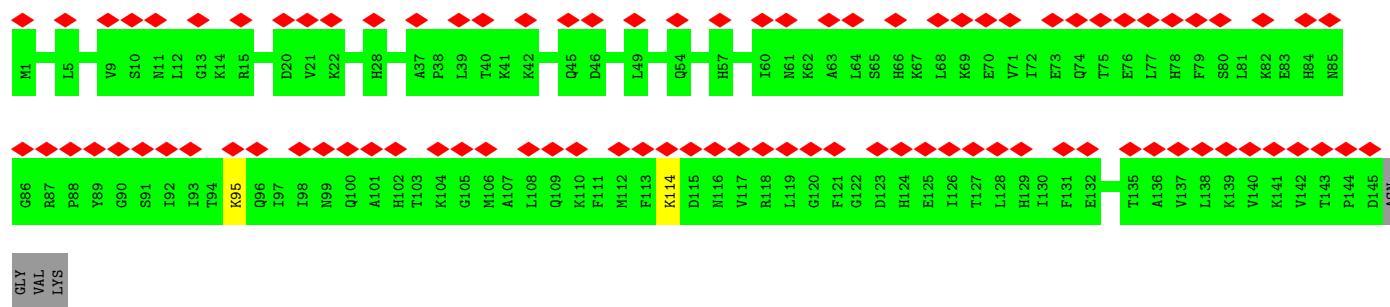


- Molecule 23: 30S ribosomal protein S21

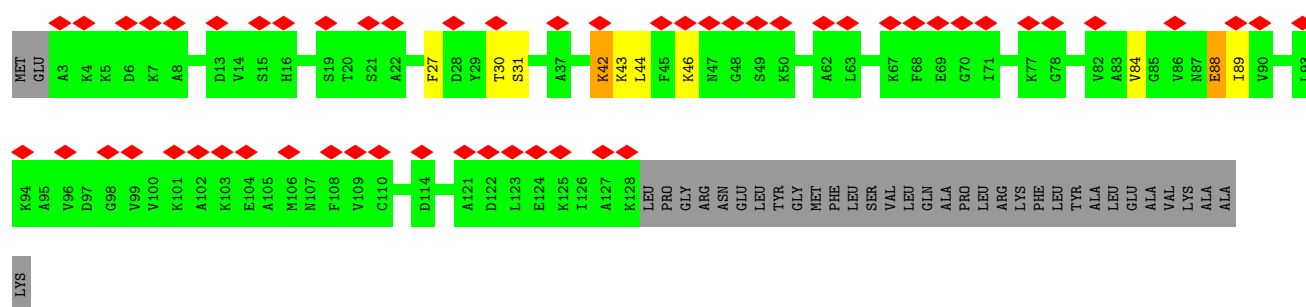




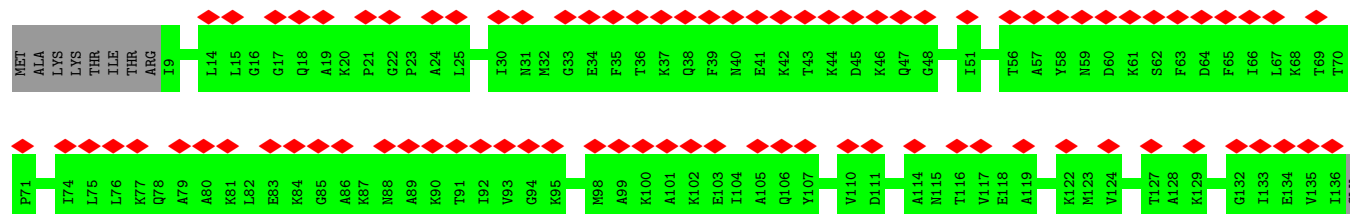
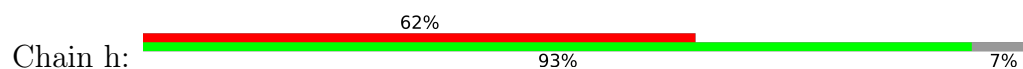




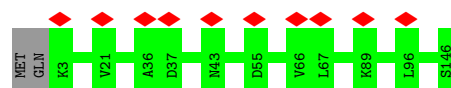
- Molecule 30: 50S ribosomal protein L10



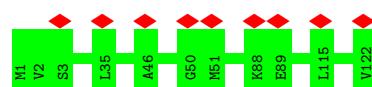
- Molecule 31: 50S ribosomal protein L11



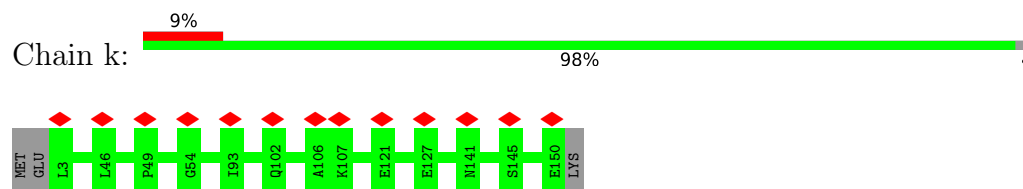
- Molecule 32: 50S ribosomal protein L13



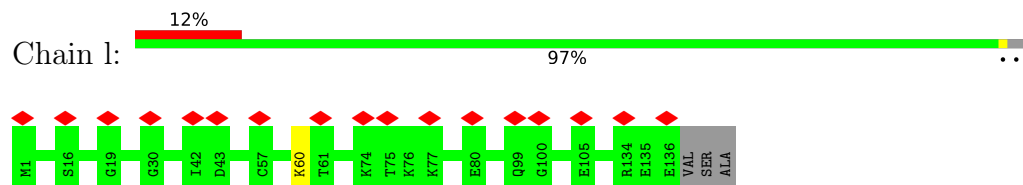
- Molecule 33: 50S ribosomal protein L14



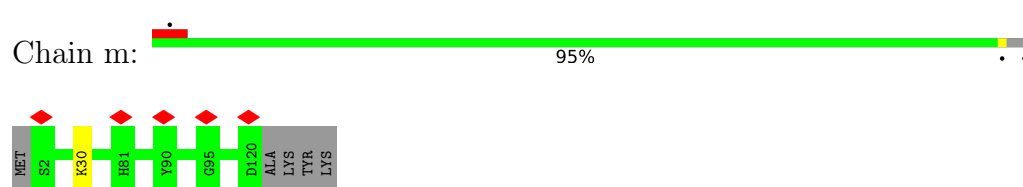
- Molecule 34: 50S ribosomal protein L15



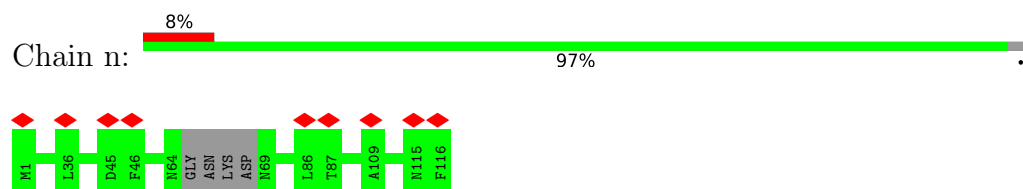
- Molecule 35: 50S ribosomal protein L16



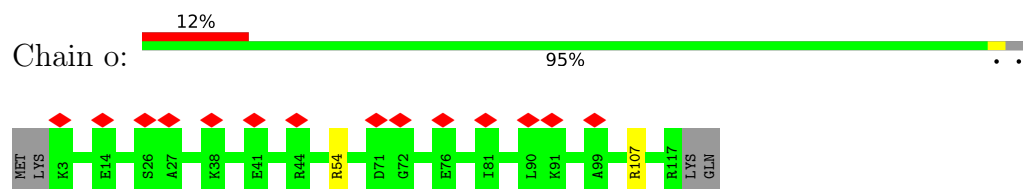
- Molecule 36: 50S ribosomal protein L17



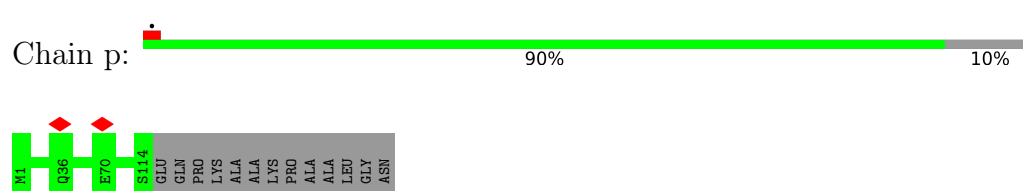
- Molecule 37: 50S ribosomal protein L18



- Molecule 38: 50S ribosomal protein L19



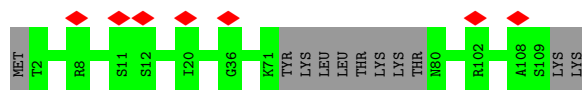
- Molecule 39: 50S ribosomal protein L20



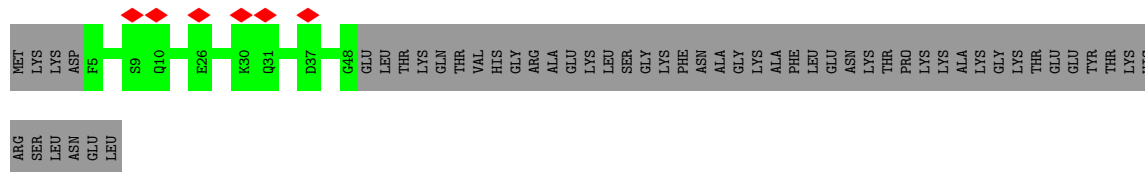
- Molecule 40: 50S ribosomal protein L21



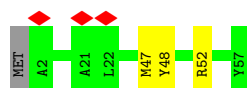
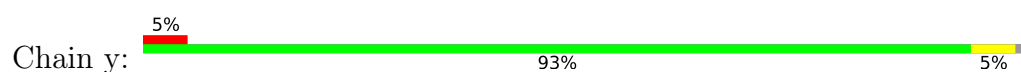




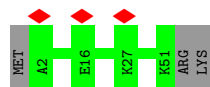
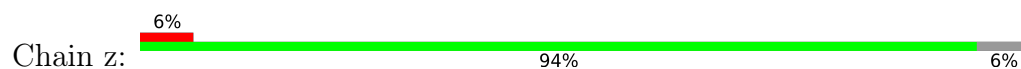
- Molecule 47: 50S ribosomal protein L31



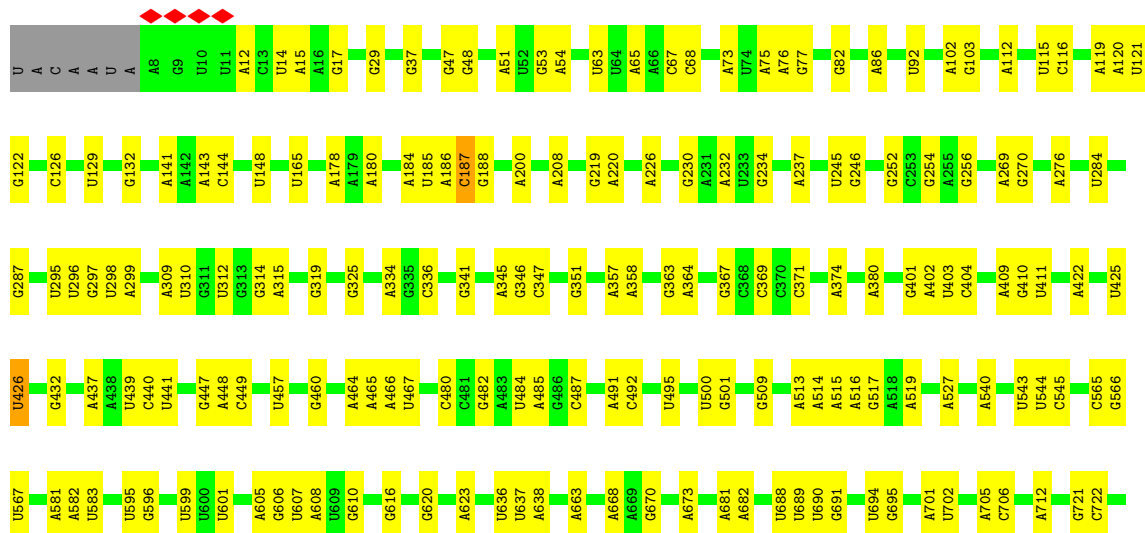
- Molecule 48: 50S ribosomal protein L32



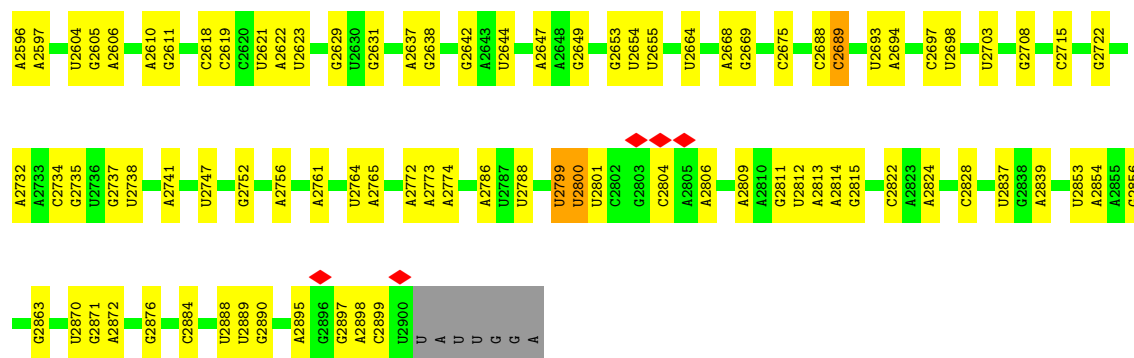
- Molecule 49: 50S ribosomal protein L33 1



- Molecule 50: 23S ribosomal RNA

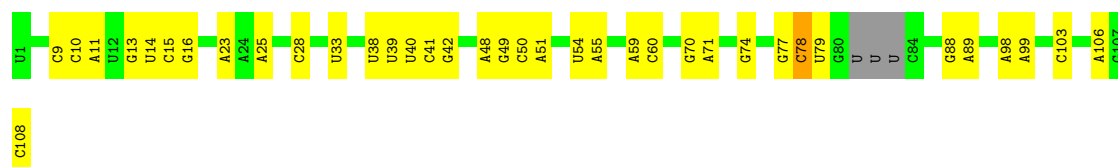


C2483	C2484	U2485	A2486	U2487	C2488	G2489	G2492	U2497	G2498	U2499	U2500	G2503	C2504	A2505	C2506	U2507	U2508	C2509	U2510	A2511	U2512	U2513	U2514	C2515	G2516	A2526	U2527	C2528	C2529	A2539	G2543	G2558	C2559	U2560	U2570	A2574	G2577	A2580	C2581	U2587	C2594	G2595	U2593	C2594	A2595																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
A2318	A2319	U2327	A2328	U2329	A2330	G2331	G2332	U2333	G2341	U2342	A2343	A2344	G2345	U2351	U2352	G2353	A2354	C2355	U2358	U2359	A2362	A2362	G2363	G2364	C2365	U2366	G2367	U2368	A2369	U2370	G2371	U2372	A2373	U2374	G2375	A2376	A2377	G2378	A2379	U2380	A2381	U2382	A2383	U2384	A2385	U2386	A2387	U2388	A2389	U2390	A2391	U2392	A2393	U2394	A2395	U2396	A2397	U2398	A2399	U2400	A2401	U2402	A2403	U2404	A2405	U2406	A2407	U2408	A2409	U2410	A2411	U2412	A2413	U2414	A2415	U2416	A2417	U2418	A2419	U2420	A2421	U2422	A2423	U2424	A2425	U2426	A2427	U2428	A2429	U2430	A2431	U2432	A2433	U2434	A2435	U2436	A2437	U2438	A2439	U2440	A2441	U2442	A2443	U2444	A2445	U2446	A2447	U2448	A2449	U2450	A2451	U2452	A2453	U2454	A2455	U2456	A2457	U2458	A2459	U2460	A2461	U2462	A2463	U2464	A2465	U2466	A2467	U2468	A2469	U2470	A2471	U2472	A2473	U2474	A2475	U2476	A2477	U2478	A2479	U2480	A2481	U2482	A2483	U2484	A2485	U2486	A2487	U2488	A2489	U2490	A2491	U2492	A2493	U2494	A2495	U2496	A2497	U2498	A2499	U2500	A2501	U2502	A2503	U2504	A2505	U2506	A2507	U2508	A2509	U2510	A2511	U2512	A2513	U2514	A2515	U2516	A2517	U2518	A2519	U2520	A2521	U2522	A2523	U2524	A2525	U2526	A2527	U2528	A2529	U2530	A2531	U2532	A2533	U2534	A2535	U2536	A2537	U2538	A2539	U2540	A2541	U2542	A2543	U2544	A2545	U2546	A2547	U2548	A2549	U2550	A2551	U2552	A2553	U2554	A2555	U2556	A2557	U2558	A2559	U2560	A2561	U2562	A2563	U2564	A2565	U2566	A2567	U2568	A2569	U2570	A2571	U2572	A2573	U2574	A2575	U2576	A2577	U2578	A2579	U2580	A2581	U2582	A2583	U2584	A2585	U2586	A2587	U2588	A2589	U2590	A2591	U2592	A2593	U2594	A2595	U2596	A2597	U2598	A2599	U2600	A2601	U2602	A2603	U2604	A2605	U2606	A2607	U2608	A2609	U2610	A2611	U2612	A2613	U2614	A2615	U2616	A2617	U2618	A2619	U2620	A2621	U2622	A2623	U2624	A2625	U2626	A2627	U2628	A2629	U2630	A2631	U2632	A2633	U2634	A2635	U2636	A2637	U2638	A2639	U2640	A2641	U2642	A2643	U2644	A2645	U2646	A2647	U2648	A2649	U2650	A2651	U2652	A2653	U2654	A2655	U2656	A2657	U2658	A2659	U2660	A2661	U2662	A2663	U2664	A2665	U2666	A2667	U2668	A2669	U2670	A2671	U2672	A2673	U2674	A2675	U2676	A2677	U2678	A2679	U2680	A2681	U2682	A2683	U2684	A2685	U2686	A2687	U2688	A2689	U2690	A2691	U2692	A2693	U2694	A2695	U2696	A2697	U2698	A2699	U2700	A2701	U2702	A2703	U2704	A2705	U2706	A2707	U2708	A2709	U2710	A2711	U2712	A2713	U2714	A2715	U2716	A2717	U2718	A2719	U2720	A2721	U2722	A2723	U2724	A2725	U2726	A2727	U2728	A2729	U2730	A2731	U2732	A2733	U2734	A2735	U2736	A2737	U2738	A2739	U2740	A2741	U2742	A2743	U2744	A2745	U2746	A2747	U2748	A2749	U2750	A2751	U2752	A2753	U2754	A2755	U2756	A2757	U2758	A2759	U2760	A2761	U2762	A2763	U2764	A2765	U2766	A2767	U2768	A2769	U2770	A2771	U2772	A2773	U2774	A2775	U2776	A2777	U2778	A2779	U2780	A2781	U2782	A2783	U2784	A2785	U2786	A2787	U2788	A2789	U2790	A2791	U2792	A2793	U2794	A2795	U2796	A2797	U2798	A2799	U2800	A2801	U2802	A2803	U2804	A2805	U2806	A2807	U2808	A2809	U2810	A2811	U2812	A2813	U2814	A2815	U2816	A2817	U2818	A2819	U2820	A2821	U2822	A2823	U2824	A2825	U2826	A2827	U2828	A2829	U2830	A2831	U2832	A2833	U2834	A2835	U2836	A2837	U2838	A2839	U2840	A2841	U2842	A2843	U2844	A2845	U2846	A2847	U2848	A2849	U2850	A2851	U2852	A2853	U2854	A2855	U2856	A2857	U2858	A2859	U2860	A2861	U2862	A2863	U2864	A2865	U2866	A2867	U2868	A2869	U2870	A2871	U2872	A2873	U2874	A2875	U2876	A2877	U2878	A2879	U2880	A2881	U2882	A2883	U2884	A2885	U2886	A2887	U2888	A2889	U2890	A2891	U2892	A2893	U2894	A2895	U2896	A2897	U2898	A2899	U2900	A2901	U2902	A2903	U2904	A2905	U2906	A2907	U2908	A2909	U2910	A2911	U2912	A2913	U2914	A2915	U2916	A2917	U2918	A2919	U2920	A2921	U2922	A2923	U2924	A2925	U2926	A2927	U2928	A2929	U2930	A2931	U2932	A2933	U2934	A2935	U2936	A2937	U2938	A2939	U2940	A2941	U2942	A2943	U2944	A2945	U2946	A2947	U2948	A2949	U2950	A2951	U2952	A2953	U2954	A2955	U2956	A2957	U2958	A2959	U2960	A2961	U2962	A2963	U2964	A2965	U2966	A2967	U2968	A2969	U2970	A2971	U2972	A2973	U2974	A2975	U2976	A2977	U2978	A2979	U2980	A2981	U2982	A2983	U2984	A2985	U2986	A2987	U2988	A2989	U2990	A2991	U2992	A2993	U2994	A2995	U2996	A2997	U2998	A2999	U3000	A3001	U3002	A3003	U3004	A3005	U3006	A3007	U3008	A3009	U3010	A3011	U3012	A3013	U3014	A3015	U3016	A3017	U3018	A3019	U3020	A3021	U3022	A3023	U3024	A3025	U3026	A3027	U3028	A3029	U3030	A3031	U3032	A3033	U3034	A3035	U3036	A3037	U3038	A3039	U3040	A3041	U3042	A3043	U3044	A3045	U3046	A3047	U3048	A3049	U3050	A3051	U3052	A3053	U3054	A3055	U3056	A3057	U3058	A3059	U3060	A3061	U3062	A3063	U3064	A3065	U3066	A3067	U3068	A3069	U3070	A3071	U3072	A3073	U3074	A3075	U3076	A3077	U3078	A3079	U3080	A3081	U3082	A3083	U3084	A3085	U3086	A3087	U3088	A3089	U3090	A3091	U3092	A3093	U3094	A3095	U3096	A3097	U3098	A3099	U3100	A3101	U3102	A3103	U3104	A3105	U3106	A3107	U3108	A3109	U3110	A3111	U3112	A3113	U3114	A3115	U3116	A3117	U3118	A3119	U3120	A3121	U3122	A3123	U3124	A3125	U3126	A3127	U3128	A3129	U3130	A3131	U3132	A3133	U3134	A3135	U3136	A3137	U3138	A3139	U3140	A3141	U3142	A3143	U3144	A3145	U3146	A3147	U3148	A3149	U3150	A3151	U3152	A3153	U3154	A3155	U3156	A3157	U3158	A3159	U3160	A3161	U3162	A3163	U3164	A3165	U3166	A3167	U3168	A3169	U3170	A3171	U3172	A3173	U3174	A3175	U3176	A3177	U3178	A3179	U3180	A3181	U3182	A3183	U3184	A3185	U3186	A3187	U3188	A3189	U3190	A3191	U3192	A3193	U3194	A3195	U3196	A3197	U3198	A3199	U3200	A3201	U3202	A3203	U3204	A3205	U3206	A3207	U3208	A3209	U3210	A3211	U3212	A3213	U3214	A3215	U3216	A3217	U3218	A3219	U3220	A3221	U3222	A3223	U3224	A3225	U3226	A3227	U3228	A3229	U3230	A3231	U3232	A3233	U3234	A3235	U3236	A3237	U3238	A3239	U3240	A3241	U3242	A3243	U3244	A3245	U3246	A3247	U3248	A3249	U3250	A3251	U3252	A3253	U3254	A3255	U3256	A3257	U3258	A3259	U3260	A3261	U3262	A3263	U3264	A3265	U3266	A3267	U3268	A3269	U3270	A3271	U3272	A3273	U3274	A3275	U3276	A3277	U3278	A3279	U3280	A3281	U3282	A3283	U3284	A3285	U3286	A3287	U3288	A3289	U3290	A3291	U3292	A3293	U3294	A3295	U3296	A3297	U3298	A3299	U3300	A3301	U3302	A3303	U3304	A3305	U3306	A3307	U3308	A3309	U3310	A3311	U3312	A3313	U3314	A3315	U3316	A3317	U3318	A3319	U3320	A3321	U3322	A3323	U3324	A3325	U3326	A3327	U3328	A3329	U3330	A3331	U3332	A3333	U3334	A3335	U3336	A3337	U3338	A3339	U3340	A3341	U3342	A3343	U3344	A3345	U3346	A3347	U3348	A3349	U3350	A3351	U3352	A3353	U3354	A3355	U3356	A3357	U3358	A3359	U3360	A3361	U3362	A3363	U3364	A3365	U3366	A3367	U3368	A3369	U3370	A3371	U3372	A3373	U3374	A3375	U3376	A3377	U3378	A3379	U3380	A3381	U3382	A3383	U3384	A3385	U3386	A3387	U3388	A3389	U3390	A3391	U3392	A3393	U3394	A3395	U3396	A3397	U3398	A3399	U3400	A3401	U3402	A3403	U3404	A3405	U3406	A3407	U3408	A3409	U3410	A3411	U3412	A3413	U3414	A3415	U3416	A3417	U3418	A3419	U3420	A3421	U3422	A3423	U3424	A3425	U3426	A3427	U3428	A3429	U3430	A3431	U3432	A3433	U3434	A3435	U3436	A3437	U3438	A3439	U3440	A3441	U3442	A3443	U3444	A3445	U3446	A3447	U3448	A3449	U3450	A3451	U3452	A3453	U3454	A3455	U3456	A3457	U3458	A3459	U3460	A3461	U3462	A3463	U3464	A3465	U3466	A3467	U3468	A3469	U3470	A3471	U3472	A3473	U3474	A3475	U3476	A3477	U3478	A3479	U3480	A3481	U3482	A3483	U3484	A3485	U3486	A3487	U3488	A3489	U3490	A3491	U3492	A3493	U3494	A3495	U3496	A3497	U3498	A3499	U3500	A3501	U3502	A3503	U3504	A3505	U3506	A3507	U3508	A3509	U3510	A3511	U3512	A3513	U3514	A3515	U3516	A3517	U3518	A3519	U3520	A3521	U3522	A3523	U3524	A3525	U3526	A3527	U3528	A3529	U3530	A3531	U3532	A3533	U3534	A3535	U3536	A3537	U3538	A3539	U3540	A3541	U3542	A3543	U3544	A3545	U3546	A3547	U3548	A3549	U3550	A3551	U3552	A3553	U3554	A3555	U3556	A3557	U3558	A3559	U3560	A3561	U3562	A3563	U3564	A3565	U3566	A3567	U3568	A3569	U3570	A3571	U3572	A3573	U3574	A3575	U3576	A3577	U3578	A3579	U3580	A3581	U3582	A3583



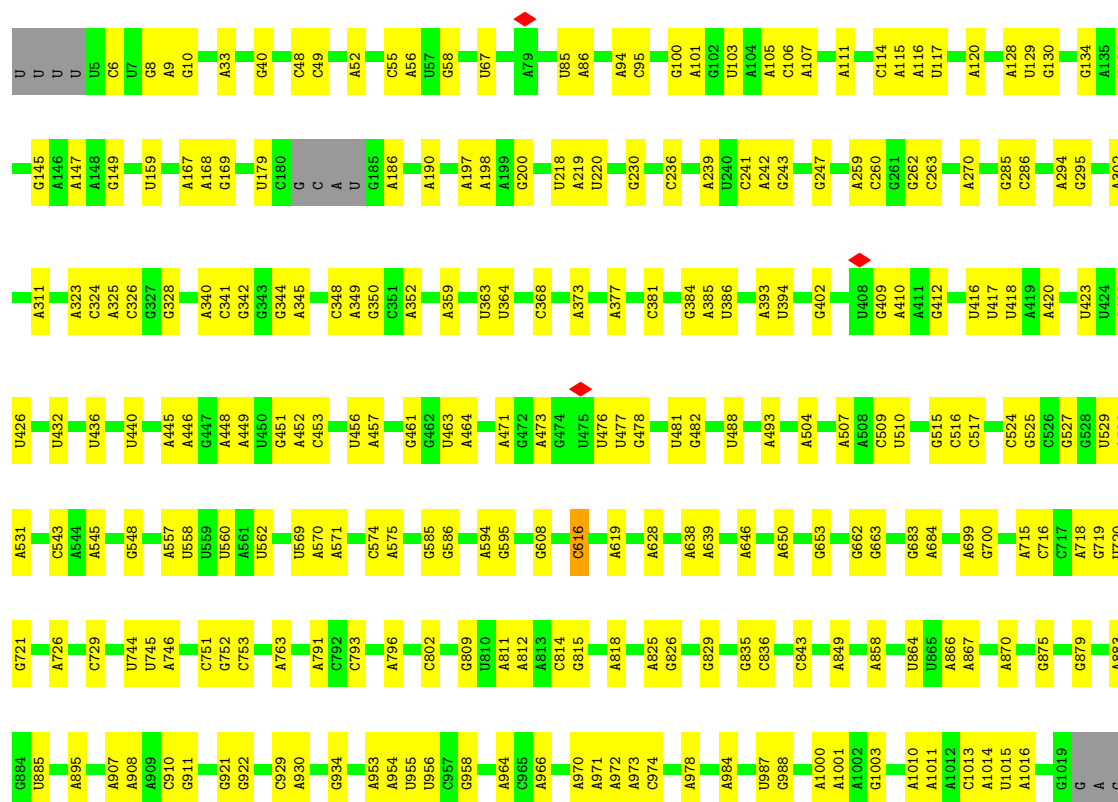
• Molecule 51: 5S ribosomal RNA

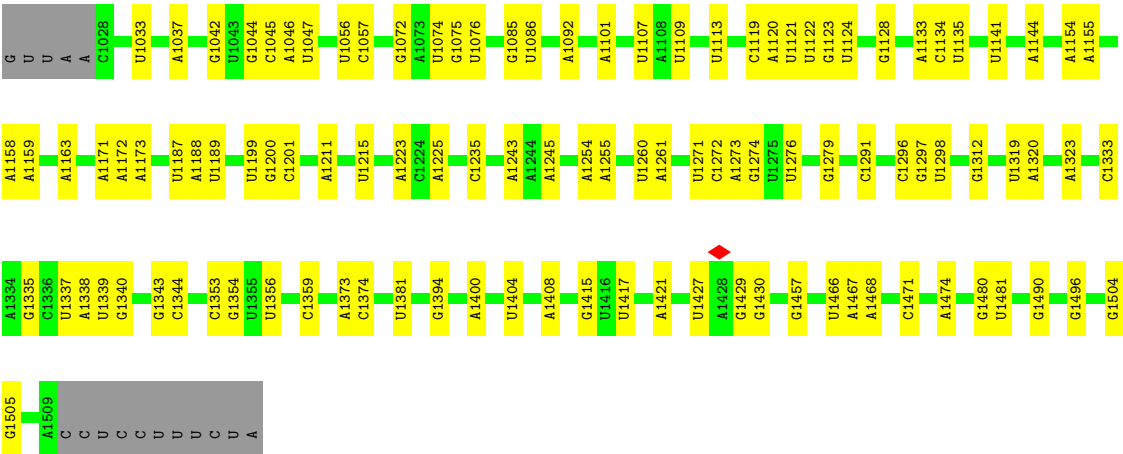
Chain 4: 63% 33%



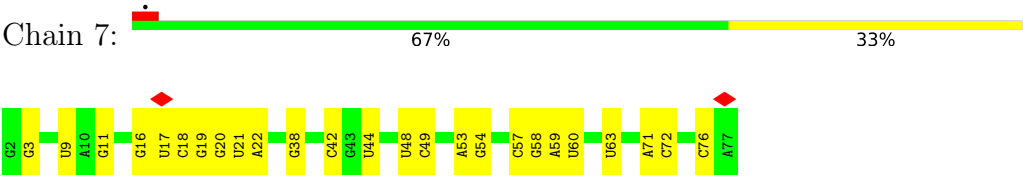
• Molecule 52: 16S ribosomal RNA

Chain 5: 75% 23%





• Molecule 53: tRNA-Phe





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	6223	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.902	Depositor
Minimum map value	-0.783	Depositor
Average map value	0.025	Depositor
Map value standard deviation	0.128	Depositor
Recommended contour level	0.47	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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	0	0.23	0/383	0.41	0/504
2	1	0.24	0/484	0.50	0/637
3	2	0.23	0/306	0.48	0/401
4	A	0.24	0/1954	0.46	0/2642
5	B	0.25	0/1721	0.50	0/2323
6	C	0.25	0/1691	0.48	0/2267
7	D	0.26	0/1188	0.51	1/1593 (0.1%)
8	E	0.24	0/1384	0.49	0/1867
9	F	0.26	0/1266	0.50	0/1700
10	G	0.25	0/1126	0.55	0/1517
11	H	0.24	0/1044	0.49	0/1395
12	I	0.25	0/820	0.54	0/1103
13	J	0.26	0/844	0.46	0/1136
14	K	0.27	0/1094	0.52	0/1468
15	L	0.27	0/962	0.49	0/1289
16	M	0.27	0/483	0.50	0/643
17	N	0.23	0/679	0.49	0/907
18	O	0.25	0/659	0.52	0/885
19	P	0.23	0/684	0.48	0/913
20	Q	0.27	0/545	0.54	0/730
21	R	0.26	0/698	0.47	0/936
22	S	0.25	0/631	0.49	0/838
23	T	0.27	0/475	0.52	0/621
24	a	0.23	0/2267	0.47	0/3044
25	b	0.26	0/1795	0.51	0/2412
26	c	0.26	0/1671	0.50	1/2246 (0.0%)
27	d	0.25	0/1409	0.47	0/1894
28	e	0.25	0/1420	0.48	0/1912
29	f	0.27	0/1183	0.55	0/1587
30	g	0.35	0/969	0.57	0/1295
31	h	0.24	0/968	0.44	0/1298
32	i	0.24	0/1186	0.47	0/1592
33	j	0.24	0/953	0.49	0/1275
34	k	0.25	0/1170	0.50	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	l	0.26	0/1104	0.49	0/1481
36	m	0.27	0/973	0.60	0/1309
37	n	0.25	0/897	0.51	0/1198
38	o	0.26	0/948	0.50	0/1262
39	p	0.26	0/961	0.47	0/1278
40	q	0.25	0/828	0.54	0/1111
41	r	0.26	0/1077	0.51	0/1441
42	s	0.24	0/732	0.47	0/988
43	t	0.24	0/879	0.49	0/1165
44	u	0.25	0/665	0.49	0/884
45	v	0.27	0/519	0.52	0/695
46	w	0.26	0/826	0.48	0/1104
47	x	0.24	0/353	0.43	0/474
48	y	0.30	0/457	0.57	0/601
49	z	0.23	0/412	0.51	0/547
50	3	0.19	0/69073	0.79	47/107710 (0.0%)
51	4	0.20	0/2505	0.81	4/3902 (0.1%)
52	5	0.18	0/35768	0.76	18/55764 (0.0%)
53	7	0.20	0/1808	0.83	0/2817
All	All	0.21	0/156897	0.71	71/234160 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	G	0	1
13	J	0	1
18	O	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	3	1718	C	N3-C2-O2	-11.00	114.20	121.90
50	3	2799	U	N3-C4-O4	-10.56	112.01	119.40
50	3	1474	C	N3-C2-O2	-9.37	115.34	121.90
50	3	2799	U	C5-C4-O4	9.14	131.38	125.90
50	3	1159	C	N3-C2-O2	-8.80	115.74	121.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	G	108	LEU	Peptide
13	J	111	HIS	Peptide
18	O	39	GLU	Peptide

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 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	0	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	A	238/294 (81%)	222 (93%)	16 (7%)	0	100	100
5	B	213/273 (78%)	196 (92%)	17 (8%)	0	100	100
6	C	201/205 (98%)	191 (95%)	10 (5%)	0	100	100
7	D	151/219 (69%)	145 (96%)	6 (4%)	0	100	100
8	E	165/215 (77%)	147 (89%)	18 (11%)	0	100	100
9	F	152/155 (98%)	135 (89%)	17 (11%)	0	100	100
10	G	139/142 (98%)	125 (90%)	14 (10%)	0	100	100
11	H	126/132 (96%)	115 (91%)	11 (9%)	0	100	100
12	I	99/108 (92%)	87 (88%)	12 (12%)	0	100	100
13	J	112/121 (93%)	105 (94%)	7 (6%)	0	100	100
14	K	134/139 (96%)	125 (93%)	9 (7%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	L	116/124 (94%)	104 (90%)	12 (10%)	0	100	100
16	M	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
17	N	81/86 (94%)	81 (100%)	0	0	100	100
18	O	78/94 (83%)	70 (90%)	8 (10%)	0	100	100
19	P	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
20	Q	63/104 (61%)	51 (81%)	12 (19%)	0	100	100
21	R	82/87 (94%)	73 (89%)	9 (11%)	0	100	100
22	S	75/87 (86%)	74 (99%)	1 (1%)	0	100	100
23	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
24	a	283/287 (99%)	265 (94%)	18 (6%)	0	100	100
25	b	227/287 (79%)	214 (94%)	13 (6%)	0	100	100
26	c	208/212 (98%)	197 (95%)	11 (5%)	0	100	100
27	d	173/180 (96%)	160 (92%)	13 (8%)	0	100	100
28	e	174/184 (95%)	166 (95%)	8 (5%)	0	100	100
29	f	143/149 (96%)	125 (87%)	18 (13%)	0	100	100
30	g	124/161 (77%)	109 (88%)	13 (10%)	2 (2%)	8	38
31	h	126/137 (92%)	114 (90%)	12 (10%)	0	100	100
32	i	142/146 (97%)	136 (96%)	6 (4%)	0	100	100
33	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
34	k	146/151 (97%)	139 (95%)	7 (5%)	0	100	100
35	l	134/139 (96%)	124 (92%)	10 (8%)	0	100	100
36	m	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
37	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
38	o	113/119 (95%)	101 (89%)	12 (11%)	0	100	100
39	p	112/127 (88%)	108 (96%)	4 (4%)	0	100	100
40	q	97/100 (97%)	90 (93%)	7 (7%)	0	100	100
41	r	137/159 (86%)	134 (98%)	3 (2%)	0	100	100
42	s	90/237 (38%)	88 (98%)	2 (2%)	0	100	100
43	t	109/111 (98%)	104 (95%)	5 (5%)	0	100	100
44	u	84/104 (81%)	81 (96%)	3 (4%)	0	100	100
45	v	61/65 (94%)	59 (97%)	2 (3%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	w	96/111 (86%)	89 (93%)	7 (7%)	0	100	100
47	x	42/97 (43%)	35 (83%)	7 (17%)	0	100	100
48	y	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
49	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	5820/6670 (87%)	5418 (93%)	400 (7%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	g	88	GLU
30	g	42	LYS

### 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	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	50 (98%)	1 (2%)	50	68
3	2	35/35 (100%)	35 (100%)	0	100	100
4	A	212/262 (81%)	211 (100%)	1 (0%)	86	89
5	B	180/232 (78%)	180 (100%)	0	100	100
6	C	181/183 (99%)	180 (99%)	1 (1%)	84	88
7	D	123/178 (69%)	122 (99%)	1 (1%)	79	85
8	E	150/196 (76%)	148 (99%)	2 (1%)	65	77
9	F	131/132 (99%)	131 (100%)	0	100	100
10	G	123/124 (99%)	122 (99%)	1 (1%)	79	85
11	H	111/115 (96%)	110 (99%)	1 (1%)	75	83
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	90 (99%)	1 (1%)	70	80
14	K	117/120 (98%)	113 (97%)	4 (3%)	32	51

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	L	100/105 (95%)	98 (98%)	2 (2%)	50	68
16	M	47/48 (98%)	47 (100%)	0	100	100
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	69 (100%)	0	100	100
19	P	73/75 (97%)	71 (97%)	2 (3%)	40	58
20	Q	56/94 (60%)	55 (98%)	1 (2%)	54	71
21	R	74/77 (96%)	74 (100%)	0	100	100
22	S	70/77 (91%)	69 (99%)	1 (1%)	62	75
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	241 (100%)	0	100	100
25	b	186/233 (80%)	185 (100%)	1 (0%)	86	89
26	c	182/184 (99%)	182 (100%)	0	100	100
27	d	150/154 (97%)	150 (100%)	0	100	100
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	123/134 (92%)	121 (98%)	2 (2%)	58	74
30	g	101/129 (78%)	91 (90%)	10 (10%)	6	21
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	126 (100%)	0	100	100
33	j	103/103 (100%)	103 (100%)	0	100	100
34	k	123/126 (98%)	123 (100%)	0	100	100
35	l	113/115 (98%)	112 (99%)	1 (1%)	75	83
36	m	105/109 (96%)	104 (99%)	1 (1%)	73	82
37	n	96/99 (97%)	96 (100%)	0	100	100
38	o	101/105 (96%)	99 (98%)	2 (2%)	50	68
39	p	100/108 (93%)	100 (100%)	0	100	100
40	q	90/91 (99%)	90 (100%)	0	100	100
41	r	116/132 (88%)	114 (98%)	2 (2%)	56	72
42	s	82/208 (39%)	82 (100%)	0	100	100
43	t	96/96 (100%)	96 (100%)	0	100	100
44	u	69/85 (81%)	69 (100%)	0	100	100
45	v	58/60 (97%)	57 (98%)	1 (2%)	56	72

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	w	87/98 (89%)	87 (100%)	0	100	100
47	x	41/86 (48%)	41 (100%)	0	100	100
48	y	48/49 (98%)	45 (94%)	3 (6%)	15	36
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5093/5751 (89%)	5051 (99%)	42 (1%)	77	85

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	46	LYS
38	o	107	ARG
30	g	84	VAL
35	l	60	LYS
41	r	126	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
24	a	62	ASN
28	e	68	HIS
42	s	19	ASN
26	c	104	ASN
28	e	72	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	733 (25%)	25 (0%)
51	4	103/108 (95%)	34 (33%)	5 (4%)
52	5	1490/1520 (98%)	349 (23%)	6 (0%)
53	7	75/76 (98%)	25 (33%)	2 (2%)
All	All	4543/4611 (98%)	1141 (25%)	38 (0%)

5 of 1141 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	12	A
50	3	14	U

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
50	3	15	A
50	3	17	G
50	3	29	G

5 of 38 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	4	59	A
52	5	1373	A
51	4	70	G
52	5	448	A
53	7	19	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](#)

There are no ligands in this entry.

## 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.

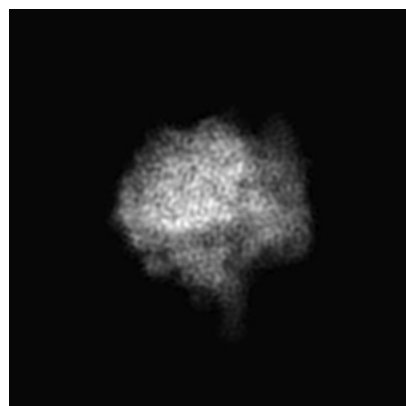
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13273. These allow visual inspection of the internal detail of the map and identification of artifacts.

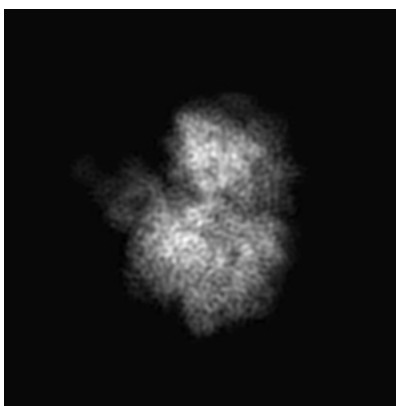
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

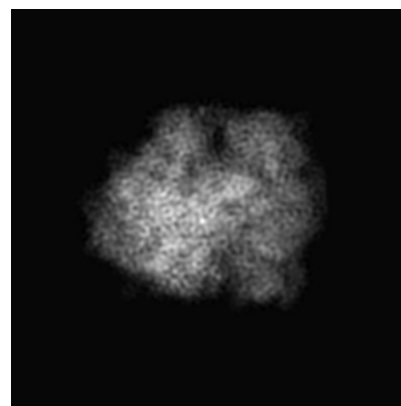
#### 6.1.1 Primary map



X

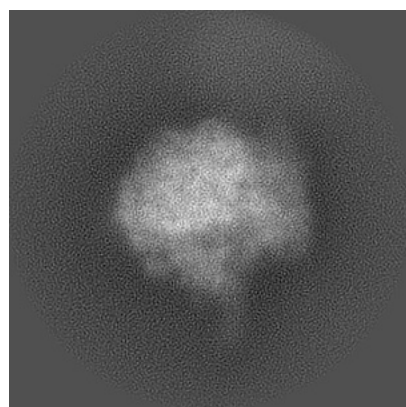


Y

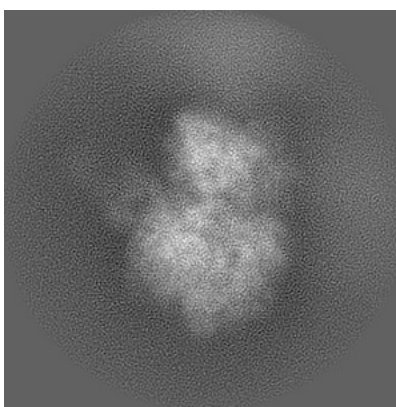


Z

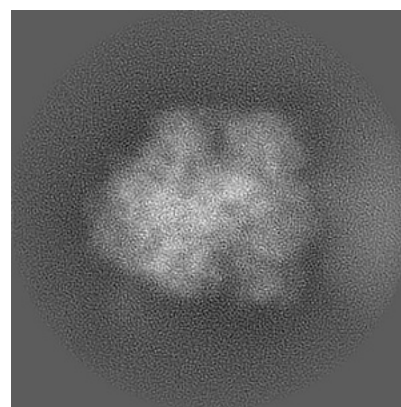
#### 6.1.2 Raw map



X



Y

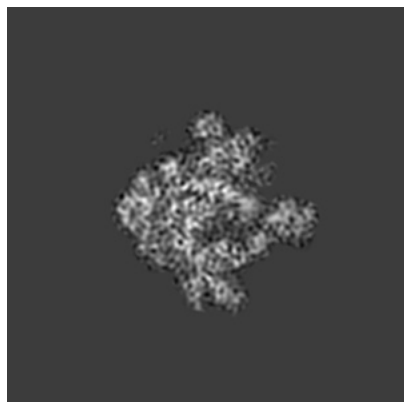


Z

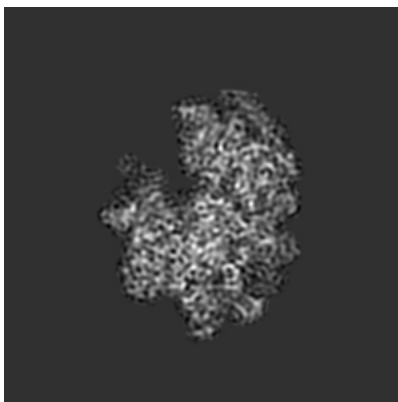
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

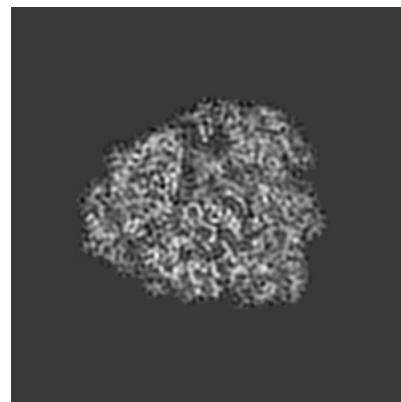
### 6.2.1 Primary map



X Index: 128

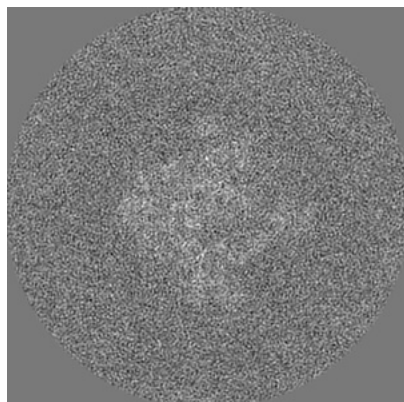


Y Index: 128

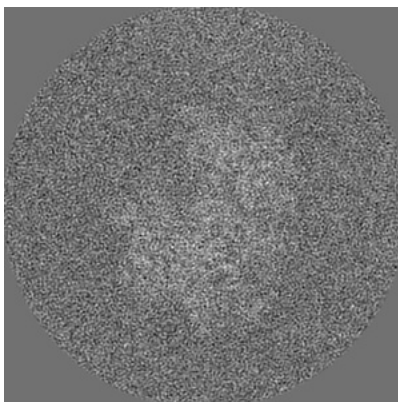


Z Index: 128

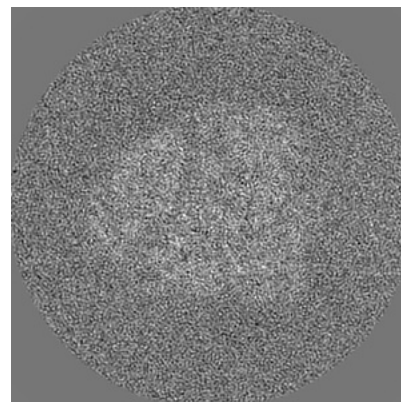
### 6.2.2 Raw map



X Index: 128



Y Index: 128

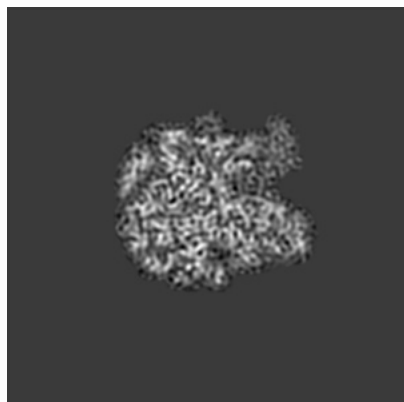


Z Index: 128

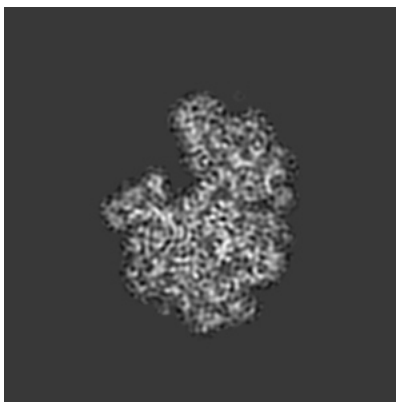
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

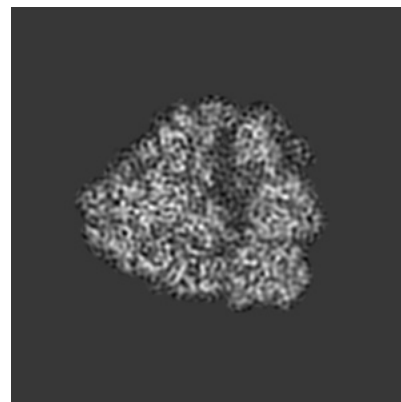
### 6.3.1 Primary map



X Index: 104

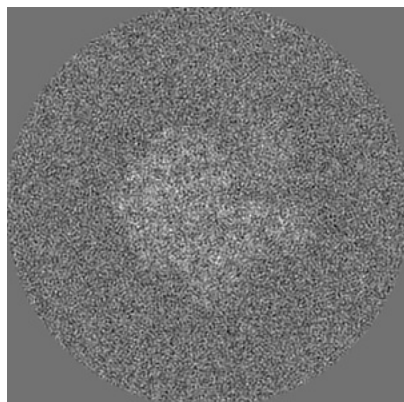


Y Index: 120

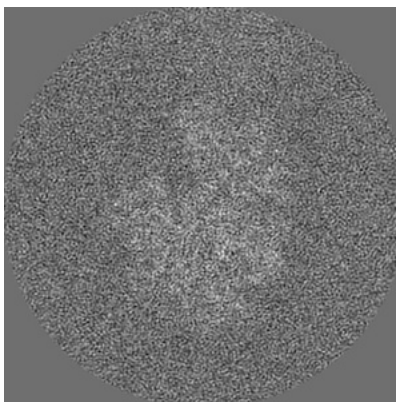


Z Index: 122

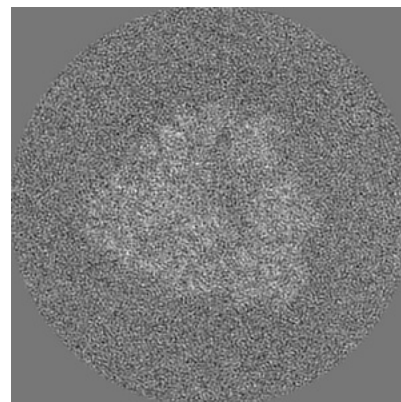
### 6.3.2 Raw map



X Index: 119



Y Index: 120

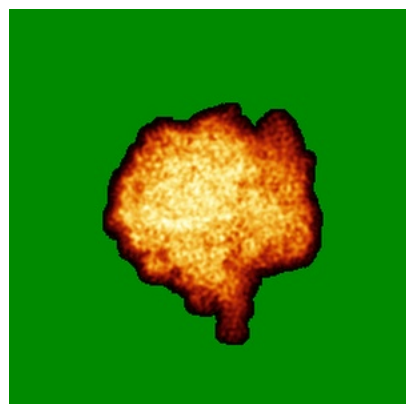


Z Index: 122

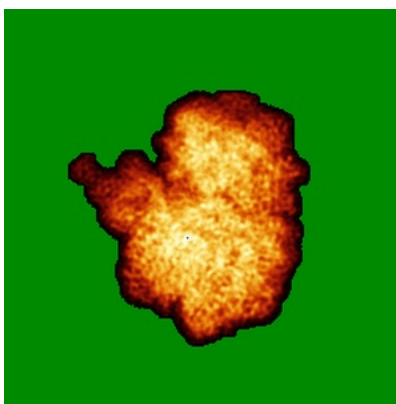
The images above show the largest variance slices of the map in three orthogonal directions.

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

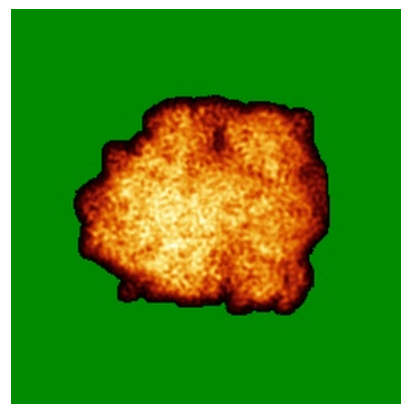
### 6.4.1 Primary map



X

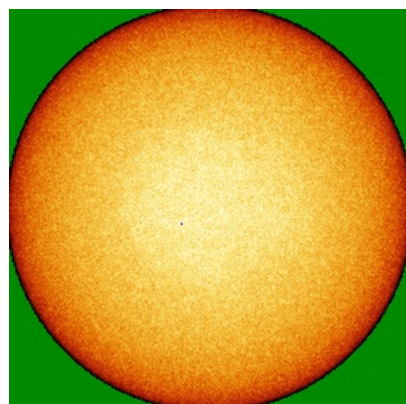


Y

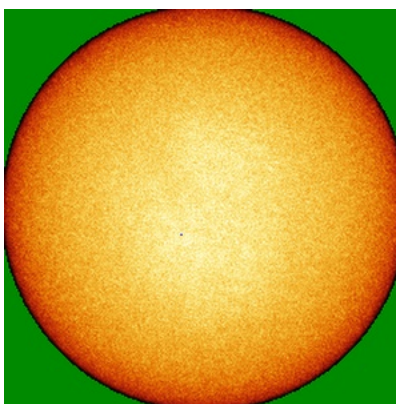


Z

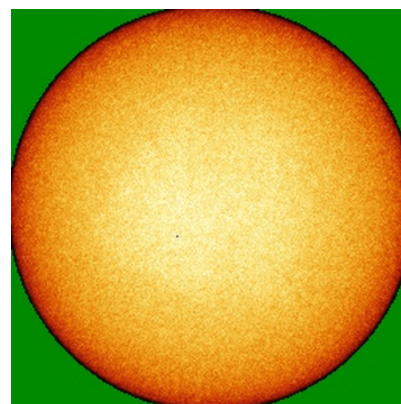
### 6.4.2 Raw map



X



Y



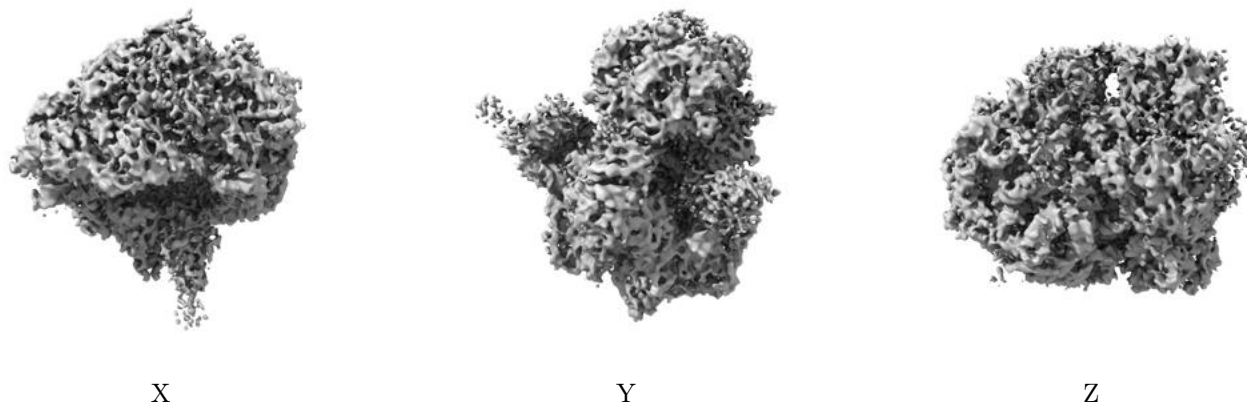
Z

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.



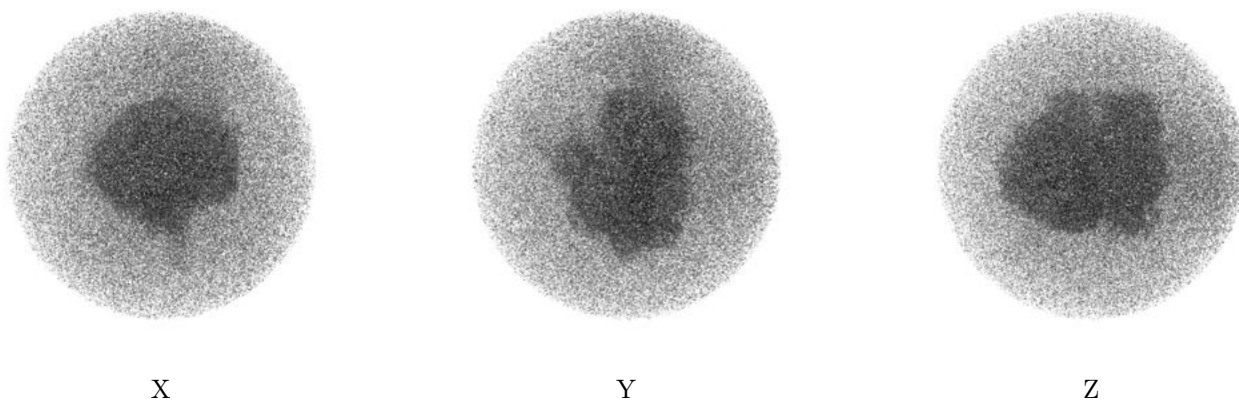
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.47. 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.

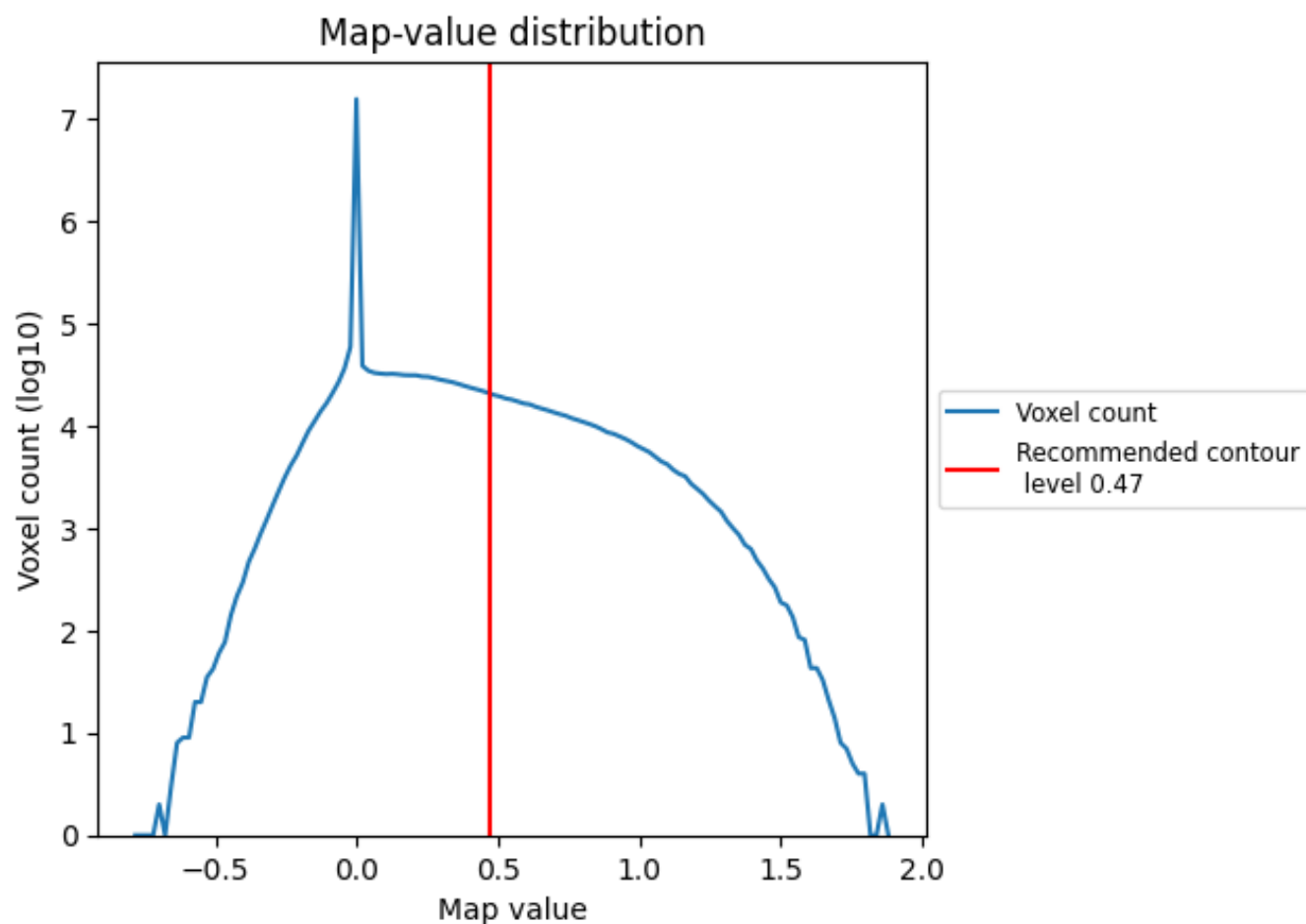
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

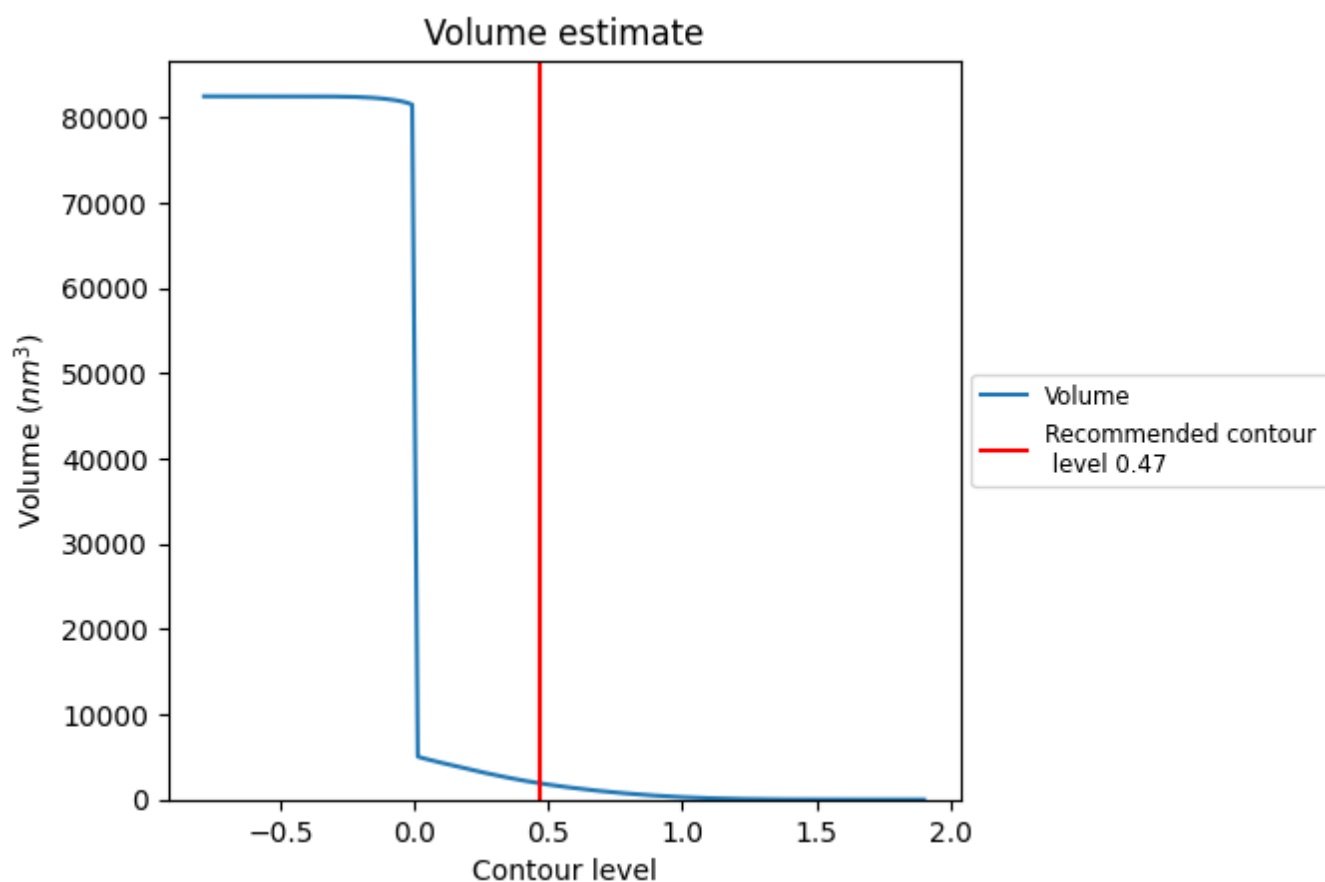
This section contains the results of statistical analysis of the map.

### 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](#)

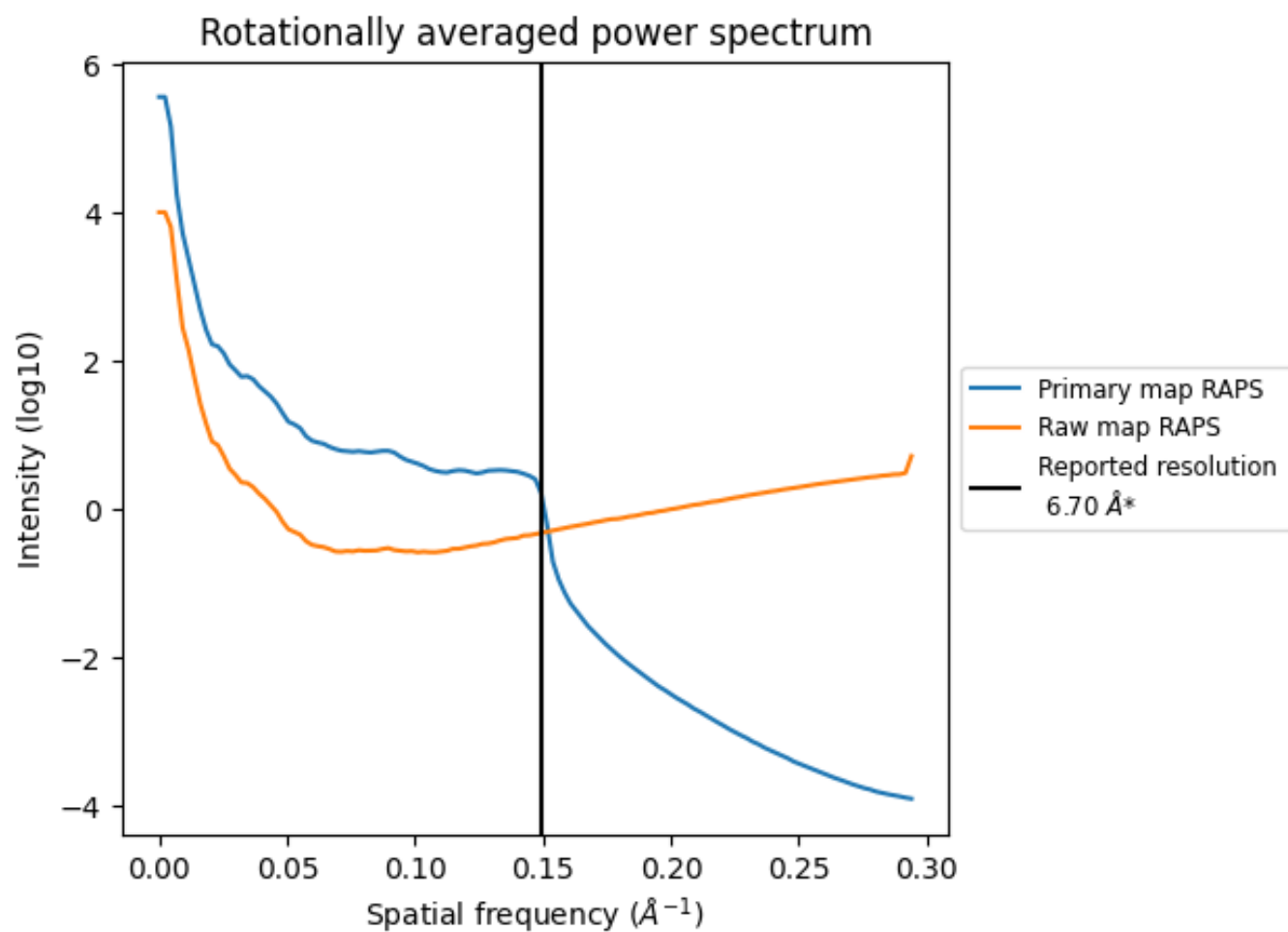


The volume at the recommended contour level is 1908  $\text{nm}^3$ ; this corresponds to an approximate mass of 1723 kDa.

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 ⓘ

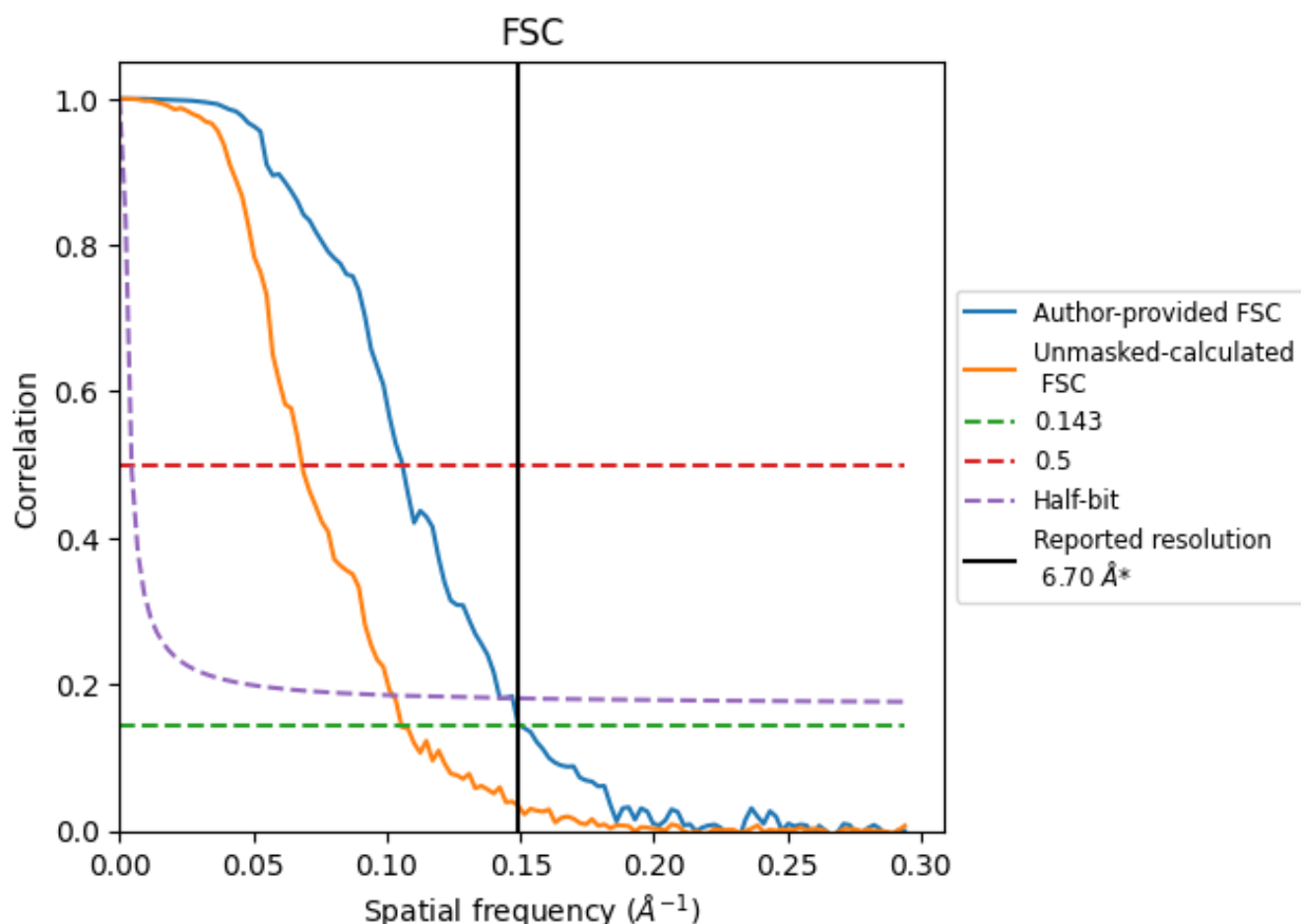


\*Reported resolution corresponds to spatial frequency of 0.149 Å<sup>-1</sup>

## 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 0.149 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

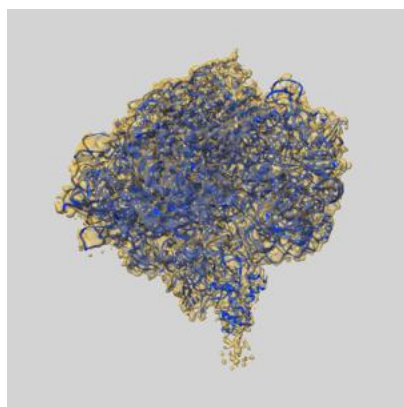
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.70	-	-
Author-provided FSC curve	6.65	9.44	7.02
Unmasked-calculated*	9.47	14.62	9.77

\*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 9.47 differs from the reported value 6.7 by more than 10 %

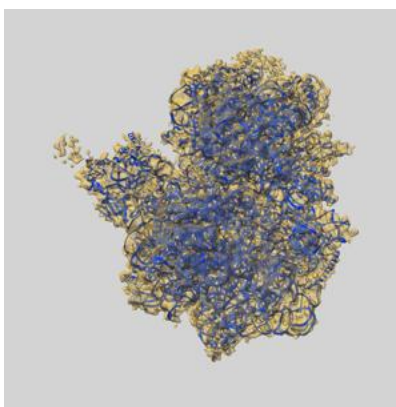
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13273 and PDB model 7PAI. Per-residue inclusion information can be found in section [3](#) on page [13](#).

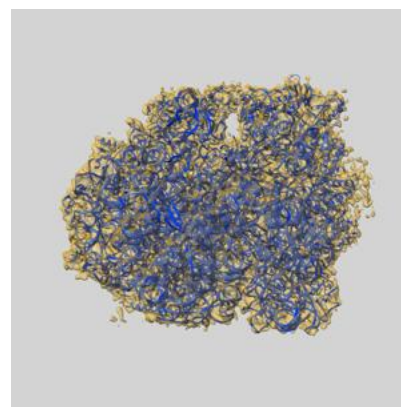
### 9.1 Map-model overlay [i](#)



X



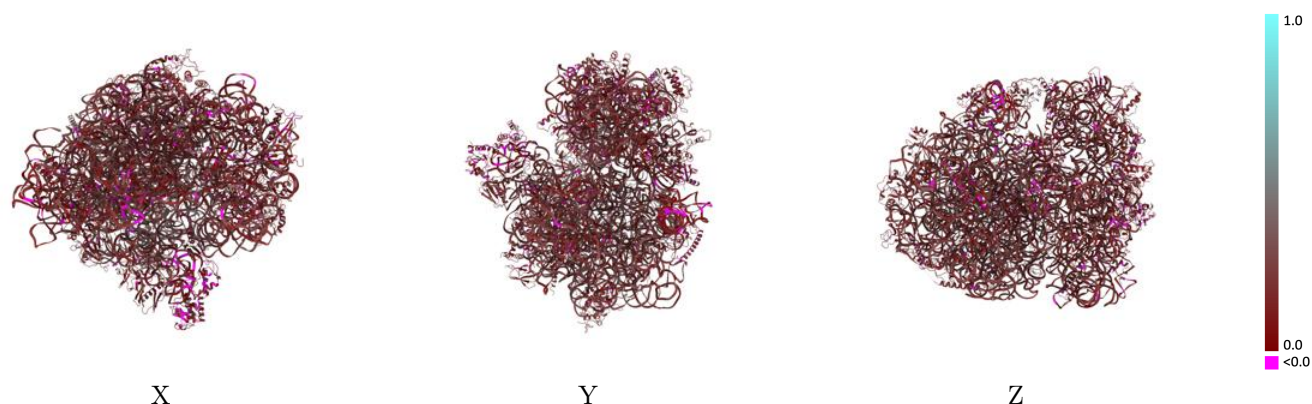
Y



Z

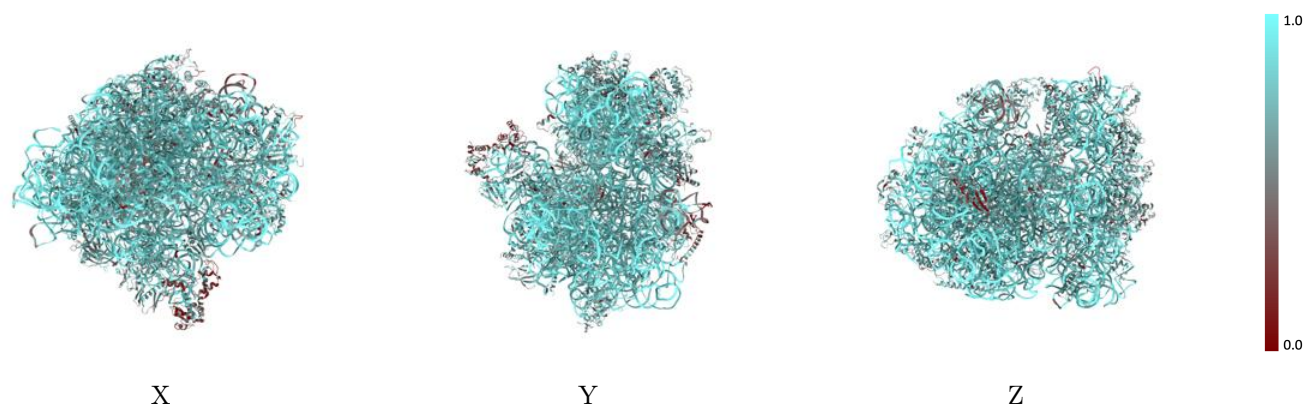
The images above show the 3D surface view of the map at the recommended contour level 0.47 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



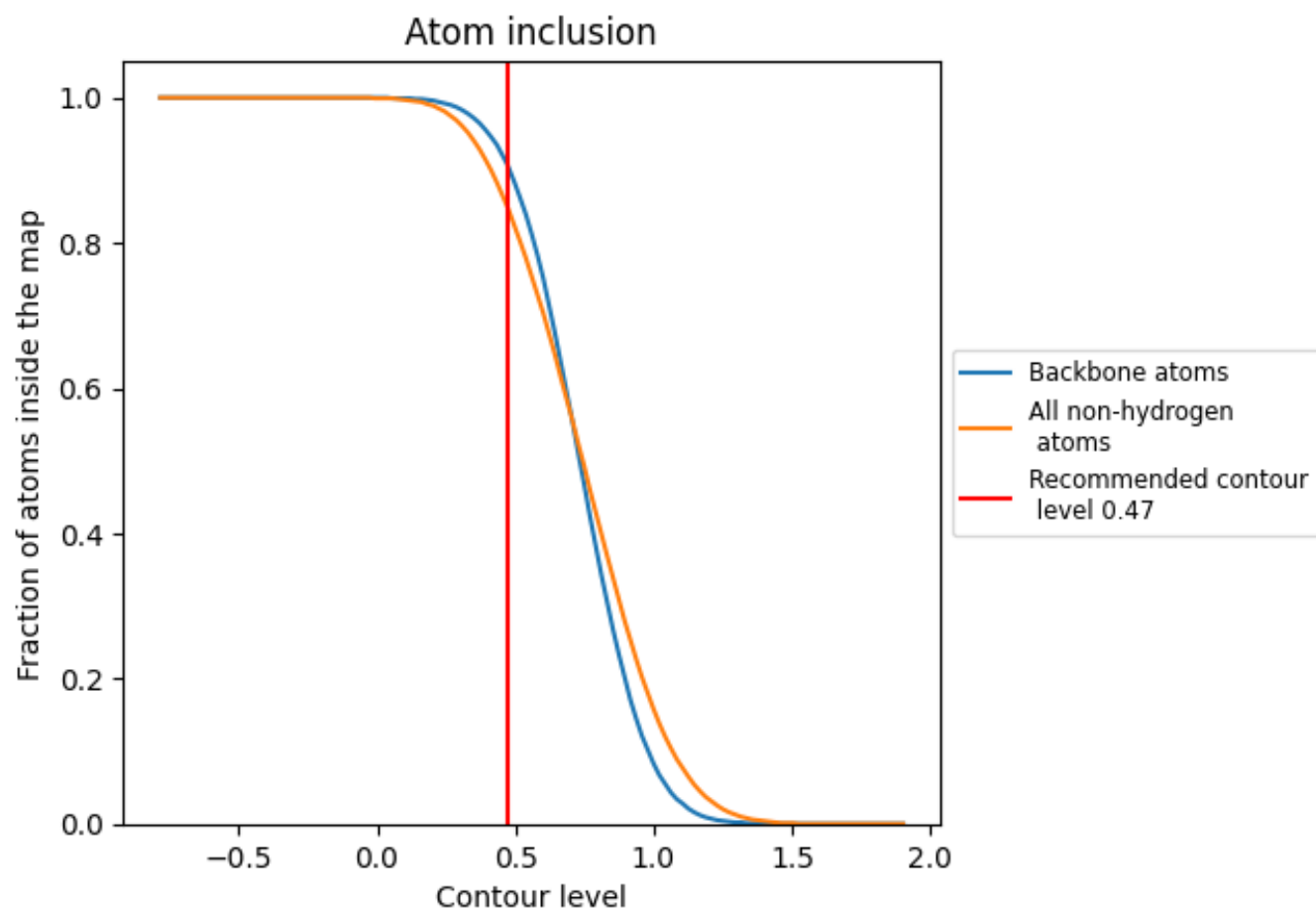
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.47).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 91% of all backbone atoms, 85% 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 (0.47) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8510	 0.2110
0	 0.7840	 0.1880
1	 0.7770	 0.2000
2	 0.7630	 0.1700
3	 0.9360	 0.2240
4	 0.9290	 0.2270
5	 0.9370	 0.2140
7	 0.8860	 0.2070
A	 0.6430	 0.1980
B	 0.6500	 0.1880
C	 0.6510	 0.1760
D	 0.6610	 0.1840
E	 0.6170	 0.2090
F	 0.6550	 0.1850
G	 0.6700	 0.1770
H	 0.6790	 0.1690
I	 0.6460	 0.1810
J	 0.6890	 0.1930
K	 0.7160	 0.2000
L	 0.6850	 0.2000
M	 0.7360	 0.1620
N	 0.6840	 0.1980
O	 0.7280	 0.1710
P	 0.6590	 0.1890
Q	 0.6960	 0.1780
R	 0.6400	 0.1800
S	 0.7390	 0.1850
T	 0.6900	 0.1980
a	 0.7540	 0.1940
b	 0.7200	 0.1870
c	 0.7240	 0.2140
d	 0.6880	 0.1920
e	 0.6460	 0.2040
f	 0.3310	 0.1710
g	 0.4420	 0.1380



*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
h	 0.3080	 0.1460
i	 0.7390	 0.1980
j	 0.6880	 0.2040
k	 0.7240	 0.2010
l	 0.7200	 0.2110
m	 0.7310	 0.2010
n	 0.7220	 0.1960
o	 0.6710	 0.1970
p	 0.7530	 0.1730
q	 0.6820	 0.1940
r	 0.7460	 0.1950
s	 0.7550	 0.2250
t	 0.6210	 0.1950
u	 0.7480	 0.1990
v	 0.7480	 0.1930
w	 0.6840	 0.1920
x	 0.6710	 0.2290
y	 0.7560	 0.2130
z	 0.7930	 0.2150