



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 12:17 AM UTC

PDB ID : 7PIT / pdb_00007pit
EMDB ID : EMD-13450
Title : 70S ribosome with EF-G, A/P- and P/E-site tRNAs in pseudouridimycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-23
Resolution : 5.70 Å (reported)
Based on initial models : 4V7D, 7OOC, 7OOD, 4V7C

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:

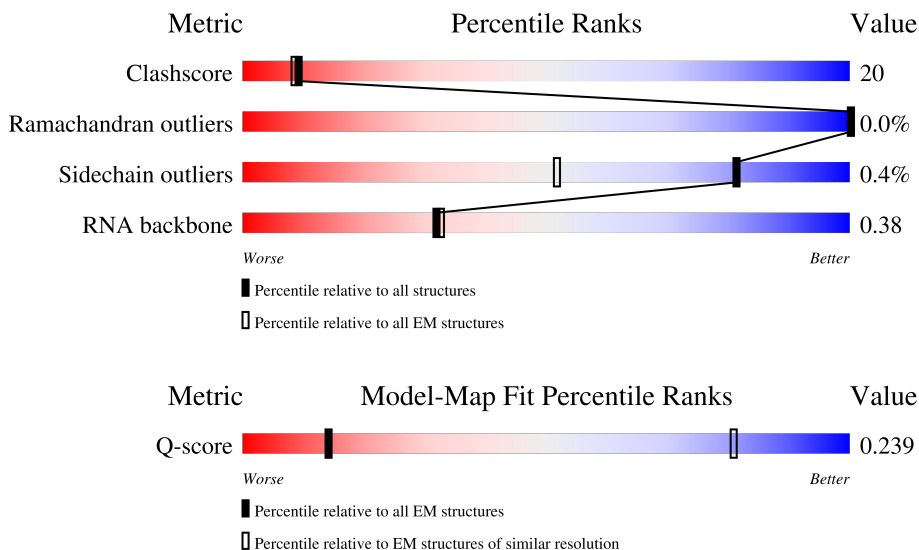
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 5.70 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)	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	503 (5.20 - 6.20)

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	0	48	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">17%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">48%</div> <div style="text-align: center;">48%</div> <div style="text-align: center;">..</div> </div>
2	1	59	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">14%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="text-align: center;">51%</div> <div style="text-align: center;">49%</div> </div>
3	2	37	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">11%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="text-align: center;">35%</div> <div style="text-align: center;">65%</div> </div>

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Mol	Chain	Length	Quality of chain
4	9	688	83% 56% 43%
5	A	294	41% 45% 36% 18%
6	B	273	39% 55% 24% 21%
7	C	205	54% 57% 42%
8	D	219	31% 38% 32% 30%
9	E	215	37% 45% 33% 22%
10	F	155	56% 67% 32%
11	G	142	32% 53% 46%
12	H	132	48% 59% 38%
13	I	108	53% 51% 43% 6%
14	J	121	30% 52% 42% 6%
15	K	139	32% 58% 40%
16	L	124	54% 60% 35% 5%
17	M	61	30% 41% 57%
18	N	86	26% 58% 38%
19	O	94	31% 46% 39% 15%
20	P	85	39% 69% 28%
21	Q	104	22% 38% 25% 38%
22	R	87	51% 54% 43%
23	S	87	23% 52% 37% 11%
24	T	60	30% 43% 43% 12%
25	W	122	56% 43% 13% 43%
26	a	287	20% 55% 45%
27	b	287	20% 48% 31% 20%
28	c	212	32% 60% 39%

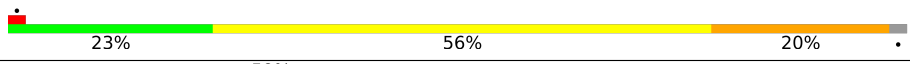


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Mol	Chain	Length	Quality of chain
29	d	180	54% 61% 37%
30	e	184	49% 60% 36%
31	f	149	81% 58% 40%
32	g	161	65% 35% 41% 22%
33	h	137	76% 51% 42% 7%
34	i	146	25% 51% 47%
35	j	122	42% 52% 48%
36	k	151	23% 62% 36%
37	l	139	29% 65% 33%
38	m	124	13% 49% 47%
39	n	116	38% 54% 42%
40	o	119	39% 45% 52%
41	p	127	18% 50% 39% 10%
42	q	100	43% 56% 43%
43	r	159	12% 51% 36% 13%
44	s	237	9% 21% 18% 61%
45	t	111	52% 55% 45%
46	u	104	25% 52% 31% 17%
47	v	65	29% 60% 37%
48	w	111	21% 52% 38% 10%
49	x	97	30% 32% 13% 55%
50	y	57	21% 49% 44% 5%
51	z	53	34% 51% 43% 6%
52	3	2907	21% 56% 22%
53	4	108	25% 42% 31%

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Mol	Chain	Length	Quality of chain
54	5	1520	
55	7	76	
55	8	76	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 151980 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
			Total	C	N	O	S		
1	0	47	380	236	81	61	2	0	0

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

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

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

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

- Molecule 4 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	9	682	5326	3369	911	1021	25	0	0

- Molecule 5 is a protein called 30S ribosomal protein S2.

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

- Molecule 6 is a protein called 30S ribosomal protein S3.

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

- Molecule 7 is a protein called 30S ribosomal protein S4.

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

- Molecule 8 is a protein called 30S ribosomal protein S5.

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

- Molecule 9 is a protein called 30S ribosomal protein S6.

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

- Molecule 10 is a protein called 30S ribosomal protein S7.

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

- Molecule 11 is a protein called 30S ribosomal protein S8.

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

- Molecule 12 is a protein called 30S ribosomal protein S9.

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

- Molecule 13 is a protein called 30S ribosomal protein S10.

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

- Molecule 14 is a protein called 30S ribosomal protein S11.

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

- Molecule 15 is a protein called 30S ribosomal protein S12.

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

- Molecule 16 is a protein called 30S ribosomal protein S13.

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

- Molecule 17 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 18 is a protein called 30S ribosomal protein S15.

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

- Molecule 19 is a protein called 30S ribosomal protein S16.

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

- Molecule 20 is a protein called 30S ribosomal protein S17.

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

- Molecule 21 is a protein called 30S ribosomal protein S18.

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

- Molecule 22 is a protein called 30S ribosomal protein S19.

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

- Molecule 23 is a protein called 30S ribosomal protein S20.

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

- Molecule 24 is a protein called 30S ribosomal protein S21.

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

- Molecule 25 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	69	Total	C	N	O	S	0	0
			534	342	87	103	2		

- Molecule 26 is a protein called 50S ribosomal protein L2.

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

- Molecule 27 is a protein called 50S ribosomal protein L3.

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

- Molecule 28 is a protein called 50S ribosomal protein L4.

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

- Molecule 29 is a protein called 50S ribosomal protein L5.

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

- Molecule 30 is a protein called 50S ribosomal protein L6.

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

- Molecule 31 is a protein called 50S ribosomal protein L9.

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

- Molecule 32 is a protein called 50S ribosomal protein L10.

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

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

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

- Molecule 46 is a protein called 50S ribosomal protein L27.

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

- Molecule 47 is a protein called 50S ribosomal protein L28.

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

- Molecule 48 is a protein called 50S ribosomal protein L29.

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

- Molecule 49 is a protein called 50S ribosomal protein L31.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L33 1.

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

- Molecule 52 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 53 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 54 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

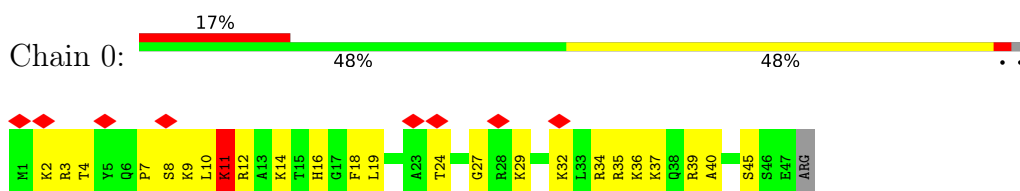
- Molecule 55 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
55	8	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

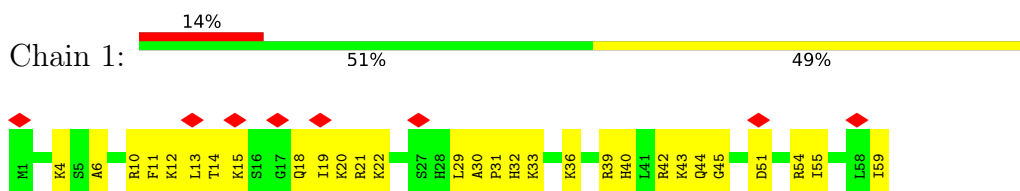
3 Residue-property plots [i](#)

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.

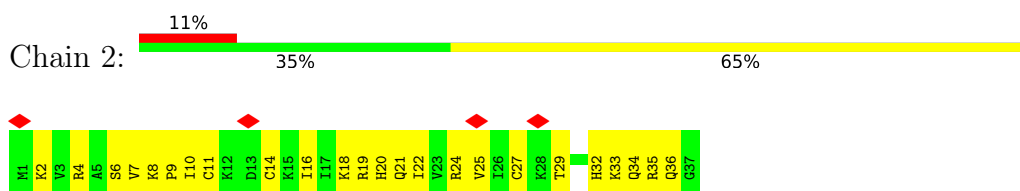
- Molecule 1: 50S ribosomal protein L34



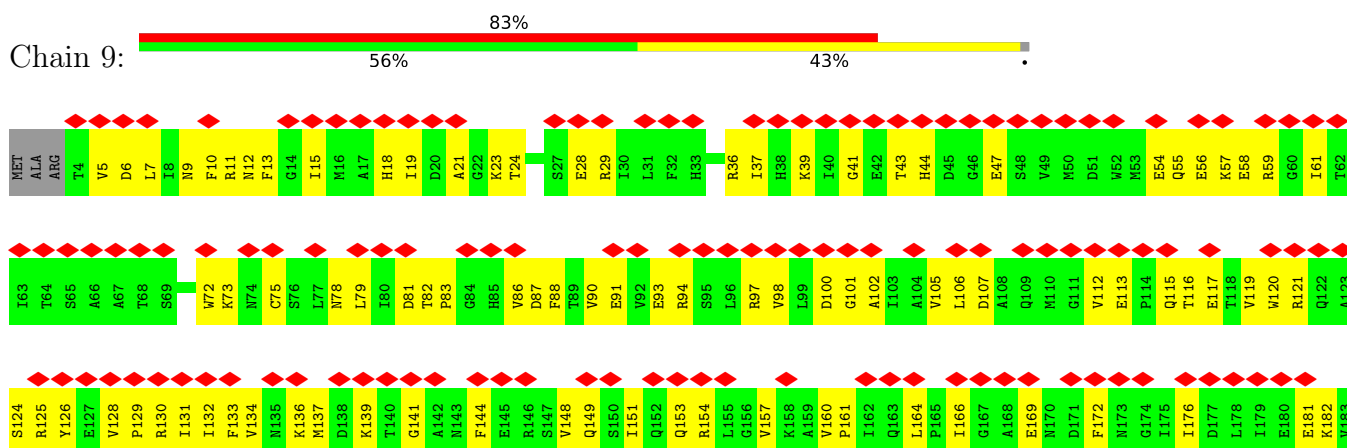
- Molecule 2: 50S ribosomal protein L35



- Molecule 3: 50S ribosomal protein L36

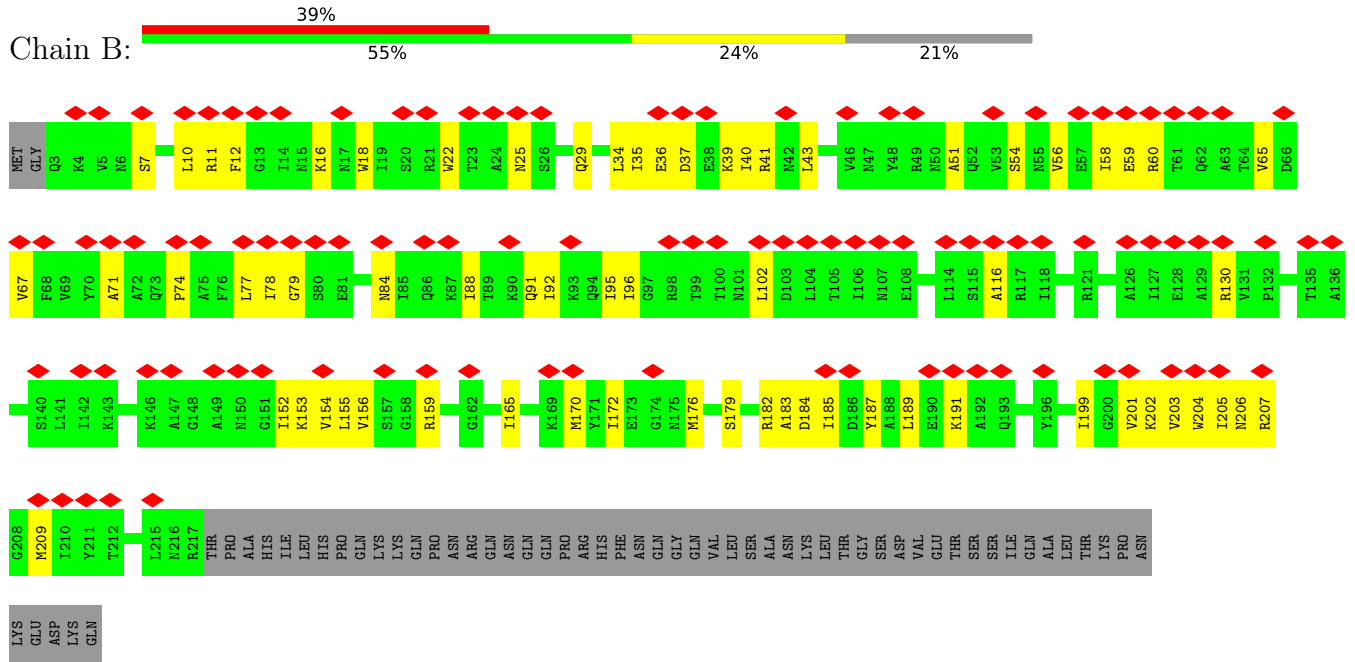


- Molecule 4: Elongation factor G

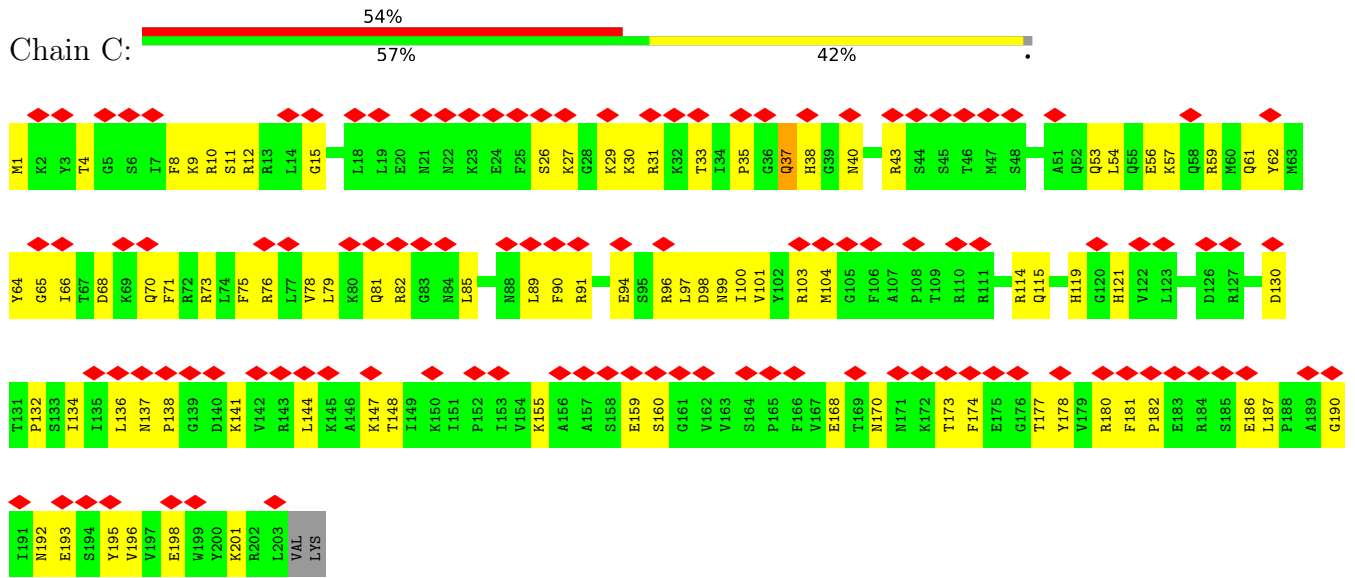


GLN
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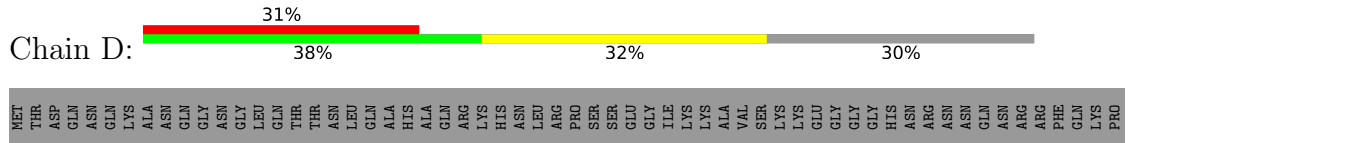
• Molecule 6: 30S ribosomal protein S3

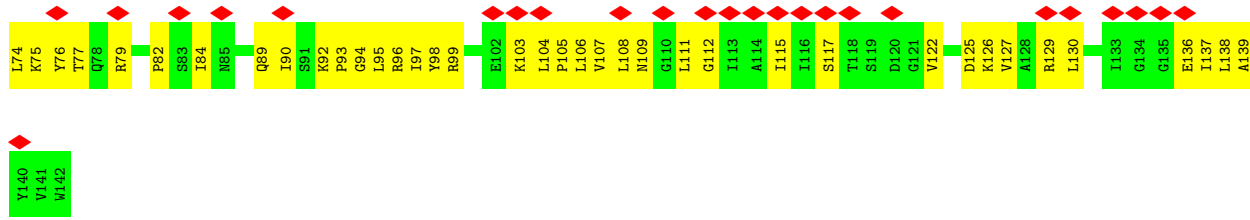


• Molecule 7: 30S ribosomal protein S4

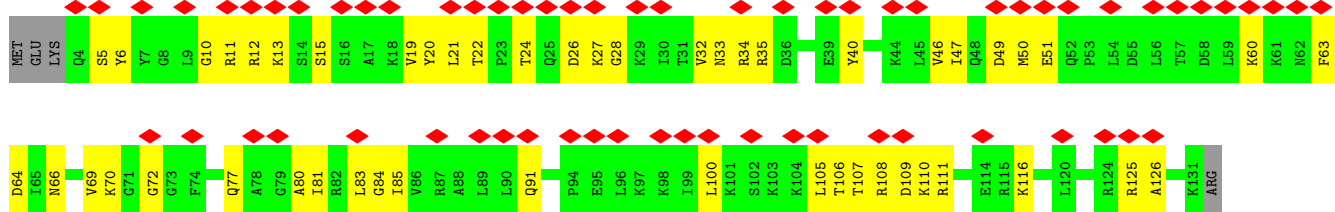


• Molecule 8: 30S ribosomal protein S5

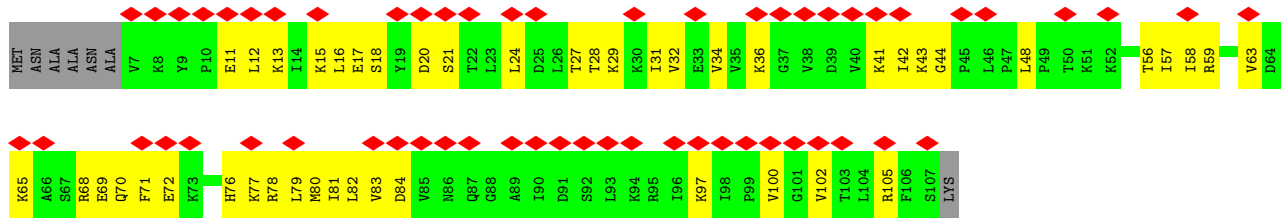




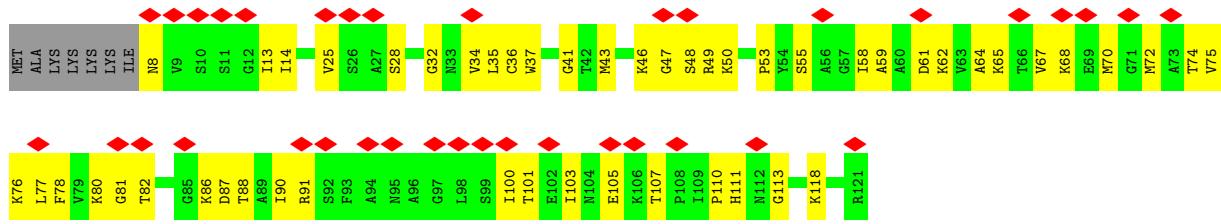
• Molecule 12: 30S ribosomal protein S9



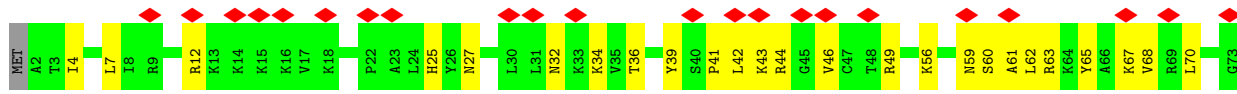
• Molecule 13: 30S ribosomal protein S10

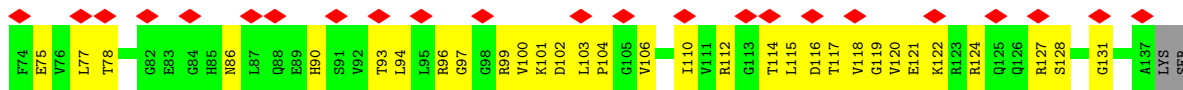


• Molecule 14: 30S ribosomal protein S11

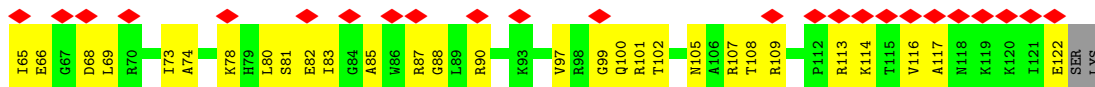


• Molecule 15: 30S ribosomal protein S12

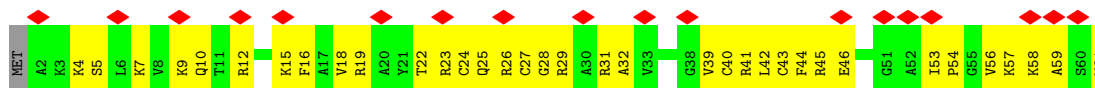




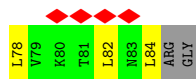
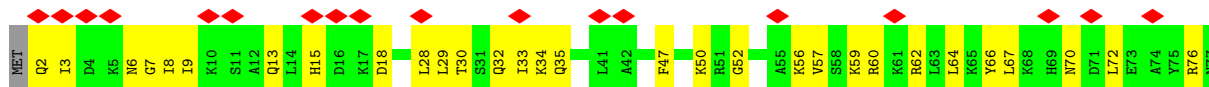
• Molecule 16: 30S ribosomal protein S13



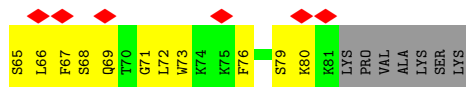
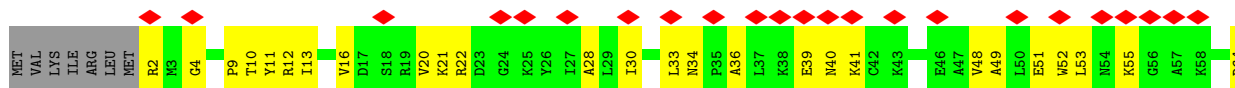
• Molecule 17: 30S ribosomal protein S14 type Z



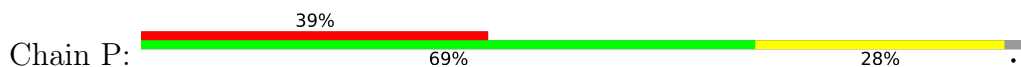
• Molecule 18: 30S ribosomal protein S15

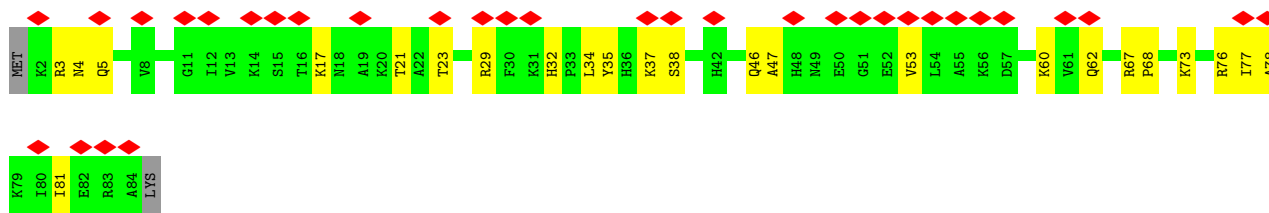


• Molecule 19: 30S ribosomal protein S16

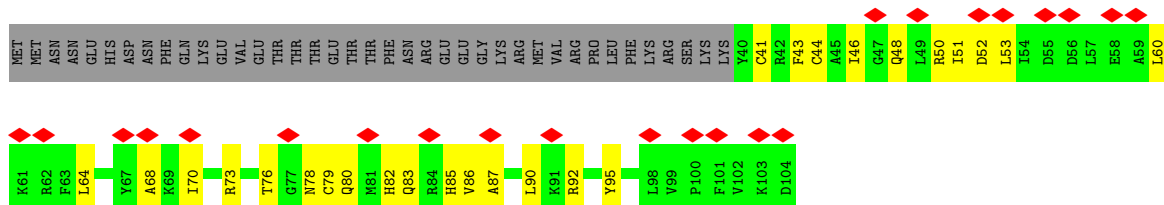


• Molecule 20: 30S ribosomal protein S17

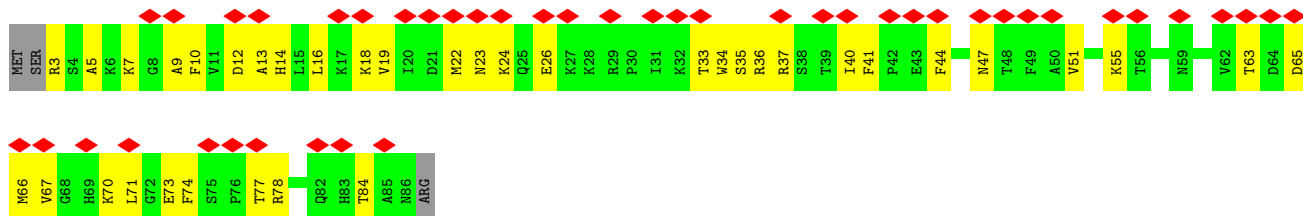




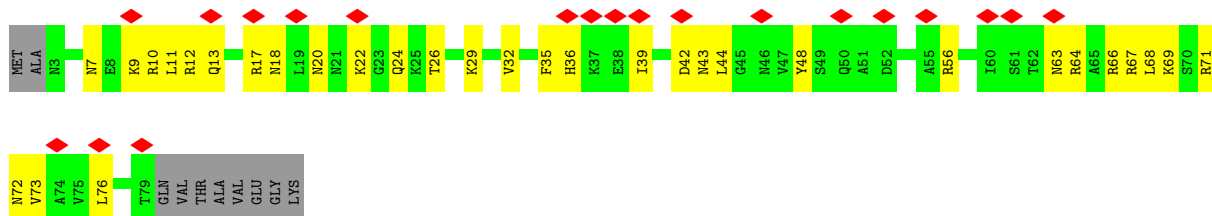
• Molecule 21: 30S ribosomal protein S18



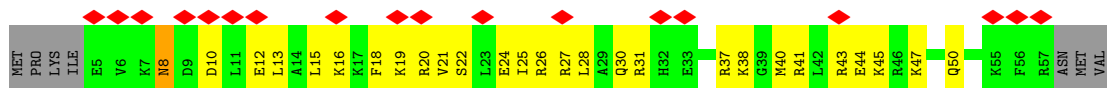
• Molecule 22: 30S ribosomal protein S19



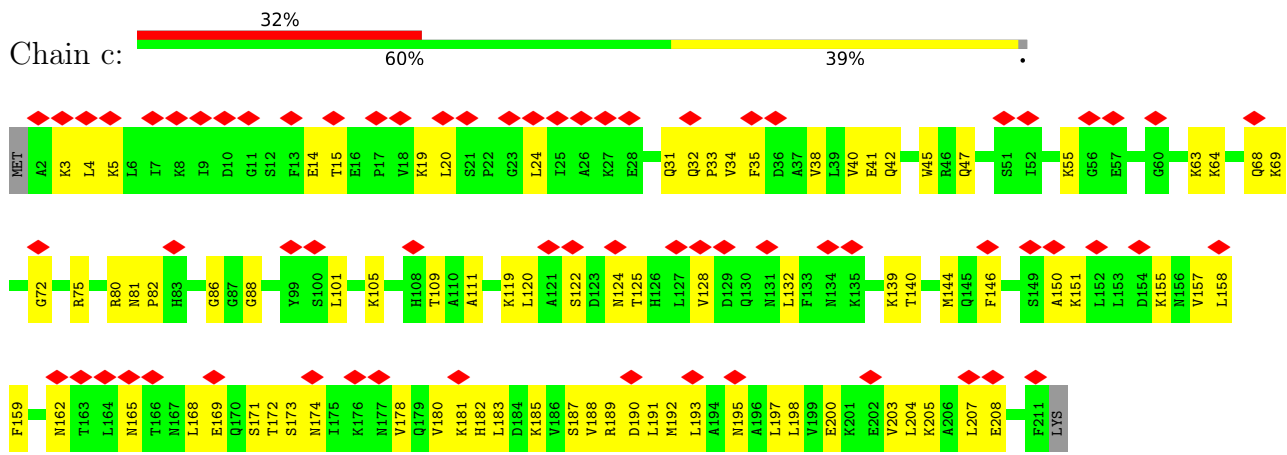
• Molecule 23: 30S ribosomal protein S20



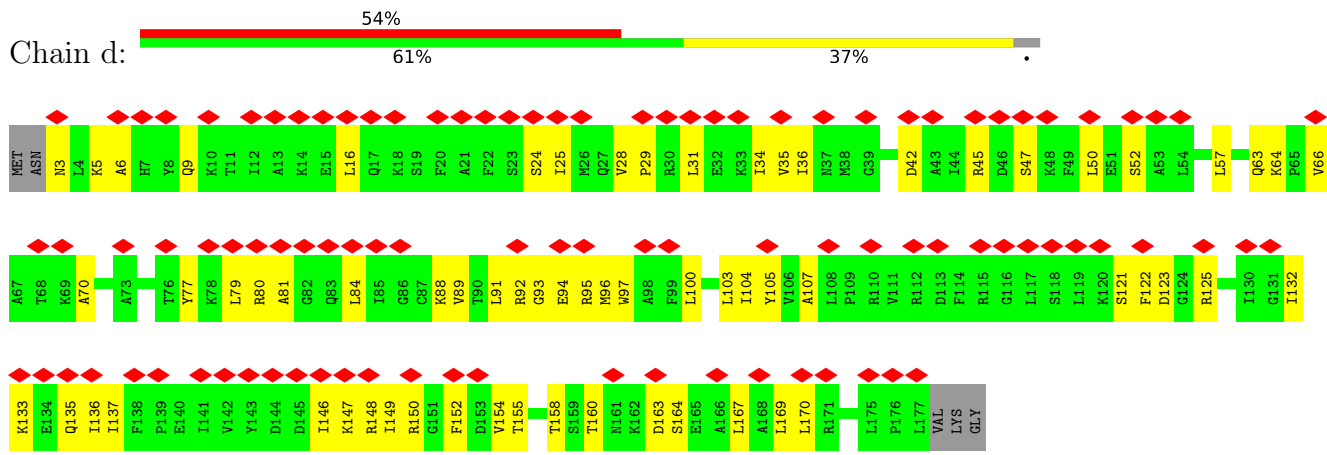
• Molecule 24: 30S ribosomal protein S21



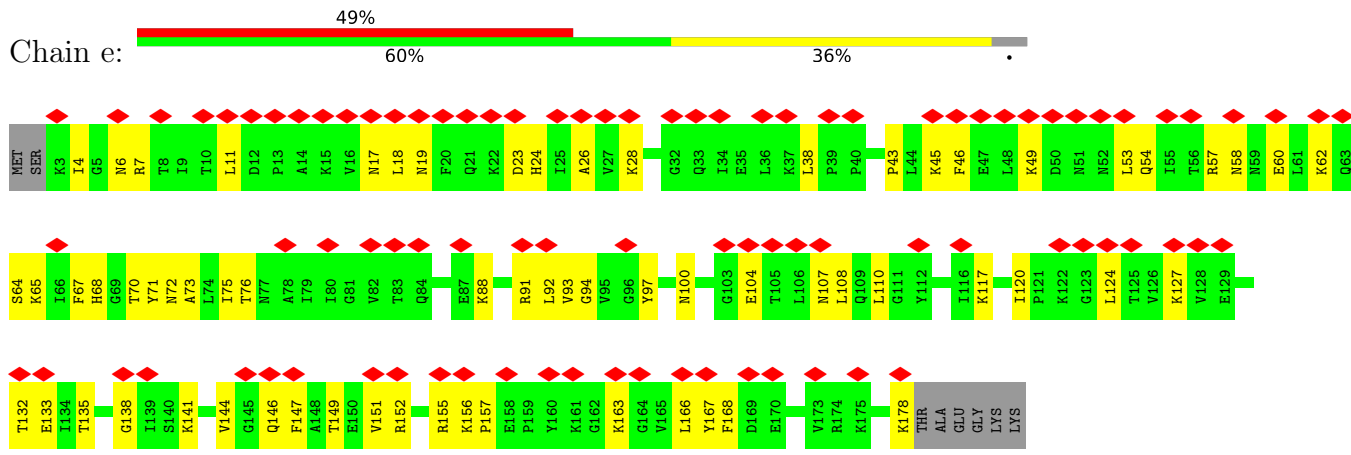
• Molecule 25: 50S ribosomal protein L7/L12



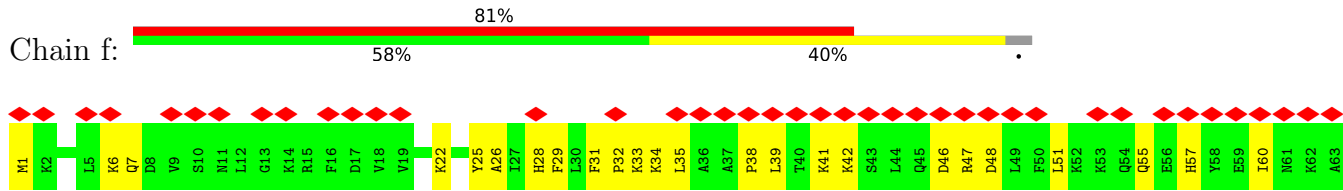
• Molecule 29: 50S ribosomal protein L5

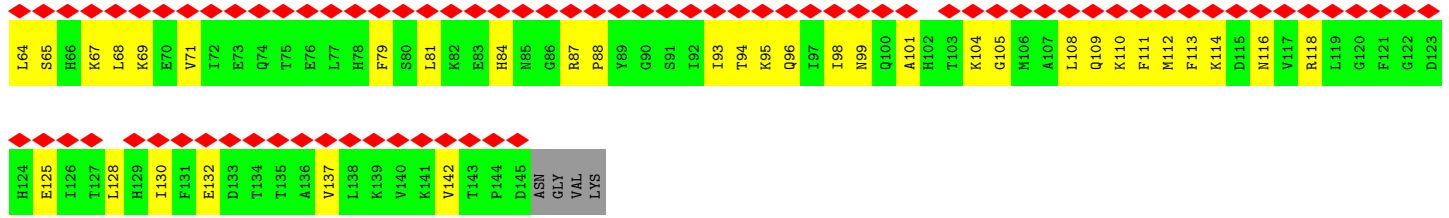


• Molecule 30: 50S ribosomal protein L6

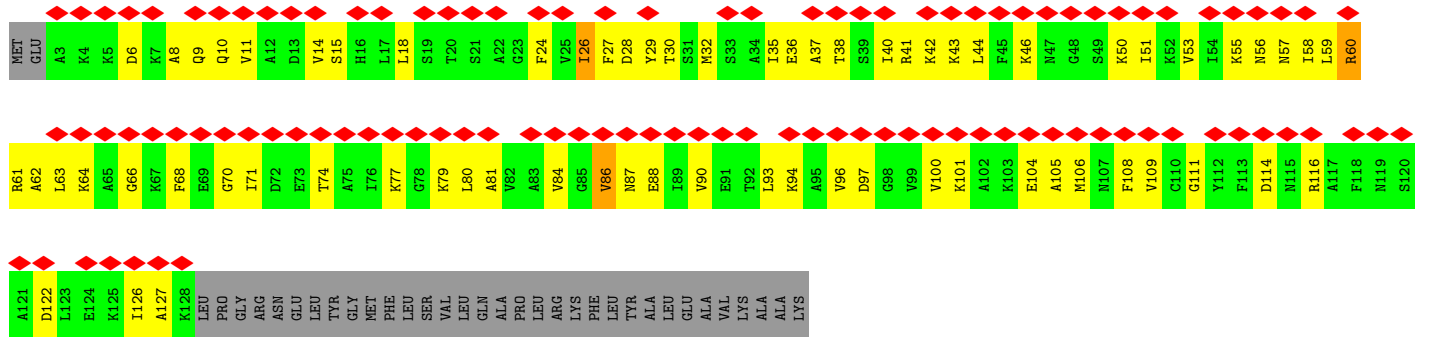


• Molecule 31: 50S ribosomal protein L9

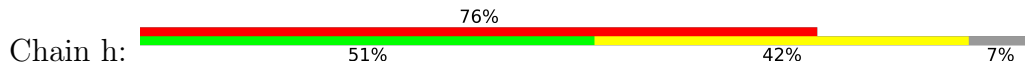




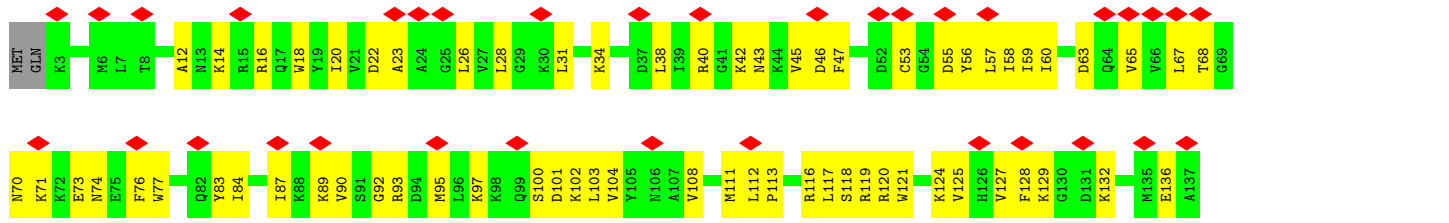
• Molecule 32: 50S ribosomal protein L10

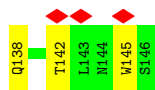


• Molecule 33: 50S ribosomal protein L11

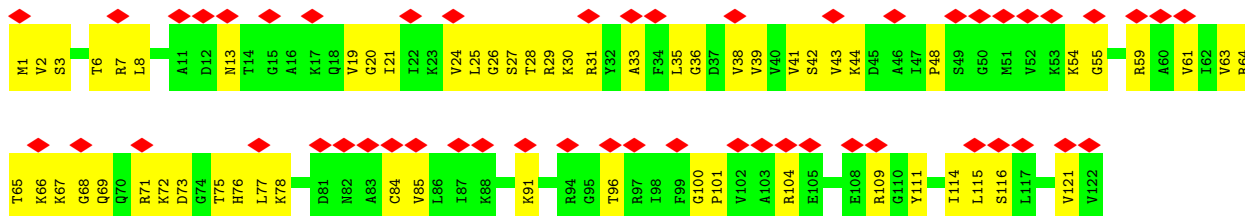
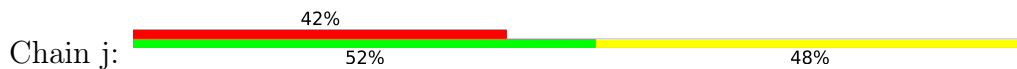


• Molecule 34: 50S ribosomal protein L13

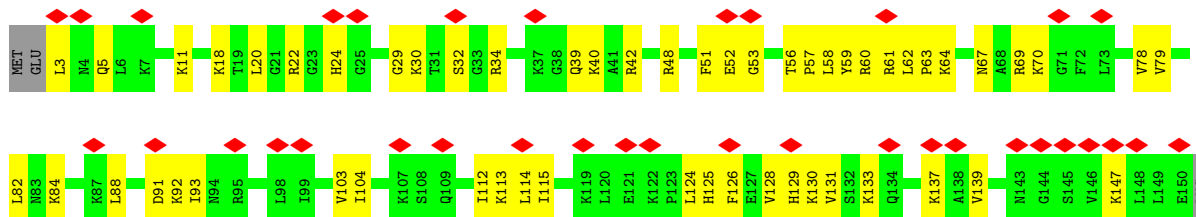




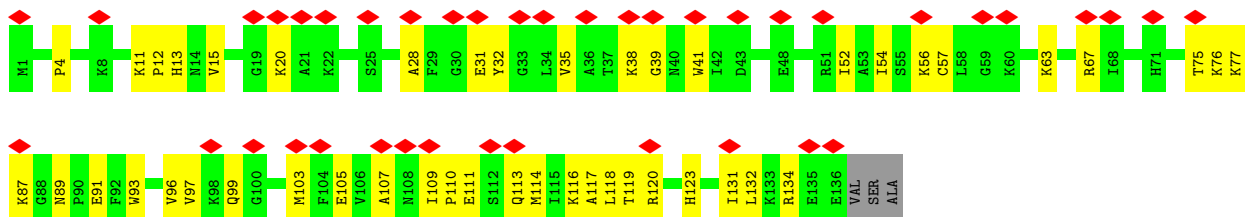
• Molecule 35: 50S ribosomal protein L14



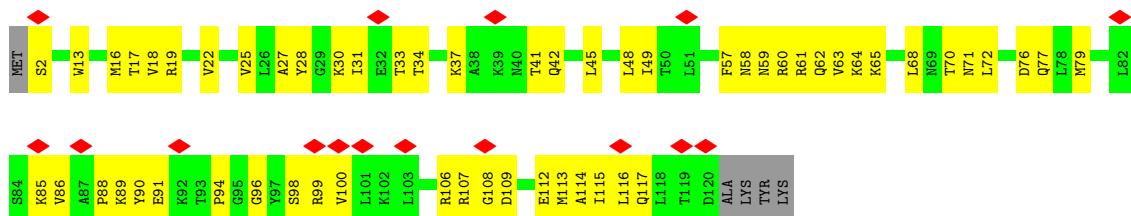
• Molecule 36: 50S ribosomal protein L15



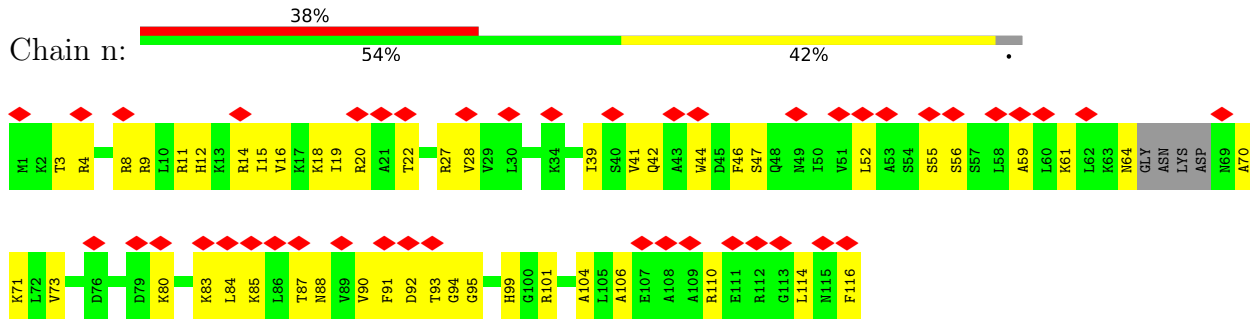
• Molecule 37: 50S ribosomal protein L16



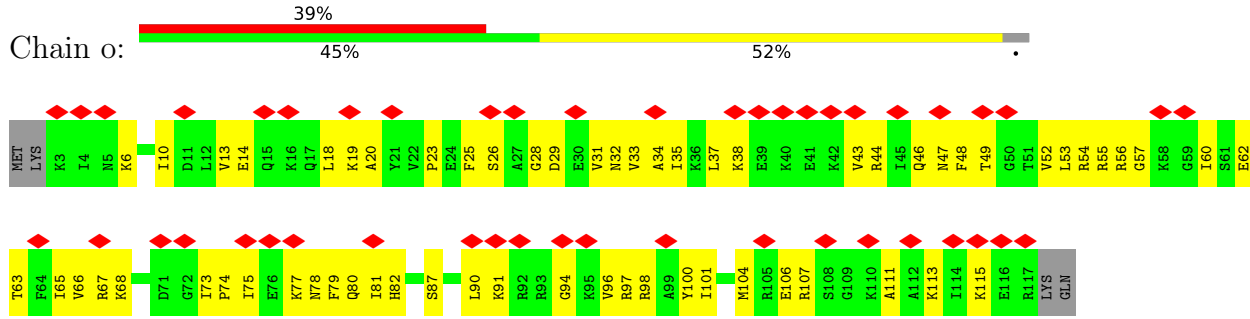
• Molecule 38: 50S ribosomal protein L17



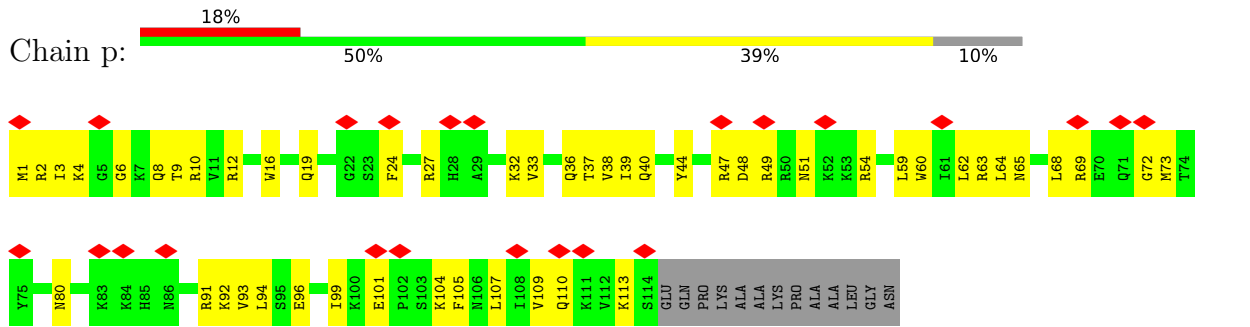
• Molecule 39: 50S ribosomal protein L18



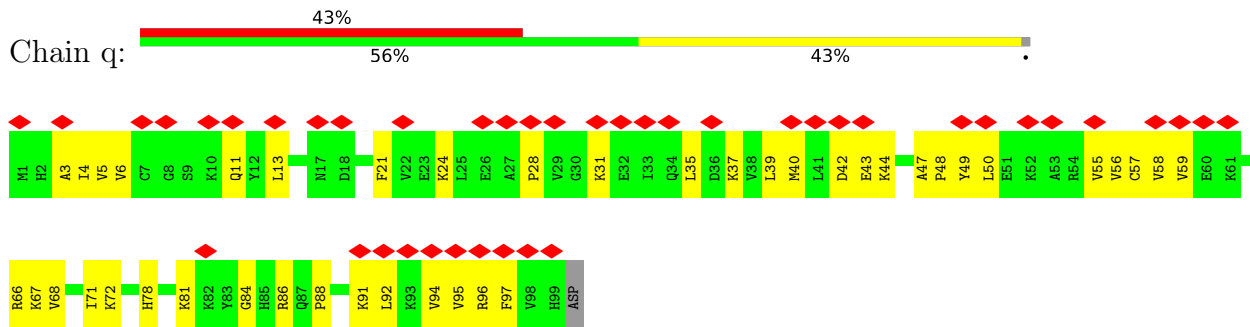
• Molecule 40: 50S ribosomal protein L19



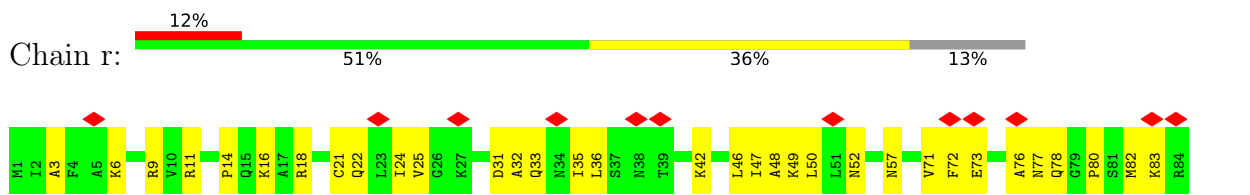
• Molecule 41: 50S ribosomal protein L20



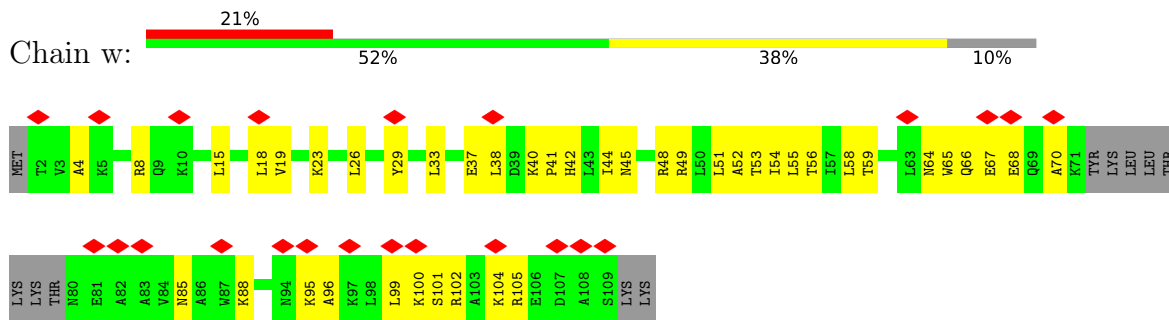
• Molecule 42: 50S ribosomal protein L21



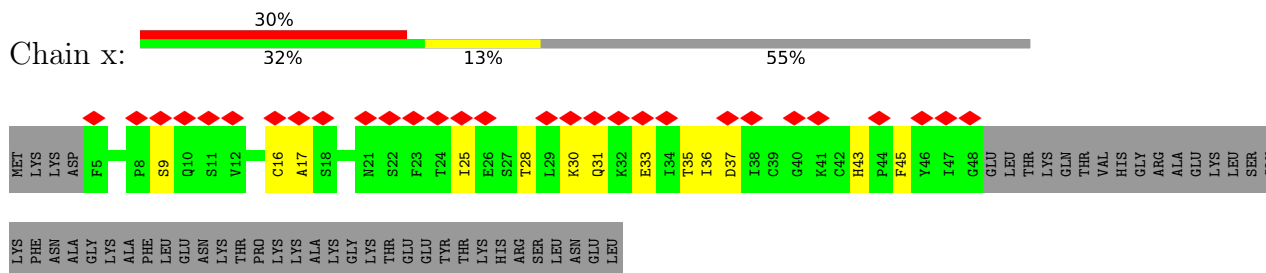
• Molecule 43: 50S ribosomal protein L22



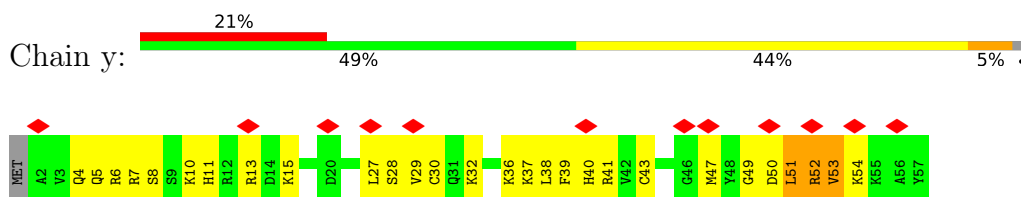
• Molecule 48: 50S ribosomal protein L29



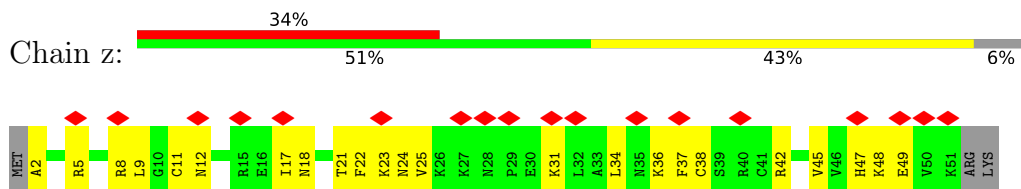
• Molecule 49: 50S ribosomal protein L31



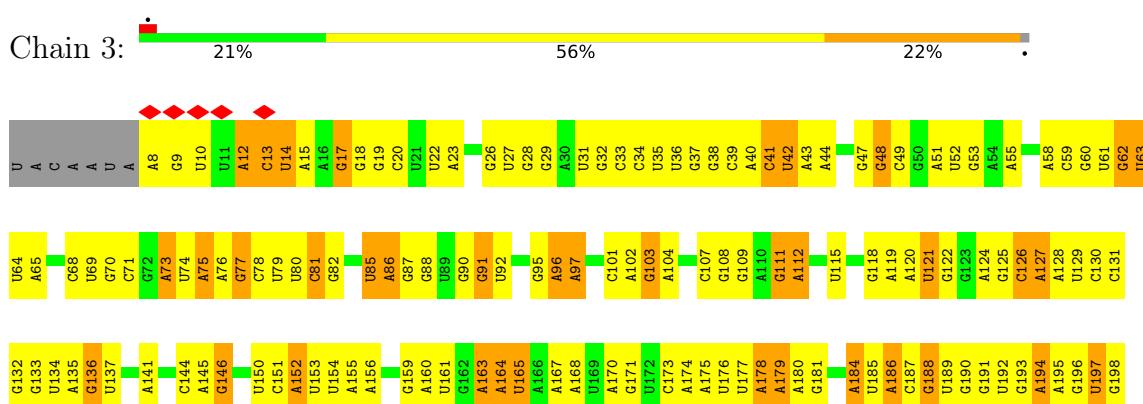
• Molecule 50: 50S ribosomal protein L32

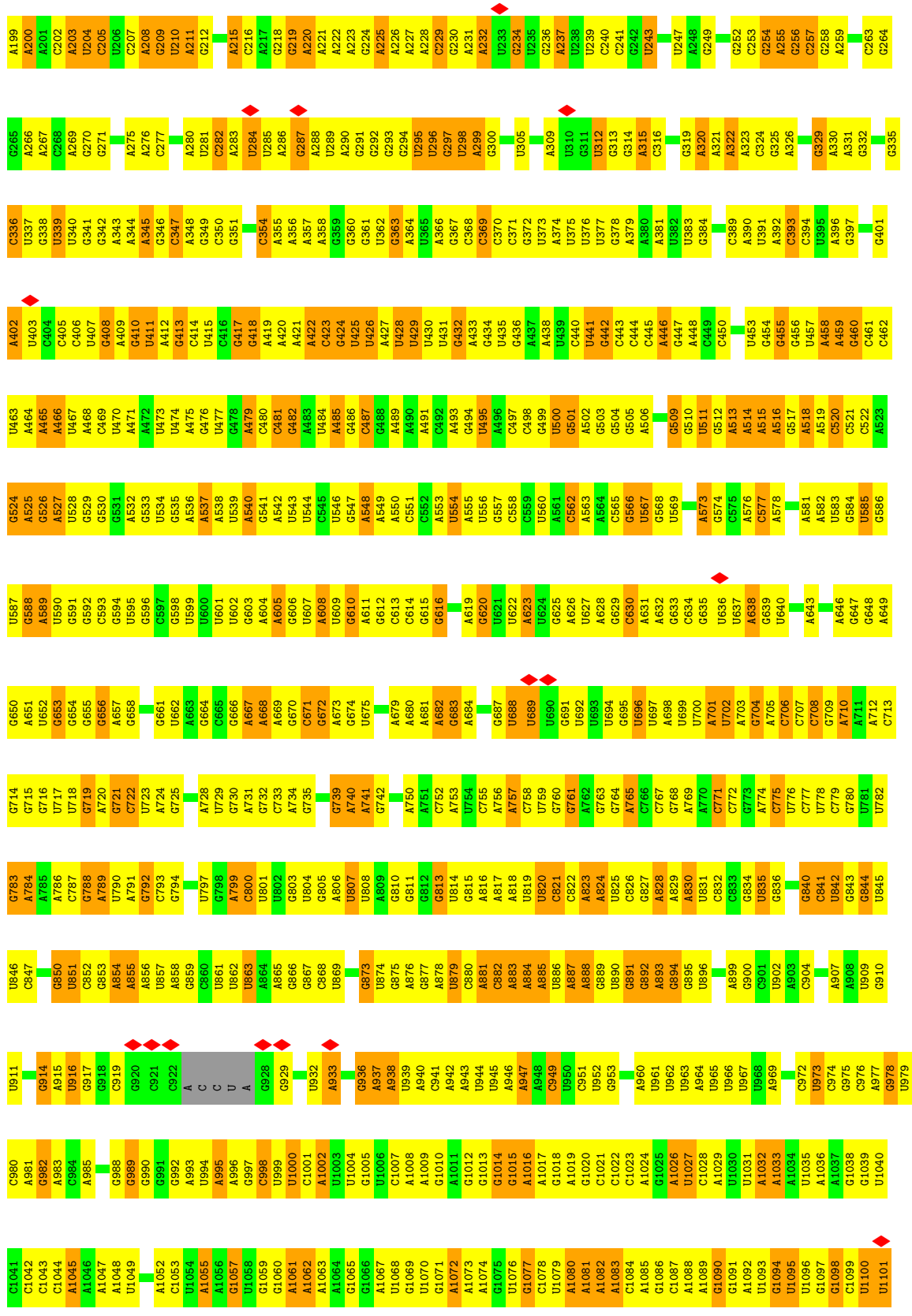


• Molecule 51: 50S ribosomal protein L33 1



• Molecule 52: 23S ribosomal RNA



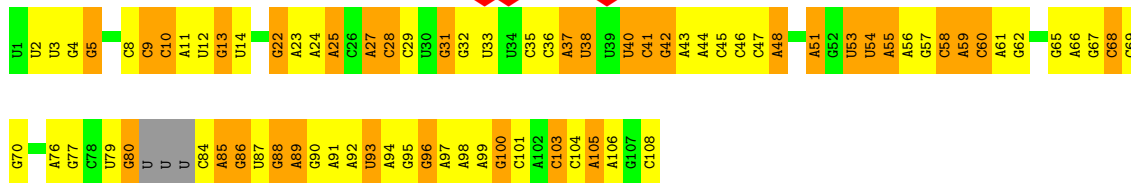
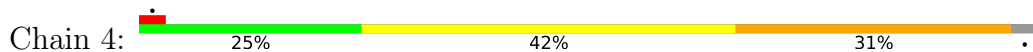


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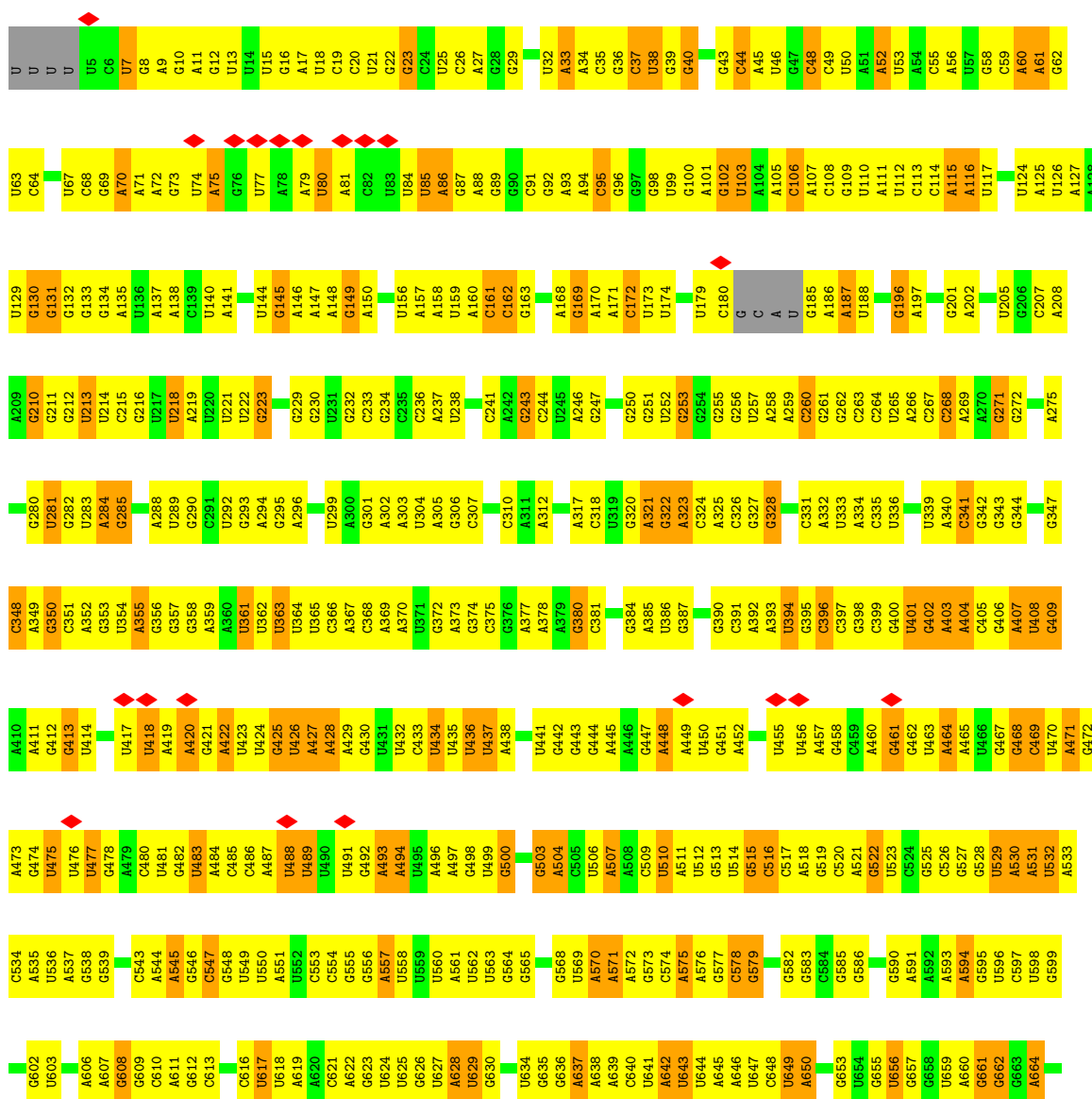
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A2719	A2720	A2721	A2722	A2723	A2724	A2725	A2726	A2727	A2728	A2729	A2730	A2731	A2732	A2733	A2734	A2735	A2736	A2737	A2738	A2739	A2740	A2741	A2742	A2743	A2744	A2745	A2746	A2747	A2748	A2749	A2750	A2751	A2752	A2753	A2754	A2755	A2756	A2757	A2758	A2759	A2760	A2761	A2762	A2763	A2764	A2765	A2766	A2767	A2768	A2769	A2770	A2771	A2772	A2773	A2774	A2775	A2776	A2777	A2778	A2779	A2780	A2781	A2782																																																																
G2518	G2519	G2520	G2521	G2522	G2523	G2524	G2525	G2526	G2527	G2528	G2529	G2530	G2531	G2532	G2533	G2534	G2535	G2536	G2537	G2538	G2539	G2540	G2541	G2542	G2543	G2544	G2545	G2546	G2547	G2548	G2549	G2550	G2551	G2552	G2553	G2554	G2555	G2556	G2557	G2558	G2559	G2560	G2561	G2562	G2563	G2564	G2565	G2566	G2567	G2568	G2569	G2570	G2571	G2572	G2573	G2574	G2575	G2576	G2577	G2578	G2579	G2580	G2581	G2582	G2583	G2584	G2585	G2586	G2587	G2588	G2589	G2590																																																							
G2454	G2455	G2456	G2457	G2458	G2459	G2460	G2461	G2462	G2463	G2464	G2465	G2466	G2467	G2468	G2469	G2470	G2471	G2472	G2473	G2474	G2475	G2476	G2477	G2478	G2479	G2480	G2481	G2482	G2483	G2484	G2485	G2486	G2487	G2488	G2489	G2490	G2491	G2492	G2493	G2494	G2495	G2496	G2497	G2498	G2499	G2500	G2501	G2502	G2503	G2504	G2505	G2506	G2507	G2508	G2509	G2510	G2511	G2512	G2513	G2514	G2515	G2516	G2517	G2518	G2519	G2520																																																													
G2390	G2391	G2392	G2393	G2394	G2395	G2396	G2397	G2398	G2399	G2400	G2401	G2402	G2403	G2404	G2405	G2406	G2407	G2408	G2409	G2410	G2411	G2412	G2413	G2414	G2415	G2416	G2417	G2418	G2419	G2420	G2421	G2422	G2423	G2424	G2425	G2426	G2427	G2428	G2429	G2430	G2431	G2432	G2433	G2434	G2435	G2436	G2437	G2438	G2439	G2440	G2441	G2442	G2443	G2444	G2445	G2446	G2447	G2448	G2449	G2450	G2451	G2452	G2453																																																																
C3321	C3322	C3323	C3324	C3325	C3326	C3327	C3328	C3329	C3330	C3331	C3332	C3333	C3334	C3335	C3336	C3337	C3338	C3339	C3340	C3341	C3342	C3343	C3344	C3345	C3346	C3347	C3348	C3349	C3350	C3351	C3352	C3353	C3354	C3355	C3356	C3357	C3358	C3359	C3360	C3361	C3362	C3363	C3364	C3365	C3366	C3367	C3368	C3369	C3370	C3371	C3372	C3373	C3374	C3375	C3376	C3377	C3378	C3379	C3380	C3381	C3382	C3383	C3384	C3385	C3386	C3387	C3388	C3389																																																											
C2356	C2357	C2358	C2359	C2360	C2361	C2362	C2363	C2364	C2365	C2366	C2367	C2368	C2369	C2370	C2371	C2372	C2373	C2374	C2375	C2376	C2377	C2378	C2379	C2380	C2381	C2382	C2383	C2384	C2385	C2386	C2387	C2388	C2389	C2390	C2391	C2392	C2393	C2394	C2395	C2396	C2397	C2398	C2399	C2400	C2401	C2402	C2403	C2404	C2405	C2406	C2407	C2408	C2409	C2410	C2411	C2412	C2413	C2414	C2415	C2416	C2417	C2418	C2419	C2420	C2421	C2422	C2423	C2424	C2425	C2426	C2427	C2428	C2429	C2430	C2431	C2432	C2433	C2434	C2435	C2436	C2437	C2438	C2439	C2440	C2441	C2442	C2443	C2444	C2445	C2446	C2447	C2448	C2449	C2450	C2451	C2452	C2453																														
U2193	U2194	U2195	U2196	U2197	U2198	U2199	U2200	U2201	U2202	U2203	U2204	U2205	U2206	U2207	U2208	U2209	U2210	U2211	U2212	U2213	U2214	U2215	U2216	U2217	U2218	U2219	U2220	U2221	U2222	U2223	U2224	U2225	U2226	U2227	U2228	U2229	U2230	U2231	U2232	U2233	U2234	U2235	U2236	U2237	U2238	U2239	U2240	U2241	U2242	U2243	U2244	U2245	U2246	U2247	U2248	U2249	U2250	U2251	U2252	U2253	U2254	U2255	U2256	U2257	U2258	U2259	U2260	U2261	U2262	U2263	U2264	U2265	U2266	U2267	U2268	U2269	U2270	U2271	U2272	U2273	U2274	U2275	U2276	U2277	U2278	U2279	U2280	U2281	U2282	U2283	U2284	U2285	U2286	U2287	U2288	U2289	U2290	U2291	U2292	U2293	U2294	U2295	U2296	U2297	U2298	U2299	U2300	U2301	U2302	U2303	U2304	U2305	U2306	U2307	U2308	U2309	U2310	U2311	U2312	U2313	U2314	U2315	U2316	U2317	U2318	U2319	U2320
A2130	A2131	A2132	A2133	A2134	A2135	A2136	A2137	A2138	A2139	A2140	A2141	A2142	A2143	A2144	A2145	A2146	A2147	A2148	A2149	A2150	A2151	A2152	A2153	A2154	A2155	A2156	A2157	A2158	A2159	A2160	A2161	A2162	A2163	A2164	A2165	A2166	A2167	A2168	A2169	A2170	A2171	A2172	A2173	A2174	A2175	A2176	A2177	A2178	A2179	A2180	A2181	A2182	A2183	A2184	A2185	A2186	A2187	A2188	A2189	A2190	A2191	A2192																																																																	
G2068	G2069	G2070	G2071	G2072	G2073	G2074	G2075	G2076	G2077	G2078	G2079	G2080	G2081	G2082	G2083	G2084	G2085	G2086	G2087	G2088	G2089	G2090	G2091	G2092	G2093	G2094	G2095	G2096	G2097	G2098	G2099	G2100	G2101	G2102	G2103	G2104	G2105	G2106	G2107	G2108	G2109	G2110	G2111	G2112	G2113	G2114	G2115	G2116	G2117	G2118	G2119	G2120	G2121	G2122	G2123	G2124	G2125	G2126	G2127	G2128	G2129																																																																		
A2008	A2009	A2010	A2011	A2012	A2013	A2014	A2015	A2016	A2017	A2018	A2019	A2020	A2021	A2022	A2023	A2024	A2025	A2026	A2027	A2028	A2029	A2030	A2031	A2032	A2033	A2034	A2035	A2036	A2037	A2038	A2039	A2040	A2041	A2042	A2043	A2044	A2045	A2046	A2047	A2048	A2049	A2050	A2051	A2052	A2053	A2054	A2055	A2056	A2057	A2058	A2059	A2060	A2061	A2062	A2063	A2064	A2065	A2066	A2067																																																																				

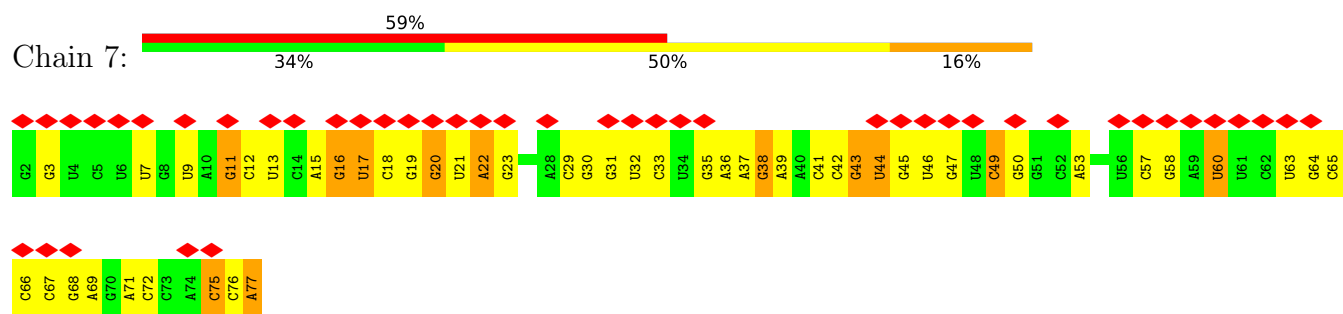
G
G
A

• Molecule 53: 5S ribosomal RNA

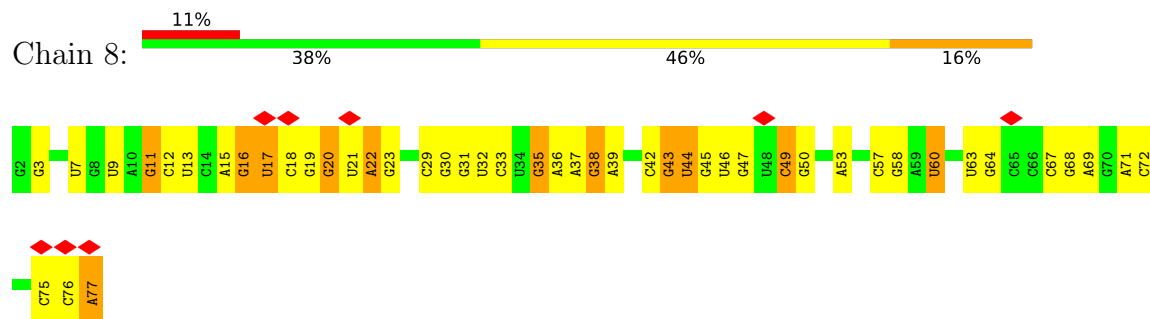


• Molecule 54: 16S ribosomal RNA





• Molecule 55: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	8730	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	1.874	Depositor
Minimum map value	-0.889	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.121	Depositor
Recommended contour level	0.54	Depositor
Map size (\AA)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.7005, 1.7005, 1.7005	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.25	0/383	0.70	1/504 (0.2%)
2	1	0.20	0/484	0.57	0/637
3	2	0.22	0/306	0.53	0/401
4	9	0.18	0/5419	0.50	0/7307
5	A	0.24	0/1954	0.61	1/2642 (0.0%)
6	B	0.19	1/1721 (0.1%)	0.42	0/2323
7	C	0.17	0/1691	0.50	0/2267
8	D	0.15	0/1188	0.47	0/1593
9	E	0.24	0/1384	0.49	0/1867
10	F	0.24	0/1266	0.52	0/1700
11	G	0.19	0/1126	0.57	0/1517
12	H	0.16	0/1044	0.43	0/1395
13	I	0.19	0/820	0.50	0/1103
14	J	0.16	0/844	0.43	0/1136
15	K	0.30	0/1094	0.62	1/1468 (0.1%)
16	L	0.17	0/962	0.52	0/1289
17	M	0.32	0/483	0.55	0/643
18	N	0.20	0/679	0.53	0/907
19	O	0.19	0/659	0.51	0/885
20	P	0.15	0/684	0.45	0/913
21	Q	0.18	0/545	0.50	0/730
22	R	0.18	0/698	0.55	0/936
23	S	0.15	0/631	0.42	0/838
24	T	0.20	0/475	0.53	0/621
25	W	0.14	0/538	0.36	0/722
26	a	0.18	0/2267	0.49	0/3044
27	b	0.17	0/1795	0.49	0/2412
28	c	0.16	0/1671	0.48	0/2246
29	d	0.15	0/1409	0.46	0/1894
30	e	0.16	0/1420	0.45	0/1912
31	f	0.20	0/1183	0.57	0/1587
32	g	0.47	0/969	0.87	2/1295 (0.2%)
33	h	0.17	0/968	0.45	0/1298
34	i	0.18	0/1186	0.48	0/1592

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	0.23	0/953	0.53	0/1275
36	k	0.16	0/1170	0.44	0/1559
37	l	0.18	0/1104	0.48	0/1481
38	m	0.17	0/973	0.46	0/1309
39	n	0.18	0/897	0.54	0/1198
40	o	0.18	0/948	0.57	0/1262
41	p	0.18	0/961	0.51	0/1278
42	q	0.31	0/828	0.62	0/1111
43	r	0.18	0/1077	0.58	0/1441
44	s	0.17	0/732	0.49	0/988
45	t	0.16	0/879	0.47	0/1165
46	u	0.17	0/665	0.46	0/884
47	v	0.18	0/519	0.60	0/695
48	w	0.27	0/826	0.51	0/1104
49	x	0.13	0/353	0.40	0/474
50	y	0.33	0/457	0.78	1/601 (0.2%)
51	z	0.14	0/412	0.46	0/547
52	3	0.11	0/69073	0.27	0/107710
53	4	0.10	0/2505	0.27	0/3902
54	5	0.11	0/35768	0.26	0/55764
55	7	0.11	0/1808	0.29	0/2817
55	8	0.11	0/1808	0.29	0/2817
All	All	0.15	1/164662 (0.0%)	0.36	6/245006 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	199	ILE	C-N	5.28	1.36	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	11	LYS	CB-CA-C	-7.03	99.74	110.92
5	A	102	ARG	CB-CG-CD	5.72	124.45	111.30
15	K	116	ASP	N-CA-C	-5.61	105.53	112.38
32	g	60	ARG	CB-CG-CD	5.33	123.57	111.30
50	y	50	ASP	N-CA-C	5.29	117.13	111.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	0	380	0	429	32	0
2	1	477	0	530	31	0
3	2	304	0	350	18	0
4	9	5326	0	5343	238	0
5	A	1921	0	1973	97	0
6	B	1698	0	1768	55	0
7	C	1660	0	1719	75	0
8	D	1173	0	1267	59	0
9	E	1362	0	1377	63	0
10	F	1246	0	1308	42	0
11	G	1110	0	1226	62	0
12	H	1028	0	1094	43	0
13	I	809	0	894	46	0
14	J	829	0	855	42	0
15	K	1076	0	1170	49	0
16	L	951	0	1014	39	0
17	M	474	0	509	37	0
18	N	673	0	730	25	0
19	O	646	0	677	28	0
20	P	675	0	728	17	0
21	Q	535	0	562	22	0
22	R	682	0	691	33	0
23	S	629	0	681	34	0
24	T	471	0	522	22	0
25	W	534	0	572	10	0
26	a	2225	0	2301	119	0
27	b	1762	0	1808	84	0
28	c	1644	0	1731	64	0
29	d	1388	0	1469	53	0
30	e	1396	0	1481	52	0
31	f	1160	0	1172	50	0
32	g	960	0	1014	56	0
33	h	959	0	1039	50	0
34	i	1164	0	1192	63	0
35	j	944	0	1019	47	0
36	k	1153	0	1256	60	0
37	l	1079	0	1134	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	958	0	1011	51	0
39	n	889	0	952	39	0
40	o	938	0	1008	63	0
41	p	947	0	1028	52	0
42	q	811	0	858	34	0
43	r	1068	0	1150	50	0
44	s	720	0	803	31	0
45	t	872	0	972	42	0
46	u	657	0	695	28	0
47	v	513	0	560	30	0
48	w	818	0	870	39	0
49	x	344	0	333	9	0
50	y	452	0	472	32	0
51	z	408	0	440	19	0
52	3	61664	0	30954	1991	0
53	4	2239	0	1137	67	0
54	5	31943	0	16058	1024	0
55	7	1618	0	821	43	0
55	8	1618	0	821	32	0
All	All	151980	0	105548	4999	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 20.

The worst 5 of 4999 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)
52:3:1382:A:H62	52:3:1405:G:N2	1.54	1.05
52:3:990:G:H1	52:3:999:U:H3	1.05	1.00
54:5:661:G:H1	54:5:738:A:N6	1.59	0.99
52:3:1382:A:N6	52:3:1405:G:H21	1.60	0.99
52:3:1504:G:H1	52:3:1539:U:H3	1.08	0.98

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	9	680/688 (99%)	625 (92%)	55 (8%)	0	100	100
5	A	238/294 (81%)	216 (91%)	22 (9%)	0	100	100
6	B	213/273 (78%)	191 (90%)	22 (10%)	0	100	100
7	C	201/205 (98%)	188 (94%)	13 (6%)	0	100	100
8	D	151/219 (69%)	145 (96%)	6 (4%)	0	100	100
9	E	165/215 (77%)	150 (91%)	15 (9%)	0	100	100
10	F	152/155 (98%)	144 (95%)	8 (5%)	0	100	100
11	G	139/142 (98%)	119 (86%)	20 (14%)	0	100	100
12	H	126/132 (96%)	109 (86%)	17 (14%)	0	100	100
13	I	99/108 (92%)	90 (91%)	9 (9%)	0	100	100
14	J	112/121 (93%)	109 (97%)	3 (3%)	0	100	100
15	K	134/139 (96%)	114 (85%)	20 (15%)	0	100	100
16	L	116/124 (94%)	99 (85%)	17 (15%)	0	100	100
17	M	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
18	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
19	O	78/94 (83%)	73 (94%)	5 (6%)	0	100	100
20	P	81/85 (95%)	76 (94%)	5 (6%)	0	100	100
21	Q	63/104 (61%)	58 (92%)	5 (8%)	0	100	100
22	R	82/87 (94%)	76 (93%)	6 (7%)	0	100	100
23	S	75/87 (86%)	74 (99%)	1 (1%)	0	100	100
24	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
25	W	67/122 (55%)	63 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	a	283/287 (99%)	252 (89%)	31 (11%)	0	100	100
27	b	227/287 (79%)	210 (92%)	17 (8%)	0	100	100
28	c	208/212 (98%)	193 (93%)	15 (7%)	0	100	100
29	d	173/180 (96%)	152 (88%)	21 (12%)	0	100	100
30	e	174/184 (95%)	162 (93%)	12 (7%)	0	100	100
31	f	143/149 (96%)	131 (92%)	12 (8%)	0	100	100
32	g	124/161 (77%)	111 (90%)	12 (10%)	1 (1%)	16	53
33	h	126/137 (92%)	113 (90%)	13 (10%)	0	100	100
34	i	142/146 (97%)	132 (93%)	10 (7%)	0	100	100
35	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
36	k	146/151 (97%)	135 (92%)	11 (8%)	0	100	100
37	l	134/139 (96%)	127 (95%)	7 (5%)	0	100	100
38	m	117/124 (94%)	115 (98%)	2 (2%)	0	100	100
39	n	108/116 (93%)	98 (91%)	10 (9%)	0	100	100
40	o	113/119 (95%)	103 (91%)	10 (9%)	0	100	100
41	p	112/127 (88%)	106 (95%)	6 (5%)	0	100	100
42	q	97/100 (97%)	86 (89%)	11 (11%)	0	100	100
43	r	137/159 (86%)	126 (92%)	11 (8%)	0	100	100
44	s	90/237 (38%)	87 (97%)	3 (3%)	0	100	100
45	t	109/111 (98%)	93 (85%)	15 (14%)	1 (1%)	14	50
46	u	84/104 (81%)	78 (93%)	6 (7%)	0	100	100
47	v	61/65 (94%)	56 (92%)	5 (8%)	0	100	100
48	w	96/111 (86%)	91 (95%)	5 (5%)	0	100	100
49	x	42/97 (43%)	38 (90%)	4 (10%)	0	100	100
50	y	54/57 (95%)	51 (94%)	2 (4%)	1 (2%)	6	31
51	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	6567/7480 (88%)	6043 (92%)	521 (8%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	g	88	GLU
50	y	53	VAL

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Mol	Chain	Res	Type
45	t	95	PRO

5.3.2 Protein sidechains [i](#)

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%)	39 (98%)	1 (2%)	42	62
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	9	579/584 (99%)	579 (100%)	0	100	100
5	A	212/262 (81%)	211 (100%)	1 (0%)	81	82
6	B	180/232 (78%)	180 (100%)	0	100	100
7	C	181/183 (99%)	180 (99%)	1 (1%)	78	82
8	D	123/178 (69%)	123 (100%)	0	100	100
9	E	150/196 (76%)	149 (99%)	1 (1%)	76	80
10	F	131/132 (99%)	130 (99%)	1 (1%)	73	79
11	G	123/124 (99%)	123 (100%)	0	100	100
12	H	111/115 (96%)	111 (100%)	0	100	100
13	I	95/99 (96%)	95 (100%)	0	100	100
14	J	91/97 (94%)	91 (100%)	0	100	100
15	K	117/120 (98%)	112 (96%)	5 (4%)	26	47
16	L	100/105 (95%)	100 (100%)	0	100	100
17	M	47/48 (98%)	47 (100%)	0	100	100
18	N	76/78 (97%)	76 (100%)	0	100	100
19	O	69/82 (84%)	69 (100%)	0	100	100
20	P	73/75 (97%)	73 (100%)	0	100	100
21	Q	56/94 (60%)	56 (100%)	0	100	100
22	R	74/77 (96%)	74 (100%)	0	100	100
23	S	70/77 (91%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	T	49/56 (88%)	48 (98%)	1 (2%)	48	66
25	W	58/98 (59%)	58 (100%)	0	100	100
26	a	241/243 (99%)	241 (100%)	0	100	100
27	b	186/233 (80%)	186 (100%)	0	100	100
28	c	182/184 (99%)	182 (100%)	0	100	100
29	d	150/154 (97%)	150 (100%)	0	100	100
30	e	153/159 (96%)	153 (100%)	0	100	100
31	f	123/134 (92%)	123 (100%)	0	100	100
32	g	101/129 (78%)	91 (90%)	10 (10%)	7	24
33	h	102/110 (93%)	102 (100%)	0	100	100
34	i	126/128 (98%)	126 (100%)	0	100	100
35	j	103/103 (100%)	103 (100%)	0	100	100
36	k	123/126 (98%)	123 (100%)	0	100	100
37	l	113/115 (98%)	113 (100%)	0	100	100
38	m	105/109 (96%)	105 (100%)	0	100	100
39	n	96/99 (97%)	96 (100%)	0	100	100
40	o	101/105 (96%)	101 (100%)	0	100	100
41	p	100/108 (93%)	100 (100%)	0	100	100
42	q	90/91 (99%)	90 (100%)	0	100	100
43	r	116/132 (88%)	116 (100%)	0	100	100
44	s	82/208 (39%)	82 (100%)	0	100	100
45	t	96/96 (100%)	96 (100%)	0	100	100
46	u	69/85 (81%)	69 (100%)	0	100	100
47	v	58/60 (97%)	58 (100%)	0	100	100
48	w	87/98 (89%)	87 (100%)	0	100	100
49	x	41/86 (48%)	41 (100%)	0	100	100
50	y	48/49 (98%)	45 (94%)	3 (6%)	16	37
51	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5730/6433 (89%)	5706 (100%)	24 (0%)	81	83

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	g	43	LYS
32	g	84	VAL
32	g	46	LYS
32	g	86	VAL
15	K	118	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 97 such sidechains are listed below:

Mol	Chain	Res	Type
26	a	276	ASN
34	i	138	GLN
27	b	95	GLN
28	c	145	GLN
36	k	67	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	2875/2907 (98%)	980 (34%)	39 (1%)
53	4	103/108 (95%)	44 (42%)	3 (2%)
54	5	1490/1520 (98%)	454 (30%)	12 (0%)
55	7	75/76 (98%)	29 (38%)	1 (1%)
55	8	75/76 (98%)	29 (38%)	1 (1%)
All	All	4618/4687 (98%)	1536 (33%)	56 (1%)

5 of 1536 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	12	A
52	3	13	C
52	3	14	U
52	3	15	A
52	3	17	G

5 of 56 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	2333	G
55	8	16	G
52	3	2764	U
55	7	16	G

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Mol	Chain	Res	Type
54	5	1037	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

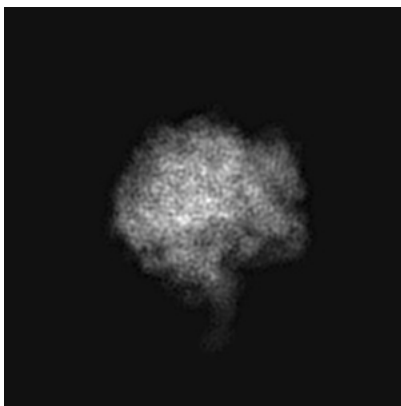
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13450. These allow visual inspection of the internal detail of the map and identification of artifacts.

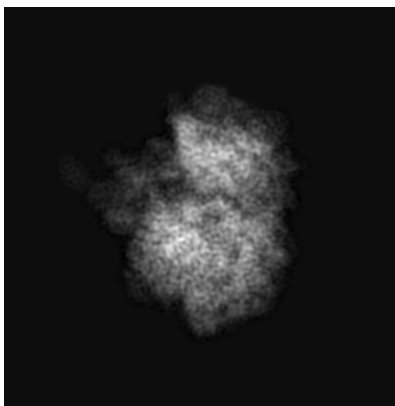
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

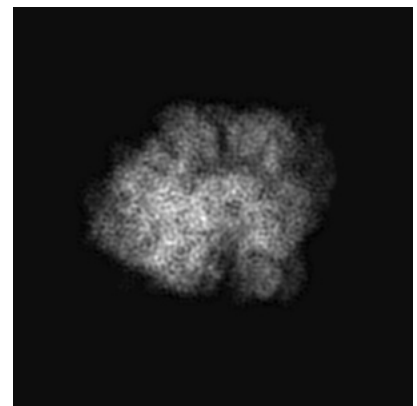
6.1.1 Primary map



X

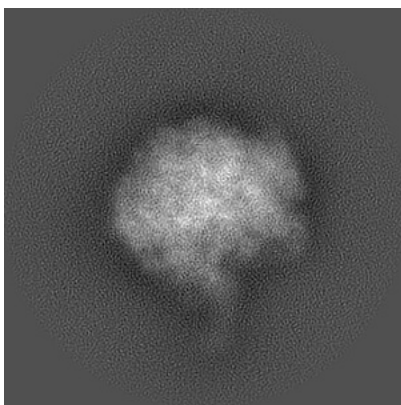


Y

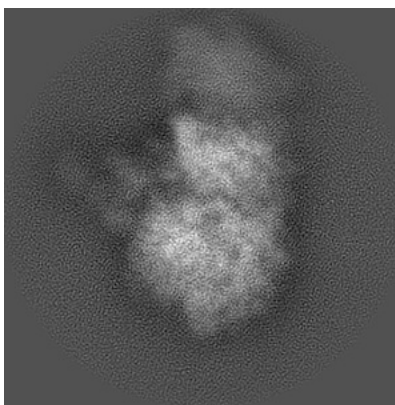


Z

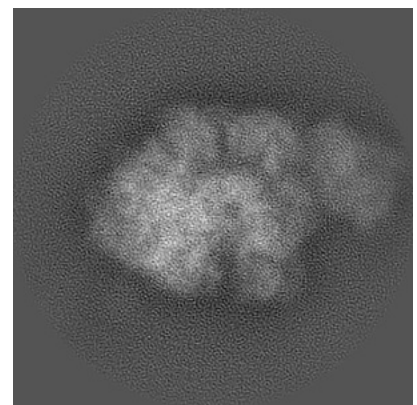
6.1.2 Raw map



X



Y

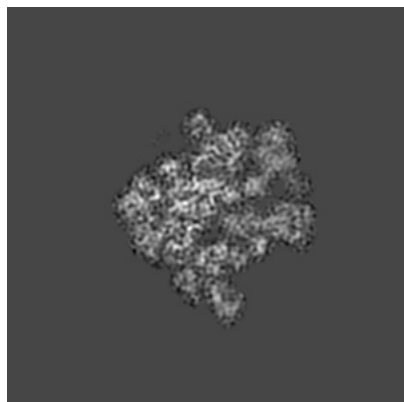


Z

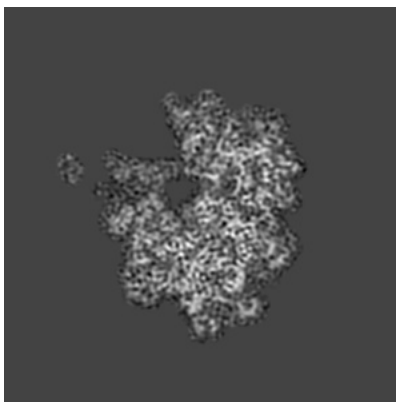
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

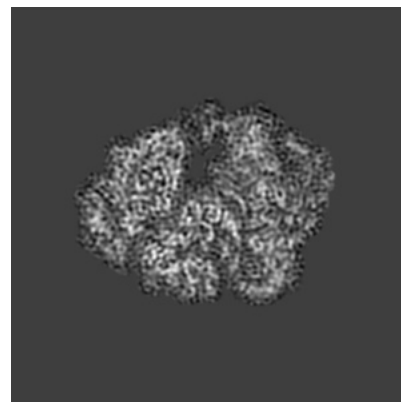
6.2.1 Primary map



X Index: 128

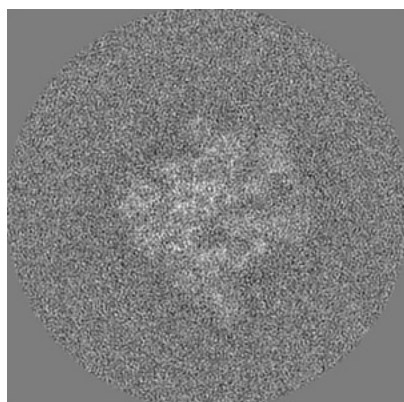


Y Index: 128

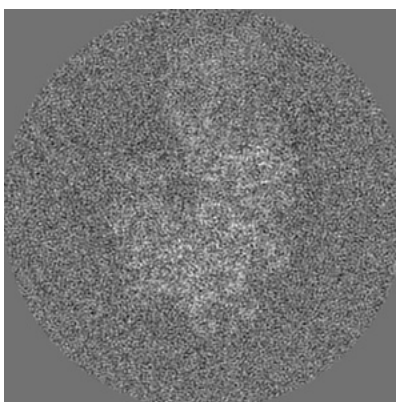


Z Index: 128

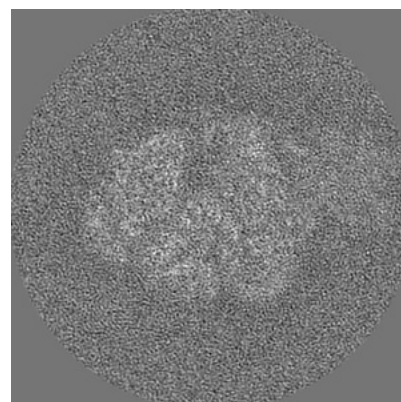
6.2.2 Raw map



X Index: 128



Y Index: 128

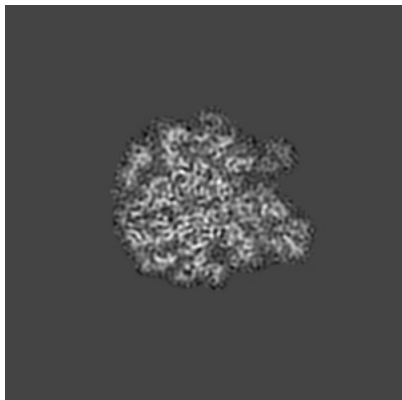


Z Index: 128

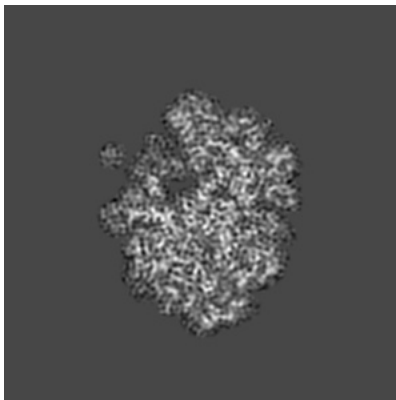
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

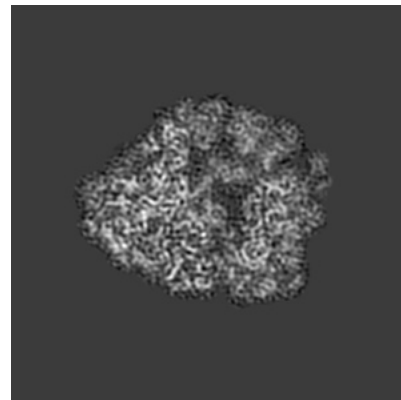
6.3.1 Primary map



X Index: 103

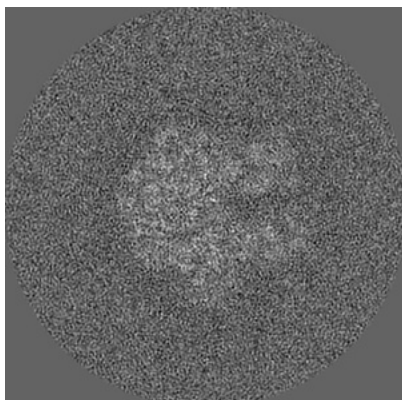


Y Index: 120

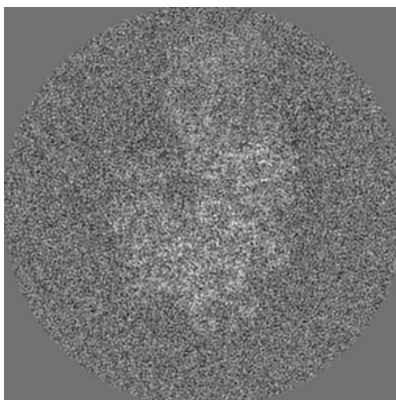


Z Index: 122

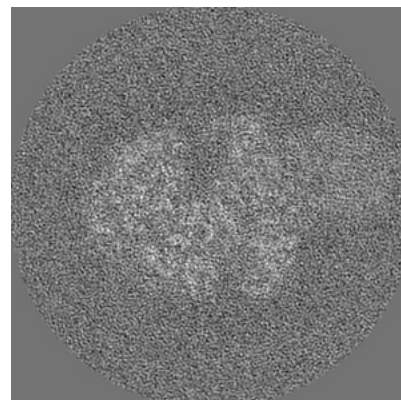
6.3.2 Raw map



X Index: 117



Y Index: 128

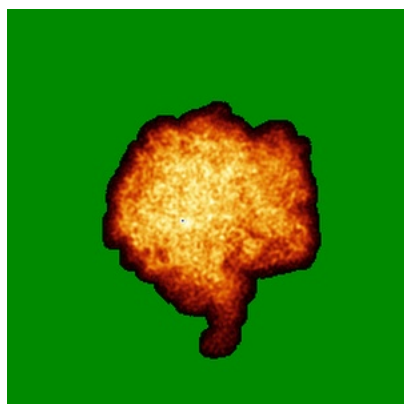


Z Index: 129

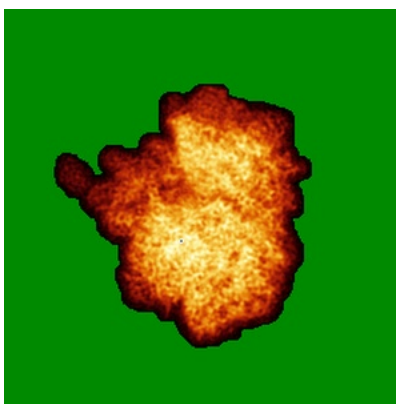
The images above show the largest variance slices of the map in three orthogonal directions.

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

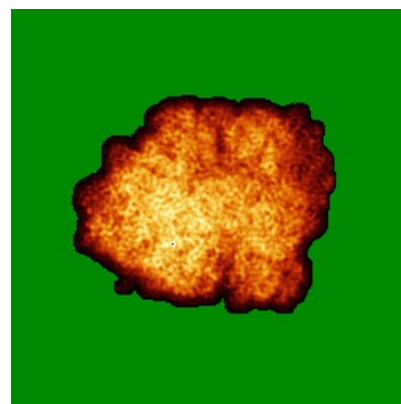
6.4.1 Primary map



X

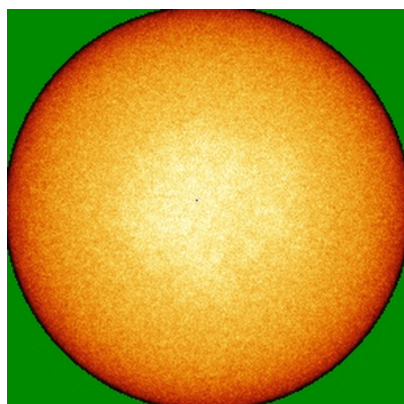


Y

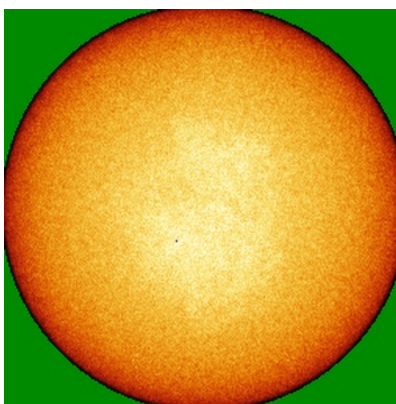


Z

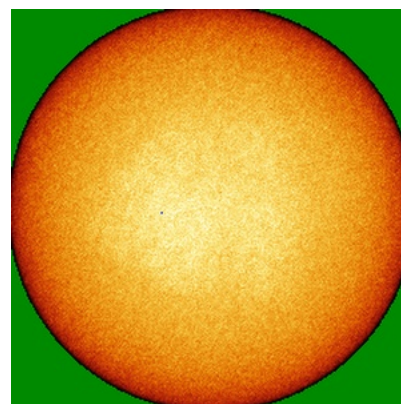
6.4.2 Raw map



X



Y

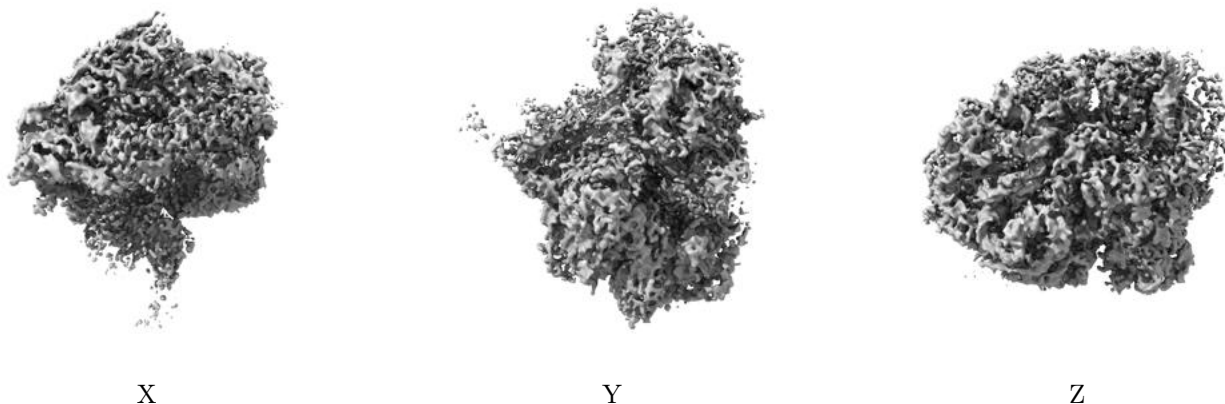


Z

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.

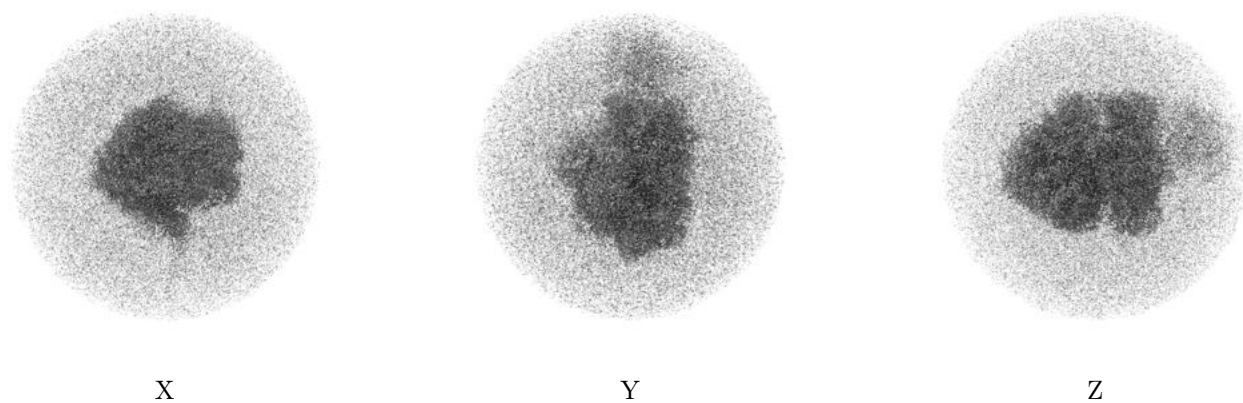
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.54. 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.

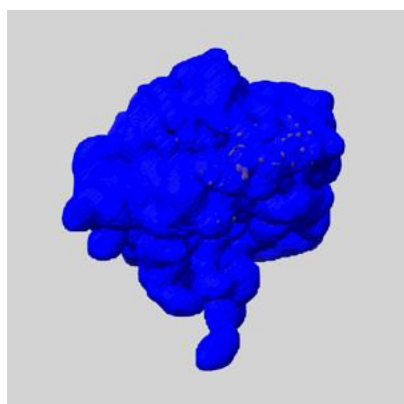
6.6 Mask visualisation [i](#)

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

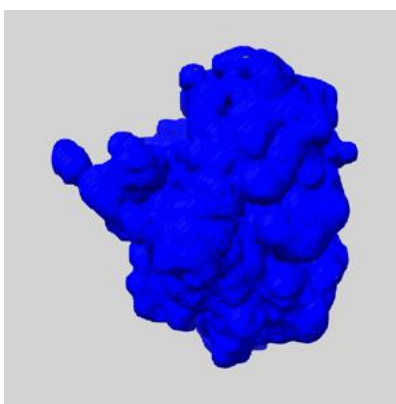
A mask typically either:

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

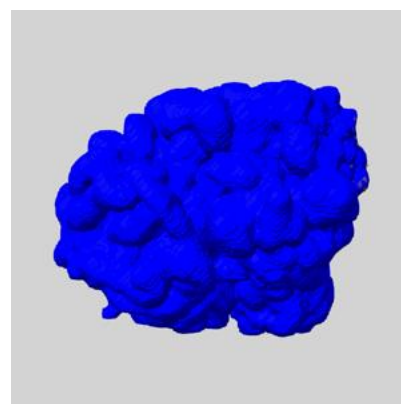
6.6.1 emd_13450_msk_1.map [i](#)



X



Y

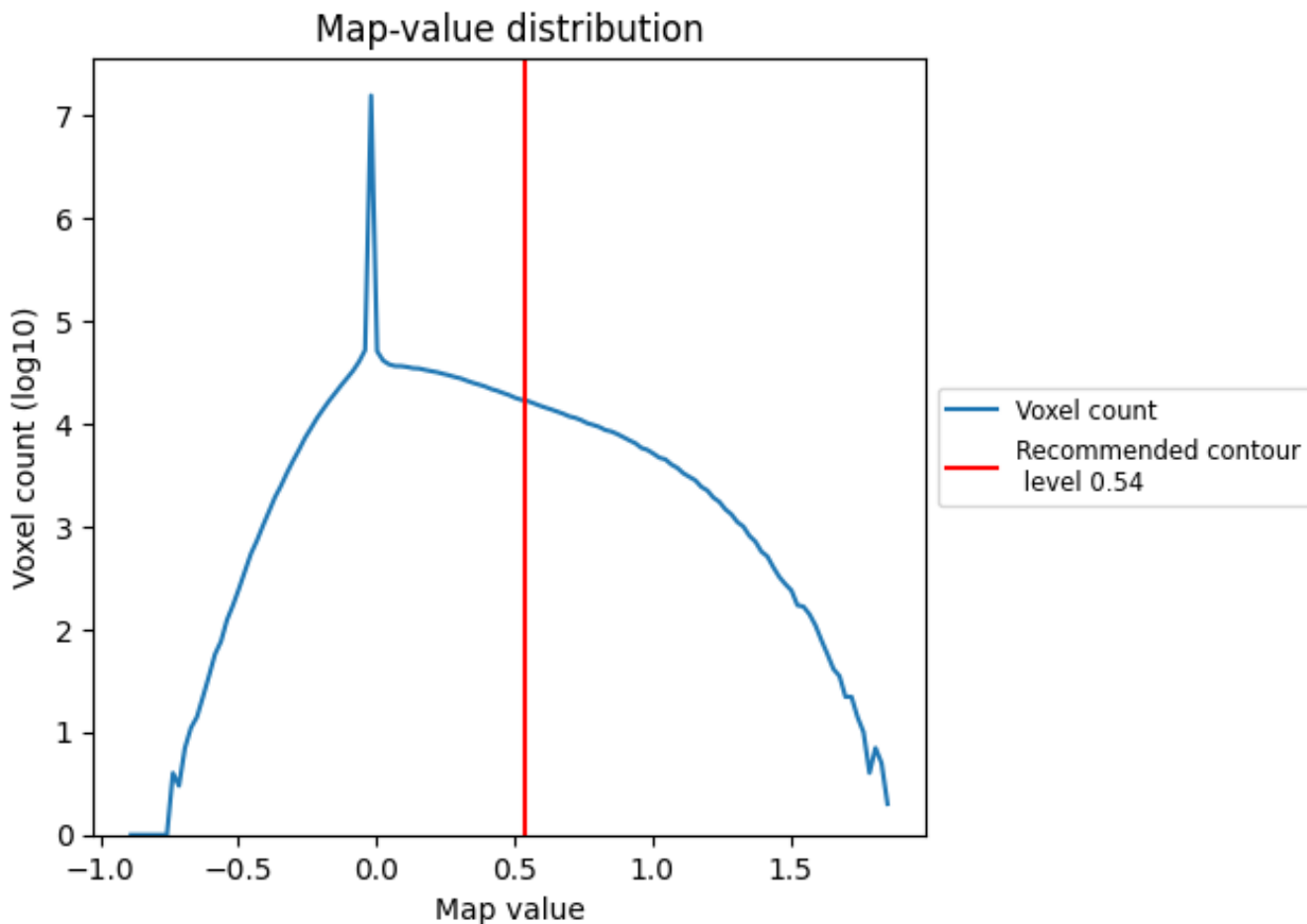


Z

7 Map analysis [i](#)

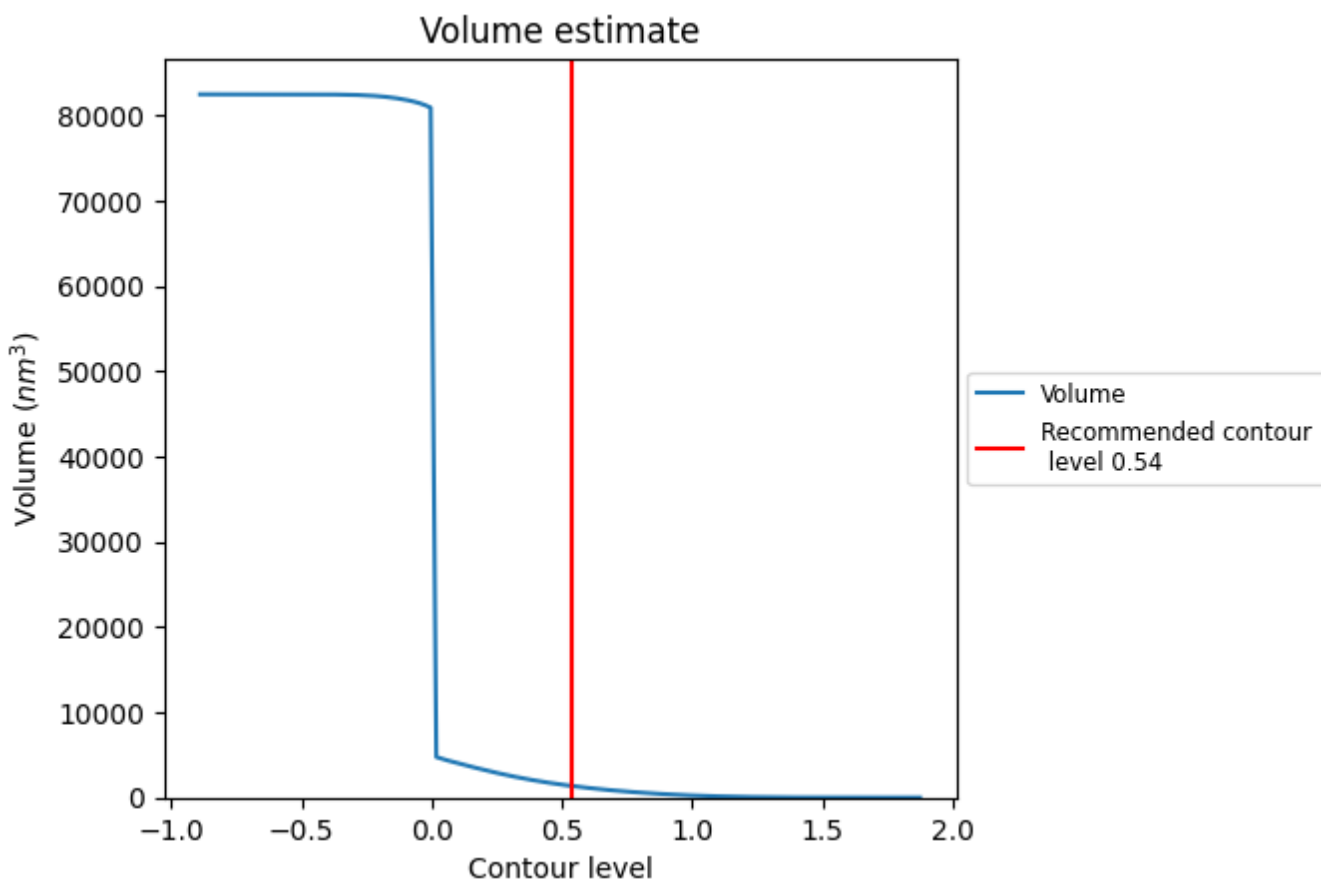
This section contains the results of statistical analysis of the map.

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.

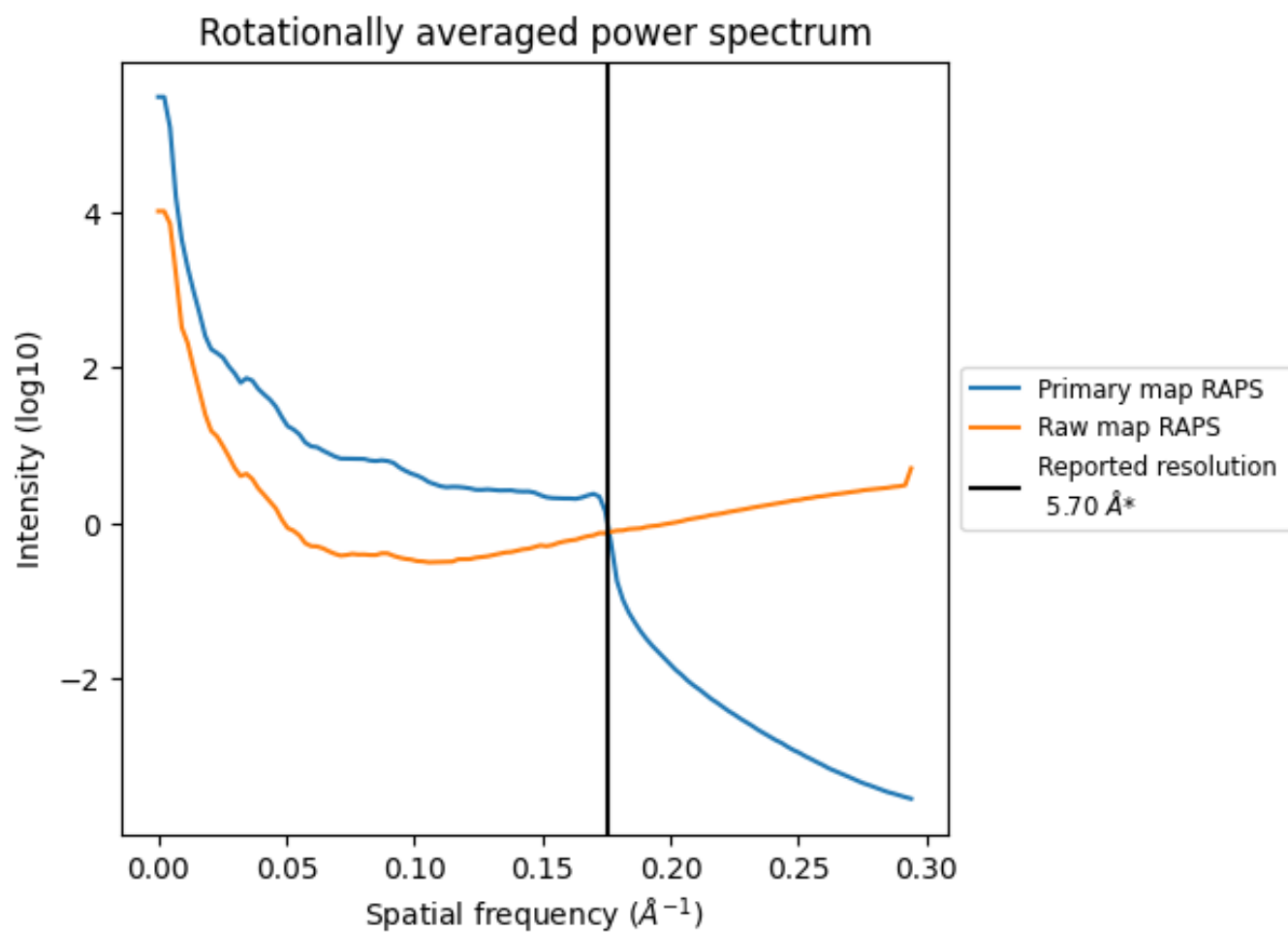
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1353 nm^3 ; this corresponds to an approximate mass of 1222 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 [i](#)

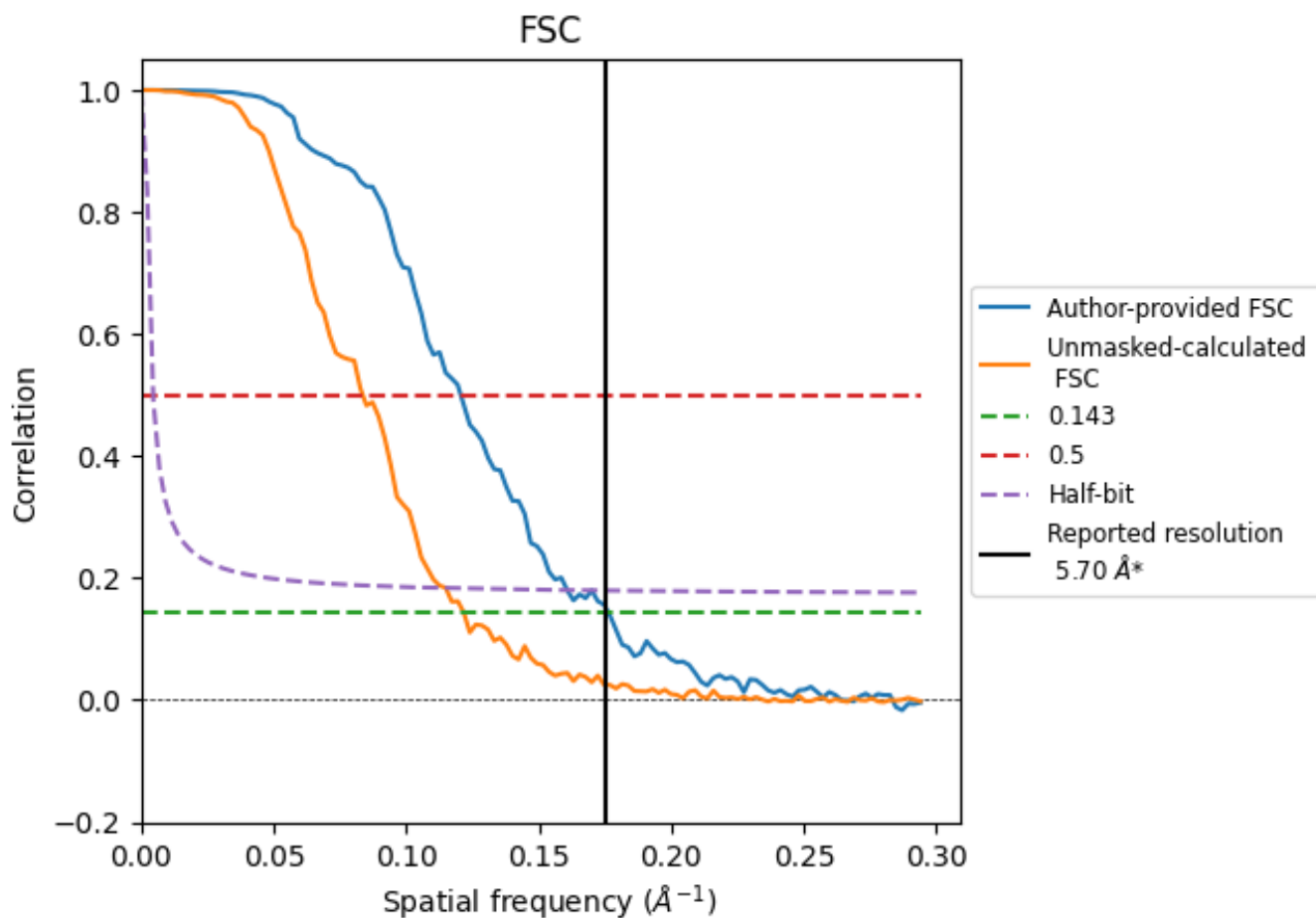


*Reported resolution corresponds to spatial frequency of 0.175 Å⁻¹

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 0.175 Å⁻¹

8.2 Resolution estimates [i](#)

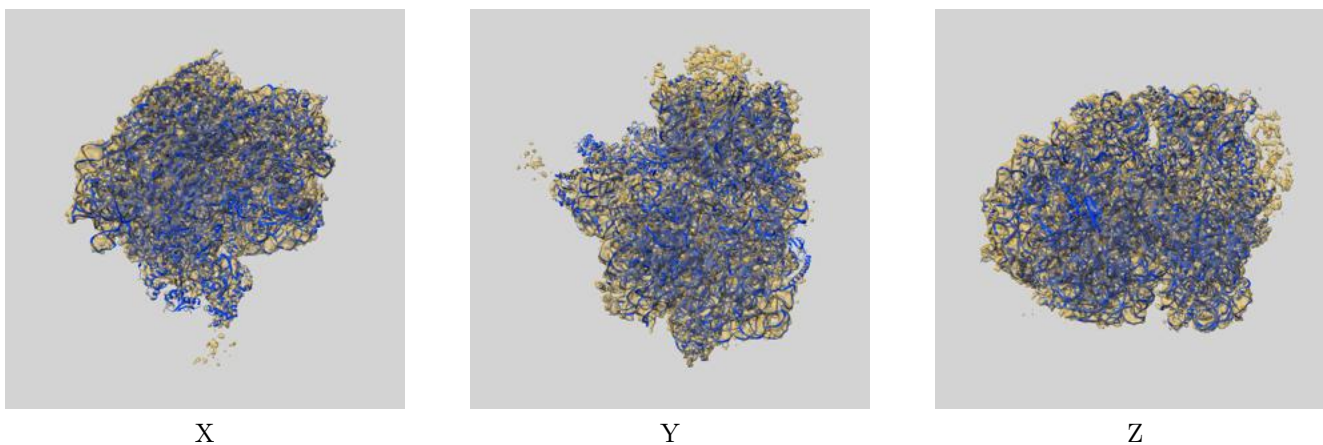
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.70	-	-
Author-provided FSC curve	5.67	8.29	6.22
Unmasked-calculated*	8.21	11.96	8.70

*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 8.21 differs from the reported value 5.7 by more than 10 %

9 Map-model fit [i](#)

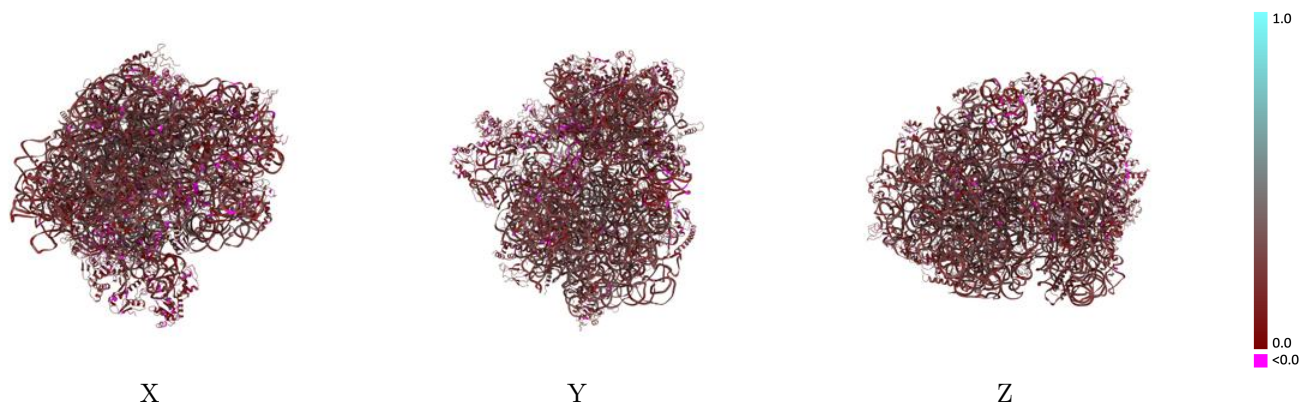
This section contains information regarding the fit between EMDB map EMD-13450 and PDB model 7PIT. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



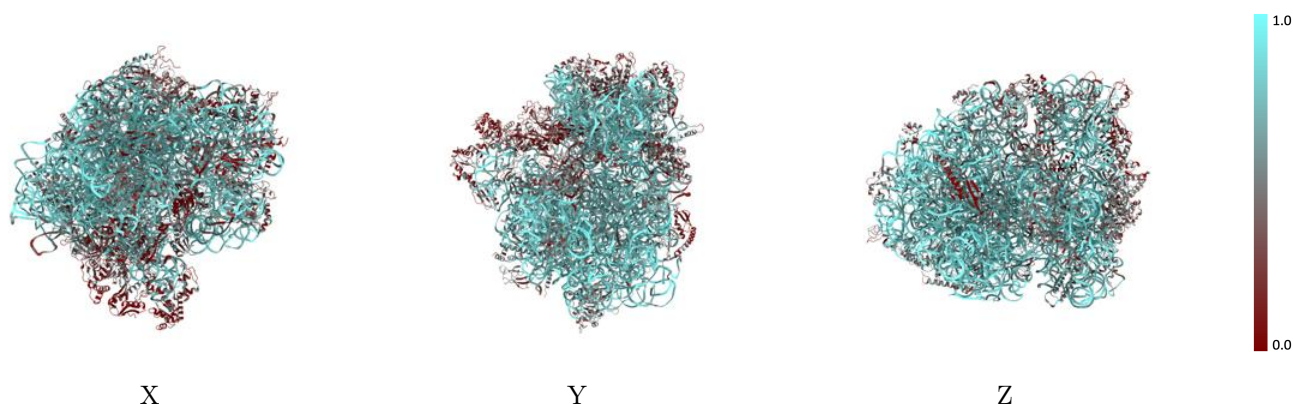
The images above show the 3D surface view of the map at the recommended contour level 0.54 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



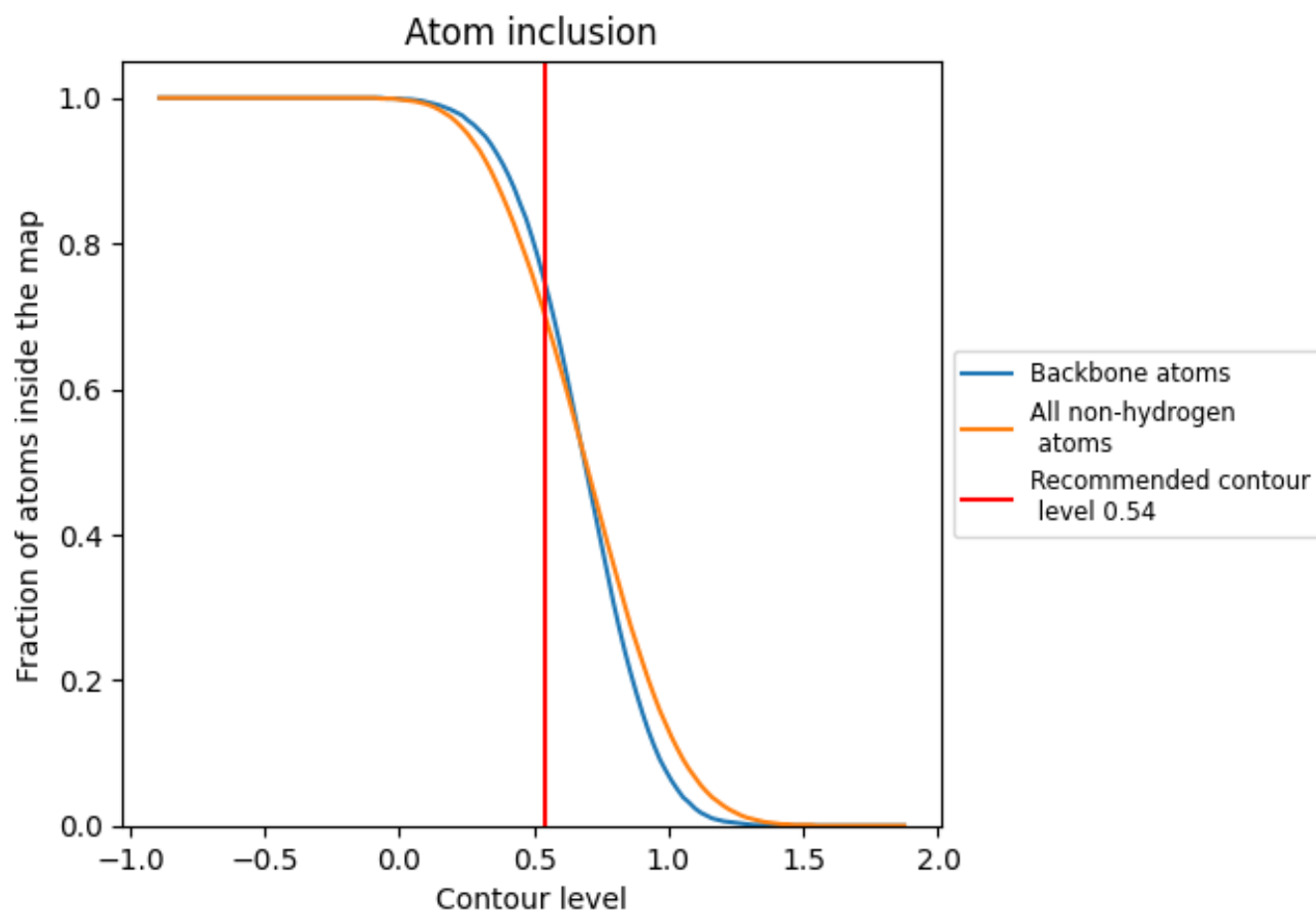
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.54).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 70% 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 (0.54) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7020	 0.2390
0	 0.5840	 0.2160
1	 0.5790	 0.2550
2	 0.6150	 0.2680
3	 0.8660	 0.2590
4	 0.8190	 0.2440
5	 0.8430	 0.2460
7	 0.3630	 0.0970
8	 0.7080	 0.1860
9	 0.1670	 0.1860
A	 0.3910	 0.2110
B	 0.4040	 0.2280
C	 0.3900	 0.2050
D	 0.4480	 0.2400
E	 0.4000	 0.2200
F	 0.3490	 0.2140
G	 0.4850	 0.2060
H	 0.4220	 0.2270
I	 0.3250	 0.2020
J	 0.5140	 0.2250
K	 0.5110	 0.2340
L	 0.3660	 0.2190
M	 0.4920	 0.2180
N	 0.5060	 0.2230
O	 0.5200	 0.2320
P	 0.4930	 0.2400
Q	 0.5150	 0.2480
R	 0.4000	 0.1700
S	 0.5340	 0.1980
T	 0.4980	 0.2310
W	 0.0450	 0.1760
a	 0.5930	 0.2410
b	 0.5340	 0.2320
c	 0.5200	 0.2460
d	 0.3910	 0.2060



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Chain	Atom inclusion	Q-score
e	 0.3800	 0.2150
f	 0.1520	 0.1850
g	 0.1850	 0.1540
h	 0.1750	 0.1750
i	 0.5520	 0.2300
j	 0.4660	 0.2410
k	 0.5450	 0.2570
l	 0.5400	 0.2300
m	 0.5980	 0.2290
n	 0.5040	 0.2230
o	 0.4600	 0.2310
p	 0.5400	 0.1950
q	 0.4880	 0.2340
r	 0.6060	 0.2290
s	 0.5440	 0.2580
t	 0.3810	 0.2270
u	 0.5230	 0.2250
v	 0.4990	 0.2050
w	 0.5260	 0.2260
x	 0.2940	 0.2420
y	 0.6180	 0.2560
z	 0.5060	 0.2420