



wwPDB EM Validation Summary Report ⓘ

Nov 13, 2024 – 03:41 PM EST

PDB ID : 3J7O
EMDB ID : EMD-2649
Title : Structure of the mammalian 60S ribosomal subunit
Authors : Voorhees, R.M.; Fernandez, I.S.; Scheres, S.H.W.; Hegde, R.S.
Deposited on : 2014-08-01
Resolution : 3.40 Å(reported)
Based on initial models : 3J3B, 3J3F

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.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

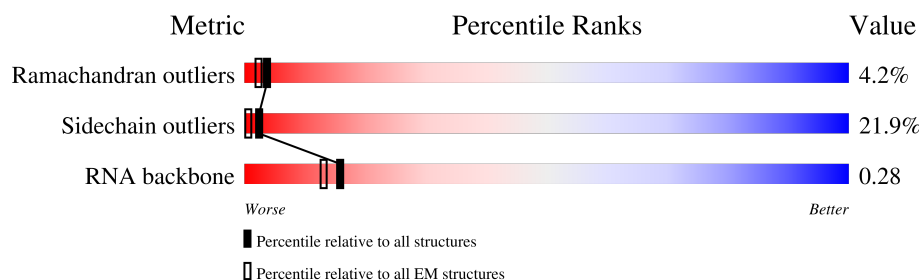
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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 ≥ 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	5	3664	<div> <div>74%</div> <div> <div>47%</div> <div>40%</div> <div>10%</div> <div>.</div> </div> </div>
2	7	120	<div> <div>64%</div> <div> <div>69%</div> <div>24%</div> <div>6%</div> <div>.</div> </div> </div>
3	8	156	<div> <div>83%</div> <div> <div>53%</div> <div>33%</div> <div>8%</div> <div>5%</div> </div> </div>
4	A	257	<div> <div>61%</div> <div> <div>71%</div> <div>18%</div> <div>5%</div> <div>5%</div> </div> </div>
5	B	394	<div> <div>73%</div> <div> <div>74%</div> <div>21%</div> <div>.</div> <div>.</div> </div> </div>
6	C	367	<div> <div>66%</div> <div> <div>77%</div> <div>19%</div> <div>.</div> <div>.</div> </div> </div>
7	D	297	<div> <div>64%</div> <div> <div>68%</div> <div>24%</div> <div>5%</div> <div>.</div> <div>.</div> </div> </div>
8	E	236	<div> <div>69%</div> <div> <div>64%</div> <div>26%</div> <div>9%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
9	F	225	
10	G	266	
11	H	192	
12	I	213	
13	J	178	
14	L	211	
15	M	213	
16	N	204	
17	O	204	
18	P	153	
19	Q	188	
20	R	196	
21	S	224	
22	T	160	
23	U	128	
24	V	140	
25	W	157	
26	X	156	
27	Y	145	
28	Z	136	
29	a	148	
30	b	160	
31	c	115	
32	d	125	
33	e	135	

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Mol	Chain	Length	Quality of chain
34	f	110	
35	g	117	
36	h	123	
37	i	105	
38	j	86	
39	k	70	
40	l	51	
41	m	128	
42	n	25	
43	o	106	
44	p	91	
45	r	125	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 136815 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called Ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 5 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

- Molecule 6 is a protein called Ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

- Molecule 7 is a protein called Ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	292	Total	C	N	O	S	0	0
			2380	1508	434	426	12		

- Molecule 8 is a protein called Ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

- Molecule 9 is a protein called Ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	241	Total	C	N	O	S	0	0
			1934	1232	372	326	4		

- Molecule 11 is a protein called Ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called Ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	213	Total	C	N	O	S	0	0
			1713	1083	331	284	15		

- Molecule 13 is a protein called Ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 14 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 15 is a protein called Ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 16 is a protein called Ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	201	Total	C	N	O	S	0	0
			1651	1063	323	260	5		

- Molecule 18 is a protein called Ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called Ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 20 is a protein called Ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 21 is a protein called Ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 22 is a protein called Ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 24 is a protein called Ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called Ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 26 is a protein called Ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 27 is a protein called Ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called Ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 30 is a protein called Ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 31 is a protein called Ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 32 is a protein called Ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called Ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called Ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called Ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 37 is a protein called Ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called Ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

- Molecule 39 is a protein called Ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 40 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 43 is a protein called Ribosomal protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 44 is a protein called Ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

- Molecule 46 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
46	5	119	Total	Mg	0
			119	119	
46	7	5	Total	Mg	0
			5	5	
46	8	4	Total	Mg	0
			4	4	
46	P	1	Total	Mg	0
			1	1	
46	V	1	Total	Mg	0
			1	1	

- Molecule 47 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	j	1	Total	Zn	0
			1	1	
47	m	1	Total	Zn	0
			1	1	

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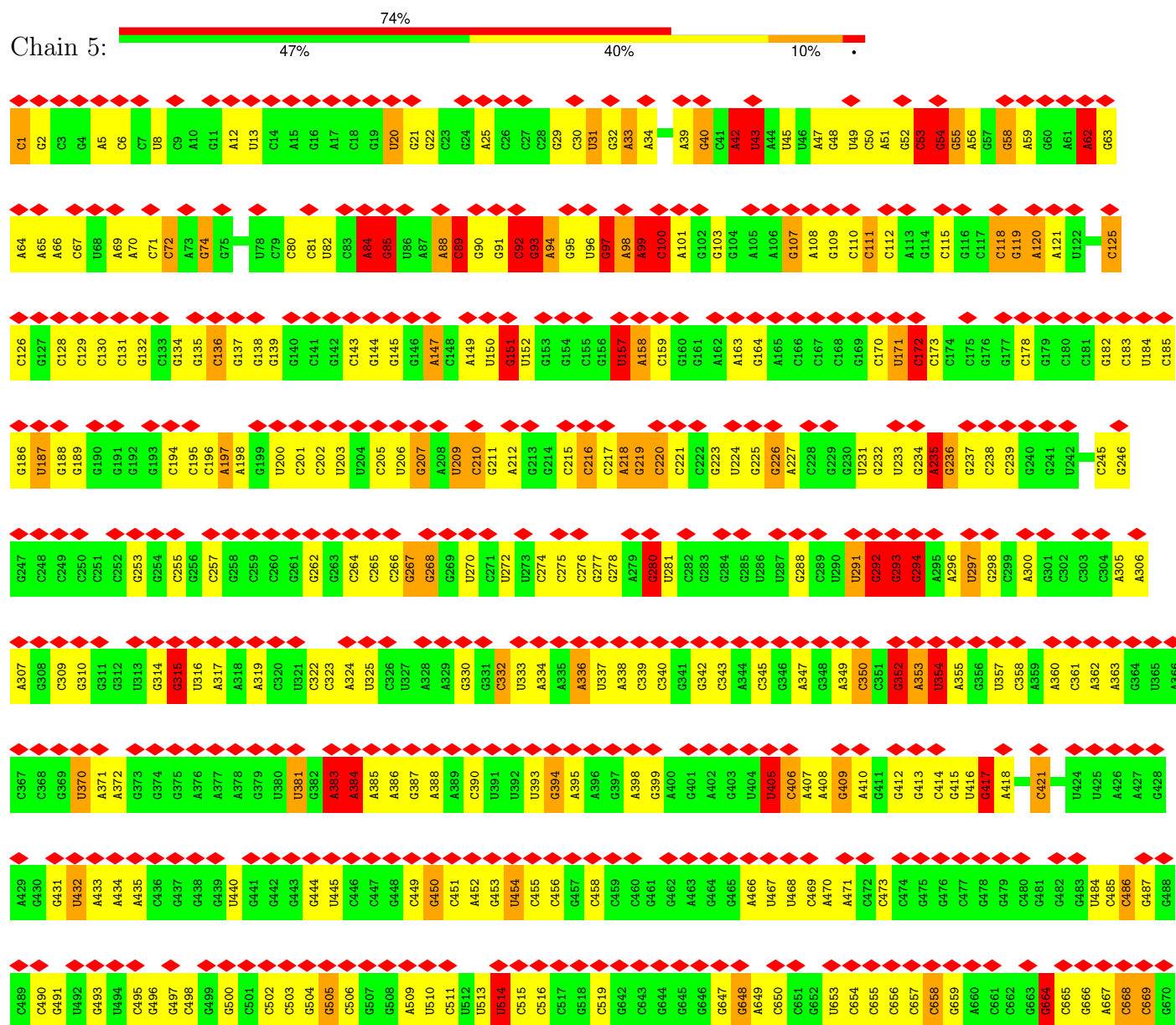
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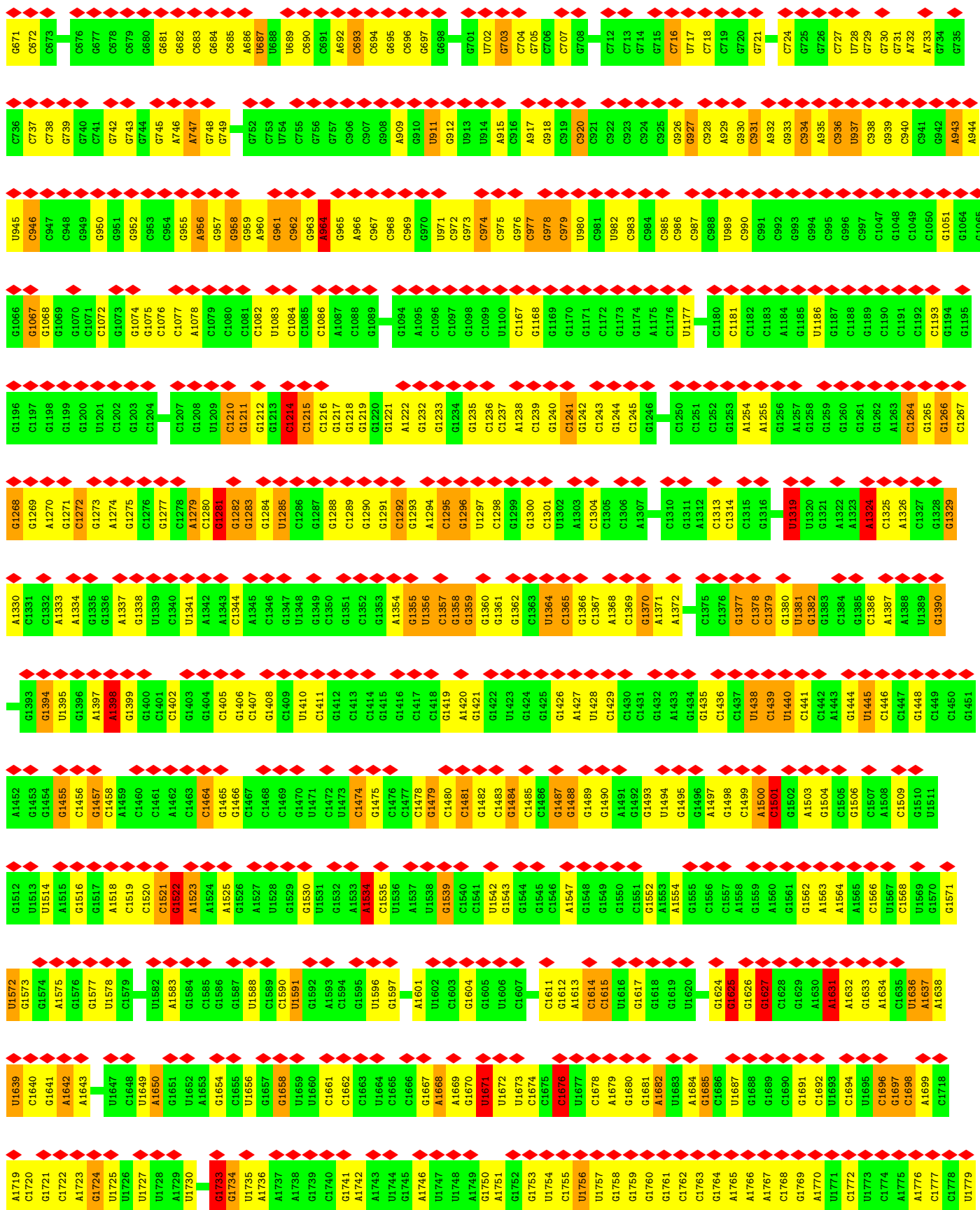
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
47	o	1	1	1	0

3 Residue-property plots

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

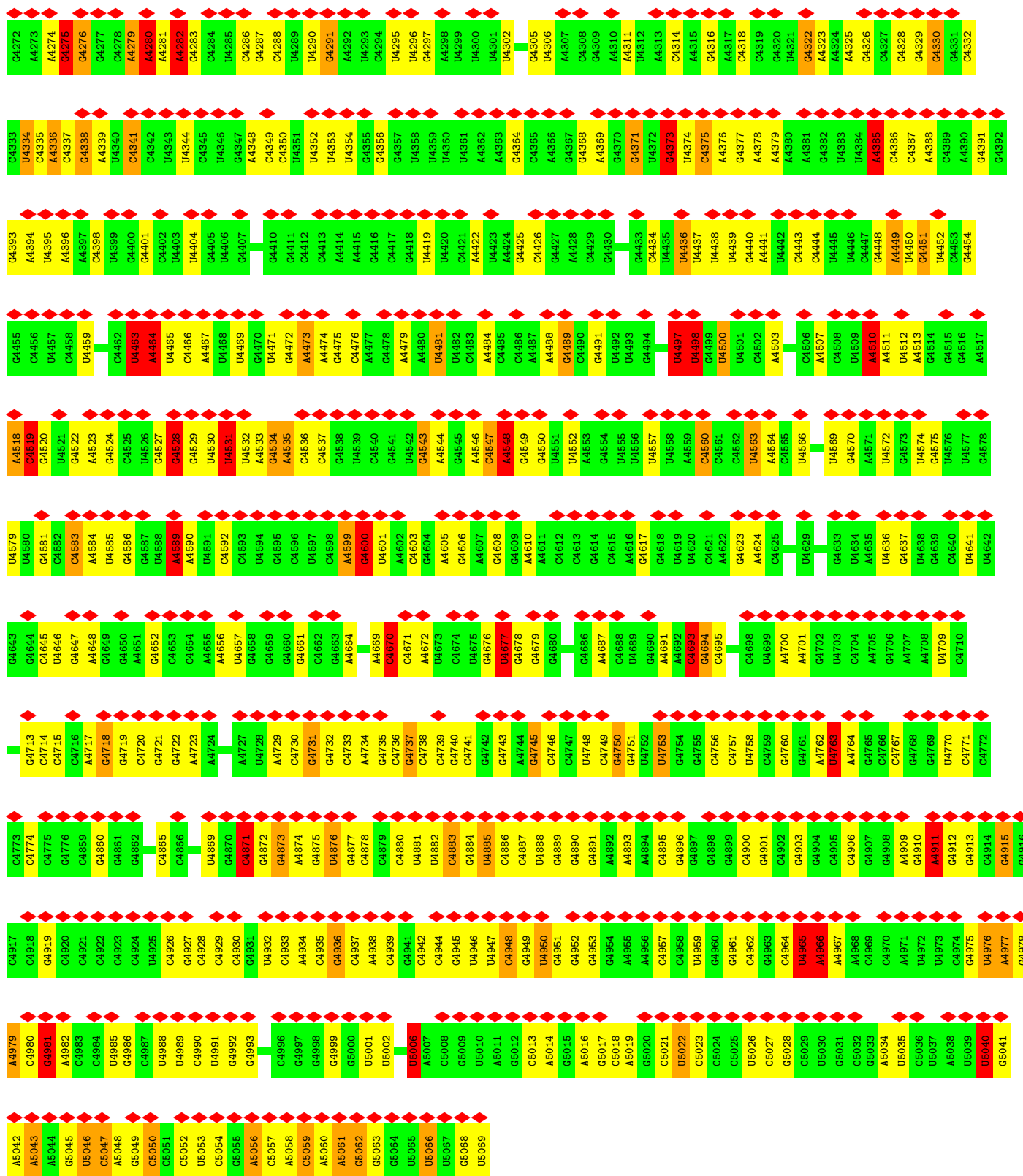
• Molecule 1: 28S ribosomal RNA





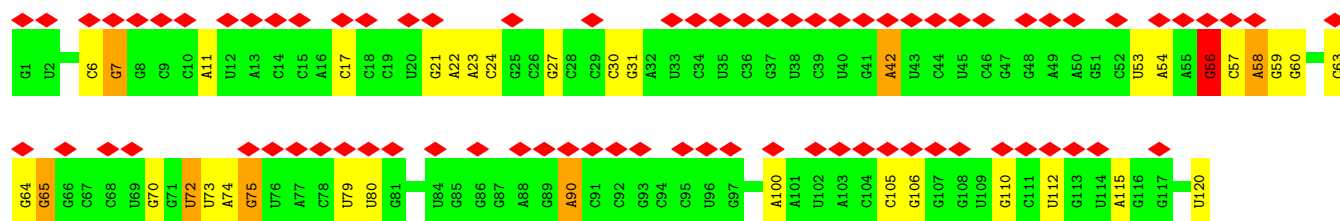
C2627	U2628	C2629	U2630	U2631	U2632	U2633	U2634	U2635	U2636	U2637	U2638	U2639	U2640	A2641	A2642	C2643	U2644	U2645	U2646	U2647	U2648	U2649	U2650	C2501	C2502	C2503	C2504	C2505	C2506	C2507	U2508	C2509	C2510	A2511	A2512	A2513	C2514	C2515	C2516	U2517	C2520	U2521	C2522	C2523	U2524	U2525	C2526	C2527	U2528	C2529	U2530	C2531	C2532	C2533	C2534	C2535	A2536	A2537	U2538	C2539	C2540	C2541	C2542	A2543	C2544	U2545	C2546	C2547	C2548	C2549	U2550	A2551	C2552	A2553	U2554	C2555	C2556	U2557	C2558	C2559	C2560	C2661	C2662	C2663	C2664	U2665	U2666	C2667	C2668	C2669	C2670	C2671	C2672	C2673	A2674	C2675	C2676	C2677	A2678	C2679	U2680	U2681	C2682	C2683	C2684	C2685																																																																
C2561	C2562	C2563	C2564	A2565	C2566	C2567	C2568	U2569	C2570	C2571	C2572	U2576	C2577	C2578	C2579	U2580	A2581	A2582	C2583	C2584	C2585	C2586	A2587	C2588	C2589	U2590	C2591	C2592	A2593	C2594	C2595	C2596	C2597	U2598	C2599	C2600	A2601	C2602	C2603	C2604	C2605	C2606	C2607	C2608	C2609	C2610	A2611	C2612	C2613	C2614	C2615	C2616	C2617	C2618	C2619	C2620	A2621	C2622	C2623	C2624	C2625	C2626	C2627	C2628	C2629	C2630	C2631	C2632	C2633	C2634	C2635	C2636	C2637	C2638	C2639	C2640	C2641	C2642	C2643	C2644	C2645	C2646	C2647	C2648	C2649																																																																																					
A2438	C2439	U2440	C2441	C2442	C2443	U2444	C2445	C2446	U2447	C2448	C2449	C2450	U2454	C2455	C2456	C2457	C2458	C2459	A2460	C2461	C2462	C2463	C2464	C2465	C2466	U2467	U2468	C2469	C2470	C2471	A2472	C2473	C2474	C2475	C2476	A2477	C2478	C2479	C2480	C2481	C2482	C2483	C2484	U2485	C2486	C2487	C2488	C2489	U2490	C2491	C2492	C2493	U2494	C2497	C2498	C2499																																																																																																																		
C2378	A2379	C2380	A2381	C2382	C2383	U2384	U2385	U2386	C2387	A2388	C2389	C2390	C2391	C2392	C2393	C2394	A2395	C2396	C2397	U2398	C2399	C2400	A2401	C2402	A2403	A2404	C2405	C2406	C2407	U2408	U2409	C2410	C2411	C2412	U2413	C2414	U2415	C2416	A2417	C2418	C2419	A2420	C2421	C2422	C2423	C2424	U2425	C2427	A2428	C2429	C2430	A2431	U2432	C2433	C2434	C2435	U2436	C2437	C2438	C2439																																																																																																														
C2319	C2320	C2321	C2322	C2323	C2324	C2325	C2326	C2327	C2328	U2329	C2330	C2331	A2332	C2333	C2334	C2335	C2336	C2337	C2338	C2339	C2340	A2341	C2342	C2343	U2344	C2345	C2346	A2347	C2348	C2349	U2350	C2351	U2352	U2353	C2354	C2355	U2356	C2357	C2358	U2359	A2360	C2361	U2362	A2363	C2364	C2365	A2366	A2367	A2368	U2369	C2370	U2371	U2372	C2373	A2374	A2375	A2376	C2377																																																																																																																
C2255	C2256	C2257	C2258	C2259	C2260	C2261	C2262	A2263	C2264	C2265	C2266	U2267	A2268	C2269	C2270	C2271	C2272	C2273	C2274	C2275	A2276	C2277	C2278	A2279	C2280	U2281	A2282	C2283	C2286	C2287	C2288	C2289	C2290	C2291	C2292	U2293	C2294	C2295	C2296	C2297	U2298	C2299	A2300	C2301	C2302	U2303	C2306	A2307	A2308	C2309	C2310	C2311	C2312	A2313	C2314	C2315	C2316																																																																																																																	
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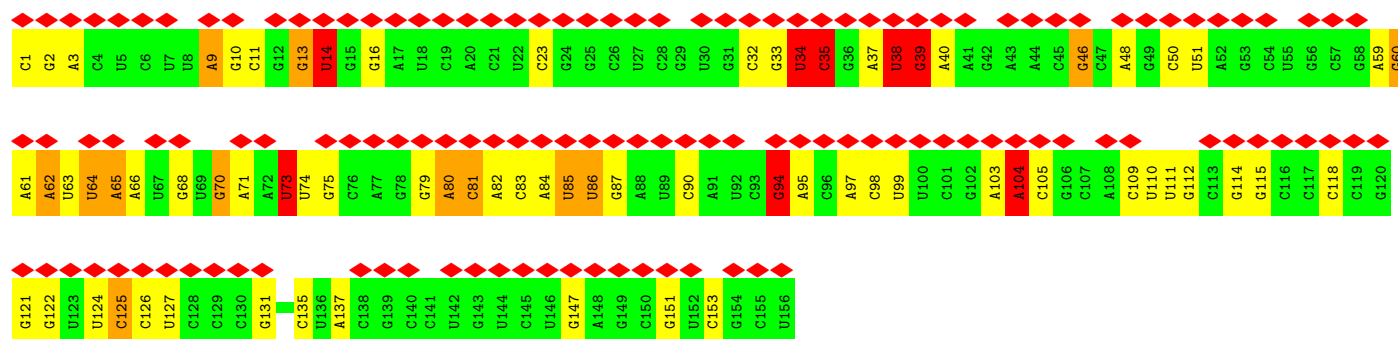
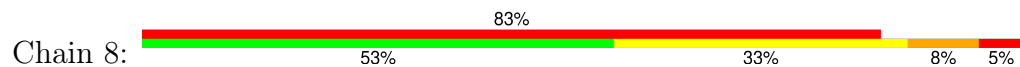


• Molecule 2: 5S ribosomal RNA

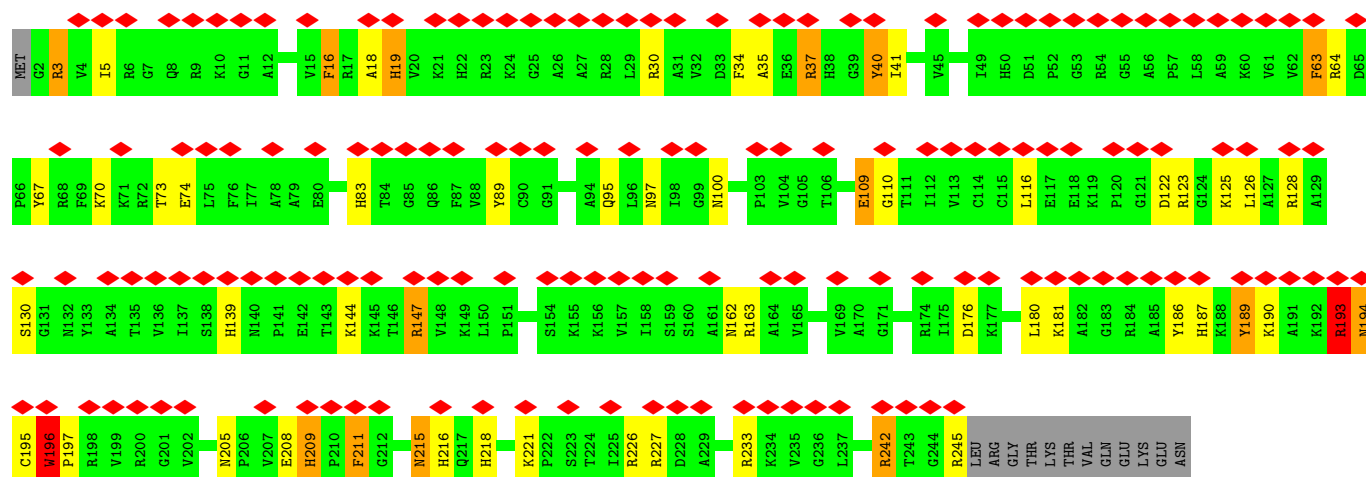




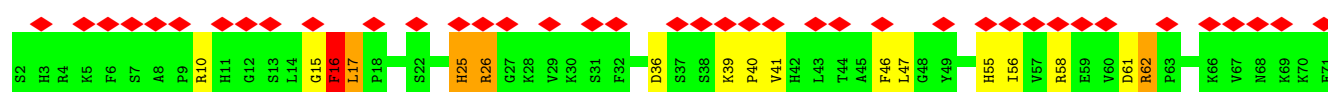
• Molecule 3: 5.8S ribosomal RNA

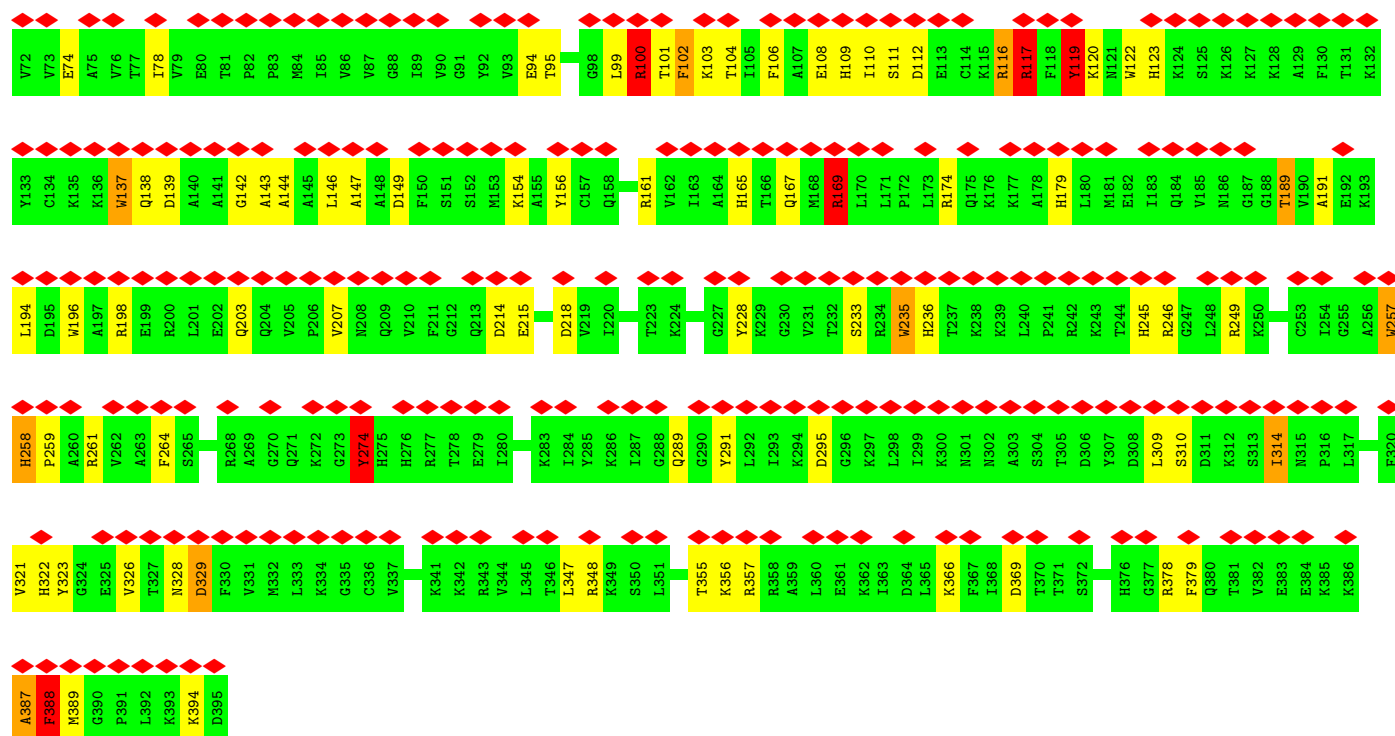


• Molecule 4: Ribosomal protein uL2

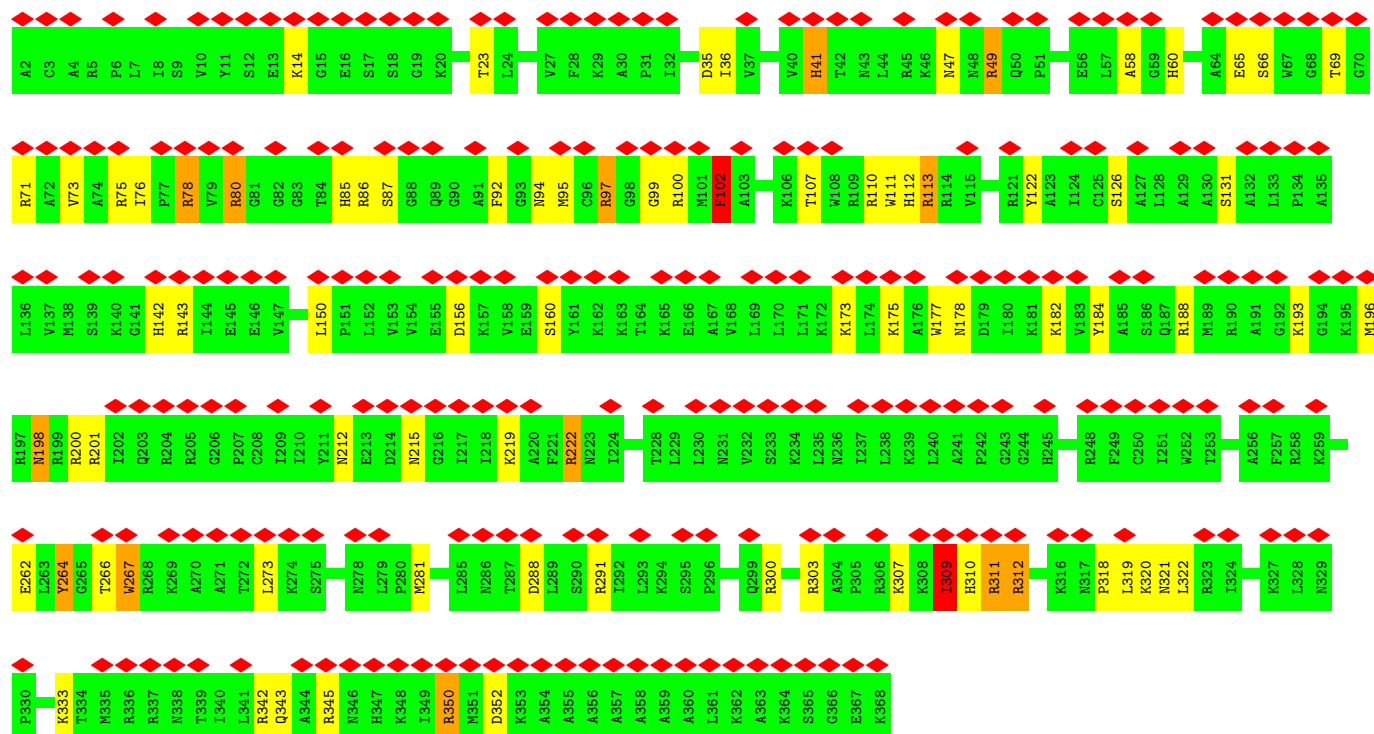
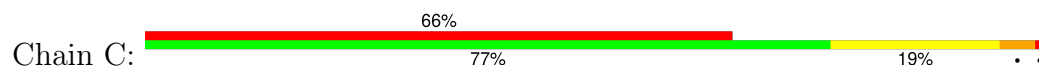


• Molecule 5: Ribosomal protein uL3



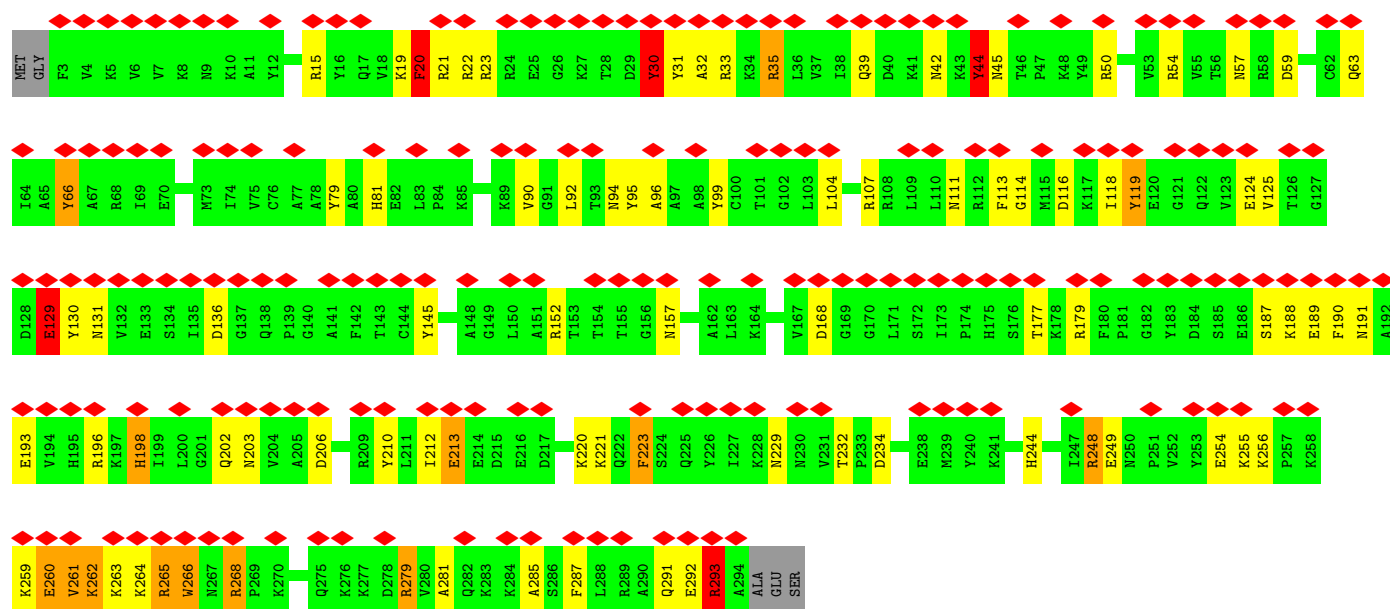


• Molecule 6: Ribosomal protein uL4



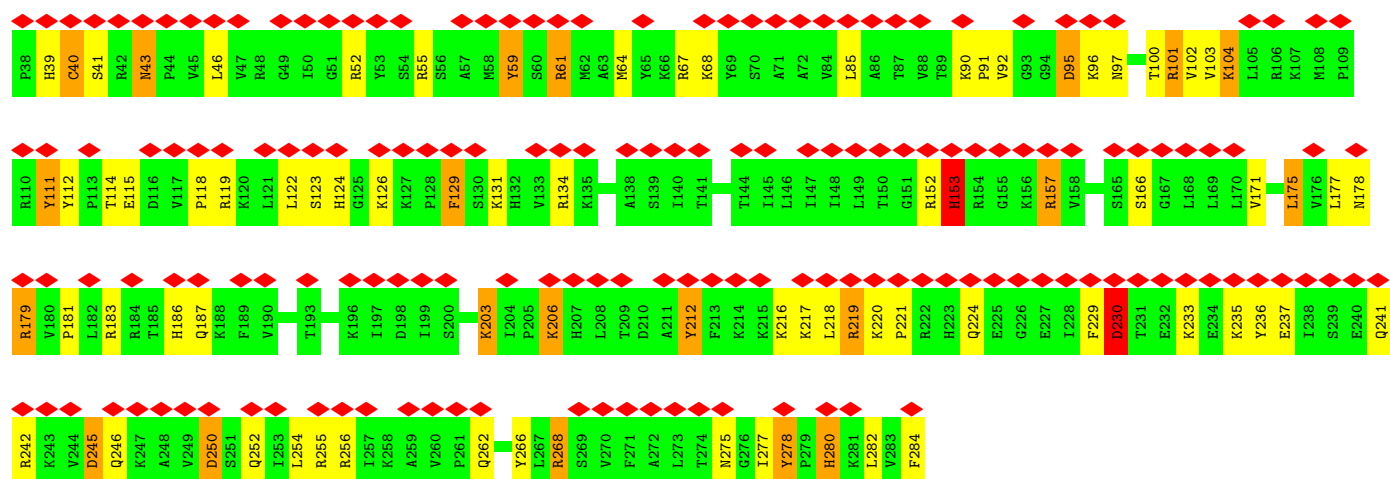
• Molecule 7: Ribosomal protein uL18

Chain D: 



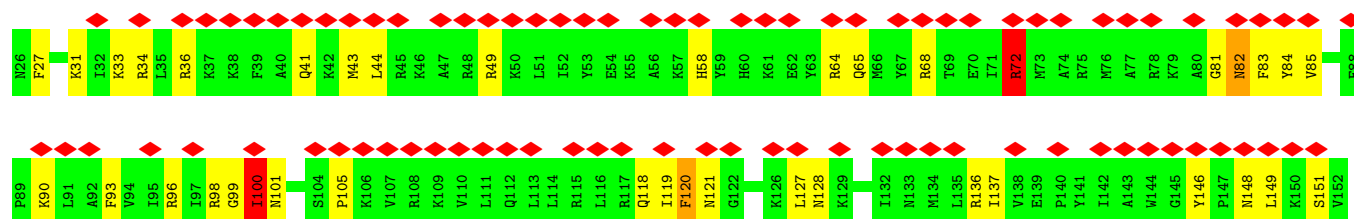
• Molecule 8: Ribosomal protein eL6

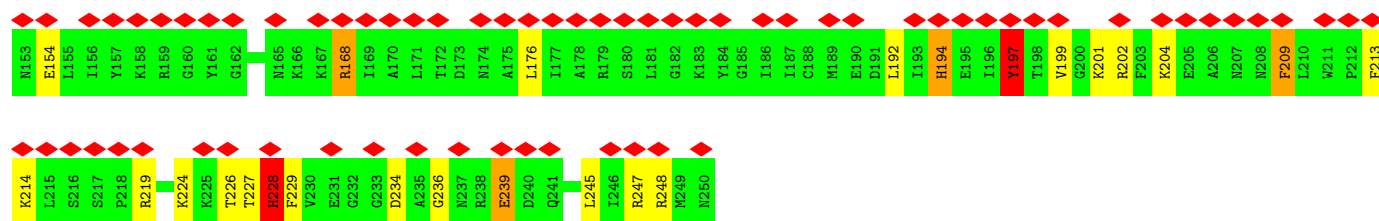
Chain E: 



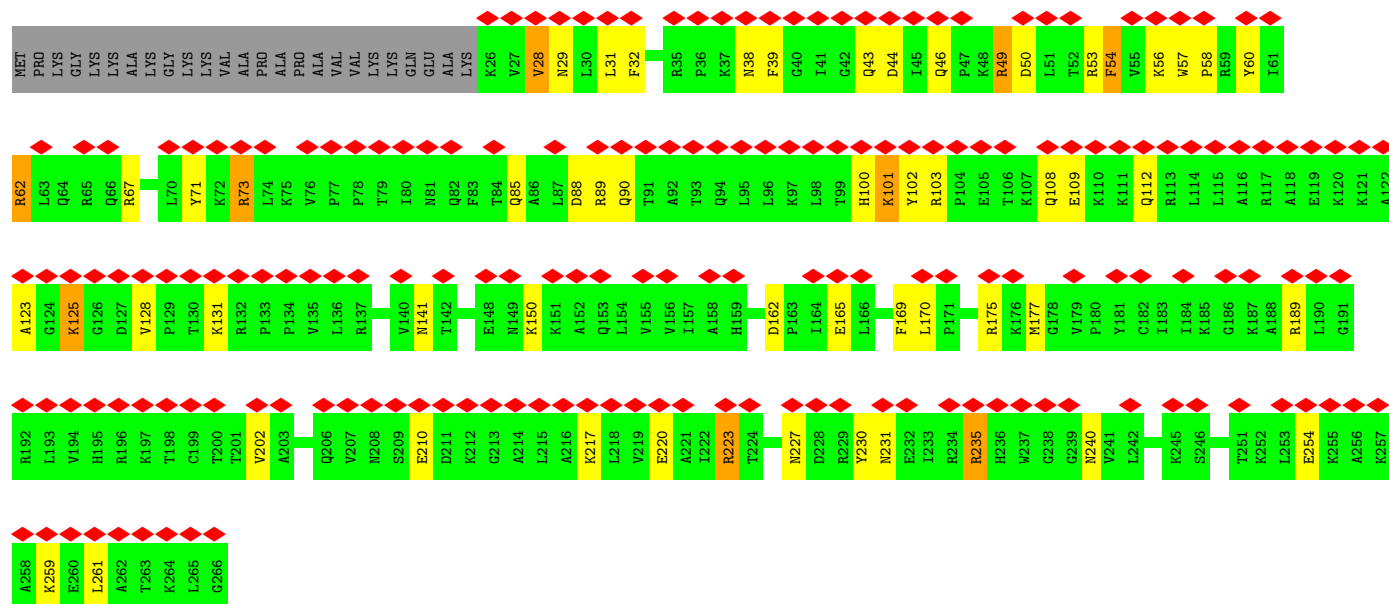
• Molecule 9: Ribosomal protein uL30

Chain F: 

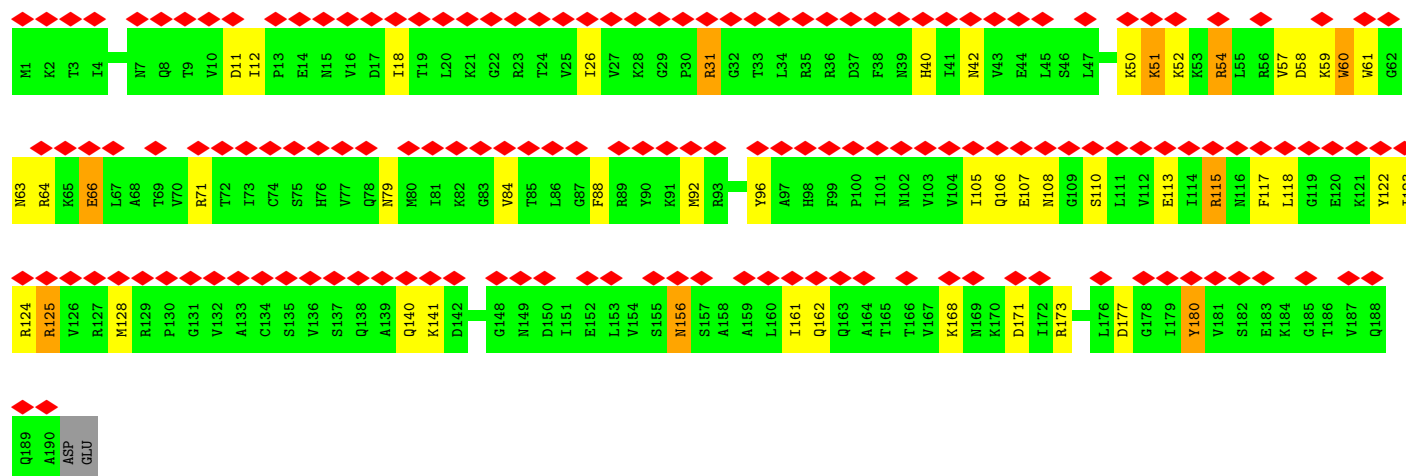
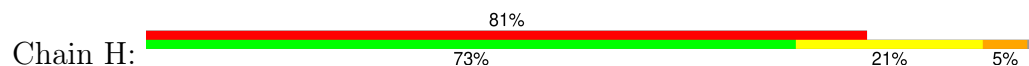




• Molecule 10: Ribosomal protein eL8

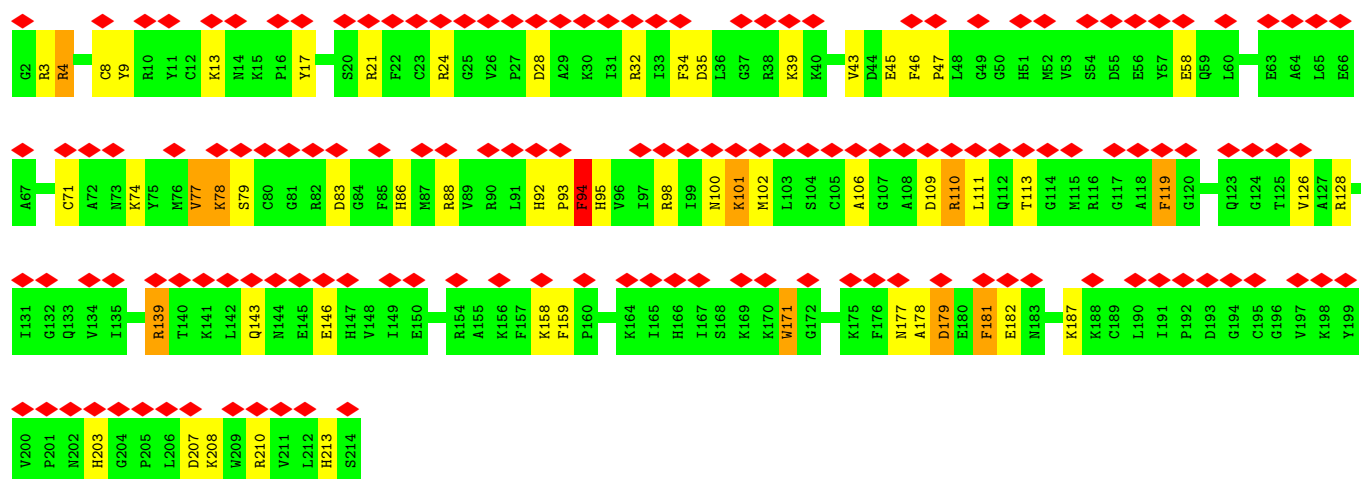


• Molecule 11: Ribosomal protein uL6




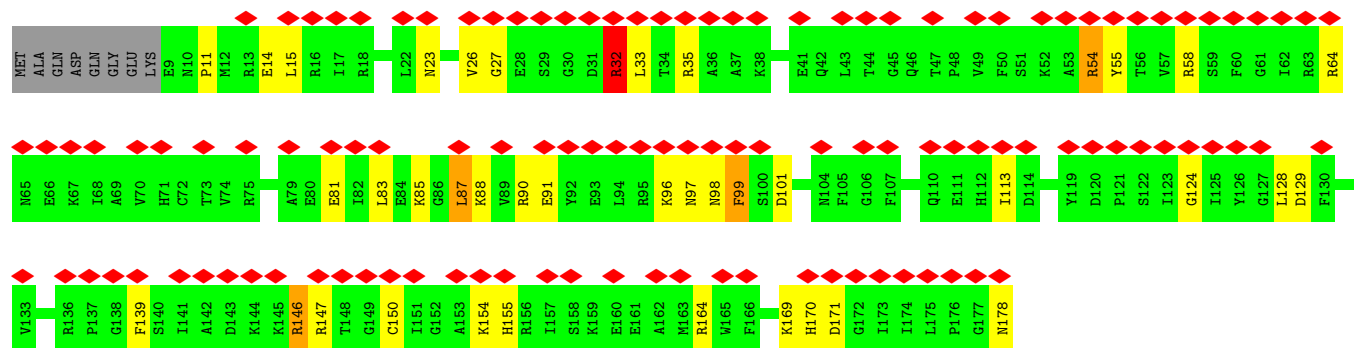
• Molecule 12: Ribosomal protein uL16

Chain I: 




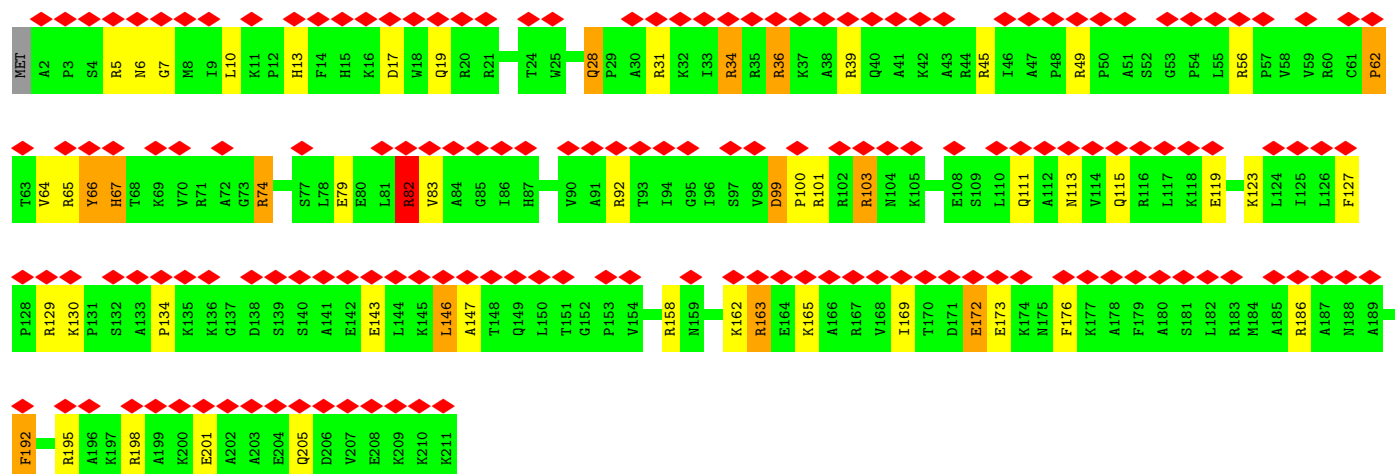
• Molecule 13: Ribosomal protein uL5

Chain J: 

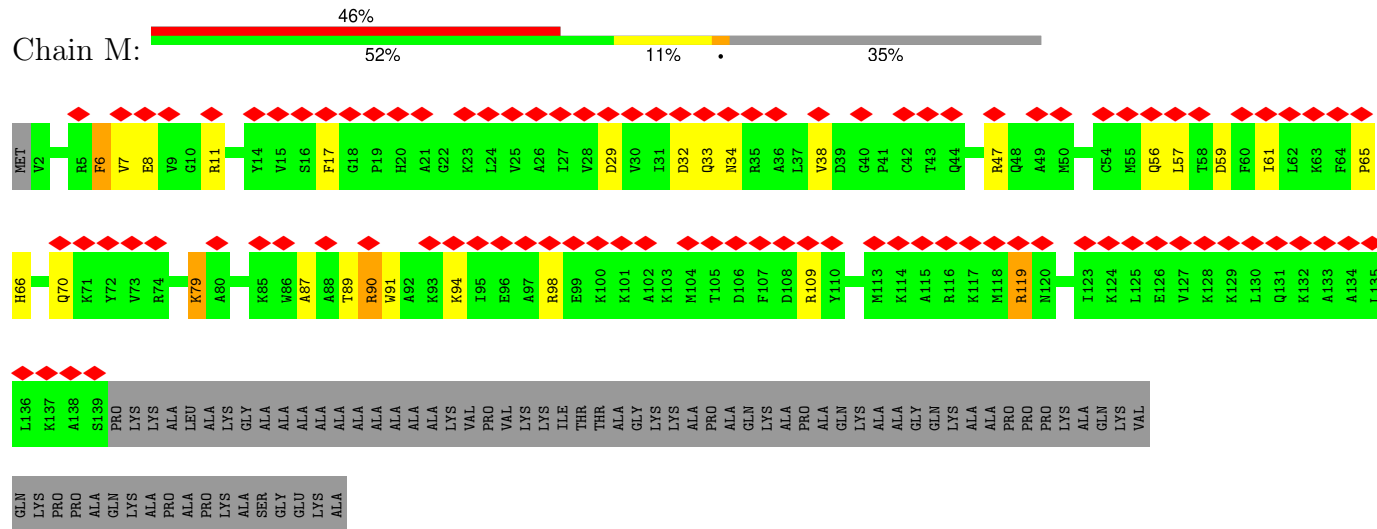


• Molecule 14: Ribosomal protein eL13

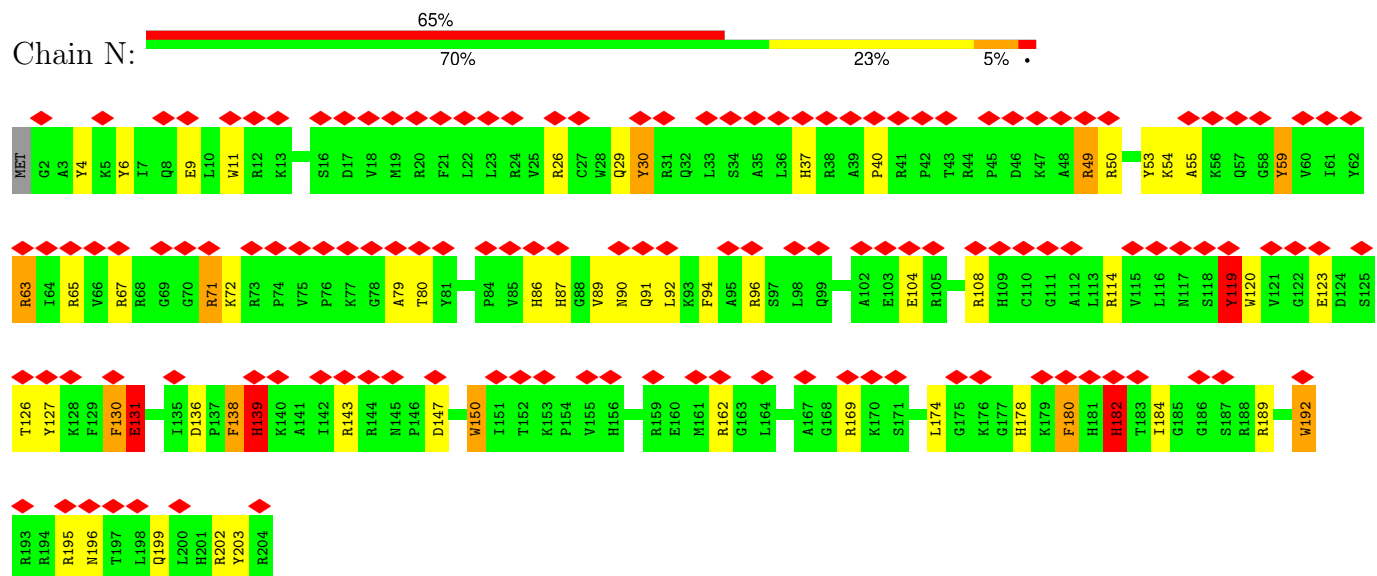
Chain L: 



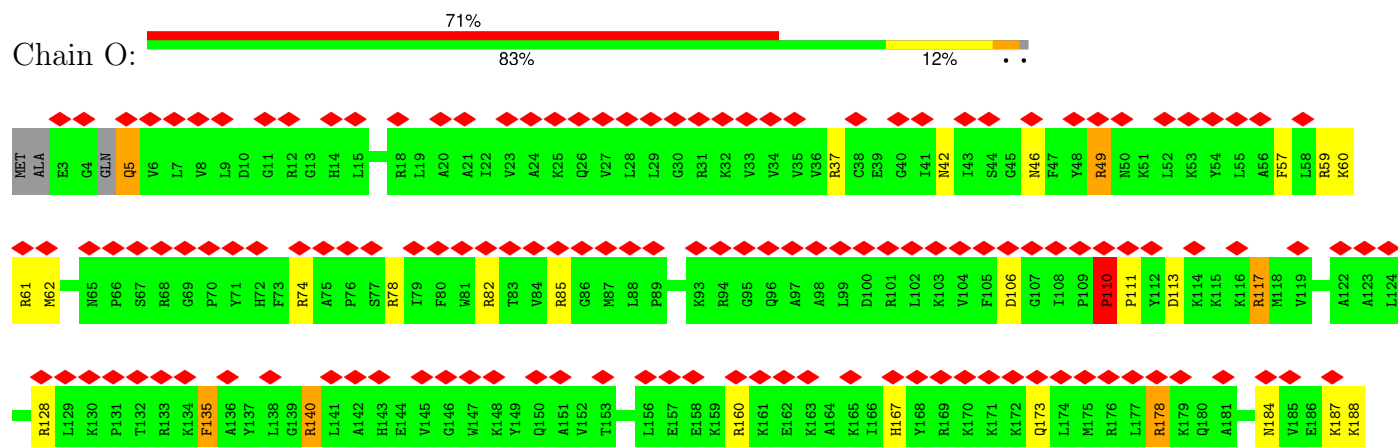
- Molecule 15: Ribosomal protein eL14

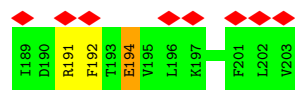


- Molecule 16: Ribosomal protein eL15

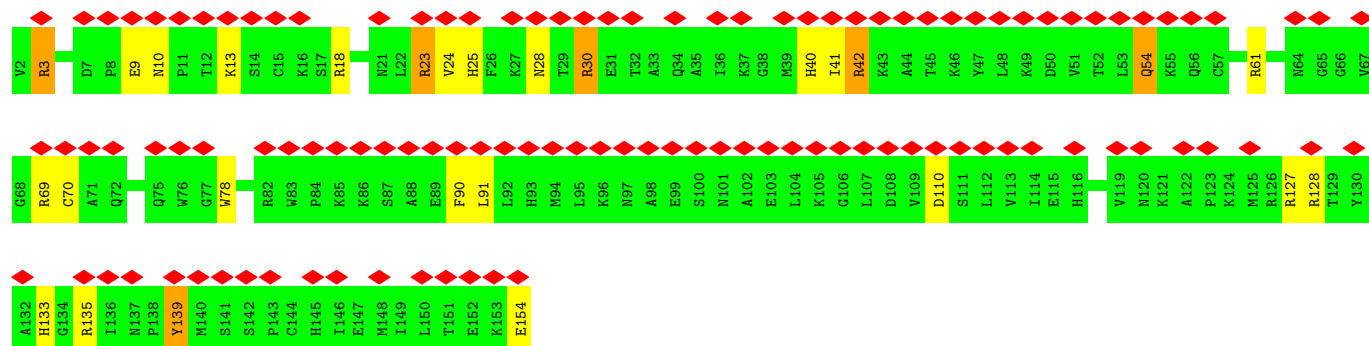
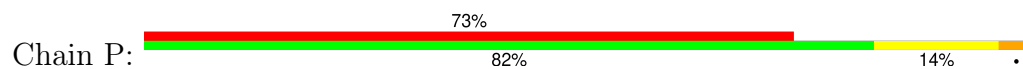


- Molecule 17: Ribosomal protein uL13

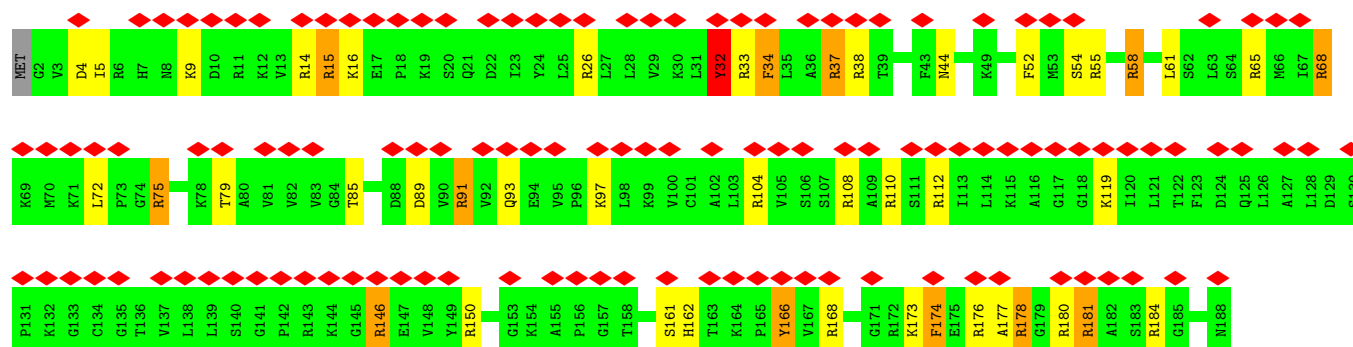
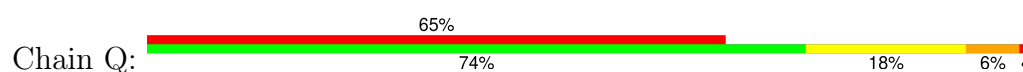




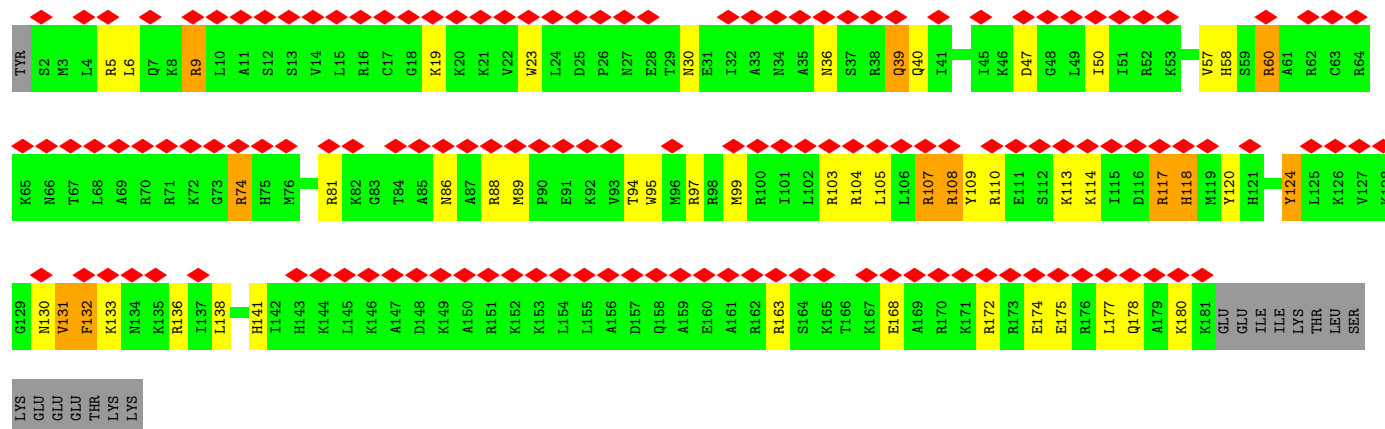
• Molecule 18: Ribosomal protein uL22



• Molecule 19: Ribosomal protein eL18



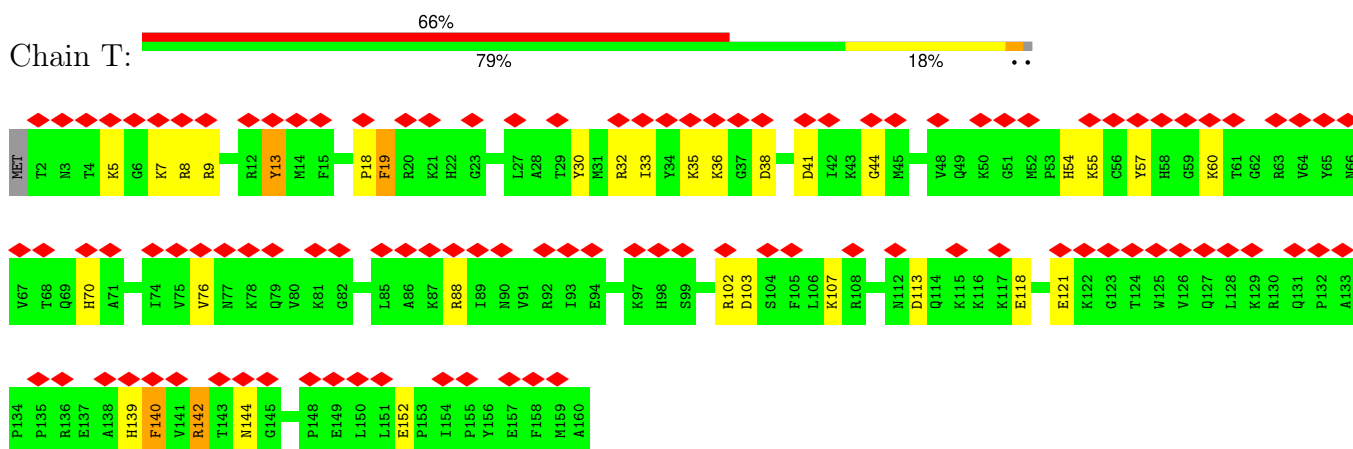
• Molecule 20: Ribosomal protein eL19



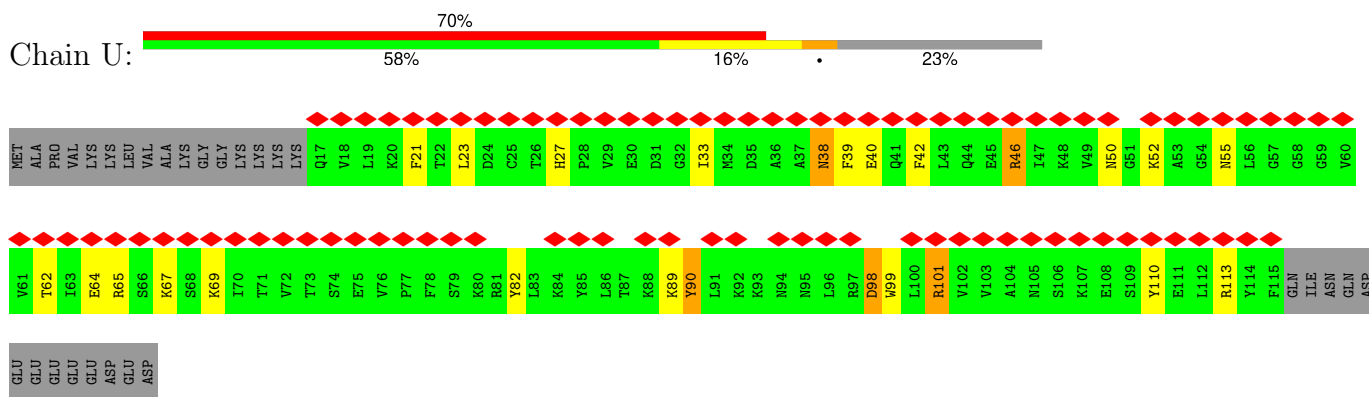
- Molecule 21: Ribosomal protein eL20



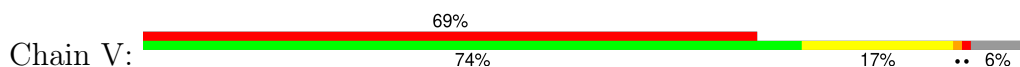
- Molecule 22: Ribosomal protein eL21

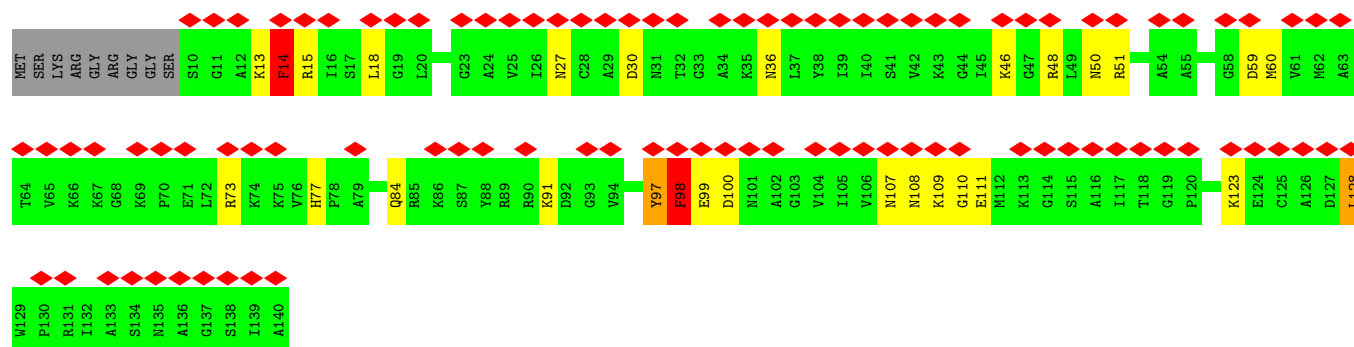


- Molecule 23: Ribosomal protein eL22

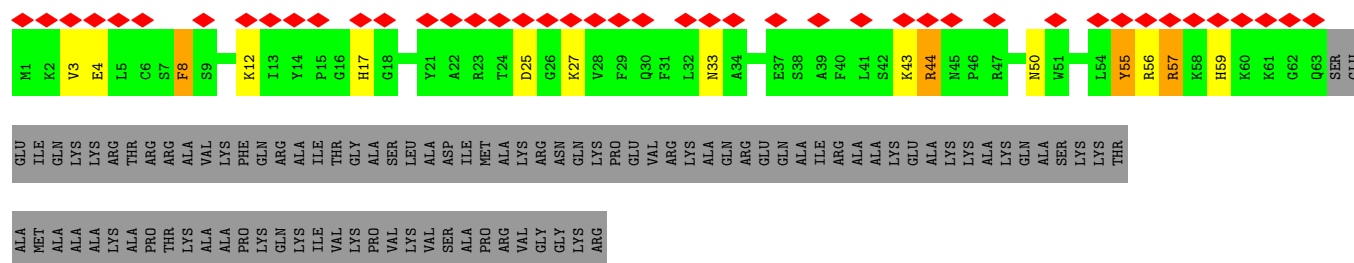


- Molecule 24: Ribosomal protein uL14

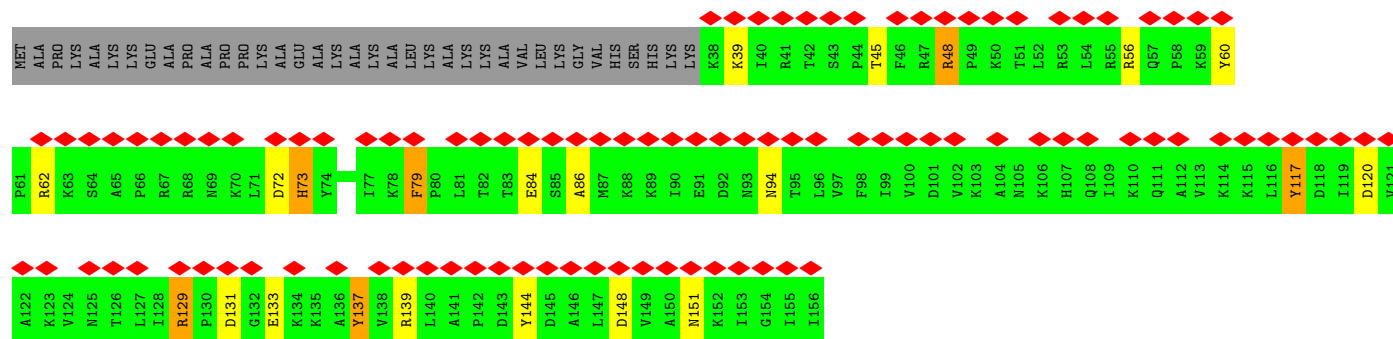




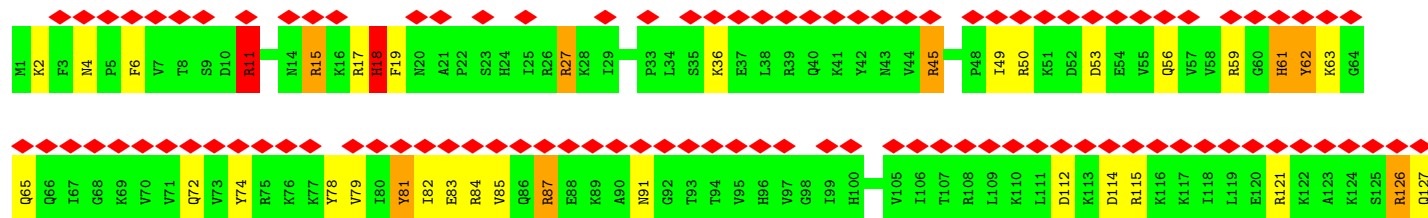
• Molecule 25: Ribosomal protein eL24



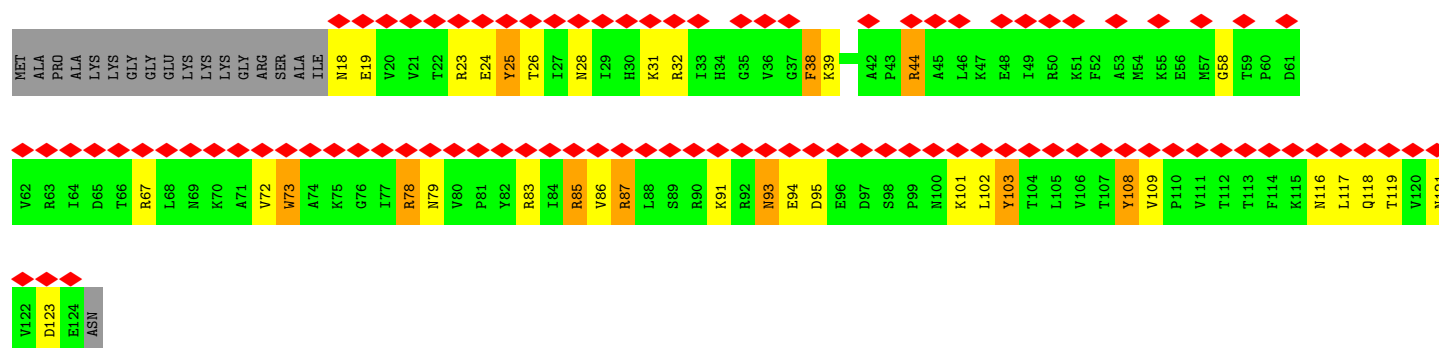
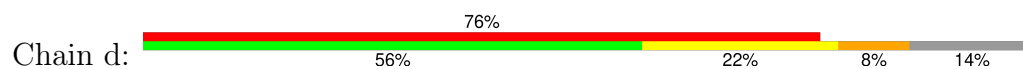
• Molecule 26: Ribosomal protein uL23



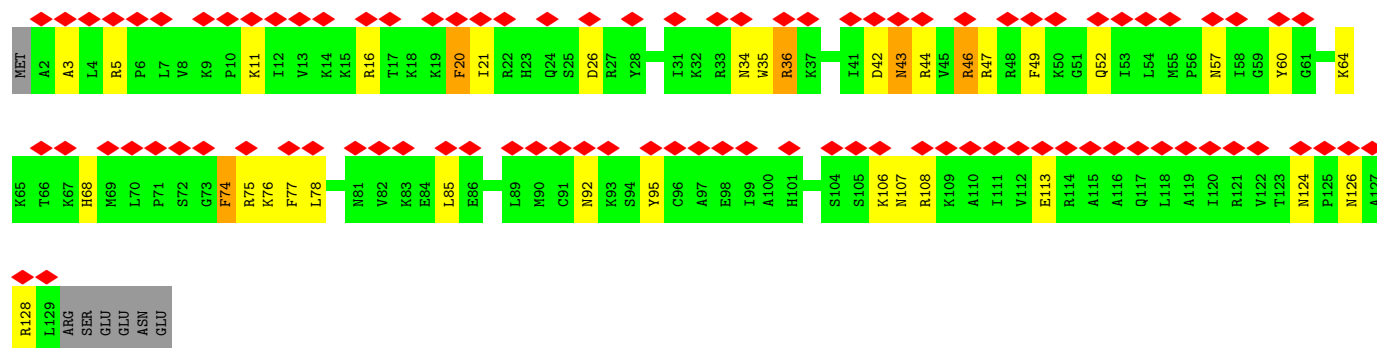
• Molecule 27: Ribosomal protein uL24



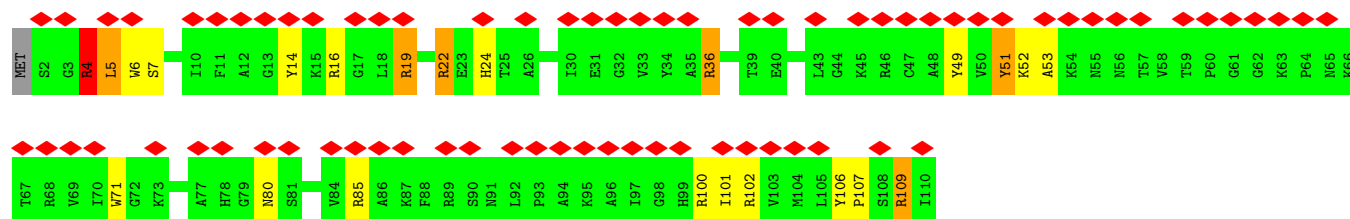
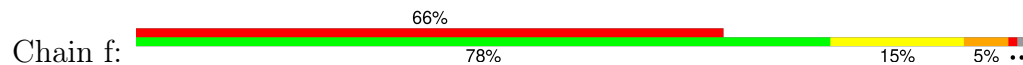
- Molecule 32: Ribosomal protein eL31



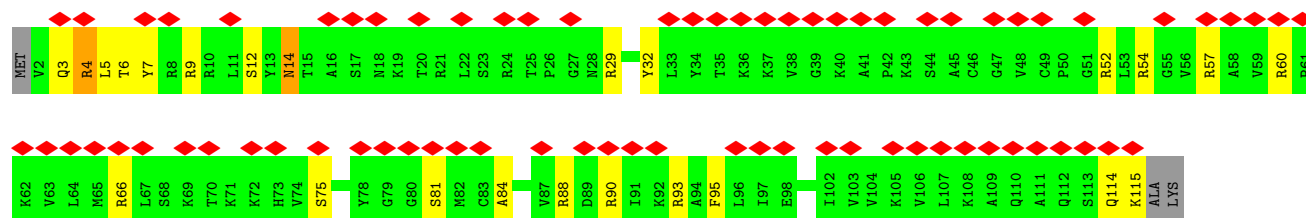
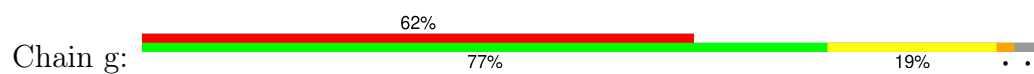
- Molecule 33: Ribosomal protein eL32



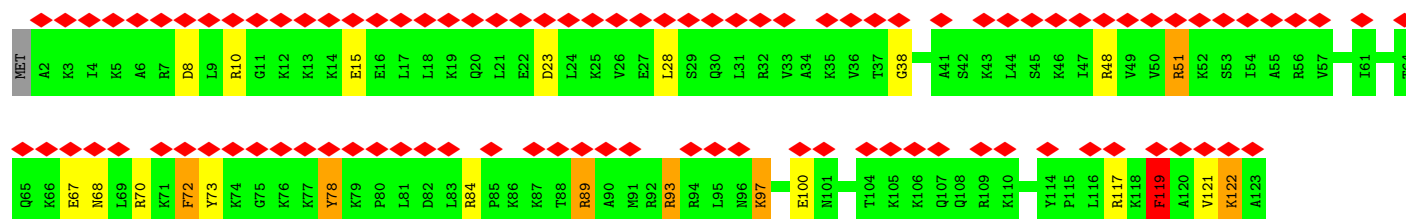
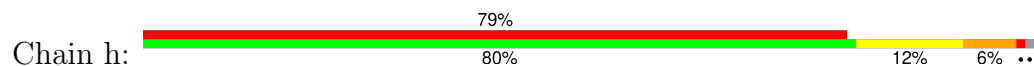
- Molecule 34: Ribosomal protein eL33



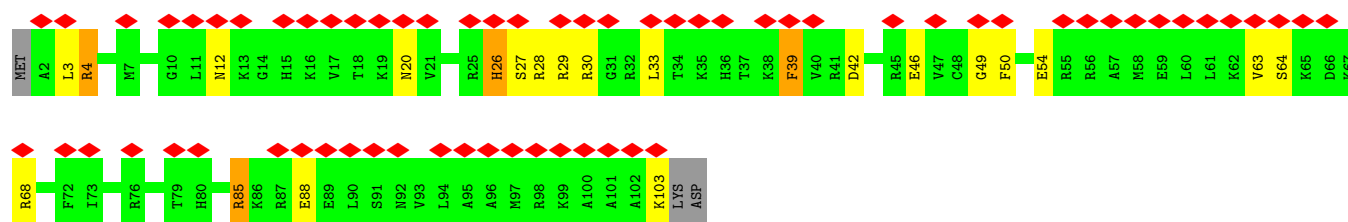
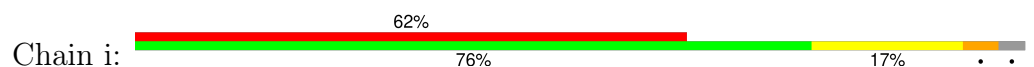
- Molecule 35: Ribosomal protein eL34



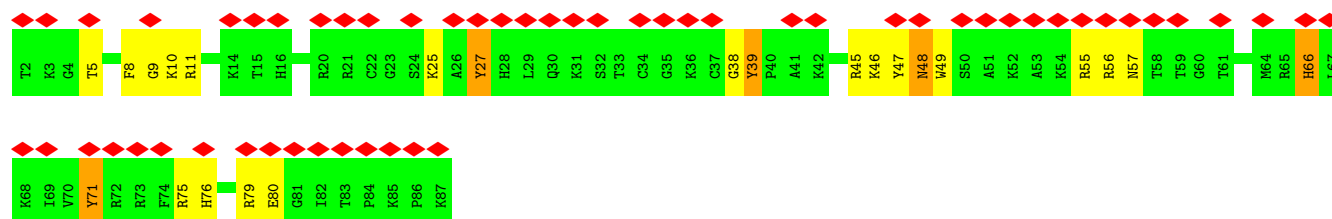
• Molecule 36: Ribosomal protein uL29



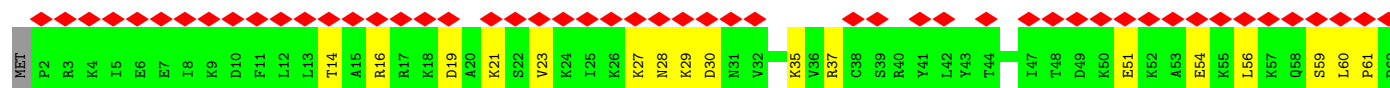
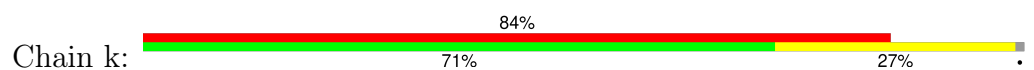
• Molecule 37: Ribosomal protein eL36

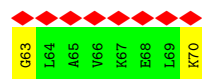


• Molecule 38: Ribosomal protein eL37

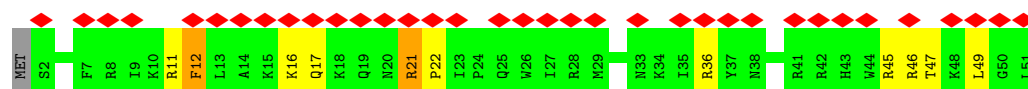
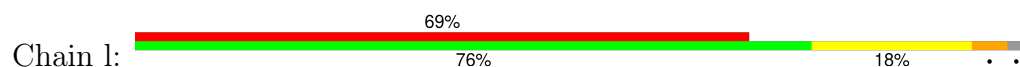


• Molecule 39: Ribosomal protein eL38

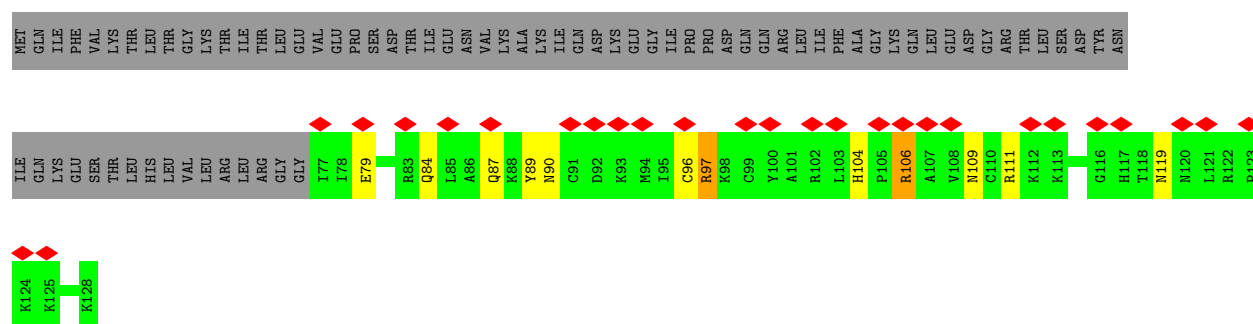




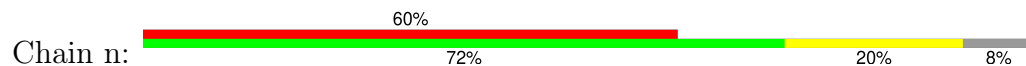
• Molecule 40: Ribosomal protein eL39



• Molecule 41: Ribosomal protein eL40



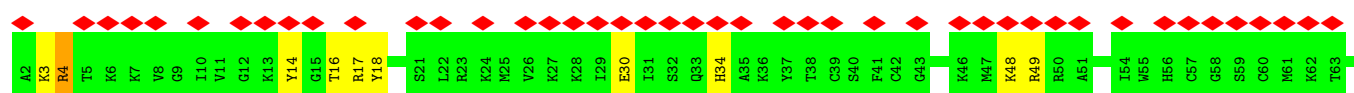
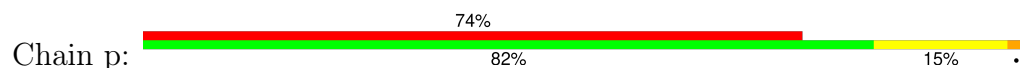
• Molecule 42: Ribosomal protein eL41

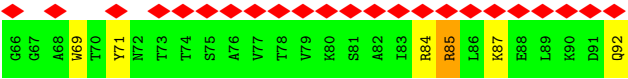


• Molecule 43: Ribosomal protein eL42

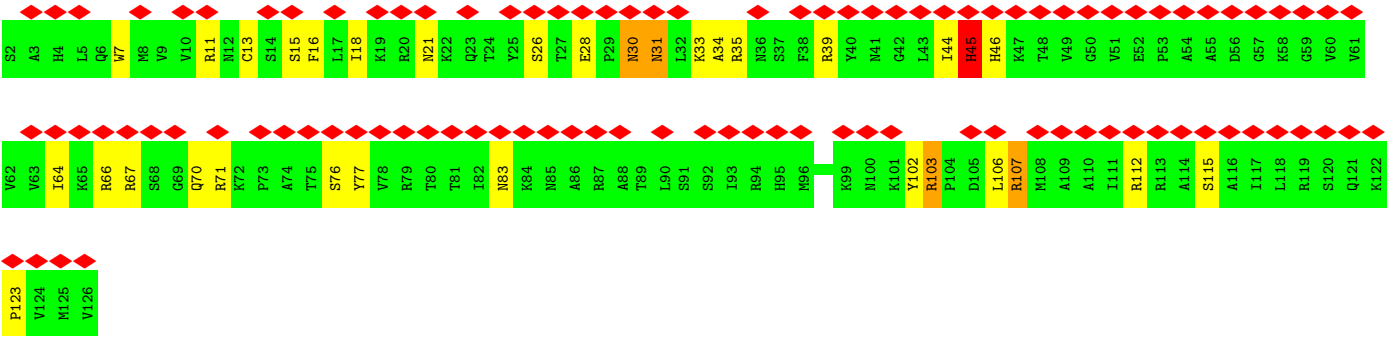
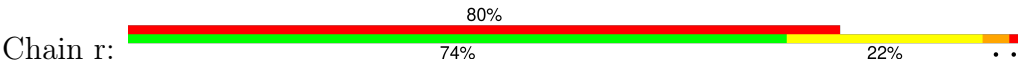


• Molecule 44: Ribosomal protein eL43





● Molecule 45: Ribosomal protein eL28



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	80019	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.933	Depositor
Minimum map value	-0.562	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.065	Depositor
Map size (\AA)	549.4, 549.4, 549.4	wwPDB
Map dimensions	410, 410, 410	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.34, 1.34, 1.34	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	5	0.64	80/87792 (0.1%)	1.13	737/136945 (0.5%)
2	7	0.53	1/2858 (0.0%)	0.96	9/4455 (0.2%)
3	8	0.68	3/3701 (0.1%)	1.19	42/5766 (0.7%)
4	A	0.80	3/1906 (0.2%)	1.26	21/2556 (0.8%)
5	B	0.81	8/3214 (0.2%)	1.16	25/4308 (0.6%)
6	C	0.73	3/2973 (0.1%)	1.12	18/3990 (0.5%)
7	D	0.73	2/2426 (0.1%)	1.23	28/3252 (0.9%)
8	E	0.73	5/1941 (0.3%)	1.21	20/2601 (0.8%)
9	F	0.80	2/1905 (0.1%)	1.27	26/2539 (1.0%)
10	G	0.76	4/1966 (0.2%)	1.09	14/2645 (0.5%)
11	H	0.77	3/1537 (0.2%)	1.17	10/2066 (0.5%)
12	I	0.66	1/1753 (0.1%)	1.11	12/2343 (0.5%)
13	J	0.63	1/1382 (0.1%)	1.04	11/1849 (0.6%)
14	L	0.70	2/1734 (0.1%)	1.12	15/2318 (0.6%)
15	M	0.76	2/1152 (0.2%)	1.11	5/1539 (0.3%)
16	N	0.84	4/1746 (0.2%)	1.33	23/2338 (1.0%)
17	O	0.72	3/1684 (0.2%)	1.11	12/2251 (0.5%)
18	P	0.74	2/1268 (0.2%)	1.10	9/1701 (0.5%)
19	Q	0.69	0/1530	1.35	31/2041 (1.5%)
20	R	0.79	3/1524 (0.2%)	1.27	20/2013 (1.0%)
21	S	0.95	8/1493 (0.5%)	1.30	20/2002 (1.0%)
22	T	0.67	1/1326 (0.1%)	1.04	7/1770 (0.4%)
23	U	0.63	1/822 (0.1%)	1.03	3/1103 (0.3%)
24	V	0.89	4/993 (0.4%)	1.11	7/1332 (0.5%)
25	W	0.71	0/541	1.23	5/720 (0.7%)
26	X	0.64	0/993	1.09	10/1334 (0.7%)
27	Y	0.72	0/1132	1.24	19/1504 (1.3%)
28	Z	0.63	0/1130	1.11	11/1507 (0.7%)
29	a	0.93	6/1192 (0.5%)	1.37	17/1591 (1.1%)
30	b	0.88	2/620 (0.3%)	1.17	5/819 (0.6%)
31	c	0.70	0/742	1.14	5/996 (0.5%)
32	d	0.84	3/903 (0.3%)	1.37	16/1216 (1.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.90	3/1071 (0.3%)	1.23	15/1429 (1.0%)
34	f	1.02	2/895 (0.2%)	1.34	17/1198 (1.4%)
35	g	0.65	0/916	1.08	5/1220 (0.4%)
36	h	0.63	0/1023	1.22	14/1350 (1.0%)
37	i	0.63	0/843	1.19	8/1115 (0.7%)
38	j	0.97	1/721 (0.1%)	1.43	11/953 (1.2%)
39	k	0.59	0/575	0.97	1/761 (0.1%)
40	l	0.70	0/454	1.14	4/599 (0.7%)
41	m	0.57	0/435	1.02	3/575 (0.5%)
42	n	0.49	0/223	1.01	0/284
43	o	0.64	0/864	1.27	9/1140 (0.8%)
44	p	0.64	1/718 (0.1%)	1.00	3/953 (0.3%)
45	r	0.68	0/1017	1.12	8/1365 (0.6%)
All	All	0.68	164/147634 (0.1%)	1.15	1311/218352 (0.6%)

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
1	5	1	155
2	7	0	2
3	8	0	11
4	A	0	6
5	B	0	13
6	C	0	5
7	D	0	8
8	E	0	12
9	F	0	5
10	G	0	3
11	H	0	3
12	I	0	5
13	J	0	2
14	L	0	5
15	M	0	4
16	N	0	11
17	O	0	3
18	P	0	1
19	Q	0	5
20	R	0	6
21	S	0	11

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
22	T	0	2
23	U	0	2
24	V	0	3
25	W	0	1
26	X	0	1
27	Y	0	4
29	a	0	9
30	b	0	1
31	c	0	2
32	d	0	4
33	e	0	4
34	f	0	2
35	g	0	1
36	h	0	3
37	i	0	3
38	j	0	4
39	k	0	1
43	o	0	6
44	p	0	1
45	r	0	5
All	All	1	335

The worst 5 of 164 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1823	G	O3'-P	41.50	2.10	1.61
10	G	109	GLU	CD-OE2	16.18	1.43	1.25
11	H	66	GLU	CD-OE1	15.80	1.43	1.25
34	f	6	TRP	CB-CG	-15.72	1.22	1.50
30	b	16	TRP	CB-CG	-13.53	1.25	1.50

The worst 5 of 1311 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	8	60	G	N9-C1'-C2'	16.18	135.03	114.00
38	j	11	ARG	NE-CZ-NH2	-13.77	113.42	120.30
19	Q	37	ARG	NE-CZ-NH2	12.86	126.73	120.30
1	5	92	C	N1-C1'-C2'	-12.64	97.57	114.00
12	I	139	ARG	CG-CD-NE	12.31	137.66	111.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	5	1992	U	C1'

5 of 335 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	22	G	Sidechain
1	5	31	U	Sidechain
1	5	42	A	Sidechain
1	5	43	U	Sidechain
1	5	53	C	Sidechain

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	
4	A	242/257 (94%)	203 (84%)	30 (12%)	9 (4%)	2	16
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	0	4
6	C	365/367 (100%)	304 (83%)	46 (13%)	15 (4%)	2	15
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	5
8	E	232/236 (98%)	150 (65%)	51 (22%)	31 (13%)	0	1
9	F	223/225 (99%)	190 (85%)	23 (10%)	10 (4%)	2	13
10	G	239/266 (90%)	200 (84%)	32 (13%)	7 (3%)	3	19
11	H	188/192 (98%)	164 (87%)	20 (11%)	4 (2%)	5	24
12	I	211/213 (99%)	168 (80%)	30 (14%)	13 (6%)	1	8
13	J	168/178 (94%)	137 (82%)	23 (14%)	8 (5%)	2	12
14	L	208/211 (99%)	172 (83%)	25 (12%)	11 (5%)	1	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	8	30
16	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	3	19
17	O	199/204 (98%)	182 (92%)	14 (7%)	3 (2%)	8	30
18	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	10	33
19	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	4	21
20	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	5	24
21	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	7	28
22	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	6	26
23	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	5	24
24	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	5	23
25	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	8	29
26	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	7	28
27	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	2	13
28	Z	133/136 (98%)	113 (85%)	16 (12%)	4 (3%)	3	19
29	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	1	10
30	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	1	10
31	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	2	14
32	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	2	15
33	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	16	44
34	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	2	12
35	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	7	27
36	h	120/123 (98%)	103 (86%)	14 (12%)	3 (2%)	4	22
37	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	6	25
38	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	2	12
39	k	67/70 (96%)	55 (82%)	7 (10%)	5 (8%)	1	5
40	l	48/51 (94%)	42 (88%)	4 (8%)	2 (4%)	2	14
41	m	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
42	n	21/25 (84%)	21 (100%)	0	0	100	100
43	o	102/106 (96%)	85 (83%)	11 (11%)	6 (6%)	1	8
44	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	12	37
45	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	2	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	6371/7060 (90%)	5341 (84%)	764 (12%)	266 (4%)	4	14

5 of 266 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	19	HIS
4	A	197	PRO
5	B	16	PHE
5	B	40	PRO
5	B	108	GLU

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	
4	A	187/199 (94%)	139 (74%)	48 (26%)	0	1
5	B	335/335 (100%)	265 (79%)	70 (21%)	1	2
6	C	305/305 (100%)	239 (78%)	66 (22%)	1	2
7	D	246/250 (98%)	178 (72%)	68 (28%)	0	1
8	E	209/209 (100%)	158 (76%)	51 (24%)	0	1
9	F	194/194 (100%)	145 (75%)	49 (25%)	0	1
10	G	206/226 (91%)	158 (77%)	48 (23%)	0	2
11	H	169/171 (99%)	125 (74%)	44 (26%)	0	1
12	I	180/180 (100%)	136 (76%)	44 (24%)	0	1
13	J	143/149 (96%)	115 (80%)	28 (20%)	1	3
14	L	176/177 (99%)	135 (77%)	41 (23%)	0	2
15	M	116/160 (72%)	95 (82%)	21 (18%)	1	5
16	N	171/172 (99%)	129 (75%)	42 (25%)	0	1
17	O	172/174 (99%)	146 (85%)	26 (15%)	2	9
18	P	134/134 (100%)	112 (84%)	22 (16%)	2	7
19	Q	163/164 (99%)	132 (81%)	31 (19%)	1	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	R	159/175 (91%)	120 (76%)	39 (24%)	0	1
21	S	156/192 (81%)	121 (78%)	35 (22%)	1	2
22	T	139/140 (99%)	112 (81%)	27 (19%)	1	3
23	U	89/114 (78%)	67 (75%)	22 (25%)	0	1
24	V	101/107 (94%)	77 (76%)	24 (24%)	0	1
25	W	55/126 (44%)	42 (76%)	13 (24%)	0	1
26	X	107/133 (80%)	89 (83%)	18 (17%)	1	7
27	Y	124/135 (92%)	96 (77%)	28 (23%)	1	2
28	Z	117/118 (99%)	94 (80%)	23 (20%)	1	3
29	a	119/120 (99%)	102 (86%)	17 (14%)	2	10
30	b	63/123 (51%)	45 (71%)	18 (29%)	0	1
31	c	79/97 (81%)	60 (76%)	19 (24%)	0	1
32	d	98/110 (89%)	66 (67%)	32 (33%)	0	0
33	e	114/121 (94%)	89 (78%)	25 (22%)	1	2
34	f	88/89 (99%)	73 (83%)	15 (17%)	1	6
35	g	98/100 (98%)	79 (81%)	19 (19%)	1	3
36	h	109/110 (99%)	92 (84%)	17 (16%)	2	8
37	i	86/89 (97%)	71 (83%)	15 (17%)	1	6
38	j	73/73 (100%)	60 (82%)	13 (18%)	1	5
39	k	64/65 (98%)	52 (81%)	12 (19%)	1	4
40	l	47/48 (98%)	39 (83%)	8 (17%)	1	6
41	m	48/116 (41%)	36 (75%)	12 (25%)	0	1
42	n	22/24 (92%)	17 (77%)	5 (23%)	0	2
43	o	92/94 (98%)	70 (76%)	22 (24%)	0	1
44	p	74/74 (100%)	61 (82%)	13 (18%)	1	6
45	r	109/109 (100%)	86 (79%)	23 (21%)	1	2
All	All	5536/6001 (92%)	4323 (78%)	1213 (22%)	2	2

5 of 1213 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	Z	122	TYR
41	m	106	ARG

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Mol	Chain	Res	Type
30	b	25	ARG
28	Z	121	ARG
34	f	5	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 176 such sidechains are listed below:

Mol	Chain	Res	Type
23	U	55	ASN
32	d	100	ASN
26	X	93	ASN
29	a	67	GLN
34	f	80	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3647/3664 (99%)	1612 (44%)	629 (17%)
2	7	119/120 (99%)	31 (26%)	9 (7%)
3	8	155/156 (99%)	61 (39%)	22 (14%)
All	All	3921/3940 (99%)	1704 (43%)	660 (16%)

5 of 1704 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	5	A
1	5	6	C
1	5	8	U
1	5	12	A

5 of 660 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	3860	A
1	5	4645	C
1	5	4084	G
1	5	3856	A
1	5	4287	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 133 ligands modelled in this entry, 133 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	13
8	E	1

The worst 5 of 14 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	72:ALA	C	84:VAL	N	23.51
1	5	4776:G	O3'	4859:C	P	17.87
1	5	757:G	O3'	906:C	P	16.89
1	5	519:C	O3'	642:G	P	16.61
1	5	2910:G	O3'	3583:U	P	16.04

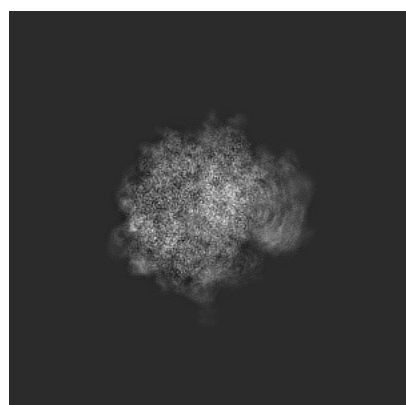
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2649. These allow visual inspection of the internal detail of the map and identification of artifacts.

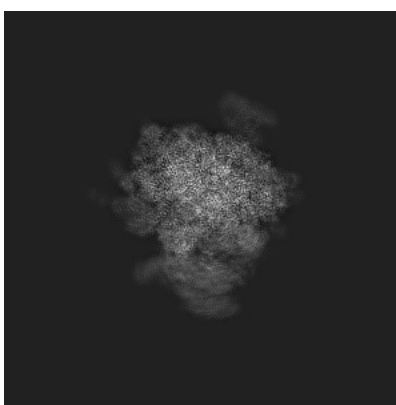
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

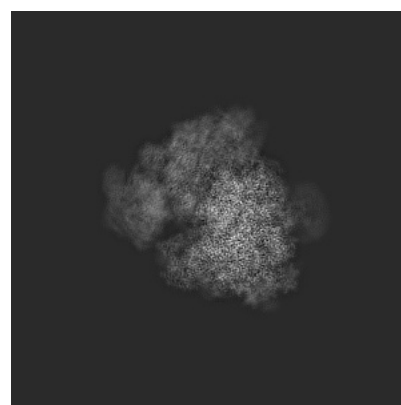
6.1.1 Primary map



X



Y

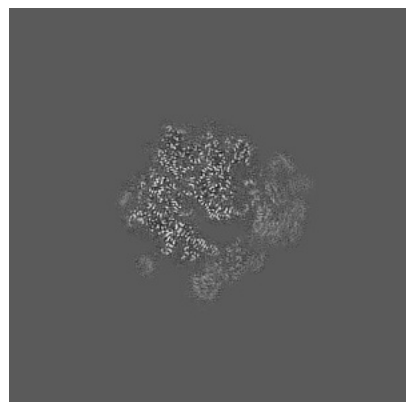


Z

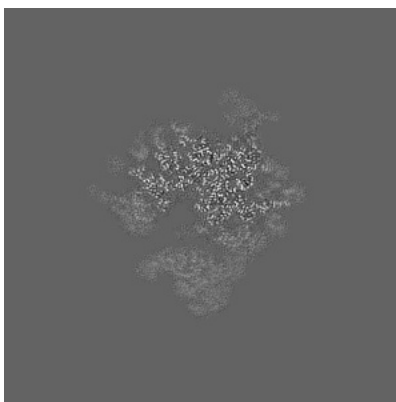
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

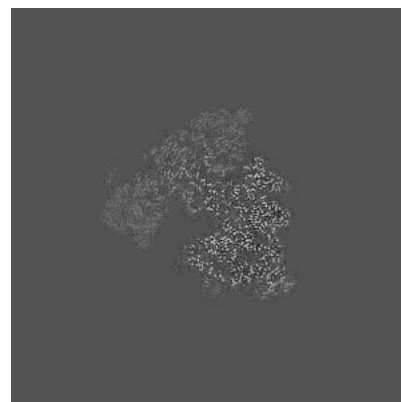
6.2.1 Primary map



X Index: 205



Y Index: 205

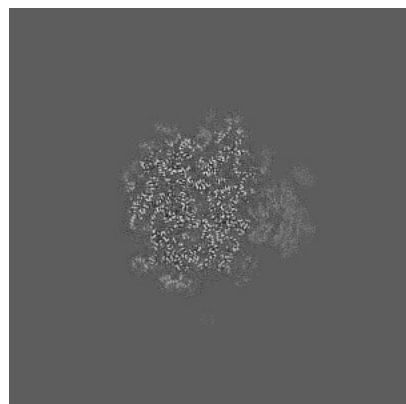


Z Index: 205

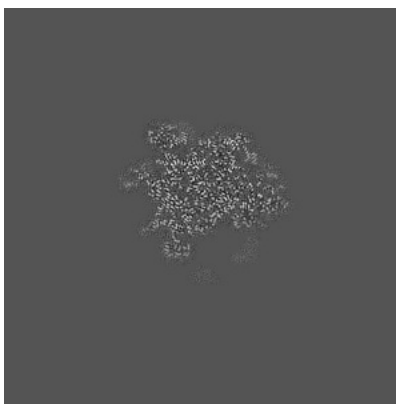
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

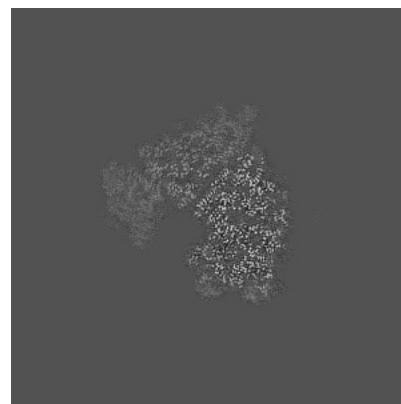
6.3.1 Primary map



X Index: 228



Y Index: 162

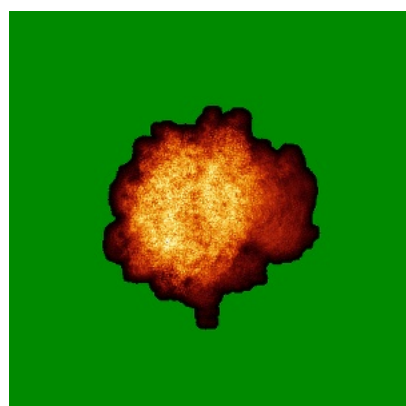


Z Index: 216

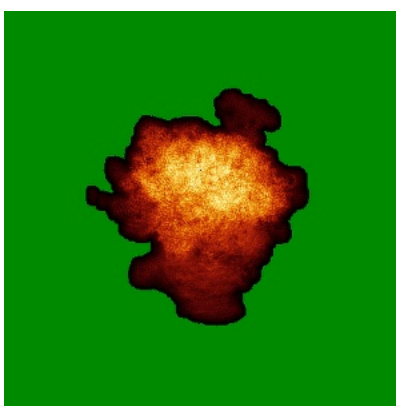
The images above show the largest variance slices of the map in three orthogonal directions.

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

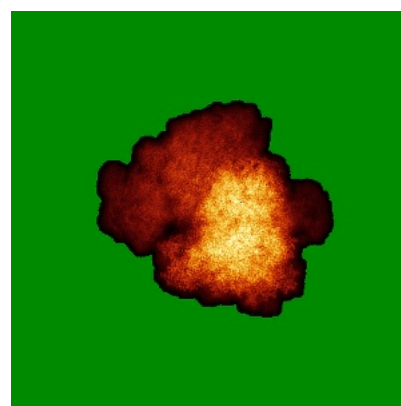
6.4.1 Primary map



X



Y

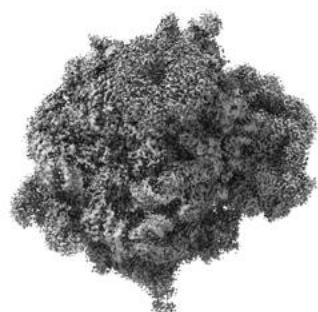


Z

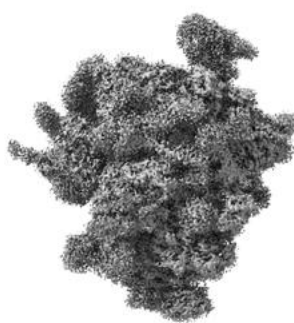
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

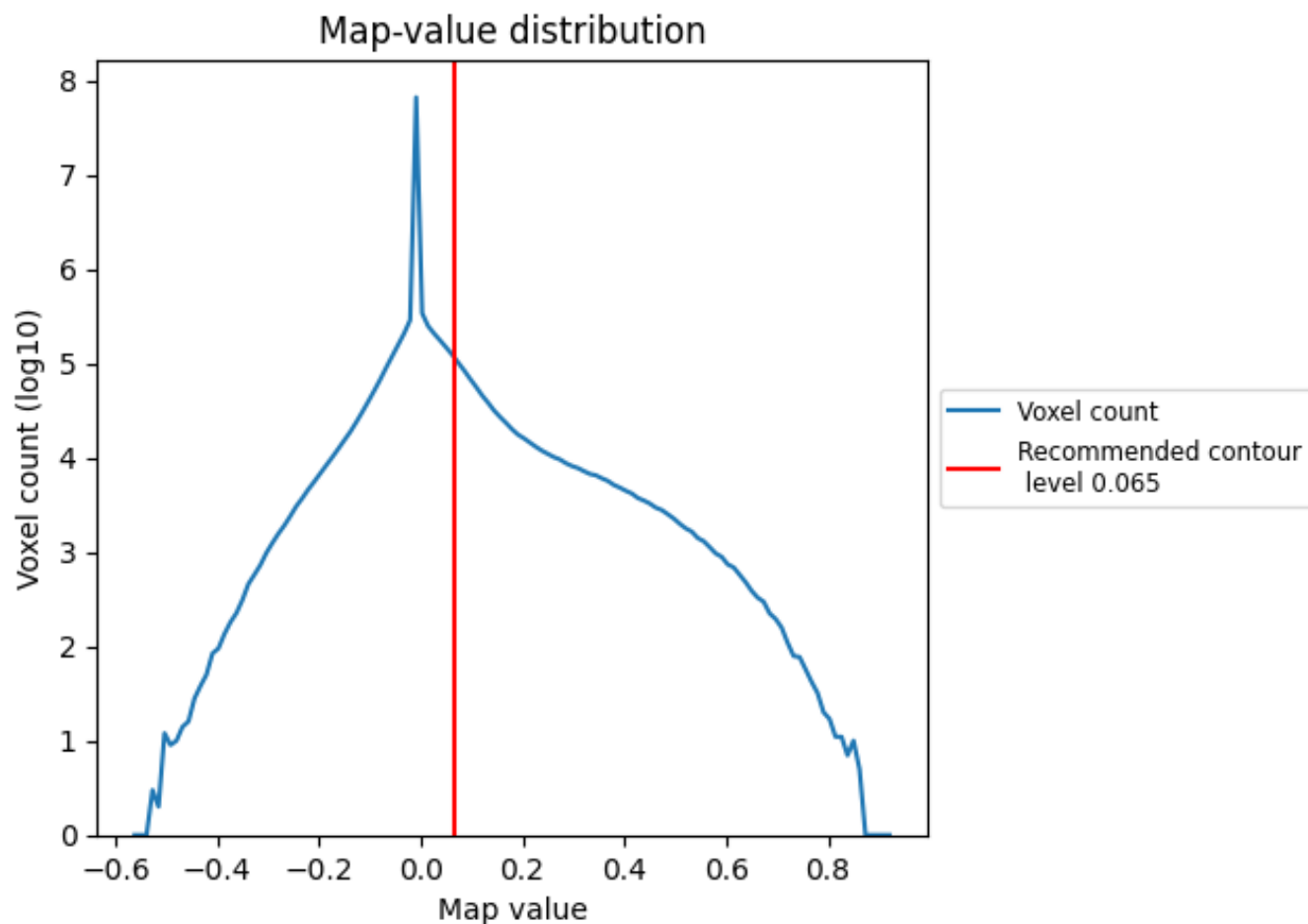
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

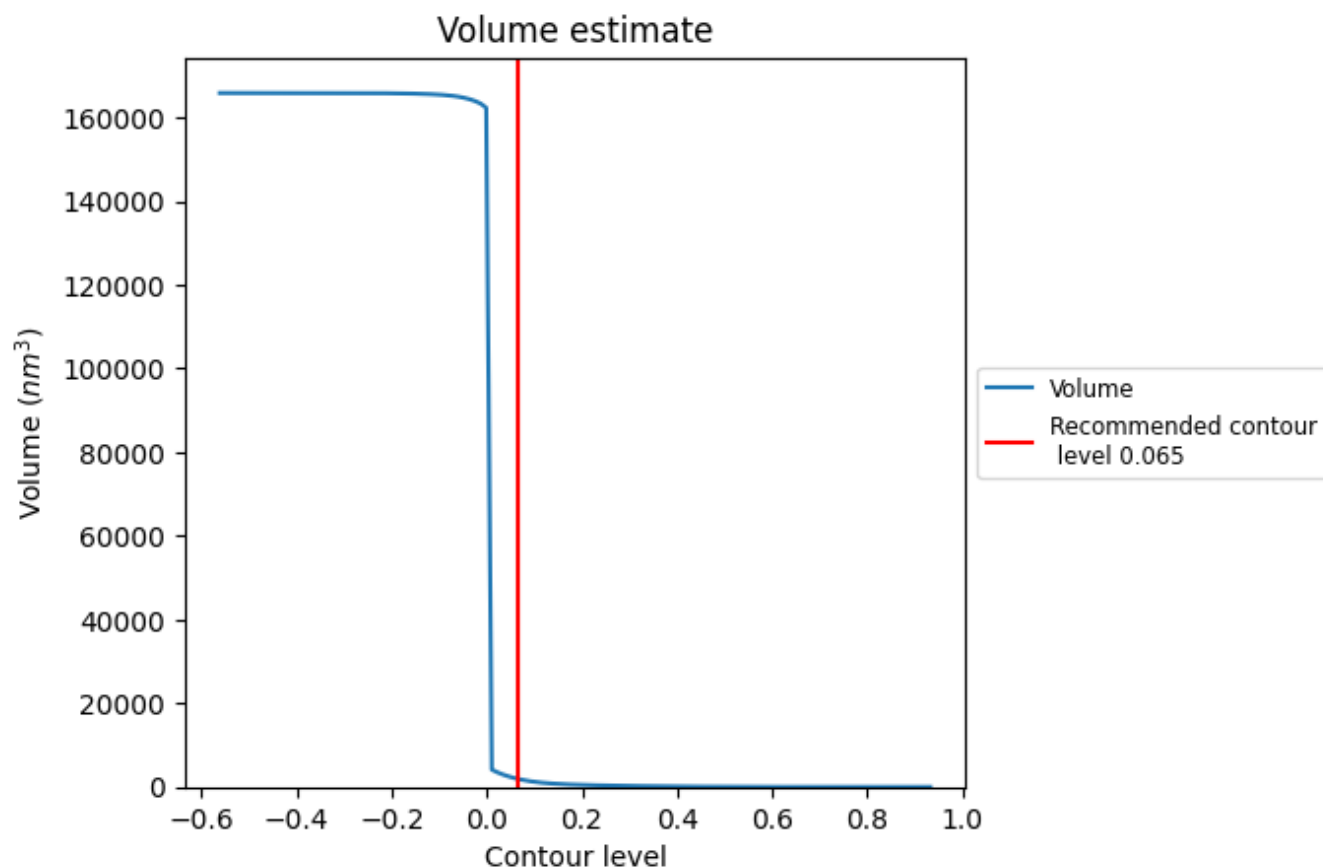
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

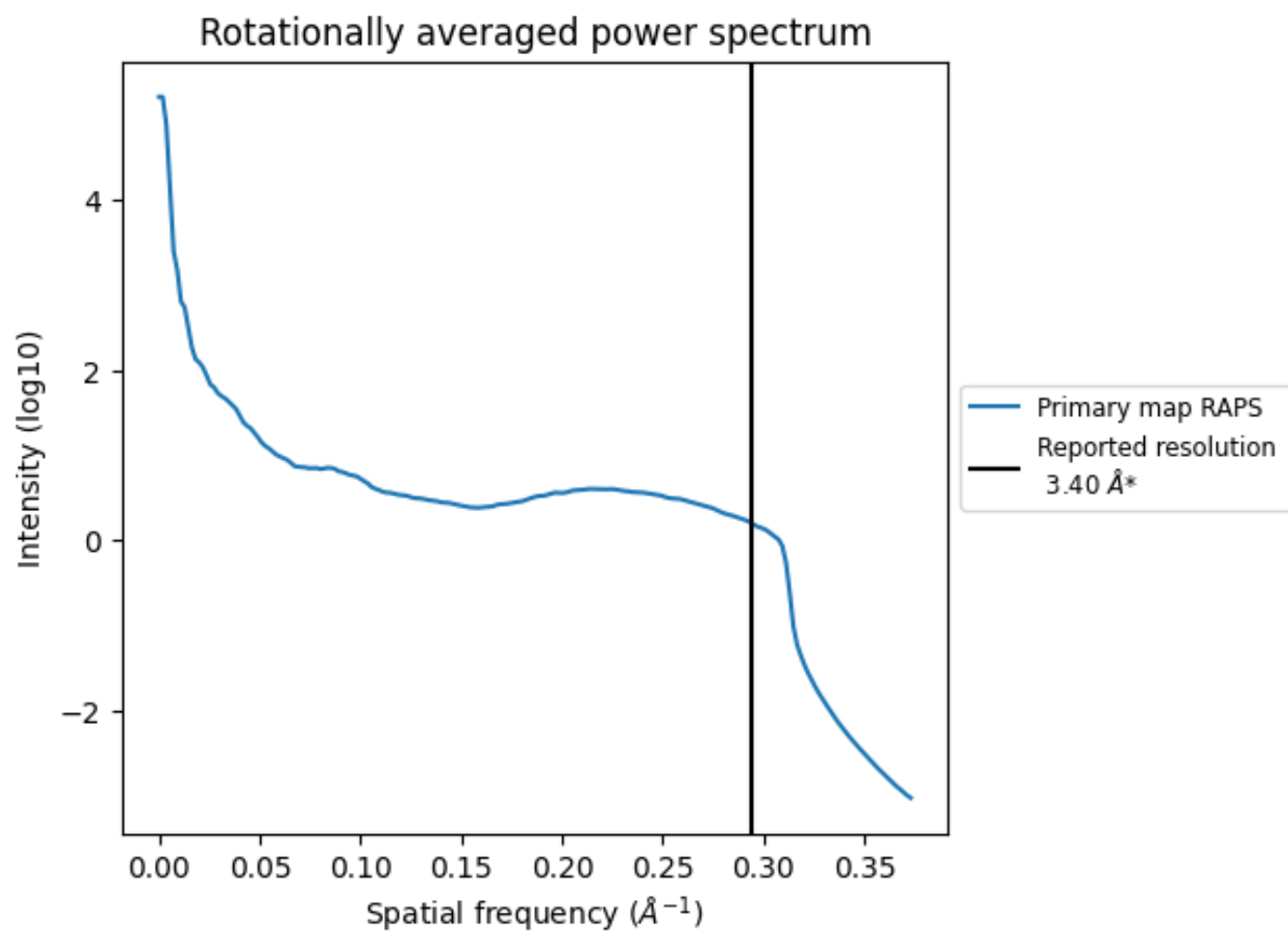
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1930 nm³; this corresponds to an approximate mass of 1743 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 0.294 Å⁻¹

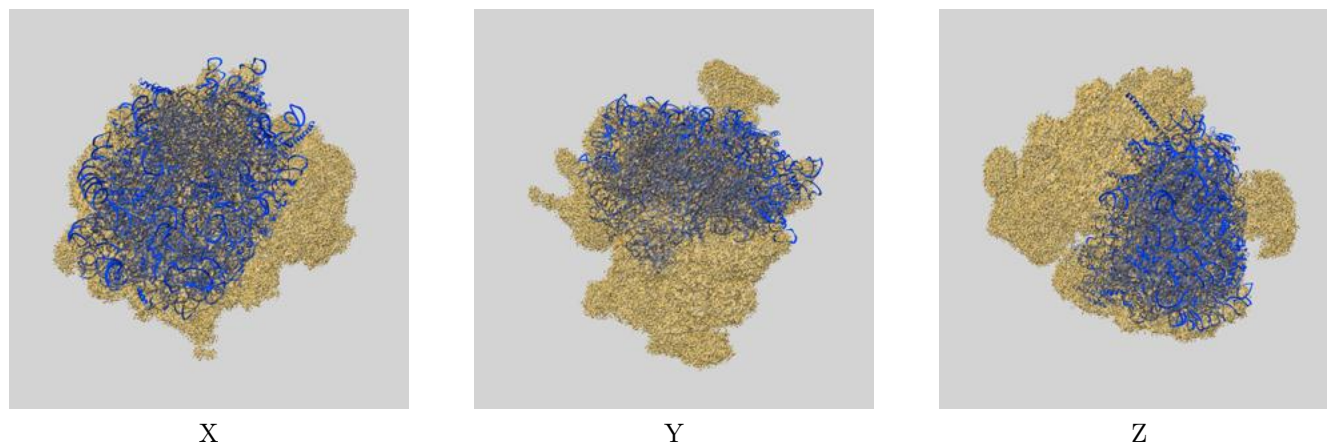
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

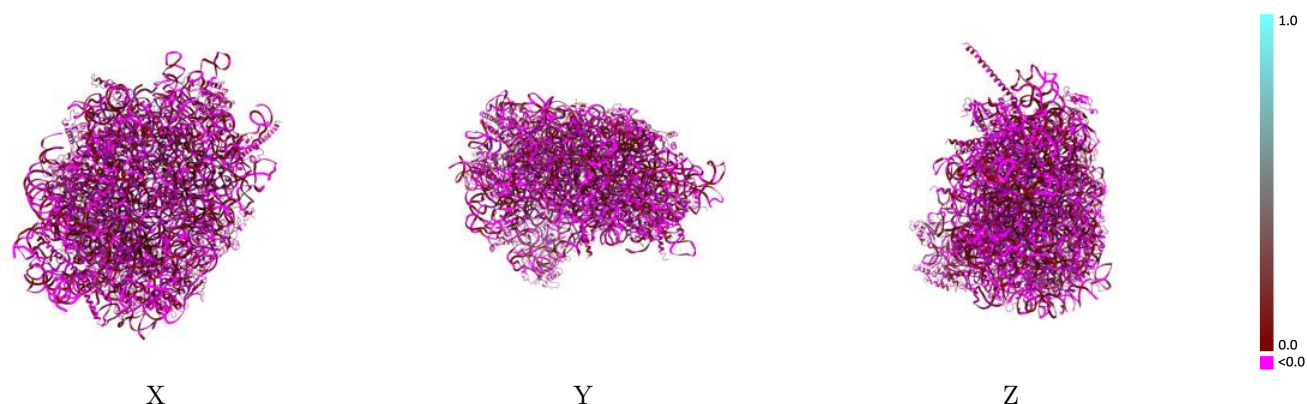
This section contains information regarding the fit between EMDB map EMD-2649 and PDB model 3J7O. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



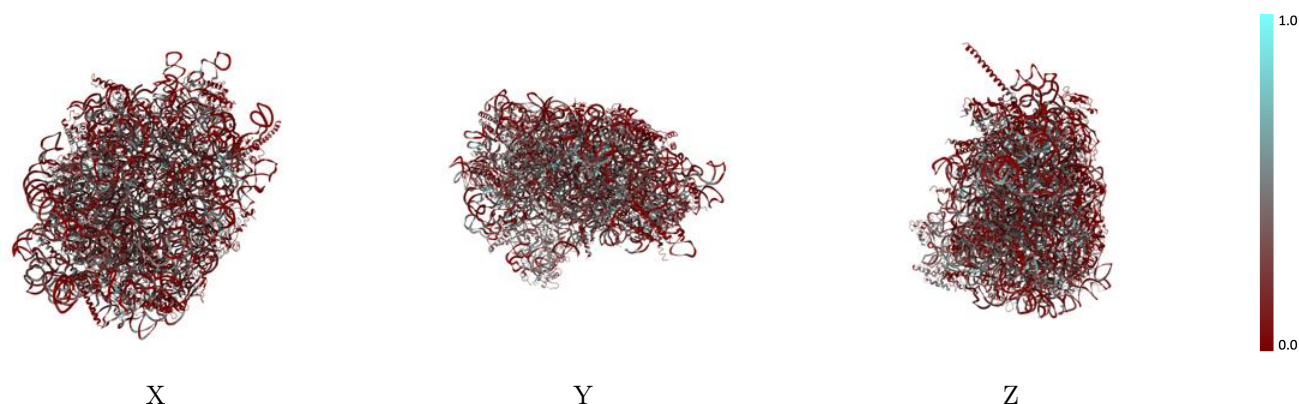
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



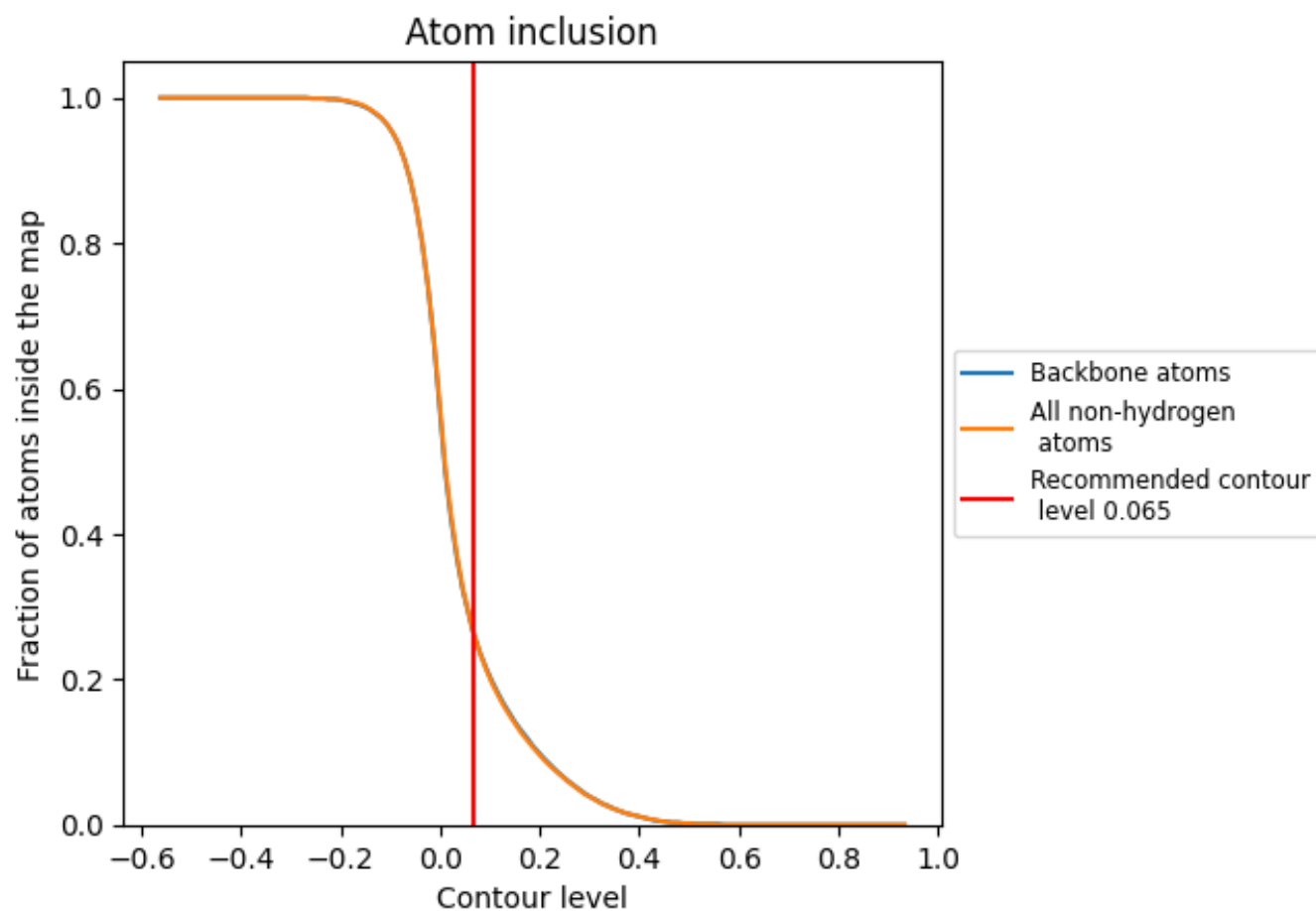
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.065).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 27% of all backbone atoms, 27% 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 (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2680	 -0.0180
5	 0.2710	 -0.0170
7	 0.3270	 -0.0110
8	 0.2350	 -0.0150
A	 0.3340	 -0.0290
B	 0.2520	 -0.0310
C	 0.3020	 -0.0240
D	 0.3080	 -0.0100
E	 0.2670	 -0.0330
F	 0.2950	 -0.0510
G	 0.2280	 -0.0110
H	 0.1740	 -0.0300
I	 0.3030	 -0.0230
J	 0.2820	 -0.0140
L	 0.2410	 -0.0100
M	 0.2610	 -0.0370
N	 0.3020	 -0.0090
O	 0.2630	 -0.0130
P	 0.2390	 -0.0130
Q	 0.3200	 -0.0230
R	 0.2100	 -0.0030
S	 0.3370	 -0.0150
T	 0.3170	 -0.0300
U	 0.1290	 -0.0120
V	 0.2640	 -0.0050
W	 0.2460	 -0.0290
X	 0.1520	 -0.0110
Y	 0.1590	 -0.0050
Z	 0.2090	 -0.0260
a	 0.3360	 -0.0120
b	 0.2070	 -0.0440
c	 0.2450	 -0.0010
d	 0.1380	 -0.0100
e	 0.2590	 -0.0370
f	 0.3140	 -0.0170



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Chain	Atom inclusion	Q-score
g	 0.3230	 -0.0210
h	 0.1840	 0.0010
i	 0.3150	 -0.0090
j	 0.3070	 -0.0070
k	 0.1180	 -0.0100
l	 0.2950	 -0.0110
m	 0.3890	 -0.0320
n	 0.2980	 -0.0330
o	 0.2410	 -0.0050
p	 0.2330	 -0.0090
r	 0.2130	 -0.0170