



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 12:05 PM UTC

PDB ID : 7PIB / pdb_00007pib
EMDB ID : EMD-13435
Title : 70S ribosome with EF-G, A/P- and P/E-site tRNAs in spectinomycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-19
Resolution : 4.70 Å (reported)
Based on initial models : 4V7D, 7OOC, 4V7C, 7OOD

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

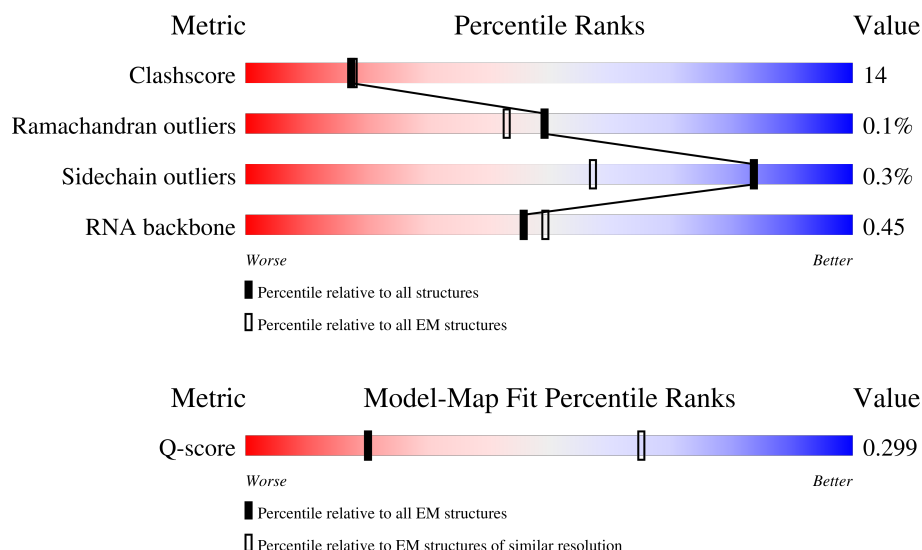
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 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	1989 (4.20 - 5.20)

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	 10% 71% 27%
2	1	59	 16% 81% 19%
3	2	37	 16% 51% 49%

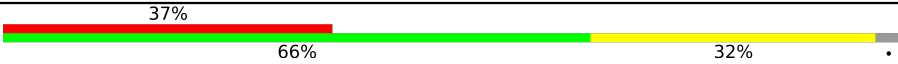
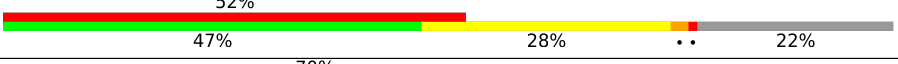
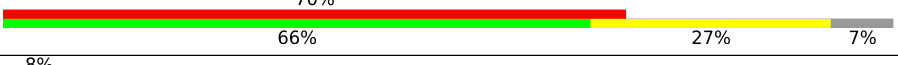
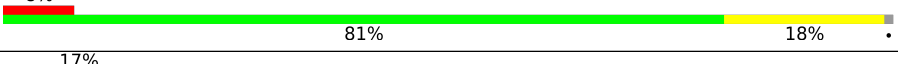
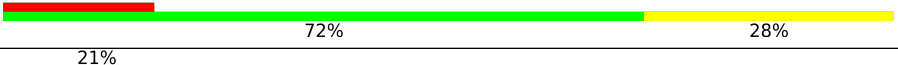
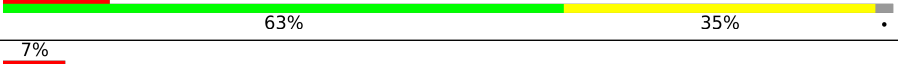
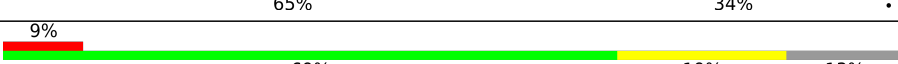
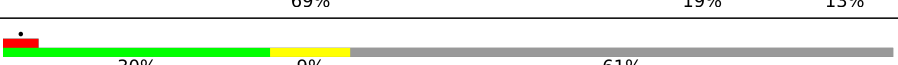
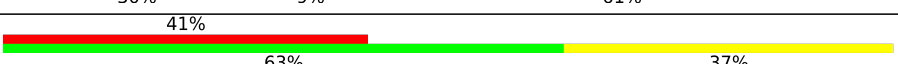
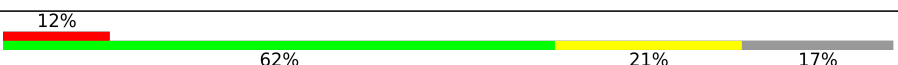
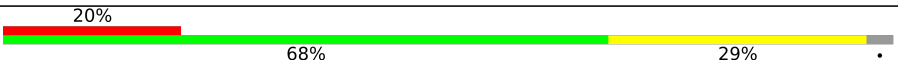
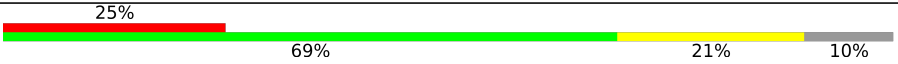
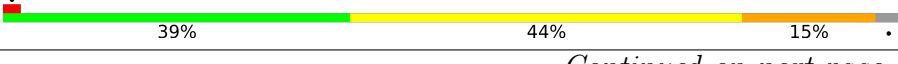
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Mol	Chain	Length	Quality of chain
4	9	688	
5	A	294	
6	B	273	
7	C	205	
8	D	219	
9	E	215	
10	F	155	
11	G	142	
12	H	132	
13	I	108	
14	J	121	
15	K	139	
16	L	124	
17	M	61	
18	N	86	
19	O	94	
20	P	85	
21	Q	104	
22	R	87	
23	S	87	
24	T	60	
25	W	122	
26	a	287	
27	b	287	
28	c	212	

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Mol	Chain	Length	Quality of chain
29	d	180	
30	e	184	
31	f	149	
32	g	161	
33	h	137	
34	i	146	
35	j	122	
36	k	151	
37	l	139	
38	m	124	
39	n	116	
40	o	119	
41	p	127	
42	q	100	
43	r	159	
44	s	237	
45	t	111	
46	u	104	
47	v	65	
48	w	111	
49	x	97	
50	y	57	
51	z	53	
52	3	2907	
53	4	108	

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Mol	Chain	Length	Quality of chain
54	5	1520	33% 53% 12%
55	7	76	34% 50% 16%
55	8	76	13% 30% 61% 8%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 152025 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L34.

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

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

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

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

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

- Molecule 4 is a protein called Elongation factor G.

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
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
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
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
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
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
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
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		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		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		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
			1182	763	206	210	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
35	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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		

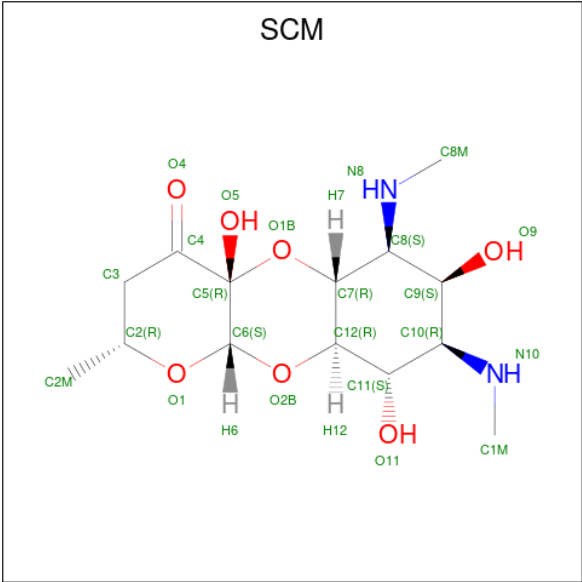
- Molecule 54 is a RNA chain called 16S ribosomal RNA.

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		

- Molecule 56 is SPECTINOMYCIN (CCD ID: SCM) (formula: $C_{14}H_{24}N_2O_7$) (labeled as "Ligand of Interest" by depositor).

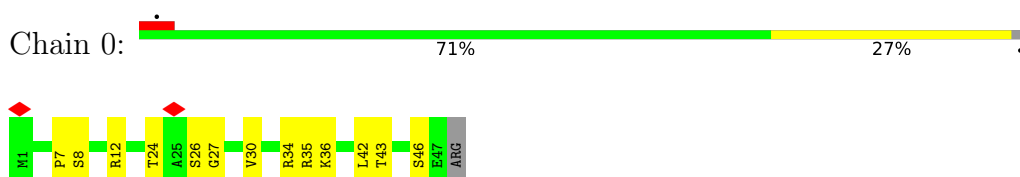


Mol	Chain	Residues	Atoms				AltConf
56	5	1	Total	C	N	O	0
			23	14	2	7	

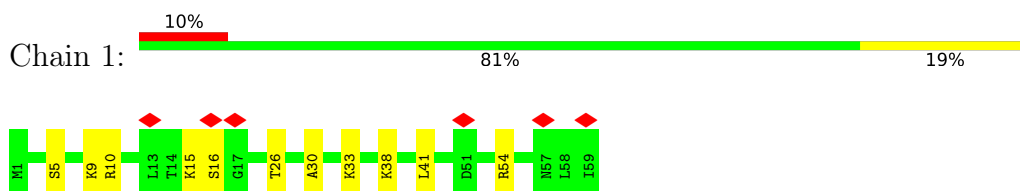
3 Residue-property plots

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

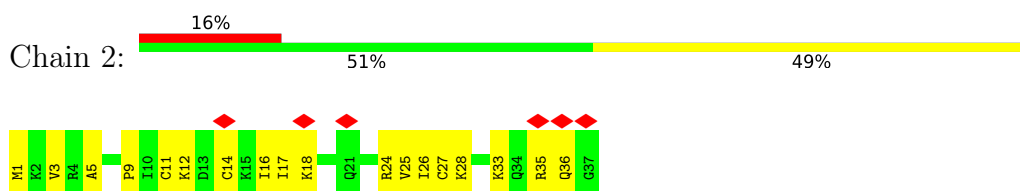
- Molecule 1: 50S ribosomal protein L34



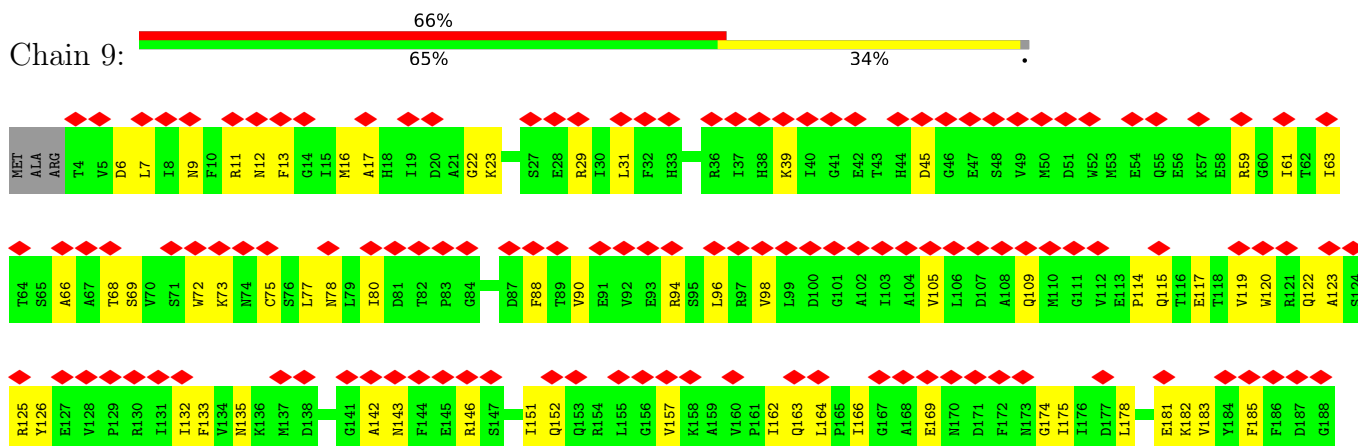
- Molecule 2: 50S ribosomal protein L35

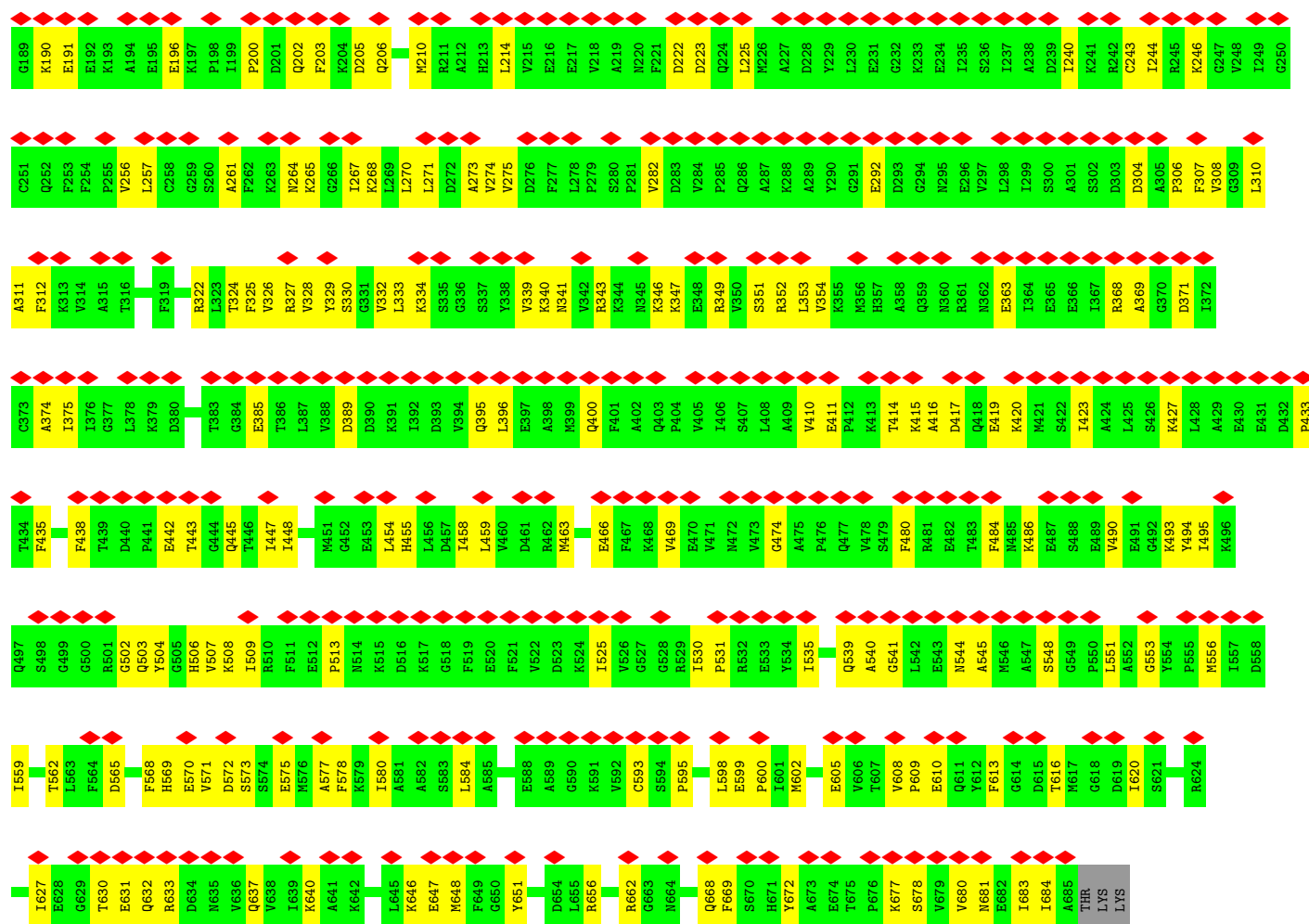


- Molecule 3: 50S ribosomal protein L36

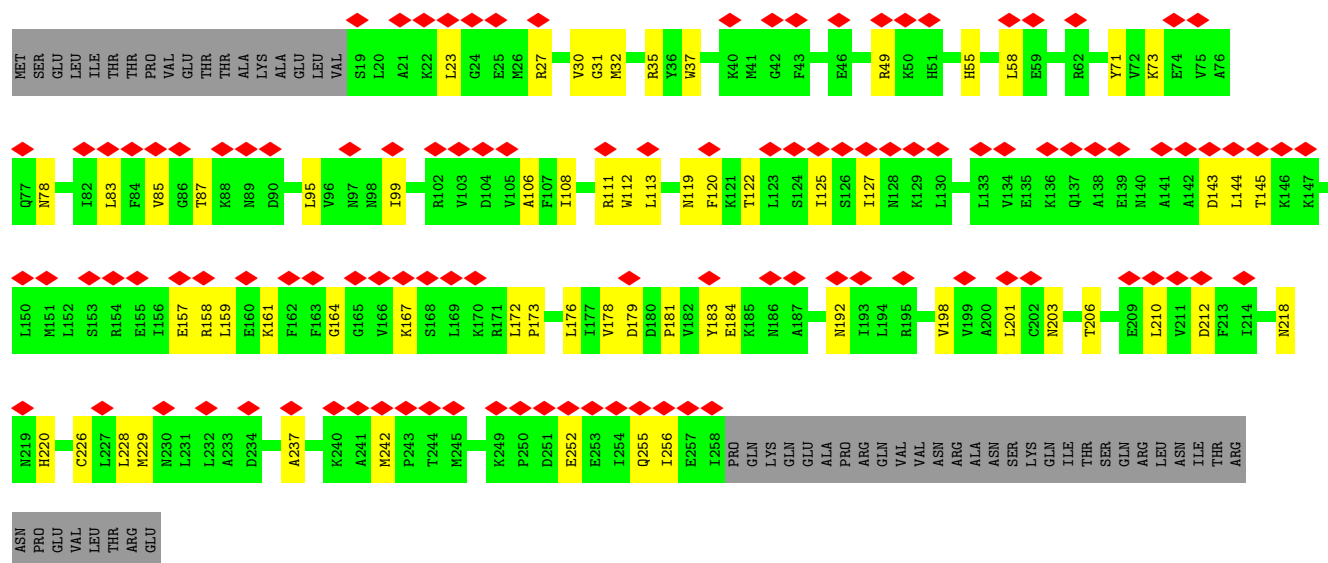


- Molecule 4: Elongation factor G

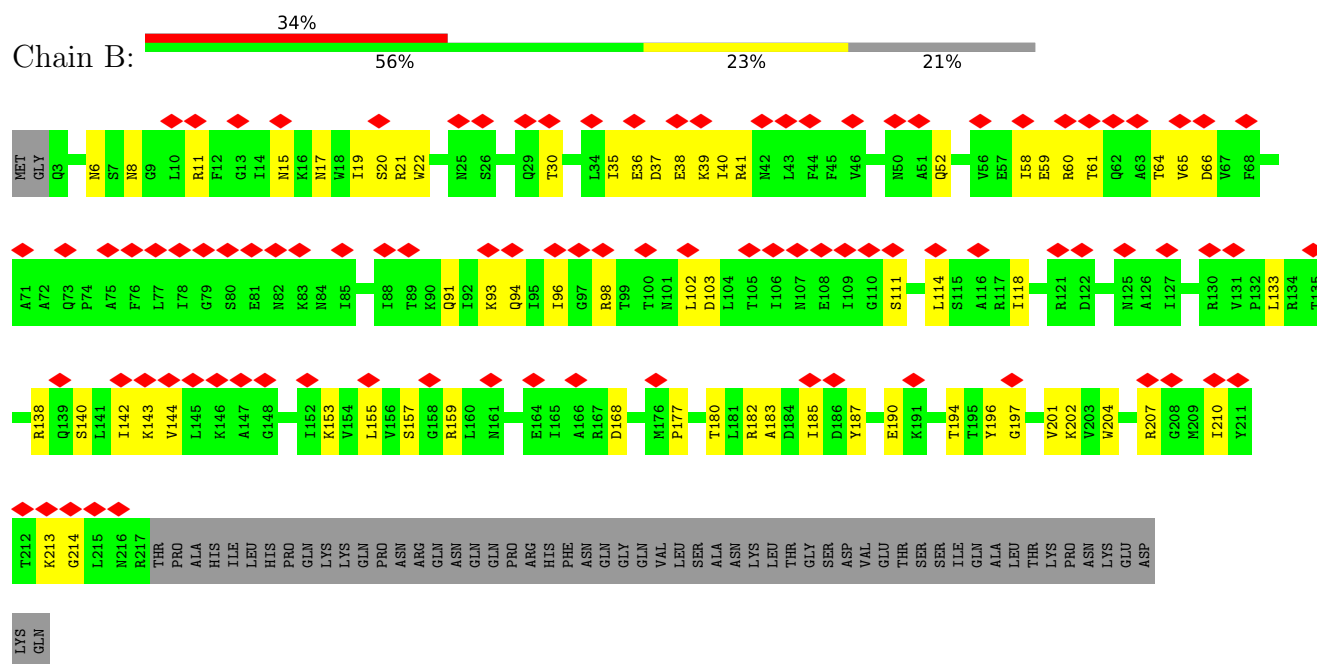




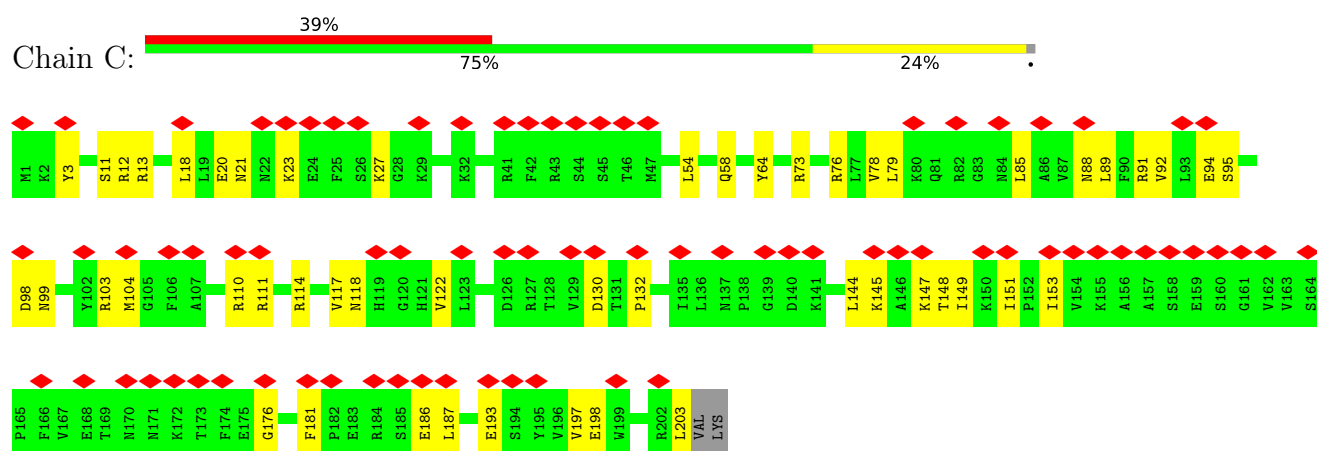
• Molecule 5: 30S ribosomal protein S2



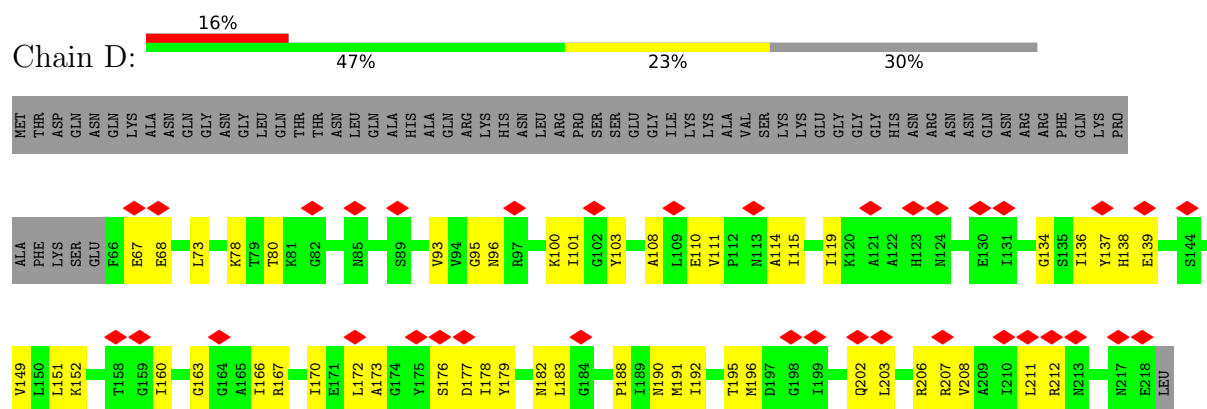
- Molecule 6: 30S ribosomal protein S3



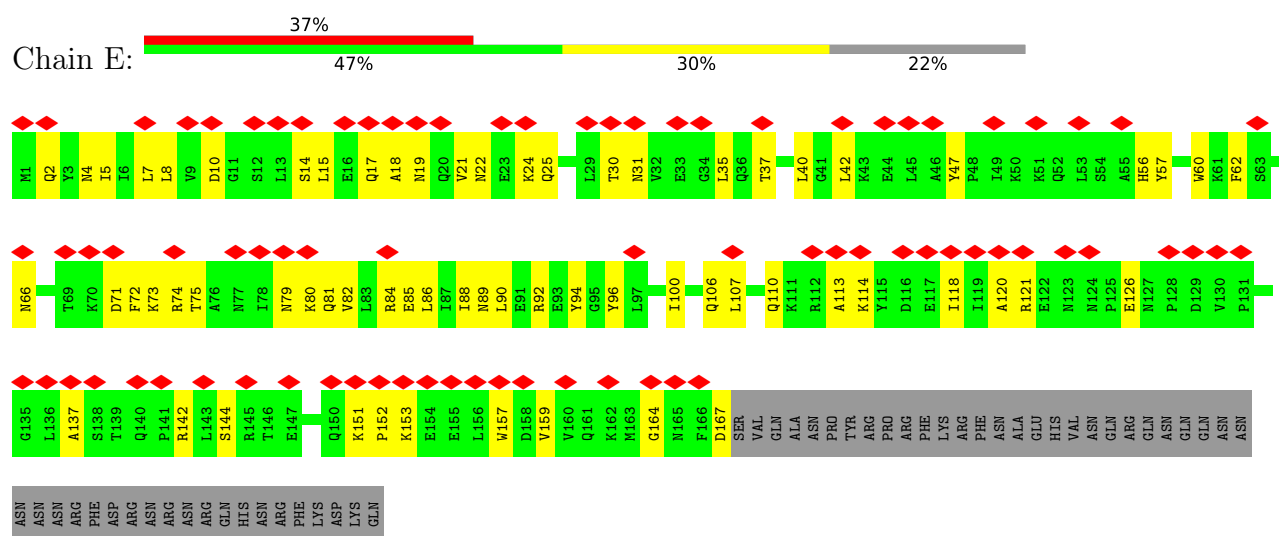
- Molecule 7: 30S ribosomal protein S4



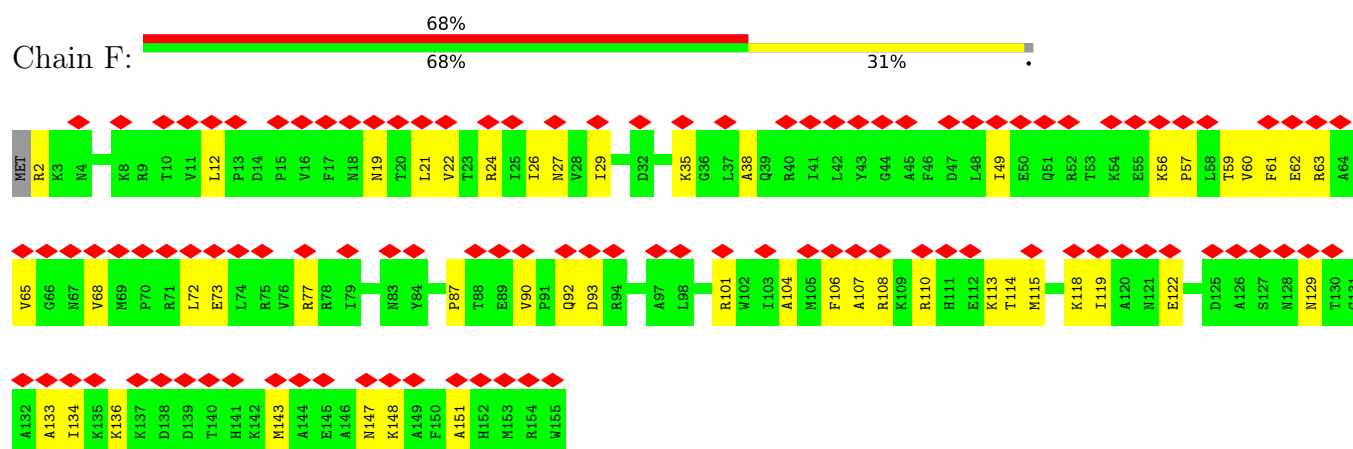
- Molecule 8: 30S ribosomal protein S5



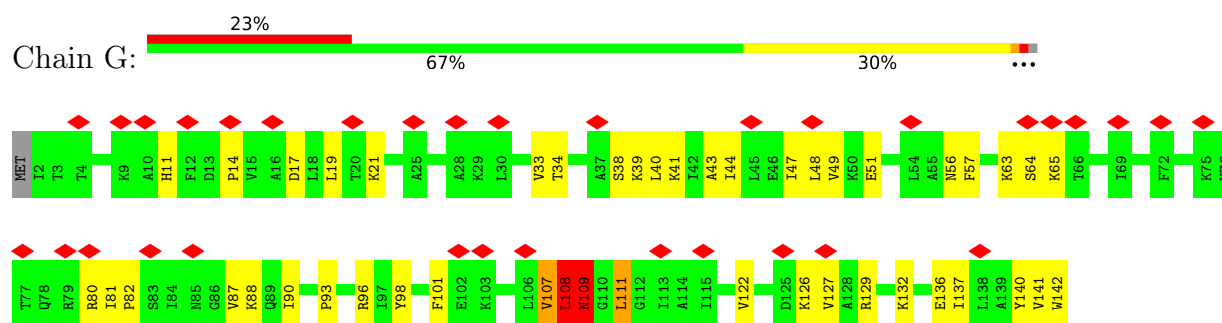
- Molecule 9: 30S ribosomal protein S6



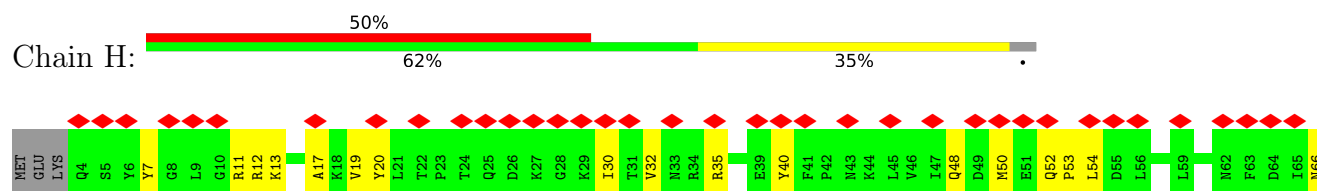
- Molecule 10: 30S ribosomal protein S7

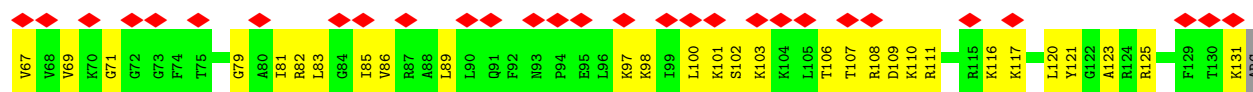


- Molecule 11: 30S ribosomal protein S8

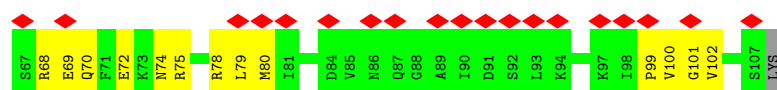
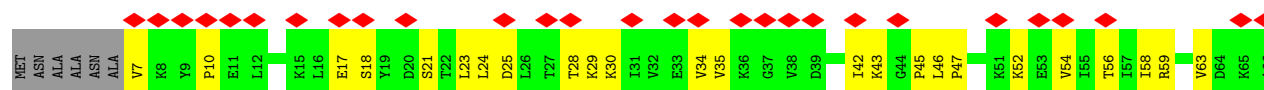
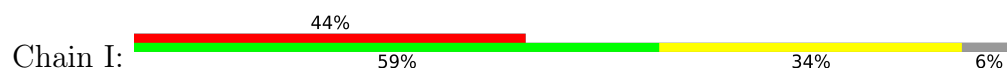


- Molecule 12: 30S ribosomal protein S9

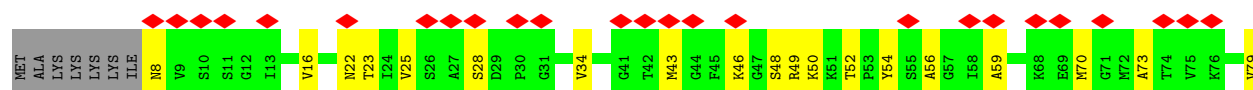




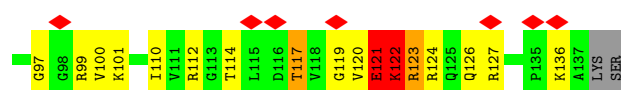
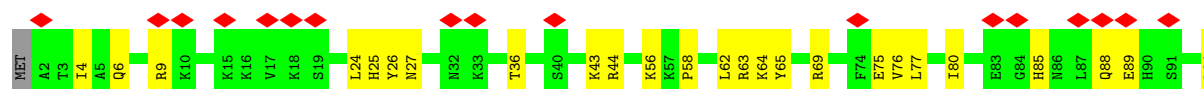
• Molecule 13: 30S ribosomal protein S10



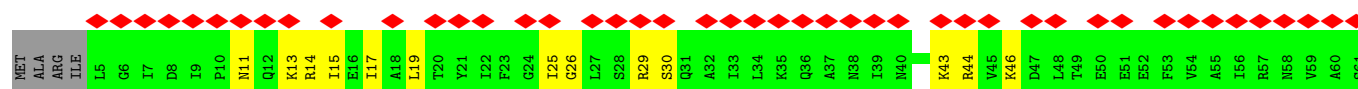
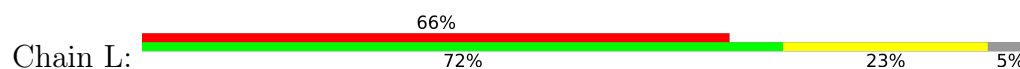
• Molecule 14: 30S ribosomal protein S11



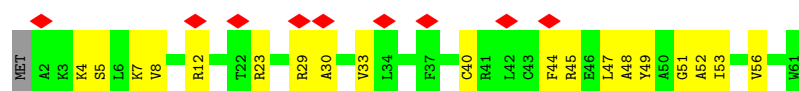
• Molecule 15: 30S ribosomal protein S12



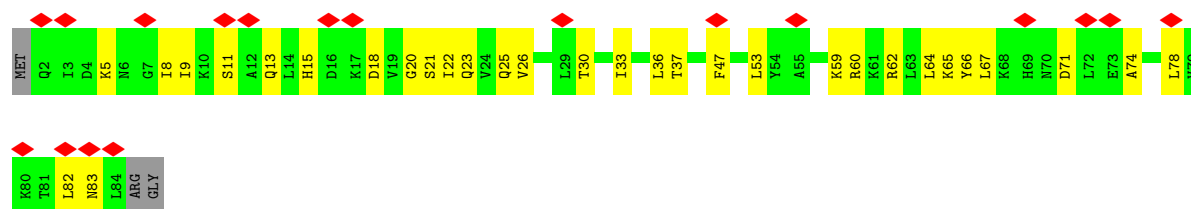
• Molecule 16: 30S ribosomal protein S13



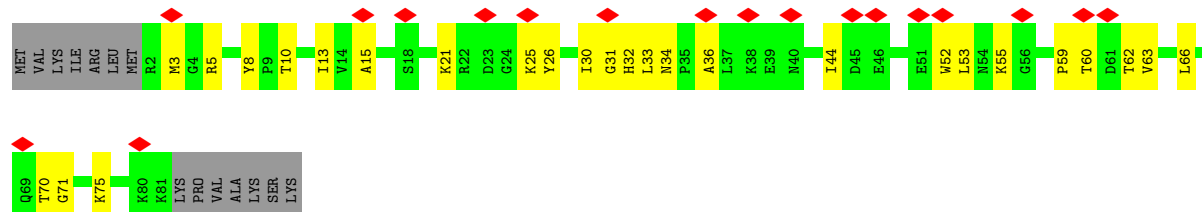
• Molecule 17: 30S ribosomal protein S14 type Z



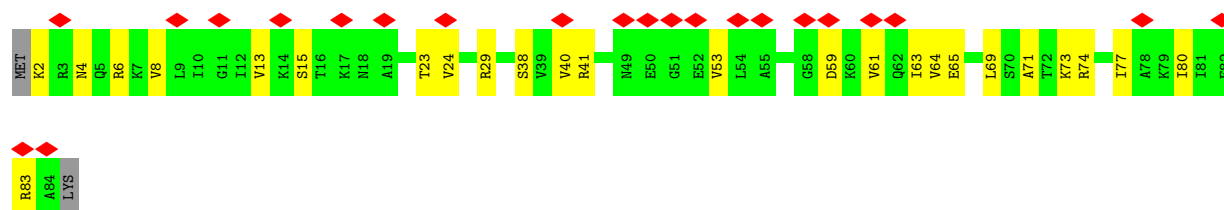
- Molecule 18: 30S ribosomal protein S15



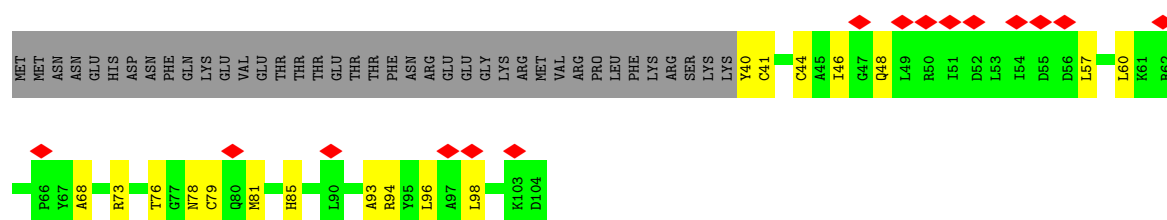
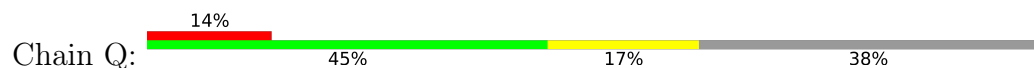
- Molecule 19: 30S ribosomal protein S16



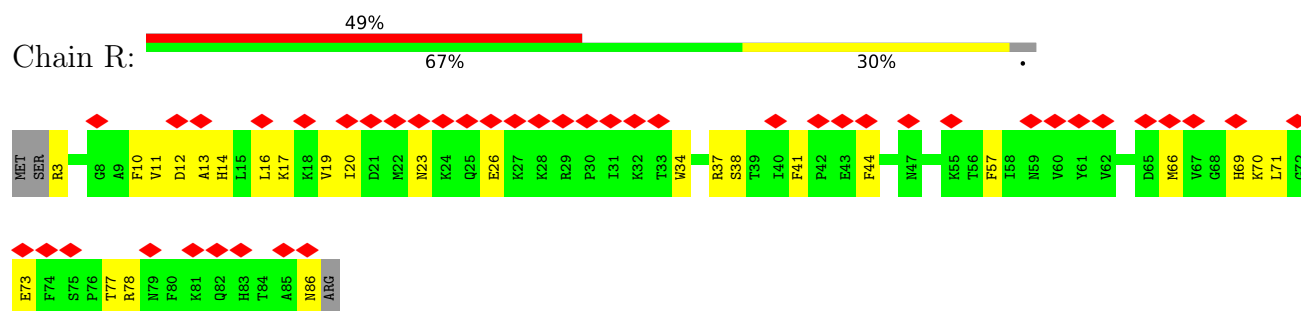
- Molecule 20: 30S ribosomal protein S17



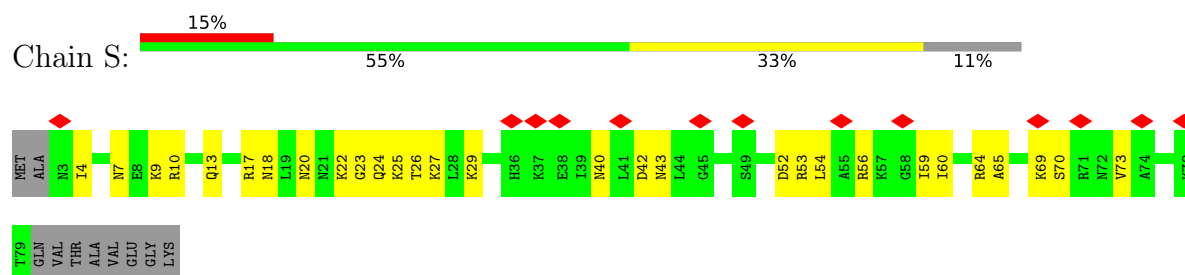
- Molecule 21: 30S ribosomal protein S18



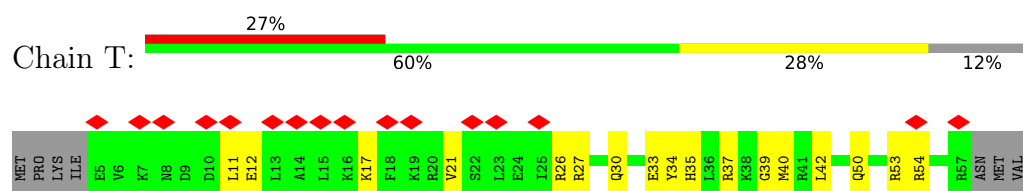
- Molecule 22: 30S ribosomal protein S19



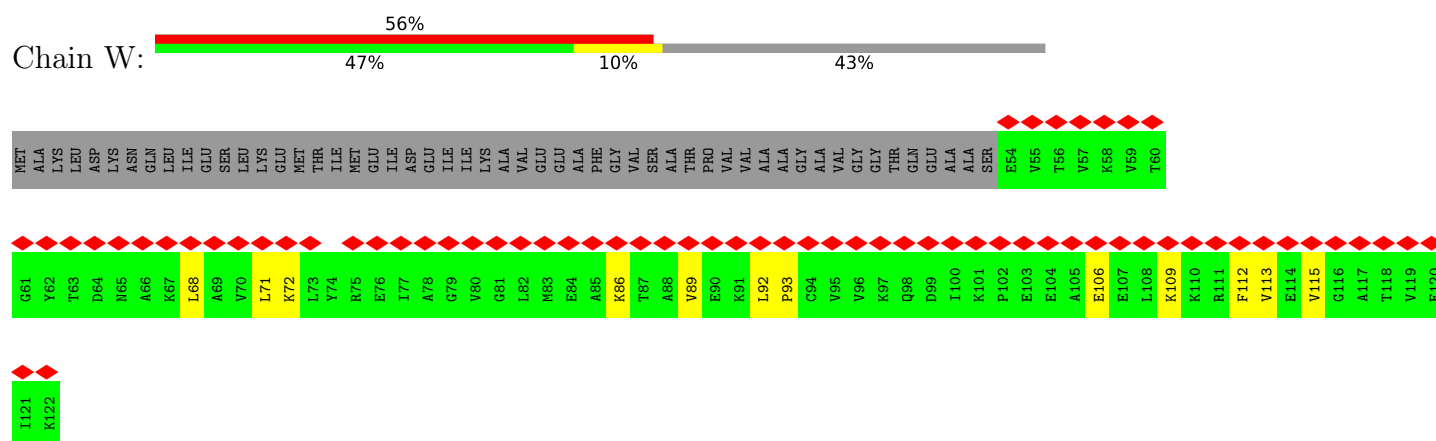
- Molecule 23: 30S ribosomal protein S20



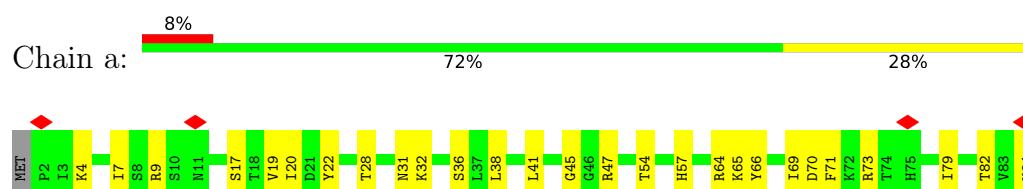
- Molecule 24: 30S ribosomal protein S21

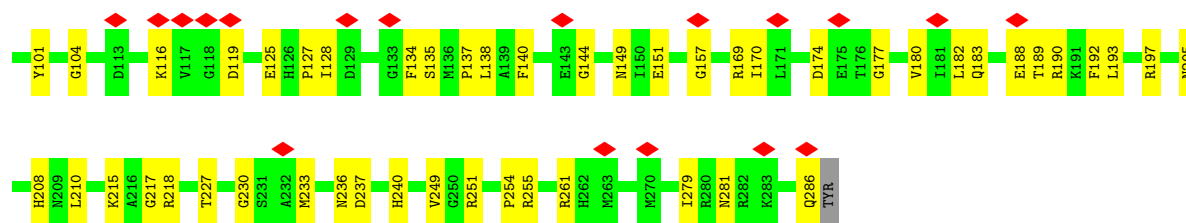


- Molecule 25: 50S ribosomal protein L7/L12

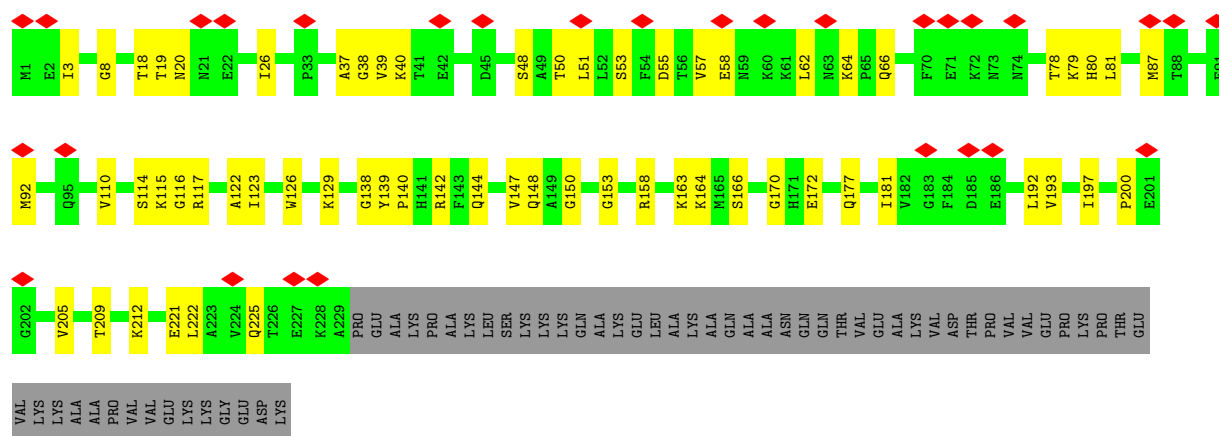


- Molecule 26: 50S ribosomal protein L2

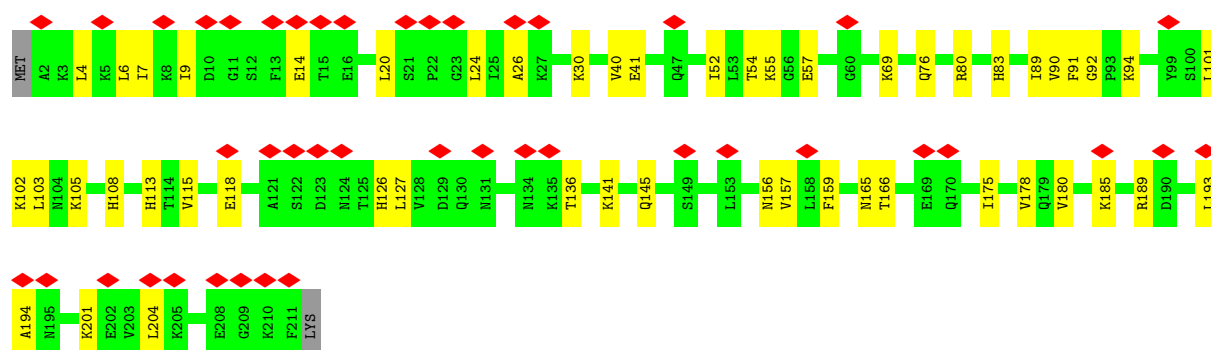
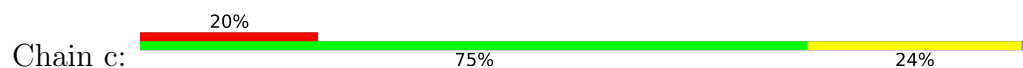




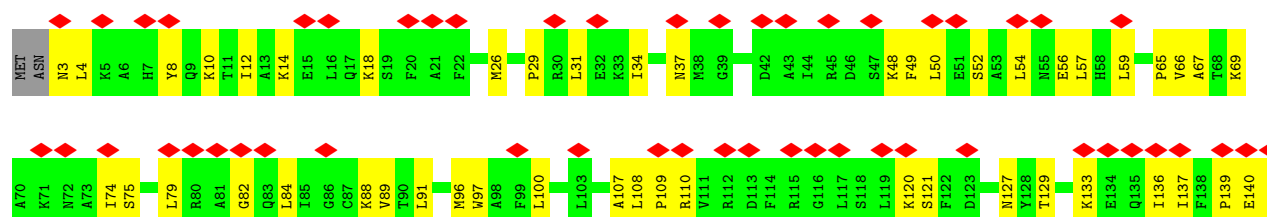
• Molecule 27: 50S ribosomal protein L3

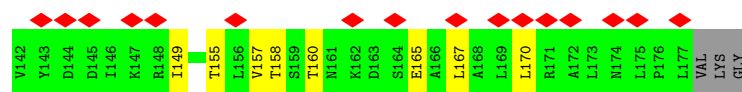


• Molecule 28: 50S ribosomal protein L4

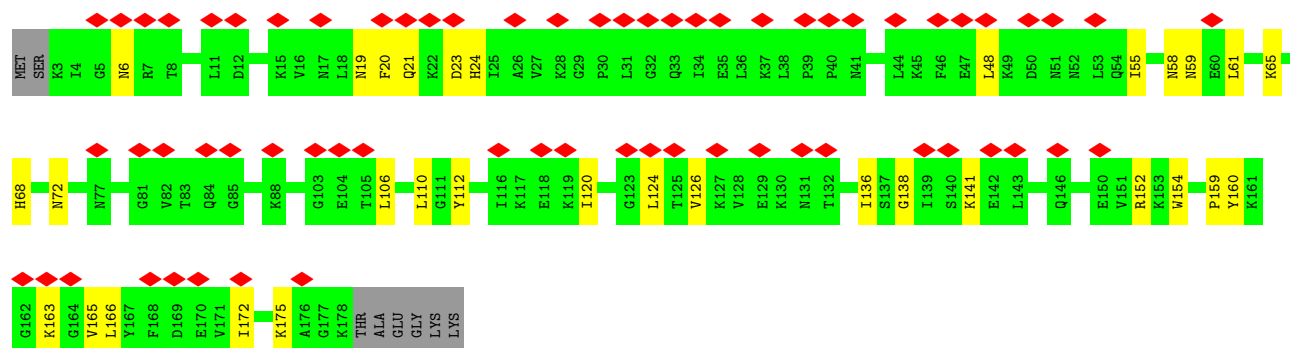
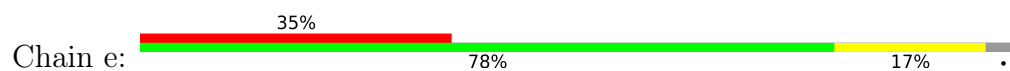


• Molecule 29: 50S ribosomal protein L5

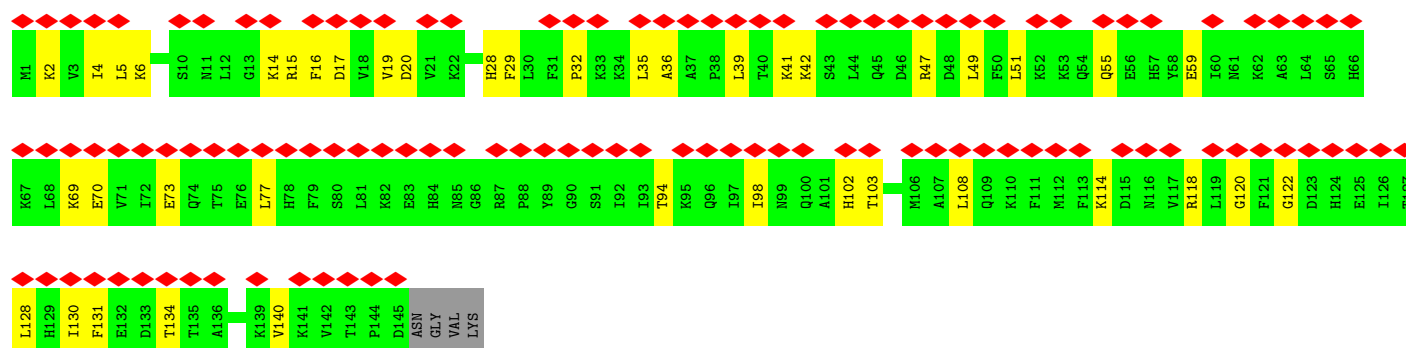
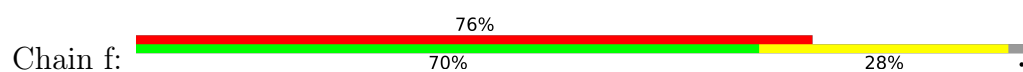




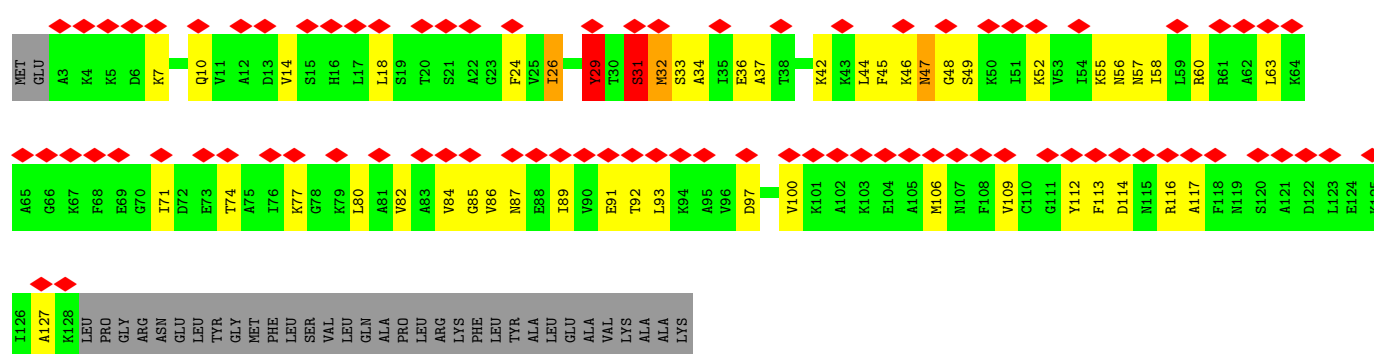
• Molecule 30: 50S ribosomal protein L6



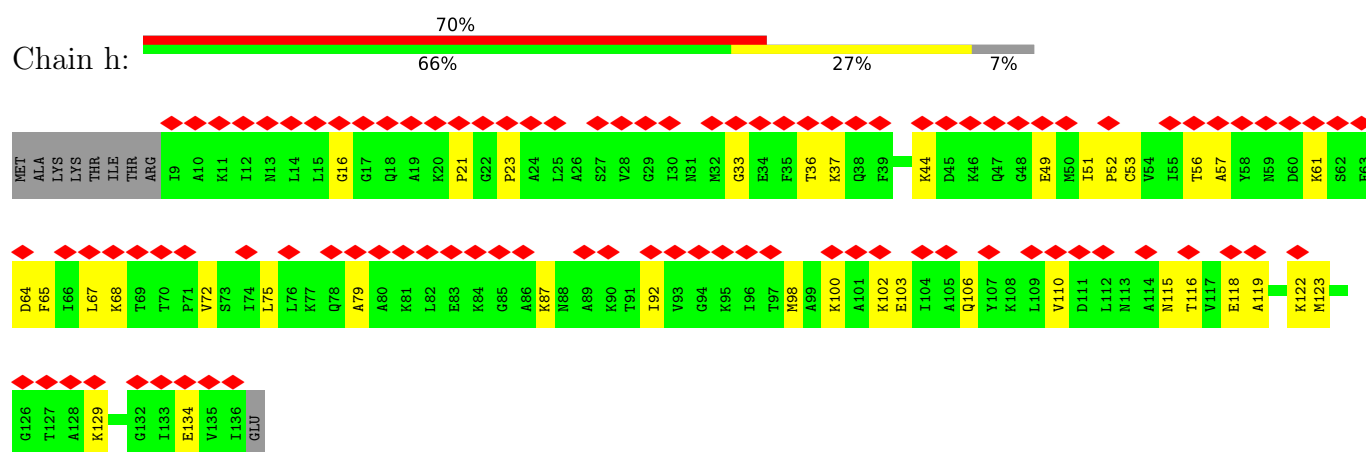
• Molecule 31: 50S ribosomal protein L9



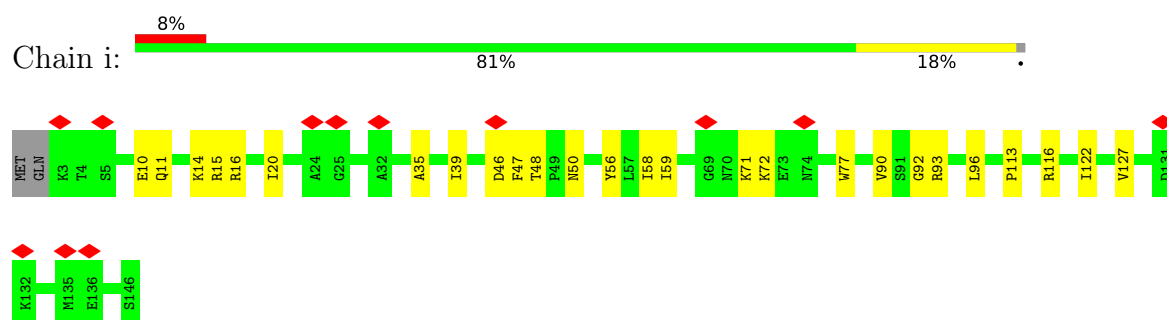
• Molecule 32: 50S ribosomal protein L10



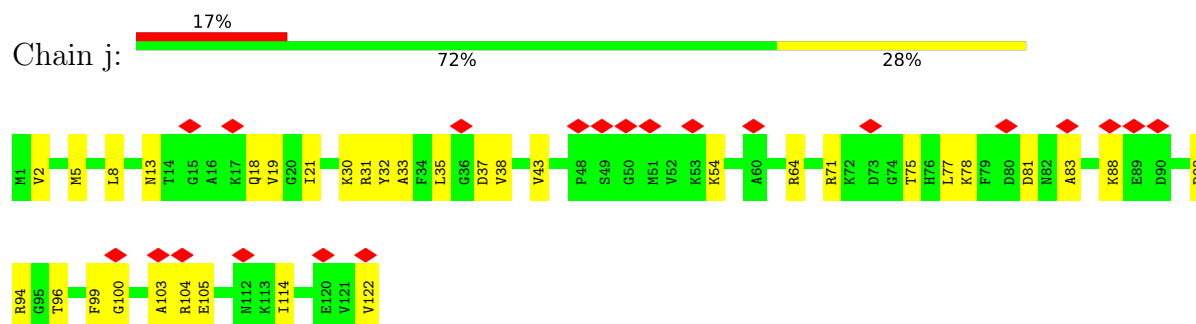
• Molecule 33: 50S ribosomal protein L11



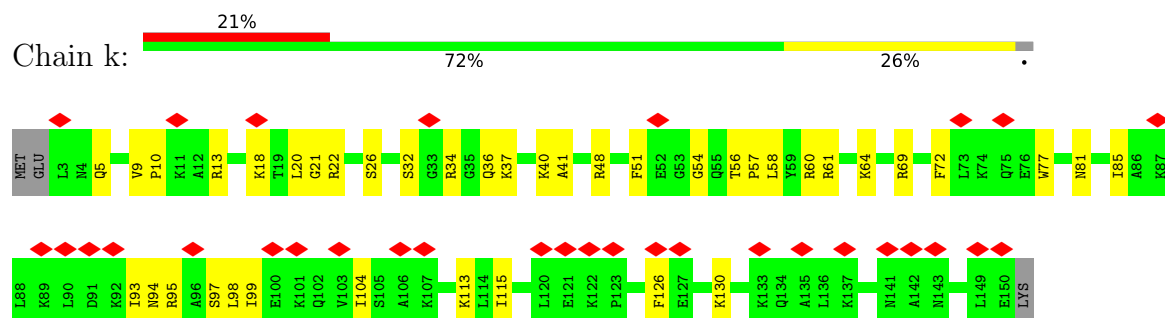
• Molecule 34: 50S ribosomal protein L13



• Molecule 35: 50S ribosomal protein L14

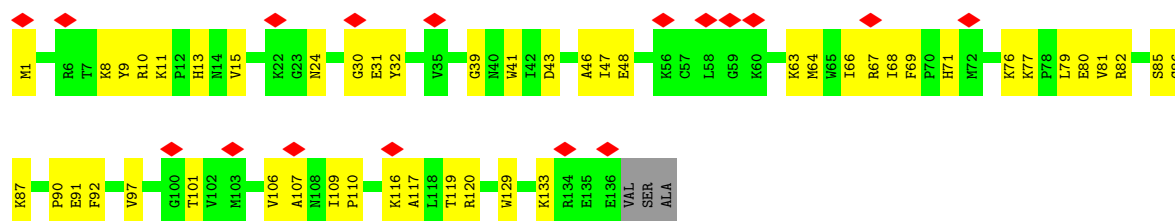


• Molecule 36: 50S ribosomal protein L15

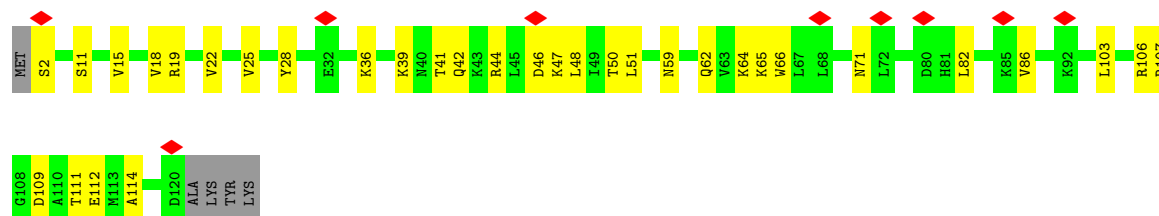


• Molecule 37: 50S ribosomal protein L16

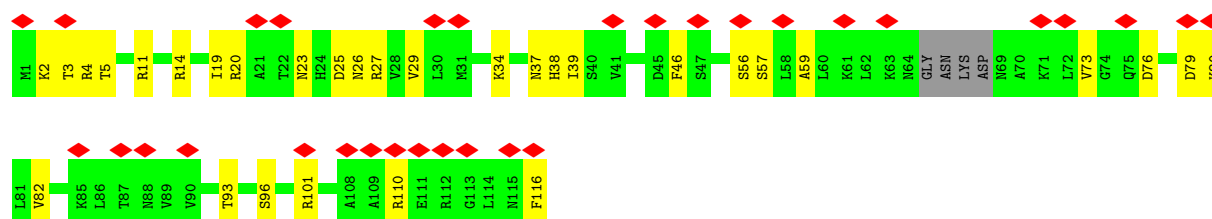




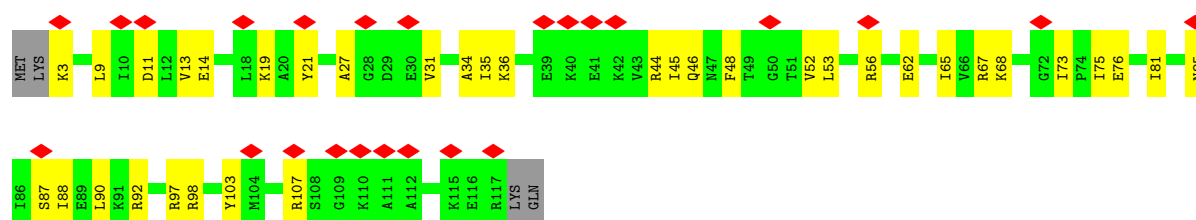
• Molecule 38: 50S ribosomal protein L17



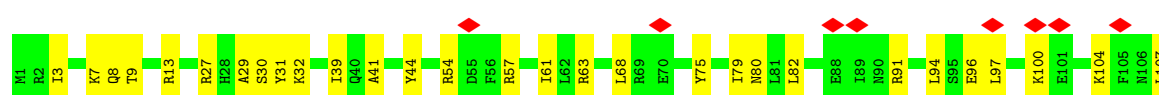
• Molecule 39: 50S ribosomal protein L18

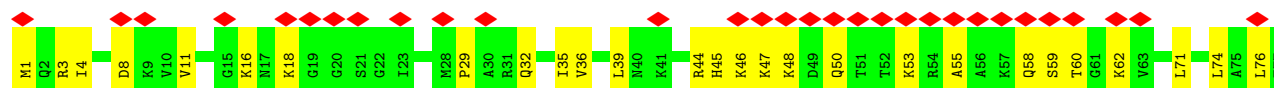


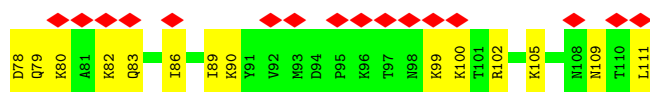
• Molecule 40: 50S ribosomal protein L19



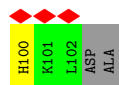
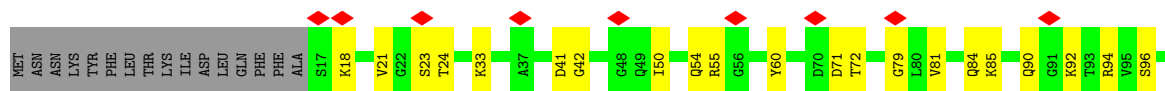
• Molecule 41: 50S ribosomal protein L20







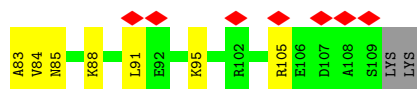
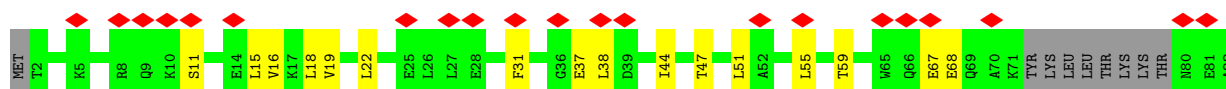
• Molecule 46: 50S ribosomal protein L27



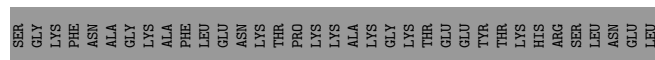
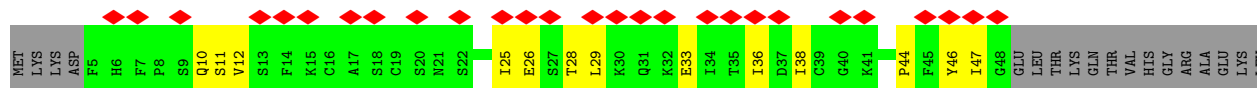
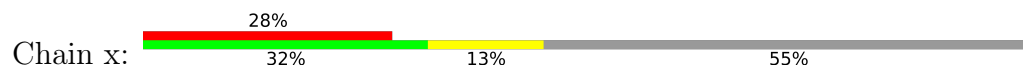
• Molecule 47: 50S ribosomal protein L28



• Molecule 48: 50S ribosomal protein L29

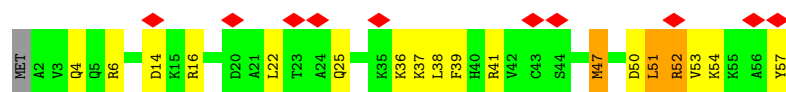


• Molecule 49: 50S ribosomal protein L31

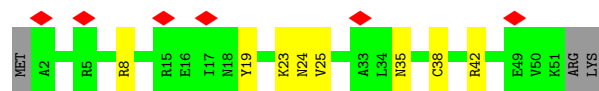
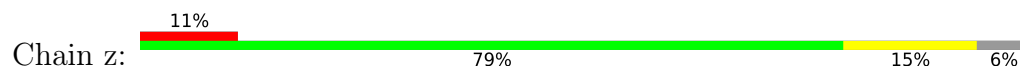


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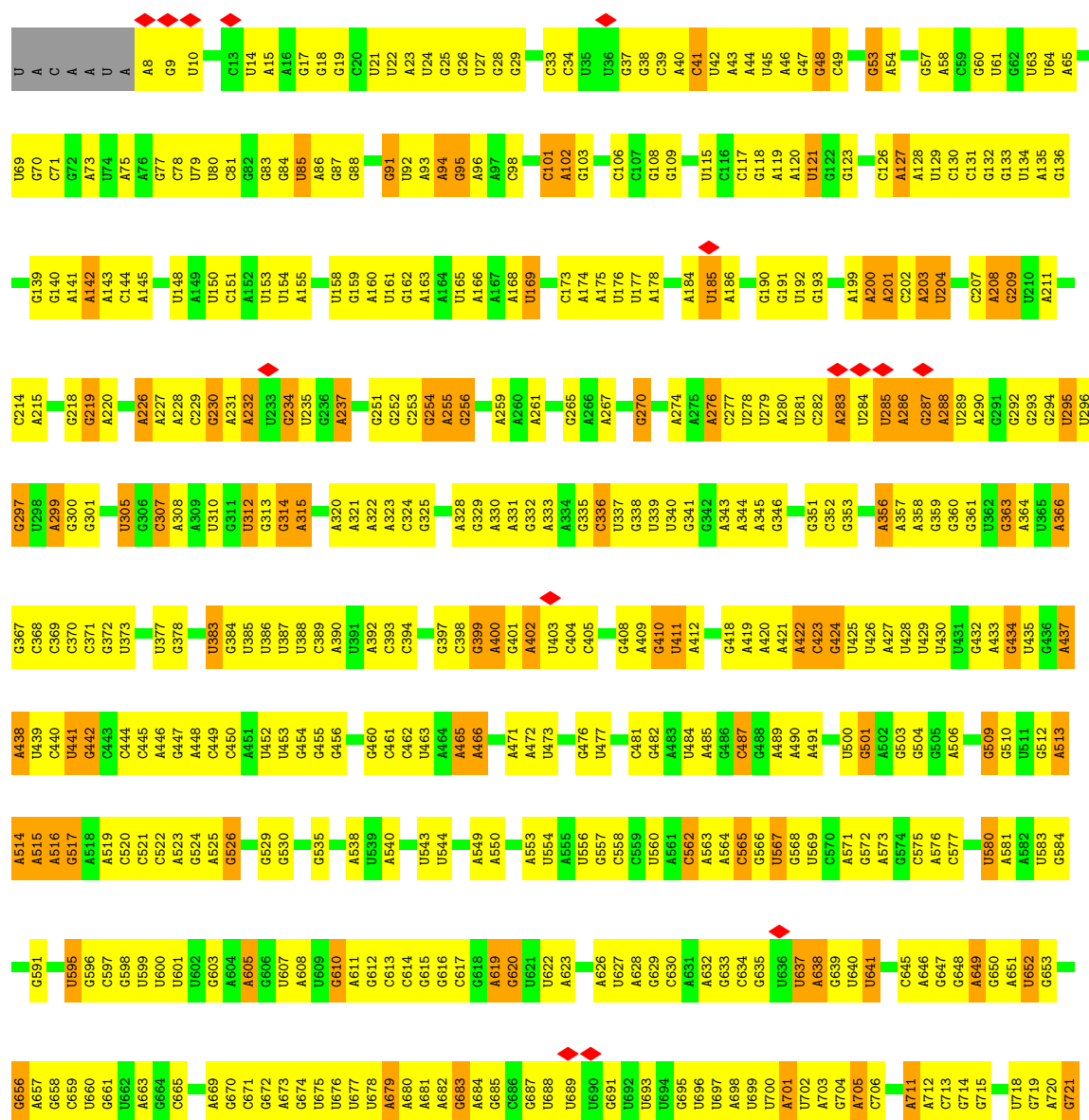




- Molecule 51: 50S ribosomal protein L33 1

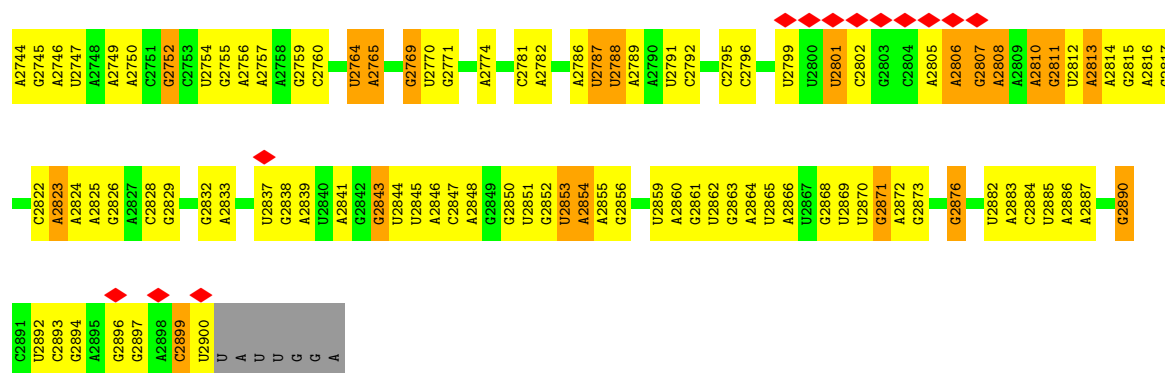


- Molecule 52: 23S ribosomal RNA

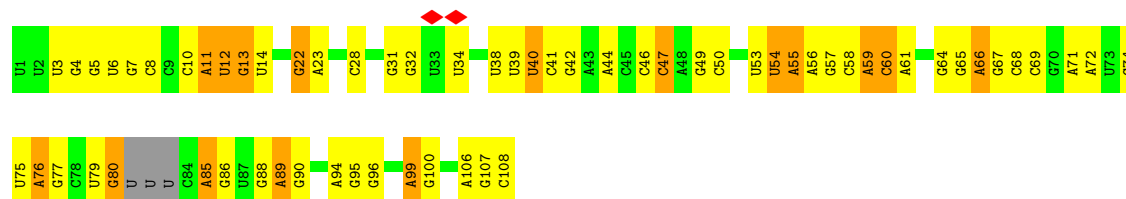


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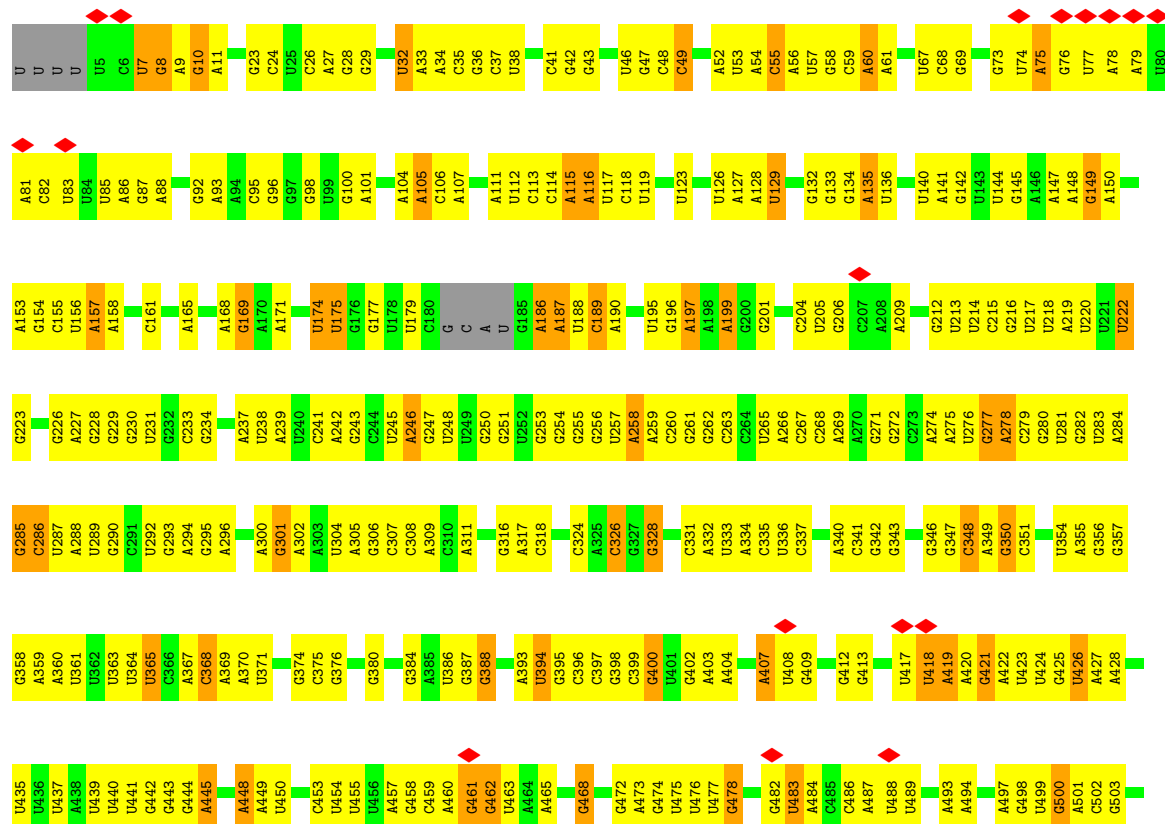
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A2685	G2604	U2522	G2455	A2385	U2175	U2110	C2044	C1965	A1897	A1822	
G2686	G2605	G2523	A2456	A2386	G2176	A2111	C2045	G1966	A1752	U1823	
A2687	A2606	U2524	U2457	G2387	G2177	U2112	U2048	U1967	G1753	G1824	
C2688	A2608	G2525	A2458	C2388	G2178	U2113	A2049	C1968	U1754	U1825	
C2689	C2609	G2526	A2459	A2389	A2179	C2114	G2050	C1969	A1826	A1826	
	A2610	U2527	A2461	G2391	U2180	G2115	G2051	G1970	U1827	G1827	
U2693	G2611	C2528	G2462	U2392	C1882	U2116	G2054	C1972	C1758	A1828	
A2694	U2612	C2529	G2463	C2393	U2181	G2117	A2055	U1973	C1759	U1829	
U2695	G2615	U2530	U2464	A2394	A2182	U2118	A2056	A1907	G1760	G1830	
G2696	U2616	G2532	U2465	U2395	C1883	G2119	C2057	A1908	C1761	U1834	
C2697	G2617	A2533	G2466	A2396	U2184	G2120	C2058	C1909	G1762	G1835	
C2698	U2618	G2534	G2467	G2397	C1884	A2121	G2059	G1979	G1763	U1836	
	U2621		C2470	G2402	C1885	G2122	G2060	U1980	U1764	G1837	
A2699	U2622	G2544	G2471	C2403	U2188	A2123	A2061	U1981	G1765	A1838	
G2700	A2701	U2545	G2472	G2404	U2189	A2124	C2062	G1982	G1766	U1839	
G2702	U2623	U2546	C2473	G2405	U2190	U2125	G2063	U1989	G1767	G1842	
U2703	C2624	A2539	G2474	G2406	G1917	A2126			A1769		
U2704	U2625		C2475	U2407	U2191		A2067	U1994	A1770		
G2705	G2629	G2547	G2476	A2385	U2192	U2129	G2068	G1995	C1771		
U2706	U2630	U2548	A2477	A2386	U2193	A2130	A2069	A1996	G1774		
A2707	G2631	G2549	G2478	U2409	U2194	G2131	C2070	C1997	G1775		
G2708	U2632	A2538	A2479	G2410	U2195	A2132	C2071	U1998	G1776		
G2709	C2633	G2552	U2482	G2338	G2196	G2133	C2072	G1999	G1777		
G2710	G2634	G2553	G2483	U2340	U2197	A2134	G2073	U2000	G1778		
C2711			A2484	G2341	C2198	G2135	C2074	C2003	G1779		
C2712	A2637	G2557	U2485	U2342	U2199	A2136	U2075	G2004	A1780		
A2713	G2638	G2558	A2486	A2415	U2200	A2137		G2005			
G2714	U2639	U2559	G2487	U2416	G2201	U2138	G2076	C2006	U1785		
U2716	A2640	G2567	G2488	G2417	U2202	C2139		U2007	U1786		
A2641	U2641	A2569	A2490	A2418	U2203	A2141	U2081	A2008	G1866		
G2717	G2642	U2570	G2492	A2419	C2204	U2142	U2082	U2009	G1867		
			U2493	A2420	U2205	G2143	U2083	A2010	A1868		
G2722	G2646	A2572	G2494	G2423	A2206	C2144	U2084	G2011	U1790		
C2723	U2649	A2573	A2495	C2424	U2207	C2145	C2085	A2012	G1870		
U2724	G2651	G2574	A2496	A2425	U2208	A2146	U2086	G2016	A1791		
				U2427	G2210	G2147	G2087	A2020	A1792		
G2727	U2652	A2580	G2498	U2427	G2211	U2148	U2088	A2021	A1793		
	G2653	C2581	U2500	G2430	U2212	U2149	A2089		C1941		
G2730	U2654	G2584	U2501	U2431	U2213	C2150		G2016	U1871		
U2731	U2655	A2585	G2502	C2432	A2214	G2151		A2024	A1872		
A2732	G2656	G2586	G2503	A2433	C2215	C2152		A2025	A1873		
A2733	C2657	U2587	C2504	G2436	U2219	U2153		A2026	A1874		
G2734	U2658	U2588	A2505	G2437	A2220	A2154		A2027	A1875		
G2735	G2659		C2506	G2438	U2221	G2155		G2028	G1876		
U2736	U2660	U2592	U2507	U2439	U2222	G2156		U2029	C1877		
G2737	A2665	G2593	U2508	U2440	U2223	U2157		A2030	A1878		
U2738	C2666	C2594	G2509	A2441	A2224	A2158		C2031	G1880		
C2739	G2667	G2595	G2510	A2441	G2225	C2159		G2032	G1881		
U2740	A2668	A2596	A2511	A2447	U2226	U2160		G2033	G1882		
A2741	U2669	A2597	U2512	U2448	U2227	G2161			A1883		
U2742	C2670	G2598	G2513	G2449	U2228	U2162			A1884		
U2743	G2671				C2229	U2163			G1885		



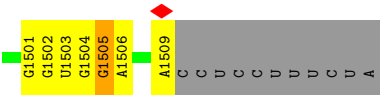
• Molecule 53: 5S ribosomal RNA



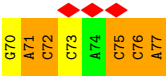
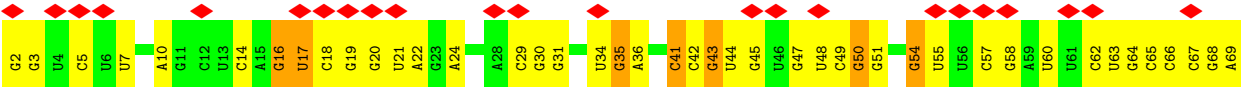
• Molecule 54: 16S ribosomal RNA



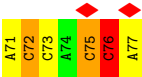
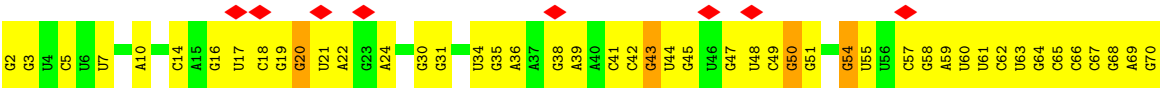
U1427	U1358	G1290	C1218	U1148	U1082	C1013	A953	U882	A806	G722	A645	A571	U506
A1428	C1359	C1291	C1219	G1149	U1085	A1014	A954	A883	A646	C723	A646	A572	A507
G1429	G1360	A1292	G1150	G1150	U1086	A1015	U955	U884	U647	G724	U647	G573	A508
G1430	G1361	A1293	A1151	G1151	U1087	A1016	U956	U885	C648	A725	C648	C574	C509
A1431	U1362	C1224	G1152	G1152	C1087	A1017	C957	A886	U649	A726	U649	A575	U510
A1432	U1363	U1295	U1363	G1153	C1088	U1018	C958	C887	A650	A731	A650	A576	A511
	C1364	C1296	A1225	A1154	U1089	G1019	A959	A888	G651	A732	G651	G577	U512
		G1297	A1227	A1155	C1090	G	C960		A652	A733	A652	G578	G513
C1436	G1367	U1298	C1228	A1156	C1091	A	C961	C891	G653	A734	G653	C579	U514
A1437	U1368	C1229	G1157	G1156	U1092	G	U962	C892	U654	A735	U654	G580	G515
U1438	A1369	C1300	G1230	A1158	A1093	G	C963	C893	C735	C736	C735	C581	C516
G1439	U1370	U1301	U1231	A1159	C1094	U	A964	A894	U736	U737	U736	A517	A517
U1440		C1302	C1232	G1160	G1095	U	C965	A895	U737	U737	U737	C518	C518
A1441		A1303	U1232	G1161	A1096	A	A966	A896	U656		U656		
A1442	C1374	U1304	A1236	G1162	G1097	A	C967	A897	G661	A738	G661	G585	G519
A1443	C1375	G1305	G1237		C1098		C968	A898	G662		G662	G586	C520
G1444	G1376			G1165	C1099		A969	A899	U657		U657	U588	A521
G1445	C1377	G1311	G1241	A1166	C1100	G1028	A970	A892	G670	U745	G670	U589	G522
A1446	C1378	G1312	U1242	G1167	A1101	G1030	A971	A893	G671	C747	G671	U590	U523
U1447	C1379	A1313	A1243	G1168		A1031	A972	C904	A672	C748	A672	C524	C524
A1448	G1380	A1314	U1169	U1168	C1104	G1032	A973	U905	A673	G749	A673	A592	G525
G1449		U1315	C1170	C1170	C1105	U1033	C974	C906	U674	A750	U674	A593	
C1450		C1316	A1171	A1171	U1106	G1034	C975	A907	U675	C751	U675	A594	G528
		A1317			U1107	A1035	U976	A908	C831	C752	U676	G595	U529
U1456	A1383	A1318	C1175	C1175	U1108	C1036	U977	A909	C677	C753	A678	U596	A530
G1457	A1384	C1319	A1176	A1176	U1109	U1040	A978	C910	U679	U754	U679	A531	A531
A1458	A1385	U1320	U1177	U1177	C1110	G1041	C979	G911	G680	U755	G680	U532	U532
U1459	C1386	A1321	C1178	C1178	C1111	G1042	C980	G912	G681	A756	G681	A533	A533
U1460	U1387	U1322	A1179	A1179	U1112	U1043	U981		C534	C757	C682	U603	
G1461	U1389	U1256	U1256	U1256	U1113	G1044	U982	G917	G683		G683		
A1462	G1390	C1257	U1187	U1187	A1114	C1045	C983	A918	U608	U760	U608	A537	U536
			A1188	A1188	C1115	A1046	A984	C919	G609	U761	G609	A538	A538
		U1260	A1189	A1189	U1116	U1047	C985	G920	G610	G762	G610	G539	G539
		A1261	U1191	U1191	U1117	G1048	C986	G921	A611	A763	A611	U540	U540
		C1262	C1192	C1192	A1118	U1049	U987	G922	G612	A764	G612	C541	C541
		U1263	U1193	U1193	C1119	U1050	U988	G923	C613	U767	C613	G542	G542
		U1265	A1194	A1194	A1120	U1051	A989	G928	A614		A614		
		U1266	G1195	G1195	U1121	G1052	C990	C929	G615		G615		
		G1267	G1196	G1196	U1122	U1053	A991	A930	A616		A616		
		U1268	G1197	G1197	U1123	C1054	U992	C931	U617		U617		
		U1269	C1198	C1198	U1124	U1056	C993	A933	G618		G618		
			U1199	U1199	U1125	U1057	C994	G934					
			G1200	G1200	C1125	C1057	U995	U935	A699		A699		
			C1201	C1201		U1058	U996	G936	G700		G700		
			A1202	A1202	G1128	A1059	U997	G937	A701		A701		
			A1203	A1203		C1060	C998	U938	U704		U704		
			A1204	A1204	A1133	U1061	C999	G939	A705		A705		
			C1205	C1205	C1134	C1062	A1000	G940	U706		U706		
			G1206	G1206	U1135	G1063	A1001	A941	A628		A628		
			U1207	U1207	G1136	U1064	A1002	G942	U629		U629		
			C1208	C1208	C1137	U1065	A1003	C943	G630		G630		
			C1209	C1209	U1138	G1066	U1004	G944	C631		C631		
			U1210	U1210	A1139	U1067	U1005	U945	A632		A632		
			A1211	A1211	A1140	C1067	U1006	G946	U633		U633		
			C1212	C1212	U1141	G1068	A1007	U947	G635		G635		
			A1213	A1213	G1142	U1069	U1008	U948	U636		U636		
			A1214	A1214	C1143	G1070	G1009	G949	U637		U637		
			U1215	U1215	A1144	A1071	G1009	U950	A638		A638		
			G1216	G1216	A1145	G1072	A1010	C950	A639		A639		
			U1217	U1217	A1146	A1073	A1011	U951	U643		U643		
					U1147		A1012	U952	U644		U644		



• Molecule 55: tRNA-Phe



• 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	8371	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 K3 (6k x 4k)	Depositor
Maximum map value	4.055	Depositor
Minimum map value	-1.778	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.164	Depositor
Recommended contour level	0.66	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.15	0/383	0.43	0/504
2	1	0.15	0/484	0.44	0/637
3	2	0.13	0/306	0.41	0/401
4	9	0.16	0/5419	0.43	0/7307
5	A	0.14	0/1954	0.39	0/2642
6	B	0.14	0/1721	0.41	0/2323
7	C	0.13	0/1691	0.41	0/2267
8	D	0.16	0/1188	0.47	0/1593
9	E	0.13	0/1384	0.39	0/1867
10	F	0.13	0/1266	0.39	0/1700
11	G	0.20	0/1126	0.55	0/1517
12	H	0.14	0/1044	0.43	0/1395
13	I	0.14	0/820	0.41	0/1103
14	J	0.13	0/844	0.36	0/1136
15	K	0.25	0/1094	0.56	1/1468 (0.1%)
16	L	0.15	0/962	0.45	0/1289
17	M	0.15	0/483	0.43	0/643
18	N	0.13	0/679	0.41	0/907
19	O	0.16	0/659	0.43	0/885
20	P	0.15	0/684	0.43	0/913
21	Q	0.15	0/545	0.39	0/730
22	R	0.15	0/698	0.43	0/936
23	S	0.12	0/631	0.39	0/838
24	T	0.13	0/475	0.40	0/621
25	W	0.13	0/538	0.40	0/722
26	a	0.15	0/2267	0.42	0/3044
27	b	0.14	0/1795	0.40	0/2412
28	c	0.15	0/1671	0.39	0/2246
29	d	0.15	0/1409	0.43	0/1894
30	e	0.14	0/1420	0.38	0/1912
31	f	0.14	0/1205	0.41	0/1616
32	g	0.39	0/969	0.78	3/1295 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.15	0/968	0.42	0/1298
34	i	0.13	0/1186	0.38	0/1592
35	j	0.15	0/953	0.46	0/1275
36	k	0.14	0/1170	0.39	0/1559
37	l	0.17	0/1104	0.44	0/1481
38	m	0.14	0/973	0.39	0/1309
39	n	0.14	0/897	0.44	0/1198
40	o	0.14	0/948	0.42	0/1262
41	p	0.13	0/961	0.37	0/1278
42	q	0.13	0/828	0.40	0/1111
43	r	0.14	0/1077	0.40	0/1441
44	s	0.13	0/732	0.43	0/988
45	t	0.14	0/879	0.42	0/1165
46	u	0.17	0/665	0.47	0/884
47	v	0.28	0/519	0.53	0/695
48	w	0.13	0/826	0.41	0/1104
49	x	0.15	0/353	0.36	0/474
50	y	0.30	0/457	0.71	0/601
51	z	0.14	0/412	0.41	0/547
52	3	0.10	0/69073	0.25	3/107710 (0.0%)
53	4	0.10	0/2505	0.26	0/3902
54	5	0.09	0/35768	0.23	1/55764 (0.0%)
55	7	0.18	0/1808	0.40	0/2817
55	8	0.18	0/1808	0.40	1/2817 (0.0%)
All	All	0.12	0/164684	0.32	9/245035 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	3	2069	A	C4'-C3'-O3'	7.39	124.09	113.00
32	g	31	SER	N-CA-C	-6.70	105.43	112.93
15	K	117	THR	CA-CB-OG1	-6.00	100.60	109.60
32	g	47	ASN	CA-CB-CG	-5.91	106.69	112.60
52	3	2070	C	C3'-C2'-O2'	5.89	119.54	110.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	380	0	429	12	0
2	1	477	0	530	8	0
3	2	304	0	350	14	0
4	9	5326	0	5343	163	0
5	A	1921	0	1973	44	0
6	B	1698	0	1768	47	0
7	C	1660	0	1719	33	0
8	D	1173	0	1267	38	0
9	E	1362	0	1377	46	0
10	F	1246	0	1308	36	0
11	G	1110	0	1226	33	0
12	H	1028	0	1094	38	0
13	I	809	0	894	27	0
14	J	829	0	855	20	0
15	K	1076	0	1170	38	0
16	L	951	0	1014	25	0
17	M	474	0	509	16	0
18	N	673	0	730	25	0
19	O	646	0	677	19	0
20	P	675	0	728	19	0
21	Q	535	0	562	17	0
22	R	682	0	691	26	0
23	S	629	0	681	23	0
24	T	471	0	522	12	0
25	W	534	0	572	8	0
26	a	2225	0	2301	60	0
27	b	1762	0	1808	43	0
28	c	1644	0	1731	38	0
29	d	1388	0	1469	49	0
30	e	1396	0	1481	24	0
31	f	1182	0	1228	68	0
32	g	960	0	1014	43	0
33	h	959	0	1039	26	0
34	i	1164	0	1192	19	0
35	j	944	0	1019	27	0
36	k	1153	0	1256	37	0
37	l	1079	0	1134	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	958	0	1011	24	0
39	n	889	0	952	22	0
40	o	938	0	1008	27	0
41	p	947	0	1028	31	0
42	q	811	0	858	24	0
43	r	1068	0	1150	23	0
44	s	720	0	803	17	0
45	t	872	0	972	30	0
46	u	657	0	695	22	0
47	v	513	0	560	22	0
48	w	818	0	870	19	0
49	x	344	0	333	10	0
50	y	452	0	472	16	0
51	z	408	0	440	7	0
52	3	61664	0	30954	1309	0
53	4	2239	0	1137	42	0
54	5	31943	0	16058	747	0
55	7	1618	0	821	41	0
55	8	1618	0	821	38	0
56	5	23	0	24	3	0
All	All	152025	0	105628	3352	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 14.

The worst 5 of 3352 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)
31:f:5:LEU:HD11	31:f:14:LYS:CG	1.26	1.62
31:f:5:LEU:CD1	31:f:14:LYS:HG3	1.26	1.54
31:f:2:LYS:HZ3	31:f:28:HIS:N	1.21	1.34
31:f:2:LYS:HE2	31:f:29:PHE:N	1.41	1.32
31:f:2:LYS:HZ3	31:f:28:HIS:CA	1.44	1.29

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%)	34 (97%)	1 (3%)	0	100	100
4	9	680/688 (99%)	622 (92%)	58 (8%)	0	100	100
5	A	238/294 (81%)	219 (92%)	19 (8%)	0	100	100
6	B	213/273 (78%)	201 (94%)	12 (6%)	0	100	100
7	C	201/205 (98%)	196 (98%)	5 (2%)	0	100	100
8	D	151/219 (69%)	147 (97%)	4 (3%)	0	100	100
9	E	165/215 (77%)	140 (85%)	25 (15%)	0	100	100
10	F	152/155 (98%)	146 (96%)	6 (4%)	0	100	100
11	G	139/142 (98%)	123 (88%)	14 (10%)	2 (1%)	9	39
12	H	126/132 (96%)	111 (88%)	15 (12%)	0	100	100
13	I	99/108 (92%)	94 (95%)	5 (5%)	0	100	100
14	J	112/121 (93%)	109 (97%)	3 (3%)	0	100	100
15	K	134/139 (96%)	121 (90%)	10 (8%)	3 (2%)	5	28
16	L	116/124 (94%)	109 (94%)	7 (6%)	0	100	100
17	M	58/61 (95%)	52 (90%)	6 (10%)	0	100	100
18	N	81/86 (94%)	78 (96%)	3 (4%)	0	100	100
19	O	78/94 (83%)	71 (91%)	7 (9%)	0	100	100
20	P	81/85 (95%)	76 (94%)	5 (6%)	0	100	100
21	Q	63/104 (61%)	57 (90%)	6 (10%)	0	100	100
22	R	82/87 (94%)	75 (92%)	7 (8%)	0	100	100
23	S	75/87 (86%)	75 (100%)	0	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%)	260 (92%)	23 (8%)	0	100	100
27	b	227/287 (79%)	213 (94%)	14 (6%)	0	100	100
28	c	208/212 (98%)	202 (97%)	6 (3%)	0	100	100
29	d	173/180 (96%)	160 (92%)	13 (8%)	0	100	100
30	e	174/184 (95%)	162 (93%)	12 (7%)	0	100	100
31	f	143/149 (96%)	132 (92%)	11 (8%)	0	100	100
32	g	124/161 (77%)	111 (90%)	11 (9%)	2 (2%)	7	37
33	h	126/137 (92%)	120 (95%)	6 (5%)	0	100	100
34	i	142/146 (97%)	134 (94%)	8 (6%)	0	100	100
35	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
36	k	146/151 (97%)	136 (93%)	10 (7%)	0	100	100
37	l	134/139 (96%)	126 (94%)	8 (6%)	0	100	100
38	m	117/124 (94%)	114 (97%)	3 (3%)	0	100	100
39	n	108/116 (93%)	101 (94%)	7 (6%)	0	100	100
40	o	113/119 (95%)	108 (96%)	5 (4%)	0	100	100
41	p	112/127 (88%)	108 (96%)	4 (4%)	0	100	100
42	q	97/100 (97%)	85 (88%)	12 (12%)	0	100	100
43	r	137/159 (86%)	129 (94%)	8 (6%)	0	100	100
44	s	90/237 (38%)	86 (96%)	4 (4%)	0	100	100
45	t	109/111 (98%)	101 (93%)	8 (7%)	0	100	100
46	u	84/104 (81%)	78 (93%)	6 (7%)	0	100	100
47	v	61/65 (94%)	58 (95%)	3 (5%)	0	100	100
48	w	96/111 (86%)	88 (92%)	8 (8%)	0	100	100
49	x	42/97 (43%)	38 (90%)	4 (10%)	0	100	100
50	y	54/57 (95%)	47 (87%)	7 (13%)	0	100	100
51	z	48/53 (91%)	45 (94%)	3 (6%)	0	100	100
All	All	6567/7480 (88%)	6123 (93%)	437 (7%)	7 (0%)	49	83

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	K	122	LYS
15	K	123	ARG

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Mol	Chain	Res	Type
11	G	108	LEU
15	K	121	GLU
32	g	45	PHE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	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%)	212 (100%)	0	100	100
6	B	180/232 (78%)	180 (100%)	0	100	100
7	C	181/183 (99%)	181 (100%)	0	100	100
8	D	123/178 (69%)	123 (100%)	0	100	100
9	E	150/196 (76%)	150 (100%)	0	100	100
10	F	131/132 (99%)	131 (100%)	0	100	100
11	G	123/124 (99%)	119 (97%)	4 (3%)	33	55
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%)	115 (98%)	2 (2%)	53	68
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	R	74/77 (96%)	74 (100%)	0	100	100
23	S	70/77 (91%)	70 (100%)	0	100	100
24	T	49/56 (88%)	49 (100%)	0	100	100
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%)	181 (100%)	1 (0%)	81	82
29	d	150/154 (97%)	150 (100%)	0	100	100
30	e	153/159 (96%)	153 (100%)	0	100	100
31	f	131/134 (98%)	131 (100%)	0	100	100
32	g	101/129 (78%)	94 (93%)	7 (7%)	14	37
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	38
51	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5738/6433 (89%)	5721 (100%)	17 (0%)	84	84

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	y	47	MET
50	y	52	ARG
32	g	26	ILE
32	g	29	TYR
32	g	31	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 74 such sidechains are listed below:

Mol	Chain	Res	Type
39	n	23	ASN
47	v	34	GLN
39	n	99	HIS
43	r	112	ASN
19	O	40	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	2875/2907 (98%)	724 (25%)	27 (0%)
53	4	103/108 (95%)	31 (30%)	2 (1%)
54	5	1490/1520 (98%)	358 (24%)	6 (0%)
55	7	75/76 (98%)	26 (34%)	2 (2%)
55	8	75/76 (98%)	26 (34%)	2 (2%)
All	All	4618/4687 (98%)	1165 (25%)	39 (0%)

5 of 1165 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	14	U
52	3	29	G
52	3	37	G
52	3	41	C
52	3	44	A

5 of 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	4	59	A
55	7	16	G

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Mol	Chain	Res	Type
54	5	60	A
54	5	988	G
55	8	16	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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
56	SCM	5	1601	-	23,25,25	1.71	8 (34%)	27,39,39	1.57	4 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	SCM	5	1601	-	-	2/4/57/57	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	5	1601	SCM	C3-C2	3.25	1.58	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	5	1601	SCM	C9-C8	3.00	1.58	1.53
56	5	1601	SCM	C3-C4	2.61	1.54	1.50
56	5	1601	SCM	C12-C7	2.41	1.57	1.52
56	5	1601	SCM	O5-C5	2.28	1.43	1.39

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	5	1601	SCM	C1M-N10-C10	-5.37	107.29	114.23
56	5	1601	SCM	O1-C2-C3	3.63	113.68	108.62
56	5	1601	SCM	C2M-C2-C3	-2.63	108.54	113.27
56	5	1601	SCM	O2B-C6-O1	2.15	109.11	107.40

There are no chirality outliers.

All (2) torsion outliers are listed below:

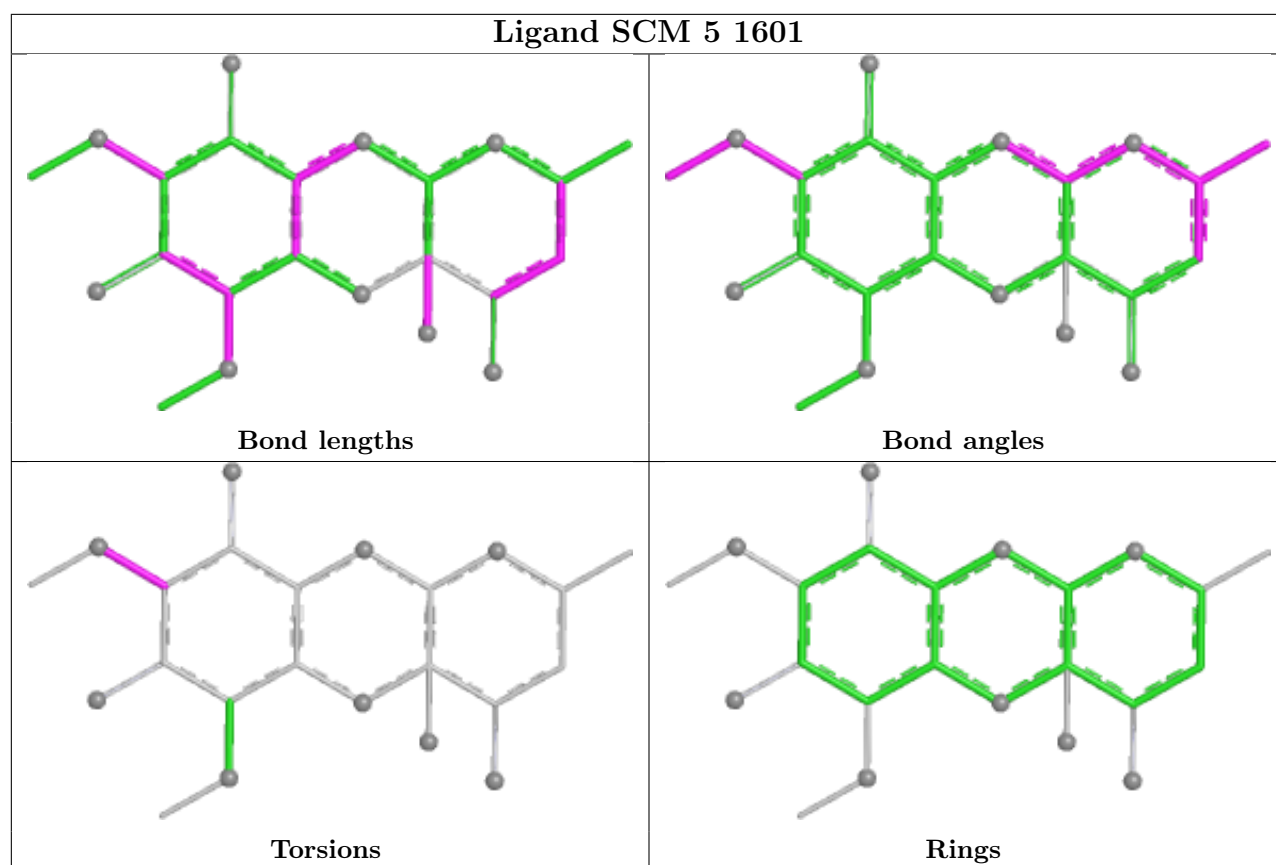
Mol	Chain	Res	Type	Atoms
56	5	1601	SCM	C9-C10-N10-C1M
56	5	1601	SCM	C11-C10-N10-C1M

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	5	1601	SCM	3	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

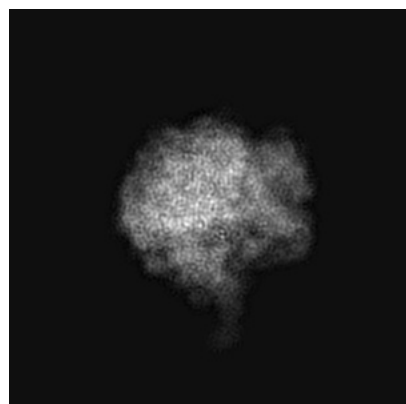
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13435. These allow visual inspection of the internal detail of the map and identification of artifacts.

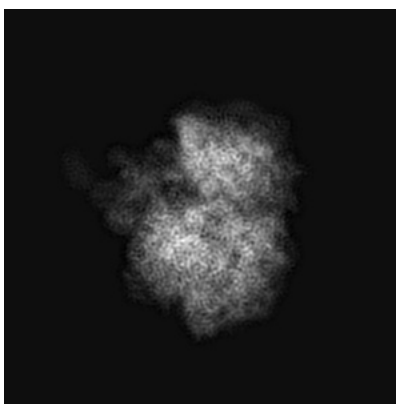
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

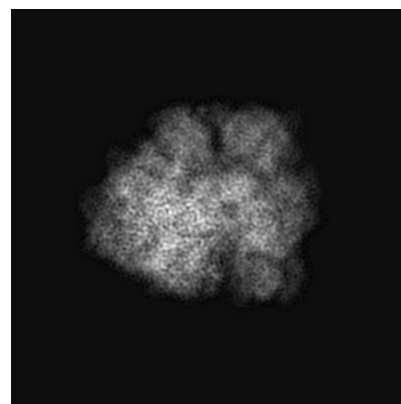
6.1.1 Primary map



X

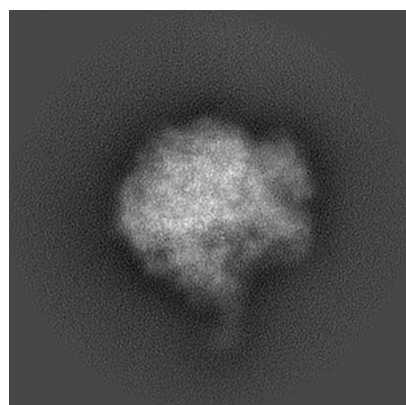


Y

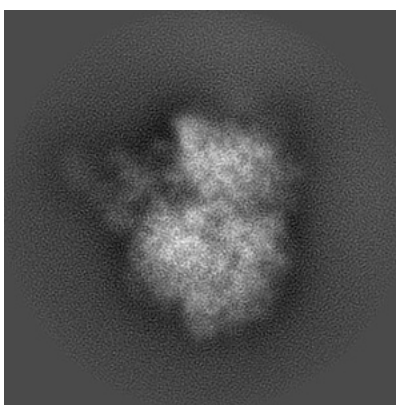


Z

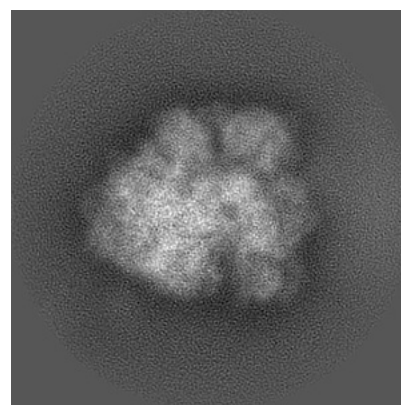
6.1.2 Raw map



X



Y

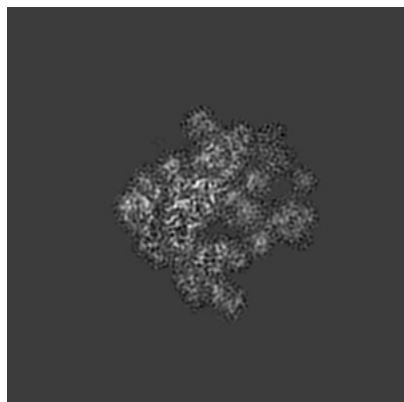


Z

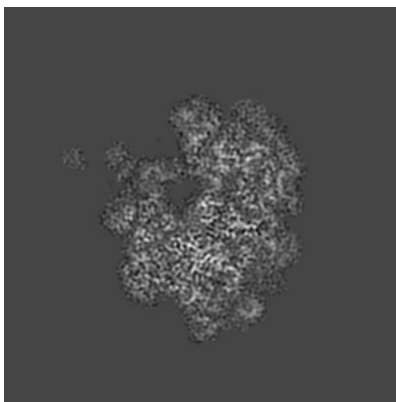
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

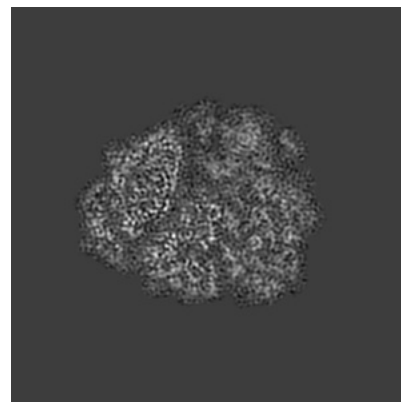
6.2.1 Primary map



X Index: 128

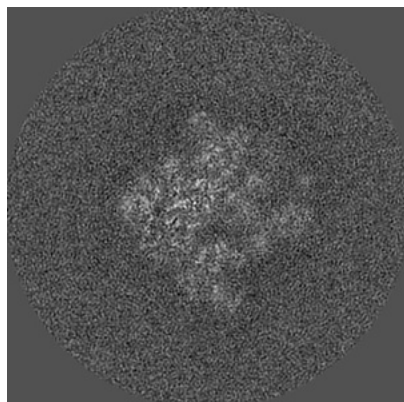


Y Index: 128

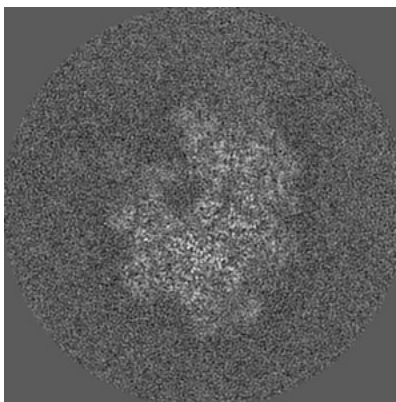


Z Index: 128

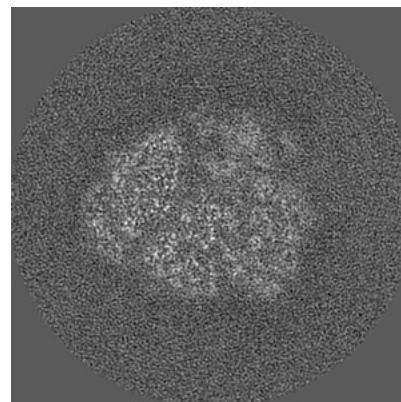
6.2.2 Raw map



X Index: 128



Y Index: 128

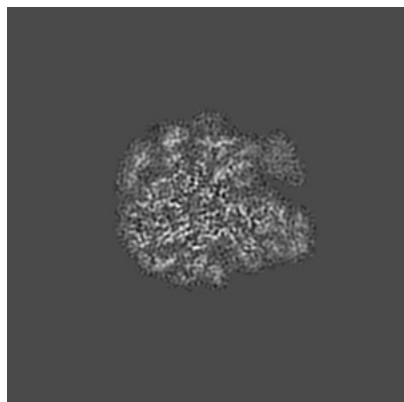


Z Index: 128

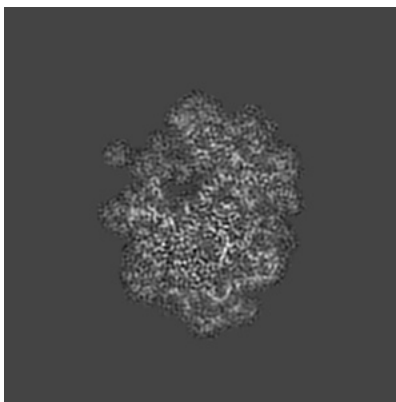
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

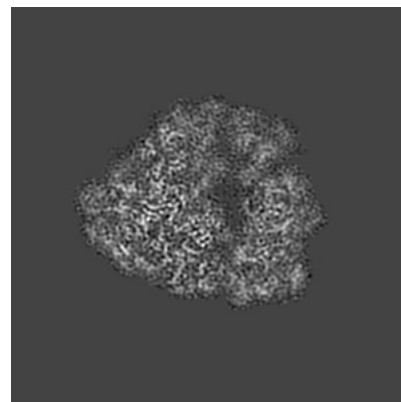
6.3.1 Primary map



X Index: 104

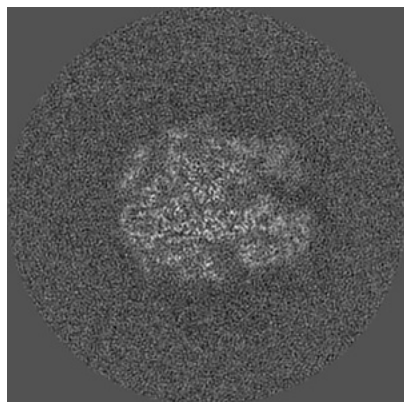


Y Index: 121

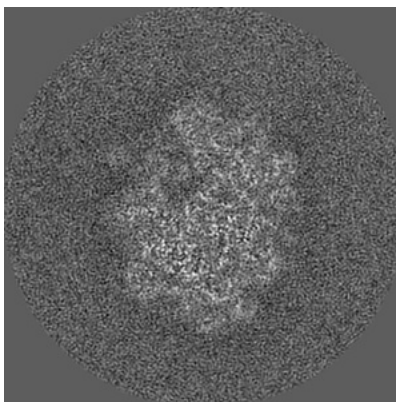


Z Index: 122

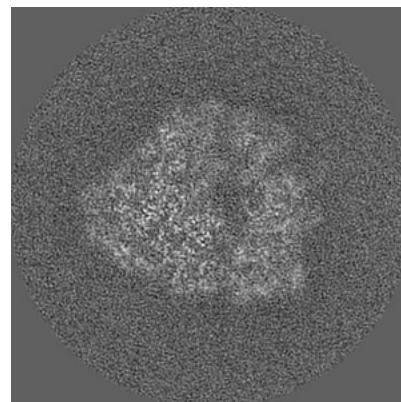
6.3.2 Raw map



X Index: 107



Y Index: 122

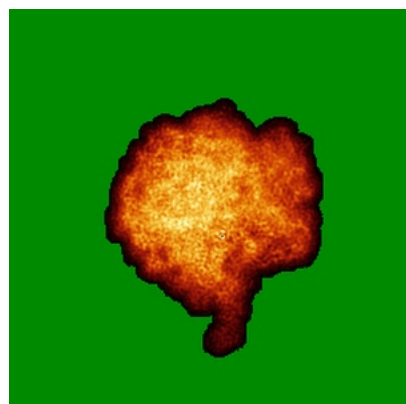


Z Index: 122

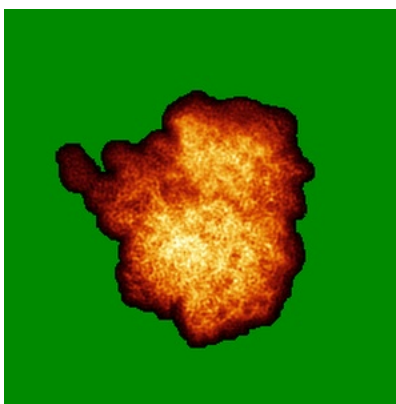
The images above show the largest variance slices of the map in three orthogonal directions.

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

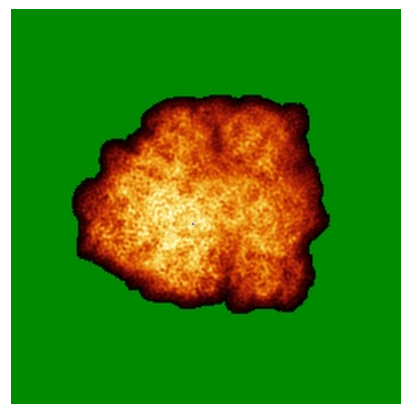
6.4.1 Primary map



X

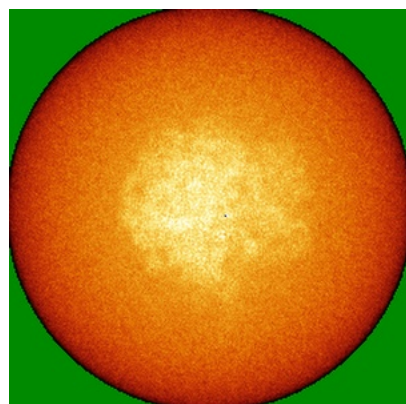


Y

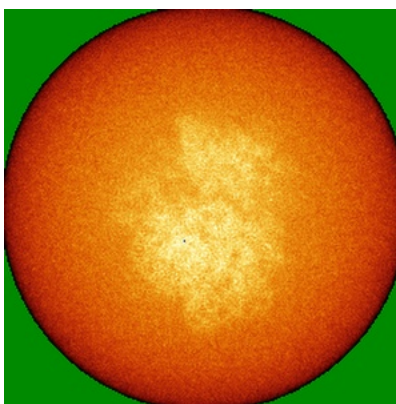


Z

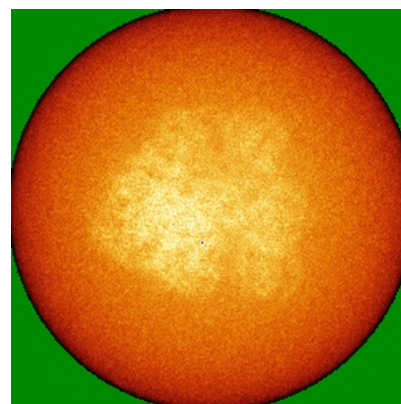
6.4.2 Raw map



X



Y

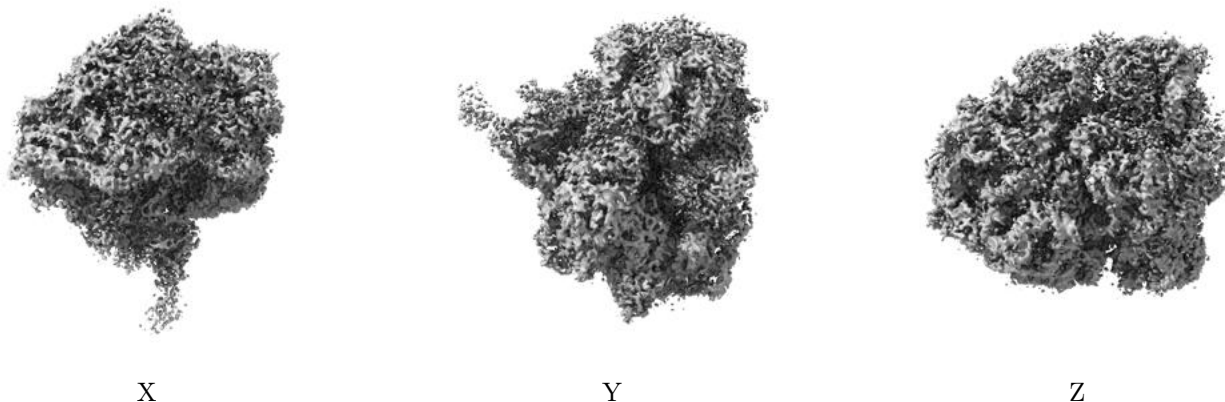


Z

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

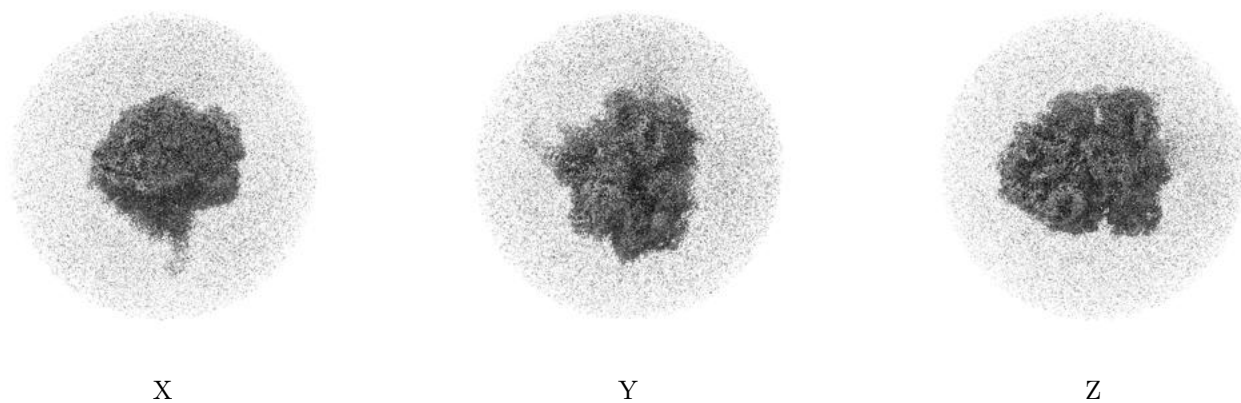
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.66. 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.

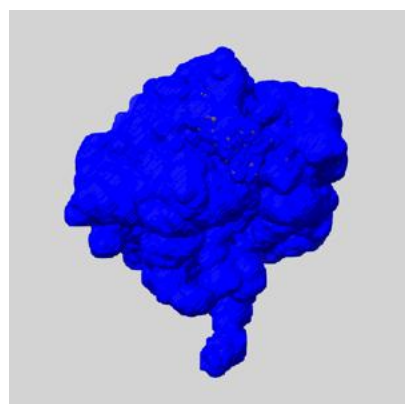
6.6 Mask visualisation [i](#)

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

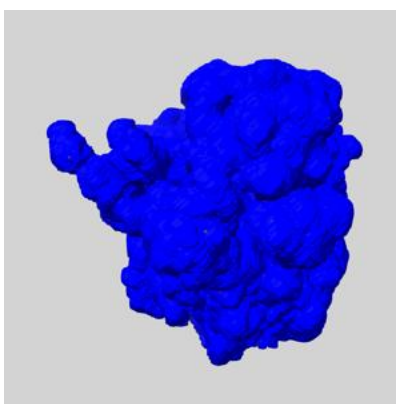
A mask typically either:

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

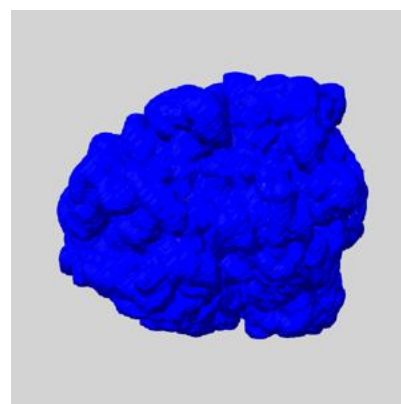
6.6.1 emd_13435_msk_1.map [i](#)



X



Y

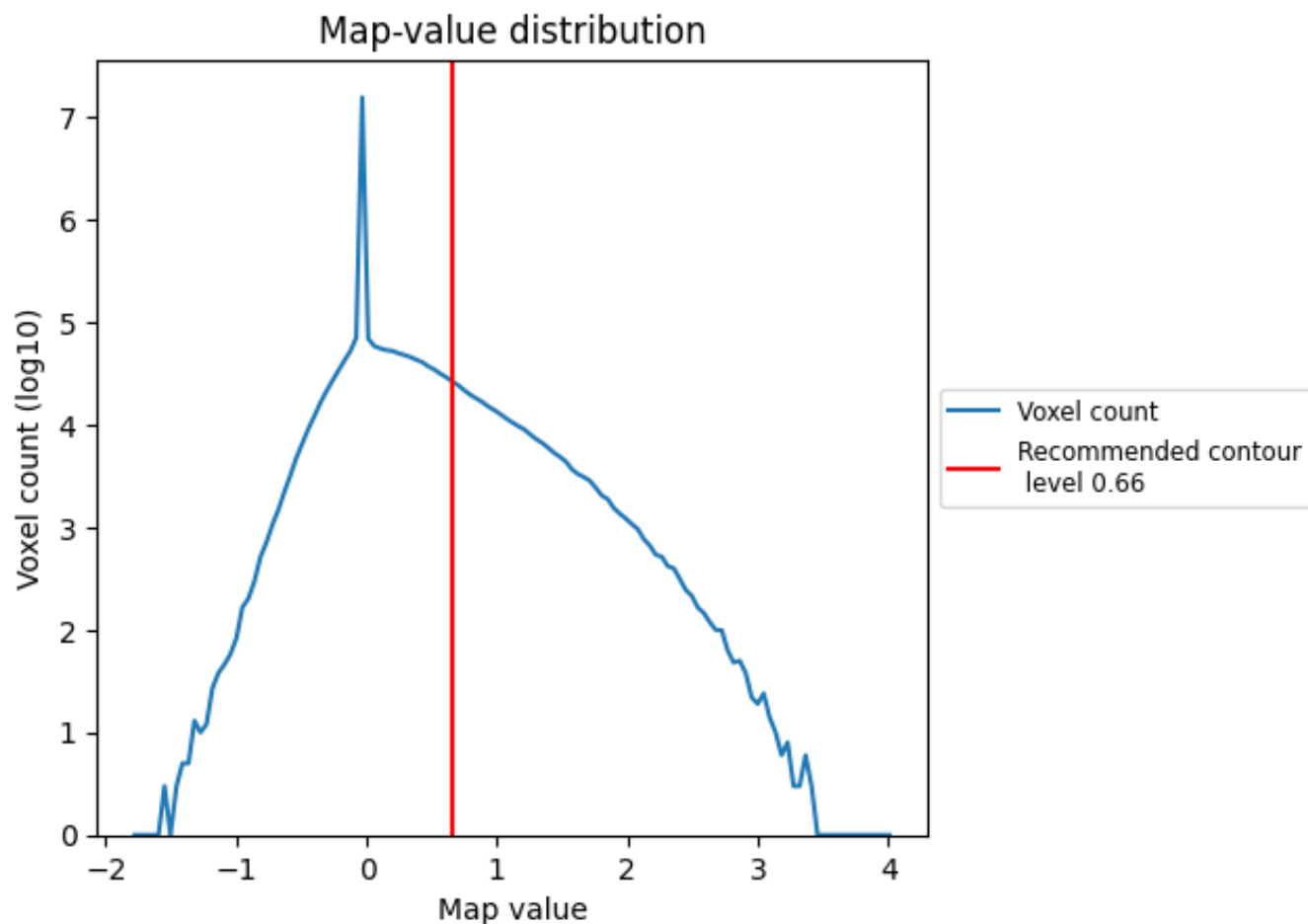


Z

7 Map analysis [i](#)

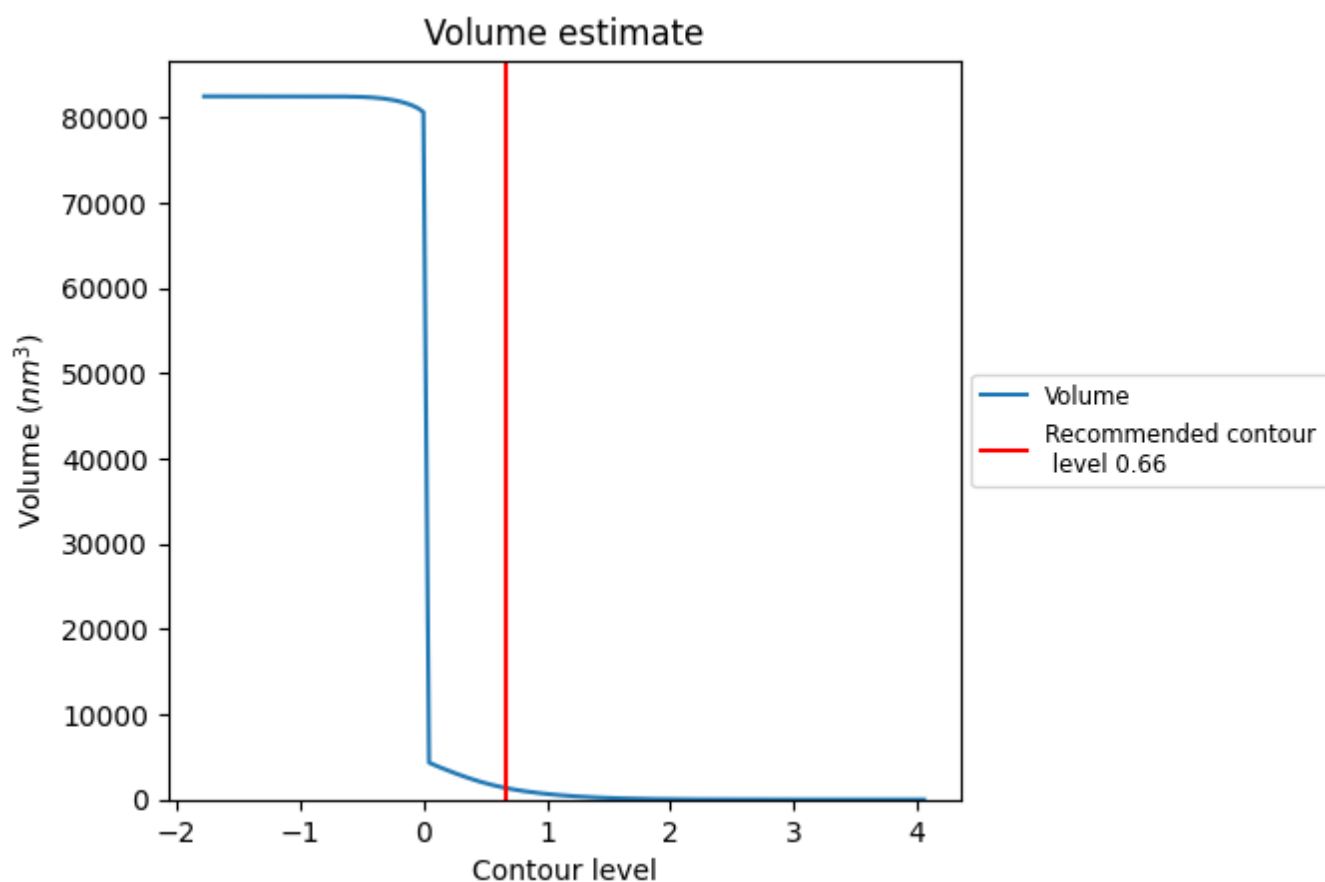
This section contains the results of statistical analysis of the map.

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.

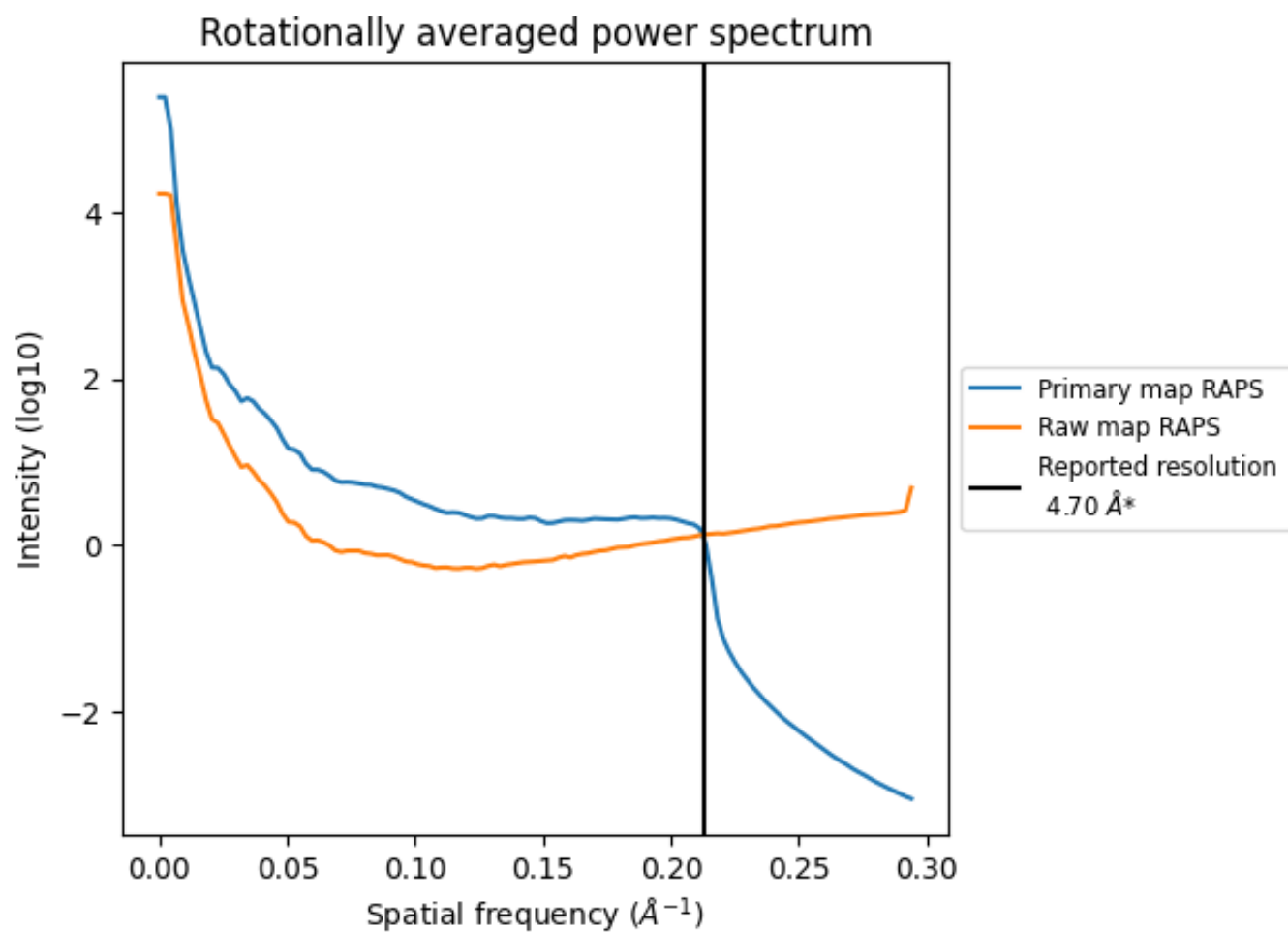
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1378 nm³; this corresponds to an approximate mass of 1245 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 ⓘ

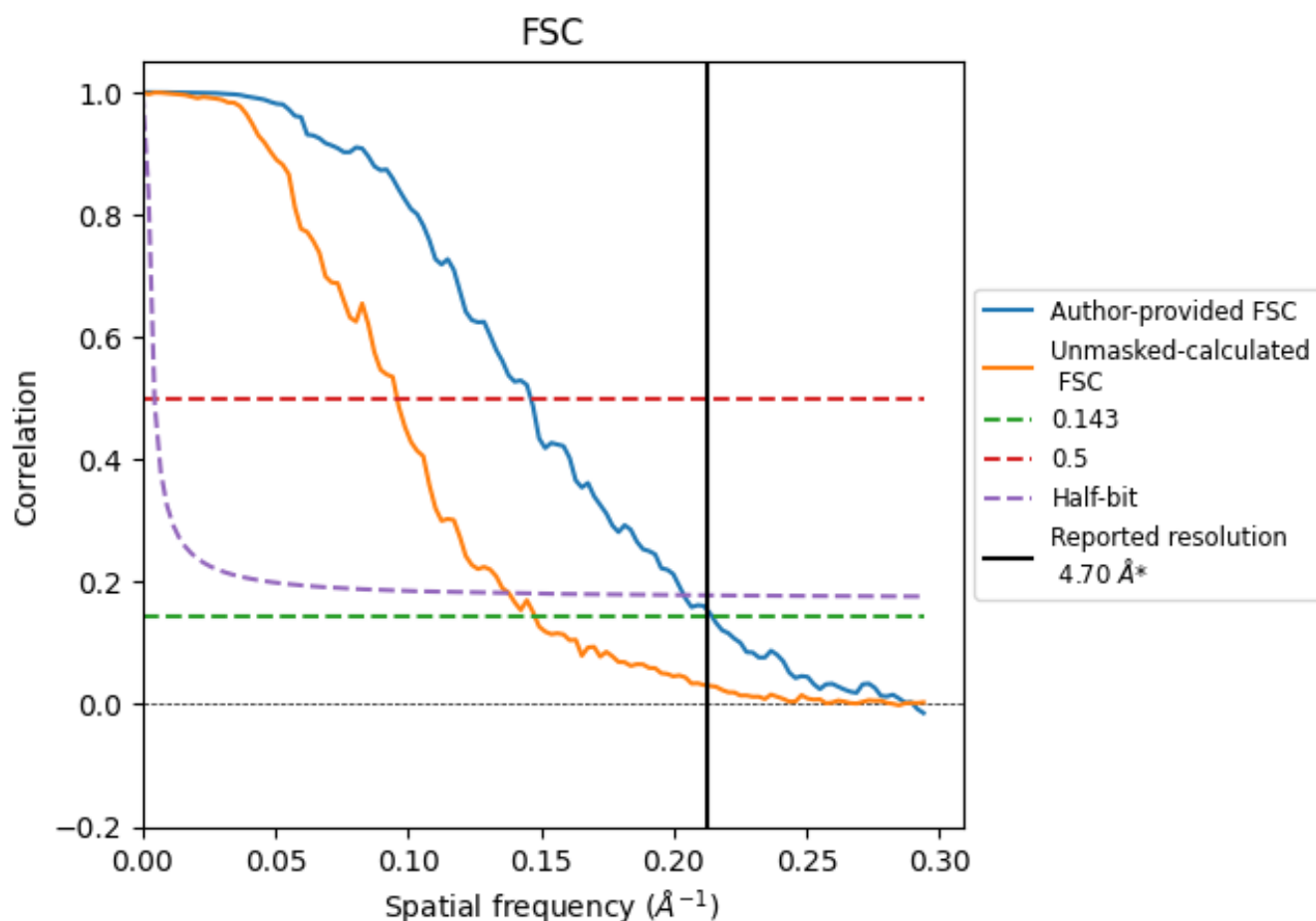


*Reported resolution corresponds to spatial frequency of 0.213 $\text{\AA}^{-1}$

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 0.213 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

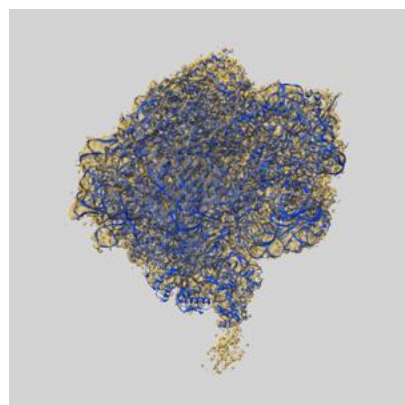
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.66	6.84	4.90
Unmasked-calculated*	6.77	10.44	7.25

*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 6.77 differs from the reported value 4.7 by more than 10 %

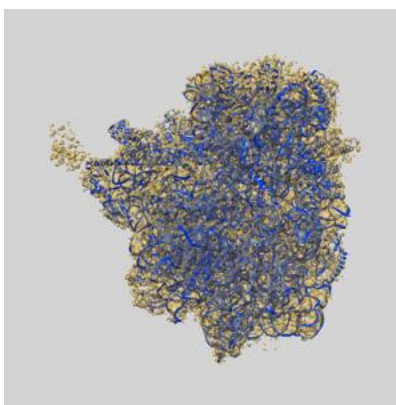
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13435 and PDB model 7PIB. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

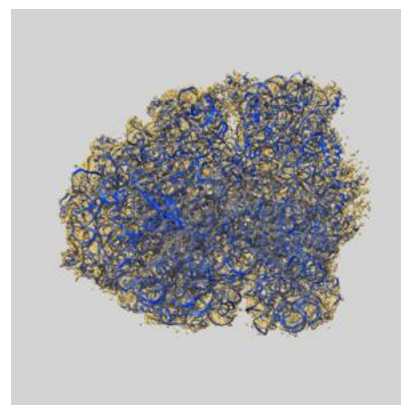
9.1 Map-model overlay [i](#)



X



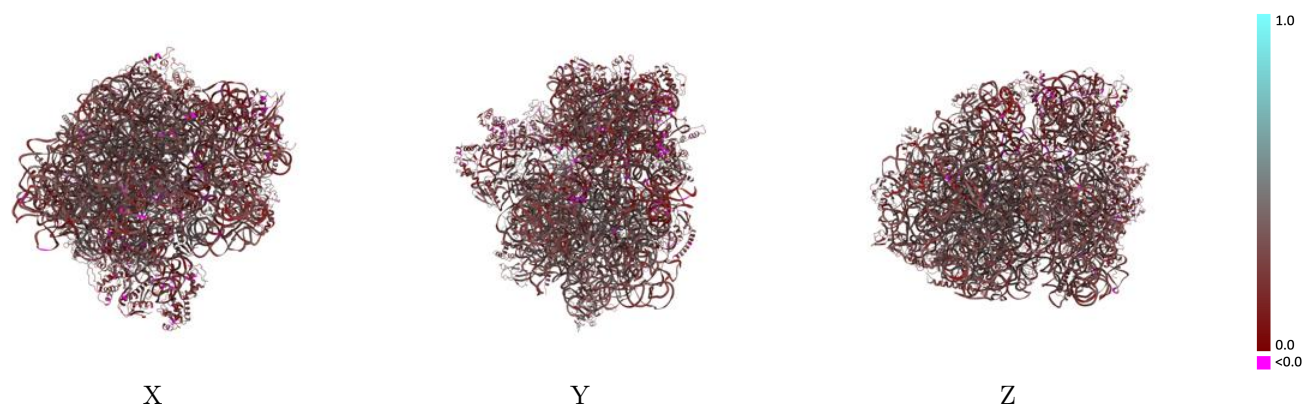
Y



Z

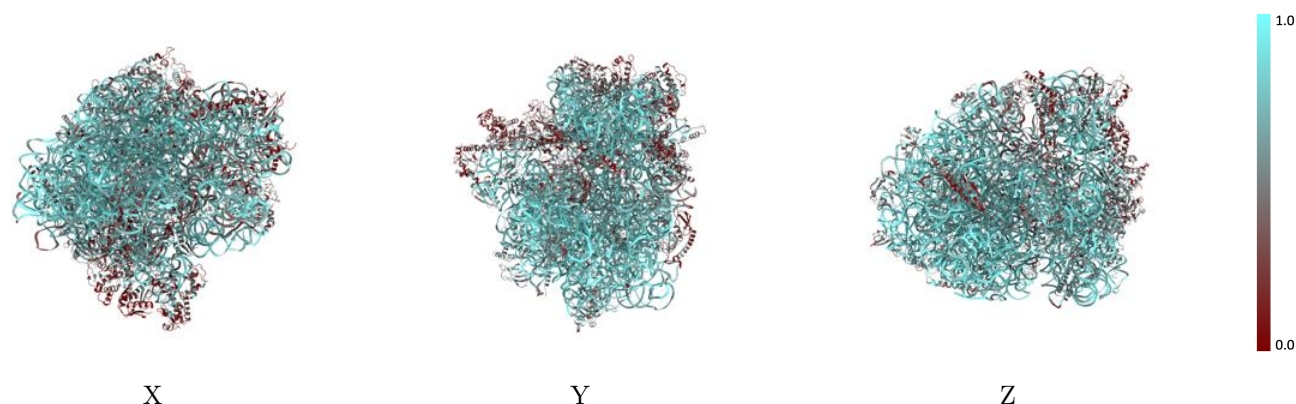
The images above show the 3D surface view of the map at the recommended contour level 0.66 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



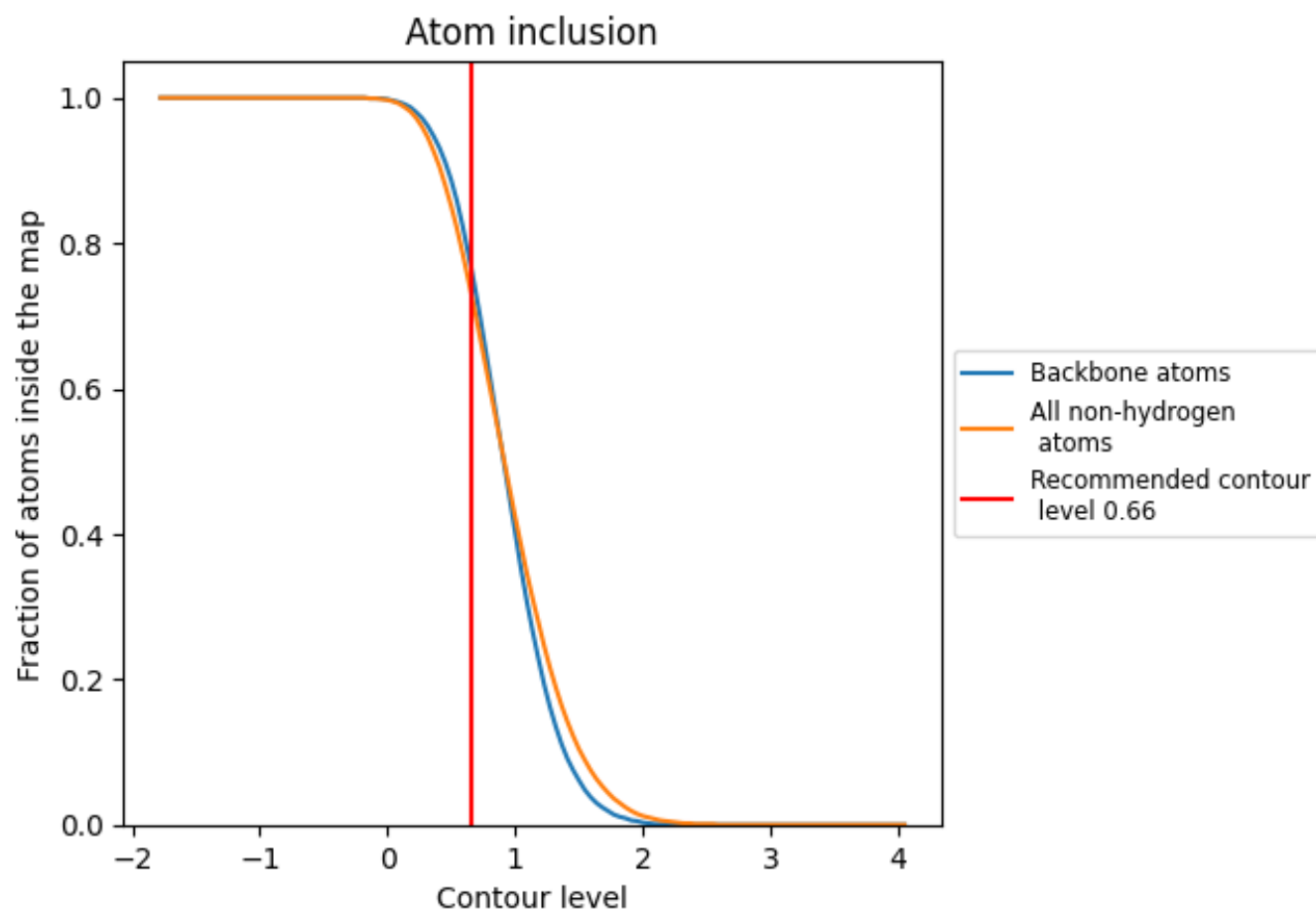
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.66).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 73% 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 (0.66) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7290	 0.2990
0	 0.7590	 0.3750
1	 0.6840	 0.3500
2	 0.6760	 0.3730
3	 0.8630	 0.3180
4	 0.8190	 0.2810
5	 0.8350	 0.2890
7	 0.5130	 0.0850
8	 0.6510	 0.1860
9	 0.3110	 0.2380
A	 0.4400	 0.2790
B	 0.4520	 0.2740
C	 0.4750	 0.2560
D	 0.5460	 0.3130
E	 0.4390	 0.2850
F	 0.2950	 0.2140
G	 0.5640	 0.3120
H	 0.3920	 0.2290
I	 0.4160	 0.2810
J	 0.5430	 0.3040
K	 0.6000	 0.3420
L	 0.3280	 0.2360
M	 0.6310	 0.3220
N	 0.5650	 0.2920
O	 0.6140	 0.3080
P	 0.5620	 0.3200
Q	 0.5580	 0.2790
R	 0.4340	 0.2350
S	 0.6070	 0.2650
T	 0.5220	 0.2980
W	 0.0890	 0.1830
a	 0.6820	 0.3520
b	 0.6410	 0.3530
c	 0.6000	 0.3380
d	 0.4750	 0.2760



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Chain	Atom inclusion	Q-score
e	 0.5180	 0.3160
f	 0.2330	 0.2220
g	 0.3070	 0.2330
h	 0.2710	 0.2180
i	 0.6710	 0.3440
j	 0.6130	 0.3560
k	 0.6130	 0.3390
l	 0.6520	 0.3370
m	 0.6740	 0.3290
n	 0.5570	 0.2990
o	 0.5820	 0.3270
p	 0.6900	 0.3270
q	 0.6270	 0.3590
r	 0.6510	 0.3320
s	 0.6600	 0.3580
t	 0.4530	 0.2900
u	 0.6550	 0.3440
v	 0.5980	 0.2990
w	 0.5740	 0.2760
x	 0.3440	 0.2400
y	 0.6310	 0.3190
z	 0.6470	 0.3470