



Full wwPDB EM Validation Report ⓘ

Oct 28, 2024 – 07:08 am GMT

PDB ID : 7PIQ
EMDB ID : EMD-13447
Title : 70S ribosome with A- and P-site tRNAs in pseudouridimycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-23
Resolution : 9.70 Å (reported)
Based on initial models : 4V7C, 7OOC, 7OOD

This is a Full wwPDB EM Validation 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

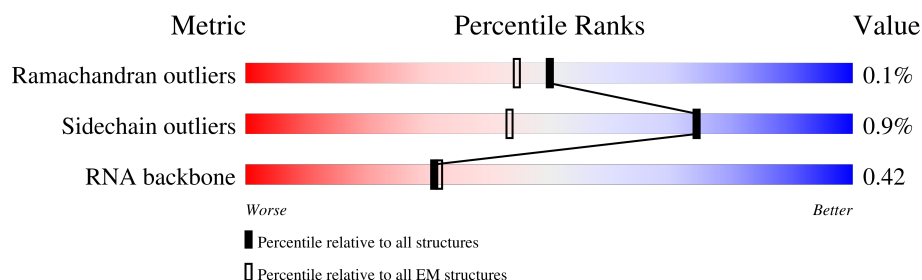
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	48	<div> <div>6%</div> <div>98%</div> <div>.</div> </div>
2	1	59	<div> <div>15%</div> <div>100%</div> </div>
3	2	37	<div> <div>22%</div> <div>97%</div> <div>.</div> </div>
4	A	294	<div> <div>33%</div> <div>81%</div> <div>18%</div> </div>
5	B	273	<div> <div>44%</div> <div>78%</div> <div>21%</div> </div>
6	C	205	<div> <div>37%</div> <div>99%</div> <div>.</div> </div>
7	D	219	<div> <div>27%</div> <div>69%</div> <div>30%</div> </div>
8	E	215	<div> <div>31%</div> <div>77%</div> <div>22%</div> </div>

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

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Mol	Chain	Length	Quality of chain
34	k	151	
35	l	139	
36	m	124	
37	n	116	
38	o	119	
39	p	127	
40	q	100	
41	r	159	
42	s	237	
43	t	111	
44	u	104	
45	v	65	
46	w	111	
47	x	97	
48	y	57	
49	z	53	
50	3	2907	
51	4	108	
52	5	1520	
53	6	76	
53	7	76	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146057 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
30	g	121	Total	C	N	O	S	0
			910	580	158	169	3	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	112	Total	C	N	O	S	0	0
			934	594	186	152	2		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

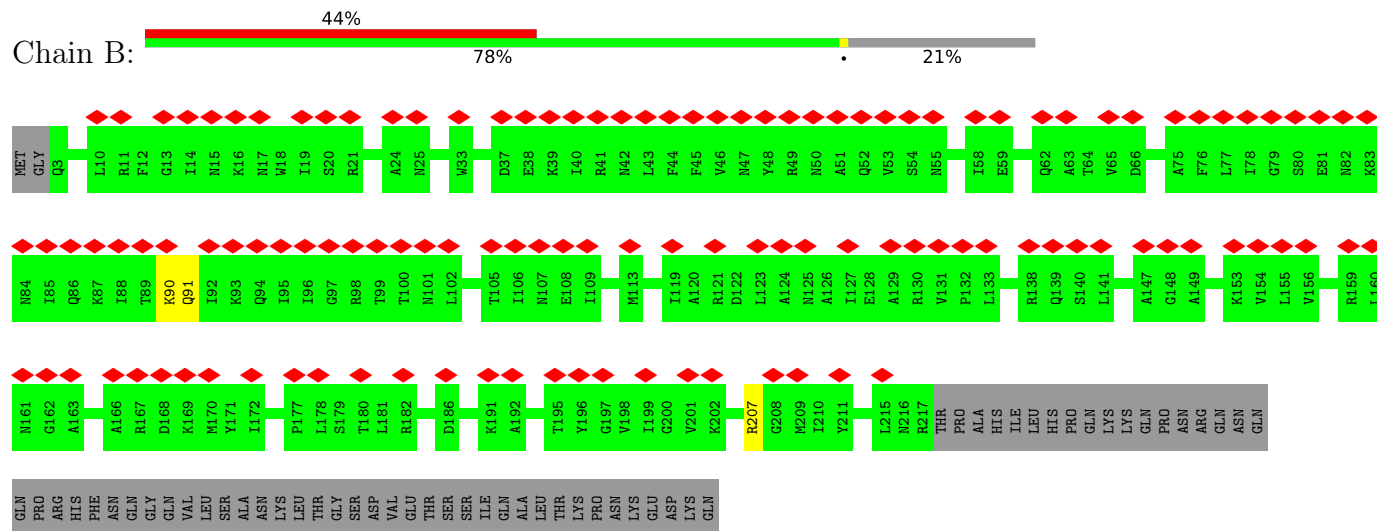
Mol	Chain	Residues	Atoms					AltConf	Trace
52	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

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

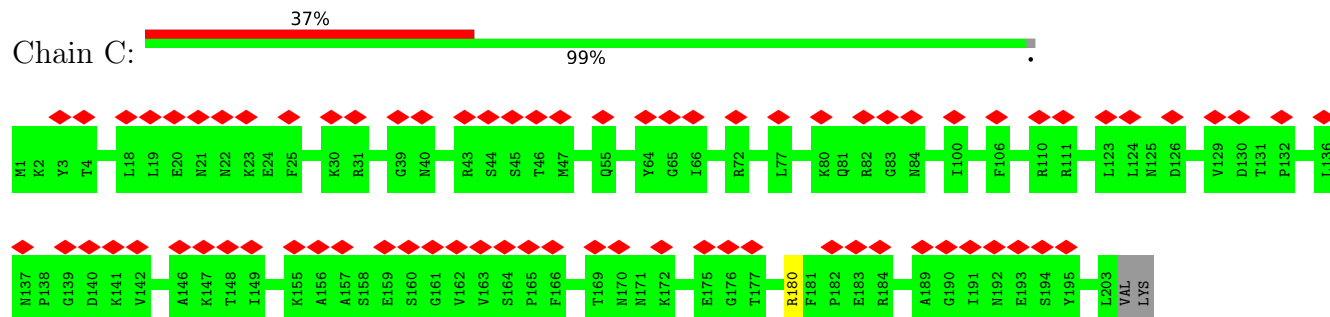
Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
53	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

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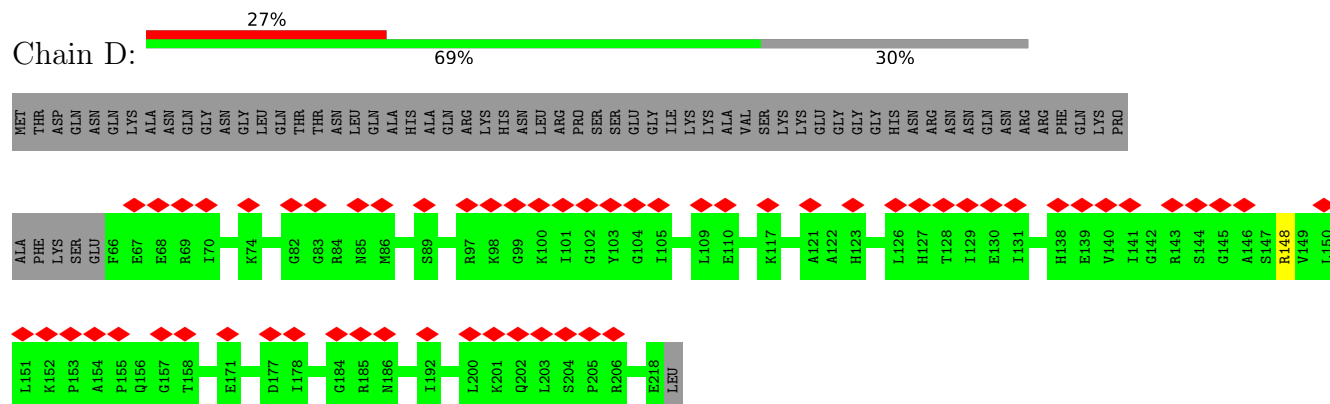
• Molecule 5: 30S ribosomal protein S3



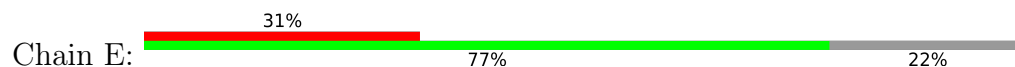
• Molecule 6: 30S ribosomal protein S4

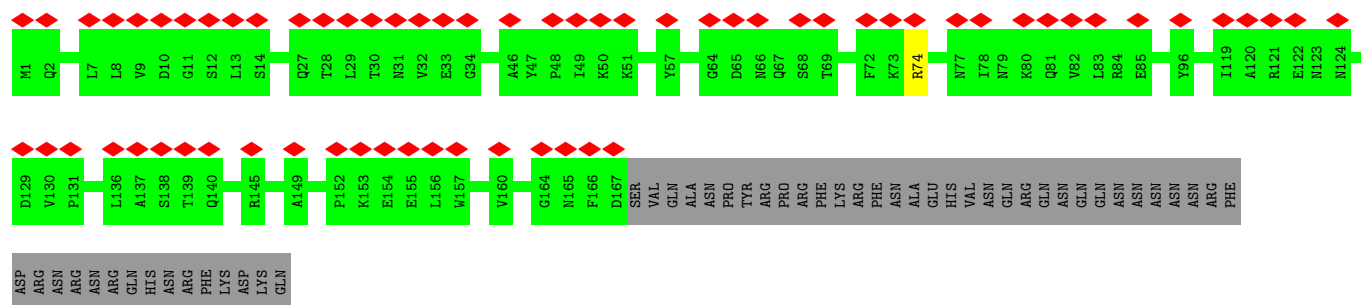


• Molecule 7: 30S ribosomal protein S5

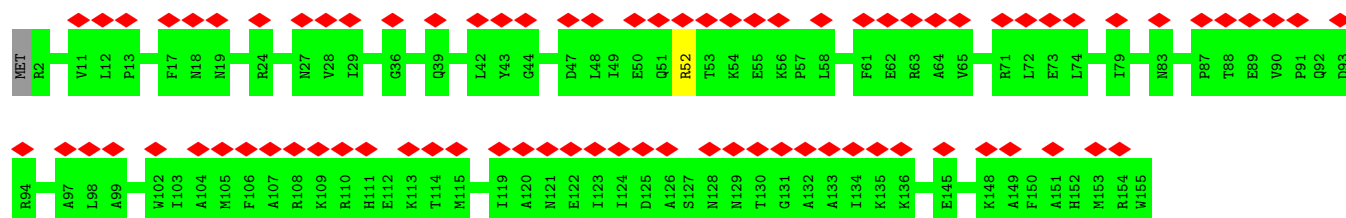


• Molecule 8: 30S ribosomal protein S6

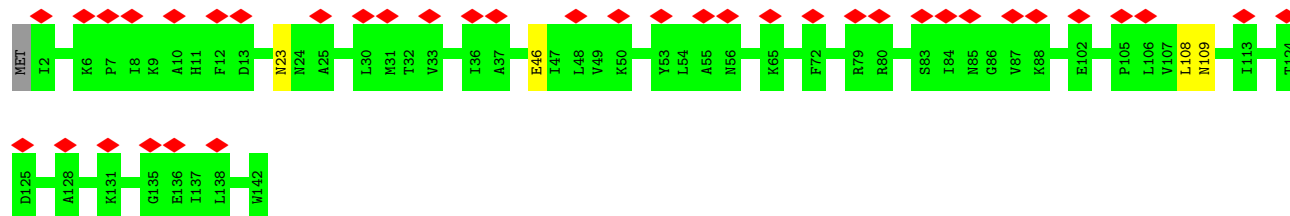




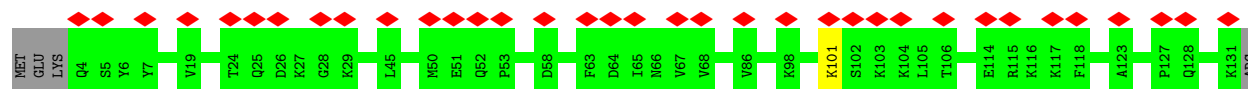
• Molecule 9: 30S ribosomal protein S7



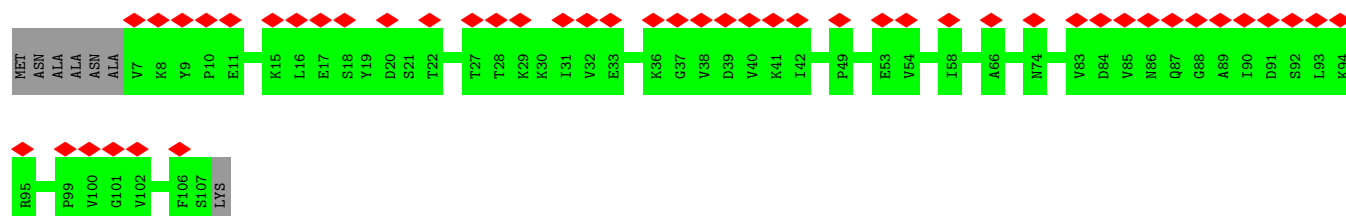
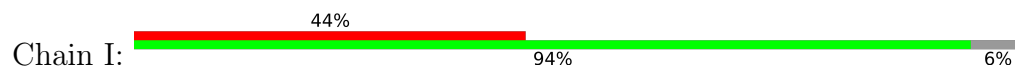
• Molecule 10: 30S ribosomal protein S8



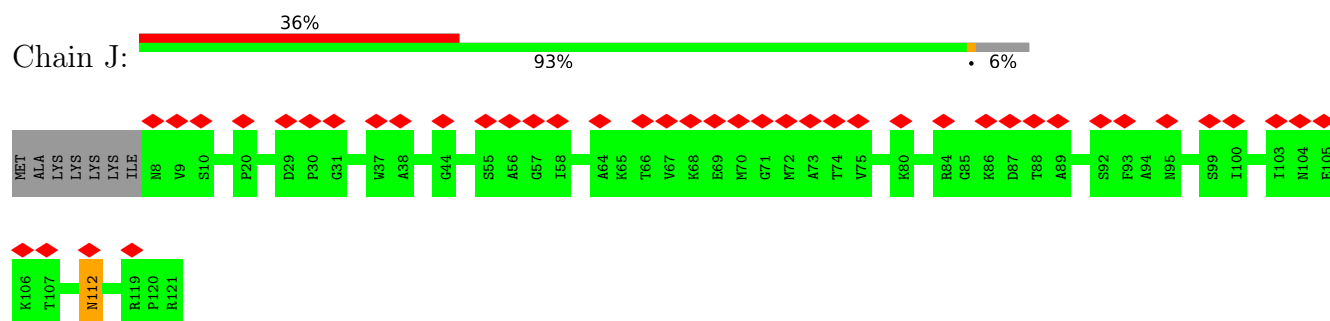
• Molecule 11: 30S ribosomal protein S9



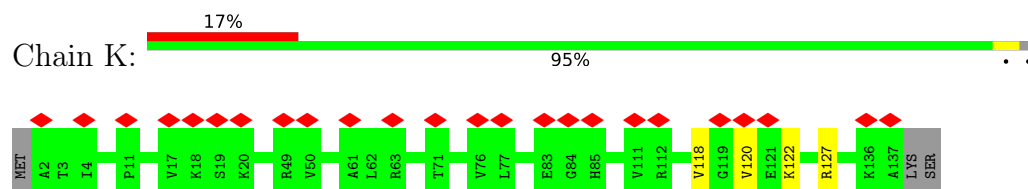
• Molecule 12: 30S ribosomal protein S10



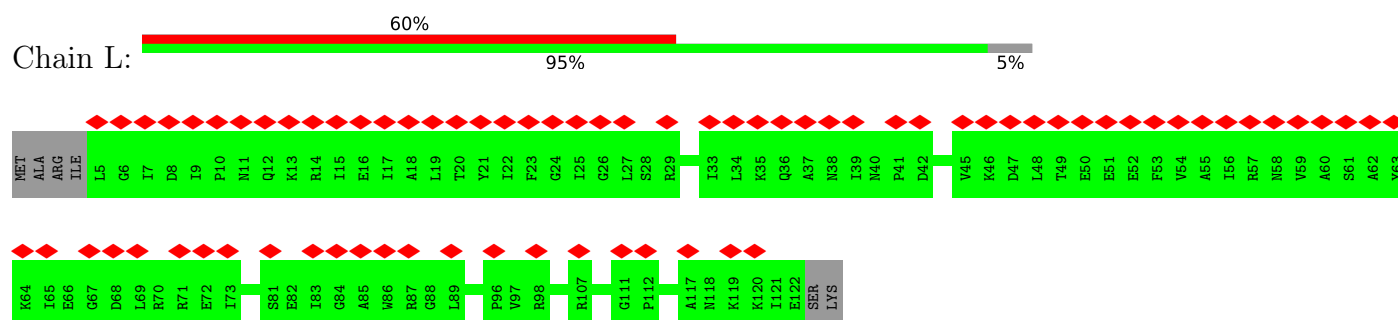
- Molecule 13: 30S ribosomal protein S11



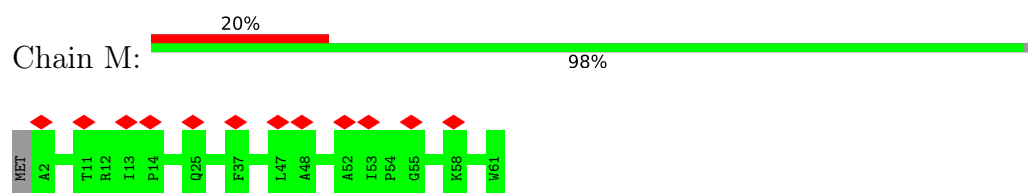
- Molecule 14: 30S ribosomal protein S12



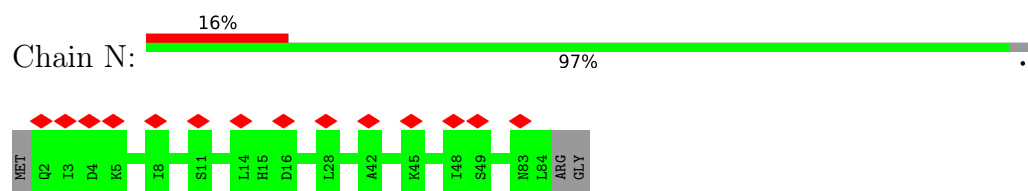
- Molecule 15: 30S ribosomal protein S13



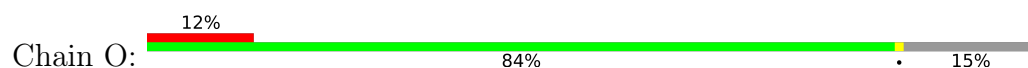
- Molecule 16: 30S ribosomal protein S14 type Z

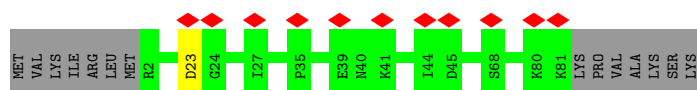


- Molecule 17: 30S ribosomal protein S15

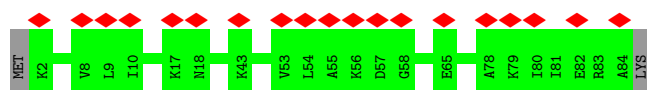


- Molecule 18: 30S ribosomal protein S16

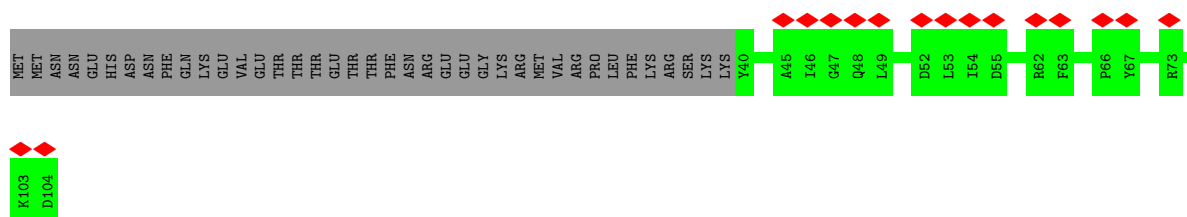




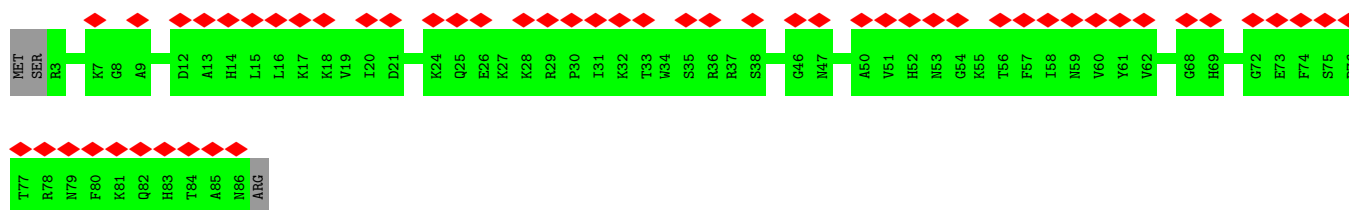
- Molecule 19: 30S ribosomal protein S17



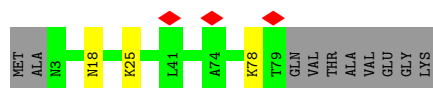
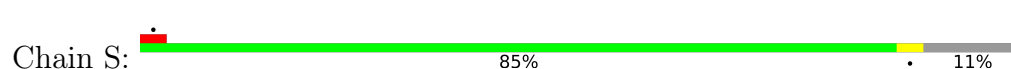
- Molecule 20: 30S ribosomal protein S18



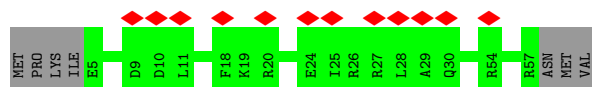
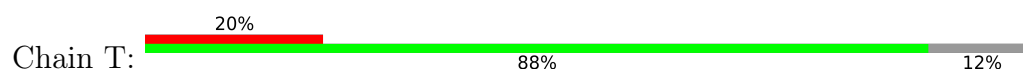
- Molecule 21: 30S ribosomal protein S19



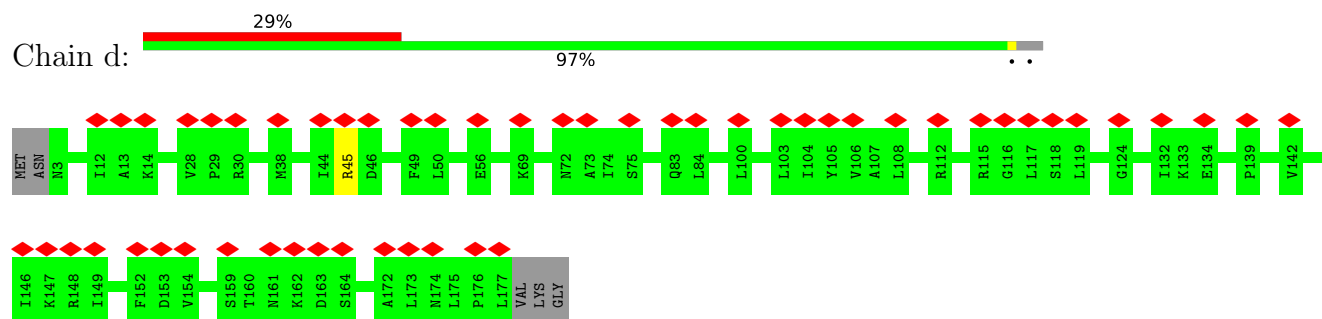
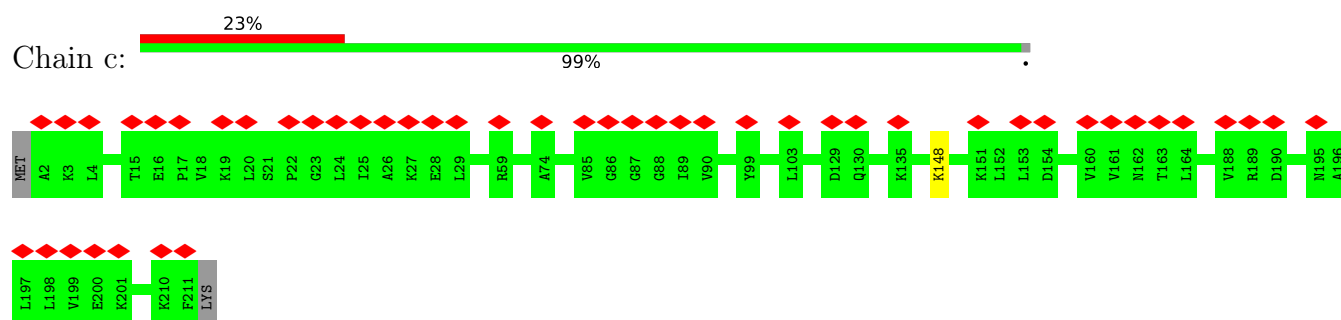
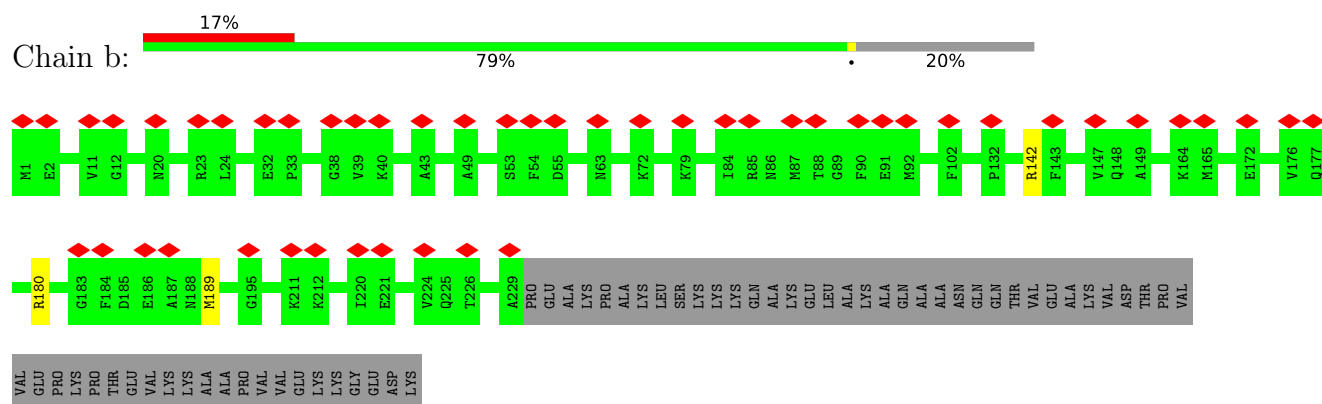
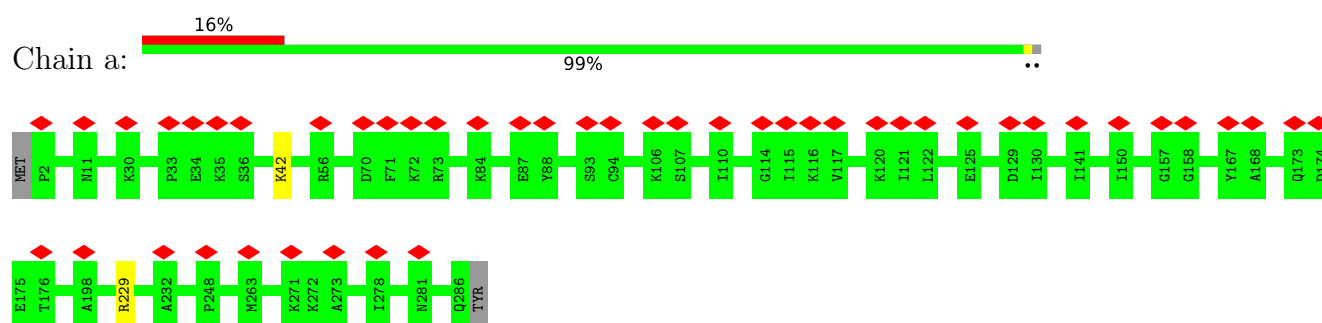
- Molecule 22: 30S ribosomal protein S20

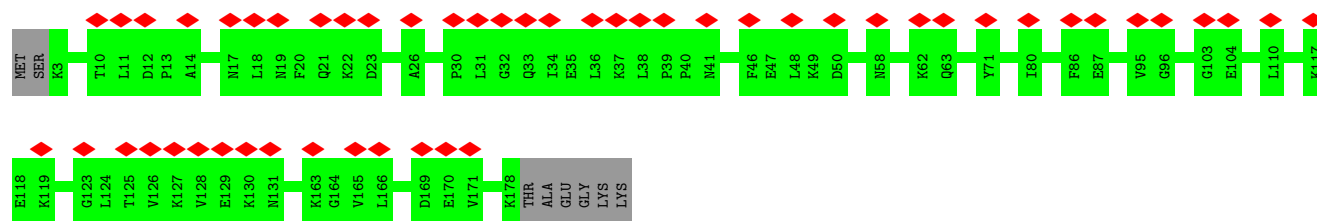


- Molecule 23: 30S ribosomal protein S21



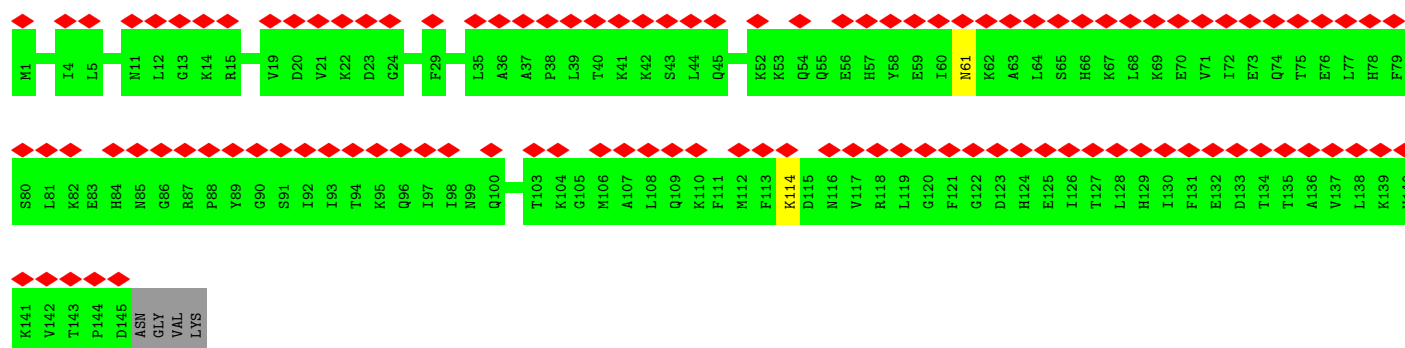
- Molecule 24: 50S ribosomal protein L2





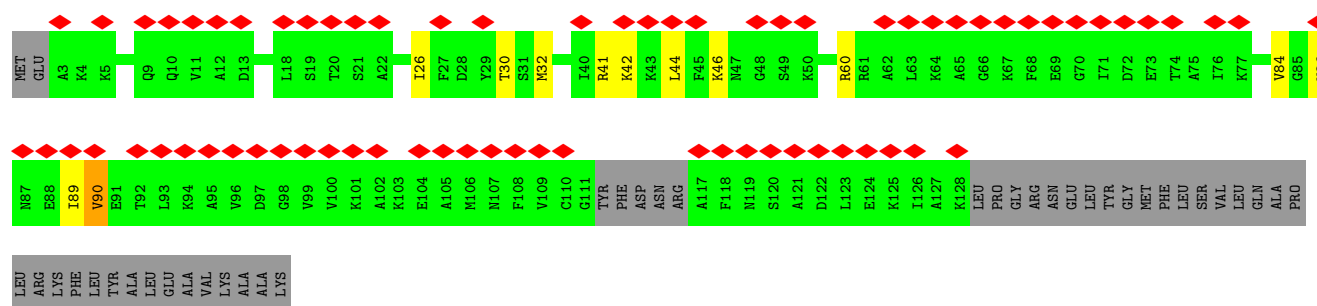
• Molecule 29: 50S ribosomal protein L9

Chain f: 74% 96%



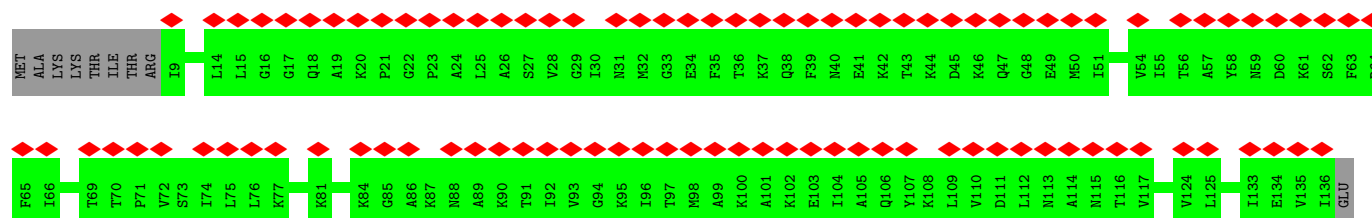
• Molecule 30: 50S ribosomal protein L10

Chain g: 44% 68% 7% 25%



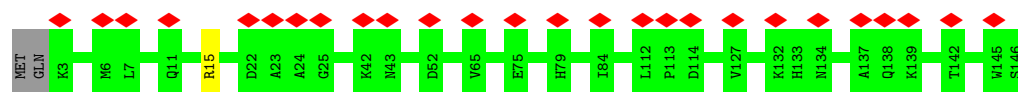
• Molecule 31: 50S ribosomal protein L11

Chain h: 71% 93% 7%

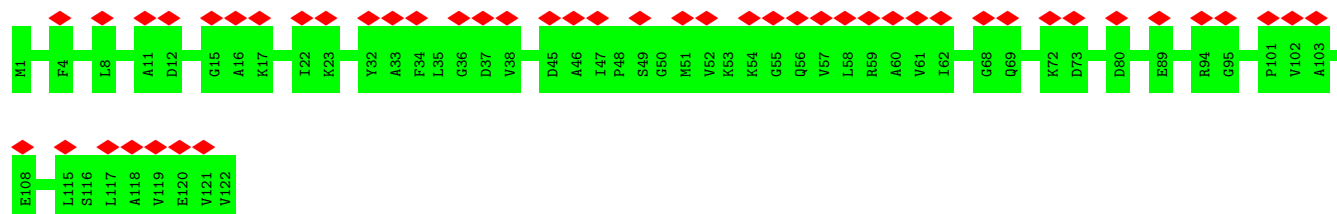
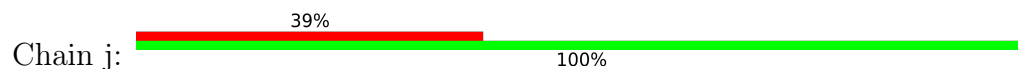


• Molecule 32: 50S ribosomal protein L13

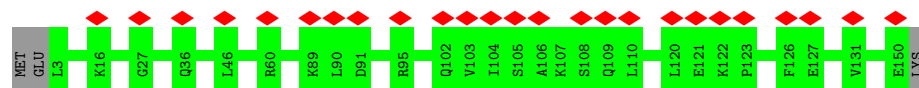
Chain i: 18% 98%



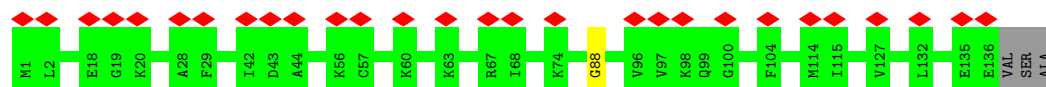
- Molecule 33: 50S ribosomal protein L14



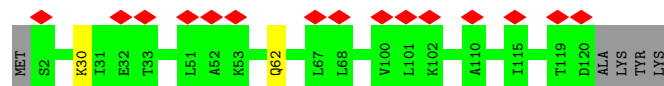
- Molecule 34: 50S ribosomal protein L15



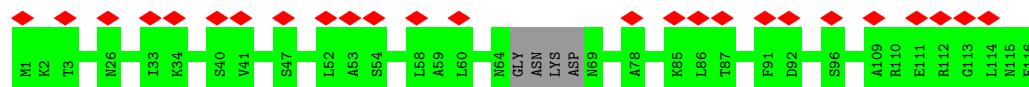
- Molecule 35: 50S ribosomal protein L16



- Molecule 36: 50S ribosomal protein L17

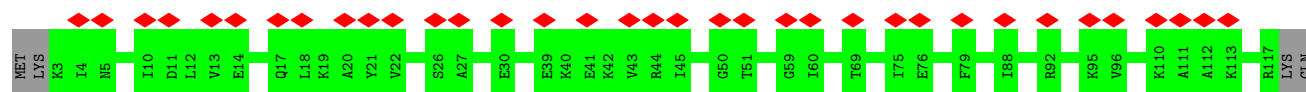


- Molecule 37: 50S ribosomal protein L18

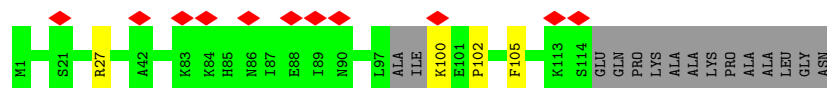
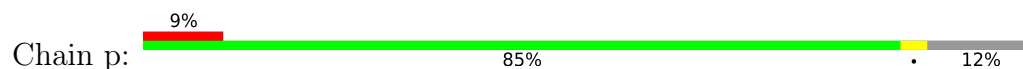


- Molecule 38: 50S ribosomal protein L19

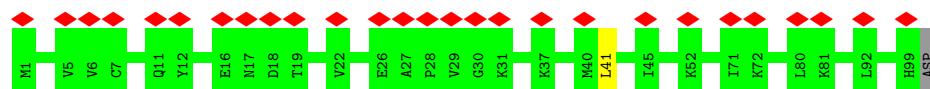




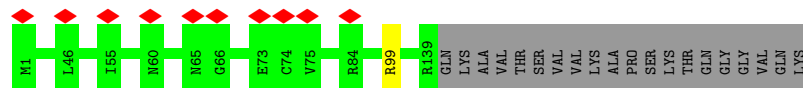
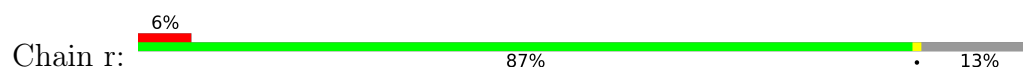
- Molecule 39: 50S ribosomal protein L20



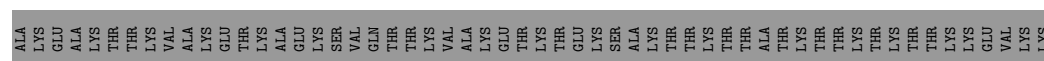
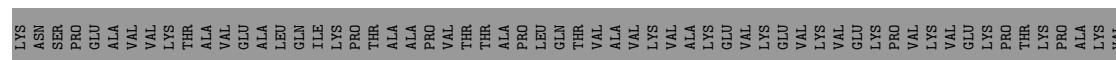
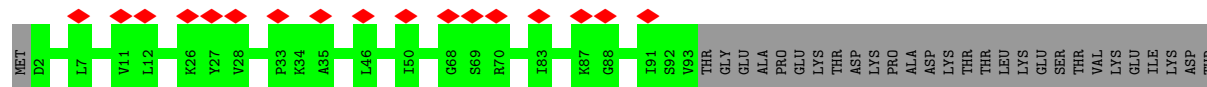
- Molecule 40: 50S ribosomal protein L21



- Molecule 41: 50S ribosomal protein L22



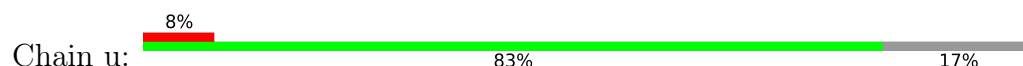
- Molecule 42: 50S ribosomal protein L23

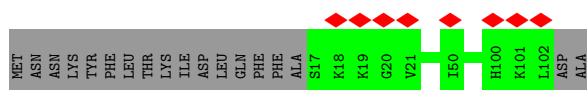


- Molecule 43: 50S ribosomal protein L24

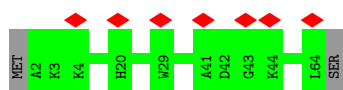


- Molecule 44: 50S ribosomal protein L27

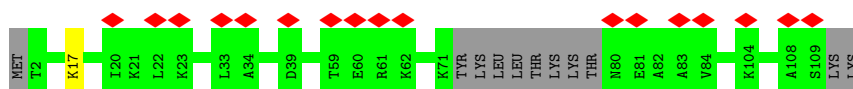
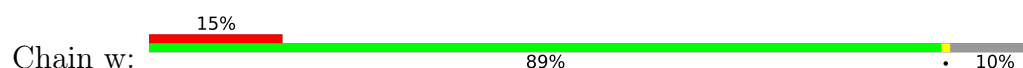




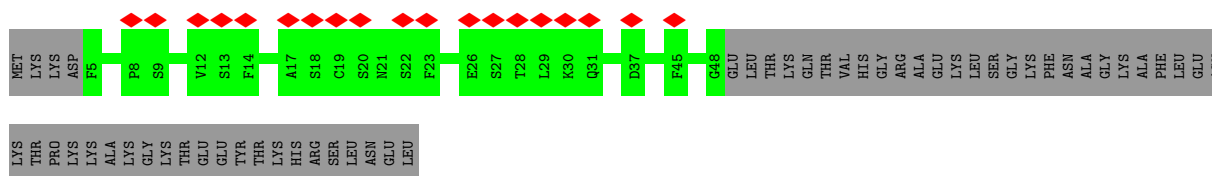
- Molecule 45: 50S ribosomal protein L28



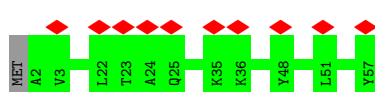
- Molecule 46: 50S ribosomal protein L29



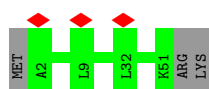
- Molecule 47: 50S ribosomal protein L31



- Molecule 48: 50S ribosomal protein L32

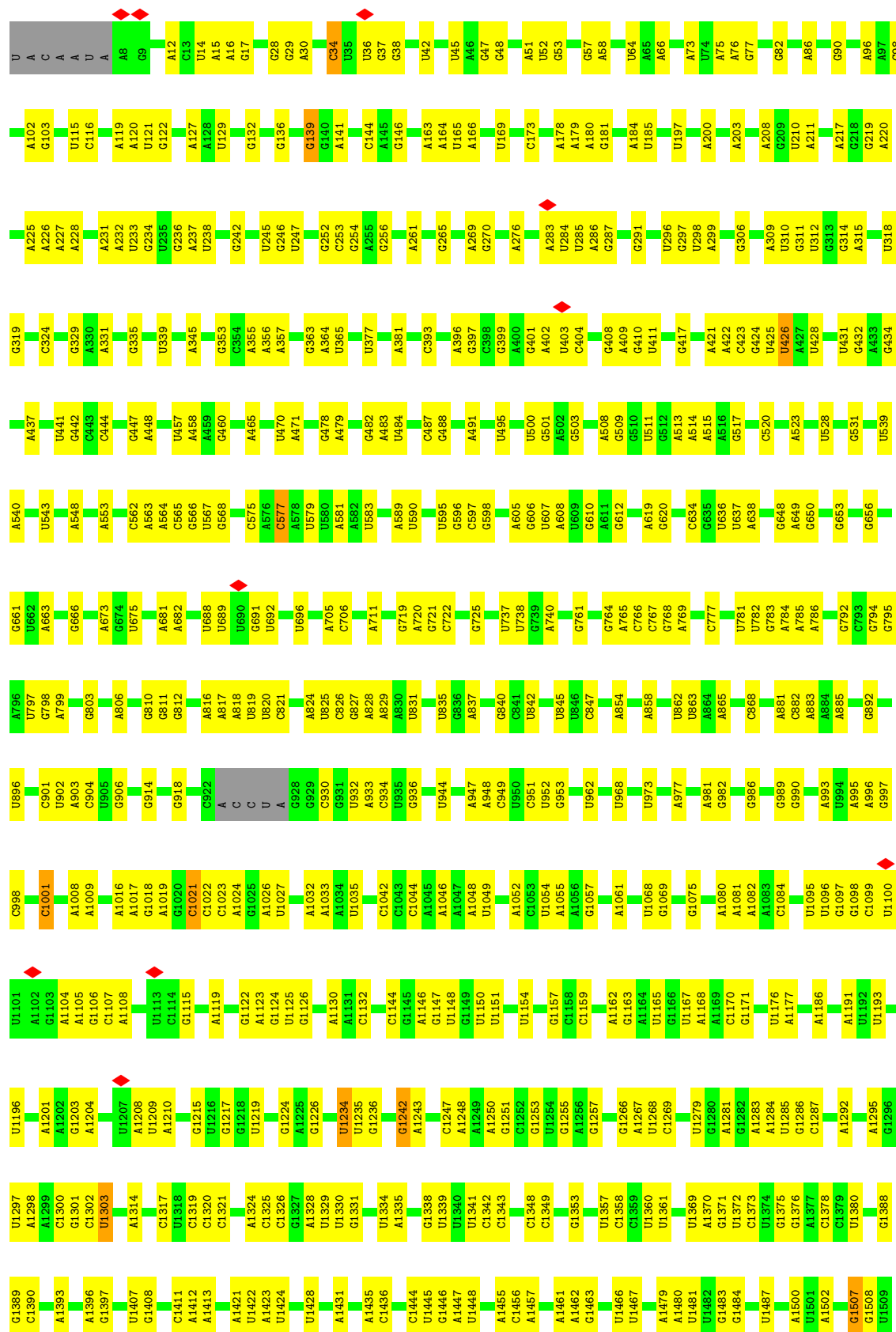


- Molecule 49: 50S ribosomal protein L33 1



- Molecule 50: 23S ribosomal RNA

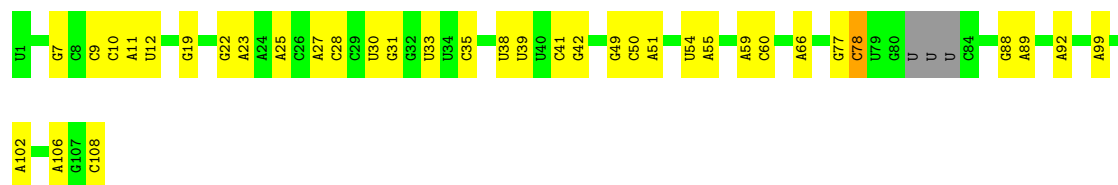




A1510	A1603	C1720	A1836	U1946	A2066	G2155	G2242	U2352	U2468	G2569	A2668	C2804
U1514	C1608	G1721	G1842	U1947	A2067	G2156	G2246	G2353	A2469	U2570	G2669	A2805
A1515	G1612	U1727	C1843	C1948	G2068	C2157	G2247	A2354	G2470	A2574	G2672	A2806
G1516	U1613	A1728	G1847	U1959	A2069	C2158	G2254	U2358	G2471	G2575	C2675	G2807
G1517	A1614	G1733	U1848	A1960	C2070	U2159	A2255	G2361	C2475	A2578	C2681	A2808
C1518	G1615	A1734	G1849	U1961	C2071	U2160	C2256	A2362	A2476	U2579	G2684	A2809
A1519	G1616	G1737	G1855	U1962	C2072	U2161	U2257	C2363	A2477	A2580	G2688	A2810
A1520	U1618	G1741	G1857	C1970	G2074	U2162	G2258	C2367	A2484	C2581	A2694	G2811
C1523	A1619	A1745	U1856	C1971	G2075	A2165	G2259	U2367	U2485	G2584	C2697	A2812
U1533	A1626	U1746	G1863	U1972	G2076	G2166	U2260	U2368	A2486	A2585	C2715	A2813
A1534	U1636	A1748	A1864	U1973	U2083	G2167	U2261	A2381	U2487	G2586	C2718	A2814
A1541	A1637	U1751	A1865	U1977	A2084	A2171	G2262	A2382	U2488	U2587	C2719	C2822
U1543	G1640	A1752	U1872	G1978	G2087	A2179	U2263	U2389	U2489	C2591	C2721	A2823
G1550	A1641	A1761	A1873	G1979	G2100	U2180	U2264	C2391	C2491	U2592	C2722	A2824
A1554	G1642	C1762	U1877	G1980	G2106	U2181	A2274	U2392	G2492	U2593	C2726	G2829
G1555	A1643	G1763	A1878	U1981	A2107	C2182	A2276	C2393	U2493	C2594	C2727	A2830
A1558	A1644	U1764	G1880	U1982	U2110	U2185	A2281	G2397	C2494	C2595	C2728	U2831
A1559	G1648	G1765	A1884	C1990	U2111	C2186	A2286	U2398	G2495	U2604	C2734	G2837
U	A1650	G1768	U1889	C1997	A2112	U2187	G2287	C2410	U2496	G2605	G2735	G2838
G	C1651	A1769	U1890	U1997	U2113	U2188	U2291	U2414	G2498	A2606	U2736	A2839
A	A1652	A1770	A1891	U1998	G2114	C2189	A2294	A2415	C2499	G2607	U2737	U2840
C	G1653	C1771	A1892	G2004	U2115	U2192	A2295	A2418	U2502	A2608	C2740	U2853
U	A1656	U1780	C1893	G2005	U2116	U2193	A2296	G2419	G2503	C2609	U2741	U2854
C	U1670	U1784	A1896	G2009	U2117	U2194	A2297	C2424	C2504	C2610	U2747	U2855
A	U1679	U1785	C1907	A2010	U2118	U2195	A2298	C2428	U2505	U2611	G2752	G2856
C	A1680	U1786	A1907	G2011	A2119	G2196	A2299	U2431	C2506	U2612	C2753	U2857
A	G1681	A1787	A1908	A2012	U2120	U2197	C2305	U2432	U2512	G2513	U2754	U2858
G1571	C1682	U1788	C1909	C2025	U2121	U2198	G2312	C2431	U2514	U2515	A2765	G2859
U1572	G1683	A1789	G1910	G2028	A2123	U2199	U2313	C2432	G2516	G2517	A2766	U2868
A1573	G1687	U1791	C1807	A2029	A2124	U2200	U2314	A2433	G2518	A2521	A2767	U2869
G1579	A1688	A1807	C1808	A2030	G2128	G2201	U2315	G2436	U2519	A2526	A2773	G2890
G1580	U1689	A1809	A1812	A2037	U2129	G2202	G2316	G2437	U2520	U2527	A2774	A2895
U1581	A1694	C1696	C1812	A2038	A2130	U2203	A2317	A2438	G2521	C2528	A2775	G2896
G1582	G1695	A1696	A1816	A2039	G2131	U2204	G2318	U2439	U2522	A2538	A2776	G2897
G1583	A1697	A1699	U1820	A2040	A2132	A2206	U2319	A2447	A2523	A2539	A2777	A2898
U1584	A1698	A1699	G1701	C2041	G2133	A2207	U2219	U2449	G2524	G2543	A2778	G2899
A1585	A1699	A1699	A1822	C2045	G2134	U2210	A2220	U2450	U2525	U2544	A2779	U2900
U1586	A1699	A1699	A1823	C2046	C2135	U2211	A2221	C2453	U2526	G2545	A2780	A
U1587	A1699	A1699	U1827	C2047	A2136	U2212	U2221	G2454	U2527	U2546	A2781	U
U1588	A1699	A1699	U1834	C2048	A2137	U2213	U2222	A2456	U2528	U2547	A2782	U
A1589	A1699	A1699	U1835	G2049	U2138	U2214	U2223	A2457	U2529	U2548	A2783	U
A1592	A1699	A1699	A1836	A2050	C2139	U2215	U2224	A2458	U2530	U2549	A2784	C
A1593	A1699	A1699	U1938	A2051	G2140	U2216	U2225	A2459	U2531	U2550	A2785	C
G1594	A1699	A1699	A1943	A2052	C2141	U2217	U2226	A2460	U2532	U2551	A2786	A
U1597	A1699	A1699	A1944	A2053	U2148	U2218	U2227	C2232	U2533	U2552	A2787	U
A1600	A1699	A1699	A1945	G2062	C2149	U2219	U2228	U2230	U2534	U2553	A2788	U
				G2063	U2150	U2220	U2229	U2231	U2535	U2554	A2789	U
				G2064	C2151	U2221	U2230	U2232	U2536	U2555	A2790	C
					C2152	U2222	U2231	U2233	U2537	U2556	U2799	A
					U2153	U2223	U2232	U2234	U2538	U2557	C2802	
					A2154	U2224	U2233	U2235	U2539	U2558	G2803	

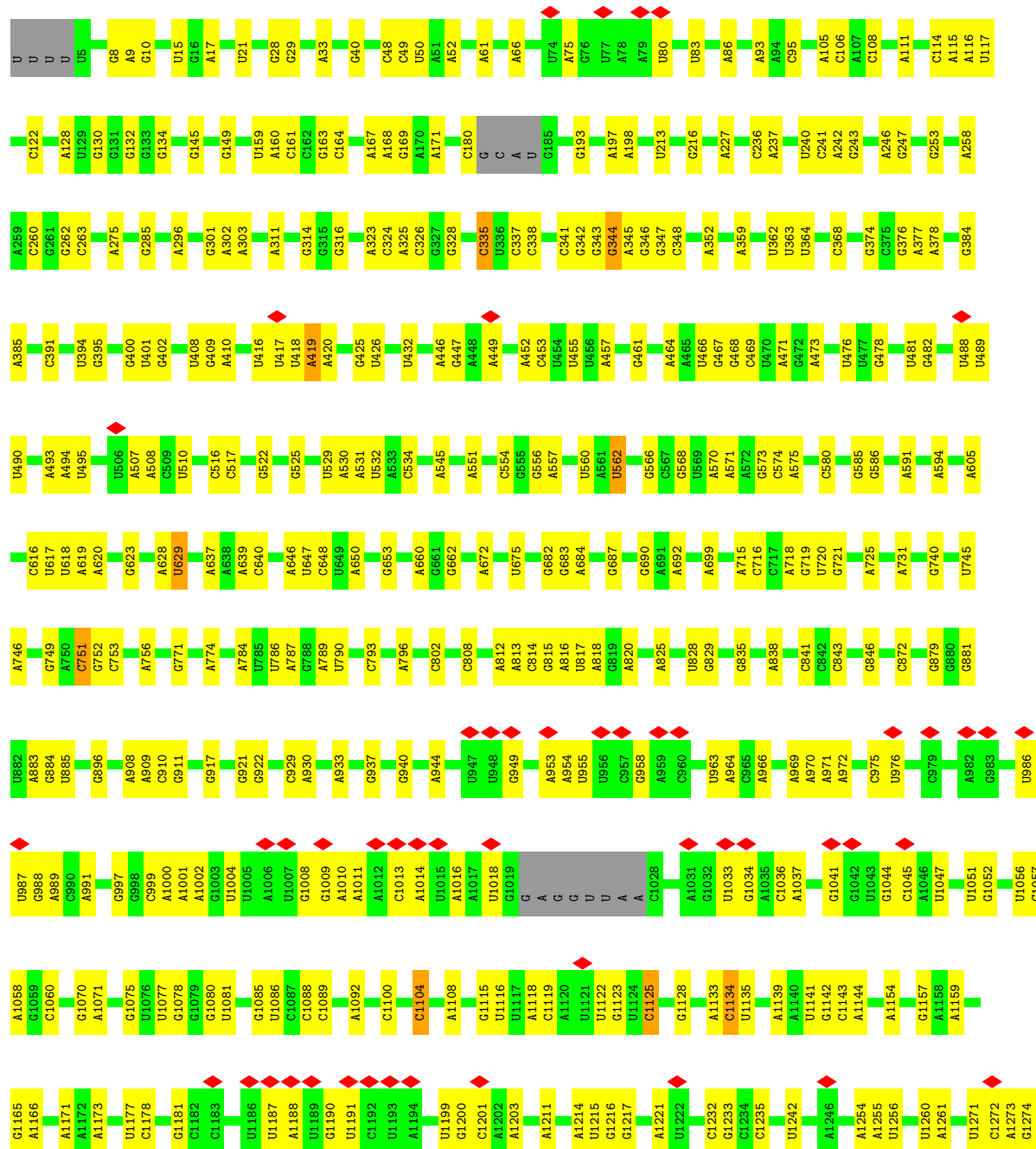
• Molecule 51: 5S ribosomal RNA

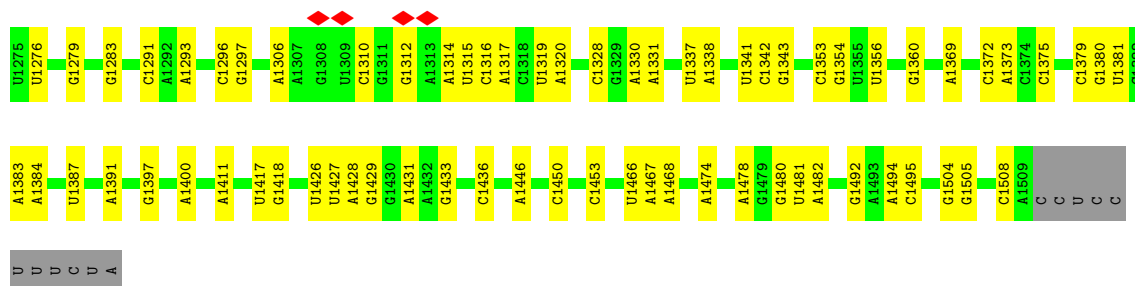
Chain 4:  64% 32%



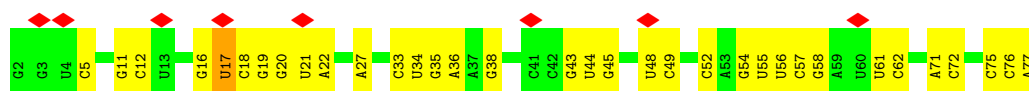
• Molecule 52: 16S ribosomal RNA

Chain 5: 69% 29%

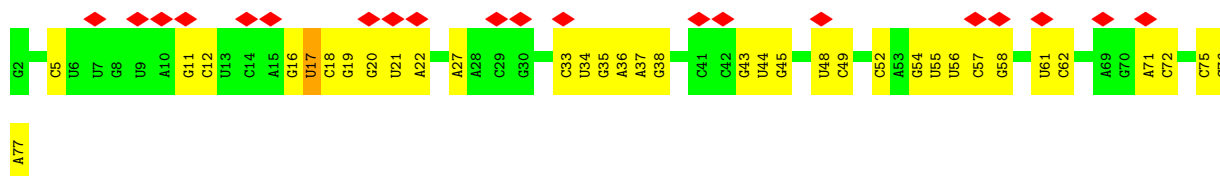




• Molecule 53: tRNA-Phe



• Molecule 53: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1534	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.401	Depositor
Minimum map value	-0.507	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.105	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.25	0/383	0.49	0/504
2	1	0.23	0/484	0.49	0/637
3	2	0.30	0/306	0.60	0/401
4	A	0.25	0/1954	0.50	0/2642
5	B	0.25	0/1721	0.54	1/2323 (0.0%)
6	C	0.28	0/1691	0.49	0/2267
7	D	0.27	0/1188	0.52	0/1593
8	E	0.29	0/1384	0.57	2/1867 (0.1%)
9	F	0.24	0/1266	0.54	0/1700
10	G	0.29	0/1126	0.54	1/1517 (0.1%)
11	H	0.25	0/1044	0.49	0/1395
12	I	0.25	0/820	0.50	0/1103
13	J	0.28	0/844	0.53	1/1136 (0.1%)
14	K	0.29	0/1094	0.53	0/1468
15	L	0.23	0/962	0.48	0/1289
16	M	0.25	0/483	0.43	0/643
17	N	0.24	0/679	0.43	0/907
18	O	0.25	0/659	0.51	1/885 (0.1%)
19	P	0.27	0/684	0.52	0/913
20	Q	0.24	0/545	0.44	0/730
21	R	0.27	0/698	0.53	0/936
22	S	0.23	0/631	0.42	0/838
23	T	0.26	0/475	0.58	0/621
24	a	0.25	0/2267	0.47	0/3044
25	b	0.29	0/1795	0.59	1/2412 (0.0%)
26	c	0.24	0/1671	0.49	0/2246
27	d	0.28	0/1409	0.52	0/1894
28	e	0.26	0/1420	0.54	0/1912
29	f	0.27	0/1183	0.55	0/1587
30	g	0.37	0/916	0.56	0/1222
31	h	0.25	0/968	0.47	0/1298
32	i	0.26	0/1186	0.45	0/1592
33	j	0.28	0/953	0.53	0/1275
34	k	0.27	0/1170	0.48	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.26	0/1104	0.52	1/1481 (0.1%)
36	m	0.27	0/973	0.51	0/1309
37	n	0.24	0/897	0.50	0/1198
38	o	0.24	0/948	0.49	0/1262
39	p	3.10	6/947 (0.6%)	0.61	2/1257 (0.2%)
40	q	0.24	0/828	0.52	1/1111 (0.1%)
41	r	0.27	0/1077	0.49	0/1441
42	s	0.25	0/732	0.49	0/988
43	t	0.25	0/879	0.49	0/1165
44	u	0.30	0/665	0.54	0/884
45	v	0.23	0/519	0.47	0/695
46	w	0.29	0/826	0.53	0/1104
47	x	0.24	0/353	0.44	0/474
48	y	0.32	0/457	0.53	0/601
49	z	0.23	0/412	0.45	0/547
50	3	0.24	0/69073	0.85	55/107710 (0.1%)
51	4	0.22	0/2505	0.84	1/3902 (0.0%)
52	5	0.22	0/35768	0.83	29/55764 (0.1%)
53	6	0.24	0/1808	0.92	4/2817 (0.1%)
53	7	0.24	0/1808	0.92	4/2817 (0.1%)
All	All	0.34	6/158638 (0.0%)	0.77	104/236883 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	p	105	PHE	CE1-CZ	44.56	2.22	1.37
39	p	105	PHE	CE2-CZ	44.52	2.21	1.37
39	p	105	PHE	CD2-CE2	42.45	2.24	1.39
39	p	105	PHE	CD1-CE1	42.10	2.23	1.39
39	p	105	PHE	CG-CD2	27.69	1.80	1.38
39	p	105	PHE	CG-CD1	26.87	1.79	1.38

All (104) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	l	88	GLY	C-N-CA	9.22	144.74	121.70
50	3	1023	C	N3-C2-O2	-9.14	115.50	121.90
52	5	843	C	N3-C2-O2	-8.36	116.05	121.90
52	5	1453	C	N3-C2-O2	-8.30	116.09	121.90
50	3	892	G	C4-C5-N7	-8.11	107.56	110.80
50	3	1786	U	N1-C2-O2	8.10	128.47	122.80
52	5	1088	C	N3-C2-O2	-7.90	116.37	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	3	1159	C	N3-C2-O2	-7.89	116.38	121.90
53	7	17	U	C2-N1-C1'	7.75	127.00	117.70
53	6	17	U	C2-N1-C1'	7.75	127.00	117.70
52	5	338	C	N3-C2-O2	-7.55	116.61	121.90
50	3	1786	U	C2-N1-C1'	7.54	126.75	117.70
53	6	17	U	N1-C2-O2	7.50	128.05	122.80
50	3	1902	C	N3-C2-O2	-7.49	116.66	121.90
50	3	1341	U	C2-N1-C1'	7.44	126.63	117.70
53	7	17	U	N1-C2-O2	7.43	128.00	122.80
8	E	74	ARG	NE-CZ-NH1	7.32	123.96	120.30
50	3	285	U	C2-N1-C1'	7.30	126.46	117.70
50	3	426	U	C2-N1-C1'	7.22	126.36	117.70
50	3	1321	C	N3-C2-O2	-7.07	116.95	121.90
50	3	1001	C	N3-C2-O2	-7.00	117.00	121.90
53	6	17	U	N3-C2-O2	-7.00	117.30	122.20
50	3	144	C	N3-C2-O2	-7.00	117.00	121.90
50	3	285	U	N1-C2-O2	6.97	127.68	122.80
50	3	34	C	N3-C2-O2	-6.96	117.03	121.90
50	3	892	G	N9-C4-C5	6.95	108.18	105.40
53	7	17	U	N3-C2-O2	-6.87	117.39	122.20
25	b	189	MET	CA-CB-CG	6.82	124.89	113.30
52	5	629	U	N3-C2-O2	-6.79	117.45	122.20
52	5	629	U	C2-N1-C1'	6.76	125.81	117.70
8	E	74	ARG	NE-CZ-NH2	-6.68	116.96	120.30
50	3	1341	U	N1-C2-O2	6.61	127.42	122.80
50	3	1697	C	N3-C2-O2	-6.60	117.28	121.90
50	3	2567	C	N3-C2-O2	-6.60	117.28	121.90
50	3	285	U	N3-C2-O2	-6.54	117.62	122.20
50	3	1247	C	N3-C2-O2	-6.46	117.38	121.90
52	5	751	C	C2-N1-C1'	6.44	125.88	118.80
52	5	562	U	C2-N1-C1'	6.32	125.28	117.70
52	5	1088	C	C6-N1-C2	-6.26	117.79	120.30
50	3	1786	U	N3-C2-O2	-6.25	117.83	122.20
52	5	629	U	N1-C2-O2	6.24	127.17	122.80
50	3	144	C	N1-C2-O2	6.16	122.59	118.90
13	J	112	ASN	CB-CA-C	6.15	122.69	110.40
50	3	1023	C	N1-C2-O2	6.13	122.58	118.90
52	5	1125	C	N3-C2-O2	-6.05	117.66	121.90
52	5	1134	C	N1-C2-O2	5.98	122.49	118.90
39	p	105	PHE	CB-CG-CD1	-5.96	116.62	120.80
50	3	1341	U	N3-C2-O2	-5.96	118.03	122.20
50	3	1303	U	C2-N1-C1'	5.94	124.83	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	5	751	C	N3-C2-O2	-5.94	117.74	121.90
52	5	335	C	N3-C2-O2	-5.93	117.75	121.90
50	3	1234	U	N3-C2-O2	-5.92	118.06	122.20
39	p	105	PHE	CD1-CG-CD2	5.88	125.94	118.30
52	5	751	C	N1-C2-O2	5.87	122.42	118.90
50	3	34	C	C6-N1-C2	-5.85	117.96	120.30
50	3	1507	G	O4'-C1'-N9	5.82	112.86	108.20
52	5	419	A	OP2-P-O3'	5.80	117.95	105.20
52	5	1134	C	C2-N1-C1'	5.79	125.17	118.80
52	5	1104	C	C2-N1-C1'	5.73	125.11	118.80
52	5	751	C	C6-N1-C2	-5.70	118.02	120.30
52	5	835	G	C5-C6-O6	5.69	132.02	128.60
51	4	78	C	O4'-C1'-N1	5.69	112.75	108.20
52	5	835	G	N1-C6-O6	-5.69	116.48	119.90
50	3	577	C	C2-N1-C1'	5.64	125.01	118.80
50	3	1021	C	N1-C2-O2	5.63	122.28	118.90
50	3	423	C	C2-N1-C1'	5.62	124.98	118.80
50	3	2005	G	C5-C6-O6	5.62	131.97	128.60
50	3	1234	U	N1-C2-O2	5.60	126.72	122.80
50	3	1159	C	C6-N1-C2	-5.58	118.07	120.30
50	3	426	U	C6-N1-C1'	-5.58	113.39	121.20
50	3	2005	G	N1-C6-O6	-5.54	116.58	119.90
50	3	2567	C	C6-N1-C2	-5.54	118.08	120.30
50	3	1321	C	C6-N1-C2	-5.53	118.09	120.30
50	3	2148	U	C2-N1-C1'	5.53	124.34	117.70
52	5	1453	C	N1-C2-O2	5.51	122.21	118.90
50	3	1371	G	C4-N9-C1'	5.48	133.62	126.50
53	7	56	U	C2-N1-C1'	5.46	124.26	117.70
50	3	1786	U	C5-C6-N1	5.45	125.42	122.70
50	3	426	U	N1-C2-O2	5.44	126.61	122.80
53	6	56	U	C2-N1-C1'	5.37	124.15	117.70
52	5	344	G	N1-C2-N2	-5.34	111.39	116.20
52	5	843	C	N1-C2-O2	5.34	122.10	118.90
50	3	2506	C	N3-C2-O2	-5.29	118.20	121.90
50	3	1242	G	O4'-C1'-N9	5.28	112.42	108.20
50	3	2000	U	N3-C2-O2	-5.28	118.51	122.20
50	3	1997	C	N3-C2-O2	-5.26	118.22	121.90
50	3	2591	G	C4-N9-C1'	5.24	133.31	126.50
52	5	419	A	P-O3'-C3'	5.23	125.98	119.70
50	3	1023	C	C6-N1-C2	-5.18	118.23	120.30
5	B	91	GLN	CA-CB-CG	5.17	124.77	113.40
50	3	1893	C	N1-C2-O2	5.15	121.99	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	3	444	C	C5-C6-N1	5.13	123.57	121.00
52	5	1125	C	N1-C2-O2	5.09	121.96	118.90
52	5	337	C	N1-C2-O2	5.09	121.95	118.90
52	5	1134	C	N3-C2-O2	-5.08	118.34	121.90
50	3	1371	G	N3-C4-N9	5.07	129.04	126.00
50	3	1303	U	N1-C2-O2	5.07	126.35	122.80
10	G	46	GLU	CA-CB-CG	5.05	124.51	113.40
50	3	1834	U	C2-N1-C1'	5.05	123.75	117.70
40	q	41	LEU	CA-CB-CG	5.04	126.90	115.30
50	3	238	U	N3-C2-O2	-5.04	118.67	122.20
52	5	1100	C	N1-C2-O2	5.02	121.91	118.90
50	3	139	G	N3-C4-N9	5.01	129.01	126.00
18	O	23	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	43 (96%)	2 (4%)	0	100	100
2	1	57/59 (97%)	52 (91%)	5 (9%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	A	238/294 (81%)	221 (93%)	17 (7%)	0	100	100
5	B	213/273 (78%)	200 (94%)	13 (6%)	0	100	100
6	C	201/205 (98%)	188 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	D	151/219 (69%)	139 (92%)	12 (8%)	0	100	100
8	E	165/215 (77%)	141 (86%)	24 (14%)	0	100	100
9	F	152/155 (98%)	130 (86%)	22 (14%)	0	100	100
10	G	139/142 (98%)	124 (89%)	14 (10%)	1 (1%)	19	57
11	H	126/132 (96%)	115 (91%)	11 (9%)	0	100	100
12	I	99/108 (92%)	87 (88%)	12 (12%)	0	100	100
13	J	112/121 (93%)	107 (96%)	4 (4%)	1 (1%)	14	52
14	K	134/139 (96%)	116 (87%)	18 (13%)	0	100	100
15	L	116/124 (94%)	109 (94%)	7 (6%)	0	100	100
16	M	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
17	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
18	O	78/94 (83%)	75 (96%)	3 (4%)	0	100	100
19	P	81/85 (95%)	72 (89%)	9 (11%)	0	100	100
20	Q	63/104 (61%)	58 (92%)	5 (8%)	0	100	100
21	R	82/87 (94%)	74 (90%)	8 (10%)	0	100	100
22	S	75/87 (86%)	75 (100%)	0	0	100	100
23	T	51/60 (85%)	49 (96%)	2 (4%)	0	100	100
24	a	283/287 (99%)	261 (92%)	22 (8%)	0	100	100
25	b	227/287 (79%)	204 (90%)	23 (10%)	0	100	100
26	c	208/212 (98%)	199 (96%)	9 (4%)	0	100	100
27	d	173/180 (96%)	155 (90%)	18 (10%)	0	100	100
28	e	174/184 (95%)	164 (94%)	10 (6%)	0	100	100
29	f	143/149 (96%)	130 (91%)	13 (9%)	0	100	100
30	g	117/161 (73%)	108 (92%)	8 (7%)	1 (1%)	14	52
31	h	126/137 (92%)	114 (90%)	12 (10%)	0	100	100
32	i	142/146 (97%)	132 (93%)	10 (7%)	0	100	100
33	j	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
34	k	146/151 (97%)	135 (92%)	11 (8%)	0	100	100
35	l	134/139 (96%)	125 (93%)	9 (7%)	0	100	100
36	m	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
37	n	108/116 (93%)	96 (89%)	12 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	o	113/119 (95%)	98 (87%)	15 (13%)	0	100	100
39	p	108/127 (85%)	100 (93%)	7 (6%)	1 (1%)	14	52
40	q	97/100 (97%)	82 (84%)	15 (16%)	0	100	100
41	r	137/159 (86%)	127 (93%)	10 (7%)	0	100	100
42	s	90/237 (38%)	81 (90%)	9 (10%)	0	100	100
43	t	109/111 (98%)	100 (92%)	9 (8%)	0	100	100
44	u	84/104 (81%)	77 (92%)	7 (8%)	0	100	100
45	v	61/65 (94%)	60 (98%)	1 (2%)	0	100	100
46	w	96/111 (86%)	90 (94%)	6 (6%)	0	100	100
47	x	42/97 (43%)	37 (88%)	5 (12%)	0	100	100
48	y	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
49	z	48/53 (91%)	46 (96%)	2 (4%)	0	100	100
All	All	5809/6670 (87%)	5335 (92%)	470 (8%)	4 (0%)	50	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	g	90	VAL
39	p	102	PRO
10	G	109	ASN
13	J	112	ASN

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%)	34 (97%)	1 (3%)	37	56
4	A	212/262 (81%)	211 (100%)	1 (0%)	86	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	B	180/232 (78%)	178 (99%)	2 (1%)	70	80
6	C	181/183 (99%)	180 (99%)	1 (1%)	84	88
7	D	123/178 (69%)	122 (99%)	1 (1%)	79	85
8	E	150/196 (76%)	150 (100%)	0	100	100
9	F	131/132 (99%)	130 (99%)	1 (1%)	79	85
10	G	123/124 (99%)	121 (98%)	2 (2%)	58	73
11	H	111/115 (96%)	110 (99%)	1 (1%)	75	83
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	91 (100%)	0	100	100
14	K	117/120 (98%)	113 (97%)	4 (3%)	32	51
15	L	100/105 (95%)	100 (100%)	0	100	100
16	M	47/48 (98%)	47 (100%)	0	100	100
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	69 (100%)	0	100	100
19	P	73/75 (97%)	73 (100%)	0	100	100
20	Q	56/94 (60%)	56 (100%)	0	100	100
21	R	74/77 (96%)	74 (100%)	0	100	100
22	S	70/77 (91%)	67 (96%)	3 (4%)	25	46
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	239 (99%)	2 (1%)	79	85
25	b	186/233 (80%)	184 (99%)	2 (1%)	70	80
26	c	182/184 (99%)	181 (100%)	1 (0%)	86	89
27	d	150/154 (97%)	149 (99%)	1 (1%)	81	87
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	123/134 (92%)	121 (98%)	2 (2%)	58	73
30	g	96/129 (74%)	84 (88%)	12 (12%)	3	15
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	125 (99%)	1 (1%)	79	85
33	j	103/103 (100%)	103 (100%)	0	100	100
34	k	123/126 (98%)	123 (100%)	0	100	100
35	l	113/115 (98%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	m	105/109 (96%)	103 (98%)	2 (2%)	52	69
37	n	96/99 (97%)	96 (100%)	0	100	100
38	o	101/105 (96%)	101 (100%)	0	100	100
39	p	99/108 (92%)	97 (98%)	2 (2%)	50	68
40	q	90/91 (99%)	90 (100%)	0	100	100
41	r	116/132 (88%)	115 (99%)	1 (1%)	75	83
42	s	82/208 (39%)	82 (100%)	0	100	100
43	t	96/96 (100%)	96 (100%)	0	100	100
44	u	69/85 (81%)	69 (100%)	0	100	100
45	v	58/60 (97%)	58 (100%)	0	100	100
46	w	87/98 (89%)	86 (99%)	1 (1%)	70	80
47	x	41/86 (48%)	41 (100%)	0	100	100
48	y	48/49 (98%)	48 (100%)	0	100	100
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5087/5751 (88%)	5043 (99%)	44 (1%)	74	83

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	2	2	LYS
4	A	27	ARG
5	B	90	LYS
5	B	207	ARG
6	C	180	ARG
7	D	148	ARG
9	F	52	ARG
10	G	23	ASN
10	G	108	LEU
11	H	101	LYS
14	K	118	VAL
14	K	120	VAL
14	K	122	LYS
14	K	127	ARG
22	S	18	ASN
22	S	25	LYS
22	S	78	LYS
24	a	42	LYS

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Mol	Chain	Res	Type
24	a	229	ARG
25	b	142	ARG
25	b	180	ARG
26	c	148	LYS
27	d	45	ARG
29	f	61	ASN
29	f	114	LYS
30	g	26	ILE
30	g	30	THR
30	g	32	MET
30	g	41	ARG
30	g	42	LYS
30	g	44	LEU
30	g	46	LYS
30	g	60	ARG
30	g	84	VAL
30	g	86	VAL
30	g	89	ILE
30	g	90	VAL
32	i	15	ARG
36	m	30	LYS
36	m	62	GLN
39	p	27	ARG
39	p	100	LYS
41	r	99	ARG
46	w	17	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
3	2	21	GLN
4	A	220	HIS
6	C	37	GLN
6	C	38	HIS
8	E	17	GLN
9	F	39	GLN
10	G	56	ASN
10	G	58	GLN
11	H	33	ASN
13	J	111	HIS
14	K	32	ASN
19	P	25	GLN

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Mol	Chain	Res	Type
19	P	62	GLN
22	S	7	ASN
22	S	14	ASN
23	T	8	ASN
24	a	15	HIS
24	a	148	HIS
24	a	240	HIS
25	b	73	ASN
25	b	225	GLN
26	c	174	ASN
27	d	27	GLN
27	d	127	ASN
28	e	107	ASN
28	e	109	GLN
36	m	21	GLN
36	m	59	ASN
37	n	42	GLN
41	r	57	ASN
42	s	56	ASN
46	w	89	GLN
48	y	40	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	975 (33%)	34 (1%)
51	4	103/108 (95%)	35 (33%)	3 (2%)
52	5	1490/1520 (98%)	440 (29%)	12 (0%)
53	6	75/76 (98%)	31 (41%)	6 (8%)
53	7	75/76 (98%)	32 (42%)	6 (8%)
All	All	4618/4687 (98%)	1513 (32%)	61 (1%)

All (1513) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	12	A
50	3	14	U
50	3	15	A
50	3	16	A
50	3	17	G
50	3	28	G

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Mol	Chain	Res	Type
50	3	29	G
50	3	30	A
50	3	34	C
50	3	36	U
50	3	37	G
50	3	38	G
50	3	42	U
50	3	45	U
50	3	48	G
50	3	51	A
50	3	52	U
50	3	53	G
50	3	57	G
50	3	58	A
50	3	64	U
50	3	66	A
50	3	73	A
50	3	75	A
50	3	76	A
50	3	77	G
50	3	82	G
50	3	86	A
50	3	90	G
50	3	96	A
50	3	98	C
50	3	102	A
50	3	103	G
50	3	115	U
50	3	116	C
50	3	119	A
50	3	120	A
50	3	121	U
50	3	122	G
50	3	127	A
50	3	129	U
50	3	132	G
50	3	136	G
50	3	139	G
50	3	141	A
50	3	146	G
50	3	163	A
50	3	164	A

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Mol	Chain	Res	Type
50	3	165	U
50	3	166	A
50	3	169	U
50	3	173	C
50	3	178	A
50	3	179	A
50	3	180	A
50	3	181	G
50	3	184	A
50	3	185	U
50	3	197	U
50	3	200	A
50	3	203	A
50	3	208	A
50	3	210	U
50	3	211	A
50	3	217	A
50	3	219	G
50	3	220	A
50	3	225	A
50	3	226	A
50	3	227	A
50	3	228	A
50	3	231	A
50	3	232	A
50	3	233	U
50	3	234	G
50	3	236	G
50	3	237	A
50	3	242	G
50	3	245	U
50	3	246	G
50	3	247	U
50	3	252	G
50	3	253	C
50	3	254	G
50	3	256	G
50	3	261	A
50	3	265	G
50	3	269	A
50	3	270	G
50	3	276	A

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Mol	Chain	Res	Type
50	3	283	A
50	3	284	U
50	3	287	G
50	3	291	G
50	3	296	U
50	3	297	G
50	3	298	U
50	3	299	A
50	3	306	G
50	3	309	A
50	3	310	U
50	3	312	U
50	3	314	G
50	3	315	A
50	3	318	U
50	3	319	G
50	3	324	C
50	3	329	G
50	3	331	A
50	3	335	G
50	3	339	U
50	3	345	A
50	3	353	G
50	3	355	A
50	3	356	A
50	3	357	A
50	3	363	G
50	3	364	A
50	3	365	U
50	3	377	U
50	3	381	A
50	3	393	C
50	3	396	A
50	3	397	G
50	3	399	G
50	3	401	G
50	3	402	A
50	3	403	U
50	3	404	C
50	3	408	G
50	3	409	A
50	3	410	G

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Mol	Chain	Res	Type
50	3	411	U
50	3	417	G
50	3	421	A
50	3	422	A
50	3	424	G
50	3	425	U
50	3	426	U
50	3	428	U
50	3	431	U
50	3	432	G
50	3	434	G
50	3	437	A
50	3	441	U
50	3	442	G
50	3	447	G
50	3	448	A
50	3	457	U
50	3	458	A
50	3	460	G
50	3	465	A
50	3	470	U
50	3	471	A
50	3	478	G
50	3	479	A
50	3	482	G
50	3	483	A
50	3	484	U
50	3	487	C
50	3	488	G
50	3	491	A
50	3	495	U
50	3	501	G
50	3	503	G
50	3	509	G
50	3	511	U
50	3	514	A
50	3	515	A
50	3	517	G
50	3	520	C
50	3	523	A
50	3	528	U
50	3	531	G

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Mol	Chain	Res	Type
50	3	539	U
50	3	540	A
50	3	543	U
50	3	548	A
50	3	553	A
50	3	562	C
50	3	563	A
50	3	564	A
50	3	565	C
50	3	566	G
50	3	567	U
50	3	568	G
50	3	575	C
50	3	577	C
50	3	579	U
50	3	581	A
50	3	583	U
50	3	589	A
50	3	590	U
50	3	595	U
50	3	596	G
50	3	597	C
50	3	598	G
50	3	605	A
50	3	606	G
50	3	607	U
50	3	608	A
50	3	610	G
50	3	612	G
50	3	619	A
50	3	620	G
50	3	634	C
50	3	636	U
50	3	637	U
50	3	638	A
50	3	648	G
50	3	649	A
50	3	650	G
50	3	653	G
50	3	656	G
50	3	661	G
50	3	663	A

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Mol	Chain	Res	Type
50	3	666	G
50	3	673	A
50	3	675	U
50	3	681	A
50	3	682	A
50	3	688	U
50	3	689	U
50	3	691	G
50	3	692	U
50	3	696	U
50	3	705	A
50	3	706	C
50	3	711	A
50	3	719	G
50	3	720	A
50	3	721	G
50	3	722	C
50	3	725	G
50	3	737	U
50	3	738	U
50	3	740	A
50	3	761	G
50	3	764	G
50	3	765	A
50	3	766	C
50	3	767	C
50	3	768	G
50	3	769	A
50	3	777	C
50	3	781	U
50	3	782	U
50	3	783	G
50	3	784	A
50	3	785	A
50	3	786	A
50	3	792	G
50	3	794	G
50	3	795	G
50	3	797	U
50	3	798	G
50	3	799	A
50	3	803	G

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Mol	Chain	Res	Type
50	3	806	A
50	3	810	G
50	3	811	G
50	3	812	G
50	3	816	A
50	3	817	A
50	3	818	A
50	3	819	U
50	3	820	U
50	3	821	C
50	3	824	A
50	3	825	U
50	3	826	C
50	3	827	G
50	3	828	A
50	3	829	A
50	3	831	U
50	3	835	U
50	3	837	A
50	3	840	G
50	3	842	U
50	3	845	U
50	3	847	C
50	3	854	A
50	3	858	A
50	3	862	U
50	3	863	U
50	3	865	A
50	3	868	C
50	3	882	C
50	3	883	A
50	3	885	A
50	3	896	U
50	3	902	U
50	3	903	A
50	3	904	C
50	3	906	G
50	3	914	G
50	3	918	G
50	3	930	C
50	3	932	U
50	3	933	A

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Mol	Chain	Res	Type
50	3	934	C
50	3	936	G
50	3	944	U
50	3	947	A
50	3	948	A
50	3	949	C
50	3	951	C
50	3	952	U
50	3	953	G
50	3	962	U
50	3	968	U
50	3	973	U
50	3	977	A
50	3	981	A
50	3	982	G
50	3	986	G
50	3	989	G
50	3	990	G
50	3	993	A
50	3	995	A
50	3	997	G
50	3	998	C
50	3	1001	C
50	3	1008	A
50	3	1009	A
50	3	1016	A
50	3	1017	A
50	3	1018	G
50	3	1019	A
50	3	1021	C
50	3	1022	C
50	3	1024	A
50	3	1026	A
50	3	1027	U
50	3	1032	A
50	3	1033	A
50	3	1035	U
50	3	1042	C
50	3	1044	C
50	3	1046	A
50	3	1049	U
50	3	1052	A

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Mol	Chain	Res	Type
50	3	1054	U
50	3	1055	A
50	3	1057	G
50	3	1061	A
50	3	1068	U
50	3	1069	G
50	3	1075	G
50	3	1080	A
50	3	1081	A
50	3	1082	A
50	3	1084	C
50	3	1095	U
50	3	1096	U
50	3	1097	G
50	3	1098	G
50	3	1099	C
50	3	1100	U
50	3	1104	A
50	3	1105	A
50	3	1106	G
50	3	1107	C
50	3	1108	A
50	3	1115	G
50	3	1119	A
50	3	1122	G
50	3	1123	A
50	3	1124	G
50	3	1125	U
50	3	1126	G
50	3	1130	A
50	3	1132	C
50	3	1144	C
50	3	1146	A
50	3	1147	G
50	3	1148	U
50	3	1150	U
50	3	1151	U
50	3	1154	U
50	3	1157	G
50	3	1162	A
50	3	1163	G
50	3	1165	U

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Mol	Chain	Res	Type
50	3	1167	U
50	3	1168	A
50	3	1170	C
50	3	1171	G
50	3	1176	U
50	3	1177	A
50	3	1186	A
50	3	1191	A
50	3	1193	U
50	3	1196	U
50	3	1201	A
50	3	1203	G
50	3	1204	A
50	3	1208	A
50	3	1209	U
50	3	1210	A
50	3	1215	G
50	3	1217	G
50	3	1219	U
50	3	1224	G
50	3	1226	G
50	3	1234	U
50	3	1235	U
50	3	1236	G
50	3	1242	G
50	3	1243	A
50	3	1248	A
50	3	1250	A
50	3	1251	G
50	3	1253	G
50	3	1255	G
50	3	1257	G
50	3	1266	G
50	3	1267	A
50	3	1268	U
50	3	1269	C
50	3	1279	U
50	3	1281	A
50	3	1283	A
50	3	1284	A
50	3	1285	U
50	3	1286	G

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Mol	Chain	Res	Type
50	3	1287	C
50	3	1292	A
50	3	1295	A
50	3	1297	U
50	3	1298	A
50	3	1300	C
50	3	1301	G
50	3	1302	C
50	3	1303	U
50	3	1314	A
50	3	1317	C
50	3	1319	C
50	3	1320	C
50	3	1324	A
50	3	1325	C
50	3	1326	C
50	3	1328	A
50	3	1329	U
50	3	1330	U
50	3	1331	G
50	3	1334	U
50	3	1335	A
50	3	1338	G
50	3	1339	U
50	3	1342	C
50	3	1343	C
50	3	1348	C
50	3	1349	C
50	3	1353	G
50	3	1357	U
50	3	1358	C
50	3	1360	U
50	3	1361	U
50	3	1369	U
50	3	1370	A
50	3	1372	U
50	3	1373	C
50	3	1375	G
50	3	1376	G
50	3	1378	C
50	3	1380	U
50	3	1388	G

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Mol	Chain	Res	Type
50	3	1389	G
50	3	1390	C
50	3	1393	A
50	3	1396	A
50	3	1397	G
50	3	1407	U
50	3	1408	G
50	3	1411	C
50	3	1412	A
50	3	1413	A
50	3	1421	A
50	3	1422	U
50	3	1423	A
50	3	1424	U
50	3	1428	U
50	3	1431	A
50	3	1435	A
50	3	1436	C
50	3	1444	C
50	3	1445	U
50	3	1446	G
50	3	1447	A
50	3	1448	U
50	3	1455	A
50	3	1456	C
50	3	1457	A
50	3	1461	A
50	3	1462	A
50	3	1463	G
50	3	1466	U
50	3	1467	U
50	3	1479	A
50	3	1480	A
50	3	1481	U
50	3	1483	G
50	3	1484	G
50	3	1487	U
50	3	1500	A
50	3	1502	A
50	3	1507	G
50	3	1508	G
50	3	1510	A

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Mol	Chain	Res	Type
50	3	1514	U
50	3	1515	A
50	3	1516	G
50	3	1517	G
50	3	1518	C
50	3	1520	A
50	3	1523	C
50	3	1533	U
50	3	1534	A
50	3	1541	A
50	3	1543	U
50	3	1550	G
50	3	1554	A
50	3	1555	G
50	3	1558	A
50	3	1571	G
50	3	1572	U
50	3	1573	A
50	3	1579	G
50	3	1580	G
50	3	1582	G
50	3	1584	U
50	3	1585	A
50	3	1586	U
50	3	1588	A
50	3	1589	A
50	3	1592	A
50	3	1594	G
50	3	1597	U
50	3	1600	A
50	3	1603	A
50	3	1608	C
50	3	1612	U
50	3	1614	G
50	3	1615	G
50	3	1618	U
50	3	1619	A
50	3	1626	C
50	3	1636	U
50	3	1637	A
50	3	1640	G
50	3	1641	A

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Mol	Chain	Res	Type
50	3	1642	G
50	3	1643	A
50	3	1644	A
50	3	1648	A
50	3	1650	A
50	3	1651	C
50	3	1652	A
50	3	1653	C
50	3	1656	A
50	3	1670	U
50	3	1679	U
50	3	1680	A
50	3	1681	G
50	3	1682	C
50	3	1683	G
50	3	1687	G
50	3	1688	A
50	3	1694	A
50	3	1695	G
50	3	1698	A
50	3	1699	A
50	3	1701	G
50	3	1702	A
50	3	1703	A
50	3	1704	C
50	3	1706	C
50	3	1707	U
50	3	1708	G
50	3	1720	C
50	3	1721	G
50	3	1727	U
50	3	1728	A
50	3	1733	G
50	3	1734	A
50	3	1737	G
50	3	1741	G
50	3	1745	A
50	3	1747	G
50	3	1748	U
50	3	1751	A
50	3	1752	A
50	3	1761	C

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Mol	Chain	Res	Type
50	3	1762	A
50	3	1763	G
50	3	1764	U
50	3	1765	G
50	3	1768	G
50	3	1769	A
50	3	1770	A
50	3	1771	C
50	3	1780	A
50	3	1784	U
50	3	1788	A
50	3	1789	C
50	3	1791	A
50	3	1807	C
50	3	1808	C
50	3	1809	A
50	3	1812	C
50	3	1816	A
50	3	1821	G
50	3	1822	A
50	3	1823	U
50	3	1827	U
50	3	1836	A
50	3	1842	G
50	3	1843	C
50	3	1847	G
50	3	1849	G
50	3	1855	A
50	3	1857	G
50	3	1863	G
50	3	1865	A
50	3	1872	U
50	3	1873	A
50	3	1876	G
50	3	1878	A
50	3	1880	G
50	3	1884	A
50	3	1889	U
50	3	1890	U
50	3	1891	A
50	3	1892	A
50	3	1896	A

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Mol	Chain	Res	Type
50	3	1906	G
50	3	1907	A
50	3	1908	A
50	3	1910	G
50	3	1913	G
50	3	1914	G
50	3	1920	A
50	3	1921	C
50	3	1925	A
50	3	1935	A
50	3	1936	G
50	3	1937	G
50	3	1938	U
50	3	1943	A
50	3	1944	A
50	3	1945	A
50	3	1946	U
50	3	1948	C
50	3	1959	A
50	3	1960	A
50	3	1962	U
50	3	1970	C
50	3	1971	G
50	3	1972	C
50	3	1973	U
50	3	1977	A
50	3	1978	U
50	3	1979	G
50	3	1980	G
50	3	1981	U
50	3	1982	G
50	3	1990	C
50	3	1998	U
50	3	1999	G
50	3	2004	G
50	3	2009	U
50	3	2010	A
50	3	2012	A
50	3	2025	C
50	3	2028	G
50	3	2030	A
50	3	2037	A

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Mol	Chain	Res	Type
50	3	2038	A
50	3	2040	A
50	3	2041	C
50	3	2045	C
50	3	2050	G
50	3	2055	A
50	3	2056	A
50	3	2059	G
50	3	2062	C
50	3	2063	G
50	3	2064	G
50	3	2066	A
50	3	2067	A
50	3	2068	G
50	3	2069	A
50	3	2070	C
50	3	2071	C
50	3	2072	C
50	3	2074	G
50	3	2075	U
50	3	2076	G
50	3	2083	U
50	3	2084	A
50	3	2087	G
50	3	2100	G
50	3	2106	G
50	3	2107	A
50	3	2110	U
50	3	2111	U
50	3	2112	A
50	3	2114	C
50	3	2115	A
50	3	2117	G
50	3	2118	U
50	3	2119	A
50	3	2123	A
50	3	2124	A
50	3	2128	G
50	3	2130	A
50	3	2132	G
50	3	2133	A
50	3	2134	G

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Mol	Chain	Res	Type
50	3	2135	C
50	3	2136	A
50	3	2139	C
50	3	2140	G
50	3	2144	C
50	3	2149	U
50	3	2151	G
50	3	2153	U
50	3	2154	A
50	3	2156	G
50	3	2159	U
50	3	2165	A
50	3	2166	U
50	3	2167	G
50	3	2171	A
50	3	2179	A
50	3	2180	U
50	3	2181	A
50	3	2182	C
50	3	2187	C
50	3	2191	G
50	3	2192	U
50	3	2193	U
50	3	2194	G
50	3	2195	U
50	3	2196	G
50	3	2198	G
50	3	2199	C
50	3	2200	U
50	3	2202	U
50	3	2203	U
50	3	2206	A
50	3	2207	A
50	3	2211	G
50	3	2212	U
50	3	2219	U
50	3	2220	A
50	3	2221	U
50	3	2222	C
50	3	2225	G
50	3	2227	U
50	3	2229	C

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Mol	Chain	Res	Type
50	3	2231	A
50	3	2232	G
50	3	2233	A
50	3	2242	G
50	3	2246	G
50	3	2247	G
50	3	2254	G
50	3	2255	A
50	3	2257	U
50	3	2258	G
50	3	2259	G
50	3	2265	U
50	3	2266	C
50	3	2267	G
50	3	2269	C
50	3	2270	U
50	3	2274	A
50	3	2276	A
50	3	2281	A
50	3	2286	A
50	3	2287	G
50	3	2291	U
50	3	2294	A
50	3	2295	A
50	3	2296	A
50	3	2305	C
50	3	2312	G
50	3	2313	U
50	3	2315	G
50	3	2316	G
50	3	2317	A
50	3	2326	G
50	3	2328	A
50	3	2329	G
50	3	2331	G
50	3	2333	G
50	3	2334	U
50	3	2335	A
50	3	2341	G
50	3	2342	U
50	3	2343	A
50	3	2345	G

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Mol	Chain	Res	Type
50	3	2352	U
50	3	2353	G
50	3	2355	C
50	3	2358	U
50	3	2361	G
50	3	2362	A
50	3	2363	C
50	3	2367	C
50	3	2380	U
50	3	2382	A
50	3	2391	G
50	3	2393	C
50	3	2397	G
50	3	2398	U
50	3	2410	C
50	3	2414	U
50	3	2415	A
50	3	2418	G
50	3	2424	C
50	3	2428	C
50	3	2431	U
50	3	2432	C
50	3	2433	A
50	3	2436	G
50	3	2438	A
50	3	2439	U
50	3	2442	A
50	3	2443	A
50	3	2447	A
50	3	2448	C
50	3	2449	U
50	3	2450	C
50	3	2453	G
50	3	2456	A
50	3	2457	U
50	3	2458	A
50	3	2460	C
50	3	2468	U
50	3	2470	C
50	3	2472	G
50	3	2475	C
50	3	2476	A

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Mol	Chain	Res	Type
50	3	2477	A
50	3	2484	A
50	3	2486	A
50	3	2488	C
50	3	2492	G
50	3	2493	G
50	3	2497	U
50	3	2499	U
50	3	2502	G
50	3	2505	A
50	3	2507	C
50	3	2509	C
50	3	2512	U
50	3	2513	G
50	3	2515	C
50	3	2517	A
50	3	2521	A
50	3	2526	A
50	3	2527	U
50	3	2528	C
50	3	2538	A
50	3	2539	A
50	3	2543	G
50	3	2560	U
50	3	2561	G
50	3	2563	U
50	3	2564	C
50	3	2565	G
50	3	2566	C
50	3	2568	G
50	3	2570	U
50	3	2574	A
50	3	2575	G
50	3	2578	A
50	3	2580	A
50	3	2581	C
50	3	2584	G
50	3	2585	A
50	3	2586	G
50	3	2587	U
50	3	2591	G
50	3	2593	U

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Mol	Chain	Res	Type
50	3	2594	C
50	3	2599	C
50	3	2605	G
50	3	2606	A
50	3	2607	G
50	3	2608	A
50	3	2610	A
50	3	2621	U
50	3	2622	A
50	3	2623	U
50	3	2627	U
50	3	2629	G
50	3	2631	G
50	3	2637	A
50	3	2638	G
50	3	2640	A
50	3	2642	G
50	3	2643	A
50	3	2647	A
50	3	2649	G
50	3	2654	U
50	3	2655	U
50	3	2662	A
50	3	2664	U
50	3	2668	A
50	3	2669	G
50	3	2672	G
50	3	2675	C
50	3	2681	G
50	3	2684	G
50	3	2694	A
50	3	2697	C
50	3	2715	C
50	3	2718	C
50	3	2720	C
50	3	2722	G
50	3	2726	G
50	3	2734	C
50	3	2735	G
50	3	2737	G
50	3	2740	U
50	3	2741	A

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Mol	Chain	Res	Type
50	3	2747	U
50	3	2752	G
50	3	2756	A
50	3	2758	A
50	3	2759	G
50	3	2765	A
50	3	2773	A
50	3	2774	A
50	3	2777	A
50	3	2786	A
50	3	2788	U
50	3	2790	A
50	3	2799	U
50	3	2803	G
50	3	2804	C
50	3	2805	A
50	3	2807	G
50	3	2808	A
50	3	2809	A
50	3	2810	A
50	3	2811	G
50	3	2813	A
50	3	2814	A
50	3	2822	C
50	3	2824	A
50	3	2829	G
50	3	2831	U
50	3	2837	U
50	3	2838	G
50	3	2839	A
50	3	2840	U
50	3	2853	U
50	3	2865	U
50	3	2871	G
50	3	2876	G
50	3	2883	A
50	3	2884	C
50	3	2887	A
50	3	2888	U
50	3	2889	U
50	3	2890	G
50	3	2895	A

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Mol	Chain	Res	Type
50	3	2897	G
50	3	2898	A
50	3	2899	C
51	4	7	G
51	4	9	C
51	4	10	C
51	4	11	A
51	4	12	U
51	4	19	G
51	4	22	G
51	4	23	A
51	4	25	A
51	4	27	A
51	4	28	C
51	4	30	U
51	4	31	G
51	4	33	U
51	4	35	C
51	4	38	U
51	4	39	U
51	4	41	C
51	4	42	G
51	4	49	G
51	4	50	C
51	4	51	A
51	4	54	U
51	4	55	A
51	4	60	C
51	4	66	A
51	4	77	G
51	4	78	C
51	4	88	G
51	4	89	A
51	4	92	A
51	4	99	A
51	4	102	A
51	4	106	A
51	4	108	C
52	5	8	G
52	5	9	A
52	5	10	G
52	5	15	U

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Mol	Chain	Res	Type
52	5	17	A
52	5	21	U
52	5	28	G
52	5	29	G
52	5	33	A
52	5	40	G
52	5	48	C
52	5	49	C
52	5	50	U
52	5	52	A
52	5	61	A
52	5	66	A
52	5	75	A
52	5	80	U
52	5	83	U
52	5	86	A
52	5	93	A
52	5	95	C
52	5	105	A
52	5	106	C
52	5	108	C
52	5	111	A
52	5	114	C
52	5	115	A
52	5	116	A
52	5	117	U
52	5	122	C
52	5	128	A
52	5	130	G
52	5	132	G
52	5	134	G
52	5	145	G
52	5	149	G
52	5	159	U
52	5	160	A
52	5	161	C
52	5	163	G
52	5	164	C
52	5	167	A
52	5	168	A
52	5	169	G
52	5	171	A

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Mol	Chain	Res	Type
52	5	180	C
52	5	193	G
52	5	197	A
52	5	198	A
52	5	213	U
52	5	216	G
52	5	227	A
52	5	236	C
52	5	237	A
52	5	240	U
52	5	241	C
52	5	242	A
52	5	243	G
52	5	246	A
52	5	247	G
52	5	253	G
52	5	258	A
52	5	260	C
52	5	262	G
52	5	263	C
52	5	275	A
52	5	285	G
52	5	296	A
52	5	301	G
52	5	302	A
52	5	303	A
52	5	311	A
52	5	314	G
52	5	316	G
52	5	323	A
52	5	324	C
52	5	325	A
52	5	326	C
52	5	328	G
52	5	335	C
52	5	341	C
52	5	342	G
52	5	343	G
52	5	344	G
52	5	345	A
52	5	346	G
52	5	347	G

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Mol	Chain	Res	Type
52	5	348	C
52	5	352	A
52	5	359	A
52	5	362	U
52	5	363	U
52	5	364	U
52	5	368	C
52	5	374	G
52	5	376	G
52	5	377	A
52	5	378	A
52	5	385	A
52	5	391	C
52	5	394	U
52	5	395	G
52	5	400	G
52	5	401	U
52	5	402	G
52	5	408	U
52	5	409	G
52	5	410	A
52	5	416	U
52	5	417	U
52	5	418	U
52	5	419	A
52	5	420	A
52	5	425	G
52	5	426	U
52	5	432	U
52	5	446	A
52	5	447	G
52	5	449	A
52	5	452	A
52	5	453	C
52	5	455	U
52	5	457	A
52	5	461	G
52	5	464	A
52	5	466	U
52	5	467	G
52	5	468	G
52	5	469	C

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Mol	Chain	Res	Type
52	5	471	A
52	5	473	A
52	5	476	U
52	5	478	G
52	5	481	U
52	5	482	G
52	5	488	U
52	5	489	U
52	5	490	U
52	5	493	A
52	5	494	A
52	5	495	U
52	5	507	A
52	5	508	A
52	5	510	U
52	5	516	C
52	5	517	C
52	5	522	G
52	5	525	G
52	5	529	U
52	5	530	A
52	5	531	A
52	5	532	U
52	5	534	C
52	5	545	A
52	5	551	A
52	5	554	C
52	5	556	G
52	5	557	A
52	5	560	U
52	5	562	U
52	5	566	G
52	5	568	G
52	5	570	A
52	5	571	A
52	5	573	G
52	5	574	C
52	5	575	A
52	5	580	C
52	5	585	G
52	5	586	G
52	5	591	A

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Mol	Chain	Res	Type
52	5	594	A
52	5	605	A
52	5	616	C
52	5	617	U
52	5	618	U
52	5	619	A
52	5	620	A
52	5	623	G
52	5	628	A
52	5	629	U
52	5	637	A
52	5	639	A
52	5	640	C
52	5	646	A
52	5	647	U
52	5	648	C
52	5	650	A
52	5	653	G
52	5	660	A
52	5	662	G
52	5	672	A
52	5	675	U
52	5	682	G
52	5	683	G
52	5	684	A
52	5	687	G
52	5	690	G
52	5	692	A
52	5	699	A
52	5	715	A
52	5	716	C
52	5	718	A
52	5	719	G
52	5	720	U
52	5	721	G
52	5	725	A
52	5	731	A
52	5	740	G
52	5	745	U
52	5	746	A
52	5	749	G
52	5	751	C

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Mol	Chain	Res	Type
52	5	752	G
52	5	753	C
52	5	756	A
52	5	771	G
52	5	774	A
52	5	784	A
52	5	786	U
52	5	787	A
52	5	789	A
52	5	790	U
52	5	793	C
52	5	796	A
52	5	802	C
52	5	808	C
52	5	812	A
52	5	813	A
52	5	814	C
52	5	815	G
52	5	816	A
52	5	817	U
52	5	818	A
52	5	820	A
52	5	825	A
52	5	828	U
52	5	829	G
52	5	838	A
52	5	841	C
52	5	846	G
52	5	872	C
52	5	879	G
52	5	881	G
52	5	883	A
52	5	884	G
52	5	885	U
52	5	896	G
52	5	908	A
52	5	909	A
52	5	910	C
52	5	911	G
52	5	917	G
52	5	921	G
52	5	922	G

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Mol	Chain	Res	Type
52	5	929	C
52	5	930	A
52	5	933	A
52	5	937	G
52	5	940	G
52	5	944	A
52	5	949	G
52	5	953	A
52	5	954	A
52	5	955	U
52	5	958	G
52	5	963	U
52	5	964	A
52	5	966	A
52	5	969	A
52	5	970	A
52	5	971	A
52	5	972	A
52	5	975	C
52	5	976	U
52	5	986	U
52	5	987	U
52	5	988	G
52	5	989	A
52	5	991	A
52	5	997	G
52	5	999	C
52	5	1000	A
52	5	1001	A
52	5	1002	A
52	5	1004	U
52	5	1008	G
52	5	1009	G
52	5	1010	A
52	5	1011	A
52	5	1013	C
52	5	1014	A
52	5	1016	A
52	5	1018	U
52	5	1033	U
52	5	1034	G
52	5	1036	C

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Mol	Chain	Res	Type
52	5	1037	A
52	5	1041	G
52	5	1044	G
52	5	1045	C
52	5	1047	U
52	5	1051	U
52	5	1052	G
52	5	1056	U
52	5	1057	C
52	5	1058	A
52	5	1060	C
52	5	1070	G
52	5	1071	A
52	5	1075	G
52	5	1077	U
52	5	1078	G
52	5	1080	G
52	5	1081	U
52	5	1085	G
52	5	1086	U
52	5	1089	C
52	5	1092	A
52	5	1104	C
52	5	1108	A
52	5	1115	G
52	5	1116	U
52	5	1118	A
52	5	1119	C
52	5	1122	U
52	5	1123	G
52	5	1125	C
52	5	1128	G
52	5	1133	A
52	5	1134	C
52	5	1135	U
52	5	1139	A
52	5	1141	U
52	5	1142	G
52	5	1143	C
52	5	1144	A
52	5	1154	A
52	5	1157	G

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Mol	Chain	Res	Type
52	5	1159	A
52	5	1165	G
52	5	1166	A
52	5	1171	A
52	5	1173	A
52	5	1178	C
52	5	1181	G
52	5	1187	U
52	5	1188	A
52	5	1190	G
52	5	1191	U
52	5	1199	U
52	5	1200	G
52	5	1201	C
52	5	1203	A
52	5	1211	A
52	5	1214	A
52	5	1215	U
52	5	1216	G
52	5	1217	G
52	5	1221	A
52	5	1232	C
52	5	1233	G
52	5	1235	C
52	5	1242	U
52	5	1254	A
52	5	1255	A
52	5	1256	U
52	5	1260	U
52	5	1261	A
52	5	1271	U
52	5	1272	C
52	5	1273	A
52	5	1274	G
52	5	1276	U
52	5	1279	G
52	5	1283	G
52	5	1291	C
52	5	1293	A
52	5	1296	C
52	5	1297	G
52	5	1306	A

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Mol	Chain	Res	Type
52	5	1310	C
52	5	1312	G
52	5	1314	A
52	5	1315	U
52	5	1316	C
52	5	1317	A
52	5	1319	U
52	5	1320	A
52	5	1328	C
52	5	1330	A
52	5	1331	A
52	5	1337	U
52	5	1338	A
52	5	1341	U
52	5	1343	G
52	5	1353	C
52	5	1354	G
52	5	1356	U
52	5	1360	G
52	5	1369	A
52	5	1372	C
52	5	1373	A
52	5	1375	C
52	5	1379	C
52	5	1380	G
52	5	1381	U
52	5	1383	A
52	5	1384	A
52	5	1387	U
52	5	1391	A
52	5	1397	G
52	5	1400	A
52	5	1411	A
52	5	1417	U
52	5	1418	G
52	5	1426	U
52	5	1427	U
52	5	1428	A
52	5	1429	G
52	5	1431	A
52	5	1433	G
52	5	1436	C

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Mol	Chain	Res	Type
52	5	1446	A
52	5	1450	C
52	5	1466	U
52	5	1467	A
52	5	1468	A
52	5	1474	A
52	5	1478	A
52	5	1480	G
52	5	1481	U
52	5	1482	A
52	5	1492	G
52	5	1494	A
52	5	1495	C
52	5	1504	G
52	5	1505	G
52	5	1508	C
53	6	5	C
53	6	11	G
53	6	12	C
53	6	17	U
53	6	18	C
53	6	19	G
53	6	20	G
53	6	21	U
53	6	22	A
53	6	27	A
53	6	33	C
53	6	34	U
53	6	35	G
53	6	36	A
53	6	38	G
53	6	43	G
53	6	44	U
53	6	45	G
53	6	48	U
53	6	49	C
53	6	52	C
53	6	54	G
53	6	55	U
53	6	57	C
53	6	58	G
53	6	61	U

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Mol	Chain	Res	Type
53	6	62	C
53	6	71	A
53	6	72	C
53	6	75	C
53	6	77	A
53	7	5	C
53	7	11	G
53	7	12	C
53	7	17	U
53	7	18	C
53	7	19	G
53	7	20	G
53	7	21	U
53	7	22	A
53	7	27	A
53	7	33	C
53	7	34	U
53	7	35	G
53	7	36	A
53	7	37	A
53	7	38	G
53	7	43	G
53	7	44	U
53	7	45	G
53	7	48	U
53	7	49	C
53	7	52	C
53	7	54	G
53	7	55	U
53	7	57	C
53	7	58	G
53	7	61	U
53	7	62	C
53	7	71	A
53	7	72	C
53	7	75	C
53	7	77	A

All (61) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	47	G

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Mol	Chain	Res	Type
50	3	286	A
50	3	296	U
50	3	311	G
50	3	410	G
50	3	425	U
50	3	500	U
50	3	508	A
50	3	513	A
50	3	605	A
50	3	688	U
50	3	881	A
50	3	901	C
50	3	903	A
50	3	996	A
50	3	1048	A
50	3	1209	U
50	3	1297	U
50	3	1507	G
50	3	1583	G
50	3	1585	A
50	3	1587	U
50	3	1588	A
50	3	1820	U
50	3	2118	U
50	3	2333	G
50	3	2491	C
50	3	2504	C
50	3	2506	C
50	3	2604	U
50	3	2668	A
50	3	2764	U
50	3	2823	A
50	3	2897	G
51	4	10	C
51	4	54	U
51	4	59	A
52	5	8	G
52	5	168	A
52	5	240	U
52	5	384	G
52	5	419	A
52	5	618	U

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Mol	Chain	Res	Type
52	5	683	G
52	5	1115	G
52	5	1133	A
52	5	1177	U
52	5	1215	U
52	5	1342	C
53	6	16	G
53	6	19	G
53	6	34	U
53	6	48	U
53	6	71	A
53	6	76	C
53	7	16	G
53	7	19	G
53	7	34	U
53	7	48	U
53	7	71	A
53	7	76	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

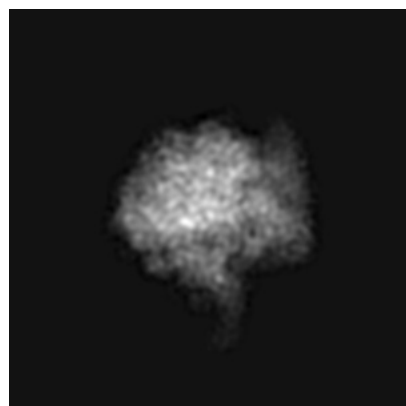
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13447. These allow visual inspection of the internal detail of the map and identification of artifacts.

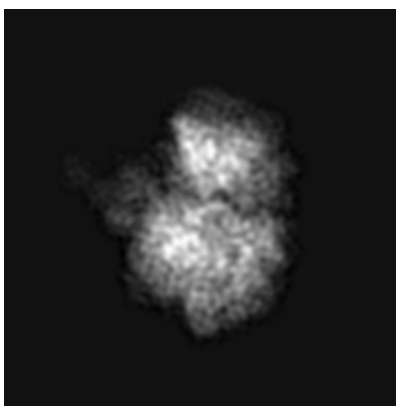
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

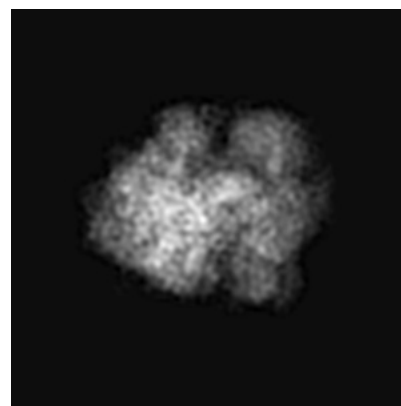
6.1.1 Primary map



X

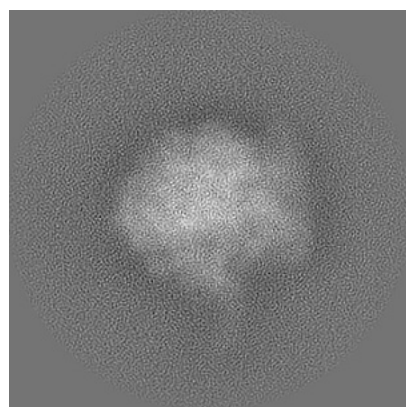


Y

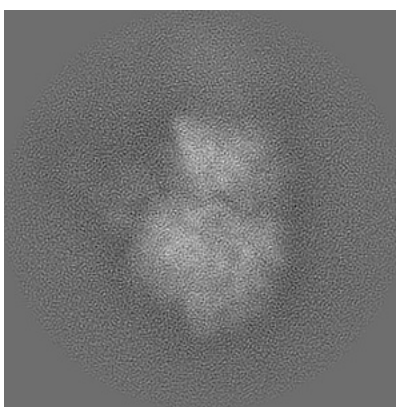


Z

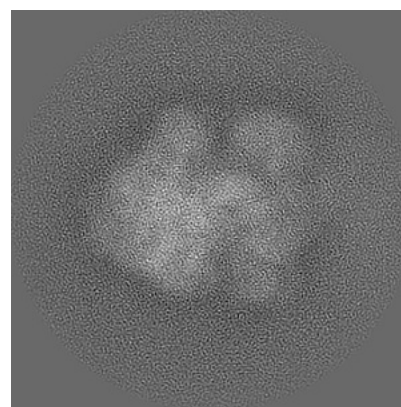
6.1.2 Raw map



X



Y

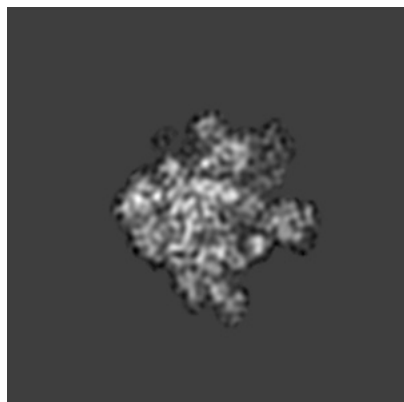


Z

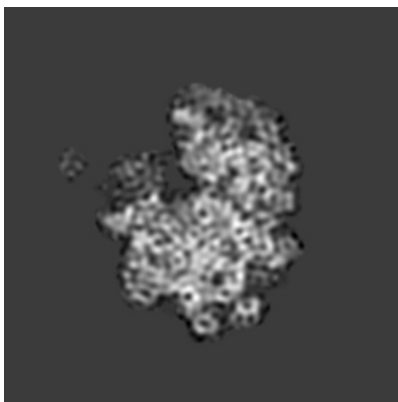
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

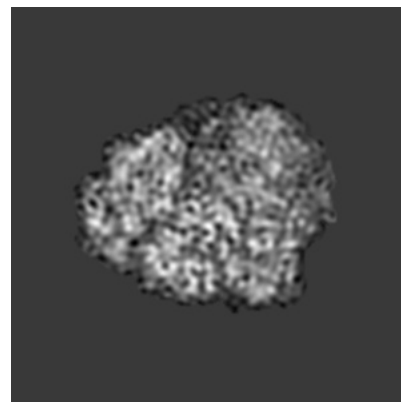
6.2.1 Primary map



X Index: 128

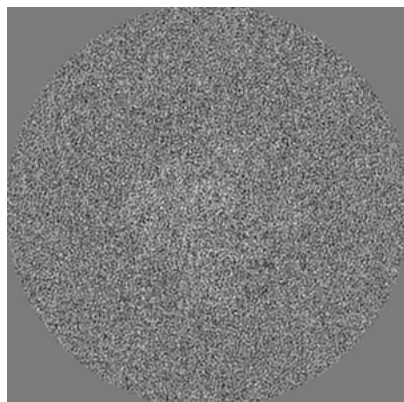


Y Index: 128

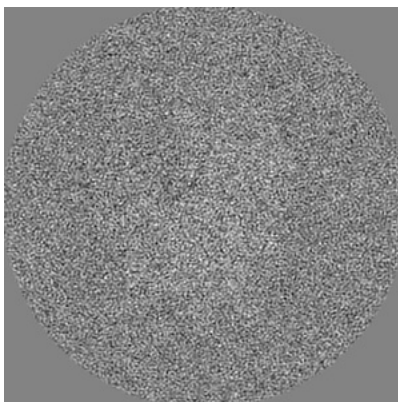


Z Index: 128

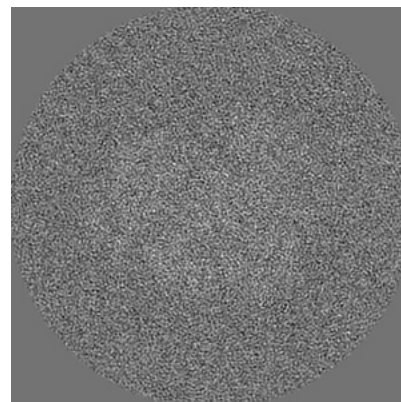
6.2.2 Raw map



X Index: 128



Y Index: 128

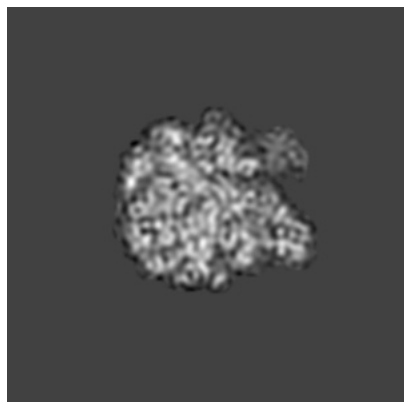


Z Index: 128

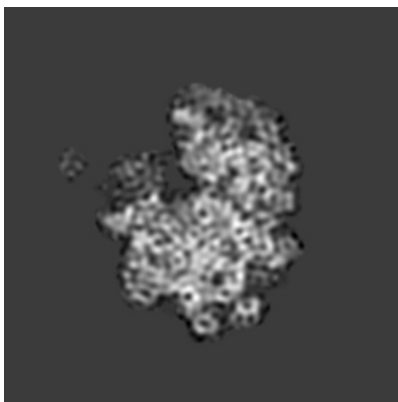
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

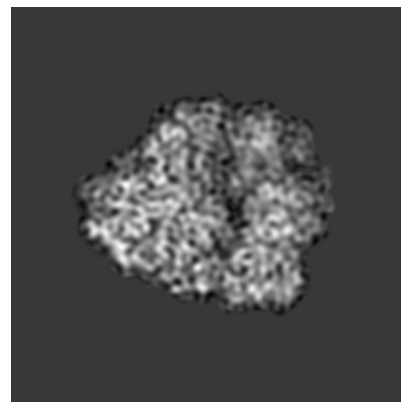
6.3.1 Primary map



X Index: 101

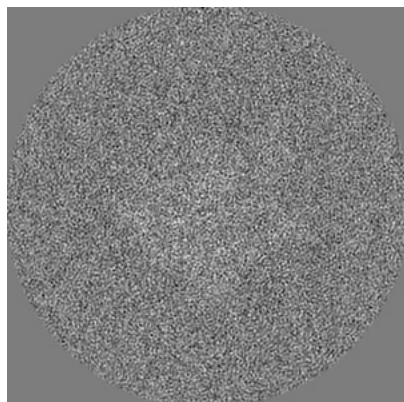


Y Index: 128

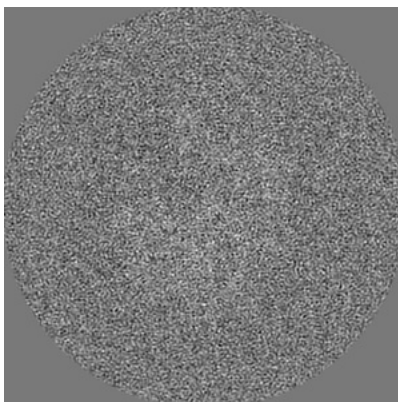


Z Index: 121

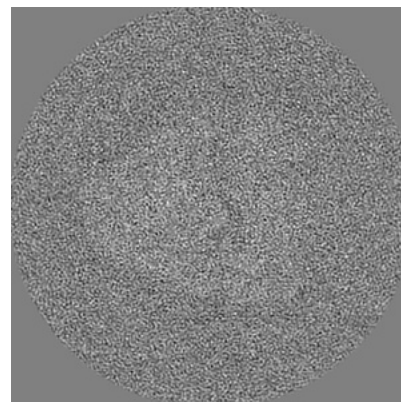
6.3.2 Raw map



X Index: 121



Y Index: 130

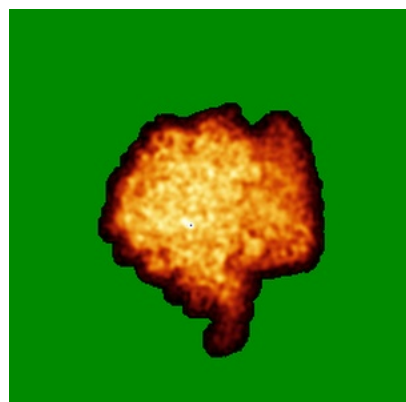


Z Index: 123

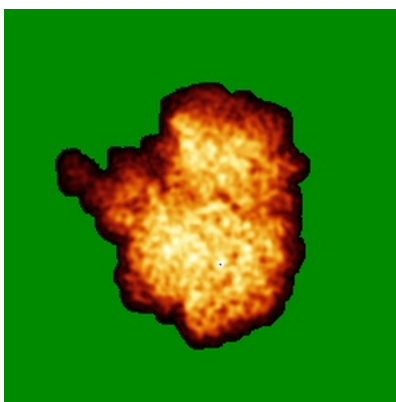
The images above show the largest variance slices of the map in three orthogonal directions.

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

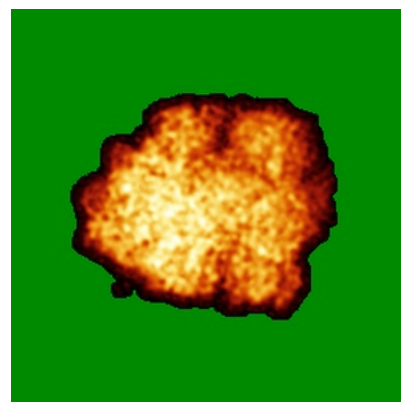
6.4.1 Primary map



X

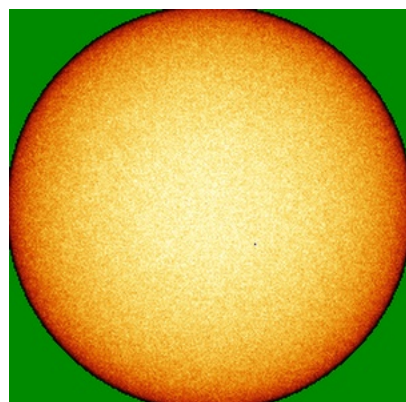


Y

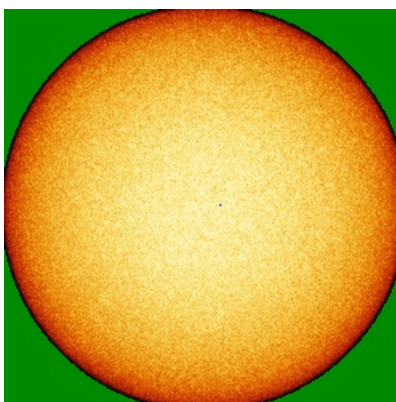


Z

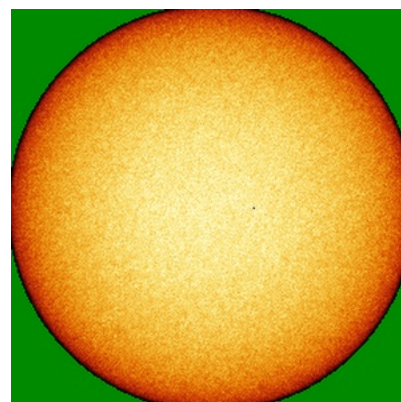
6.4.2 Raw map



X



Y



Z

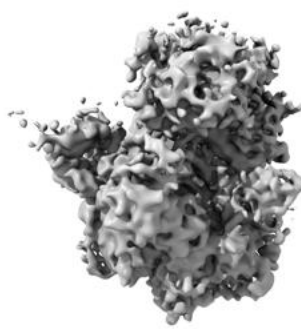
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

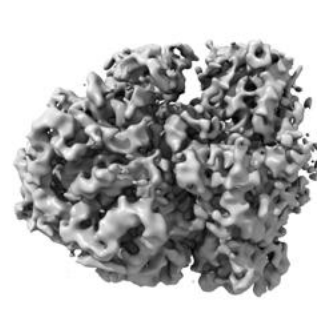
6.5.1 Primary map



X



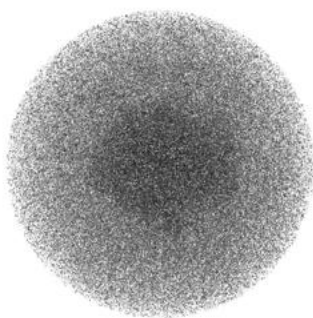
Y



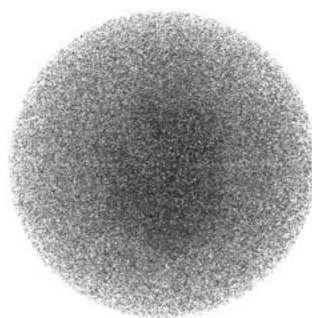
Z

The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

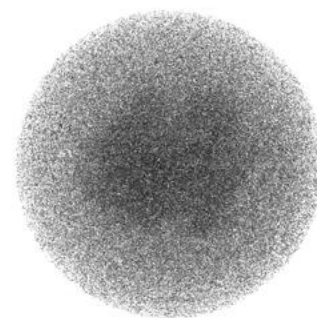
6.5.2 Raw map



X



Y



Z

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.

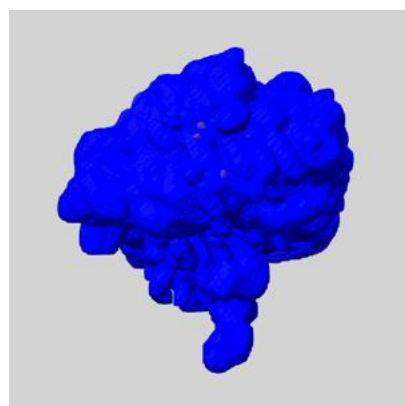
6.6 Mask visualisation [i](#)

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

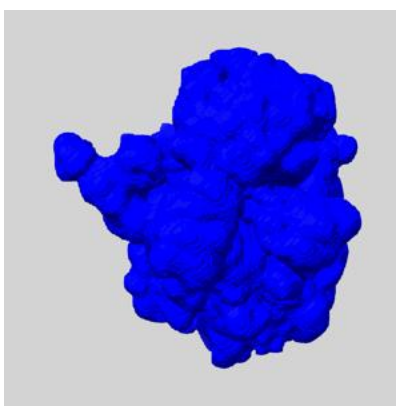
A mask typically either:

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

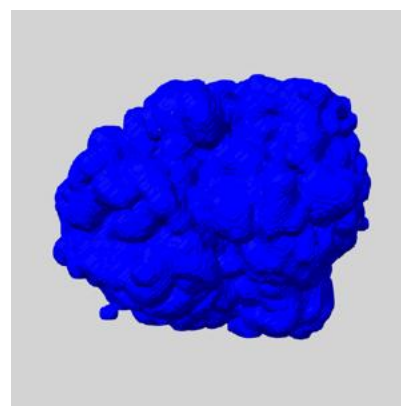
6.6.1 emd_13447_msk_1.map [i](#)



X



Y

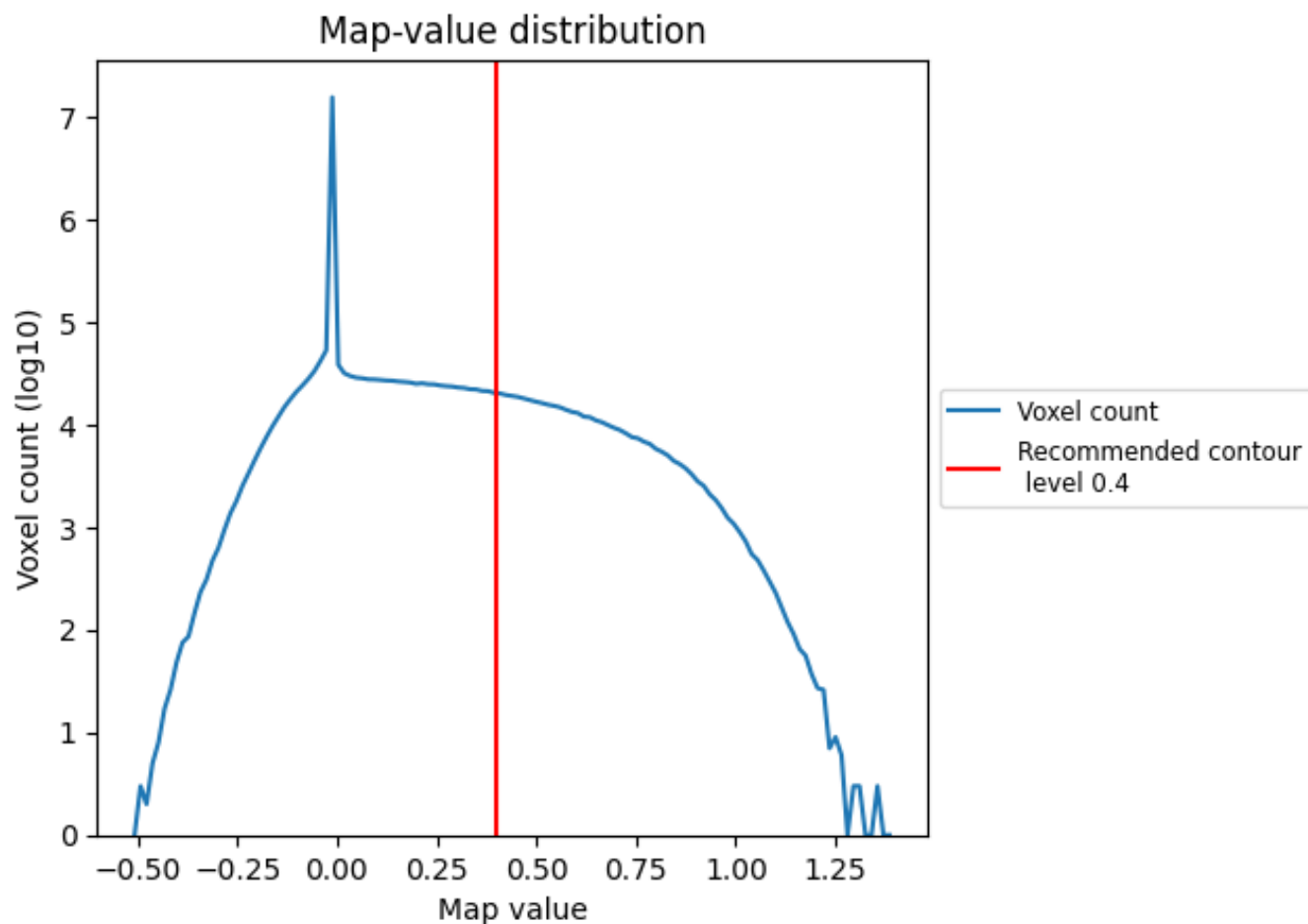


Z

7 Map analysis [i](#)

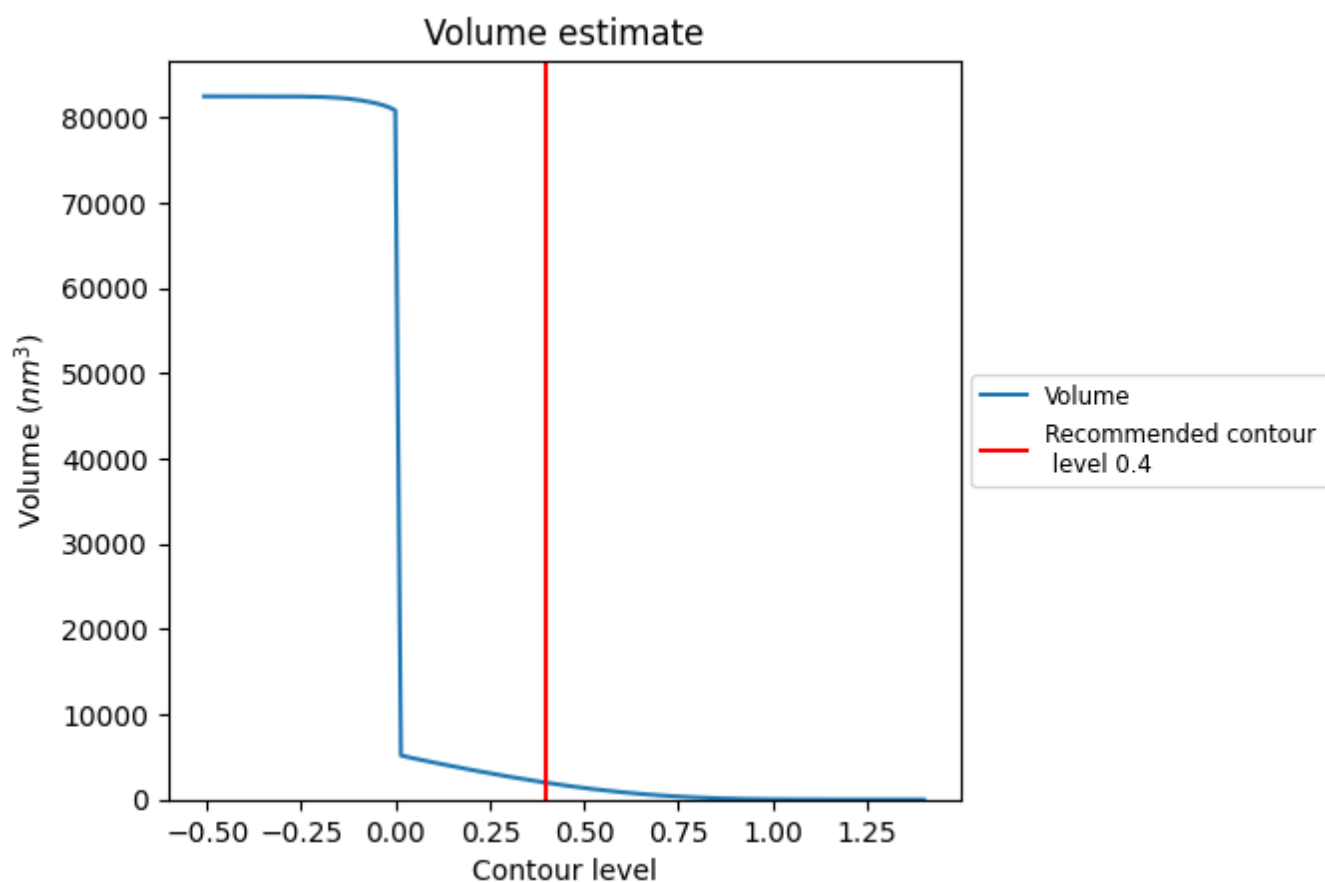
This section contains the results of statistical analysis of the map.

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.

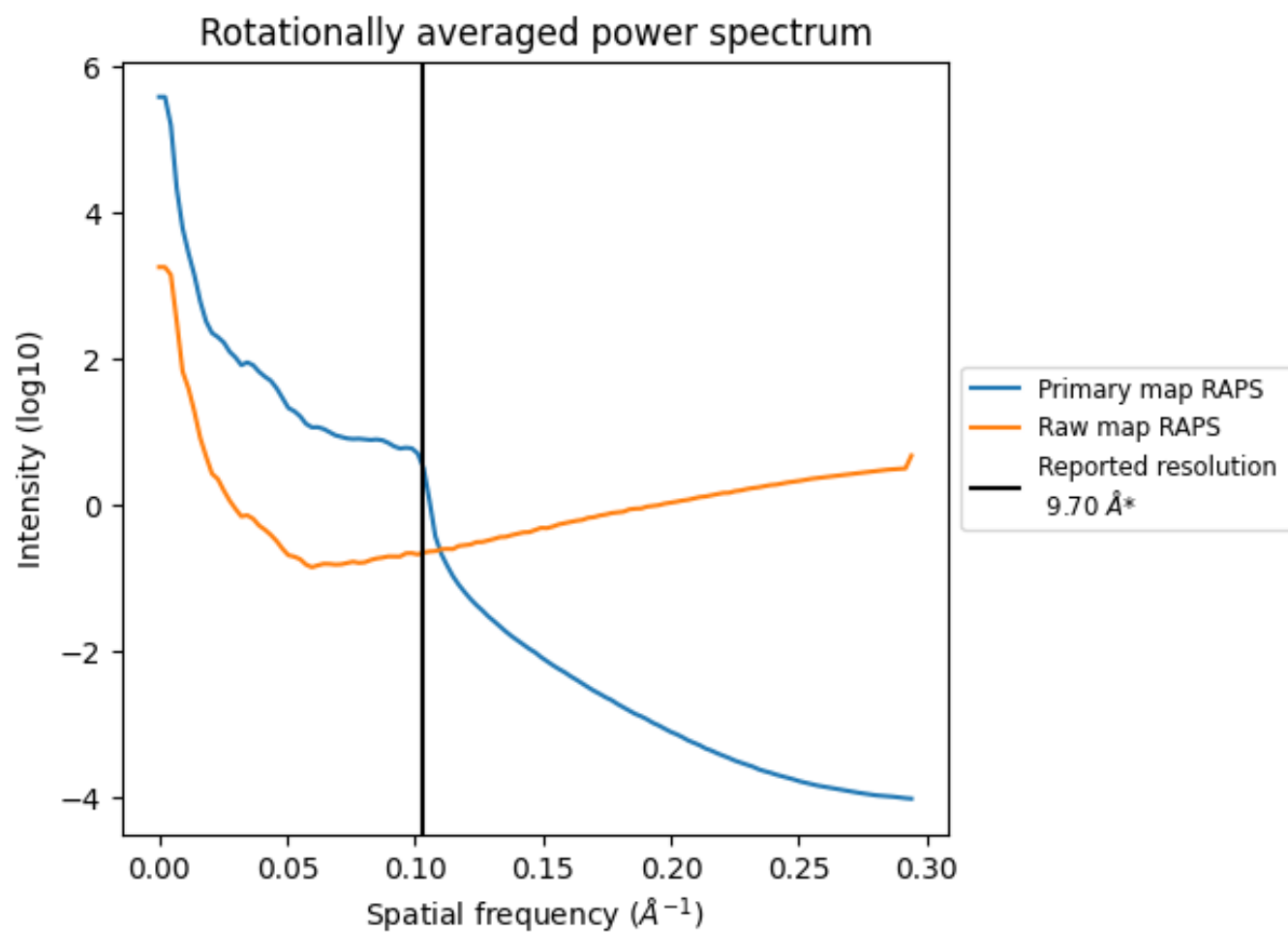
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 19,750 nm³; this corresponds to an approximate mass of 1784 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 ⓘ

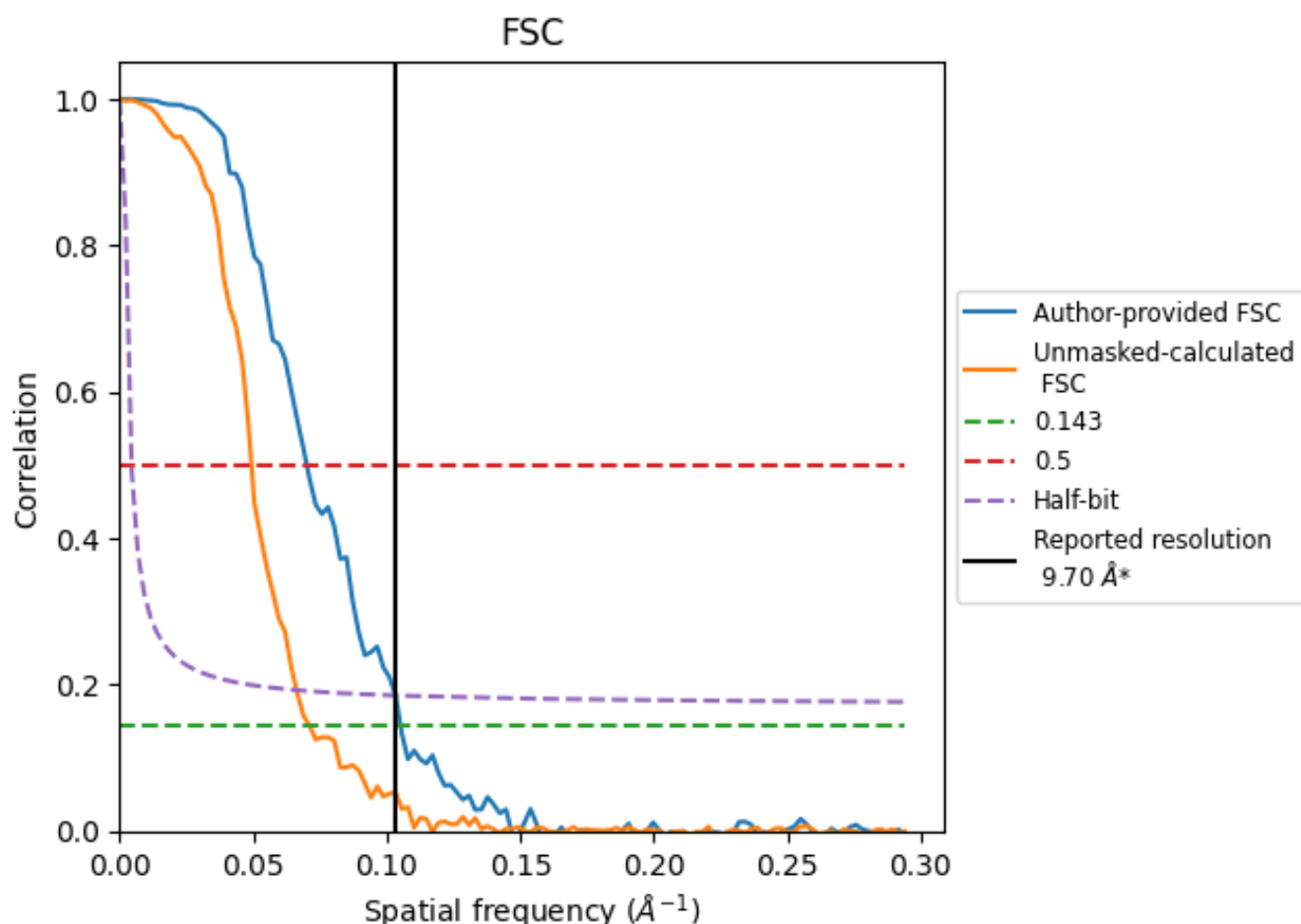


*Reported resolution corresponds to spatial frequency of 0.103 \AA^{-1}

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 0.103 Å⁻¹

8.2 Resolution estimates [i](#)

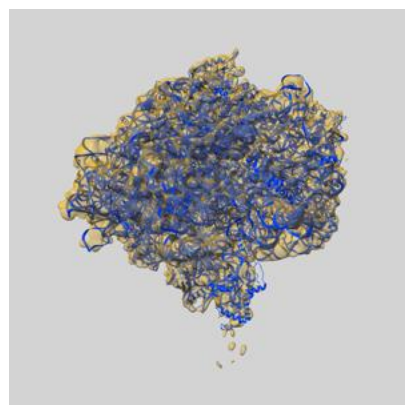
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.70	-	-
Author-provided FSC curve	9.51	14.27	9.67
Unmasked-calculated*	14.04	20.24	15.08

*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 14.04 differs from the reported value 9.7 by more than 10 %

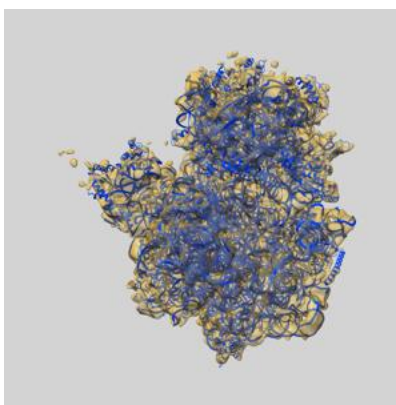
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13447 and PDB model 7PIQ. Per-residue inclusion information can be found in section [3](#) on page [13](#).

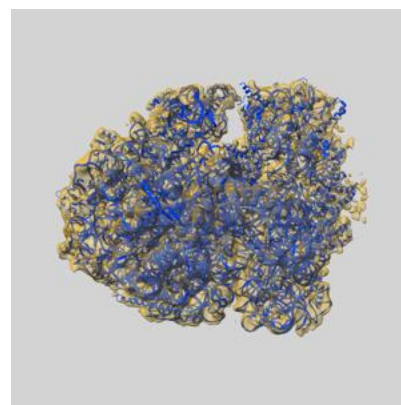
9.1 Map-model overlay [i](#)



X



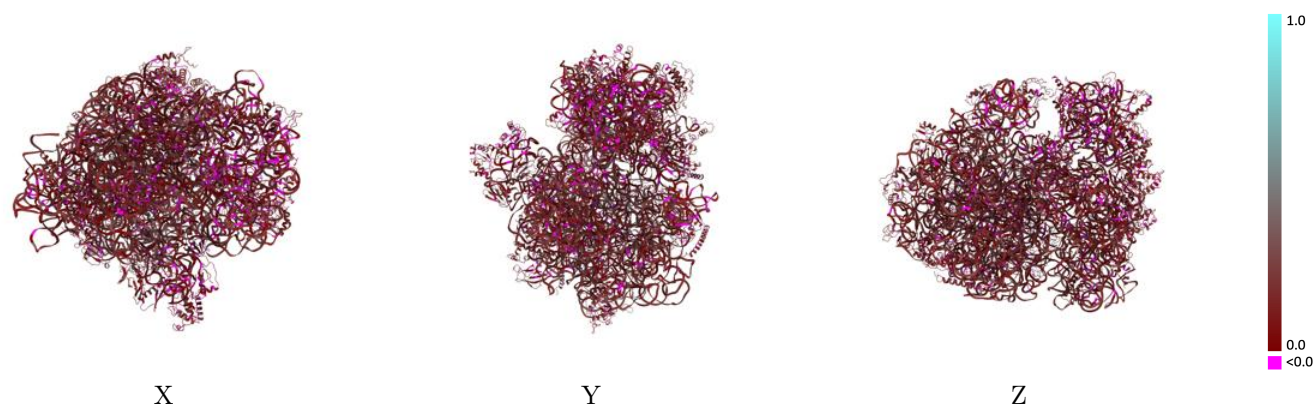
Y



Z

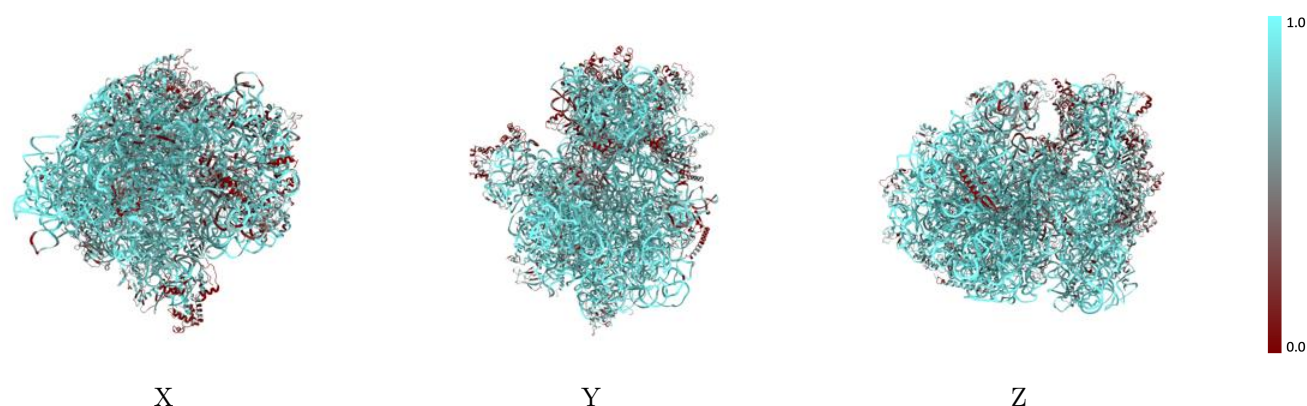
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



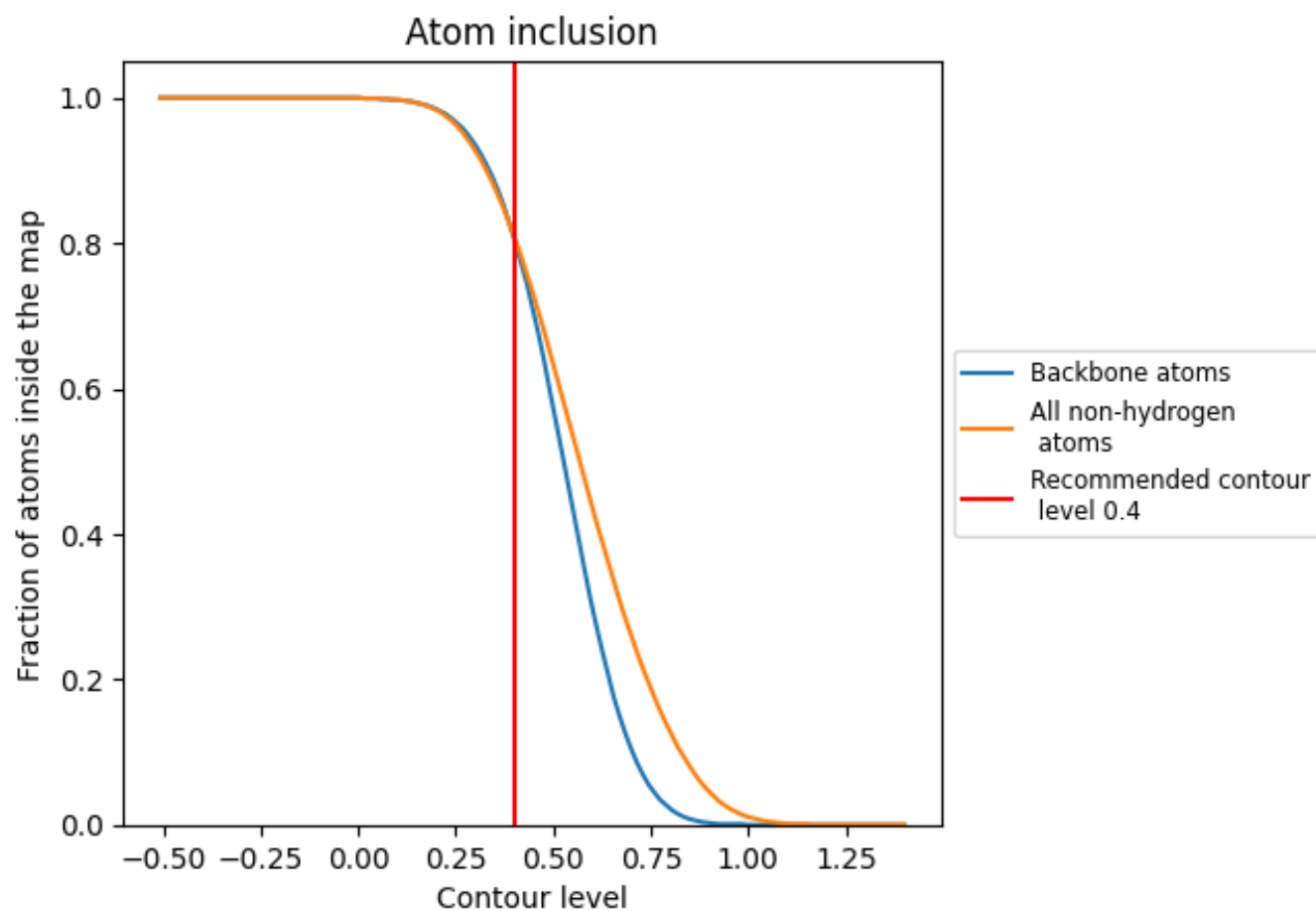
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 81% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8090	 0.1480
0	 0.7810	 0.1420
1	 0.7320	 0.1210
2	 0.7160	 0.0980
3	 0.9400	 0.1620
4	 0.9430	 0.1680
5	 0.8970	 0.1510
6	 0.7050	 0.1480
7	 0.5640	 0.0990
A	 0.4780	 0.1600
B	 0.3780	 0.1200
C	 0.5500	 0.1090
D	 0.5000	 0.1210
E	 0.4690	 0.1550
F	 0.3960	 0.1110
G	 0.6030	 0.1150
H	 0.5990	 0.0970
I	 0.4670	 0.1130
J	 0.5350	 0.1120
K	 0.6720	 0.1080
L	 0.3390	 0.1190
M	 0.6610	 0.0600
N	 0.6770	 0.1470
O	 0.7230	 0.1400
P	 0.6270	 0.1240
Q	 0.6510	 0.1280
R	 0.3160	 0.0610
S	 0.7690	 0.1500
T	 0.6000	 0.1780
a	 0.7070	 0.1120
b	 0.6070	 0.1140
c	 0.6410	 0.1390
d	 0.5650	 0.1250
e	 0.5680	 0.1410
f	 0.2250	 0.1420



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Chain	Atom inclusion	Q-score
g	 0.3650	 0.1190
h	 0.2300	 0.0950
i	 0.7070	 0.1370
j	 0.5080	 0.1200
k	 0.7110	 0.1360
l	 0.6810	 0.1260
m	 0.7320	 0.1240
n	 0.6640	 0.1370
o	 0.5680	 0.1440
p	 0.7450	 0.1280
q	 0.6080	 0.1260
r	 0.7730	 0.1540
s	 0.6540	 0.1430
t	 0.5520	 0.1100
u	 0.7470	 0.1130
v	 0.7290	 0.1120
w	 0.6580	 0.1800
x	 0.4780	 0.1610
y	 0.6960	 0.0940
z	 0.7980	 0.1460