



wwPDB EM Validation Summary Report ⓘ

Jun 26, 2026 – 06:19 AM EDT

PDB ID : 6V39 / pdb_00006v39
EMDB ID : EMD-21030
Title : Cryo-EM structure of the Acinetobacter baumannii Ribosome: 70S with P-site tRNA
Authors : Morgan, C.E.; Yu, E.W.
Deposited on : 2019-11-25
Resolution : 3.04 Å(reported)
Based on initial model : 5AFI

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
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

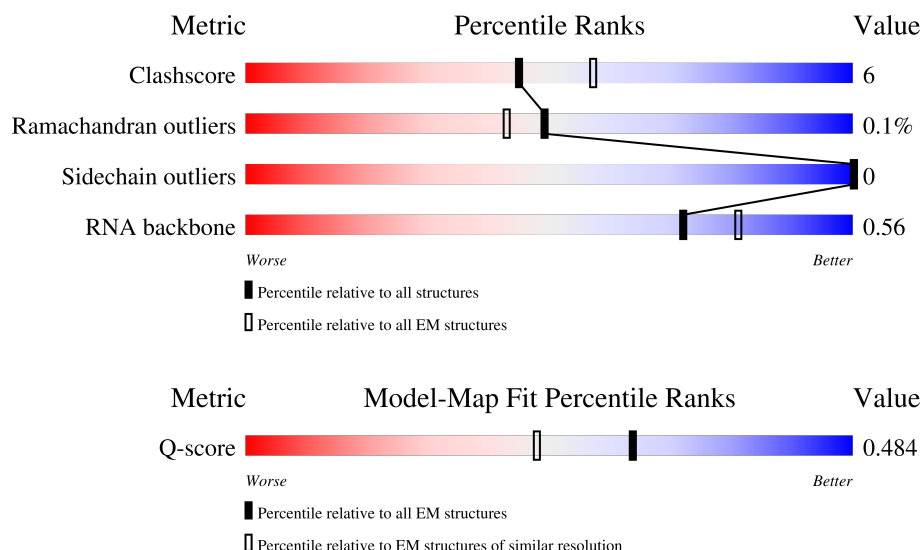
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.04 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	13952 (2.54 - 3.54)

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	51	
2	1	44	
3	2	64	

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Mol	Chain	Length	Quality of chain
4	3	38	
5	AN1	2918	
6	B	115	
7	C	274	
8	D	212	
9	E	200	
10	F	178	
11	G	177	
12	H	148	
13	I	142	
14	J	122	
15	K	146	
16	L	137	
17	M	125	
18	N	116	
19	O	122	
20	P	119	
21	Q	103	
22	R	109	
23	S	106	
24	T	105	
25	U	98	
26	V	85	
27	W	78	
28	X	65	

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Mol	Chain	Length	Quality of chain
29	Y	58	
30	Z	61	
31	sN1	1544	
32	b	250	
33	c	250	
34	d	208	
35	e	165	
36	f	127	
37	g	156	
38	h	131	
39	i	128	
40	j	103	
41	k	128	
42	l	124	
43	m	118	
44	n	101	
45	o	89	
46	p	101	
47	q	85	
48	r	75	
49	s	91	
50	t	88	
51	u	71	
52	v	77	
53	w	3	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 141897 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 L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	51	Total	C	N	O	S	0	0
			427	274	77	73	3		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	44	Total	C	N	O	S	0	0
			363	222	85	54	2		

- Molecule 3 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	63	Total	C	N	O	S	0	0
			509	319	110	76	4		

- Molecule 4 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			295	179	64	48	4		

- Molecule 5 is a RNA chain called 23s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AN1	2892	Total	C	N	O	P	0	0
			62023	27689	11345	20098	2891		

- Molecule 6 is a RNA chain called 5s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	115	Total	C	N	O	P	0	0
			2450	1095	440	800	115		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	270	Total	C	N	O	S	0	0
			2096	1291	434	363	8		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	211	Total	C	N	O	S	0	0
			1572	972	297	300	3		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	186	Total	C	N	O	S	0	0
			1419	893	265	257	4		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	175	Total	C	N	O	S	0	0
			1381	877	247	249	8		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	174	Total	C	N	O	S	0	0
			1318	832	236	249	1		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	60	Total	C	N	O	S	0	0
			458	287	84	86	1		

- Molecule 13 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	142	Total	C	N	O	S	0	0
			1125	718	200	203	4		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	122	Total	C	N	O	S	0	0
			946	592	180	169	5		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	146	Total	C	N	O	S	0	0
			1089	673	215	200	1		

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	137	Total	C	N	O	S	0	0
			1087	687	210	185	5		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	119	Total	C	N	O	S	0	0
			942	590	186	163	3		

- Molecule 18 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	114	Total	C	N	O	S	0	0
			857	528	173	155	1		

- Molecule 19 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	O	117	Total	C	N	O	0	0
			919	578	177	164		

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	117	Total	C	N	O	S	0	0
			934	589	197	146	2		

- Molecule 21 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	103	Total	C	N	O	S	0	0
			807	506	155	143	3		

- Molecule 22 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	109	Total	C	N	O	S	0	0
			826	514	158	150	4		

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	90	Total	C	N	O		0	0
			702	447	127	128			

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	100	Total	C	N	O		0	0
			749	465	139	145			

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	97	Total	C	N	O	S	0	0
			760	477	143	139	1		

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	80	Total	C	N	O	S	0	0
			598	370	115	111	2		

- Molecule 27 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	77	Total	C	N	O	S	0	0
			632	395	130	105	2		

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	62	Total	C	N	O	S	0	0
			498	308	96	93	1		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	58	Total	C	N	O	S	0	0
			463	286	88	85	4		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	55	Total	C	N	O	S	0	0
			456	271	102	82	1		

- Molecule 31 is a RNA chain called 16s Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	sN1	1528	Total	C	N	O	P	0	0
			32782	14631	5994	10630	1527		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	225	Total	C	N	O	S	0	0
			1769	1110	328	325	6		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	215	Total	C	N	O	S	0	0
			1690	1065	318	299	8		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	207	Total	C	N	O	S	0	0
			1631	1017	313	299	2		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	155	Total	C	N	O	S	0	0
			1129	700	217	207	5		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	94	Total	C	N	O	S	0	0
			793	499	147	143	4		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	141	Total	C	N	O	S	0	0
			1111	696	210	199	6		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	130	Total	C	N	O	S	0	0
			985	615	177	187	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	127	Total	C	N	O	S	0	0
			995	621	198	175	1		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	100	Total	C	N	O	S	0	0
			801	500	150	148	3		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	117	Total	C	N	O	S	0	0
			862	535	167	159	1		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	122	Total	C	N	O	S	0	0
			945	580	193	167	5		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	115	Total	C	N	O	S	0	0
			903	558	184	158	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	100	Total	C	N	O	S	0	0
			792	493	158	137	4		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	88	Total	C	N	O	S	0	0
			705	434	144	126	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	83	Total	C	N	O	S	0	0
			649	406	129	113	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	80	Total	C	N	O	S	0	0
			630	396	118	115	1		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	r	53	Total	C	N	O	0	0
			438	282	75	81		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	82	Total	C	N	O	S	0	0
			646	412	125	107	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	85	Total	C	N	O	S	0	0
			658	406	138	112	2		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	u	21	Total	C	N	O	0	0
			182	115	37	30		

- Molecule 52 is a RNA chain called tRNA-met.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	v	77	Total	C	N	O	P	S	0	0
			1636	733	291	535	76	1		

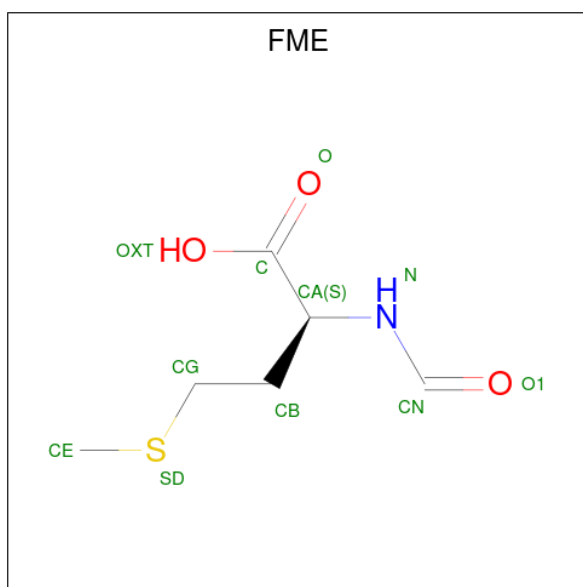
- Molecule 53 is a RNA chain called mRNA 5'-AUG-3'.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	3	Total	C	N	O	P	0	0
			65	29	12	21	3		

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
54	3	1	Total	Zn	0
			1	1	

- Molecule 55 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



Mol	Chain	Residues	Atoms					AltConf
55	AN1	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	AN1	59	Total	Mg	0
			59	59	
56	sN1	55	Total	Mg	0
			55	55	

- Molecule 57 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
57	AN1	1	Total	Na	0
			1	1	

- Molecule 58 is water.

Mol	Chain	Residues	Atoms		AltConf
58	1	1	Total	O	0
			1	1	
58	AN1	193	Total	O	0
			193	193	
58	B	1	Total	O	0
			1	1	

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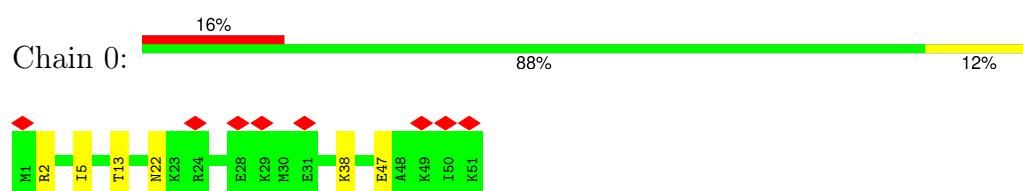
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Mol	Chain	Residues	Atoms		AltConf
58	C	2	Total 2	O 2	0
58	D	2	Total 2	O 2	0
58	K	2	Total 2	O 2	0
58	Z	1	Total 1	O 1	0
58	sN1	63	Total 63	O 63	0
58	h	1	Total 1	O 1	0
58	j	1	Total 1	O 1	0
58	m	1	Total 1	O 1	0
58	q	1	Total 1	O 1	0
58	s	3	Total 3	O 3	0
58	t	1	Total 1	O 1	0

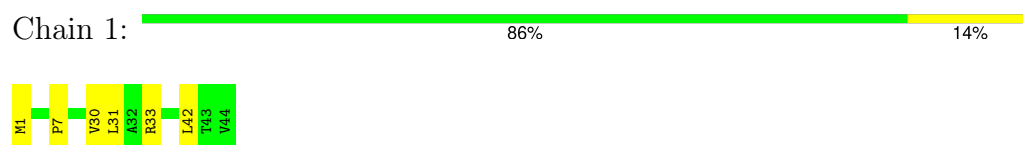
3 Residue-property plots [i](#)

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

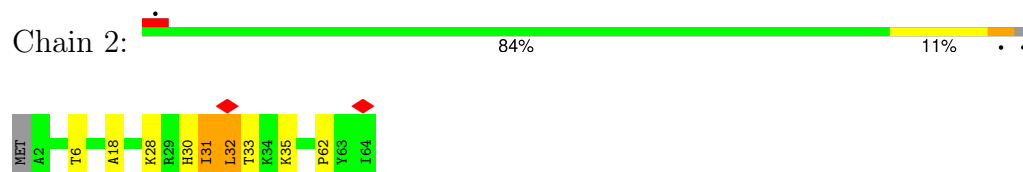
- Molecule 1: 50S ribosomal protein L33



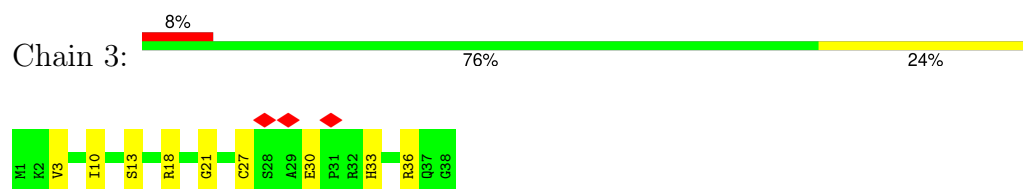
- Molecule 2: 50S ribosomal protein L34



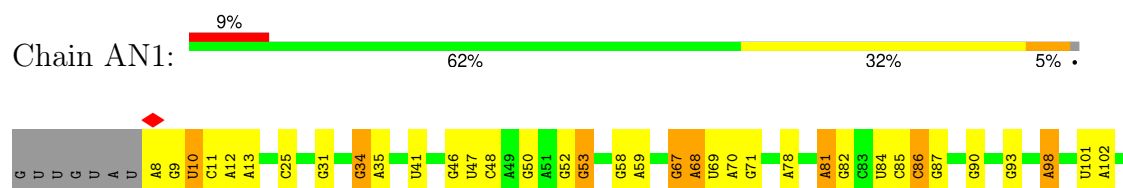
- Molecule 3: 50S ribosomal protein L35

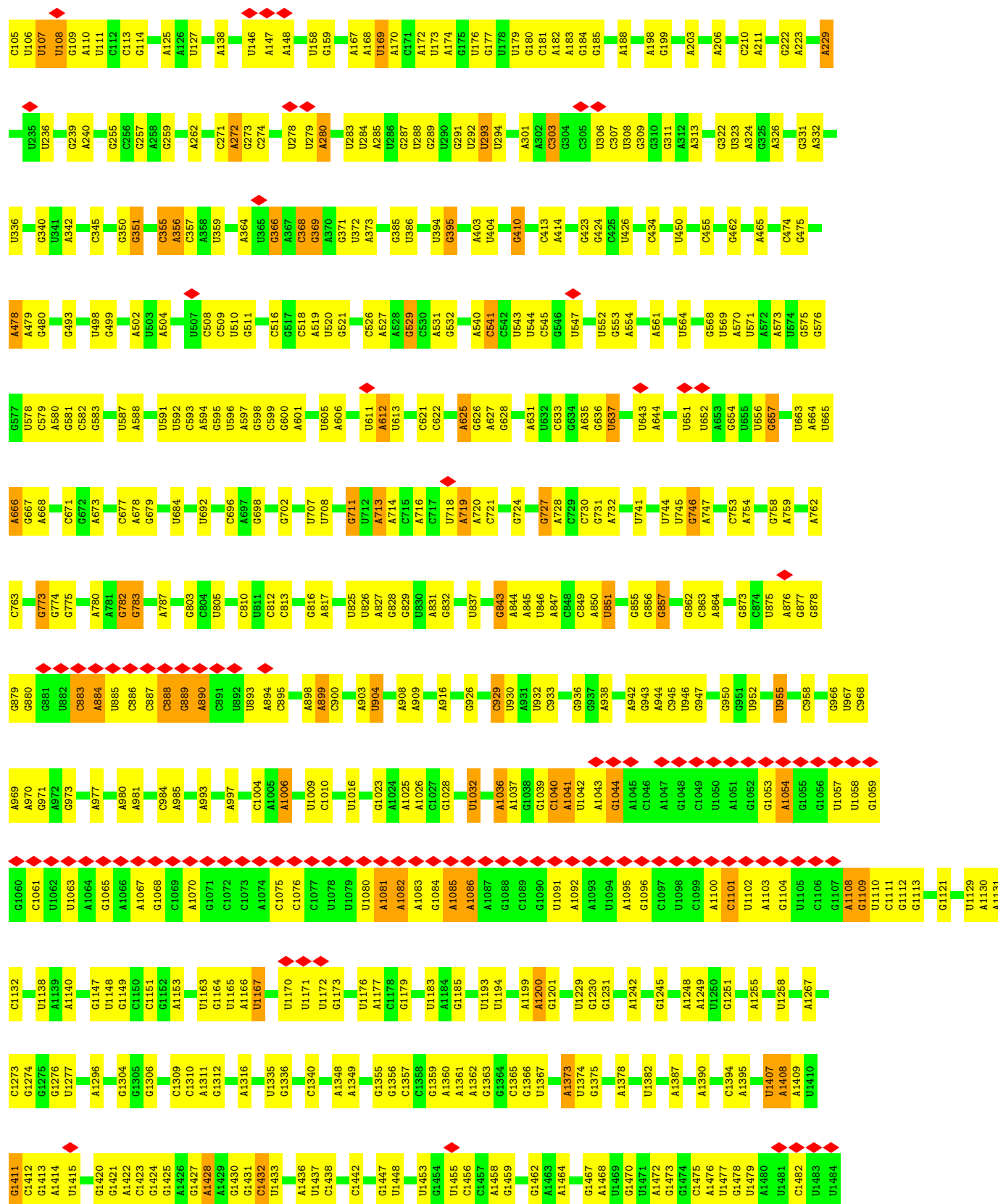


- Molecule 4: 50S ribosomal protein L36



- Molecule 5: 23S ribosomal RNA





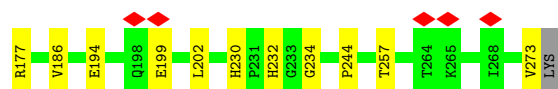
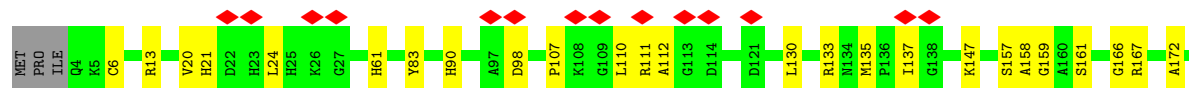
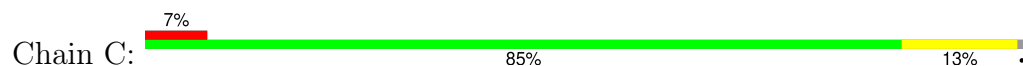
A2730	U2601	U2485	G2387	U2261	A2166	G2106	G2020	C1905	C1796	G1665	U1560	A1485
A2734	U2605	G2486	C2399	A2262	A2167	U2107	C2021	G1906	A1797	G1680	U1561	A1486
U2735	C2606	U2487	U2401	A2263	U2168	G2108	U2022	A1908	A1798	G1672	C1562	G1487
A2737	C2608	C2494	G2401	A2274	A2169	U2109	G2025	A1909	A1799	C1673	A1564	C1488
U2743	U2603	C2495	U2402	G2275	C2170	U2110	A2026	C1910	A1805	U1681	A1567	A1489
A2744	A2611	G2498	A2407	G2276	A2172	G2111	A2027	3TD1911	G1810	U1682	A1568	A1490
A2753	C2622	U2500	A2408	A2280	C2173	G2112	G2028	A1912	A1811	C1683	A1569	A1491
A2754	G2623	U2502	G2418	G2281	C2174	A2113	U2030	U1913	C1812	C1684	U1574	U1492
U2760	C2624	C2503	U2419	G2282	C2175	U2114	C2039	A1914	A1825	C1575	C1576	C1493
A2761	U2625	A2514	C2420	A2283	U2176	G2116	C2043	G1917	C1828	U1691	U1577	C1494
G2762	U2633	U2515	C2423	A2284	G2177	G2117	G2044	U1918	A1829	U1712	U1578	G1495
U2769	G2634	C2516	G2424	G2287	U2178	U2118	G2049	U1919	U1713	U1710	G1579	G1496
A2774	A2635	G2519	G2425	U2288	G2179	G2119	A2050	C1920	A1843	G1714	C1580	G1497
U2775	G2636	G2525	G2426	G2289	A2180	G2120	C2051	U1921	A1844	G1717	U1581	U1499
A2776	A2637	G2526	U2427	C2296	A2181	G2121	G2052	A1923	G1845	U1718	U1582	A1500
C2784	U2641	A2527	A2428	G2297	U2182	A2122	A2055	G1925	U1847	U1719	C1583	C1501
G2785	C2642	G2528	A2430	U2301	G2185	G2123	G2057	G1926	A1850	U1725	A1584	U1502
U2786	U2643	C2530	A2431	C2302	G2188	G2124	A2058	U1932	U1857	C1726	U1587	C1503
G2787	G2644	U2533	U2437	G2304	G2189	C2125	G2059	A1933	A1854	G1727	A1588	U1504
A2788	C2645	C2534	G2438	A2305	U2190	U2126	C2060	A1934	A1855	C1731	A1589	U1505
U2791	U2646	G2536	U2439	A2306	U2191	U2127	C2061	U1935	C1732	U1733	C1591	U1506
U2792	C2647	A2543	G2441	U2307	U2192	U2128	G2062	U1936	G1858	C1732	C1592	G1507
U2793	U2648	U2544	G2442	U2308	U2193	G2129	U2064	C1937	G1859	U1734	G1593	C1508
U2794	G2655	U2545	G2443	C2311	A2194	A2130	G2065	C1938	U1860	G1735	G1594	U1509
U2795	A2656	G2548	A2444	G2312	A2195	G2132	A2066	U1939	A1861	U1739	A1595	G1510
G2796	C2657	U2549	U2445	G2313	C2196	G2132	C2067	U1942	G1862	C1741	A1596	A1511
U2797	A2658	U2550	A2446	G2314	G2200	C2133	C2068	C1943	G1863	G1742	C1602	G1512
U2798	C2659	G2552	G2447	U2315	C2204	U2134	U2070	U1951	U1866	C1743	G1605	G1517
C2799	G2660	A2562	A2448	A2316	G2207	G2135	U2071	G1958	A1867	C1744	A1606	U1518
C2800	A2661	G2564	G2450	G2317	G2207	G2136	U2072	C1959	A1868	A1745	A1607	U1519
A2804	U2674	U2568	U2453	A2321	G2212	A2137	C2077	U1959	G1869	G1746	A1608	G1521
A2806	A2675	G2572	G2454	U2322	G2213	C2138	A2078	C1960	C1870	G1749	A1616	C1522
U2811	U2683	A2573	U2455	A2323	U2219	C2139	U2088	G1961	G1871	C1750	A1617	A1523
C2815	G2684	G2574	A2456	A2325	G2222	G2140	G2089	C1962	A1872	G1752	C1623	G1524
G2816	U2685	U2575	C2463	G2326	C2222	C2141	C2092	C1963	U1876	C1752	A1624	G1525
A2817	A2686	G2576	A2464	C2346	U2225	U2142	U2093	A1966	U1877	G1760	A1630	C1526
U2829	G2694	G2577	G2467	C2355	G2226	A2143	U2094	U1967	C1877	C1767	A1634	G1527
A2831	A2695	A2578	G2468	A2356	U2229	G2144	U2095	G1968	U1878	A1768	A1635	G1528
G2834	C2697	U2579	U2469	A2357	G2230	U2145	G2096	U1978	A1885	A1769	C1642	U1529
G2835	U2710	G2591	C2471	A2373	G2234	U2146	A2097	U1987	U1888	U1775	C1642	U1530
U2841	U2722	A2594	A2473	U2376	G2235	C2148	C2098	G1988	C1888	A1776	U1645	U1531
G2842	G2727	G2598	U2474	A2377	U2239	A2149	U2100	U1989	A1895	A1780	U1646	G1532
U2843	U2728	U2600	G2483	G2378	U2241	G2150	U2101	C1992	A1895	U1792	G1647	U1533
			G2484	U2379	G2242	A2102	A2103	C1993	G1889	C1793	U1657	G1534
				C2381	A2243	G2152	U2104	U2018	U1902	U1794	A1662	U1535
					G2247	G2153	U2105	C2019	G1902	G1795		U1536
					C2254	A2154						G1537
						C2156						A1538
						C2157						G1539
						G2158						C1540
						U2159						G1541
						C2160						A1542
						U2162						G1543
						U2163						G1544
						G2164						U1545
						A2165						C1559



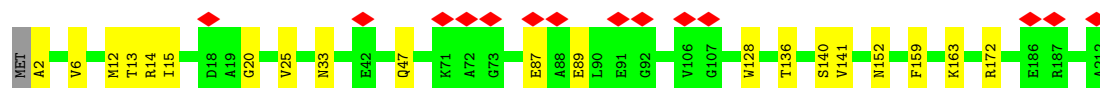
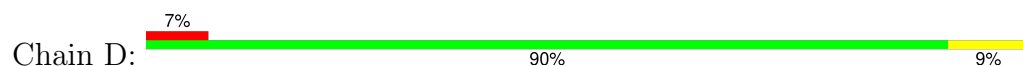
• Molecule 6: 5s ribosomal RNA



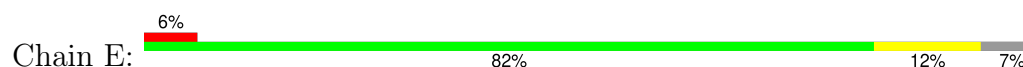
• Molecule 7: 50S ribosomal protein L2



• Molecule 8: 50S ribosomal protein L3

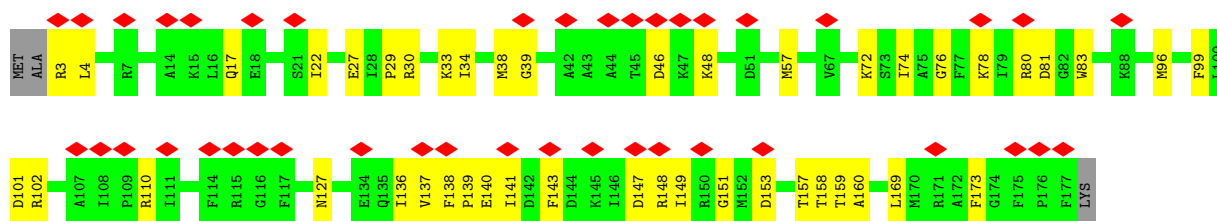


• Molecule 9: 50S ribosomal protein L4

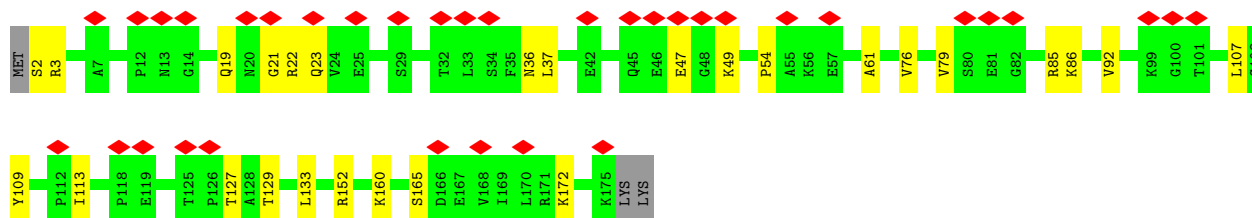
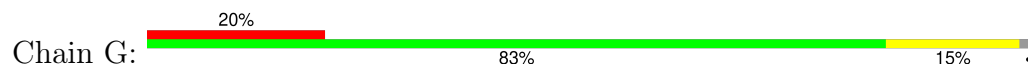


• Molecule 10: 50S ribosomal protein L5

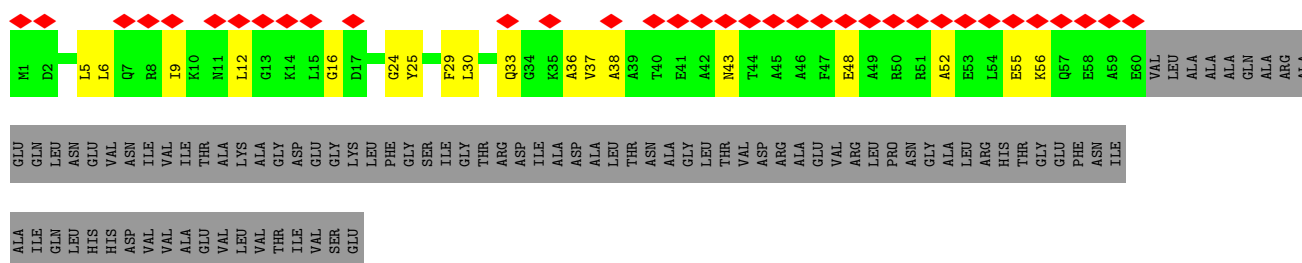




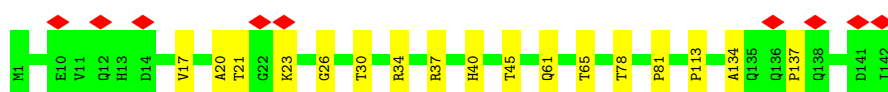
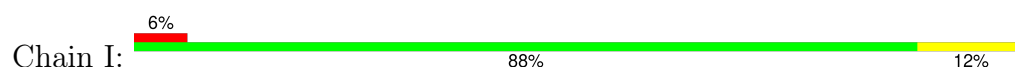
• Molecule 11: 50S ribosomal protein L6



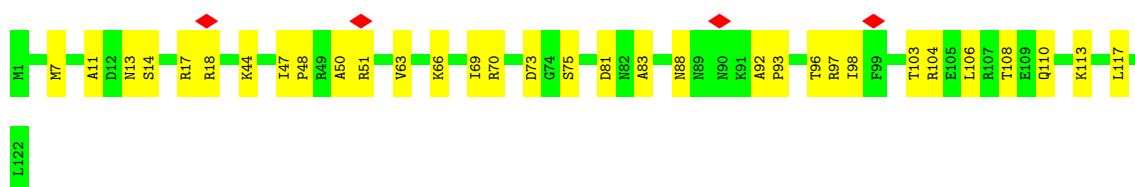
• Molecule 12: 50S ribosomal protein L9



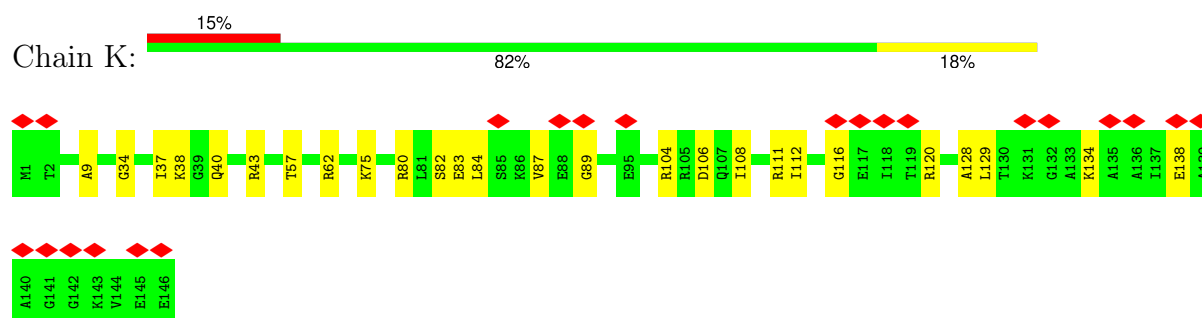
• Molecule 13: 50S ribosomal protein L13



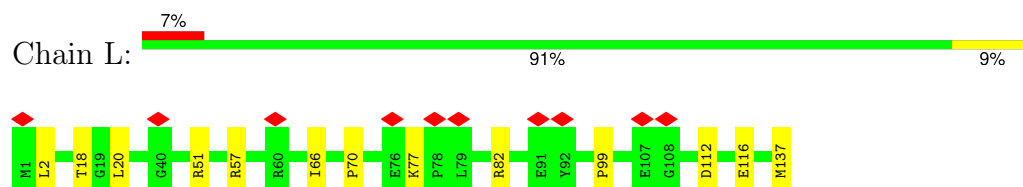
• Molecule 14: 50S ribosomal protein L14



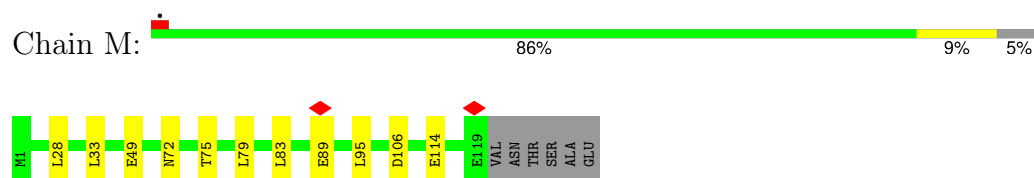
• Molecule 15: 50S ribosomal protein L15



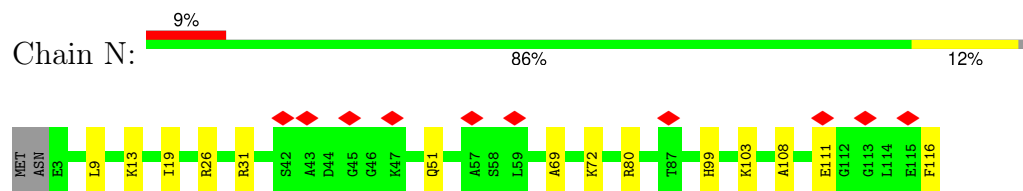
- Molecule 16: 50S ribosomal protein L16



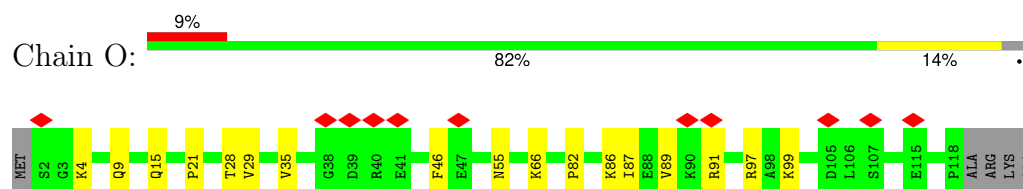
- Molecule 17: 50S ribosomal protein L17



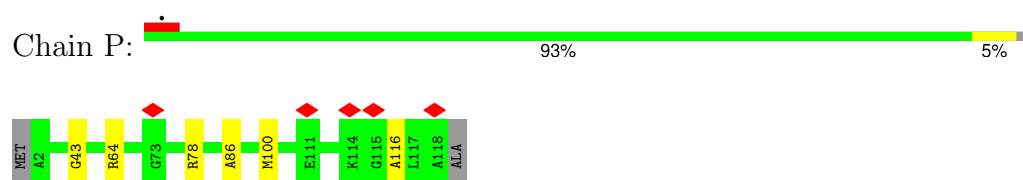
- Molecule 18: 50S ribosomal protein L18



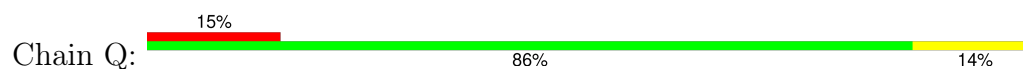
- Molecule 19: 50S ribosomal protein L19

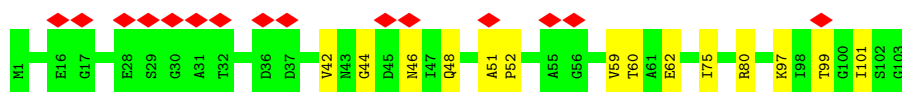


- Molecule 20: 50S ribosomal protein L20

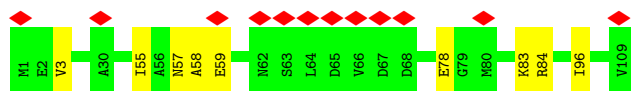
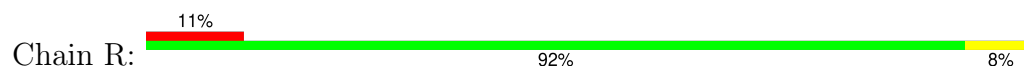


- Molecule 21: 50S ribosomal protein L21

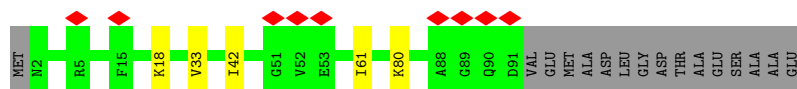




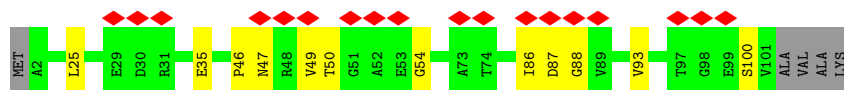
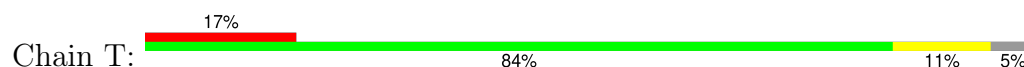
- Molecule 22: 50S ribosomal protein L22



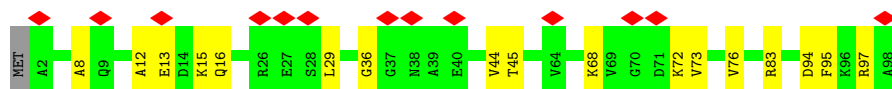
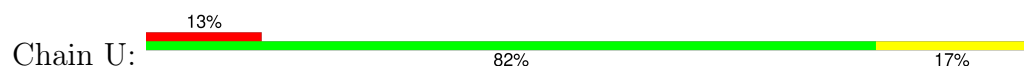
- Molecule 23: 50S ribosomal protein L23



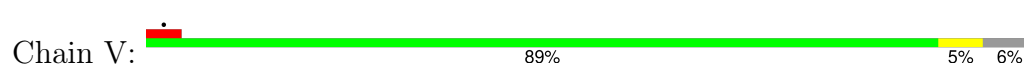
- Molecule 24: 50S ribosomal protein L24



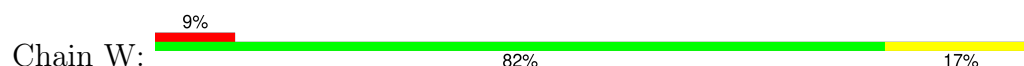
- Molecule 25: 50S ribosomal protein L25



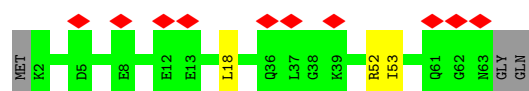
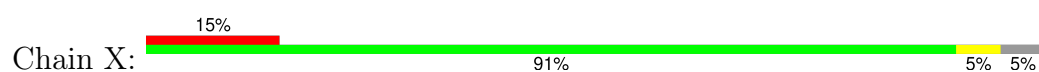
- Molecule 26: 50S ribosomal protein L27



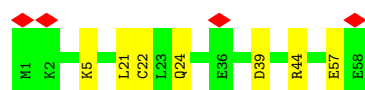
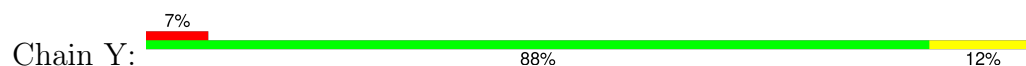
- Molecule 27: 50S ribosomal protein L28



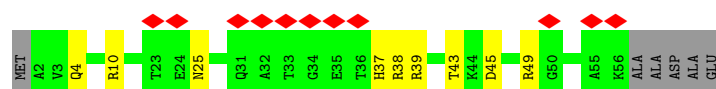
- Molecule 28: 50S ribosomal protein L29



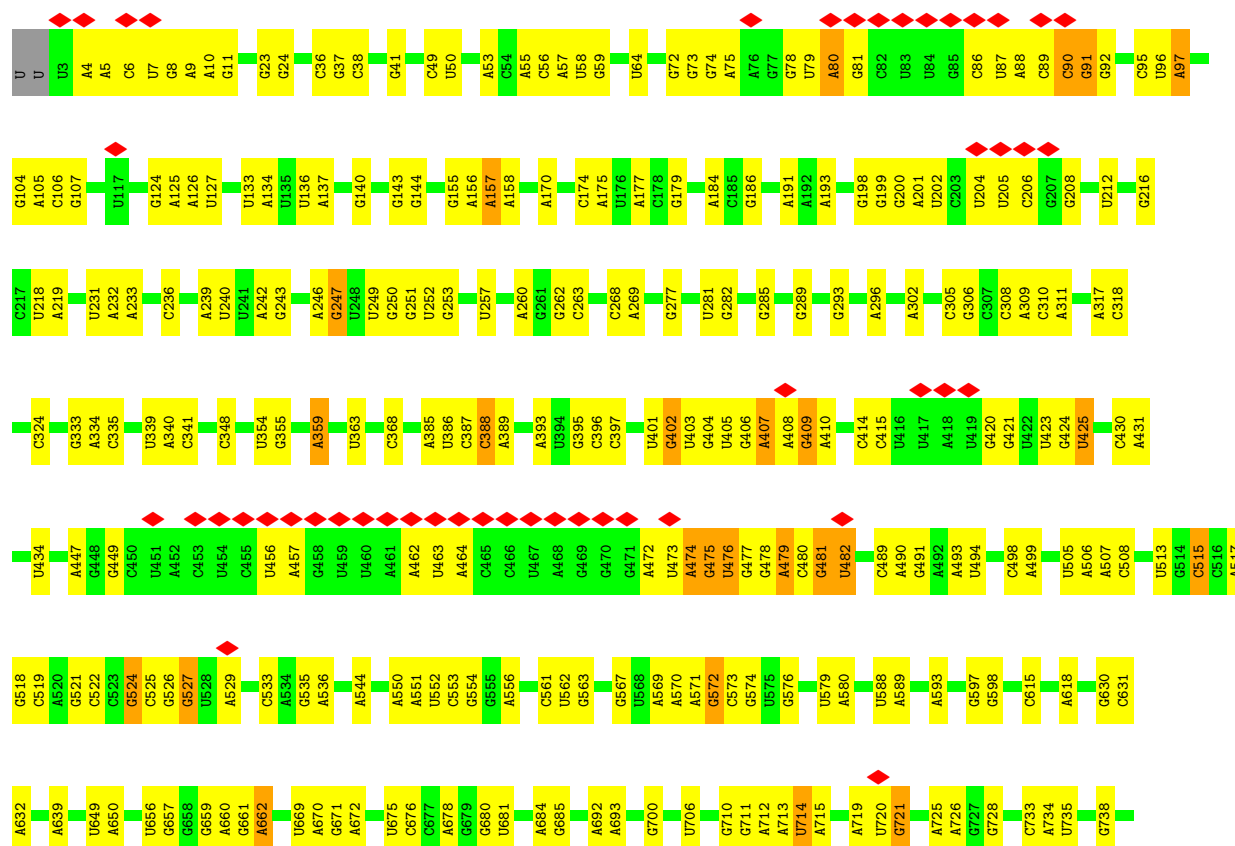
- Molecule 29: 50S ribosomal protein L30

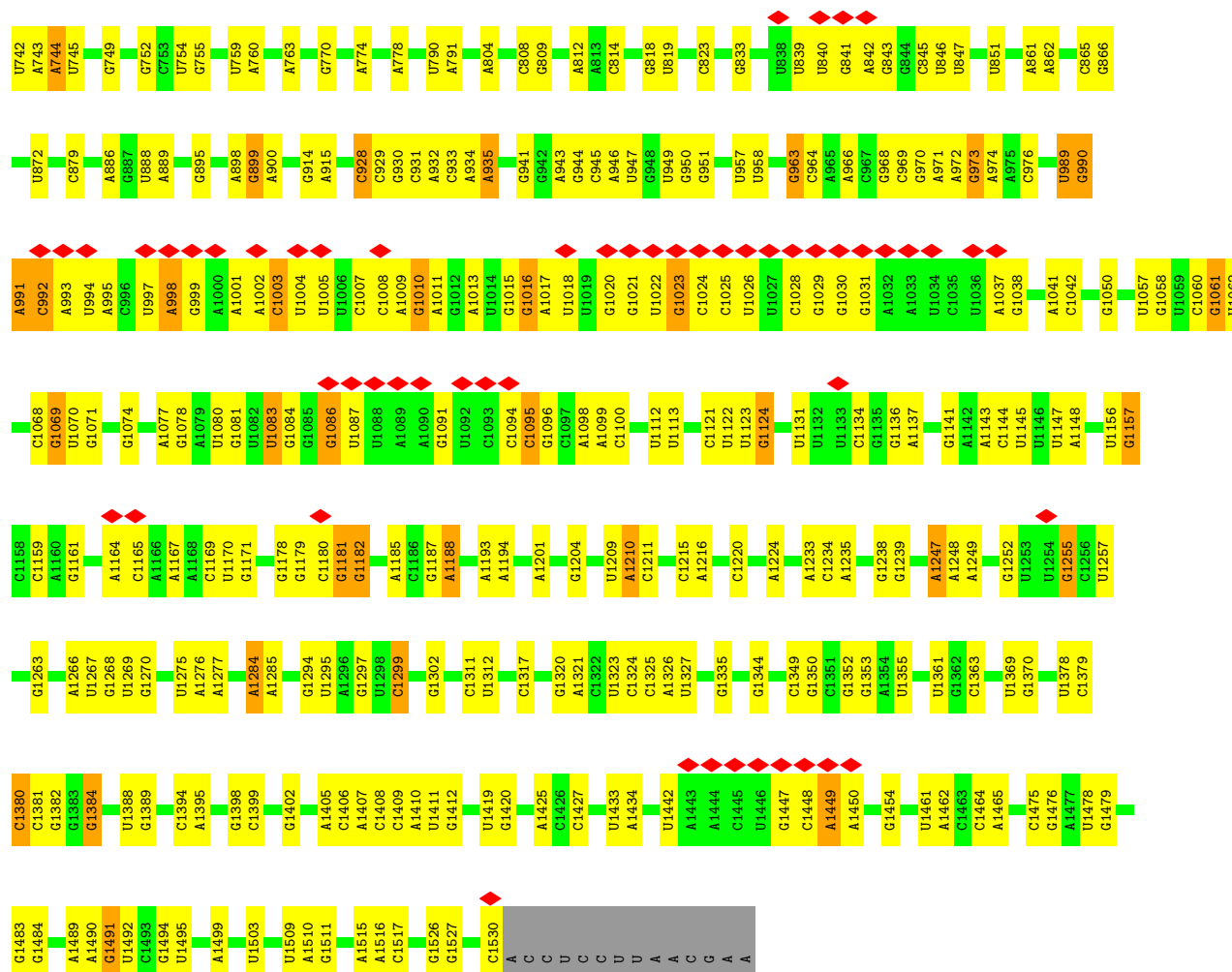


- Molecule 30: 50S ribosomal protein L32



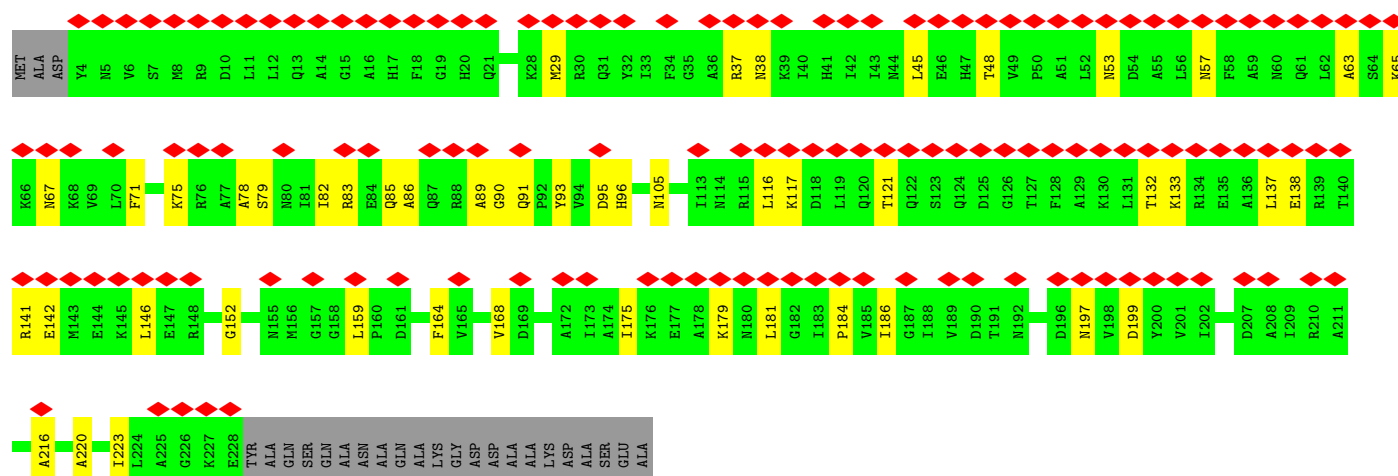
- Molecule 31: 16s Ribosomal RNA





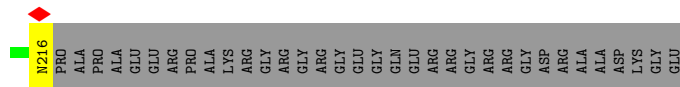
• Molecule 32: 30S ribosomal protein S2

Chain b:



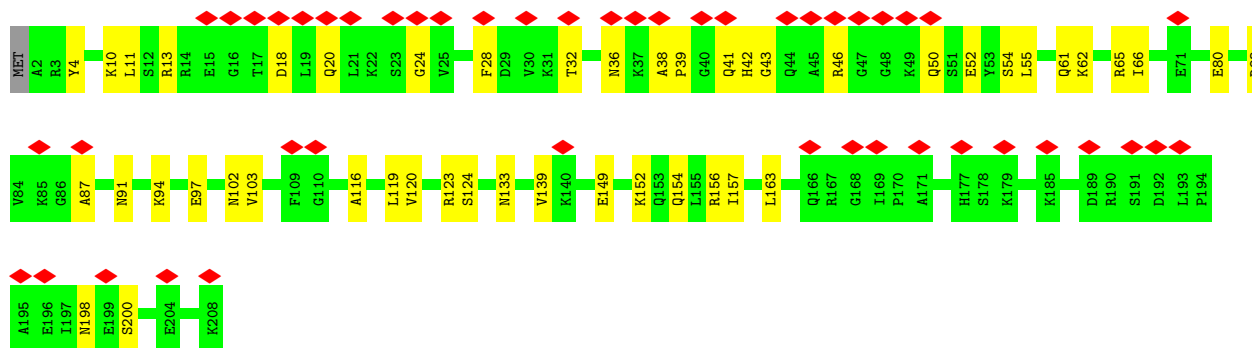
• Molecule 33: 30S ribosomal protein S3

Frequency	Percentage
Daily	74%
Weekly	12%
Monthly	14%



- Molecule 34: 30S ribosomal protein S4

Frequency	Percentage
Daily	23%
Weekly	77%
Monthly	23%



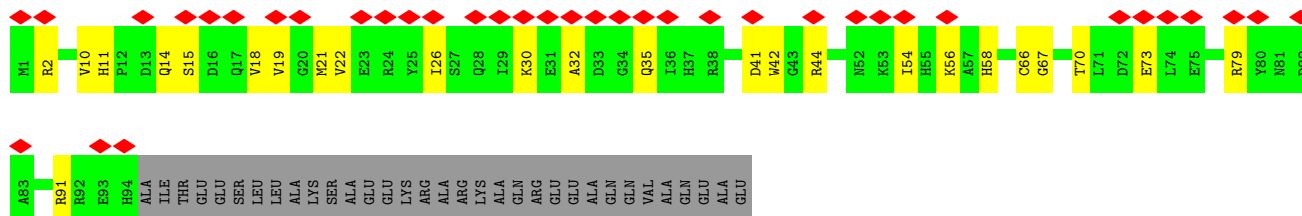
- Molecule 35: 30S ribosomal protein S5

Response	Percentage
Yes	83%
No	11%
Don't know	6%



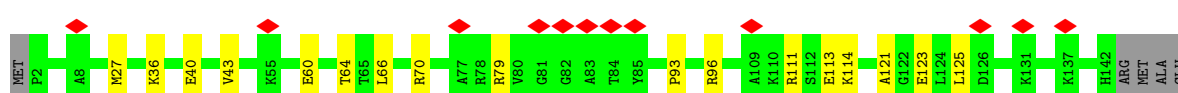
- Molecule 36: 30S ribosomal protein S6

Response	Percentage
Current government is the best	30%
Opposition is the best	54%
Neither is the best	20%
No answer	26%



- Molecule 37: 30S ribosomal protein S7

Frequency	Percentage
Very often	8%
Often	79%
Sometimes	11%
Never	10%



ALA
ASN
LYS
ALA
PHE
SER
HIS
TYR
ARG
PHE

- Molecule 38: 30S ribosomal protein S8

Chain h:  92% 8%

MET S2 M3 R15 N16 K22 A37 E43 V49 E55 Y66 I102 S131

- Molecule 39: 30S ribosomal protein S9

Chain i:  88% 11%

MET A2 Y5 R10 K11 T14 L19 K25 D60 L61 T82 D89 L96 R104 D105 R117 R128

- Molecule 40: 30S ribosomal protein S10

Chain j:  13% 72% 25%

MET SER N3 Q4 R7 I8 R16 A22 V26 E27 R31 V36 C37 G38 M42 H56 V57 N58 K59 D63 E66 I67 R68 K71 R72 L73 I74 T80 D81 K82 T83 V84 D85 K89 L90 D91 L92 A101 L102 GLY

- Molecule 41: 30S ribosomal protein S11

Chain k:  17% 66% 25% 9%

MET ALA LYS ASP THR ARG THR ARG LYS VAL T12 R13 S16 E17 G18 V19 A20 H21 T32 T33 T34 D35 N36 Q37 G38 G50 F51 R52 R55 T58 P59 F60 V64 E67 V68 K71 L74 D75 L78 R79 N80 L81 D82 V83 L84 R92 A98

L99 G100 A101 V102 G103 Y104 K105 I106 N107 S108 I109 T110 D111 N118 G119 K125 V128

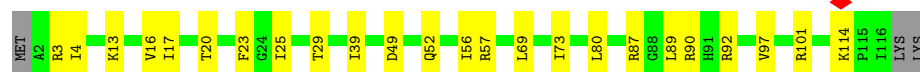
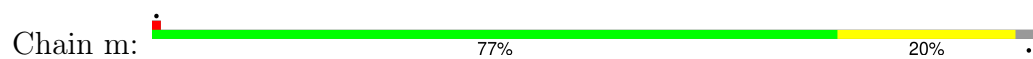
- Molecule 42: 30S ribosomal protein S12

Chain l:  19% 83% 15%

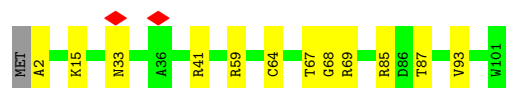
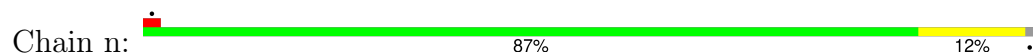
MET A2 L15 V16 E17 K18 L24 C27 R30 C34 T35 R36 T41 P42 K43 K44 P45 M46 S47 A48 M49 R50 R51 V52 C53 R54 G60 F61 E62 E70 H73 L74 Q75 E76 H77 G85 R86 V87 K88 D89 L90 P91 G92 H95 R99 G100 S101 L102

D109 R114 Y117 K123 LYS

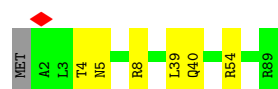
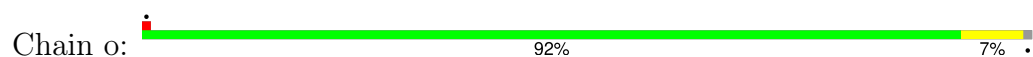
- Molecule 43: 30S ribosomal protein S13



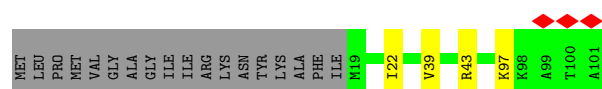
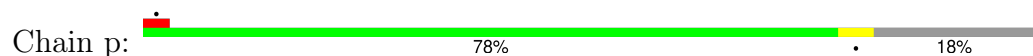
- Molecule 44: 30S ribosomal protein S14



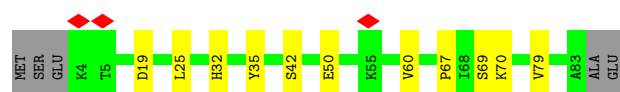
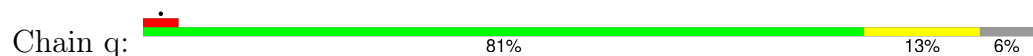
- Molecule 45: 30S ribosomal protein S15



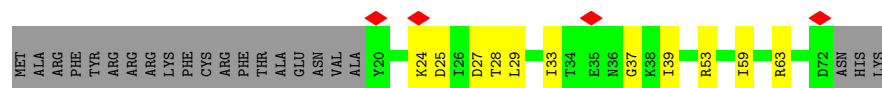
- Molecule 46: 30S ribosomal protein S16



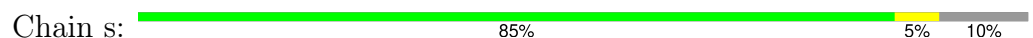
- Molecule 47: 30S ribosomal protein S17



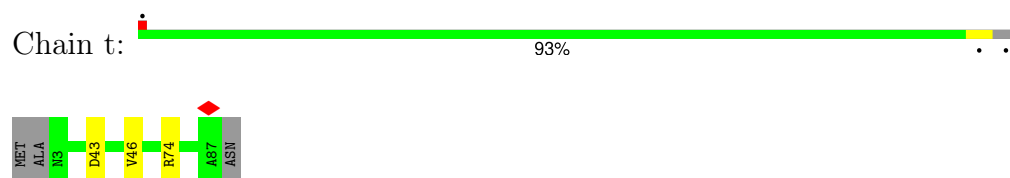
- Molecule 48: 30S ribosomal protein S18



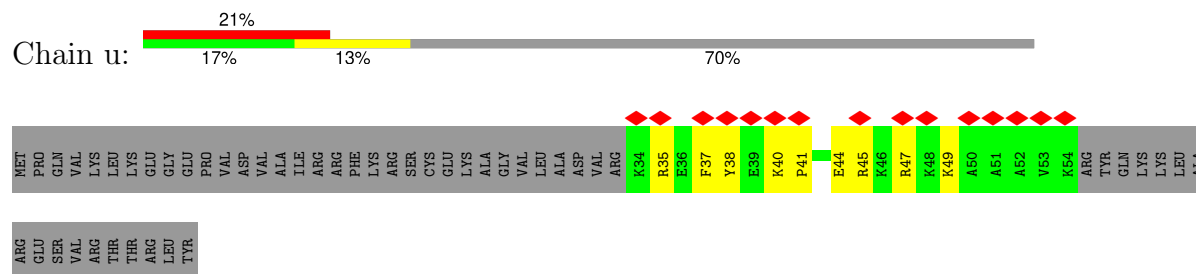
- Molecule 49: 30S ribosomal protein S19



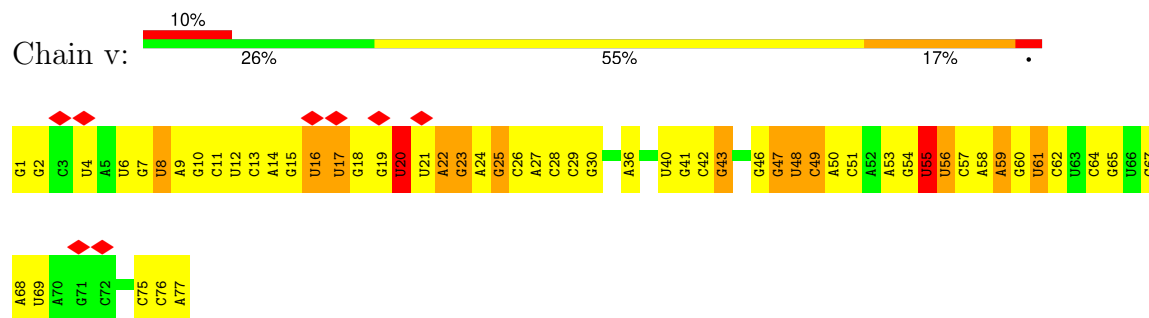
- Molecule 50: 30S ribosomal protein S20



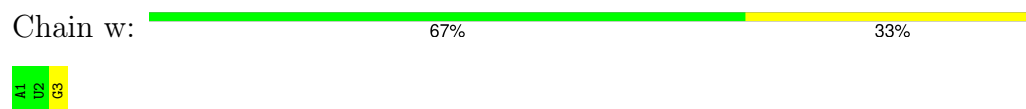
- Molecule 51: 30S ribosomal protein S21



- Molecule 52: tRNA-met



- Molecule 53: mRNA 5'-AUG-3'



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24306	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.512	Depositor
Minimum map value	-1.632	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.091	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	544.768, 544.768, 544.768	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.064, 1.064, 1.064	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, 6MZ, 2MG, 4SU, MA6, 7MG, ZN, OMU, 5MU, MG, 5MC, FME, UR3, H2U, 3TD, 4OC, OMG, PSU, NA

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	0.13	0/434	0.33	0/573
2	1	0.13	0/367	0.36	0/481
3	2	0.14	0/515	0.44	0/678
4	3	0.16	0/296	0.50	0/389
5	AN1	0.10	0/69101	0.23	0/107780
6	B	0.09	0/2739	0.21	0/4266
7	C	0.13	0/2136	0.35	0/2869
8	D	0.13	0/1590	0.31	0/2142
9	E	0.11	0/1440	0.30	0/1944
10	F	0.15	0/1401	0.43	0/1877
11	G	0.13	0/1337	0.36	0/1807
12	H	0.15	0/461	0.42	0/616
13	I	0.13	0/1151	0.32	0/1551
14	J	0.13	0/956	0.35	0/1286
15	K	0.13	0/1097	0.38	0/1461
16	L	0.12	0/1104	0.31	0/1475
17	M	0.15	0/956	0.38	0/1282
18	N	0.12	0/865	0.31	0/1156
19	O	0.13	0/931	0.33	0/1249
20	P	0.13	0/947	0.31	0/1262
21	Q	0.14	0/818	0.37	0/1094
22	R	0.13	0/831	0.32	0/1113
23	S	0.12	0/708	0.31	0/947
24	T	0.14	0/753	0.39	0/1010
25	U	0.13	0/770	0.34	0/1036
26	V	0.12	0/606	0.31	0/810
27	W	0.12	0/642	0.31	0/856
28	X	0.11	0/499	0.29	0/662
29	Y	0.13	0/468	0.34	0/624
30	Z	0.12	0/462	0.33	0/615
31	sN1	0.09	1/36476 (0.0%)	0.20	0/56895

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	b	0.15	0/1799	0.41	0/2429
33	c	0.11	0/1714	0.31	0/2304
34	d	0.11	0/1653	0.32	0/2213
35	e	0.12	0/1141	0.33	0/1537
36	f	0.12	0/808	0.38	0/1089
37	g	0.11	0/1127	0.31	0/1511
38	h	0.12	0/993	0.31	0/1331
39	i	0.13	0/1006	0.36	0/1346
40	j	0.15	0/811	0.38	0/1096
41	k	0.13	0/878	0.37	0/1189
42	l	0.14	0/958	0.42	0/1284
43	m	0.14	0/913	0.41	0/1226
44	n	0.11	0/803	0.30	0/1071
45	o	0.10	0/715	0.28	0/958
46	p	0.10	0/660	0.31	0/886
47	q	0.12	0/637	0.34	0/858
48	r	0.11	0/445	0.33	0/601
49	s	0.11	0/664	0.34	0/897
50	t	0.13	0/664	0.28	0/885
51	u	0.24	0/184	0.37	0/240
52	v	0.17	1/1739 (0.1%)	0.27	0/2709
53	w	0.08	0/72	0.16	0/110
All	All	0.11	2/153241 (0.0%)	0.26	0/229576

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	v	8	4SU	O3'-P	5.37	1.61	1.56
31	sN1	1495	UR3	O3'-P	5.02	1.61	1.56

There are no bond angle outliers.

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	427	0	462	4	0
2	1	363	0	401	5	0
3	2	509	0	566	8	0
4	3	295	0	327	6	0
5	AN1	62023	0	31191	563	0
6	B	2450	0	1241	39	0
7	C	2096	0	2157	27	0
8	D	1572	0	1610	16	0
9	E	1419	0	1464	19	0
10	F	1381	0	1433	35	0
11	G	1318	0	1373	16	0
12	H	458	0	480	11	0
13	I	1125	0	1148	12	0
14	J	946	0	1007	20	0
15	K	1089	0	1159	16	0
16	L	1087	0	1162	8	0
17	M	942	0	987	7	0
18	N	857	0	899	9	0
19	O	919	0	973	14	0
20	P	934	0	997	5	0
21	Q	807	0	842	9	0
22	R	826	0	894	6	0
23	S	702	0	756	3	0
24	T	749	0	797	8	0
25	U	760	0	783	12	0
26	V	598	0	600	3	0
27	W	632	0	667	9	0
28	X	498	0	537	2	0
29	Y	463	0	488	4	0
30	Z	456	0	448	7	0
31	sN1	32782	0	16505	333	0
32	b	1769	0	1787	33	0
33	c	1690	0	1774	20	0
34	d	1631	0	1691	28	0
35	e	1129	0	1174	11	0
36	f	793	0	788	15	0
37	g	1111	0	1163	10	0
38	h	985	0	1047	7	0
39	i	995	0	1053	12	0
40	j	801	0	832	18	0
41	k	862	0	877	24	0
42	l	945	0	996	12	0
43	m	903	0	962	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	n	792	0	833	9	0
45	o	705	0	712	6	0
46	p	649	0	660	3	0
47	q	630	0	678	8	0
48	r	438	0	456	7	0
49	s	646	0	663	4	0
50	t	658	0	710	2	0
51	u	182	0	198	9	0
52	v	1636	0	831	40	0
53	w	65	0	33	1	0
54	3	1	0	0	0	0
55	AN1	10	0	10	0	0
56	AN1	59	0	0	0	0
56	sN1	55	0	0	0	0
57	AN1	1	0	0	0	0
58	1	1	0	0	0	0
58	AN1	193	0	0	2	0
58	B	1	0	0	0	0
58	C	2	0	0	0	0
58	D	2	0	0	0	0
58	K	2	0	0	0	0
58	Z	1	0	0	0	0
58	h	1	0	0	0	0
58	j	1	0	0	0	0
58	m	1	0	0	0	0
58	q	1	0	0	0	0
58	s	3	0	0	0	0
58	sN1	63	0	0	1	0
58	t	1	0	0	0	0
All	All	141897	0	94282	1398	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 6.

The worst 5 of 1398 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)
5:AN1:1462:G:H1	5:AN1:1520:A:N6	1.44	1.12
31:sN1:1442:U:H3	31:sN1:1454:G:H1	1.08	1.02
6:B:70:G:H21	6:B:101:A:H62	0.97	0.97
6:B:70:G:N2	6:B:101:A:H62	1.64	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:sN1:1069:G:O6	31:sN1:1081:G:N2	1.99	0.95

There are no symmetry-related clashes.

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	49/51 (96%)	47 (96%)	2 (4%)	0	100	100
2	1	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
3	2	61/64 (95%)	54 (88%)	5 (8%)	2 (3%)	3	15
4	3	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
7	C	268/274 (98%)	259 (97%)	9 (3%)	0	100	100
8	D	209/212 (99%)	205 (98%)	4 (2%)	0	100	100
9	E	184/200 (92%)	184 (100%)	0	0	100	100
10	F	173/178 (97%)	158 (91%)	14 (8%)	1 (1%)	21	53
11	G	172/177 (97%)	167 (97%)	5 (3%)	0	100	100
12	H	58/148 (39%)	53 (91%)	5 (9%)	0	100	100
13	I	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
14	J	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
15	K	144/146 (99%)	141 (98%)	3 (2%)	0	100	100
16	L	135/137 (98%)	135 (100%)	0	0	100	100
17	M	117/125 (94%)	117 (100%)	0	0	100	100
18	N	112/116 (97%)	111 (99%)	1 (1%)	0	100	100
19	O	115/122 (94%)	112 (97%)	3 (3%)	0	100	100
20	P	115/119 (97%)	114 (99%)	1 (1%)	0	100	100
21	Q	101/103 (98%)	94 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	R	107/109 (98%)	106 (99%)	1 (1%)	0	100	100
23	S	88/106 (83%)	88 (100%)	0	0	100	100
24	T	98/105 (93%)	97 (99%)	1 (1%)	0	100	100
25	U	95/98 (97%)	94 (99%)	1 (1%)	0	100	100
26	V	78/85 (92%)	77 (99%)	1 (1%)	0	100	100
27	W	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
28	X	60/65 (92%)	60 (100%)	0	0	100	100
29	Y	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
30	Z	53/61 (87%)	51 (96%)	2 (4%)	0	100	100
32	b	223/250 (89%)	216 (97%)	7 (3%)	0	100	100
33	c	213/250 (85%)	205 (96%)	8 (4%)	0	100	100
34	d	205/208 (99%)	201 (98%)	4 (2%)	0	100	100
35	e	153/165 (93%)	153 (100%)	0	0	100	100
36	f	92/127 (72%)	88 (96%)	4 (4%)	0	100	100
37	g	139/156 (89%)	138 (99%)	1 (1%)	0	100	100
38	h	128/131 (98%)	123 (96%)	5 (4%)	0	100	100
39	i	125/128 (98%)	123 (98%)	2 (2%)	0	100	100
40	j	98/103 (95%)	94 (96%)	4 (4%)	0	100	100
41	k	115/128 (90%)	110 (96%)	5 (4%)	0	100	100
42	l	120/124 (97%)	113 (94%)	7 (6%)	0	100	100
43	m	113/118 (96%)	110 (97%)	3 (3%)	0	100	100
44	n	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
45	o	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
46	p	81/101 (80%)	80 (99%)	1 (1%)	0	100	100
47	q	78/85 (92%)	76 (97%)	2 (3%)	0	100	100
48	r	51/75 (68%)	51 (100%)	0	0	100	100
49	s	80/91 (88%)	79 (99%)	1 (1%)	0	100	100
50	t	83/88 (94%)	82 (99%)	1 (1%)	0	100	100
51	u	19/71 (27%)	17 (90%)	2 (10%)	0	100	100
All	All	5361/5872 (91%)	5223 (97%)	135 (2%)	3 (0%)	49	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	2	31	ILE
3	2	32	LEU
10	F	139	PRO

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	47/47 (100%)	47 (100%)	0	100	100
2	1	36/36 (100%)	36 (100%)	0	100	100
3	2	52/53 (98%)	52 (100%)	0	100	100
4	3	33/33 (100%)	33 (100%)	0	100	100
7	C	216/220 (98%)	216 (100%)	0	100	100
8	D	166/167 (99%)	166 (100%)	0	100	100
9	E	144/155 (93%)	144 (100%)	0	100	100
10	F	145/147 (99%)	145 (100%)	0	100	100
11	G	139/142 (98%)	139 (100%)	0	100	100
12	H	45/112 (40%)	45 (100%)	0	100	100
13	I	118/118 (100%)	118 (100%)	0	100	100
14	J	103/103 (100%)	103 (100%)	0	100	100
15	K	108/108 (100%)	108 (100%)	0	100	100
16	L	113/113 (100%)	113 (100%)	0	100	100
17	M	96/101 (95%)	96 (100%)	0	100	100
18	N	83/85 (98%)	83 (100%)	0	100	100
19	O	99/102 (97%)	99 (100%)	0	100	100
20	P	85/86 (99%)	85 (100%)	0	100	100
21	Q	84/84 (100%)	84 (100%)	0	100	100
22	R	88/88 (100%)	88 (100%)	0	100	100
23	S	76/87 (87%)	76 (100%)	0	100	100
24	T	82/85 (96%)	82 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	U	79/80 (99%)	79 (100%)	0	100	100
26	V	60/64 (94%)	60 (100%)	0	100	100
27	W	69/70 (99%)	69 (100%)	0	100	100
28	X	54/56 (96%)	54 (100%)	0	100	100
29	Y	54/54 (100%)	54 (100%)	0	100	100
30	Z	47/50 (94%)	47 (100%)	0	100	100
32	b	185/200 (92%)	185 (100%)	0	100	100
33	c	175/198 (88%)	175 (100%)	0	100	100
34	d	170/171 (99%)	170 (100%)	0	100	100
35	e	113/120 (94%)	113 (100%)	0	100	100
36	f	86/111 (78%)	86 (100%)	0	100	100
37	g	116/128 (91%)	116 (100%)	0	100	100
38	h	108/109 (99%)	108 (100%)	0	100	100
39	i	99/100 (99%)	99 (100%)	0	100	100
40	j	89/91 (98%)	89 (100%)	0	100	100
41	k	88/98 (90%)	88 (100%)	0	100	100
42	l	104/106 (98%)	104 (100%)	0	100	100
43	m	95/98 (97%)	95 (100%)	0	100	100
44	n	81/82 (99%)	81 (100%)	0	100	100
45	o	71/72 (99%)	71 (100%)	0	100	100
46	p	63/77 (82%)	63 (100%)	0	100	100
47	q	72/76 (95%)	72 (100%)	0	100	100
48	r	47/66 (71%)	47 (100%)	0	100	100
49	s	70/78 (90%)	70 (100%)	0	100	100
50	t	65/67 (97%)	65 (100%)	0	100	100
51	u	18/62 (29%)	18 (100%)	0	100	100
All	All	4436/4756 (93%)	4436 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 108 such sidechains are listed below:

Mol	Chain	Res	Type
32	b	96	HIS
34	d	154	GLN
45	o	42	HIS
32	b	111	GLN
33	c	18	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	sN1	1527/1544 (98%)	213 (13%)	0
5	AN1	2891/2918 (99%)	490 (16%)	8 (0%)
52	v	76/77 (98%)	29 (38%)	0
53	w	2/3 (66%)	0	0
6	B	114/115 (99%)	20 (17%)	1 (0%)
All	All	4610/4657 (98%)	752 (16%)	9 (0%)

5 of 752 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	AN1	10	U
5	AN1	34	G
5	AN1	41	U
5	AN1	50	G
5	AN1	53	G

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	AN1	2379	G
6	B	108	C
5	AN1	478	A
5	AN1	782	G
5	AN1	1538	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

28 non-standard protein/DNA/RNA residues are 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
52	5MU	v	55	52	19,22,23	5.05	7 (36%)	27,32,35	3.75	9 (33%)
5	PSU	AN1	2576	5	18,21,22	1.10	1 (5%)	21,30,33	1.89	5 (23%)
31	2MG	sN1	1204	31	23,26,27	2.90	8 (34%)	33,38,41	2.20	11 (33%)
31	MA6	sN1	1516	31	23,26,27	1.38	4 (17%)	33,38,41	3.29	12 (36%)
5	PSU	AN1	2500	5	18,21,22	1.15	1 (5%)	21,30,33	1.90	4 (19%)
31	4OC	sN1	1399	31	20,23,24	3.21	8 (40%)	25,32,35	0.88	1 (4%)
31	UR3	sN1	1495	31	19,22,23	2.94	6 (31%)	26,32,35	1.61	3 (11%)
5	PSU	AN1	2453	5	18,21,22	1.11	1 (5%)	21,30,33	1.94	6 (28%)
5	6MZ	AN1	2026	5	22,25,26	2.47	4 (18%)	29,36,39	3.41	13 (44%)
5	OMU	AN1	2548	5	19,22,23	3.10	8 (42%)	25,31,34	1.81	4 (16%)
5	2MA	AN1	2499	56,5	22,25,26	3.98	9 (40%)	32,37,40	2.75	11 (34%)
5	PSU	AN1	2601	5	18,21,22	1.10	1 (5%)	21,30,33	1.93	5 (23%)
5	5MU	AN1	1935	5	19,22,23	4.99	7 (36%)	27,32,35	3.64	9 (33%)
5	7MG	AN1	2065	5	23,26,27	3.54	10 (43%)	27,39,42	2.15	9 (33%)
52	PSU	v	56	52	18,21,22	1.13	1 (5%)	21,30,33	1.71	4 (19%)
5	PSU	AN1	1913	5	18,21,22	1.12	1 (5%)	21,30,33	1.83	5 (23%)
31	5MC	sN1	964	31	19,22,23	3.90	8 (42%)	26,32,35	0.97	2 (7%)
52	4SU	v	8	52	18,21,22	4.47	8 (44%)	25,30,33	2.25	5 (20%)
52	H2U	v	20	52	18,21,22	3.21	4 (22%)	19,30,33	1.33	3 (15%)
31	2MG	sN1	963	31	23,26,27	2.91	8 (34%)	33,38,41	2.23	10 (30%)
31	PSU	sN1	513	31	18,21,22	1.16	1 (5%)	21,30,33	1.63	4 (19%)
31	MA6	sN1	1515	31	23,26,27	1.38	4 (17%)	33,38,41	3.31	12 (36%)
5	OMG	AN1	2247	52,5	23,26,27	2.35	8 (34%)	32,38,41	1.84	8 (25%)
5	PSU	AN1	952	5	18,21,22	1.12	1 (5%)	21,30,33	1.91	4 (19%)
31	7MG	sN1	524	31	23,26,27	3.63	11 (47%)	27,39,42	2.18	9 (33%)
5	3TD	AN1	1911	5	19,22,23	4.32	7 (36%)	23,32,35	1.81	3 (13%)
5	PSU	AN1	1907	5	18,21,22	1.14	1 (5%)	21,30,33	1.87	4 (19%)
5	2MG	AN1	2441	5	23,26,27	2.89	8 (34%)	33,38,41	2.21	11 (33%)

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
52	5MU	v	55	52	-	6/7/25/26	0/2/2/2
5	PSU	AN1	2576	5	-	0/7/25/26	0/2/2/2
31	2MG	sN1	1204	31	-	0/9/27/28	0/3/3/3
31	MA6	sN1	1516	31	-	4/11/29/30	0/3/3/3
5	PSU	AN1	2500	5	-	0/7/25/26	0/2/2/2
31	4OC	sN1	1399	31	-	2/9/29/30	0/2/2/2
31	UR3	sN1	1495	31	-	0/7/25/26	0/2/2/2
5	PSU	AN1	2453	5	-	0/7/25/26	0/2/2/2
5	6MZ	AN1	2026	5	-	2/9/27/28	0/3/3/3
5	OMU	AN1	2548	5	-	2/9/27/28	0/2/2/2
5	2MA	AN1	2499	56,5	-	1/7/25/26	0/3/3/3
5	PSU	AN1	2601	5	-	0/7/25/26	0/2/2/2
5	5MU	AN1	1935	5	-	0/7/25/26	0/2/2/2
5	7MG	AN1	2065	5	-	0/7/37/38	0/3/3/3
52	PSU	v	56	52	-	2/7/25/26	0/2/2/2
5	PSU	AN1	1913	5	-	2/7/25/26	0/2/2/2
31	5MC	sN1	964	31	-	0/7/25/26	0/2/2/2
52	4SU	v	8	52	-	4/7/25/26	0/2/2/2
52	H2U	v	20	52	-	4/7/38/39	0/2/2/2
31	2MG	sN1	963	31	-	0/9/27/28	0/3/3/3
31	PSU	sN1	513	31	-	0/7/25/26	0/2/2/2
31	MA6	sN1	1515	31	-	3/11/29/30	0/3/3/3
5	OMG	AN1	2247	52,5	-	0/9/27/28	0/3/3/3
5	PSU	AN1	952	5	-	0/7/25/26	0/2/2/2
31	7MG	sN1	524	31	-	3/7/37/38	0/3/3/3
5	3TD	AN1	1911	5	-	3/7/25/26	0/2/2/2
5	PSU	AN1	1907	5	-	1/7/25/26	0/2/2/2
5	2MG	AN1	2441	5	-	1/9/27/28	0/3/3/3

The worst 5 of 146 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	AN1	1911	3TD	C6-C5	12.81	1.49	1.35
5	AN1	2499	2MA	C4-N3	12.19	1.50	1.34
52	v	55	5MU	C2-N1	11.66	1.56	1.38
5	AN1	1935	5MU	C2-N1	11.58	1.56	1.38
52	v	55	5MU	C6-N1	11.24	1.57	1.38

The worst 5 of 186 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	v	55	5MU	C5-C4-N3	12.65	126.32	115.32
31	sN1	1515	MA6	N1-C6-N6	-12.22	101.97	116.86
31	sN1	1516	MA6	N1-C6-N6	-12.06	102.16	116.86
5	AN1	1935	5MU	C5-C4-N3	11.90	125.67	115.32
5	AN1	2026	6MZ	C4-N9-C1'	-9.90	103.47	126.63

There are no chirality outliers.

5 of 40 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	AN1	1911	3TD	O4'-C4'-C5'-O5'
5	AN1	1913	PSU	O4'-C1'-C5-C6
5	AN1	2548	OMU	O4'-C4'-C5'-O5'
31	sN1	1515	MA6	C5-C6-N6-C9
52	v	8	4SU	O4'-C1'-N1-C2

There are no ring outliers.

7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
52	v	55	5MU	2	0
5	AN1	2026	6MZ	2	0
5	AN1	2499	2MA	3	0
52	v	56	PSU	1	0
52	v	8	4SU	2	0
52	v	20	H2U	1	0
5	AN1	1911	3TD	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 117 ligands modelled in this entry, 116 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
55	FME	AN1	3001	-	8,9,10	0.99	0	8,9,11	0.90	0

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
55	FME	AN1	3001	-	-	3/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	AN1	3001	FME	O1-CN-N-CA
55	AN1	3001	FME	C-CA-CB-CG
55	AN1	3001	FME	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

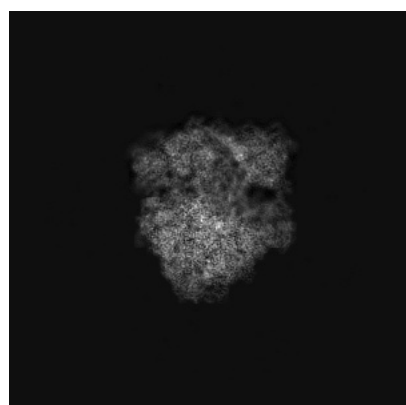
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21030. These allow visual inspection of the internal detail of the map and identification of artifacts.

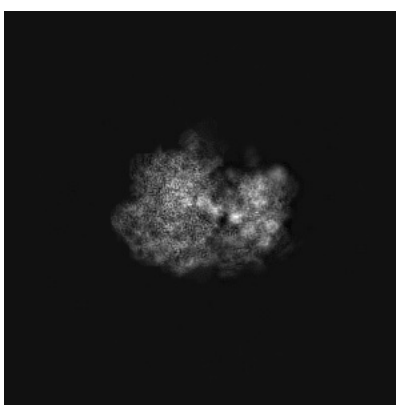
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

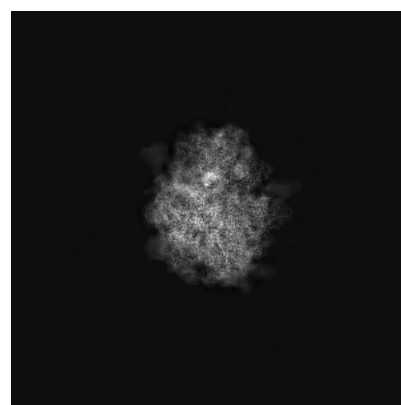
6.1.1 Primary map



X



Y

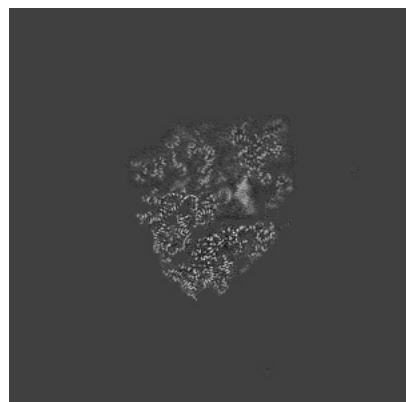


Z

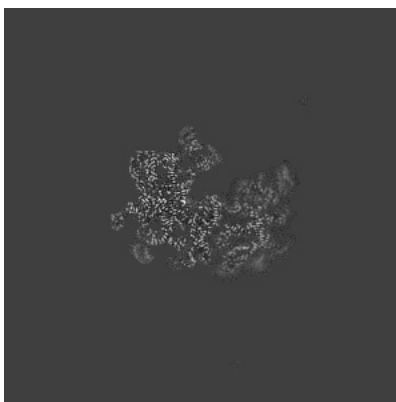
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

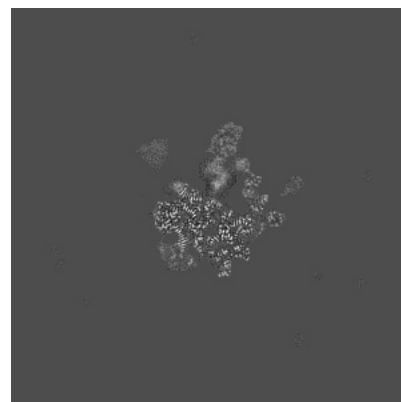
6.2.1 Primary map



X Index: 256



Y Index: 256

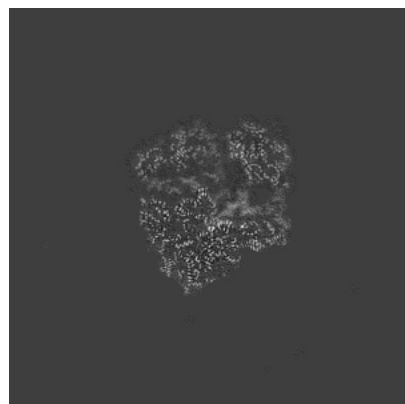


Z Index: 256

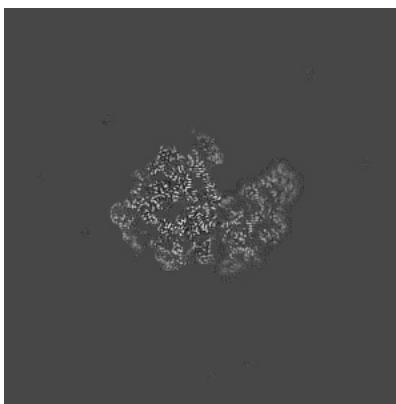
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

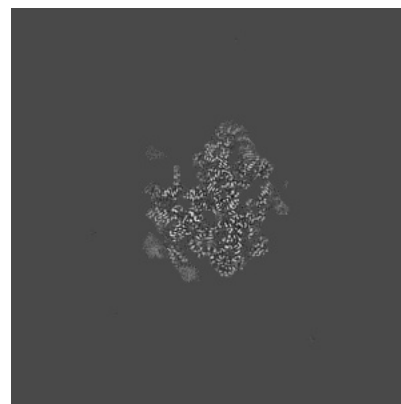
6.3.1 Primary map



X Index: 264



Y Index: 240

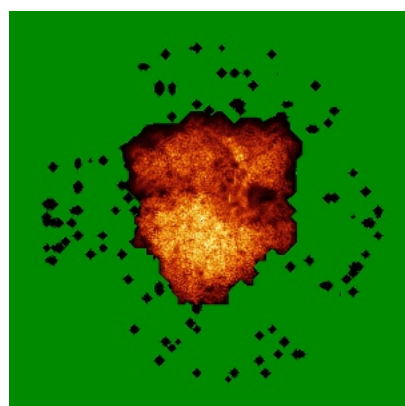


Z Index: 227

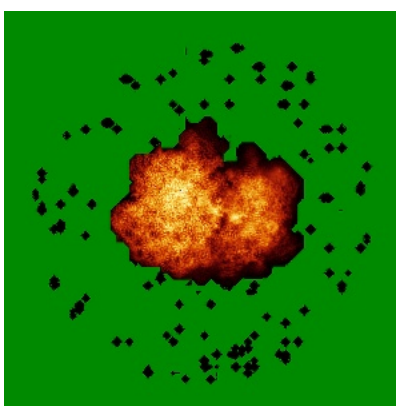
The images above show the largest variance slices of the map in three orthogonal directions.

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

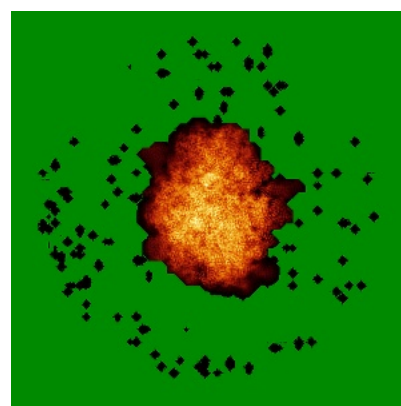
6.4.1 Primary map



X



Y

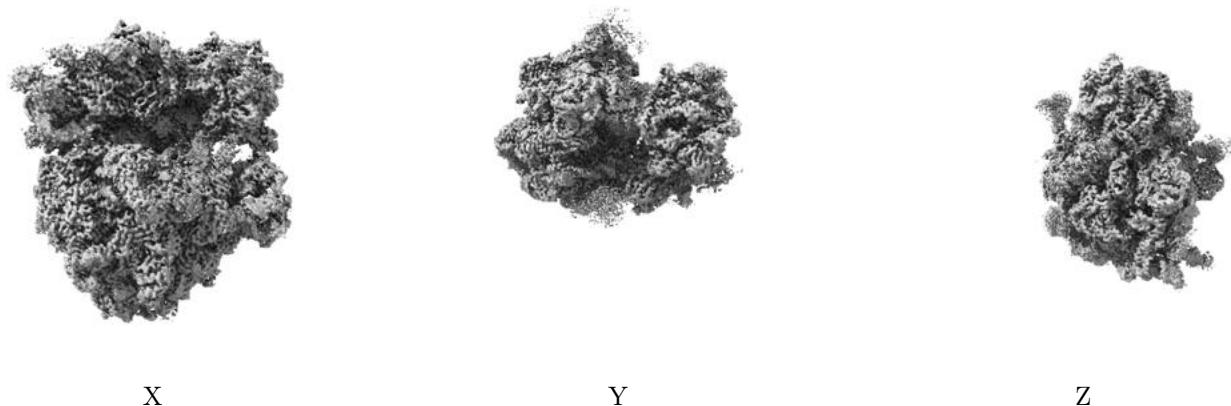


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

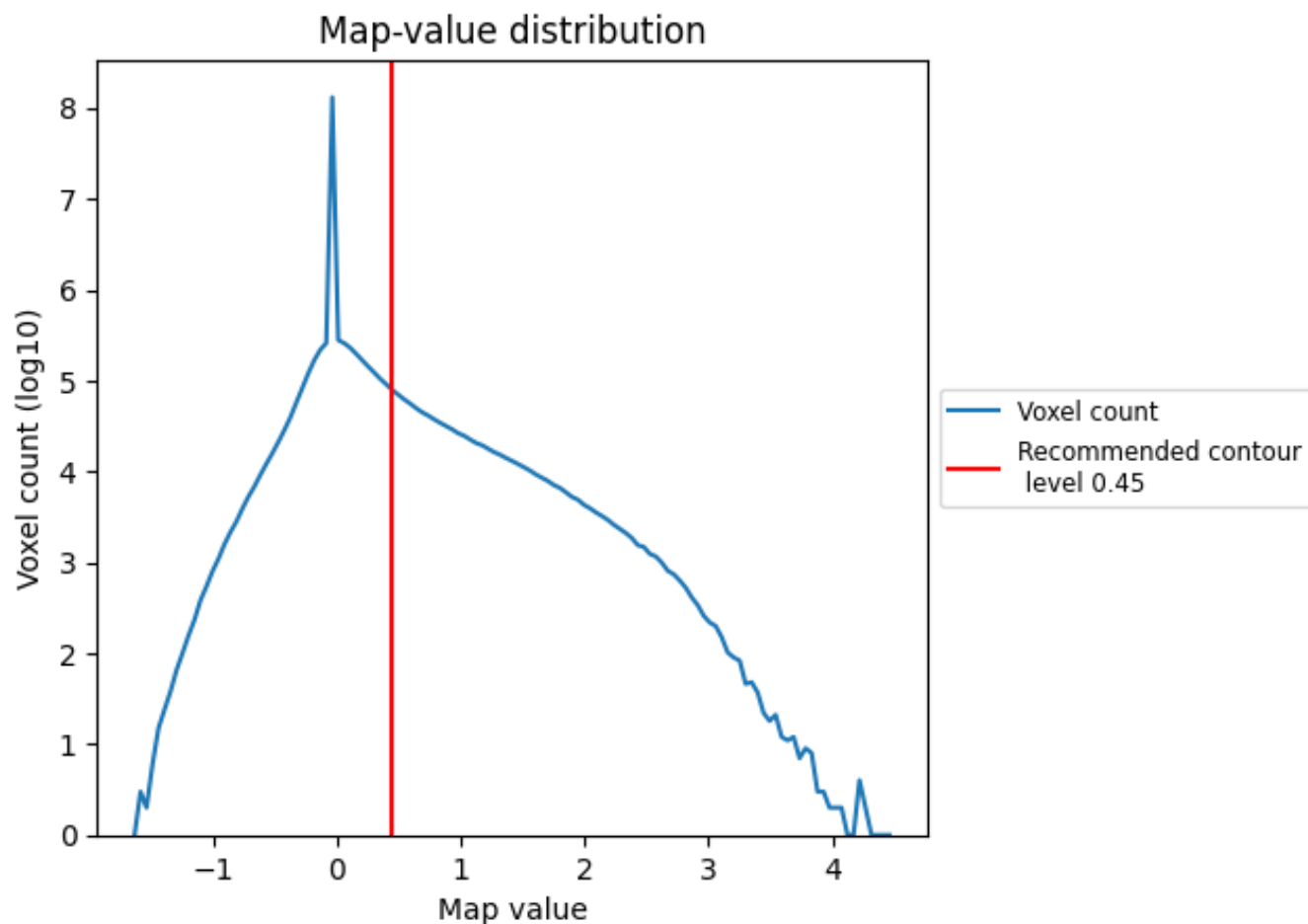
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

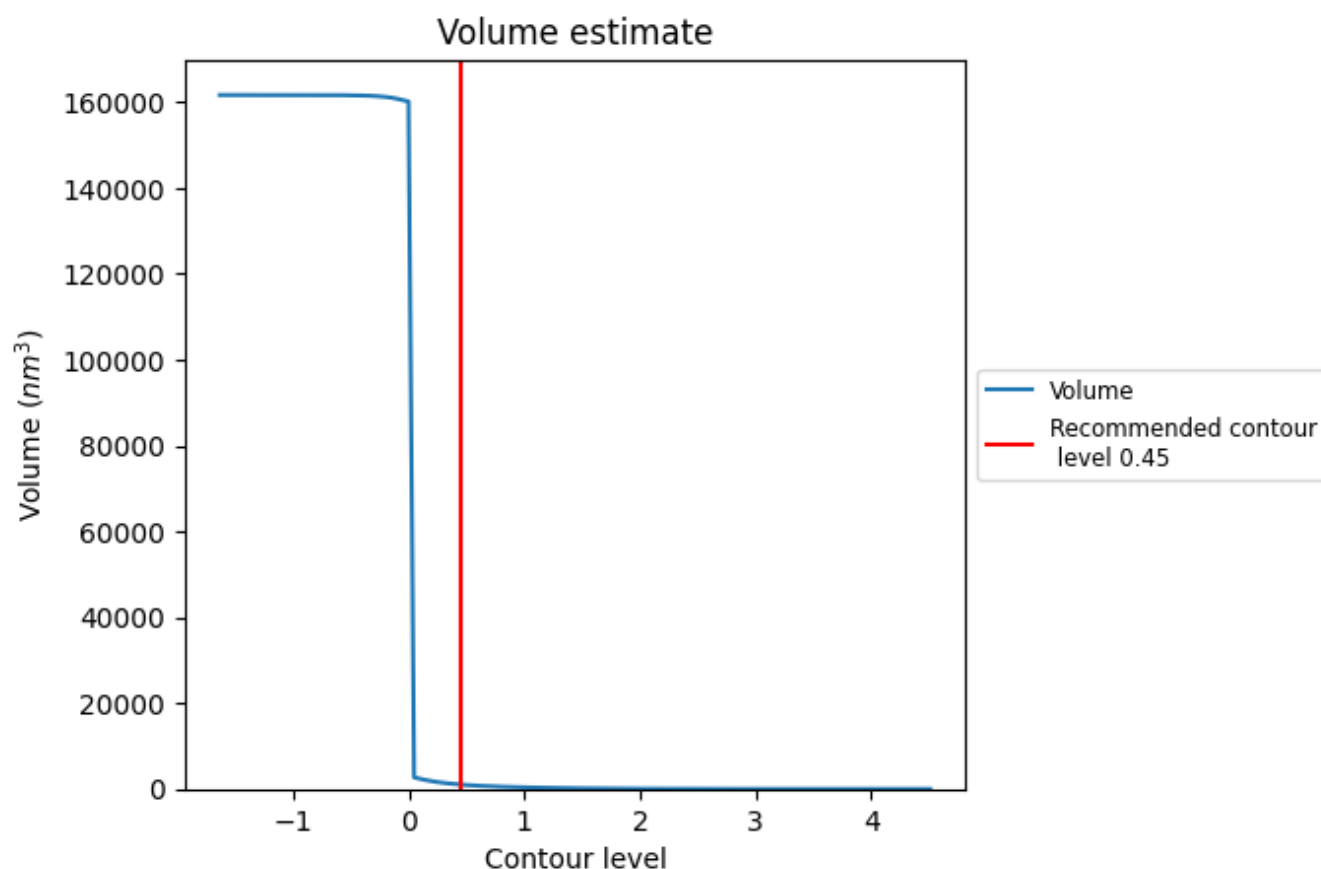
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

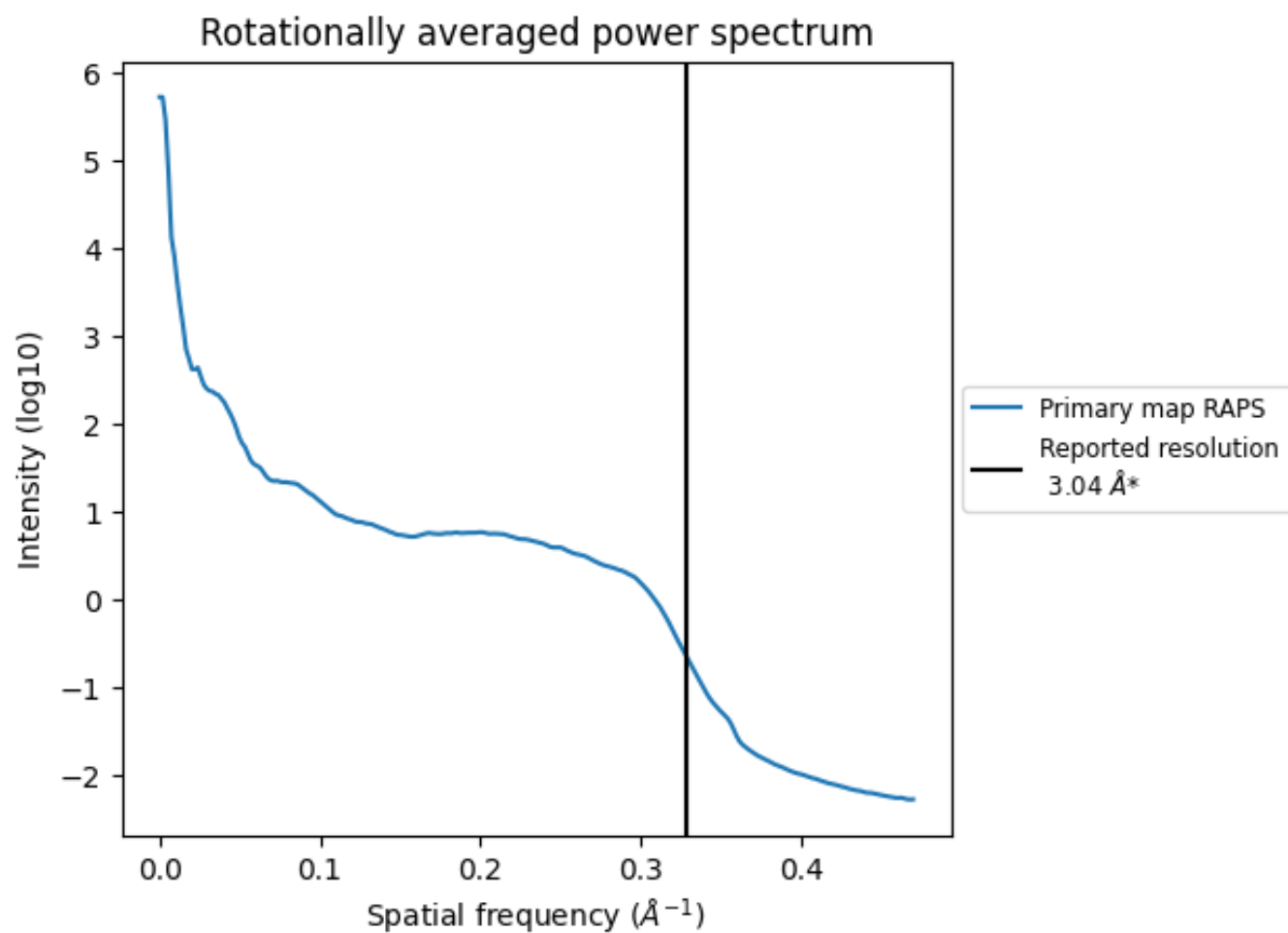
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1023 nm^3 ; this corresponds to an approximate mass of 924 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 0.329 Å⁻¹

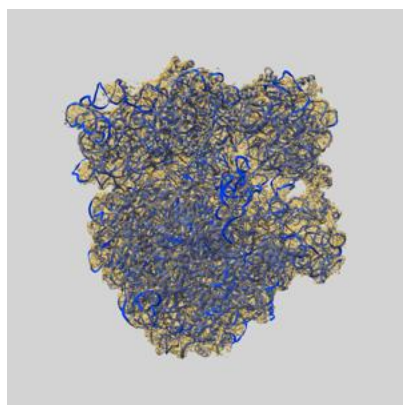
8 Fourier-Shell correlation

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

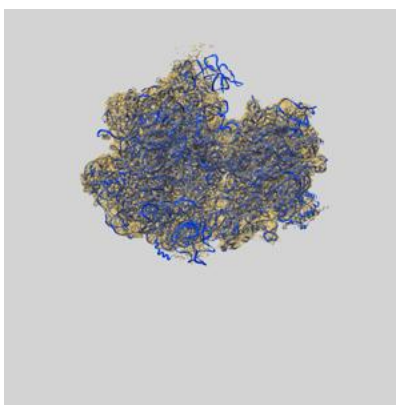
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21030 and PDB model 6V39. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

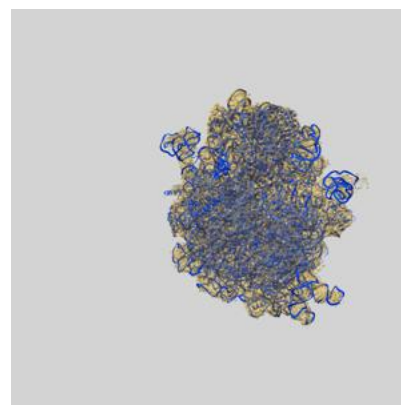
9.1 Map-model overlay [i](#)



X



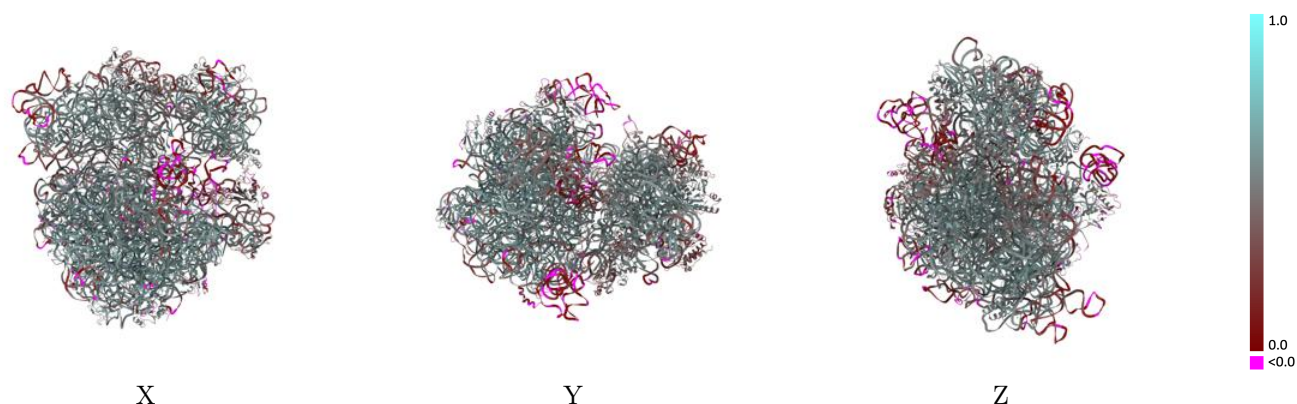
Y



Z

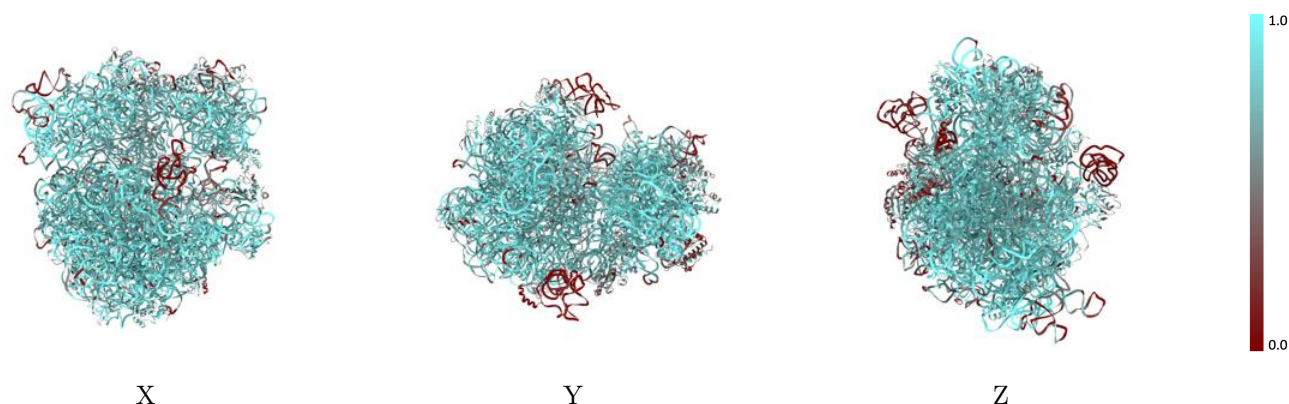
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



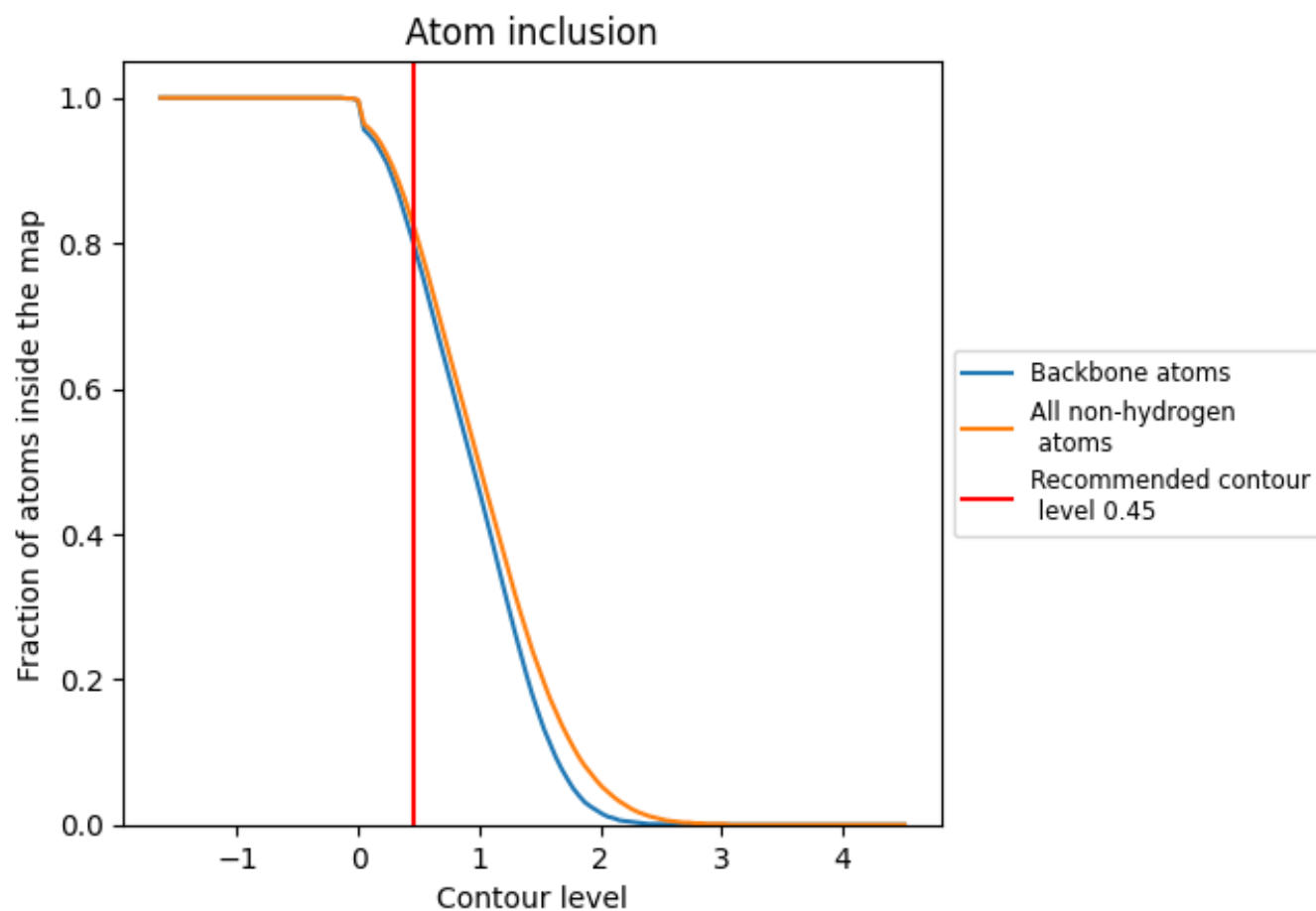
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 83% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8280	 0.4840
0	 0.7220	 0.4830
1	 0.9270	 0.6020
2	 0.8670	 0.5560
3	 0.8150	 0.4980
AN1	 0.8580	 0.4980
B	 0.8540	 0.4270
C	 0.8510	 0.5470
D	 0.8650	 0.5480
E	 0.8440	 0.5340
F	 0.5660	 0.2930
G	 0.6270	 0.3870
H	 0.3410	 0.2940
I	 0.8590	 0.5390
J	 0.8510	 0.5460
K	 0.7990	 0.5010
L	 0.8110	 0.5150
M	 0.9170	 0.5820
N	 0.8000	 0.4650
O	 0.8050	 0.5050
P	 0.9070	 0.5650
Q	 0.8160	 0.5080
R	 0.7970	 0.5200
S	 0.7700	 0.5020
T	 0.6830	 0.4360
U	 0.7680	 0.4900
V	 0.8990	 0.5670
W	 0.8190	 0.5330
X	 0.6720	 0.4230
Y	 0.8480	 0.5280
Z	 0.7860	 0.5100
b	 0.3210	 0.3450
c	 0.7760	 0.5010
d	 0.5800	 0.3910
e	 0.8180	 0.5110



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Chain	Atom inclusion	Q-score
f	 0.4910	 0.3610
g	 0.7150	 0.4250
h	 0.8440	 0.5420
i	 0.8550	 0.5390
j	 0.7190	 0.5010
k	 0.5970	 0.4050
l	 0.6000	 0.4670
m	 0.8120	 0.4960
n	 0.8160	 0.5410
o	 0.8300	 0.5100
p	 0.8530	 0.5470
q	 0.7890	 0.5240
r	 0.7120	 0.4740
s	 0.8560	 0.5250
sN1	 0.8740	 0.4730
t	 0.8590	 0.5210
u	 0.3200	 0.4040
v	 0.8250	 0.2140
w	 1.0000	 0.4340