



wwPDB EM Validation Summary Report ⓘ

Sep 17, 2026 – 04:24 AM EDT

PDB ID : 6V3B / pdb_00006v3b
EMDB ID : EMD-21032
Title : Cryo-EM structure of the Acinetobacter baumannii Ribosome: 70S in Empty state
Authors : Morgan, C.E.; Yu, E.W.
Deposited on : 2019-11-25
Resolution : 2.91 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.dev133
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) : 2.50

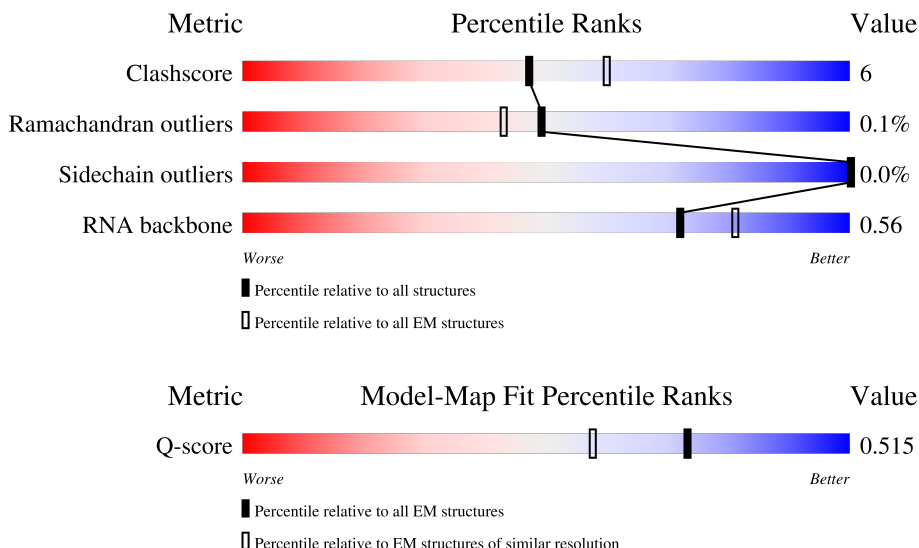
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.91 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	12972 (2.41 - 3.41)

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	8% 92% 8%
2	1	44	86% 14%
3	2	64	77% 17% ...

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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	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 140290 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 ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	3	1	Total	Zn	0
			1	1	

- Molecule 53 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
53	AN1	52	Total	Mg	0
			52	52	
53	sN1	41	Total	Mg	0
			41	41	

- Molecule 54 is SODIUM ION (CCD ID: NA) (formula: Na).

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

- Molecule 55 is water.

Mol	Chain	Residues	Atoms		AltConf
55	3	1	Total	O	0
			1	1	
55	AN1	253	Total	O	0
			253	253	

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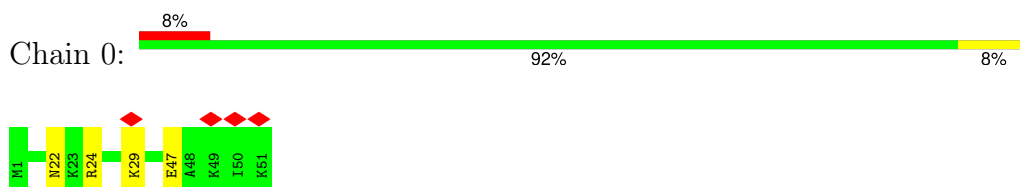
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Mol	Chain	Residues	Atoms		AltConf
55	B	5	Total 5	O 5	0
55	C	3	Total 3	O 3	0
55	D	3	Total 3	O 3	0
55	E	2	Total 2	O 2	0
55	K	3	Total 3	O 3	0
55	M	1	Total 1	O 1	0
55	P	1	Total 1	O 1	0
55	Q	3	Total 3	O 3	0
55	R	1	Total 1	O 1	0
55	V	2	Total 2	O 2	0
55	Y	1	Total 1	O 1	0
55	Z	1	Total 1	O 1	0
55	sN1	107	Total 107	O 107	0
55	g	1	Total 1	O 1	0
55	h	1	Total 1	O 1	0
55	i	2	Total 2	O 2	0
55	m	2	Total 2	O 2	0
55	n	1	Total 1	O 1	0
55	s	3	Total 3	O 3	0
55	t	1	Total 1	O 1	0

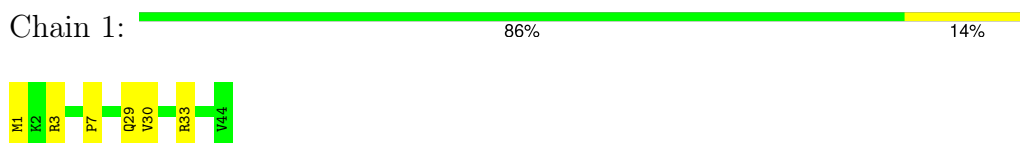
3 Residue-property plots [i](#)

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.

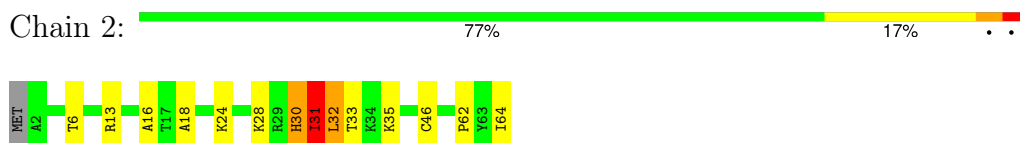
- Molecule 1: 50S ribosomal protein L33



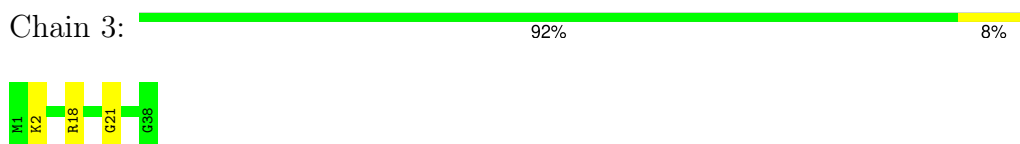
- Molecule 2: 50S ribosomal protein L34



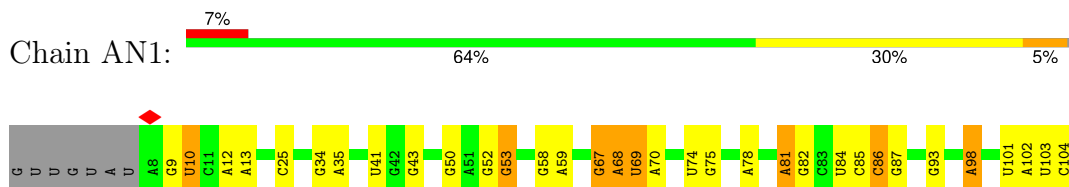
- Molecule 3: 50S ribosomal protein L35



- Molecule 4: 50S ribosomal protein L36



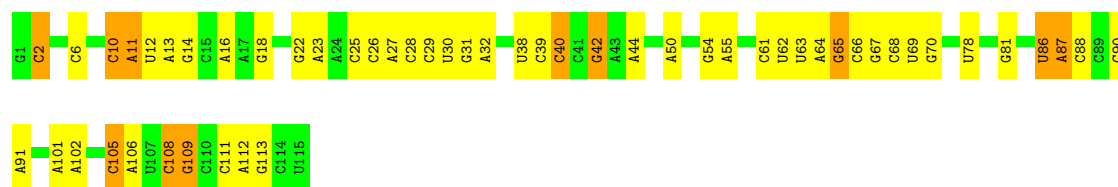
- Molecule 5: 23s ribosomal RNA





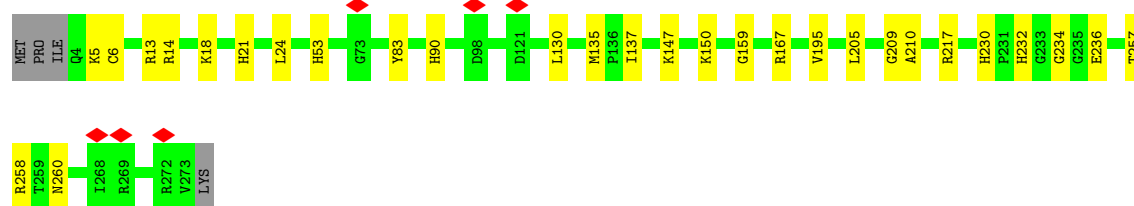
U	C2815	U2685	G2577	U2473	C2346	G2230	C2147	A2078	U1959	C1870	C1767	C1623
U	G2816	A2686	C2587	C2479	C2355	G2234	C2148	G2089	G1960	G1871	A1768	A1624
G	G2817	U2694	G2588	C2479	A2356	G2235	A2149	A2090	C1961	A1872	A1769	A1630
	G2818	C2695	G2591	C2482	A2357	U2239	G2150	C2091	C1963	C1875	U1775	G1634
	G2830	A2696	U2487	U2488	A2373	U2240	U2151	C2092	A1966	U1876	A1776	A1635
	A2831	C2697	U2489	U2489	G2374	U2241	G2152	U2093	U1967	U1877		
	G2842	C2698	U2490	U2490	G2375	U2242	G2153	U2094	G1968	U1878		
	U2843	A2699	U2491	U2491	G2376	A2243	G2154	G2096	U1978	A1780		
	G2844	C2495	G2377	C2495	A2377	C2244	G2155	A2097	U1792	U1792		
	G2845	C2496	G2378	C2496	A2378	U2247	G2156	C2098	C1793	U1645		
		U2800	G2379	C2497	U2380	G2247	C2157	C2098	U1987	U1646		
	G2848	U2501	U2381	U2498	U2381	C2254	C2158	C2099	G1988	G1647		
	G2728	U2500	U2382	U2499	U2382	C2254	C2159	U2100	U1989			
	G2729	U2501	U2383	U2500	U2383	U2261	U2160	U2101	G1992	A1662		
	A2730	U2502	C2389	G2501	C2389	A2262	G2161	A2102	C1993	A1797		
	G2731	U2503	U2400	U2502	U2400	A2263	C2162	G2103	U1994	A1798		
	U2734	U2504	G2401	U2503	G2401	U2273	U2163	C2104	G1995	A1799		
	U2735	U2505	U2402	U2504	U2402	G2274	U2164	U2105	U1996			
	A2736	U2506	A2407	U2505	A2407	G2275	G2165	G2106	C2019			
	A2737	U2507	A2408	U2506	A2408	G2276	A2166	U2107	G2020			
		U2508		U2507		U2279	A2167	G2108	C2021			
	G2740	U2509	C2416	U2508	C2416	A2283	A2168	U2109	U2022			
	G2741	U2510	G2417	U2509	G2417	U2287	U2169	A2110	A1909			
	U2742	U2511	G2418	U2510	G2418	U2288	U2170	G2111	C1910			
	A2743	U2512	C2423	U2511	C2423	U2289	U2171	G2112	A2025			
	A2744	U2513	G2424	U2512	G2424	U2290	C2172	A2113	A2026			
	G2747	U2514	G2425	U2513	G2425	U2291	C2173	U2114	A2027			
	A2753	U2515	A2426	U2514	A2426	G2296	U2174	A2115	G2028			
	A2754	U2516	A2427	U2515	A2427	C2297	U2175	A2116	A2029			
	A2755	U2517	A2428	U2516	A2428	C2298	U2176	G2117	U2030			
	G2761	U2518	A2429	U2517	A2429	U2301	U2177	U2118	C2039			
	G2762	U2519	A2430	U2518	A2430	U2302	U2178	G2119	A2048			
	A2774	U2520	A2431	U2519	A2431	A2303	U2179	U2120	G2049			
	U2775	U2521	U2437	U2520	U2437	A2304	U2180	G2121	A2050			
	A2776	U2522	U2438	U2521	U2438	A2305	U2181	A2122	C2051			
	C2784	U2523	G2441	U2522	G2441	A2306	U2182	G2123	G2052			
	C2785	U2524	G2442	U2523	G2442	A2307	U2183	U2124	A2053			
	U2786	U2525	G2443	U2524	G2443	A2308	U2184	C2125	A2054			
	A2787	U2526	G2444	U2525	G2444	A2309	U2185	U2126	C2055			
	G2788	U2527	G2445	U2526	G2445	A2310	U2186	U2127	G2056			
	C2791	U2528	U2446	U2527	U2446	G2312	U2187	U2128	A2057			
	U2792	U2529	U2447	U2528	U2447	G2313	U2188	G2129	G2058			
	U2793	U2530	U2448	U2529	U2448	G2314	U2189	U2130	C2059			
	U2794	U2531	U2449	U2530	U2449	G2315	U2190	A2131	A1932			
	A2795	U2532	U2450	U2531	U2450	G2316	U2191	A1933	A1934			
	C2800	U2533	U2451	U2532	U2451	G2317	U2192	U1935	U1936			
	A2804	U2534	U2452	U2533	U2452	A2321	U2193	G2132	G1937			
	A2805	U2535	U2453	U2534	U2453	U2322	U2194	U2070	C1938			
		U2536	U2454	U2535	U2454	A2323	U2195	C2069	U1939			
		U2537	U2455	U2536	U2455	A2324	U2196	U2071	U1942			
		U2538	U2456	U2537	U2456	A2325	U2197	U2072	C1943			
		U2539	U2457	U2538	U2457	G2326	U2198	G1950	U1951			
		U2540	U2458	U2539	U2458	A2341	U2199	G1865				
		U2541	U2459	U2540	U2459		U2200	U1866				
		U2542	U2460	U2541	U2460		G2204	A1867				
		U2543	U2461	U2542	U2461		G2212	G1868				
		U2544	U2462	U2543	U2462		G2213	G1869				
		U2545	U2463	U2544	U2463		A2221					
		U2546	U2464	U2545	U2464		G2224					
		U2547	U2465	U2546	U2465		U2225					
		U2548	U2466	U2547	U2466		G2226					
		U2549	U2467	U2548	U2467		U2229					
		U2550	U2468	U2549	U2468							
		U2551	U2469	U2550	U2469							
		U2552	U2470	U2551	U2470							
		U2553	U2471	U2552	U2471							
		U2554	U2472	U2553	U2472							
		U2555	U2473	U2554	U2473							
		U2556	U2474	U2555	U2474							
		U2557	U2475	U2556	U2475							
		U2558	U2476	U2557	U2476							
		U2559	U2477	U2558	U2477							
		U2560	U2478	U2559	U2478							
		U2561	U2479	U2560	U2479							
		U2562	U2480	U2561	U2480							
		U2563	U2481	U2562	U2481							
		U2564	U2482	U2563	U2482							
		U2565	U2483	U2564	U2483							
		U2566	U2484	U2565	U2484							
		U2567	U2485	U2566	U2485							
		U2568	U2486	U2567	U2486							
		U2569	U2487	U2568	U2487							
		U2570	U2488	U2569	U2488							
		U2571	U2489	U2570	U2489							
		U2572	U2490	U2571	U2490							
		U2573	U2491	U2572	U2491							
		U2574	U2492	U2573	U2492							
		U2575	U2493	U2574	U2493							
		U2576	U2494	U2575	U2494							
		U2577	U2495	U2576	U2495							
		U2578	U2496	U2577	U2496							
		U2579	U2497	U2578	U2497							
		U2580	U2498	U2579	U2498							
		U2581	U2499	U2580	U2499							
		U2582	U2500	U2581	U2500							
		U2583	U2501	U2582	U2501							
		U2584	U2502	U2583	U2502							
		U2585	U2503	U2584	U2503							
		U2586	U2504	U2585	U2504							
		U2587	U2505	U2586	U2505							
		U2588	U2506	U2587	U2506							
		U2589	U2507	U2588	U2507							
		U2590	U2508	U2589	U2508							
		U2591	U2509	U2590	U2509							
		U2592	U2510	U2591	U2510							
		U2593	U2511	U2592	U2511							
		U2594	U2512	U2593	U2512							
		U2595	U2513	U2594	U2513							
		U2596	U2514	U2595	U2514							
		U2597	U2515	U2596	U2515							
		U2598	U2516	U2597	U2516							
		U2599	U2517	U2598	U2517							
		U2600	U2518	U2599	U2518							
		U2601	U2519	U2600	U2519							
		U2602	U2520	U2601	U2520							
		U2603	U2521	U2602	U2521							
		U2604	U2522	U2603	U2522							
		U2605	U2523	U2604	U2523							
		U2606	U2524	U2605	U2524							
		U2607	U2525	U2606	U2525							
		U2608	U2526	U2607	U2526							
		U2609	U2527	U2608	U2527							
		U2610	U2528	U2609	U2528							
		U2611	U2529	U2610	U2529							
		U2612	U2530	U2611	U2530							
		U2613	U2531	U2612	U2531							
		U2614	U2532	U2613	U2532							
		U2615	U2533	U2614	U2533							
		U2616	U2534	U2615	U2534							
		U2617	U2535	U2616	U2535							
		U2618	U2536	U2617	U2536							

Chain B: 



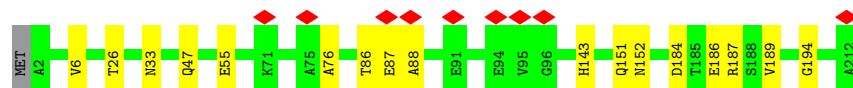
- Molecule 7: 50S ribosomal protein L2

Chain C: 



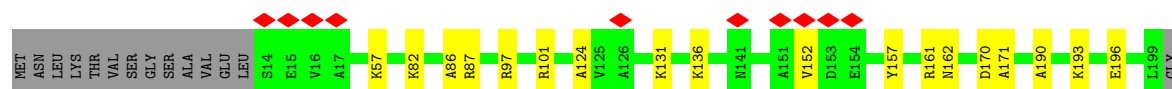
- Molecule 8: 50S ribosomal protein L3

Chain D: 



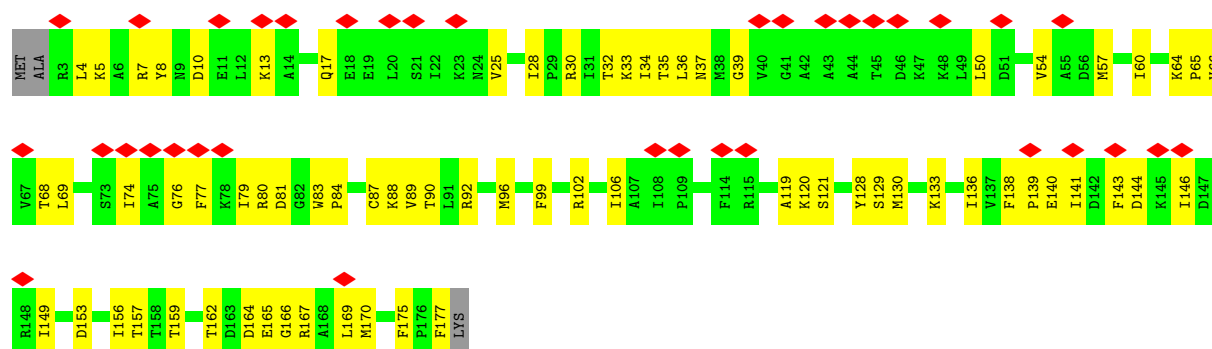
- Molecule 9: 50S ribosomal protein L4

Chain E: 

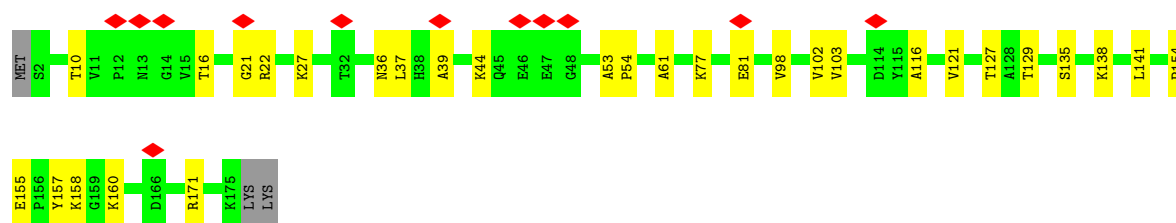
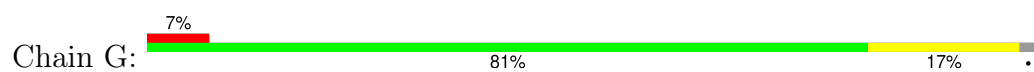


- Molecule 10: 50S ribosomal protein L5

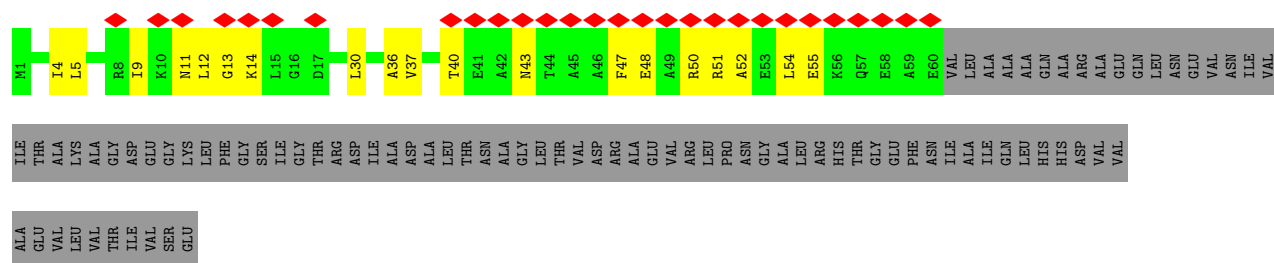
Chain F: 



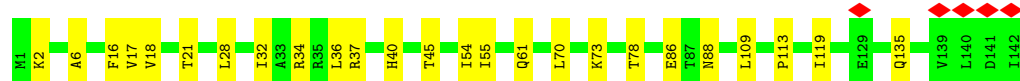
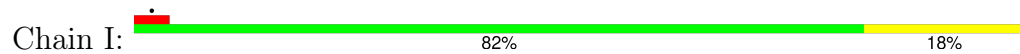
- Molecule 11: 50S ribosomal protein L6



- Molecule 12: 50S ribosomal protein L9



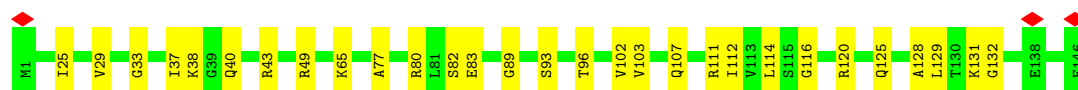
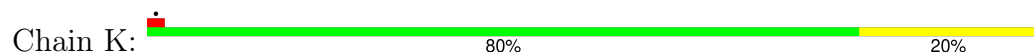
- Molecule 13: 50S ribosomal protein L13



- Molecule 14: 50S ribosomal protein L14



- Molecule 15: 50S ribosomal protein L15



- Molecule 16: 50S ribosomal protein L16





- Molecule 17: 50S ribosomal protein L17

Chain M: 90% 5% 5%



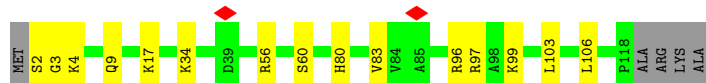
- Molecule 18: 50S ribosomal protein L18

Chain N: 7% 84% 14% .



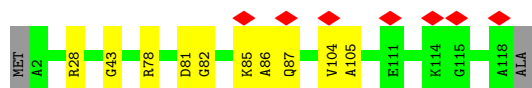
- Molecule 19: 50S ribosomal protein L19

Chain O: 84% 12% .



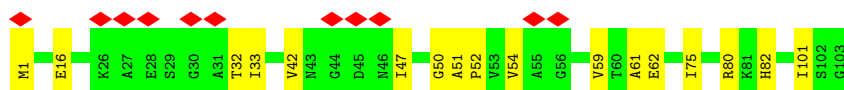
- Molecule 20: 50S ribosomal protein L20

Chain P: 6% 90% 8% .



- Molecule 21: 50S ribosomal protein L21

Chain Q: 11% 83% 17%

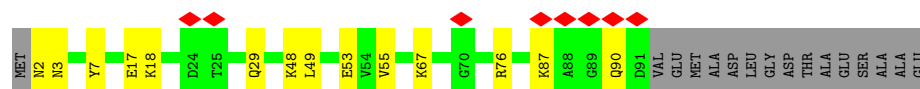


- Molecule 22: 50S ribosomal protein L22

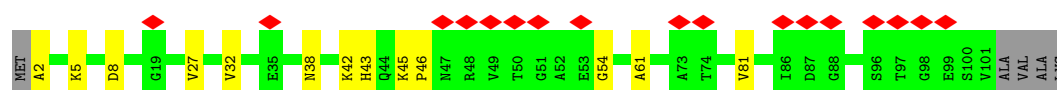
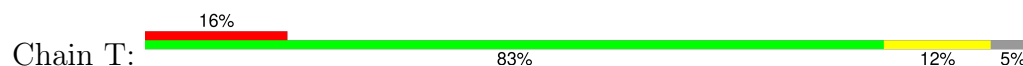
Chain R: 93% 7%



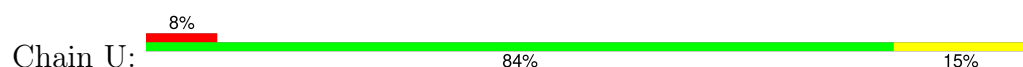
- Molecule 23: 50S ribosomal protein L23



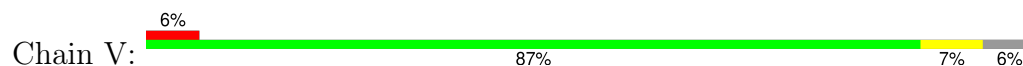
- Molecule 24: 50S ribosomal protein L24



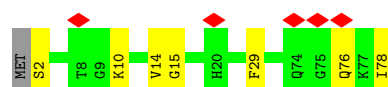
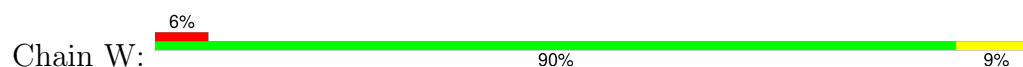
- Molecule 25: 50S ribosomal protein L25



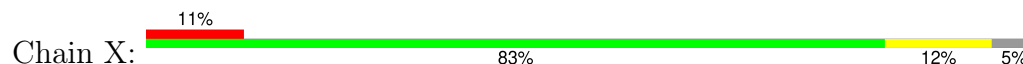
- Molecule 26: 50S ribosomal protein L27



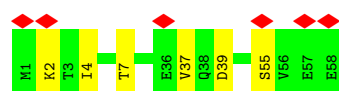
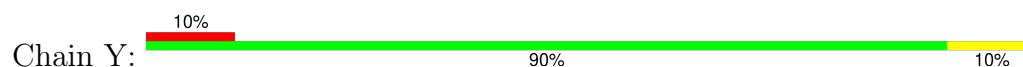
- Molecule 27: 50S ribosomal protein L28

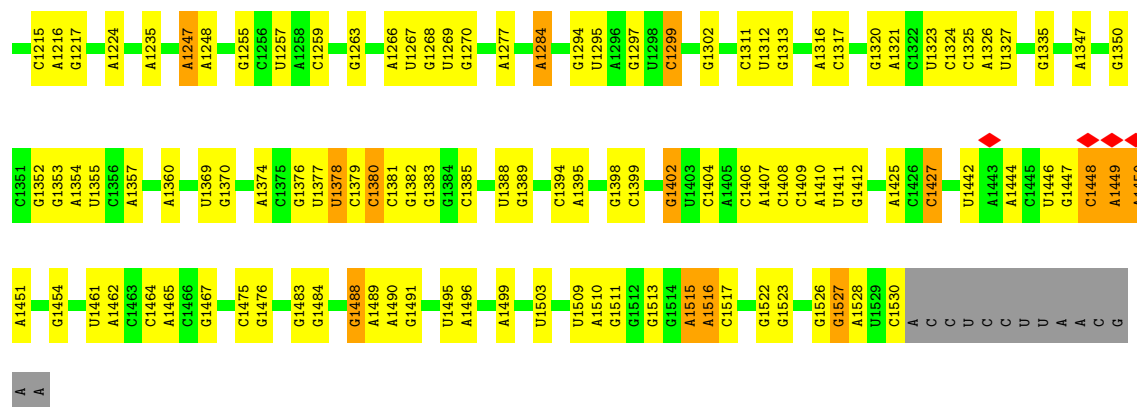


- Molecule 28: 50S ribosomal protein L29

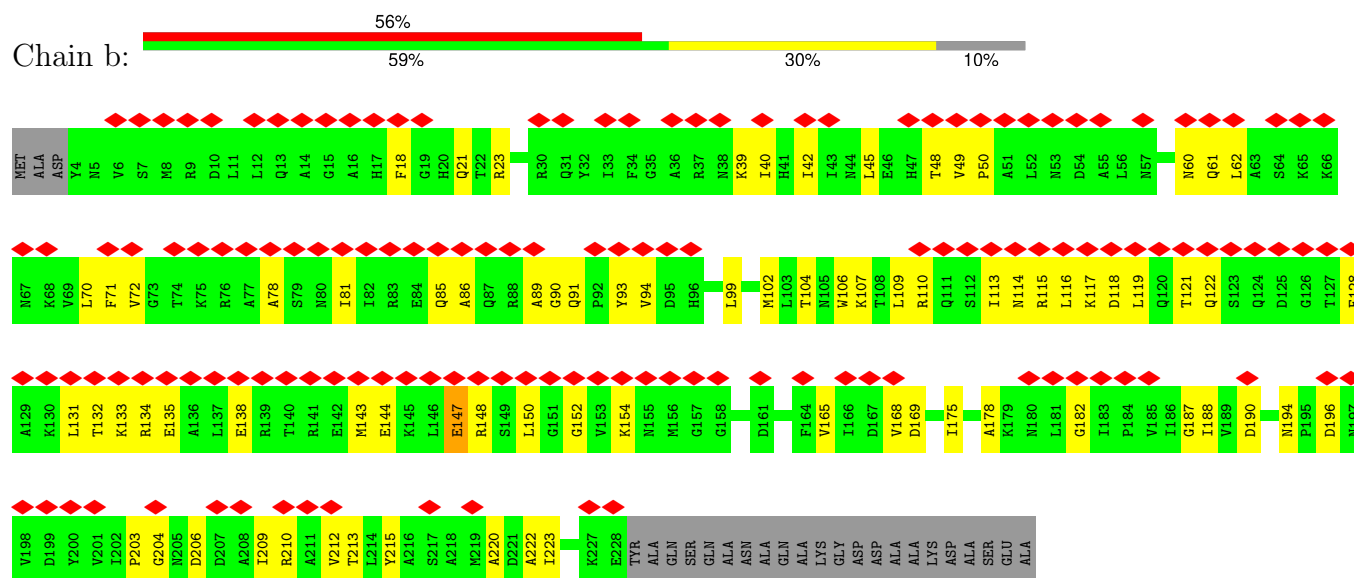


- Molecule 29: 50S ribosomal protein L30

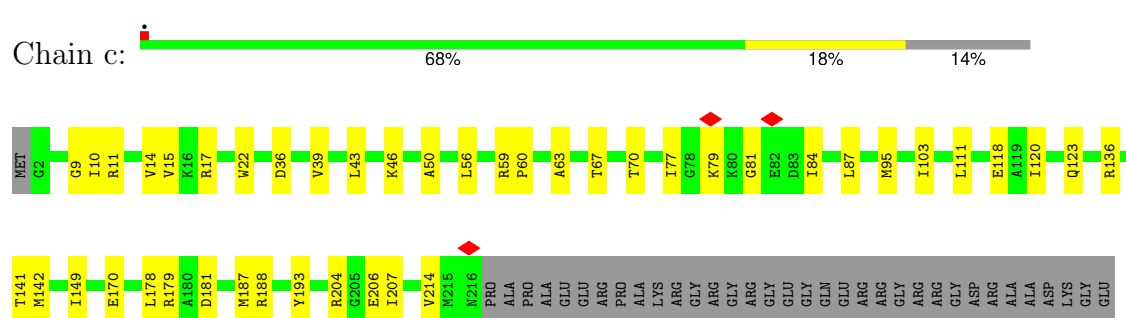




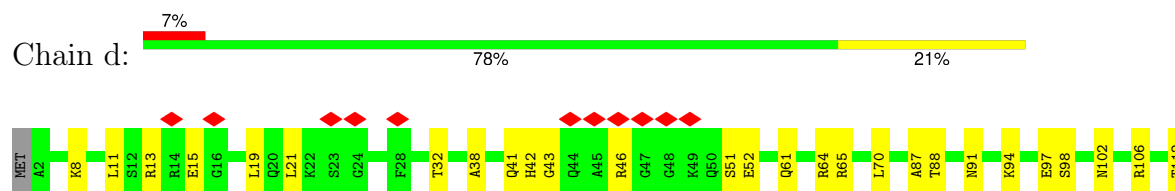
• Molecule 32: 30S ribosomal protein S2



• Molecule 33: 30S ribosomal protein S3



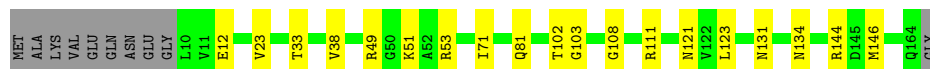
• Molecule 34: 30S ribosomal protein S4





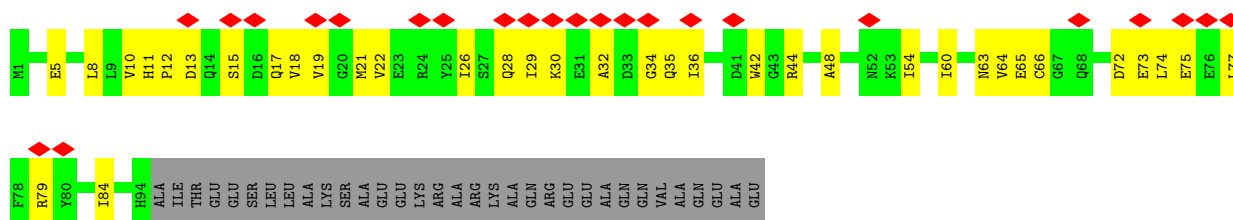
- Molecule 35: 30S ribosomal protein S5

Chain e: 82% 12% 6%



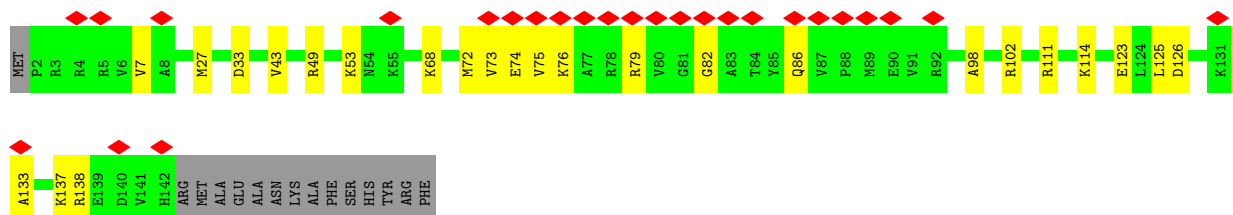
- Molecule 36: 30S ribosomal protein S6

Chain f: 19% 46% 28% 26%



- Molecule 37: 30S ribosomal protein S7

Chain g: 17% 74% 17% 10%



- Molecule 38: 30S ribosomal protein S8

Chain h: 84% 15%

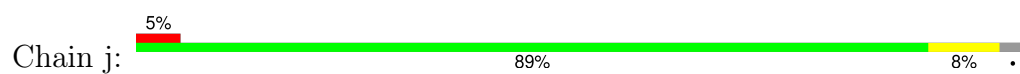


- Molecule 39: 30S ribosomal protein S9

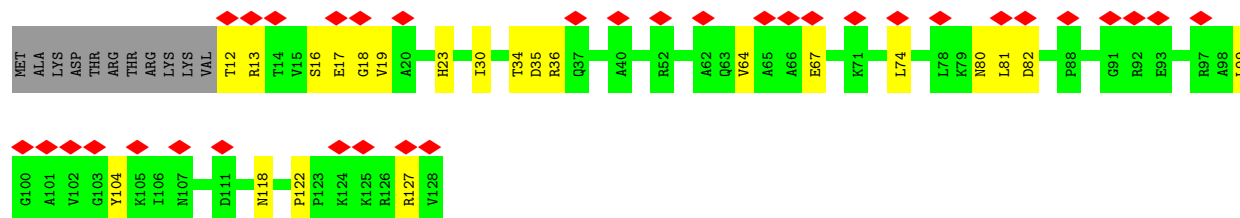
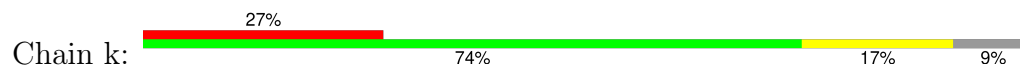
Chain i: 90% 9%



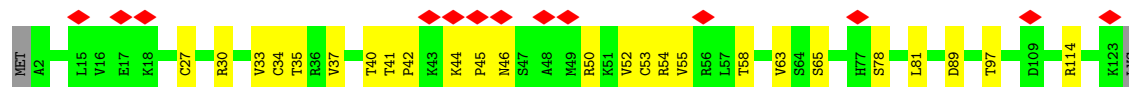
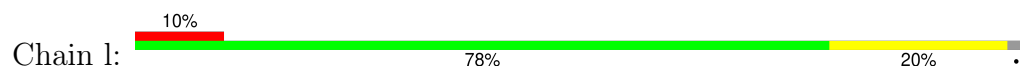
- Molecule 40: 30S ribosomal protein S10



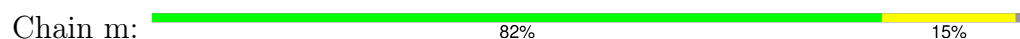
- Molecule 41: 30S ribosomal protein S11



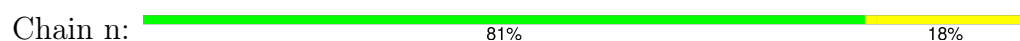
- Molecule 42: 30S ribosomal protein S12



- Molecule 43: 30S ribosomal protein S13



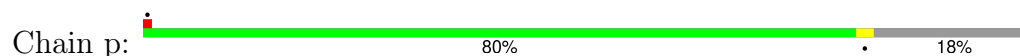
- Molecule 44: 30S ribosomal protein S14

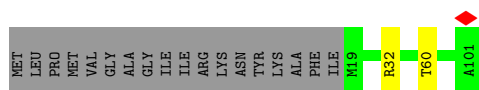


- Molecule 45: 30S ribosomal protein S15

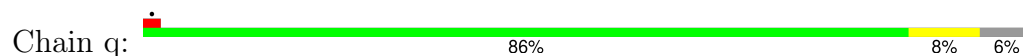


- Molecule 46: 30S ribosomal protein S16





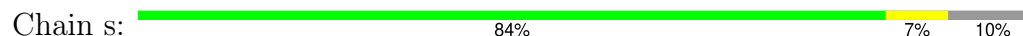
- Molecule 47: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S18



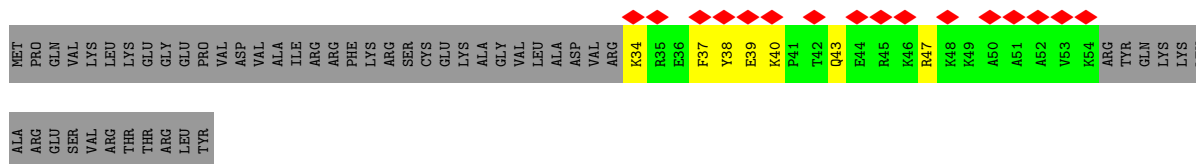
- Molecule 49: 30S ribosomal protein S19



- Molecule 50: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	66318	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	5.794	Depositor
Minimum map value	-2.515	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.106	Depositor
Recommended contour level	0.4	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, PSU, 3TD, MG, OMG, 6MZ, 4OC, UR3, 5MC, MA6, 7MG, OMU, ZN, 2MG, NA, 5MU

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	0.14	0/434	0.36	0/573
2	1	0.13	0/367	0.36	0/481
3	2	0.17	0/515	0.51	0/678
4	3	0.15	0/296	0.46	0/389
5	AN1	0.10	0/69101	0.24	0/107780
6	B	0.09	0/2739	0.22	0/4266
7	C	0.13	0/2136	0.36	0/2869
8	D	0.13	0/1590	0.33	0/2142
9	E	0.12	0/1440	0.31	0/1944
10	F	0.19	0/1401	0.53	0/1877
11	G	0.15	0/1337	0.41	2/1807 (0.1%)
12	H	0.18	0/461	0.57	0/616
13	I	0.13	0/1151	0.32	0/1551
14	J	0.13	0/956	0.36	0/1286
15	K	0.13	0/1097	0.40	0/1461
16	L	0.13	0/1104	0.32	0/1475
17	M	0.14	0/956	0.37	0/1282
18	N	0.13	0/865	0.37	0/1156
19	O	0.13	0/931	0.34	0/1249
20	P	0.14	0/947	0.33	0/1262
21	Q	0.15	0/818	0.37	0/1094
22	R	0.11	0/831	0.31	0/1113
23	S	0.13	0/708	0.31	0/947
24	T	0.15	0/753	0.47	0/1010
25	U	0.13	0/770	0.35	0/1036
26	V	0.13	0/606	0.34	0/810
27	W	0.12	0/642	0.33	0/856
28	X	0.12	0/499	0.30	0/662
29	Y	0.13	0/468	0.35	0/624
30	Z	0.13	0/462	0.36	0/615
31	sN1	0.09	0/36476	0.21	0/56895
32	b	0.19	0/1799	0.50	0/2429

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.13	0/1714	0.35	0/2304
34	d	0.12	0/1653	0.35	0/2213
35	e	0.12	0/1141	0.32	0/1537
36	f	0.16	0/808	0.49	0/1089
37	g	0.14	0/1127	0.36	0/1511
38	h	0.12	0/993	0.30	0/1331
39	i	0.13	0/1006	0.36	0/1346
40	j	0.14	0/811	0.37	0/1096
41	k	0.15	0/878	0.42	0/1189
42	l	0.16	0/958	0.46	0/1284
43	m	0.16	0/913	0.41	0/1226
44	n	0.12	0/803	0.32	0/1071
45	o	0.10	0/715	0.27	0/958
46	p	0.11	0/660	0.31	0/886
47	q	0.13	0/637	0.34	0/858
48	r	0.15	0/445	0.38	0/601
49	s	0.12	0/664	0.33	0/897
50	t	0.14	0/664	0.30	0/885
51	u	0.27	0/184	0.68	0/240
All	All	0.11	0/151430	0.27	2/226757 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	2	0	1
12	H	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	G	10	THR	CA-C-N	-5.11	118.91	122.59
11	G	10	THR	C-N-CA	-5.11	118.91	122.59

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	2	30	HIS	Peptide
12	H	47	PHE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	427	0	462	2	0
2	1	363	0	401	5	0
3	2	509	0	566	12	0
4	3	295	0	326	2	0
5	AN1	62023	0	31194	500	0
6	B	2450	0	1241	44	0
7	C	2096	0	2157	20	0
8	D	1572	0	1610	13	0
9	E	1419	0	1464	16	0
10	F	1381	0	1433	56	0
11	G	1318	0	1373	20	0
12	H	458	0	480	13	0
13	I	1125	0	1148	16	0
14	J	946	0	1007	6	0
15	K	1089	0	1159	18	0
16	L	1087	0	1162	7	0
17	M	942	0	987	4	0
18	N	857	0	899	10	0
19	O	919	0	973	9	0
20	P	934	0	997	8	0
21	Q	807	0	842	16	0
22	R	826	0	894	6	0
23	S	702	0	756	11	0
24	T	749	0	797	9	0
25	U	760	0	783	11	0
26	V	598	0	600	4	0
27	W	632	0	667	6	0
28	X	498	0	537	6	0
29	Y	463	0	488	3	0
30	Z	456	0	448	6	0
31	sN1	32782	0	16507	310	0
32	b	1769	0	1787	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	c	1690	0	1774	28	0
34	d	1631	0	1691	30	0
35	e	1129	0	1174	11	0
36	f	793	0	788	24	0
37	g	1111	0	1163	15	0
38	h	985	0	1047	12	0
39	i	995	0	1053	7	0
40	j	801	0	832	5	0
41	k	862	0	877	15	0
42	l	945	0	996	16	0
43	m	903	0	962	15	0
44	n	792	0	833	15	0
45	o	705	0	712	2	0
46	p	649	0	660	1	0
47	q	630	0	678	5	0
48	r	438	0	456	11	0
49	s	646	0	663	3	0
50	t	658	0	710	2	0
51	u	182	0	198	7	0
52	3	1	0	0	0	0
53	AN1	52	0	0	0	0
53	sN1	41	0	0	0	0
54	AN1	1	0	0	0	0
55	3	1	0	0	0	0
55	AN1	253	0	0	2	0
55	B	5	0	0	1	0
55	C	3	0	0	0	0
55	D	3	0	0	0	0
55	E	2	0	0	0	0
55	K	3	0	0	0	0
55	M	1	0	0	0	0
55	P	1	0	0	1	0
55	Q	3	0	0	0	0
55	R	1	0	0	0	0
55	V	2	0	0	0	0
55	Y	1	0	0	0	0
55	Z	1	0	0	0	0
55	g	1	0	0	0	0
55	h	1	0	0	0	0
55	i	2	0	0	0	0
55	m	2	0	0	0	0
55	n	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	s	3	0	0	0	0
55	sN1	107	0	0	1	0
55	t	1	0	0	0	0
All	All	140290	0	93412	1323	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 1323 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	1.43	1.16
31:sN1:1157:G:N7	31:sN1:1179:G:N2	2.18	0.91
5:AN1:2096:G:H1	5:AN1:2185:U:H3	0.91	0.90
6:B:70:G:H21	6:B:101:A:H62	1.11	0.89
6:B:2:C:O2	6:B:113:G:N2	2.08	0.86

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	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%)	58 (95%)	1 (2%)	2 (3%)	3	11
4	3	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
7	C	268/274 (98%)	260 (97%)	8 (3%)	0	100	100
8	D	209/212 (99%)	203 (97%)	6 (3%)	0	100	100
9	E	184/200 (92%)	184 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	F	173/178 (97%)	151 (87%)	21 (12%)	1 (1%)	21	50
11	G	172/177 (97%)	166 (96%)	6 (4%)	0	100	100
12	H	58/148 (39%)	55 (95%)	3 (5%)	0	100	100
13	I	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
14	J	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
15	K	144/146 (99%)	140 (97%)	4 (3%)	0	100	100
16	L	135/137 (98%)	134 (99%)	1 (1%)	0	100	100
17	M	117/125 (94%)	116 (99%)	1 (1%)	0	100	100
18	N	112/116 (97%)	111 (99%)	1 (1%)	0	100	100
19	O	115/122 (94%)	111 (96%)	4 (4%)	0	100	100
20	P	115/119 (97%)	115 (100%)	0	0	100	100
21	Q	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
22	R	107/109 (98%)	107 (100%)	0	0	100	100
23	S	88/106 (83%)	85 (97%)	3 (3%)	0	100	100
24	T	98/105 (93%)	96 (98%)	2 (2%)	0	100	100
25	U	95/98 (97%)	94 (99%)	1 (1%)	0	100	100
26	V	78/85 (92%)	78 (100%)	0	0	100	100
27	W	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
28	X	60/65 (92%)	58 (97%)	2 (3%)	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%)	211 (95%)	12 (5%)	0	100	100
33	c	213/250 (85%)	204 (96%)	9 (4%)	0	100	100
34	d	205/208 (99%)	204 (100%)	1 (0%)	0	100	100
35	e	153/165 (93%)	152 (99%)	1 (1%)	0	100	100
36	f	92/127 (72%)	88 (96%)	4 (4%)	0	100	100
37	g	139/156 (89%)	137 (99%)	2 (1%)	0	100	100
38	h	128/131 (98%)	124 (97%)	4 (3%)	0	100	100
39	i	125/128 (98%)	123 (98%)	2 (2%)	0	100	100
40	j	98/103 (95%)	93 (95%)	5 (5%)	0	100	100
41	k	115/128 (90%)	109 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	l	120/124 (97%)	112 (93%)	8 (7%)	0	100	100
43	m	113/118 (96%)	109 (96%)	4 (4%)	0	100	100
44	n	98/101 (97%)	95 (97%)	3 (3%)	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%)	77 (99%)	1 (1%)	0	100	100
48	r	51/75 (68%)	51 (100%)	0	0	100	100
49	s	80/91 (88%)	80 (100%)	0	0	100	100
50	t	83/88 (94%)	83 (100%)	0	0	100	100
51	u	19/71 (27%)	16 (84%)	3 (16%)	0	100	100
All	All	5361/5872 (91%)	5203 (97%)	155 (3%)	3 (0%)	49	76

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%)	51 (98%)	1 (2%)	50	78
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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%)	184 (100%)	1 (0%)	81	93
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	4434 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	2	31	ILE
32	b	147	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

Mol	Chain	Res	Type
32	b	60	ASN
36	f	11	HIS
32	b	85	GLN
34	d	102	ASN
37	g	32	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	sN1	1527/1544 (98%)	211 (13%)	0
5	AN1	2891/2918 (99%)	495 (17%)	10 (0%)
6	B	114/115 (99%)	18 (15%)	1 (0%)
All	All	4532/4577 (99%)	724 (15%)	11 (0%)

5 of 724 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	AN1	10	U
5	AN1	41	U
5	AN1	50	G
5	AN1	53	G
5	AN1	58	G

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	AN1	1538	A
5	AN1	2170	C
6	B	108	C
5	AN1	2379	G
5	AN1	782	G

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

24 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
5	2MG	AN1	2441	5	23,26,27	2.89	8 (34%)	33,38,41	2.22	11 (33%)
5	6MZ	AN1	2026	5	22,25,26	2.47	4 (18%)	29,36,39	3.40	10 (34%)
5	PSU	AN1	2601	5	18,21,22	1.09	1 (5%)	21,30,33	1.88	4 (19%)
5	OMU	AN1	2548	5	19,22,23	3.12	8 (42%)	25,31,34	1.80	5 (20%)
31	MA6	sN1	1515	31	23,26,27	1.37	4 (17%)	33,38,41	3.26	12 (36%)
5	PSU	AN1	2500	5	18,21,22	1.12	1 (5%)	21,30,33	1.91	4 (19%)
31	2MG	sN1	1204	31	23,26,27	2.91	8 (34%)	33,38,41	2.21	12 (36%)
31	MA6	sN1	1516	31	23,26,27	1.37	4 (17%)	33,38,41	3.32	12 (36%)
5	PSU	AN1	1907	5	18,21,22	1.15	1 (5%)	21,30,33	1.90	4 (19%)
5	7MG	AN1	2065	5	23,26,27	3.53	10 (43%)	27,39,42	2.17	9 (33%)
31	7MG	sN1	524	31	23,26,27	3.63	11 (47%)	27,39,42	2.16	9 (33%)
5	PSU	AN1	1913	5	18,21,22	1.13	1 (5%)	21,30,33	1.81	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
31	PSU	sN1	513	31	18,21,22	1.20	1 (5%)	21,30,33	1.62	4 (19%)
5	PSU	AN1	952	5	18,21,22	1.09	1 (5%)	21,30,33	1.96	5 (23%)
31	4OC	sN1	1399	31	20,23,24	3.23	8 (40%)	25,32,35	0.92	1 (4%)
31	UR3	sN1	1495	31	19,22,23	2.96	6 (31%)	26,32,35	1.59	3 (11%)
31	2MG	sN1	963	31	23,26,27	2.93	8 (34%)	33,38,41	2.21	12 (36%)
5	PSU	AN1	2576	5	18,21,22	1.11	1 (5%)	21,30,33	1.93	5 (23%)
31	5MC	sN1	964	31	19,22,23	3.94	8 (42%)	26,32,35	0.99	2 (7%)
5	3TD	AN1	1911	5	19,22,23	4.30	7 (36%)	23,32,35	1.82	3 (13%)
5	PSU	AN1	2453	5	18,21,22	1.10	1 (5%)	21,30,33	1.94	6 (28%)
5	2MA	AN1	2499	53,5	22,25,26	3.99	9 (40%)	32,37,40	2.78	11 (34%)
5	5MU	AN1	1935	5	19,22,23	4.98	7 (36%)	27,32,35	3.62	9 (33%)
5	OMG	AN1	2247	5	23,26,27	2.38	8 (34%)	32,38,41	1.90	8 (25%)

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
5	2MG	AN1	2441	5	-	1/9/27/28	0/3/3/3
5	6MZ	AN1	2026	5	-	2/9/27/28	0/3/3/3
5	PSU	AN1	2601	5	-	0/7/25/26	0/2/2/2
5	OMU	AN1	2548	5	-	2/9/27/28	0/2/2/2
31	MA6	sN1	1515	31	-	0/11/29/30	0/3/3/3
5	PSU	AN1	2500	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	1907	5	-	1/7/25/26	0/2/2/2
5	7MG	AN1	2065	5	-	2/7/37/38	0/3/3/3
31	7MG	sN1	524	31	-	3/7/37/38	0/3/3/3
5	PSU	AN1	1913	5	-	3/7/25/26	0/2/2/2
31	PSU	sN1	513	31	-	0/7/25/26	0/2/2/2
5	PSU	AN1	952	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	-	2/7/25/26	0/2/2/2
31	2MG	sN1	963	31	-	0/9/27/28	0/3/3/3
5	PSU	AN1	2576	5	-	0/7/25/26	0/2/2/2
31	5MC	sN1	964	31	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	3TD	AN1	1911	5	-	4/7/25/26	0/2/2/2
5	PSU	AN1	2453	5	-	0/7/25/26	0/2/2/2
5	2MA	AN1	2499	53,5	-	3/7/25/26	0/3/3/3
5	5MU	AN1	1935	5	-	0/7/25/26	0/2/2/2
5	OMG	AN1	2247	5	-	0/9/27/28	0/3/3/3

The worst 5 of 126 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	12.26	1.50	1.34
5	AN1	1935	5MU	C2-N1	11.53	1.56	1.38
5	AN1	1935	5MU	C6-N1	10.89	1.56	1.38
5	AN1	1935	5MU	C4-C5	10.19	1.61	1.44

The worst 5 of 166 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	sN1	1516	MA6	N1-C6-N6	-12.18	102.02	116.86
5	AN1	1935	5MU	C5-C4-N3	11.93	125.69	115.32
31	sN1	1515	MA6	N1-C6-N6	-11.82	102.46	116.86
5	AN1	2026	6MZ	C4-N9-C1'	-9.78	103.75	126.63
5	AN1	1935	5MU	C5-C6-N1	-9.63	112.85	123.31

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	AN1	1913	PSU	O4'-C1'-C5-C4
5	AN1	1913	PSU	O4'-C1'-C5-C6
5	AN1	2548	OMU	O4'-C4'-C5'-O5'
31	sN1	1516	MA6	C5-C6-N6-C9
5	AN1	2548	OMU	C3'-C4'-C5'-O5'

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	AN1	2026	6MZ	2	0
31	sN1	1515	MA6	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
31	sN1	1516	MA6	1	0
5	AN1	1913	PSU	1	0
5	AN1	1911	3TD	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 95 ligands modelled in this entry, 95 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

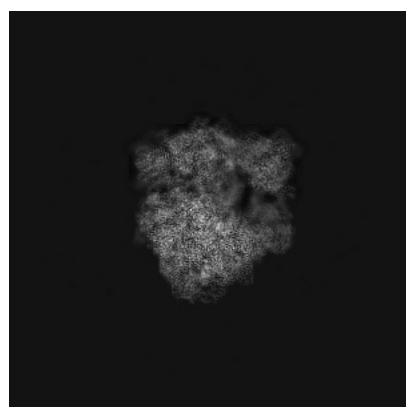
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21032. These allow visual inspection of the internal detail of the map and identification of artifacts.

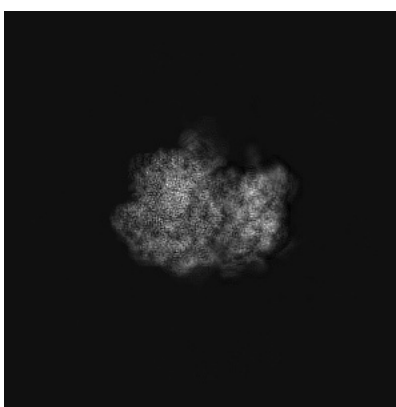
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

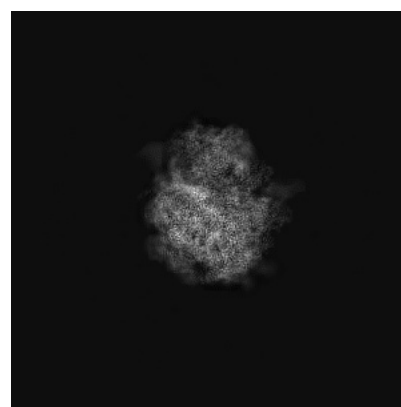
6.1.1 Primary map



X



Y

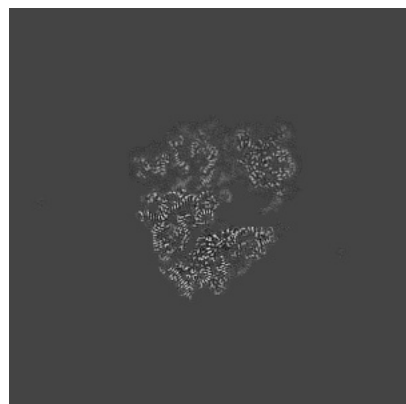


Z

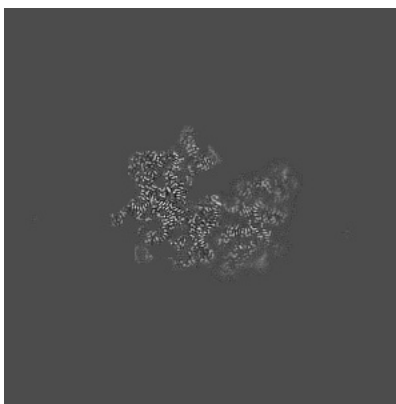
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

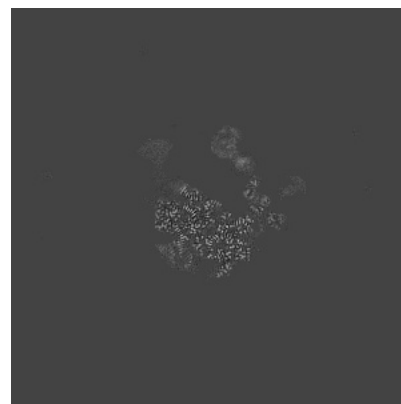
6.2.1 Primary map



X Index: 256



Y Index: 256

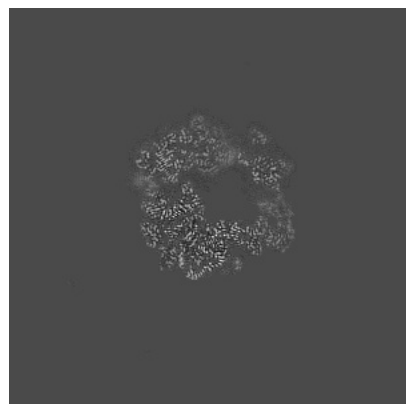


Z Index: 256

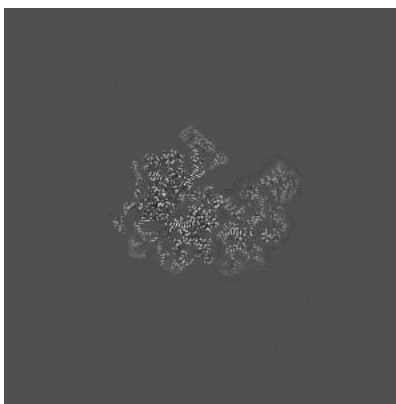
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

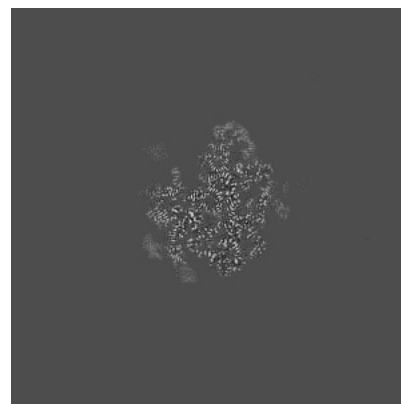
6.3.1 Primary map



X Index: 277



Y Index: 245

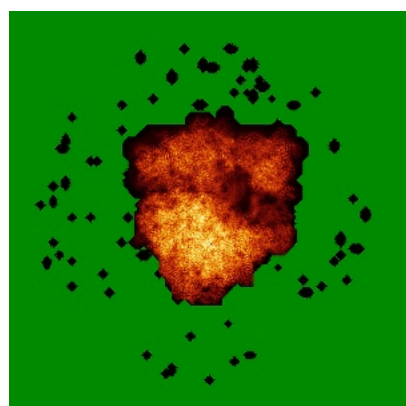


Z Index: 227

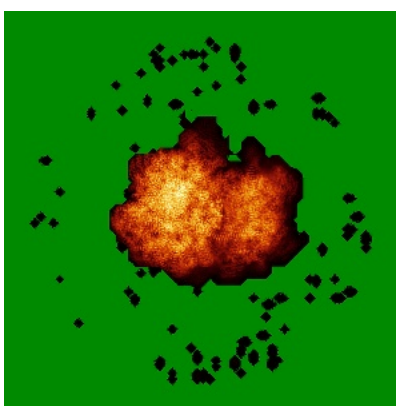
The images above show the largest variance slices of the map in three orthogonal directions.

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

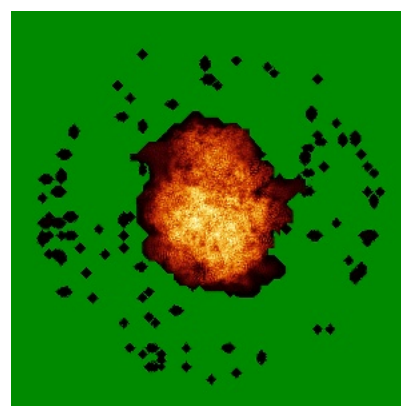
6.4.1 Primary map



X



Y

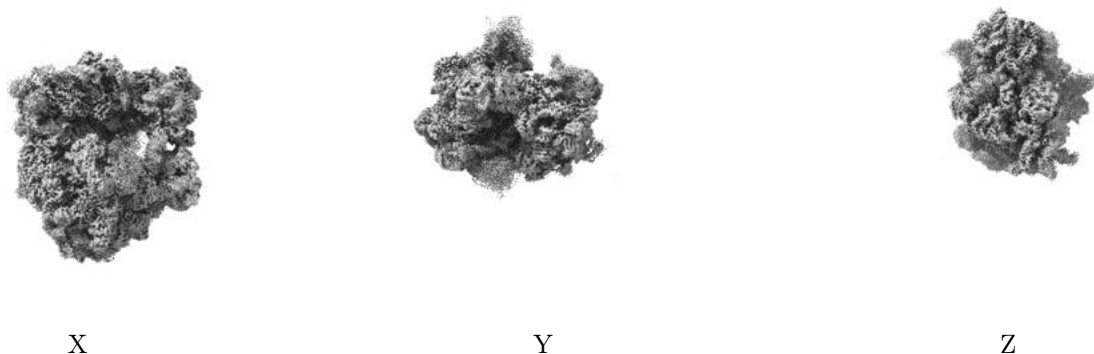


Z

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 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

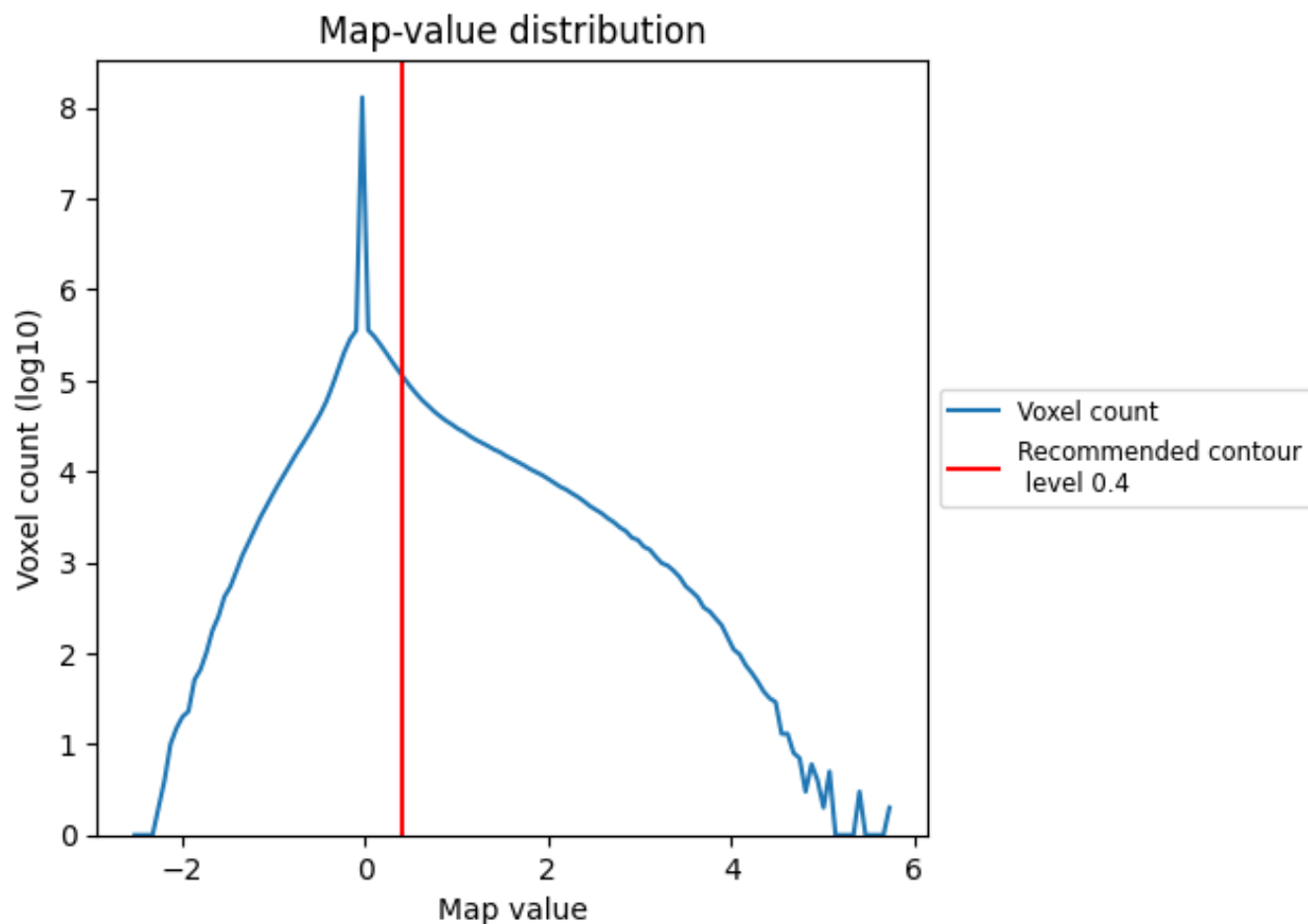
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

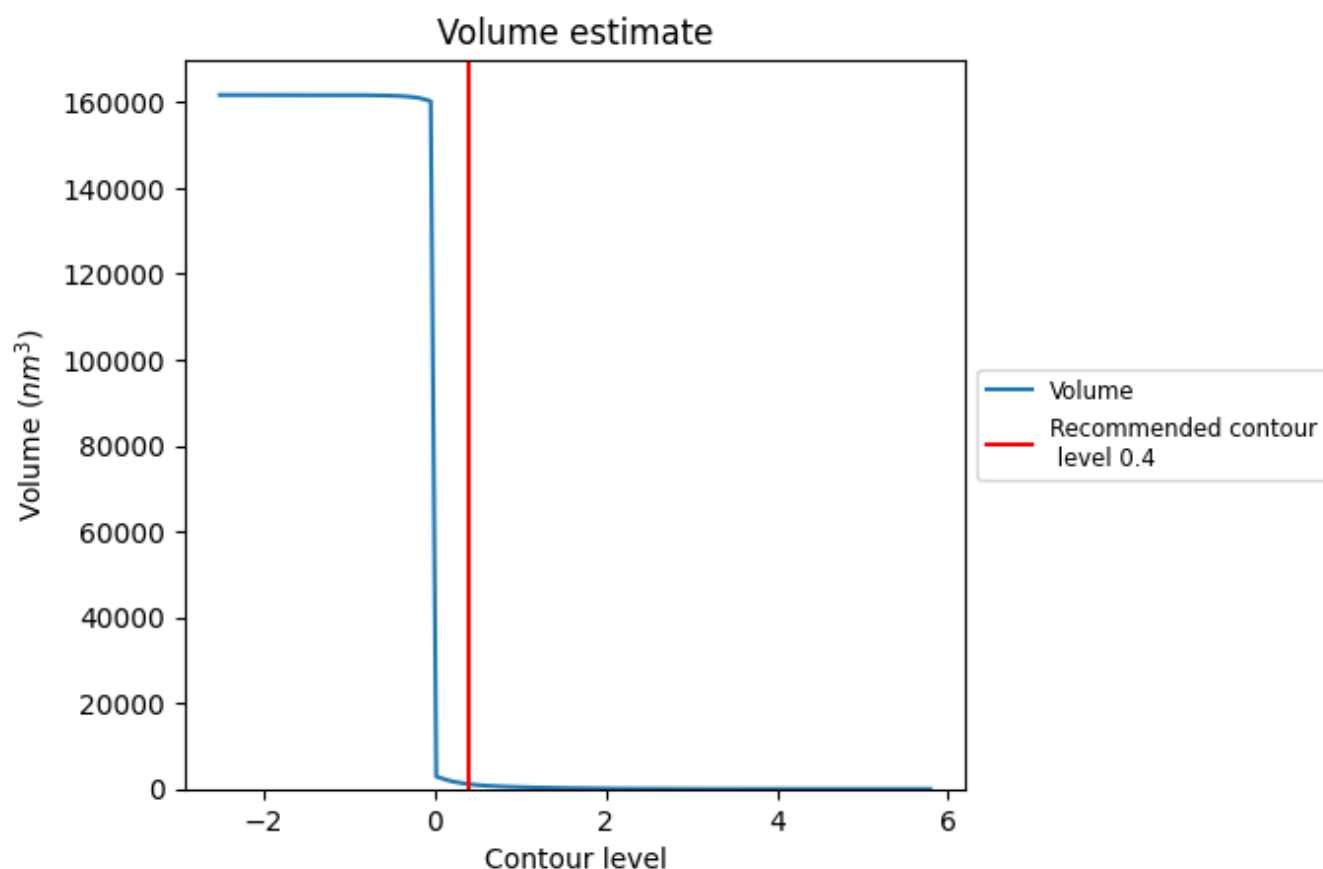
This section contains the results of statistical analysis of the map.

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.

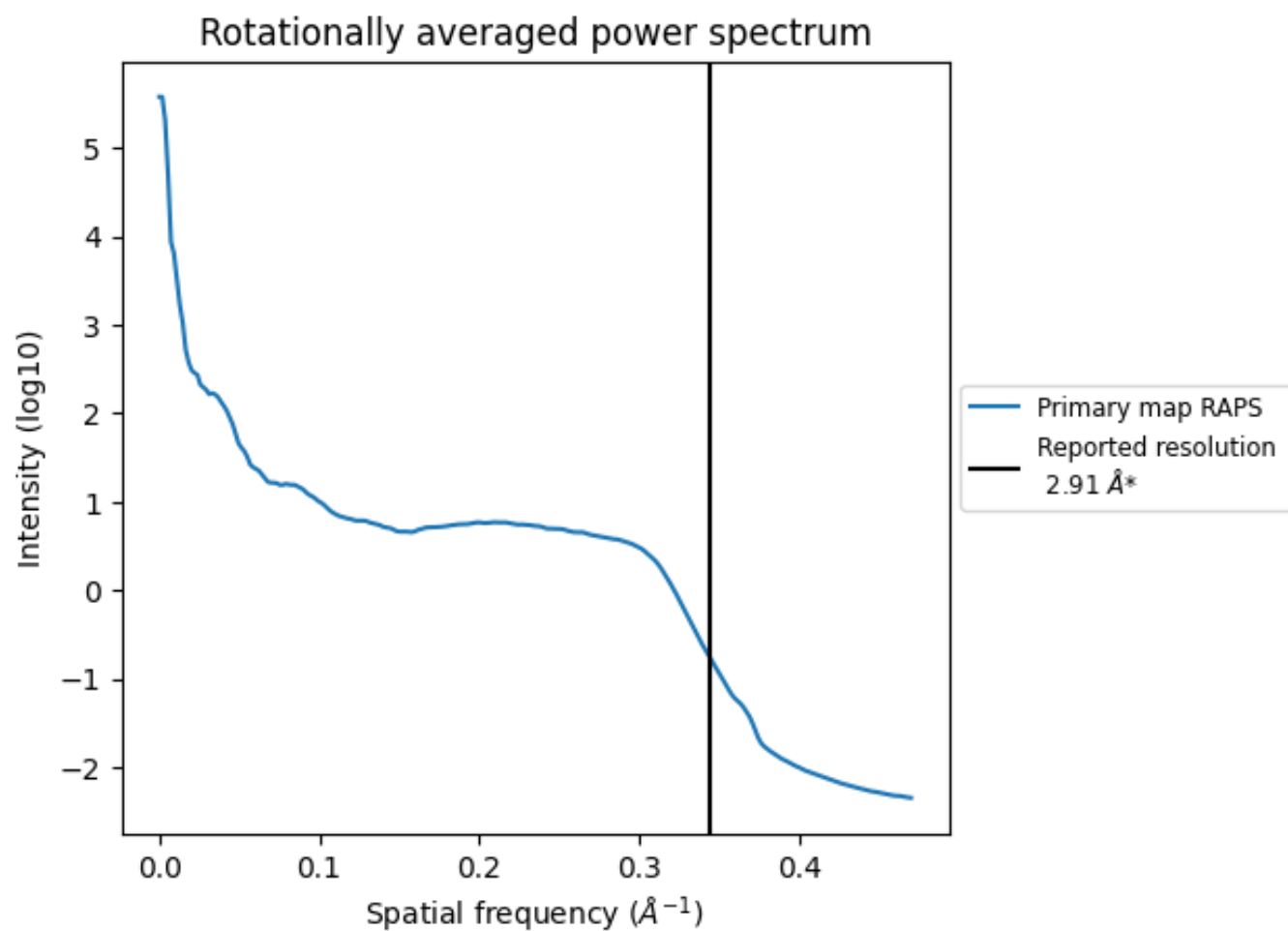
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1118 nm³; this corresponds to an approximate mass of 1010 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 0.344 Å⁻¹

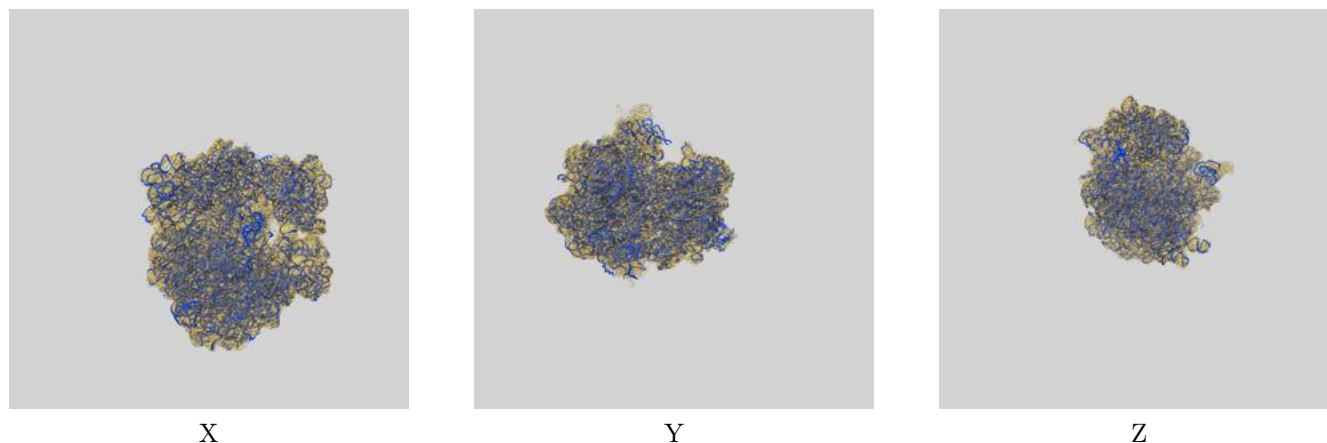
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

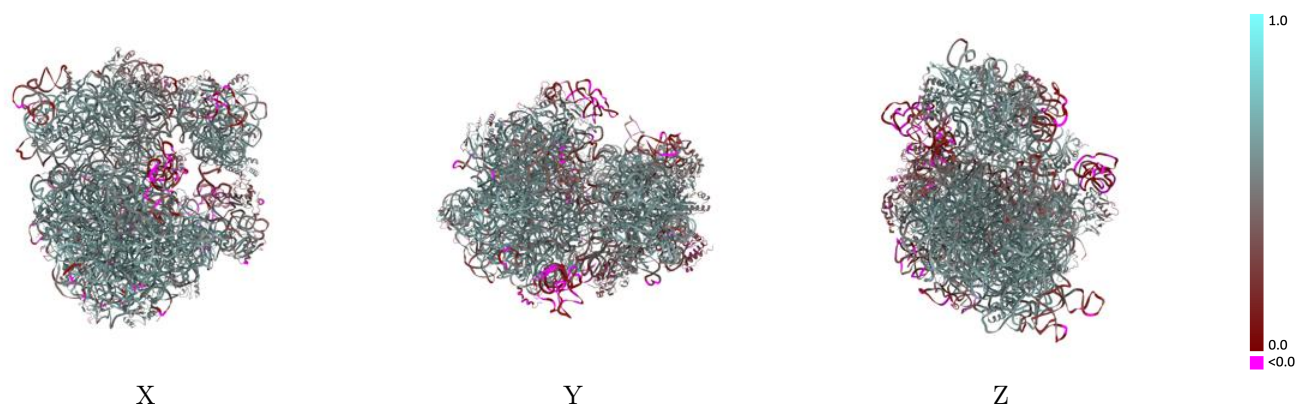
This section contains information regarding the fit between EMDB map EMD-21032 and PDB model 6V3B. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



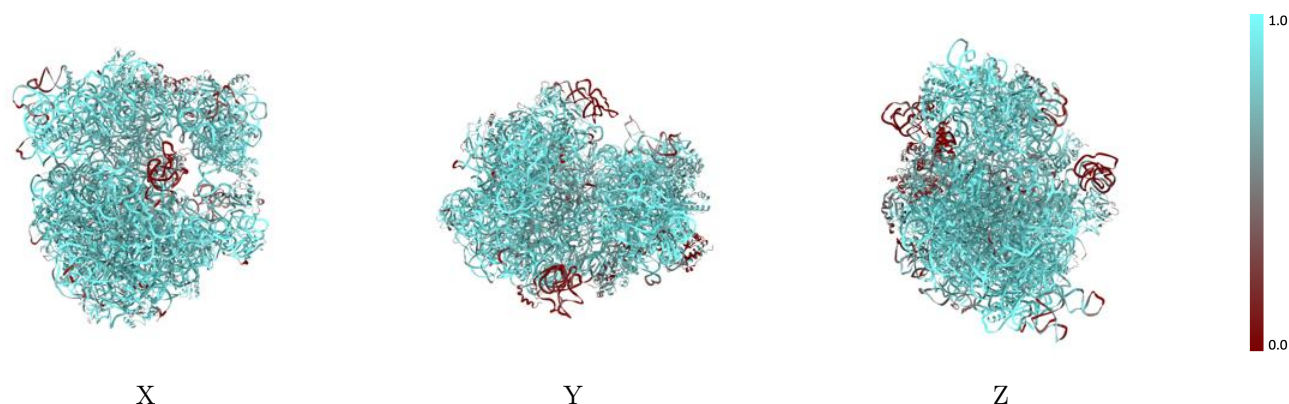
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



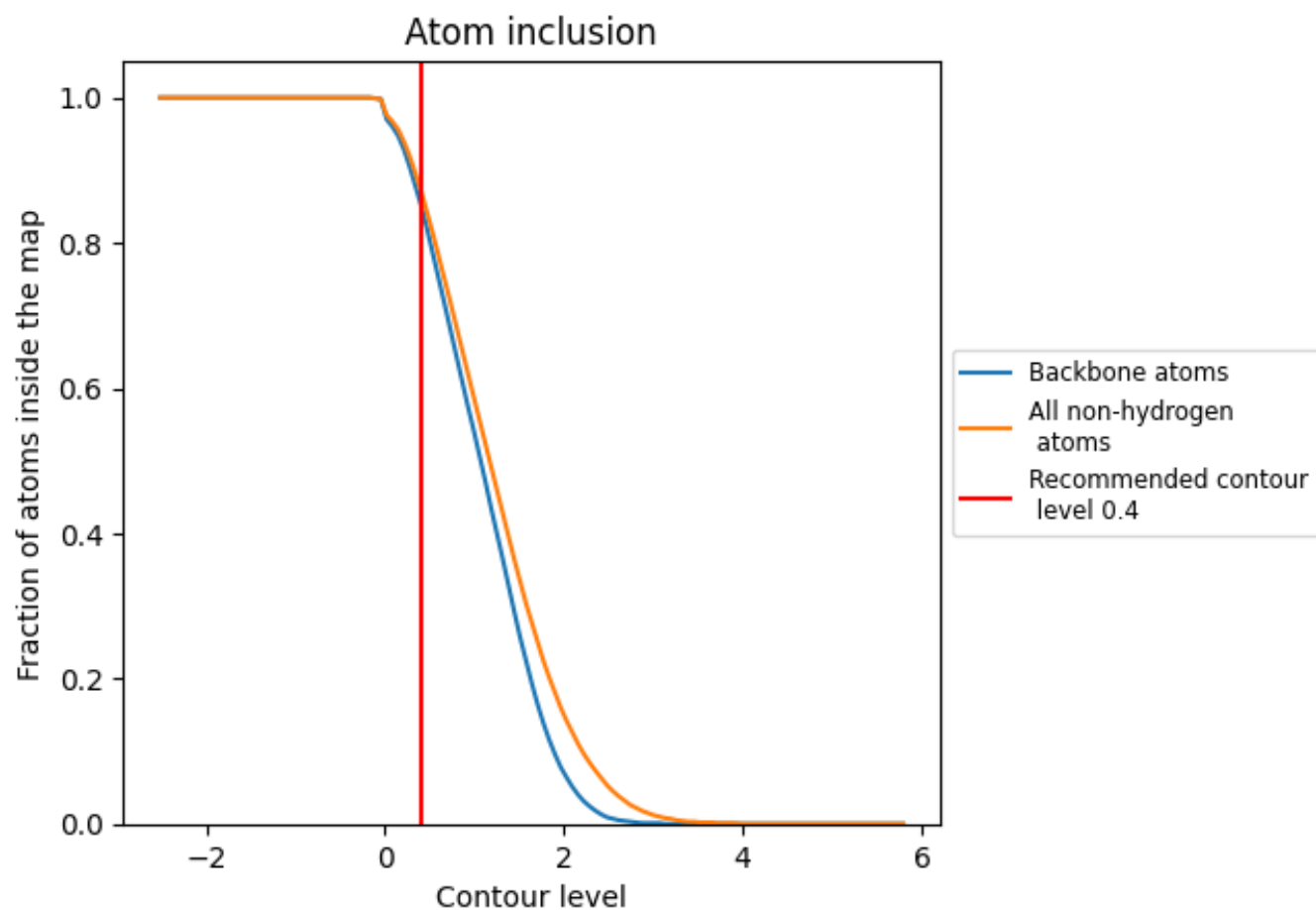
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 85% of all backbone atoms, 87% 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	 0.8720	 0.5150
0	 0.8230	 0.5200
1	 0.9500	 0.6270
2	 0.9390	 0.5900
3	 0.9480	 0.5550
AN1	 0.8900	 0.5260
B	 0.9240	 0.4750
C	 0.9200	 0.5830
D	 0.9220	 0.5850
E	 0.8830	 0.5540
F	 0.6360	 0.2780
G	 0.7610	 0.4330
H	 0.4830	 0.3220
I	 0.9000	 0.5640
J	 0.9260	 0.5850
K	 0.9090	 0.5680
L	 0.8670	 0.5480
M	 0.9620	 0.6090
N	 0.8530	 0.4870
O	 0.9090	 0.5670
P	 0.9150	 0.5830
Q	 0.8550	 0.5360
R	 0.9100	 0.5820
S	 0.8450	 0.5230
T	 0.7270	 0.4330
U	 0.8260	 0.5200
V	 0.8900	 0.5820
W	 0.8710	 0.5560
X	 0.7560	 0.4410
Y	 0.8410	 0.5200
Z	 0.8250	 0.5230
b	 0.3130	 0.2870
c	 0.8500	 0.5230
d	 0.7580	 0.4480
e	 0.8950	 0.5240



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Chain	Atom inclusion	Q-score
f	 0.5740	 0.3610
g	 0.6900	 0.4250
h	 0.9140	 0.5670
i	 0.9080	 0.5650
j	 0.8150	 0.5210
k	 0.5720	 0.3400
l	 0.7370	 0.5040
m	 0.8790	 0.5340
n	 0.8810	 0.5580
o	 0.9020	 0.5320
p	 0.9150	 0.5720
q	 0.8640	 0.5420
r	 0.7620	 0.4600
s	 0.9360	 0.5700
sN1	 0.9110	 0.5080
t	 0.9150	 0.5560
u	 0.2740	 0.3110