



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 05:00 PM UTC

PDB ID : 7ZS5 / pdb_00007zs5
EMDB ID : EMD-14926
Title : Structure of 60S ribosomal subunit from *S. cerevisiae* with eIF6 and tRNA
Authors : Best, K.M.; Ikeuchi, K.; Kater, L.; Best, D.M.; Musial, J.; Matsuo, Y.; Berninghausen, O.; Becker, T.; Inada, T.; Beckmann, R.
Deposited on : 2022-05-06
Resolution : 3.20 Å (reported)
Based on initial models : 6SNT, 6HD7, 1G62

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
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

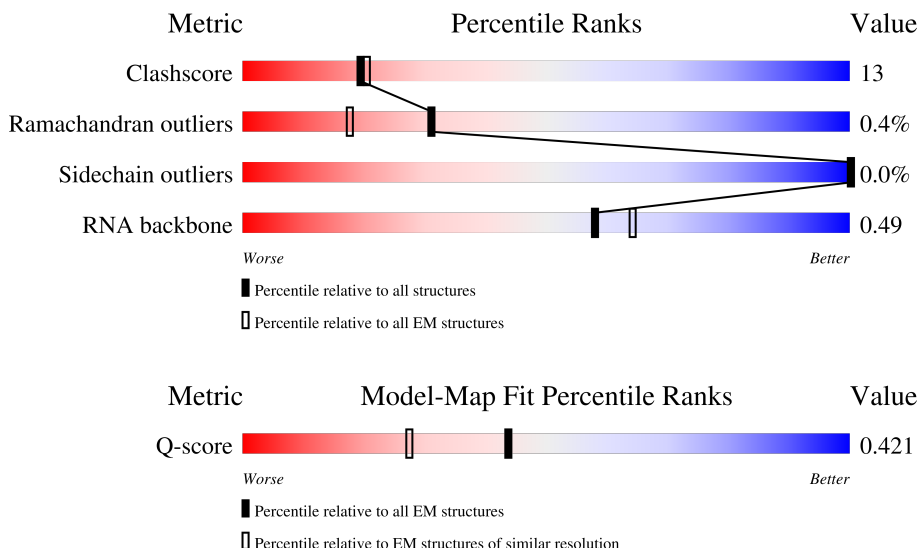
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	1	3396	
2	3	121	
3	4	158	

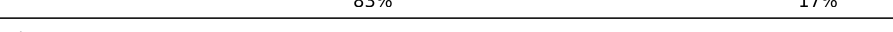
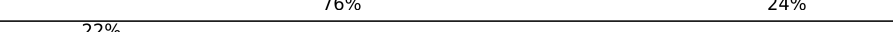
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Mol	Chain	Length	Quality of chain
4	A	224	
5	2	76	
6	BA	105	
7	BB	91	
8	BC	252	
9	BD	386	
10	BE	361	
11	BF	296	
12	BG	176	
13	BH	222	
14	BI	233	
15	BJ	191	
16	BL	169	
17	BM	193	
18	BN	136	
19	BO	203	
20	BP	197	
21	BQ	183	
22	BR	185	
23	BS	160	
24	BT	172	
25	BU	159	
26	BV	100	
27	BW	136	
28	BX	69	

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Mol	Chain	Length	Quality of chain
29	BY	121	 83% 17%
30	BZ	127	 77% 17% 6%
31	Ba	135	 71% 29%
32	Bb	148	 68% 31%
33	Bc	58	 64% 36%
34	Bd	97	 75% 25%
35	Be	109	 82% 18%
36	Bf	127	 82% 18%
37	Bg	106	 71% 29%
38	Bh	112	 5% 71% 29%
39	Bi	119	 76% 24%
40	Bj	99	 76% 23%
41	Bk	87	 67% 33%
42	Bl	77	 64% 36%
43	Bm	50	 66% 34%
44	Bn	52	 83% 17%
45	BK	220	 76% 24%
46	B	23	 22% 100%

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 127849 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3248	Total	C	N	O	P	0	0
			69452	31022	12494	22688	3248		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	224	Total	C	N	O	S	0	0
			1633	1019	279	328	7		

- Molecule 5 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	2	76	Total	C	N	O	P	0	0
			1619	722	288	533	76		

- Molecule 6 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	BA	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 7 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	BB	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 8 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	BC	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 9 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BD	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 10 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	BE	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 11 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BF	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 12 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BG	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 13 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BH	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 14 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BI	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 15 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BJ	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 16 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BL	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 17 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BM	193	Total	C	N	O		0	0
			1543	962	315	266			

- Molecule 18 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BN	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BO	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 20 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BP	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	BQ	183	Total	C	N	O	0	0
			1420	882	281	257		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BR	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	BS	160	Total	C	N	O	0	0
			1286	797	269	220		

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BT	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 25 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BU	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 26 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	BV	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BW	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 28 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BX	69	Total	C	N	O	S	0	0
			553	355	108	89	1		

- Molecule 29 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BY	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 30 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BZ	120	Total	C	N	O		0	0
			939	591	179	169			

- Molecule 31 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ba	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 32 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bb	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 33 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Bc	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bd	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 35 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Be	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 36 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Bf	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 37 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Bg	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 38 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Bh	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 39 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Bi	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 40 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Bj	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 41 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Bk	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 42 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	Bl	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 43 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Bm	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 44 is a protein called 60S ribosomal protein L40-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Bn	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 45 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BK	220	Total	C	N	O	S	0	0
			1770	1121	335	307	7		

- Molecule 46 is a protein called Unknown chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	B	23	Total	C	N	O	0	0
			115	69	23	23		

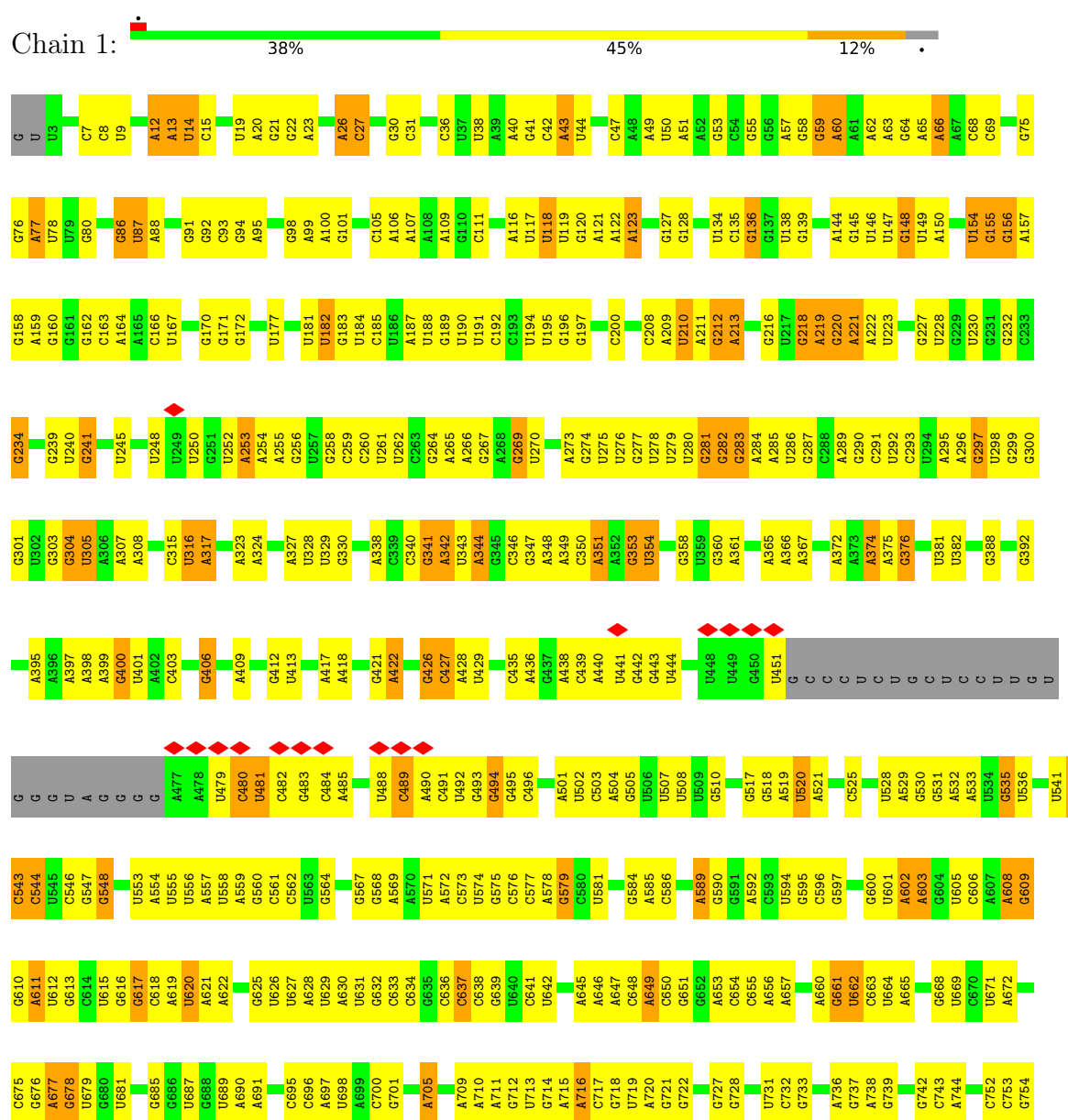
- Molecule 47 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
47	2	1	Total	Mg	0
			1	1	

3 Residue-property plots [i](#)

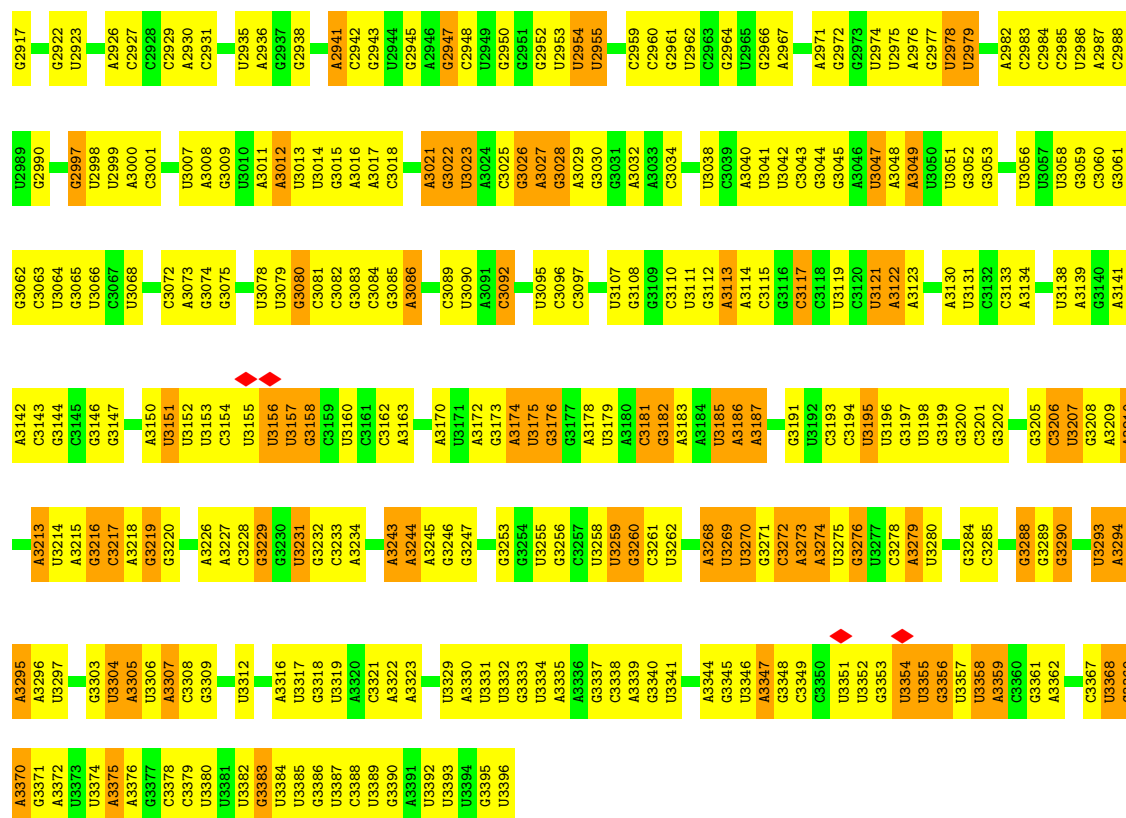
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 25S ribosomal RNA



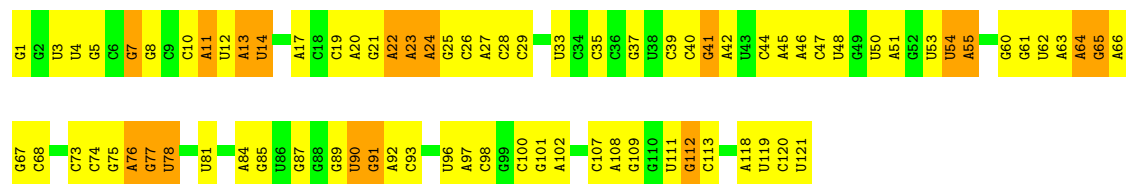


G2745	G2837	G2675	G2603	G2530	A2397	U2318	A2168	A2100	C	G	G1899	G1822
A2746	A2837	A2676	U2604	C2531	A2402	U2319	G2169	C2101	U2040	C	A1900	G1829
A2747	G2605	G2677	G2606	G2533	G2403	A2320	U2176	U2102	U2041	G	G1902	G1830
G2748	G2607	A2679	G2608	G2537	C2405	U2328	G2178	A2104	U2042	C	G1906	U1831
U2750	G2609	U2537	A2608	U2538	C2406	G2329	A2178	A2107	U2043	G	C1907	U1834
G2751	U2610	U2538	U2611	C2539	C2407	U2334	G2179	C2108	U2044	G	A1908	A1835
U2752	U2612	U2683	U2613	G2540	U2408	G2335	G2180	U2109	G2045	G	A1909	G1836
G2753	U2614	C2684	U2615	U2541	U2411	U2336	U2185	G2110	U2046	C	A1910	U1837
C2755	U2616	C2685	G2617	U2542	G2412	C2337	G2186	U2112	A2047	U	A1911	G1838
U2756	G2618	U2686	G2619	U2543	A2413	C2338	U2187	U2113	U2048	U	A1912	A1839
A2758	U2620	U2687	U2621	U2544	A2414	U2340	A2188	C2114	A2049	U	A1913	U1840
G2761	U2622	U2688	U2623	U2545	G2417	U2344	U2189	G2115	C2050	G	A1914	A1841
U2762	U2624	A2689	U2625	A2547	U2418	U2345	U2190	U2116	G2051	G	C1843	C1842
U2763	G2626	C2548	U2627	C2548	A2419	A2345	U2191	A2117	G1927	C	C1846	G1847
A2769	G2628	U2550	G2629	C2549	C2420	U2349	C2192	C2118	G1928	A	U1847	G1848
G2770	G2631	U2551	U2630	U2552	U2423	C2350	U2193	G2121	U1931	C	G1849	G1849
C2772	U2632	C2552	U2633	C2553	A2424	U2351	G2194	G2122	U1932	C	G1850	G1851
C2773	U2634	C2553	U2635	U2554	G2425	A2352	C2196	A2125	G1940	U	U1851	G1852
U2776	U2636	G2555	U2637	U2555	U2426	G2353	A2197	U2126	G2058	G	C1941	U1853
G2777	U2638	C2556	U2638	U2556	U2427	G2354	A2198	U2127	U2059	G	U1942	U1853
G2778	U2642	A2557	U2643	U2557	U2428	A2355	C2202	G2128	A	U	C1943	G1863
A2779	U2644	U2558	U2644	C2558	G2429	A2357	U2205	G2130	G1952	G	U1944	A1864
G2787	U2647	U2559	U2647	C2559	C2431	A2358	U2206	A2131	G1953	C	A1858	C1866
U2794	U2651	U2560	U2652	U2560	U2432	A2361	A2208	C2136	U1954	C	A1859	G1867
U2795	U2652	U2561	U2653	U2561	U2433	A2362	U2209	U2137	U1955	U	G1868	G1868
C2796	U2653	U2562	U2654	U2562	U2434	A2363	G2210	A2138	U1956	G	C1869	C1870
U2797	U2654	U2563	U2655	U2563	U2435	A2364	A2213	U2142	U1957	C	U1873	U1873
U2798	U2655	U2564	U2656	U2564	U2436	C2365	A2214	A2143	G1958	C	U1958	U1878
G2800	U2656	U2565	U2657	U2565	U2437	C2366	G2215	A2144	A1960	G	A1960	G1879
A2801	U2657	U2566	U2658	U2566	U2438	A2367	A2216	A2145	G1961	C	G1961	U1880
A2802	U2658	U2567	U2659	U2567	U2439	A2368	A2217	C2146	U1962	C	U1883	A1883
A2803	U2659	U2568	U2660	U2568	U2440	A2369	A2218	A2147	U1963	C	A1884	U1885
U2807	U2660	U2569	U2661	U2569	U2441	G2370	A2219	U2148	C1964	C	U1885	U1886
A2808	U2662	U2570	U2662	U2570	U2442	G2371	A2220	A2149	U1965	C	A1886	A1887
C2809	U2663	U2571	U2663	U2571	U2443	A2372	A2221	A2150	U1966	C	U1887	U1890
U2810	U2664	U2572	U2664	U2572	U2444	A2373	A2222	C2151	U1967	C	U1890	U1890
C2811	U2665	U2573	U2665	U2573	U2445	A2374	A2223	A2152	G1968	U	G1968	A1893
U2812	U2666	U2574	U2666	U2574	U2446	C2375	A2224	U2153	U1969	C	U1969	U1894
A2813	U2667	U2575	U2667	U2575	U2447	A2376	A2225	U2154	U1970	C	U1970	A1895
U2814	U2668	U2576	U2668	U2576	U2448	U2377	U2226	U2155	U1971	C	A1971	U1896
G2815	U2669	U2577	U2669	U2577	U2449	U2378	U2227	G2156	A2088	C	U1972	G1897
A2816	U2670	U2578	U2670	U2578	U2450	U2379	A2228	A2157	U2081	C	A1973	A1974
U2817	U2671	U2579	U2671	U2579	U2451	U2380	A2229	G2158	U2082	C	U1975	C1975
A2818	U2672	U2580	U2672	U2580	U2452	A2381	G2234	G2159	U2083	C	G1976	C1976
U2819	U2673	U2581	U2673	U2581	U2453	A2382	U2241	A2160	U2084	C	A1977	A
G2823	U2674	U2582	U2674	U2582	U2454	A2383	U2242	U2161	U2085	C	U1977	A
U2827	U2675	U2583	U2675	U2583	U2455	A2384	A2243	G2162	A2086	C	U1977	A
G2828	U2676	U2584	U2676	U2584	U2456	A2385	A2244	C2163	U2087	C	U1977	A
U2909	U2677	U2585	U2677	U2585	U2457	A2386	U2245	U2163	A2088	C	U1977	A
A2910	U2678	U2586	U2678	U2586	U2458	A2387	U2246	C2164	A2089	C	U1977	A
G2911	U2679	U2587	U2679	U2587	U2459	A2388	U2247	U2165	U2090	C	U1977	A
C2912	U2680	U2588	U2680	U2588	U2460	A2389	U2248	A2166	U2091	C	U1977	A
U2913	U2681	U2589	U2681	U2589	U2461	A2390	U2249	A2167	A2092	C	U1977	A
G2914	U2682	U2590	U2682	U2590	U2462	A2391	U2250	A2168	A2093	C	U1977	A
U2915	U2683	U2591	U2683	U2591	U2463	A2392	U2251	A2169	G2095	C	U1977	A
U2916	U2684	U2592	U2684	U2592	U2464	A2393	U2252	A2170	A2096	C	U1977	A
U2917	U2685	U2593	U2685	U2593	U2465	A2394	U2253	A2171	U2097	C	U1977	A
U2918	U2686	U2594	U2686	U2594	U2466	A2395	U2254	A2172	A2098	C	U1977	A
U2919	U2687	U2595	U2687	U2595	U2467	A2396	U2255	A2173	U2099	C	U1977	A
U2920	U2688	U2596	U2688	U2596	U2468	A2397	U2256	A2174	A2100	C	U1977	A
U2921	U2689	U2597	U2689	U2597	U2469	A2398	U2257	A2175	A2101	C	U1977	A
U2922	U2690	U2598	U2690	U2598	U2470	A2399	U2258	A2176	A2102	C	U1977	A
U2923	U2691	U2599	U2691	U2599	U2471	A2400	U2259	A2177	A2103	C	U1977	A
U2924	U2692	U2600	U2692	U2600	U2472	A2401	U2260	A2178	A2104	C	U1977	A
U2925	U2693	A2601	U2693	A2601	U2473	A2402	U2261	A2179	A2105	C	U1977	A
U2926	U2694	G2602	U2694	G2602	U2474	A2403	U2262	A2180	A2106	C	U1977	A
U2927	U2695	U2603	U2695	U2603	U2475	A2404	U2263	A2181	A2107	C	U1977	A
U2928	U2696	U2604	U2696	U2604	U2476	A2405	U2264	A2182	A2108	C	U1977	A
U2929	U2697	U2605	U2697	U2605	U2477	A2406	U2265	A2183	A2109	C	U1977	A
U2930	U2698	U2606	U2698	U2606	U2478	A2407	U2266	A2184	A2110	C	U1977	A
U2931	U2699	U2607	U2699	U2607	U2479	A2408	U2267	A2185	A2111	C	U1977	A
U2932	U2700	U2608	U2700	U2608	U2480	A2409	U2268	A2186	A2112	C	U1977	A
U2933	U2701	U2609	U2701	U2609	U2481	A2410	U2269	A2187	A2113	C	U1977	A
U2934	U2702	U2610	U2702	U2610	U2482	A2411	U2270	A2188	A2114	C	U1977	A
U2935	U2703	U2611	U2703	U2611	U2483	A2412	U2271	A2189	A2115	C	U1977	A
U2936	U2704	U2612	U2704	U2612	U2484	A2413	U2272	A2190	A2116	C	U1977	A
U2937	U2705	U2613	U2705	U2613	U2485	A2414	U2273	A2191	A2117	C	U1977	A
U2938	U2706	U2614	U2706	U2614	U2486	A2415	U2274	A2192	A2118	C	U1977	A
U2939	U2707	U2615	U2707	U2615	U2487	A2416	U2275	A2193	A2119	C	U1977	A
U2940	U2708	U2616	U2708	U2616	U2488	A2417	U2276	A2194	A2120	C	U1977	A
U2941	U2709	U2617	U2709	U2617	U2489	A2418	U2277	A2195	A2121	C	U1977	A
U2942	U2710	U2618	U2710	U2618	U2490	A2419	U2278	A2196	A2122	C	U1977	A
U2943	U2711	U2619	U2711	U2619	U2491	A2420	U2279	A2197	A2123	C	U1977	A
U2944	U2712	U2620	U2712	U2620	U2492	A2421	U2280	A2198	A2124	C	U1977	A
U2945	U2713	U2621	U2713	U2621	U2493	A2422	U2281	A2199	A2125	C	U1977	A
U2946	U2714	U2622	U2714	U2622	U2494	A2423	U2282	A2200	A2126	C	U1977	A
U2947	U2715	U2623	U2715	U2623	U2495	A2424	U2283	A2201	A2127	C	U1977	A
U2948	U2716	U2624	U2716	U2624	U2496	A2425	U2284	A2202	A2128	C	U1977	A
U2949	U2717	U2625	U2717	U2625	U2497	A2426	U2285	A2203	A2129	C	U1977	A
U2950	U2718	U2626	U2718	U2626	U2498	A2427	U2286	A2204	A2130	C	U1977	A
U2951	U2719	U2627	U2719	U2627	U2499	A2428	U2287	A2205	A2131	C	U1977	A
U2952	U2720	U2628	U2720	U2628	U2500	A2429	U2288	A2206	A2132	C	U1977	A
U2953	U2721	U2629	U2721	U2629	U2501	A2430	U2289	A2207	A2133	C	U1977	A
U2954	U2722	U2630	U2722	U2630	U2502	A2431	U2290	A2208	A2134	C	U1977	A
U2955	U2723	U2631	U2723	U2631	U2503	A2432	U2291	A2209	A2135	C	U1977	A
U2956	U2724	U2632	U2724	U2632	U2504	A2433	U2292	A2210	A2136	C	U1977	A
U2957	U2725	U2633	U2725	U2633	U2505	A2434	U2293	A2211	A2137	C	U1977	A
U2958	U2726	U2634	U2726	U2634	U2506	A2435	U2294	A2212	A2138	C	U1977	A
U2959	U2727	U2635	U2727	U2635	U2507	A2436	U2295	A2213	A2139	C	U1977	A
U2960	U2728	U2636	U2728	U2636	U2508	A2437	U2296	A2214	A2140	C	U1977	A
U2961	U2729	U2637	U2729	U2637	U2							



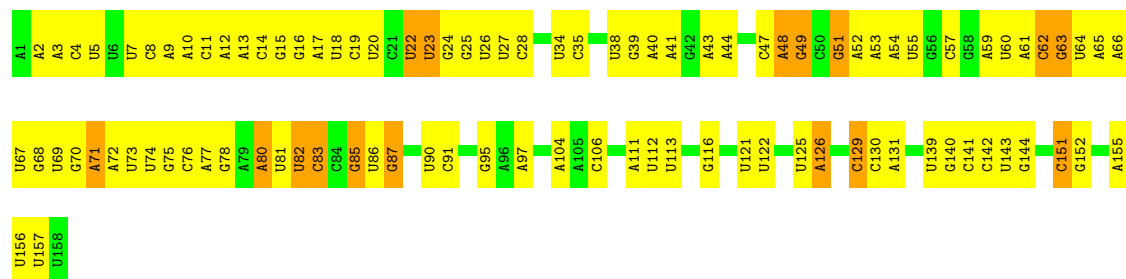
• Molecule 2: 5S ribosomal RNA

Chain 3: 34% 51% 15%



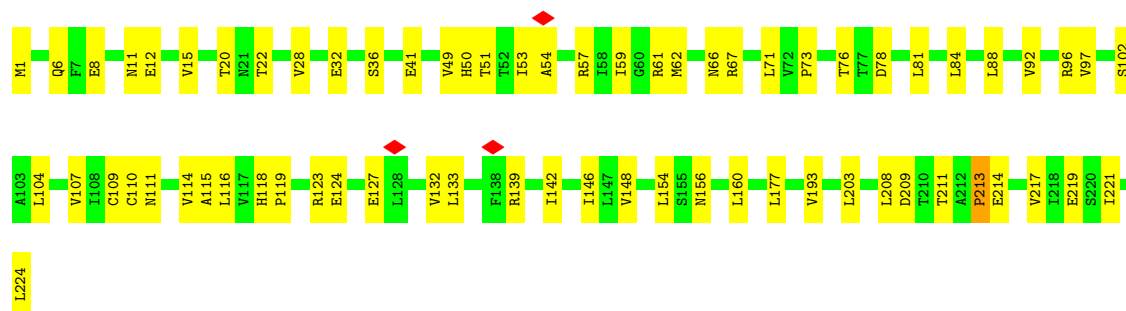
• Molecule 3: 5.8S ribosomal RNA

Chain 4: 39% 51% 10%

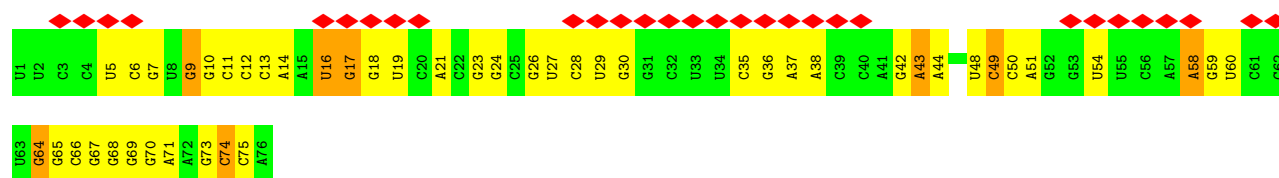


• Molecule 4: Eukaryotic translation initiation factor 6

Chain A: 70% 30%



- Molecule 5: tRNA



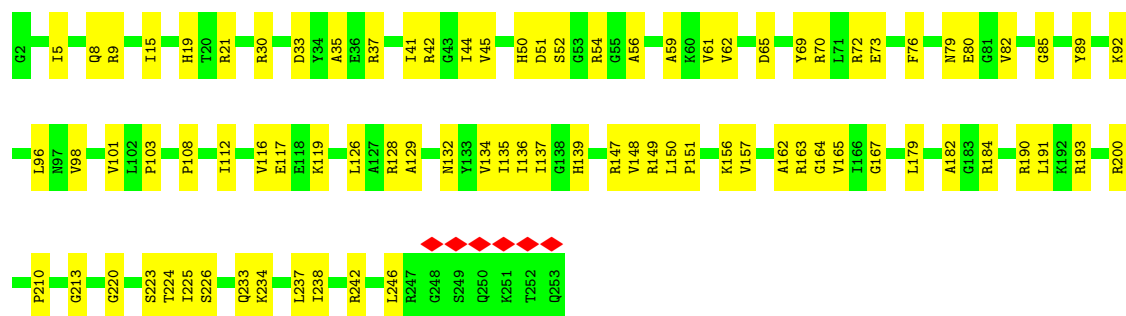
- Molecule 6: 60S ribosomal protein L42-A



- Molecule 7: 60S ribosomal protein L43-A



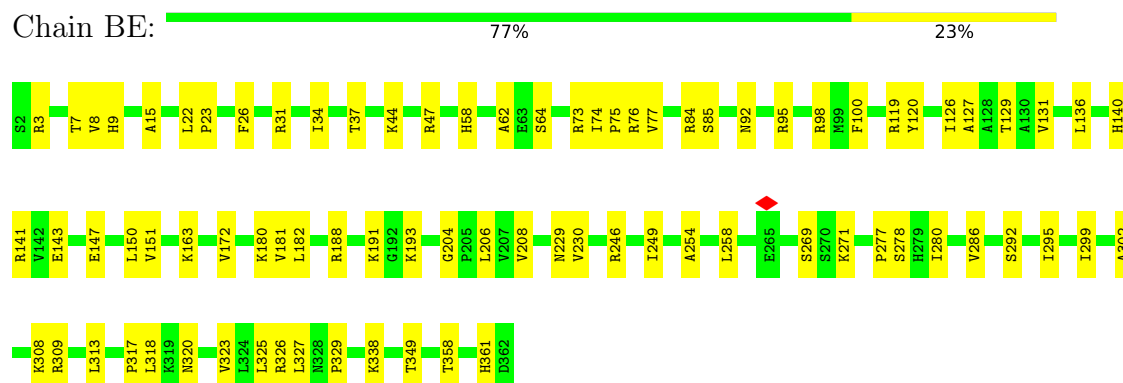
- Molecule 8: 60S ribosomal protein L2-A



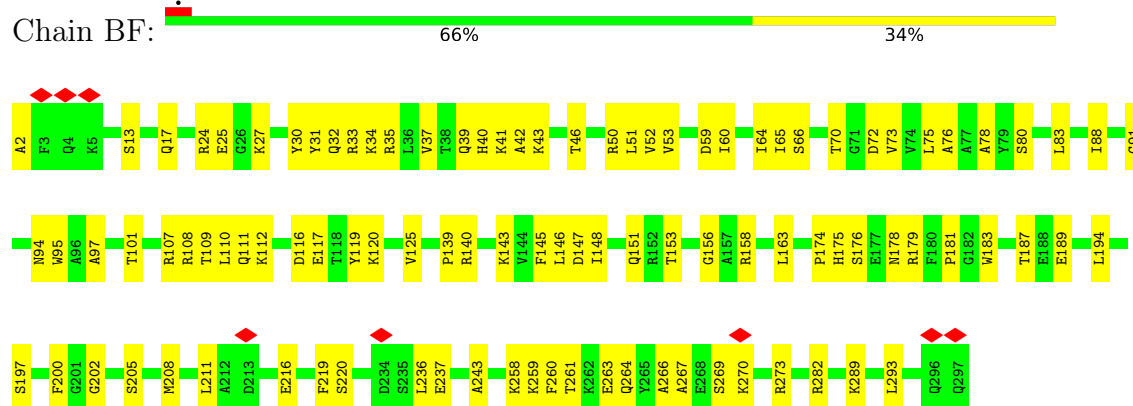
- Molecule 9: 60S ribosomal protein L3



- Molecule 10: 60S ribosomal protein L4-A

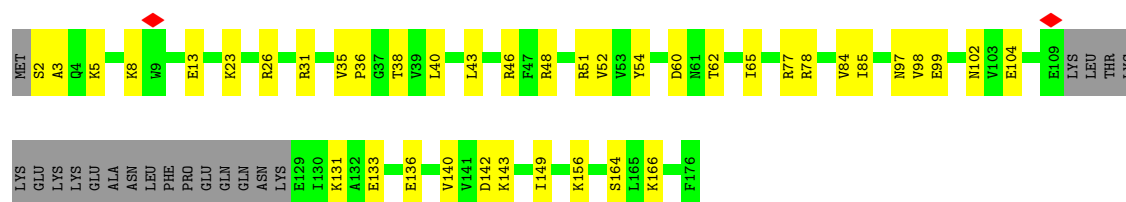


- Molecule 11: 60S ribosomal protein L5

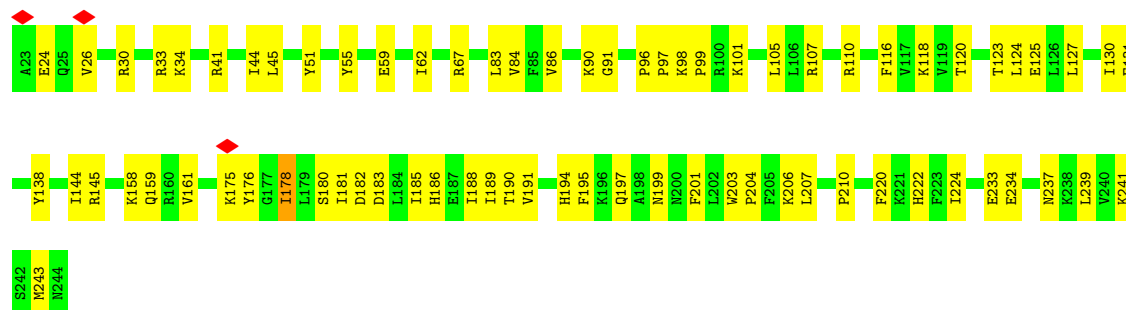


- Molecule 12: 60S ribosomal protein L6-A

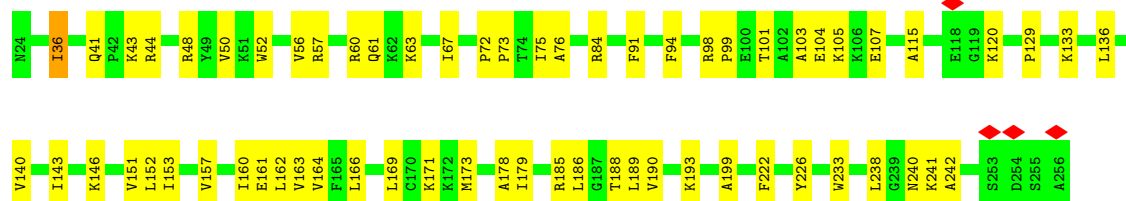




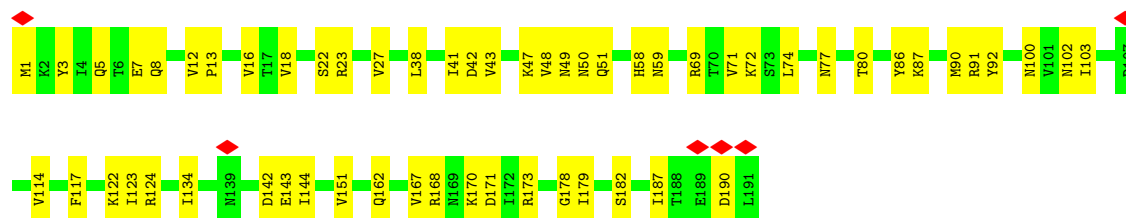
• Molecule 13: 60S ribosomal protein L7-A



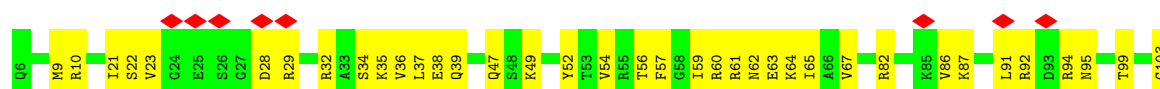
• Molecule 14: 60S ribosomal protein L8-A



• Molecule 15: 60S ribosomal protein L9-A

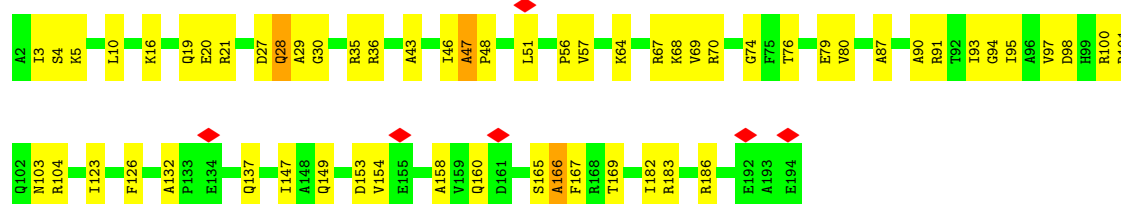


• Molecule 16: 60S ribosomal protein L11-B

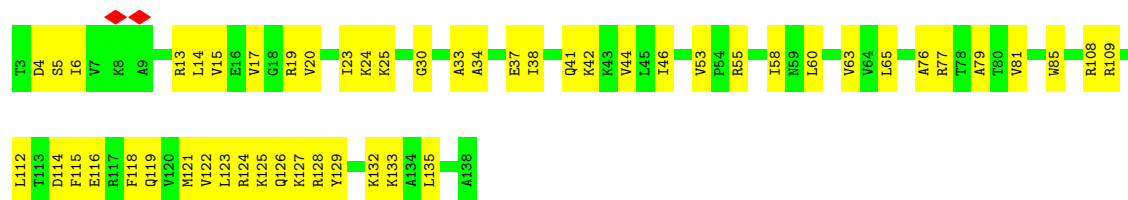




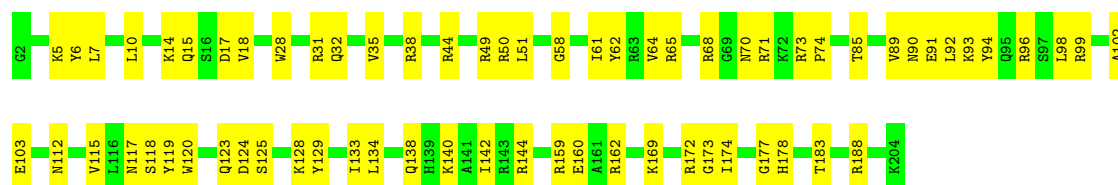
- Molecule 17: 60S ribosomal protein L13-A



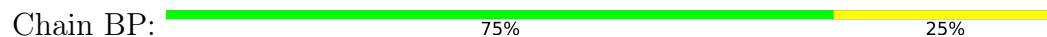
- Molecule 18: 60S ribosomal protein L14-A



- Molecule 19: 60S ribosomal protein L15-A

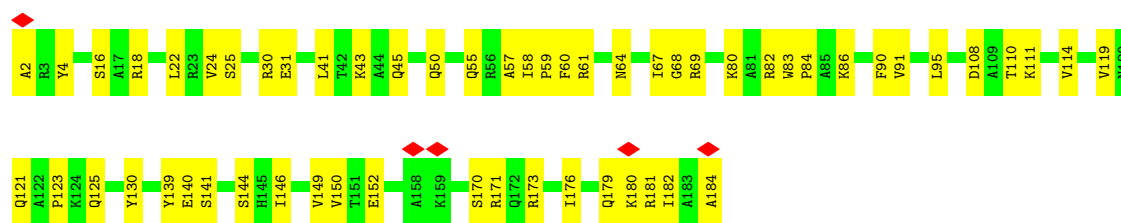


- Molecule 20: 60S ribosomal protein L16-A

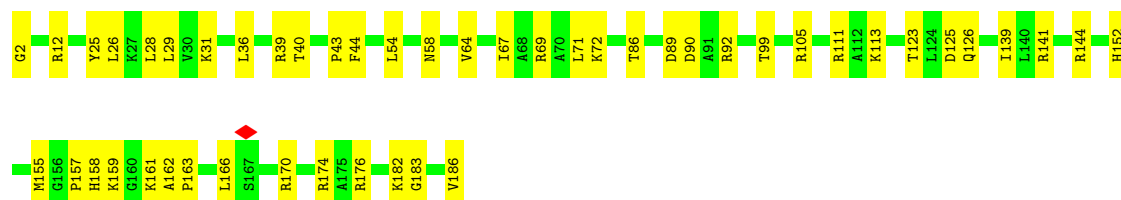
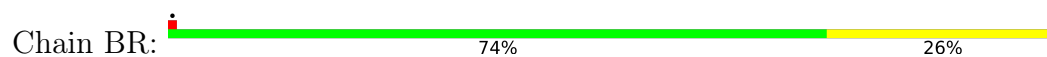


- Molecule 21: 60S ribosomal protein L17-A

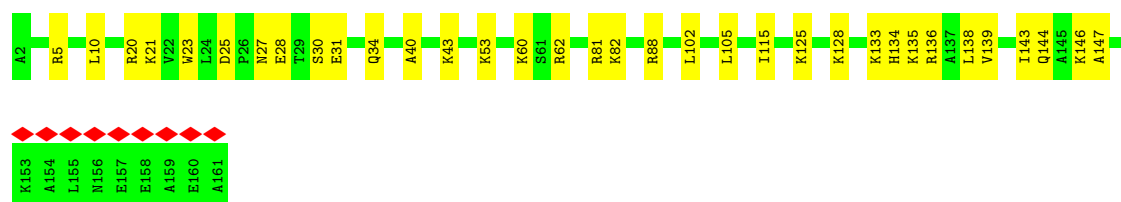
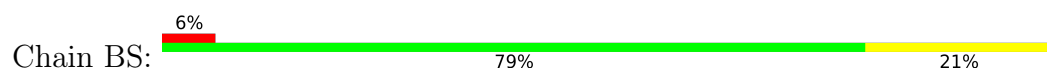




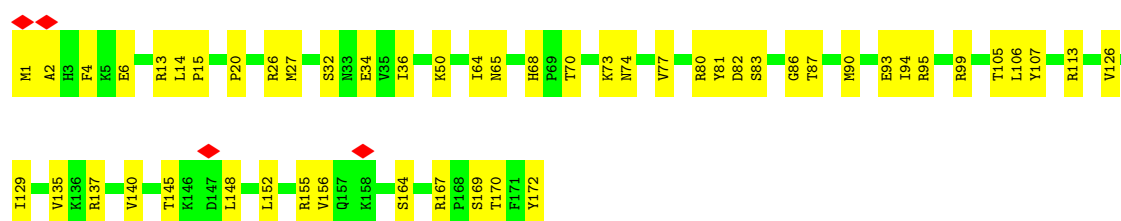
- Molecule 22: 60S ribosomal protein L18-A



- Molecule 23: 60S ribosomal protein L19-A



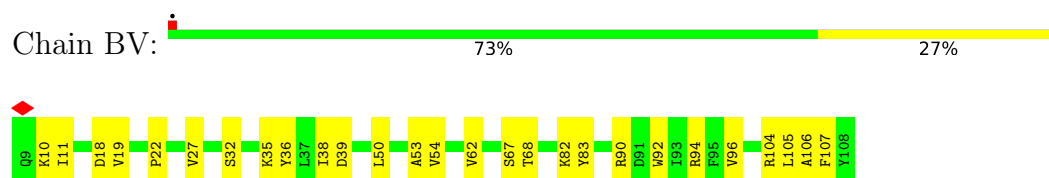
- Molecule 24: 60S ribosomal protein L20-A



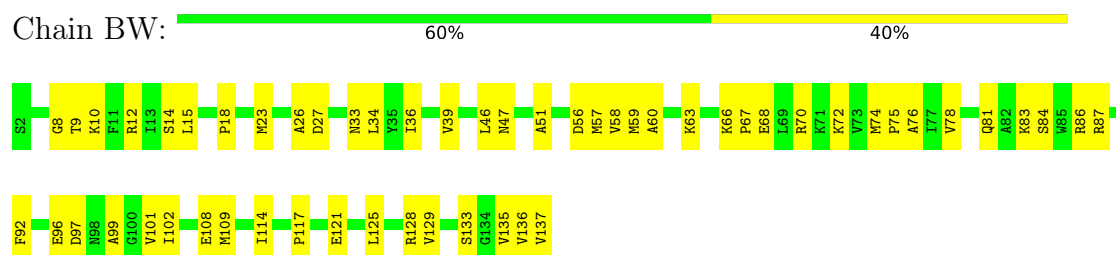
- Molecule 25: 60S ribosomal protein L21-A



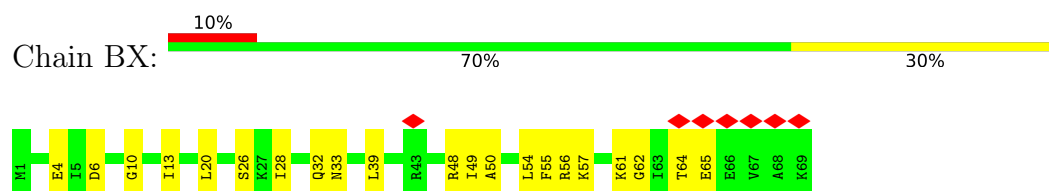
- Molecule 26: 60S ribosomal protein L22-A



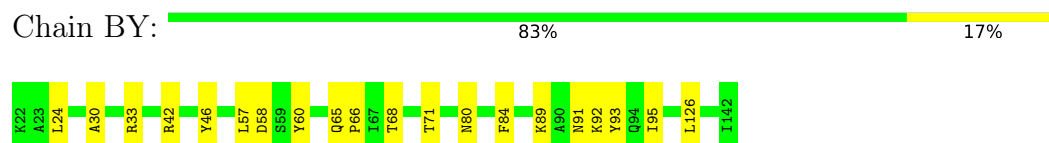
- Molecule 27: 60S ribosomal protein L23-A



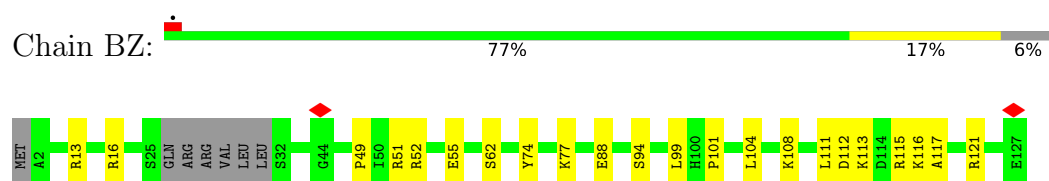
- Molecule 28: 60S ribosomal protein L24-A



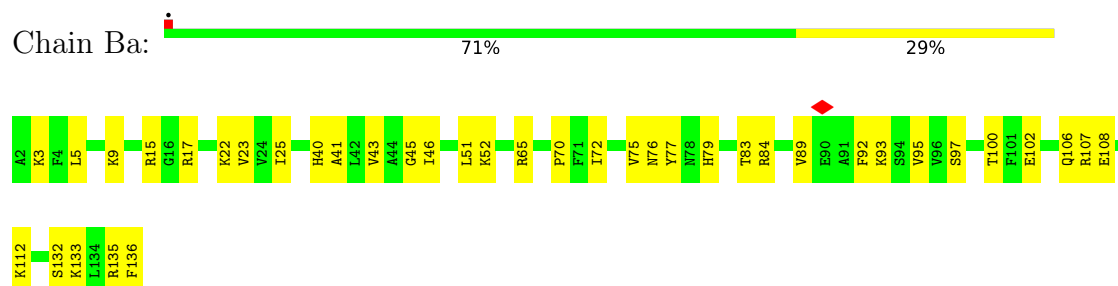
- Molecule 29: 60S ribosomal protein L25



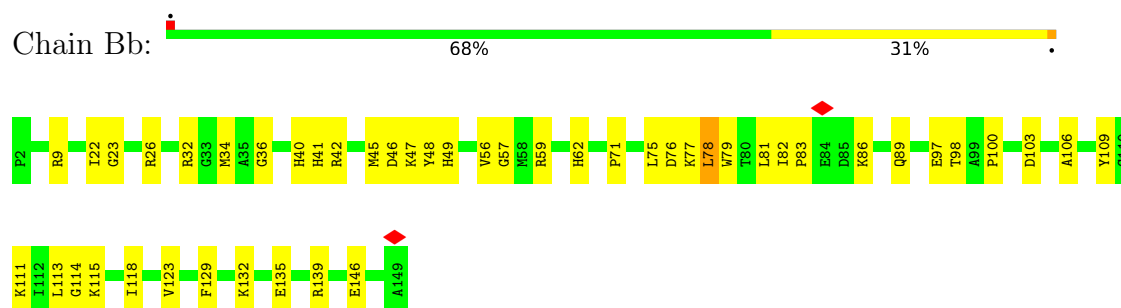
- Molecule 30: 60S ribosomal protein L26-A



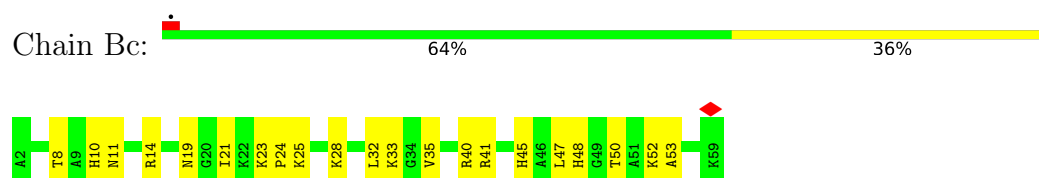
- Molecule 31: 60S ribosomal protein L27-A



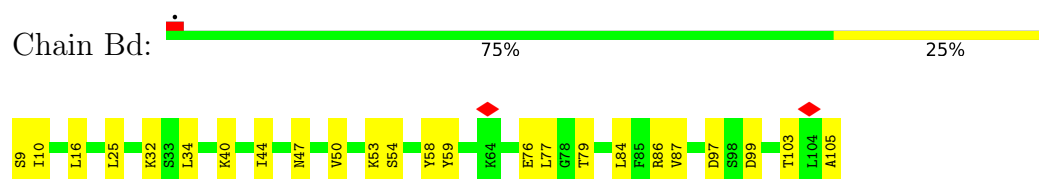
- Molecule 32: 60S ribosomal protein L28



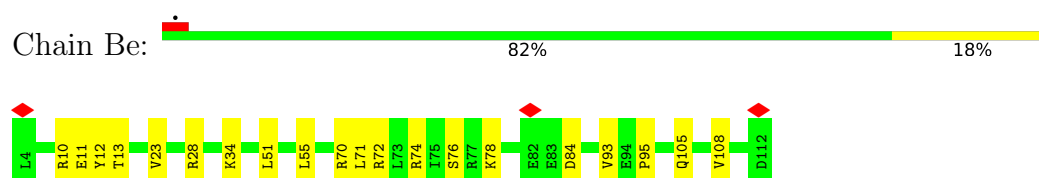
- Molecule 33: 60S ribosomal protein L29



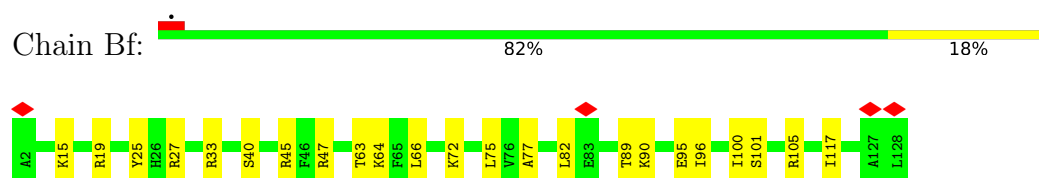
- Molecule 34: 60S ribosomal protein L30



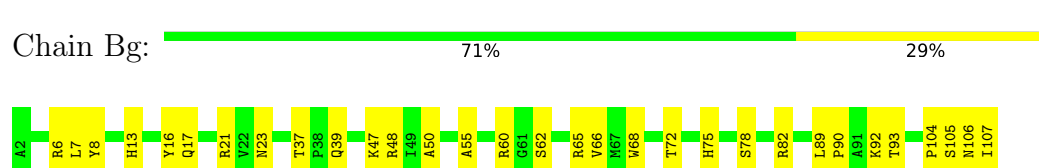
- Molecule 35: 60S ribosomal protein L31-A



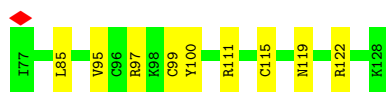
- Molecule 36: 60S ribosomal protein L32



- Molecule 37: 60S ribosomal protein L33-A

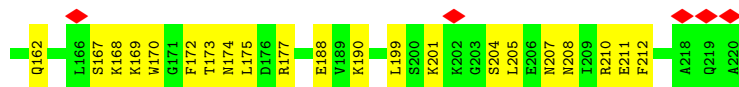


- Molecule 38: 60S ribosomal protein L34-A



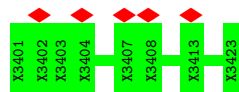
- Molecule 45: 60S ribosomal protein L10

Chain BK: 76% 24%



- Molecule 46: Unknown chain

Chain B: 22% 100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	25072	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 ($e^-/\text{\AA}^2$)	43.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.151	Depositor
Minimum map value	-1.485	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.070	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	585.19995, 585.19995, 585.19995	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.11	0/77733	0.28	1/121186 (0.0%)
2	3	0.09	0/2883	0.26	0/4491
3	4	0.11	0/3746	0.24	0/5832
4	A	0.13	0/1653	0.38	1/2255 (0.0%)
5	2	0.09	0/1808	0.21	0/2816
6	BA	0.11	0/860	0.33	0/1136
7	BB	0.12	0/701	0.37	0/934
8	BC	0.12	0/1948	0.32	0/2617
9	BD	0.11	0/3146	0.32	0/4228
10	BE	0.10	0/2800	0.32	0/3790
11	BF	0.10	0/2425	0.32	1/3271 (0.0%)
12	BG	0.12	0/1260	0.32	0/1694
13	BH	0.12	0/1821	0.32	0/2451
14	BI	0.13	0/1836	0.35	0/2481
15	BJ	0.11	0/1539	0.31	0/2073
16	BL	0.17	0/1374	0.44	1/1842 (0.1%)
17	BM	0.12	0/1568	0.35	0/2106
18	BN	0.10	0/1068	0.33	0/1438
19	BO	0.10	0/1757	0.29	0/2354
20	BP	0.10	0/1585	0.29	0/2128
21	BQ	0.12	0/1443	0.35	0/1944
22	BR	0.09	0/1465	0.30	0/1965
23	BS	0.11	0/1303	0.33	0/1740
24	BT	0.12	0/1481	0.34	0/1990
25	BU	0.11	0/1300	0.34	0/1743
26	BV	0.11	0/812	0.32	0/1099
27	BW	0.16	0/1018	0.36	0/1369
28	BX	0.15	0/565	0.42	0/752
29	BY	0.10	0/979	0.30	0/1321
30	BZ	0.12	0/949	0.33	0/1266
31	Ba	0.13	0/1118	0.35	0/1497
32	Bb	0.15	0/1204	0.44	0/1612

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Bc	0.16	0/473	0.46	0/629
34	Bd	0.14	0/751	0.36	0/1008
35	Be	0.10	0/890	0.30	0/1196
36	Bf	0.10	0/1041	0.30	0/1394
37	Bg	0.10	0/868	0.31	0/1168
38	Bh	0.10	0/890	0.32	0/1189
39	Bi	0.12	0/978	0.31	0/1301
40	Bj	0.12	0/778	0.33	0/1034
41	Bk	0.11	0/696	0.34	0/923
42	Bl	0.14	0/618	0.33	0/826
43	Bm	0.20	0/443	0.34	0/588
44	Bn	0.18	0/423	0.42	0/562
45	BK	0.11	0/1807	0.32	0/2425
All	All	0.11	0/137804	0.30	4/203664 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	213	PRO	CA-N-CD	-8.22	100.49	112.00
16	BL	173	ASP	CB-CA-C	-5.59	110.11	116.54
1	1	2269	U	O4'-C1'-C2'	-5.54	102.06	107.60
11	BF	260	PHE	CB-CA-C	-5.12	109.69	115.79

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	1	69452	0	34903	1524	0
2	3	2579	0	1304	72	0
3	4	3353	0	1695	80	0
4	A	1633	0	1596	48	0
5	2	1619	0	821	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	BA	847	0	918	25	0
7	BB	694	0	738	28	0
8	BC	1914	0	1981	66	0
9	BD	3075	0	3142	98	0
10	BE	2748	0	2859	61	0
11	BF	2375	0	2325	78	0
12	BG	1239	0	1326	31	0
13	BH	1784	0	1862	59	0
14	BI	1804	0	1877	53	0
15	BJ	1518	0	1587	46	0
16	BL	1353	0	1383	45	0
17	BM	1543	0	1608	48	0
18	BN	1053	0	1149	41	0
19	BO	1720	0	1779	58	0
20	BP	1555	0	1659	37	0
21	BQ	1420	0	1437	46	0
22	BR	1441	0	1543	37	0
23	BS	1286	0	1364	28	0
24	BT	1445	0	1487	43	0
25	BU	1276	0	1323	39	0
26	BV	796	0	812	19	0
27	BW	1003	0	1048	39	0
28	BX	553	0	571	16	0
29	BY	964	0	1025	19	0
30	BZ	939	0	1015	19	0
31	Ba	1092	0	1155	29	0
32	Bb	1173	0	1215	41	0
33	Bc	462	0	491	13	0
34	Bd	743	0	797	22	0
35	Be	876	0	912	14	0
36	Bf	1020	0	1090	22	0
37	Bg	850	0	880	24	0
38	Bh	880	0	945	25	0
39	Bi	969	0	1078	28	0
40	Bj	771	0	849	25	0
41	Bk	681	0	687	26	0
42	Bl	612	0	682	19	0
43	Bm	436	0	475	16	0
44	Bn	417	0	459	8	0
45	BK	1770	0	1808	43	0
46	B	115	0	35	0	0
47	2	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	127849	0	91695	2702	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 13.

The worst 5 of 2702 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)
1:1:196:G:N2	1:1:219:A:H61	1.46	1.12
1:1:196:G:H21	1:1:219:A:N6	1.61	0.98
1:1:3232:G:H1	1:1:3255:U:H3	1.10	0.98
1:1:1564:U:H3	1:1:1576:G:H1	1.00	0.97
1:1:1385:C:HO2'	12:BG:2:SER:N	1.61	0.97

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	
4	A	222/224 (99%)	218 (98%)	4 (2%)	0	100	100
6	BA	103/105 (98%)	101 (98%)	2 (2%)	0	100	100
7	BB	89/91 (98%)	87 (98%)	2 (2%)	0	100	100
8	BC	250/252 (99%)	247 (99%)	3 (1%)	0	100	100
9	BD	384/386 (100%)	375 (98%)	6 (2%)	3 (1%)	16	50
10	BE	359/361 (99%)	343 (96%)	14 (4%)	2 (1%)	21	56
11	BF	294/296 (99%)	288 (98%)	4 (1%)	2 (1%)	18	52
12	BG	152/176 (86%)	151 (99%)	1 (1%)	0	100	100
13	BH	220/222 (99%)	213 (97%)	5 (2%)	2 (1%)	14	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	BI	231/233 (99%)	225 (97%)	4 (2%)	2 (1%)	14	47
15	BJ	189/191 (99%)	186 (98%)	3 (2%)	0	100	100
16	BL	167/169 (99%)	154 (92%)	12 (7%)	1 (1%)	21	56
17	BM	191/193 (99%)	179 (94%)	9 (5%)	3 (2%)	7	36
18	BN	134/136 (98%)	130 (97%)	3 (2%)	1 (1%)	18	52
19	BO	201/203 (99%)	198 (98%)	3 (2%)	0	100	100
20	BP	195/197 (99%)	191 (98%)	4 (2%)	0	100	100
21	BQ	181/183 (99%)	175 (97%)	6 (3%)	0	100	100
22	BR	183/185 (99%)	178 (97%)	5 (3%)	0	100	100
23	BS	158/160 (99%)	155 (98%)	3 (2%)	0	100	100
24	BT	170/172 (99%)	163 (96%)	7 (4%)	0	100	100
25	BU	157/159 (99%)	150 (96%)	6 (4%)	1 (1%)	21	56
26	BV	98/100 (98%)	92 (94%)	5 (5%)	1 (1%)	12	45
27	BW	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
28	BX	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
29	BY	119/121 (98%)	118 (99%)	1 (1%)	0	100	100
30	BZ	116/127 (91%)	113 (97%)	3 (3%)	0	100	100
31	Ba	133/135 (98%)	128 (96%)	4 (3%)	1 (1%)	16	50
32	Bb	146/148 (99%)	140 (96%)	5 (3%)	1 (1%)	18	52
33	Bc	56/58 (97%)	55 (98%)	0	1 (2%)	6	34
34	Bd	95/97 (98%)	95 (100%)	0	0	100	100
35	Be	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
36	Bf	125/127 (98%)	122 (98%)	3 (2%)	0	100	100
37	Bg	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
38	Bh	110/112 (98%)	108 (98%)	1 (1%)	1 (1%)	14	47
39	Bi	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
40	Bj	97/99 (98%)	91 (94%)	5 (5%)	1 (1%)	12	45
41	Bk	85/87 (98%)	85 (100%)	0	0	100	100
42	Bl	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
43	Bm	48/50 (96%)	47 (98%)	0	1 (2%)	5	31
44	Bn	50/52 (96%)	50 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	BK	218/220 (99%)	209 (96%)	9 (4%)	0	100	100
All	All	6330/6443 (98%)	6148 (97%)	158 (2%)	24 (0%)	31	62

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	BF	259	LYS
17	BM	28	GLN
17	BM	166	ALA
31	Ba	102	GLU
38	Bh	82	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	177/192 (92%)	177 (100%)	0	100	100
6	BA	90/90 (100%)	90 (100%)	0	100	100
7	BB	71/71 (100%)	71 (100%)	0	100	100
8	BC	193/194 (100%)	193 (100%)	0	100	100
9	BD	320/322 (99%)	320 (100%)	0	100	100
10	BE	288/288 (100%)	288 (100%)	0	100	100
11	BF	244/244 (100%)	244 (100%)	0	100	100
12	BG	134/153 (88%)	134 (100%)	0	100	100
13	BH	186/186 (100%)	186 (100%)	0	100	100
14	BI	187/191 (98%)	187 (100%)	0	100	100
15	BJ	171/171 (100%)	171 (100%)	0	100	100
16	BL	147/147 (100%)	147 (100%)	0	100	100
17	BM	154/154 (100%)	154 (100%)	0	100	100
18	BN	107/107 (100%)	107 (100%)	0	100	100
19	BO	175/175 (100%)	175 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	BP	160/160 (100%)	160 (100%)	0	100	100
21	BQ	140/145 (97%)	140 (100%)	0	100	100
22	BR	150/150 (100%)	150 (100%)	0	100	100
23	BS	131/131 (100%)	131 (100%)	0	100	100
24	BT	156/156 (100%)	156 (100%)	0	100	100
25	BU	136/136 (100%)	136 (100%)	0	100	100
26	BV	87/87 (100%)	87 (100%)	0	100	100
27	BW	104/104 (100%)	104 (100%)	0	100	100
28	BX	56/60 (93%)	56 (100%)	0	100	100
29	BY	104/105 (99%)	104 (100%)	0	100	100
30	BZ	103/110 (94%)	103 (100%)	0	100	100
31	Ba	115/115 (100%)	115 (100%)	0	100	100
32	Bb	118/118 (100%)	118 (100%)	0	100	100
33	Bc	46/46 (100%)	46 (100%)	0	100	100
34	Bd	81/81 (100%)	81 (100%)	0	100	100
35	Be	92/96 (96%)	92 (100%)	0	100	100
36	Bf	109/109 (100%)	109 (100%)	0	100	100
37	Bg	90/90 (100%)	90 (100%)	0	100	100
38	Bh	95/95 (100%)	94 (99%)	1 (1%)	65	79
39	Bi	104/104 (100%)	104 (100%)	0	100	100
40	Bj	81/81 (100%)	81 (100%)	0	100	100
41	Bk	70/70 (100%)	70 (100%)	0	100	100
42	Bl	68/68 (100%)	68 (100%)	0	100	100
43	Bm	45/45 (100%)	45 (100%)	0	100	100
44	Bn	47/47 (100%)	47 (100%)	0	100	100
45	BK	184/186 (99%)	184 (100%)	0	100	100
All	All	5316/5380 (99%)	5315 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	Bh	69	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
17	BM	12	ASN
37	Bg	88	ASN
20	BP	65	ASN
37	Bg	77	ASN
43	Bm	4	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3243/3396 (95%)	755 (23%)	79 (2%)
2	3	120/121 (99%)	27 (22%)	3 (2%)
3	4	157/158 (99%)	34 (21%)	3 (1%)
5	2	75/76 (98%)	16 (21%)	0
All	All	3595/3751 (95%)	832 (23%)	85 (2%)

5 of 832 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	12	A
1	1	13	A
1	1	15	C
1	1	22	G
1	1	26	A

5 of 85 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2538	U
1	1	3216	G
1	1	2549	G
1	1	3022	G
1	1	3246	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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.

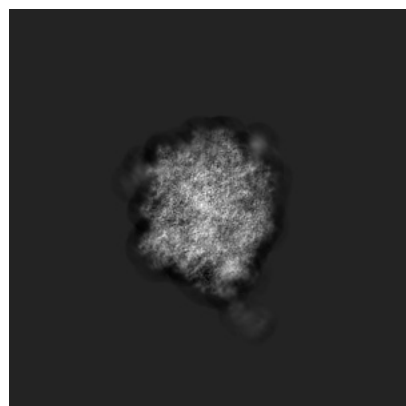
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14926. These allow visual inspection of the internal detail of the map and identification of artifacts.

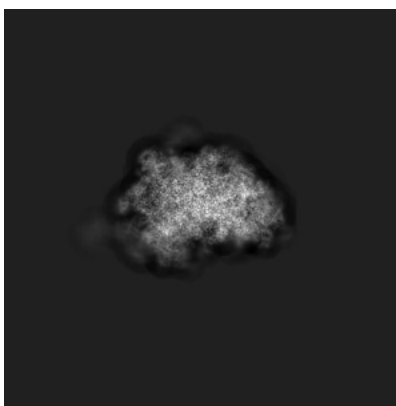
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

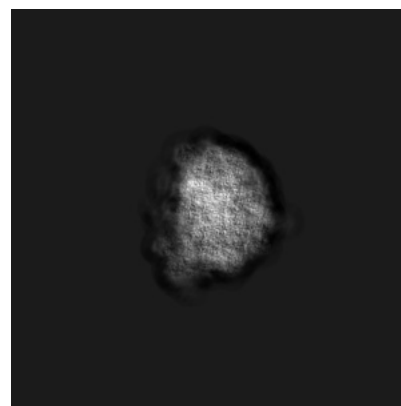
6.1.1 Primary map



X

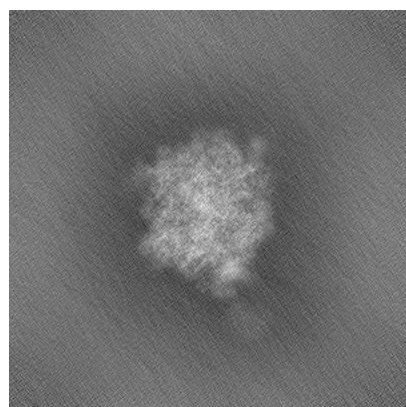


Y

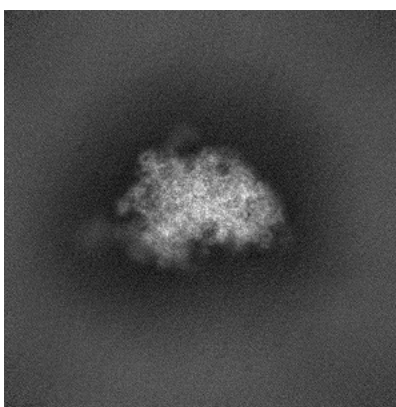


Z

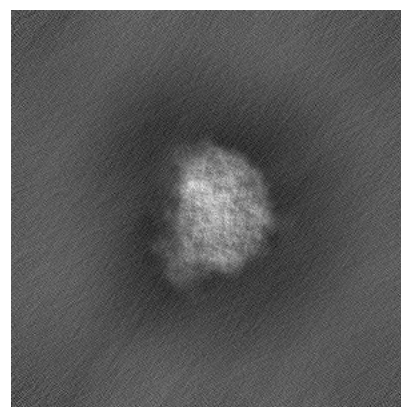
6.1.2 Raw map



X



Y

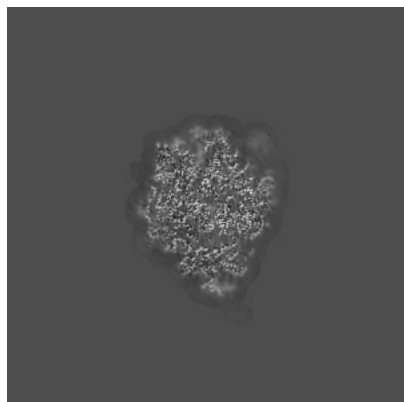


Z

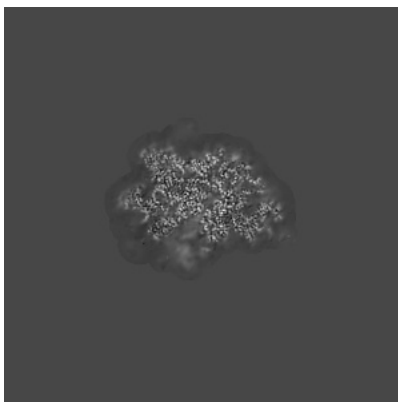
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

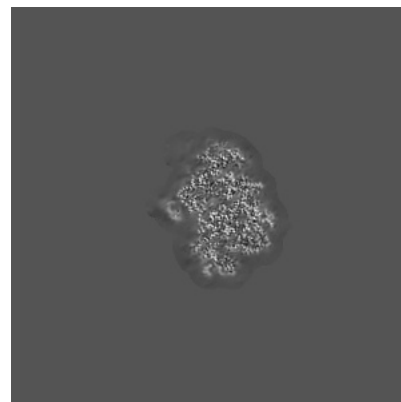
6.2.1 Primary map



X Index: 280

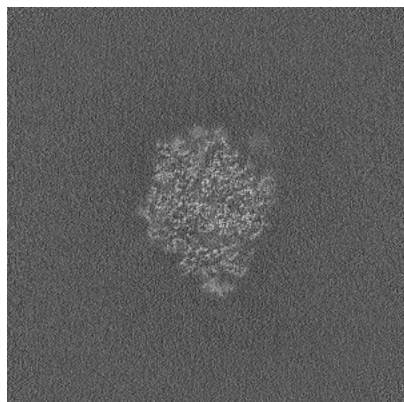


Y Index: 280

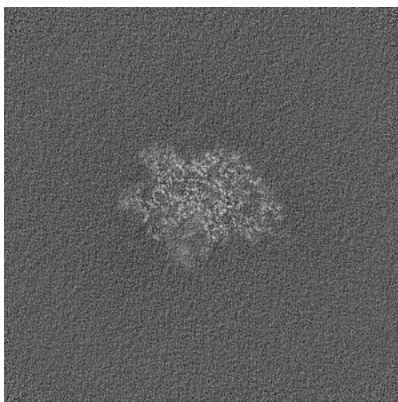


Z Index: 280

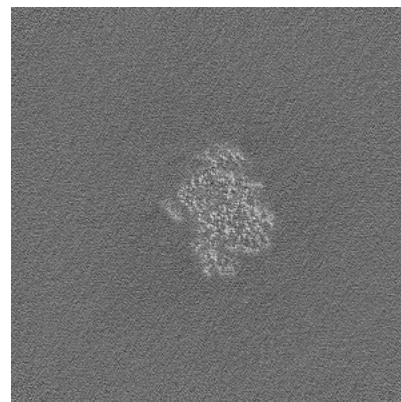
6.2.2 Raw map



X Index: 280



Y Index: 280

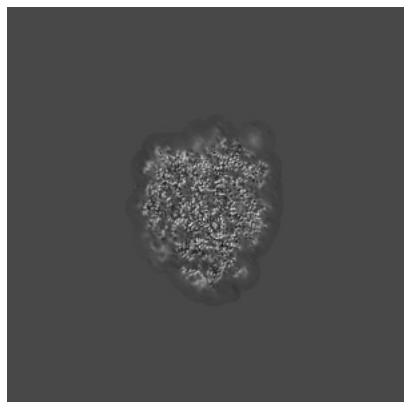


Z Index: 280

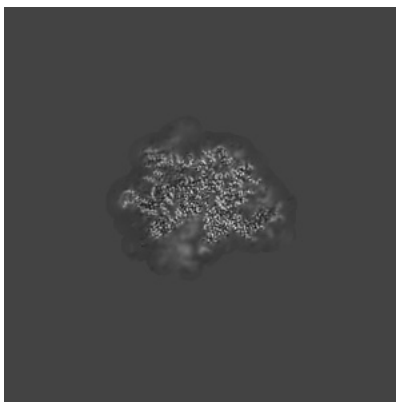
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

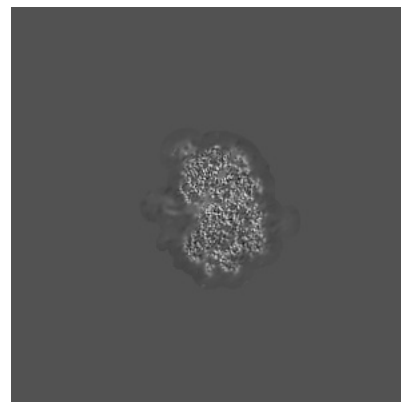
6.3.1 Primary map



X Index: 300

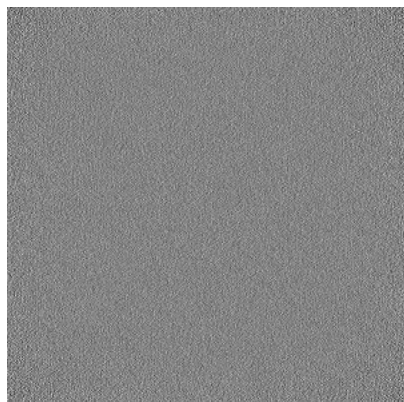


Y Index: 275

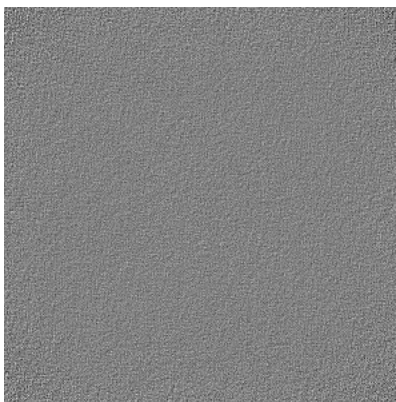


Z Index: 271

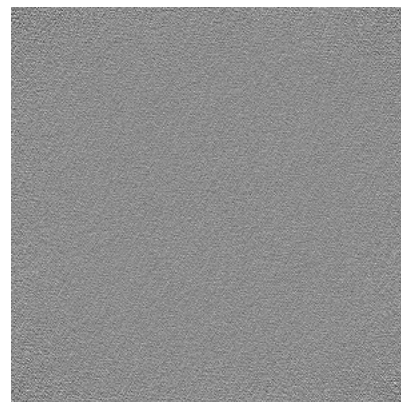
6.3.2 Raw map



X Index: 0



Y Index: 0

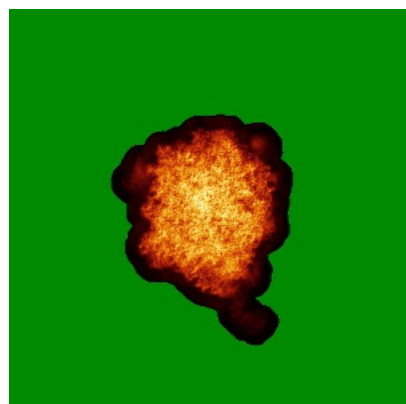


Z Index: 0

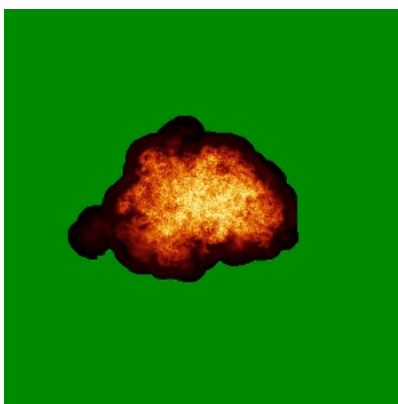
The images above show the largest variance slices of the map in three orthogonal directions.

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

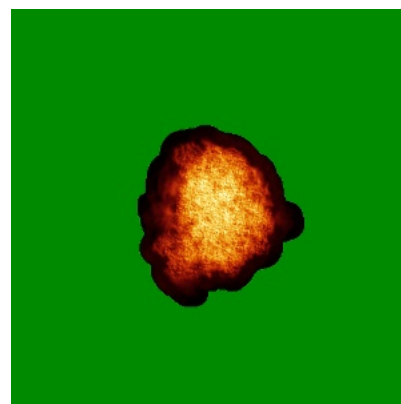
6.4.1 Primary map



X

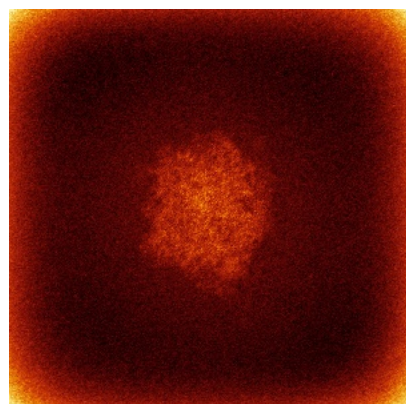


Y

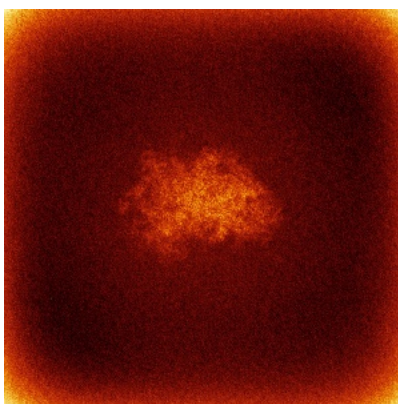


Z

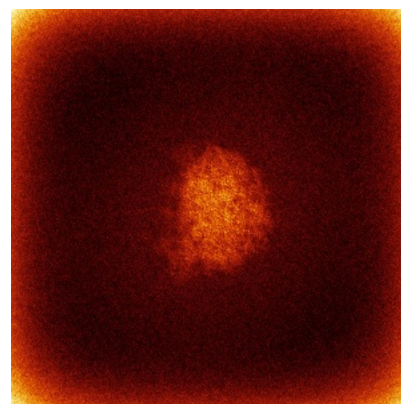
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



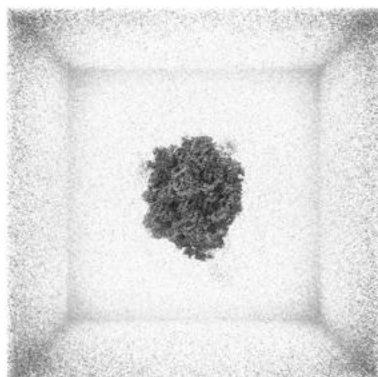
Y



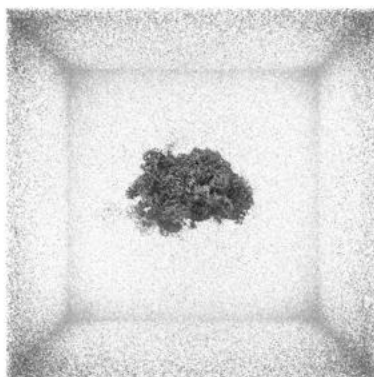
Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

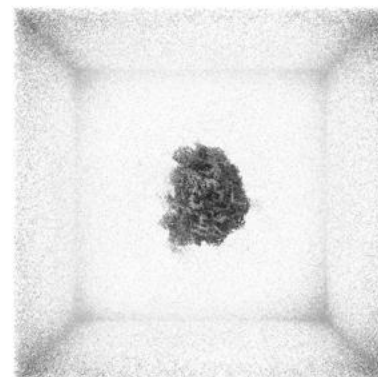
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

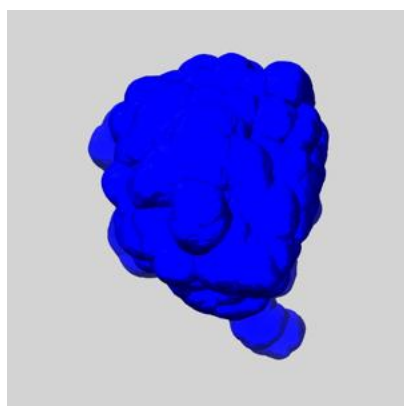
6.6 Mask visualisation [i](#)

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

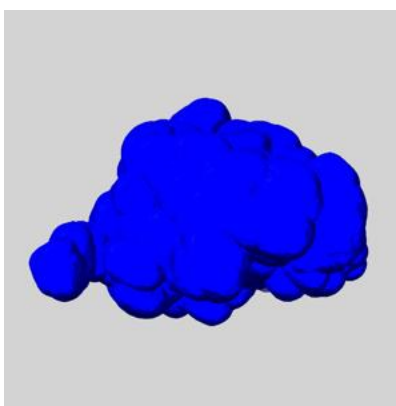
A mask typically either:

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

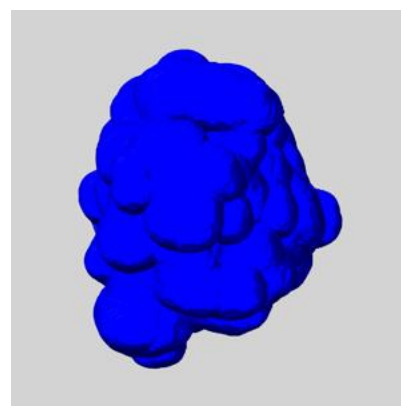
6.6.1 emd_14926_msk_1.map [i](#)



X



Y

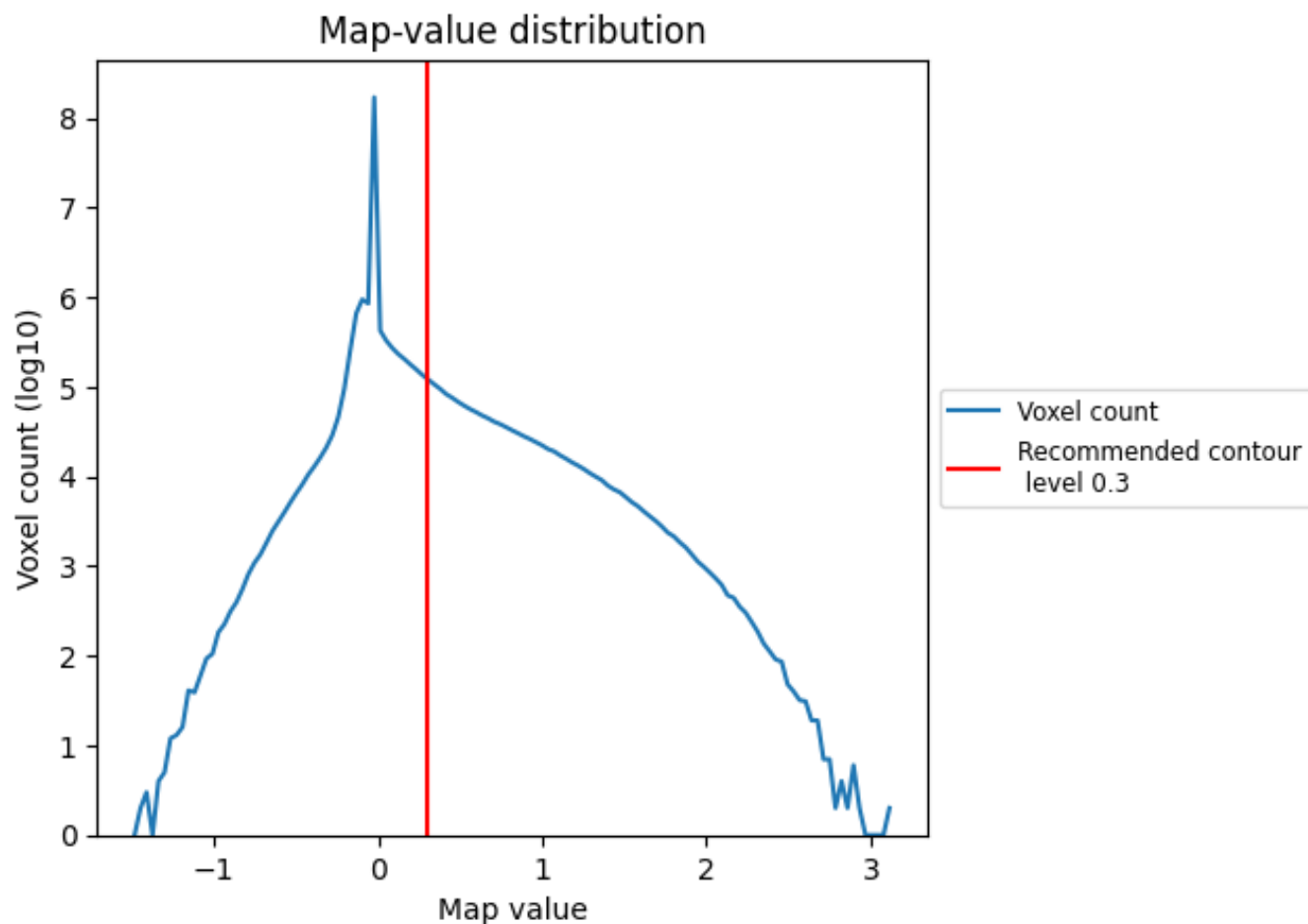


Z

7 Map analysis [i](#)

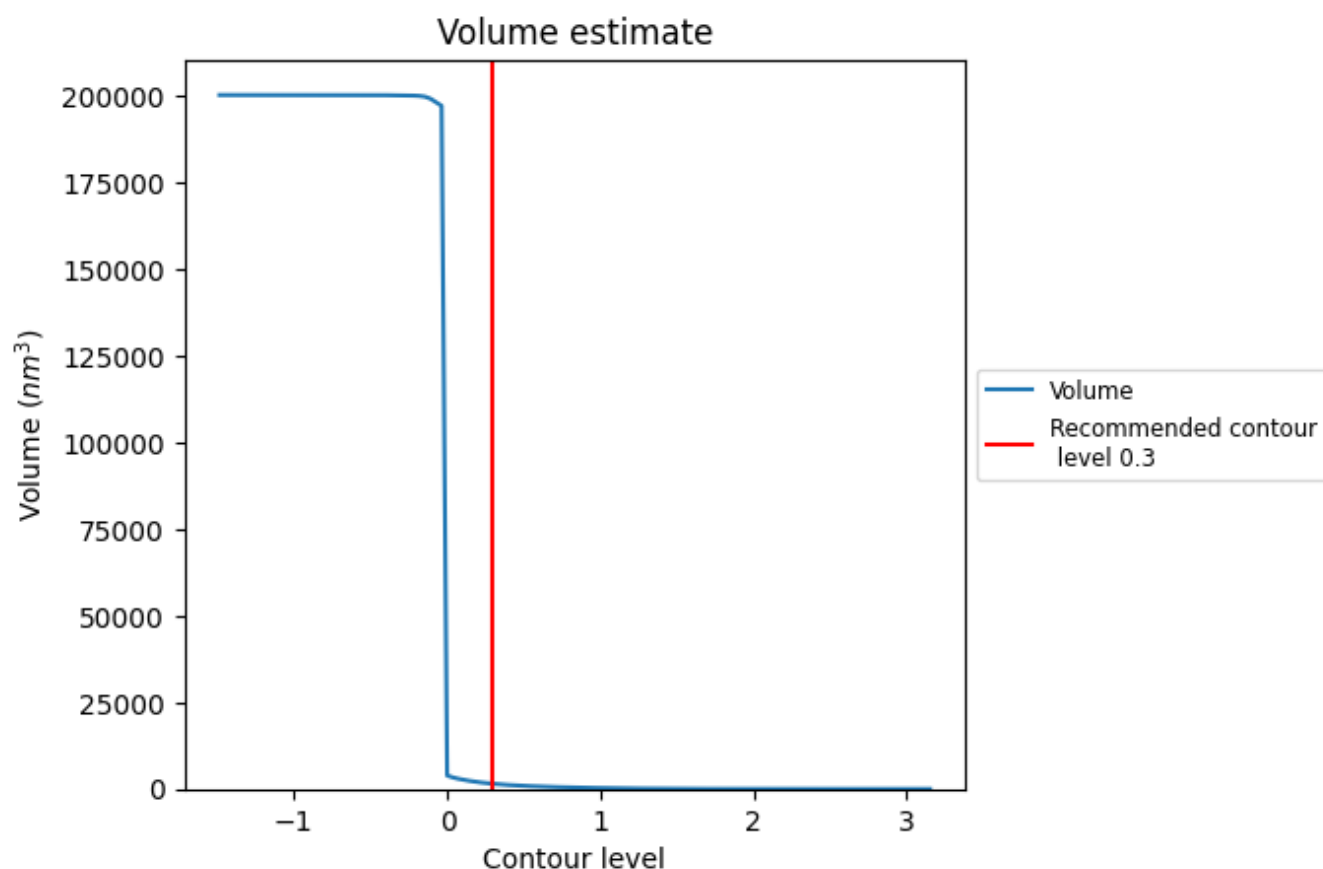
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

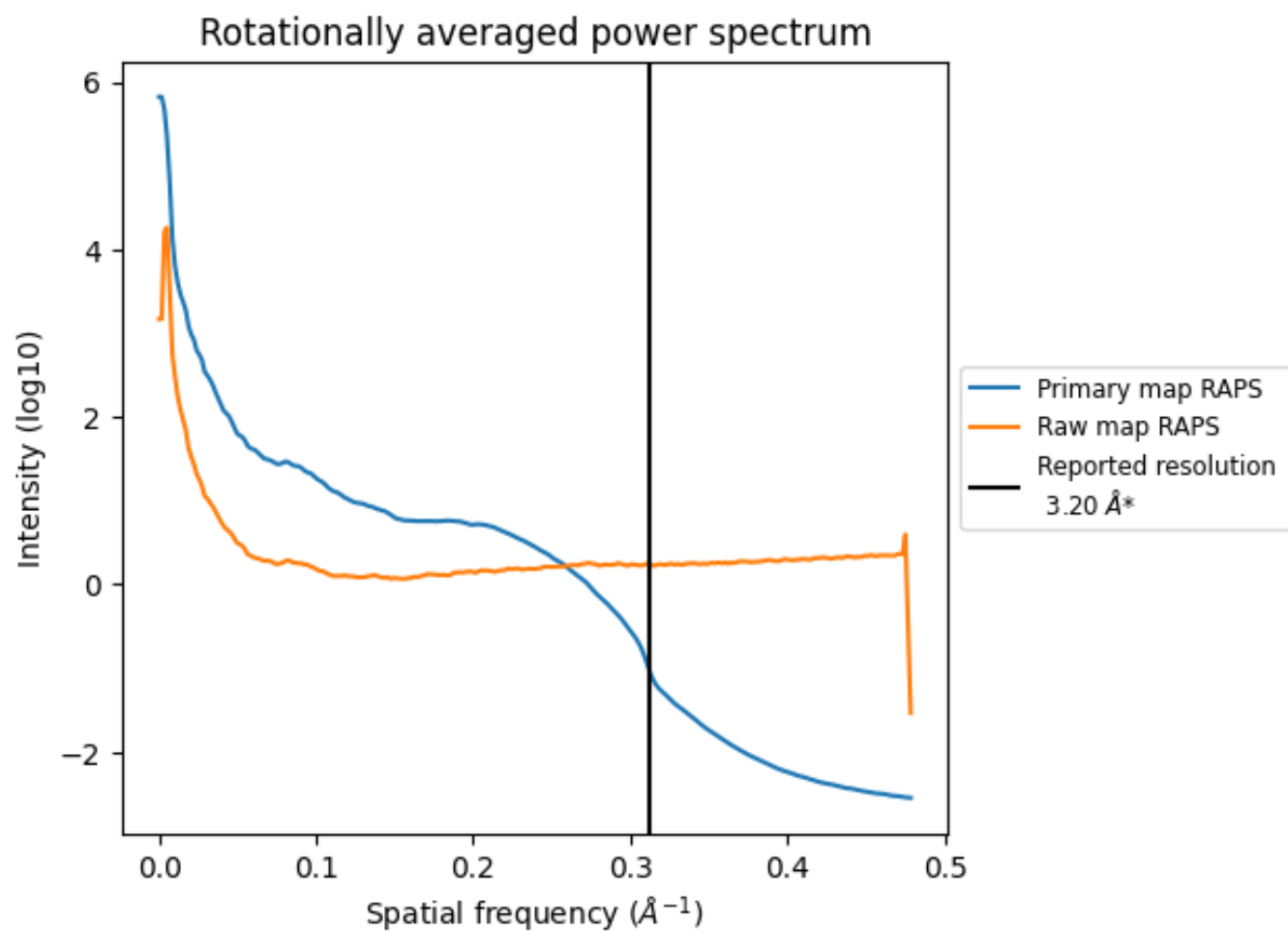
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1499 nm³; this corresponds to an approximate mass of 1354 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 ⓘ

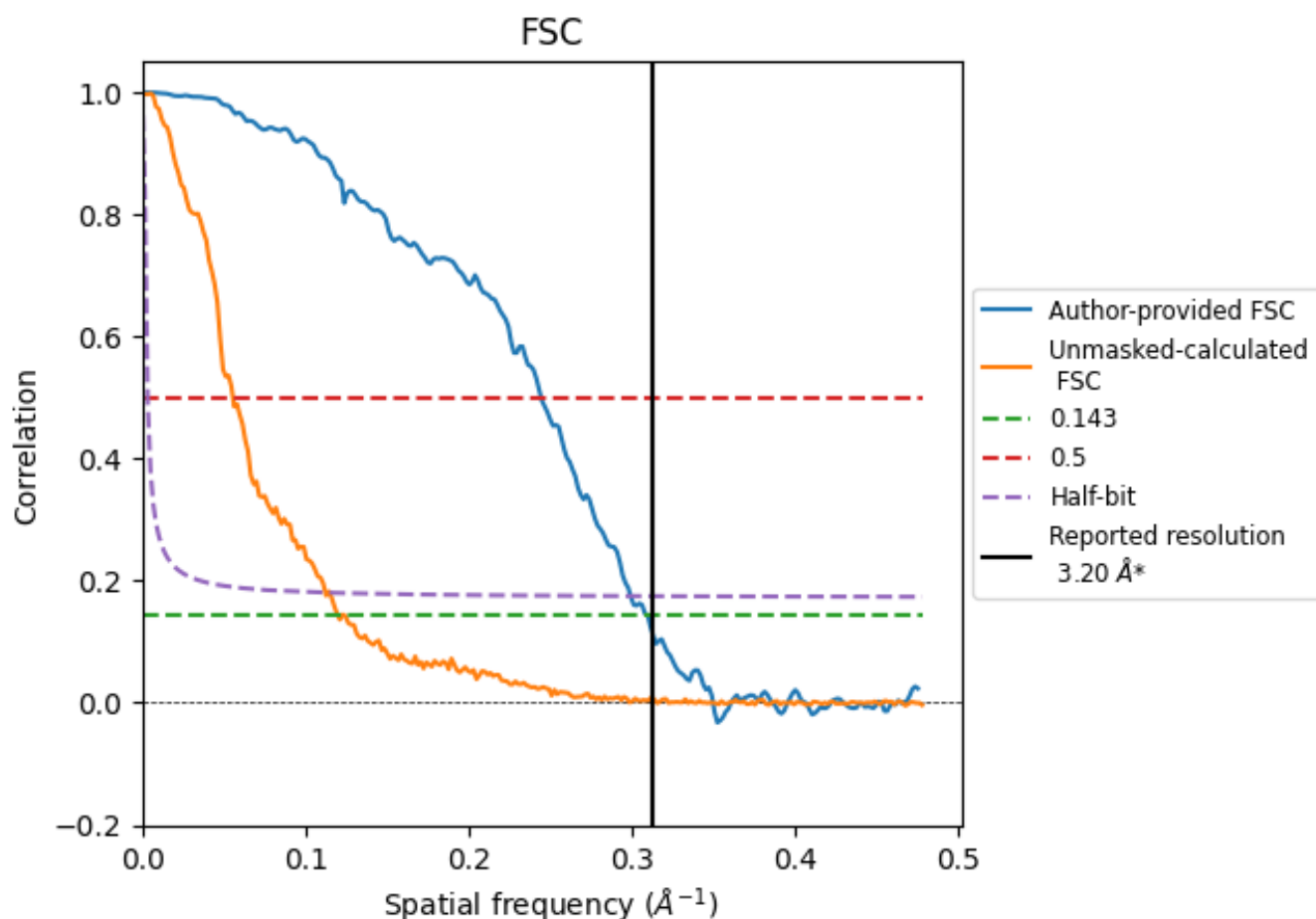


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.312 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

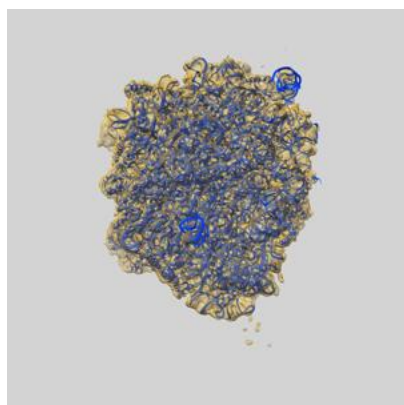
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.22	4.08	3.34
Unmasked-calculated*	8.33	17.99	8.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.33 differs from the reported value 3.2 by more than 10 %

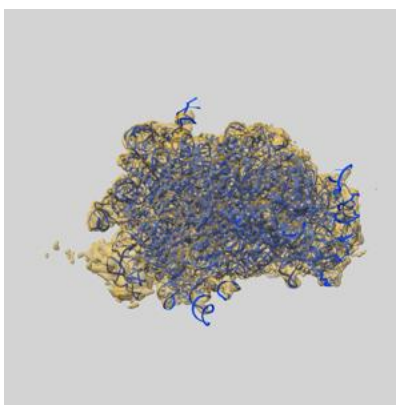
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14926 and PDB model 7ZS5. Per-residue inclusion information can be found in section 3 on page 12.

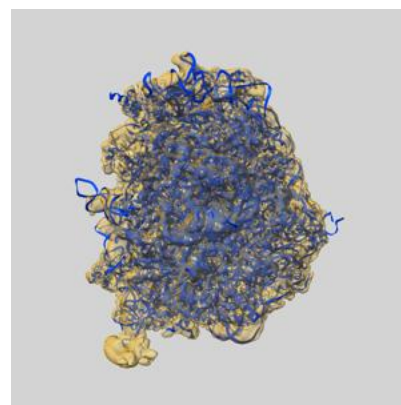
9.1 Map-model overlay [i](#)



X



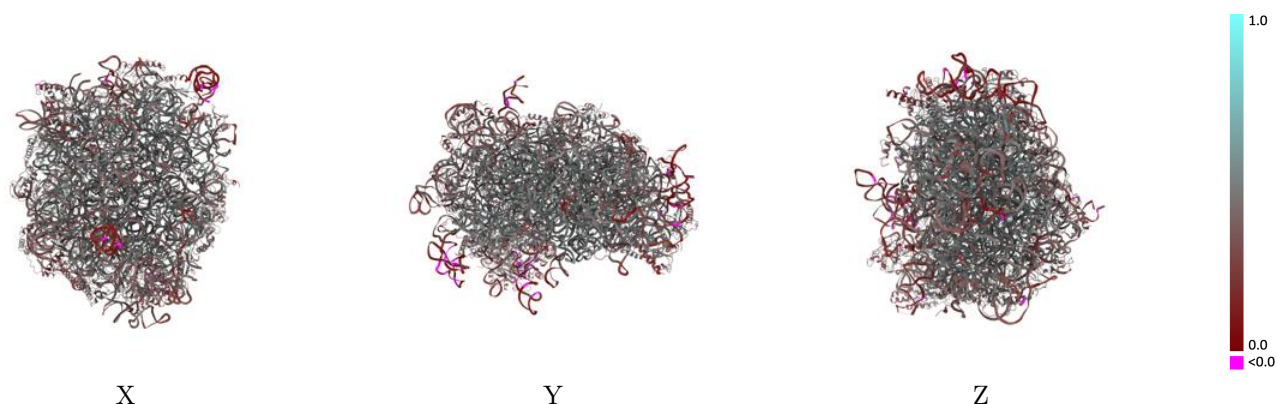
Y



Z

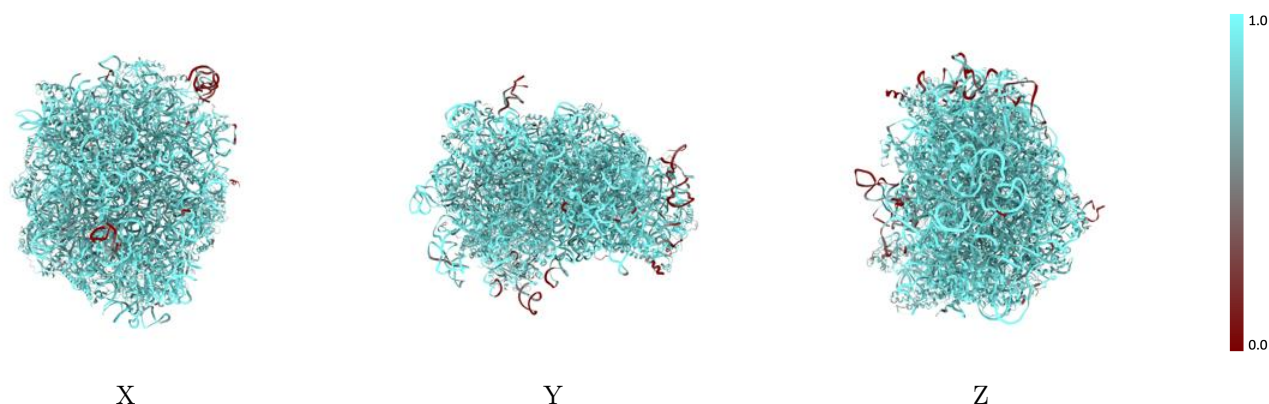
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



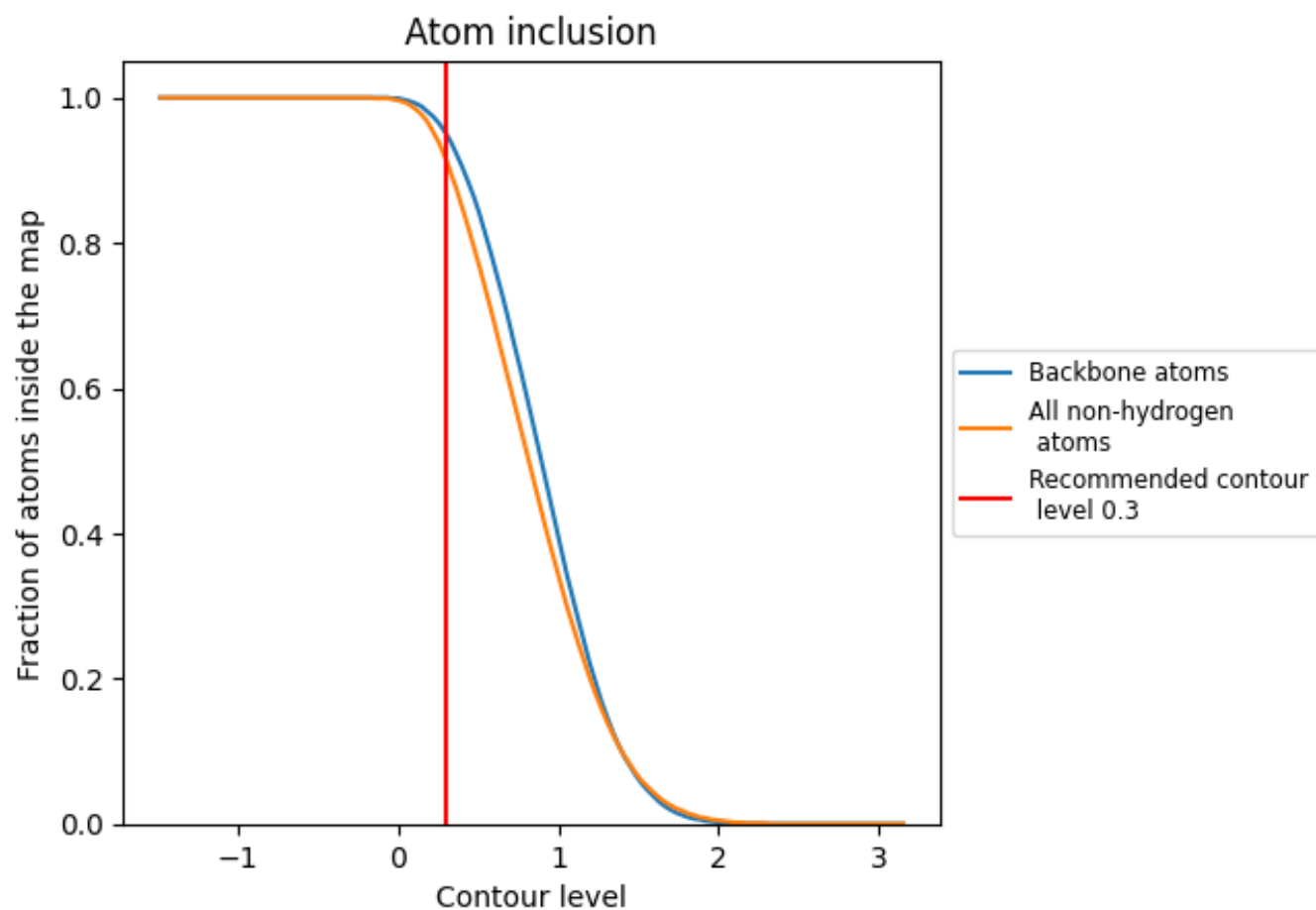
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 91% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9140	 0.4210
1	 0.9390	 0.4160
2	 0.5330	 0.1110
3	 0.9620	 0.4120
4	 0.9780	 0.4490
A	 0.8320	 0.3510
B	 0.7560	 0.3320
BA	 0.8560	 0.4560
BB	 0.9190	 0.4630
BC	 0.9110	 0.4740
BD	 0.9180	 0.4570
BE	 0.9190	 0.4580
BF	 0.8490	 0.3730
BG	 0.8310	 0.3830
BH	 0.8890	 0.4470
BI	 0.8770	 0.3950
BJ	 0.8560	 0.4280
BK	 0.8610	 0.4220
BL	 0.8000	 0.3220
BM	 0.8720	 0.4410
BN	 0.8470	 0.3940
BO	 0.9440	 0.4970
BP	 0.9230	 0.4640
BQ	 0.9170	 0.4450
BR	 0.8930	 0.4620
BS	 0.8820	 0.4380
BT	 0.8730	 0.4500
BU	 0.8740	 0.4400
BV	 0.8820	 0.4000
BW	 0.9140	 0.4720
BX	 0.8550	 0.4210
BY	 0.9400	 0.4720
BZ	 0.8700	 0.4380
Ba	 0.8710	 0.4240
Bb	 0.9110	 0.4600



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Chain	Atom inclusion	Q-score
Bc	 0.8940	 0.4210
Bd	 0.8540	 0.4150
Be	 0.8810	 0.4630
Bf	 0.8880	 0.4570
Bg	 0.9030	 0.4710
Bh	 0.8720	 0.4410
Bi	 0.9120	 0.4320
Bj	 0.8730	 0.4210
Bk	 0.9450	 0.5100
Bl	 0.7910	 0.4030
Bm	 0.9300	 0.4780
Bn	 0.9130	 0.4600