



## wwPDB EM Validation Summary Report ⓘ

Jan 29, 2025 – 10:33 pm GMT

PDB ID : 7ZS5  
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 : 1G62, 6SNT, 6HD7

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

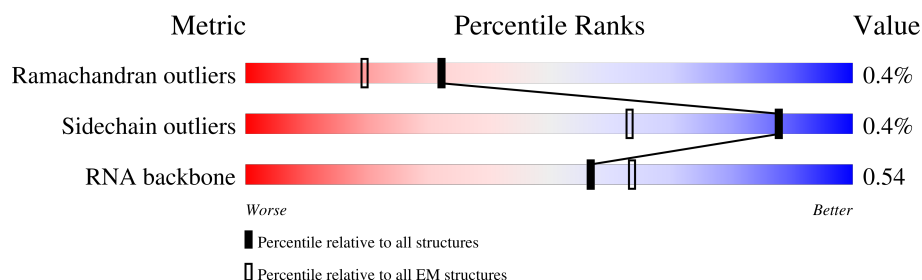
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*




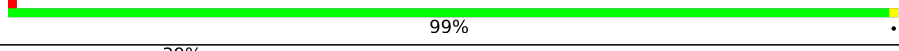

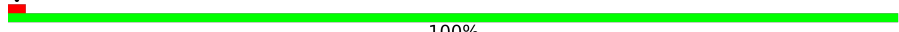
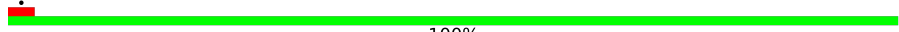

The reported resolution of this entry is 3.20 Å.

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.



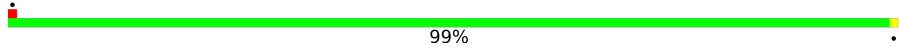
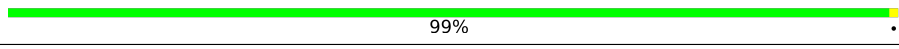
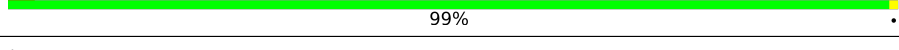

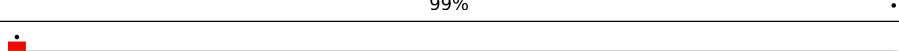
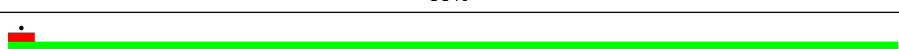
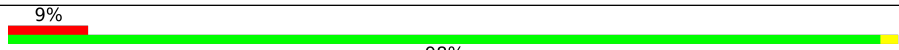

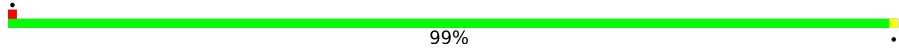
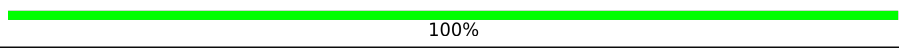
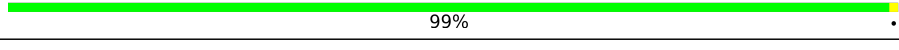
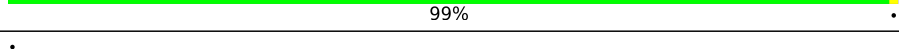
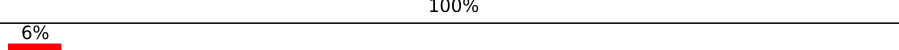
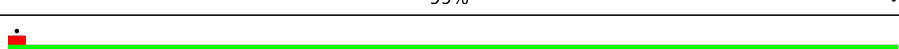


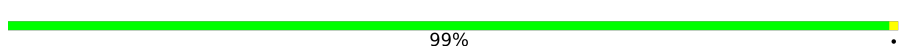
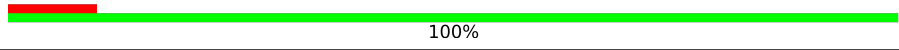
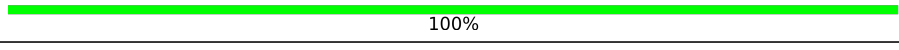
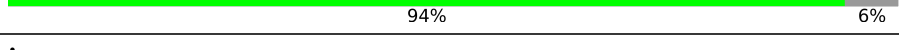
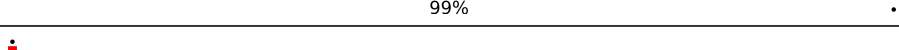
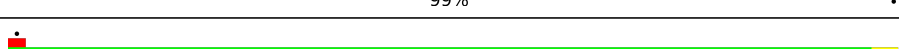



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	
4	A	224	
5	2	76	
6	BA	105	
7	BB	91	
8	BC	252	

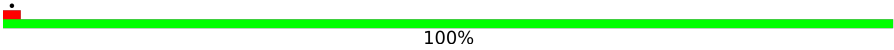
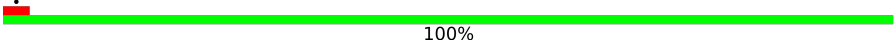
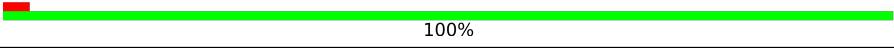
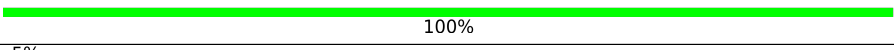
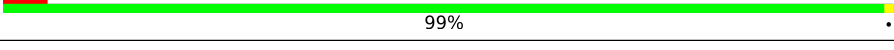
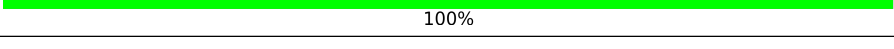
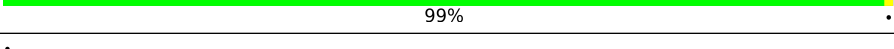
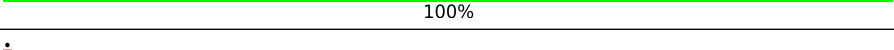
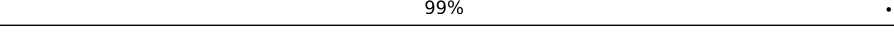
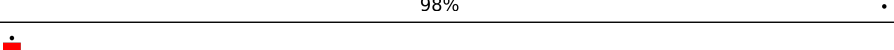
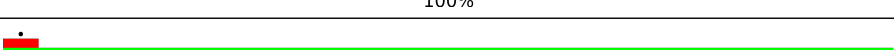
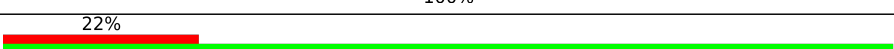
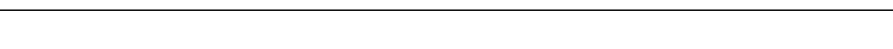
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Mol	Chain	Length	Quality of chain
9	BD	386	 99%
10	BE	361	 99%
11	BF	296	 99%
12	BG	176	 89% 11%
13	BH	222	 99%
14	BI	233	 99%
15	BJ	191	 100%
16	BL	169	 9% 98%
17	BM	193	 98%
18	BN	136	 99%
19	BO	203	 100%
20	BP	197	 99%
21	BQ	183	 99%
22	BR	185	 100%
23	BS	160	 6% 99%
24	BT	172	 100%
25	BU	159	 99%
26	BV	100	 99%
27	BW	136	 99%
28	BX	69	 10% 100%
29	BY	121	 100%
30	BZ	127	 94% 6%
31	Ba	135	 99%
32	Bb	148	 99%
33	Bc	58	 97%

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Mol	Chain	Length	Quality of chain
34	Bd	97	 100%
35	Be	109	 100%
36	Bf	127	 100%
37	Bg	106	 100%
38	Bh	112	 5% 99%
39	Bi	119	 100%
40	Bj	99	 99%
41	Bk	87	 100%
42	Bl	77	 99%
43	Bm	50	 98%
44	Bn	52	 100%
45	BK	220	 100%
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		

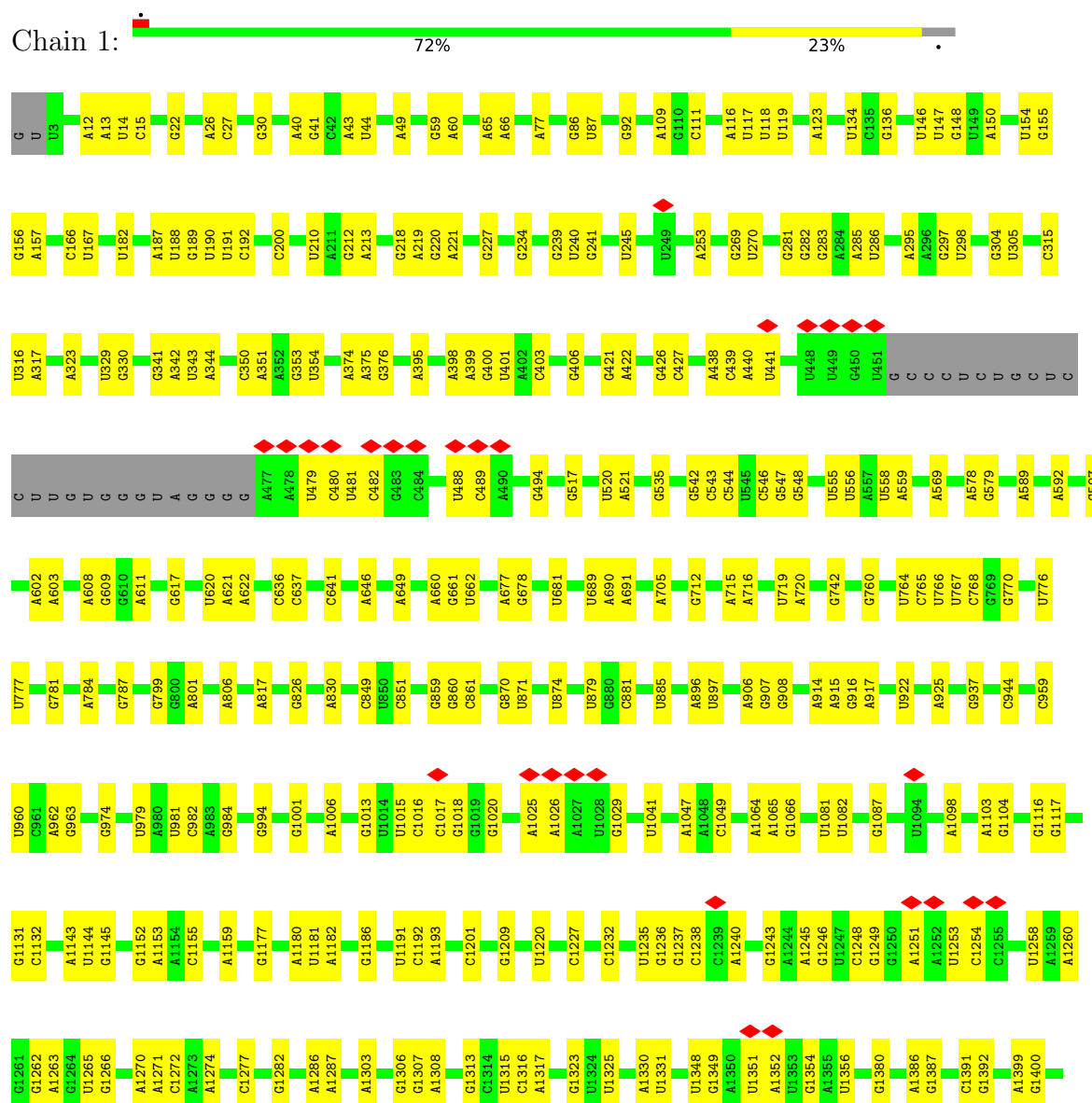
- Molecule 47 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

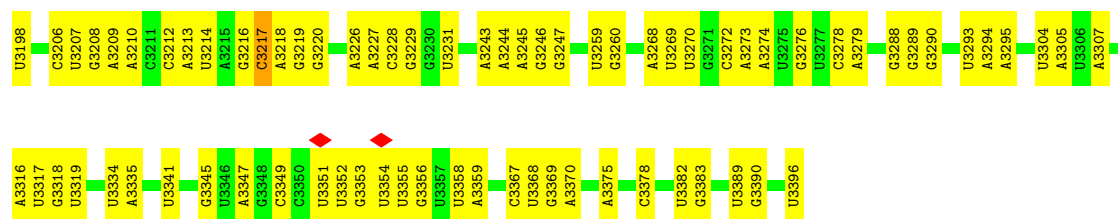
### 3 Residue-property plots

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

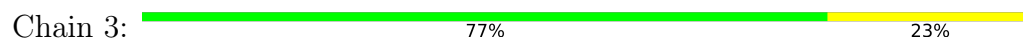
#### • Molecule 1: 25S ribosomal RNA



A3048	A3049	U3056	U3057	U3058	G3059	U3078	U3079	G3080	A3086	C3092	A3113	C3117	U3121	A3122	A3130	A3131	A3141	A3142	C3143	G3144	U3151	U3152	C3154	U3155	U3156	U3157	G3158	A3170	U3171	A3172	G3173	A3174	U3175	G3176	U3179	A3180	C3181	G3182	U3185	A3186	A3187	U3189	U3196	U3197																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
U2846	A2847	C2867	G2871	U2872	U2873	G2874	U2888	C2889	G2898	C2899	A2911	G2912	U2923	U2935	A2936	G2937	G2938	A2941	C2942	C3143	G2947	U2954	U2955	C2956	G2957	U2958	U2959	G2960	A2961	C2962	G2963	G2964	G2965	G2966	G2967	G2968	G2969	G2970	G2971	G2972	G2973	G2974	G2975	G2976	G2977	G2978	G2979	G2980	A2801	A2802	A2803	C2810	G2814	G2815	G2816	G2817	G2818	U2842	U2843	C2844	A2845																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
U2544	A2547	C2548	U2549	U2550	U2551	C2552	G2555	U2558	U2559	C2560	C2568	U2571	C2572	C2582	G2585	A2593	C2600	G2606	G2607	G2608	G2609	G2610	G2611	G2612	G2613	G2614	G2615	G2616	G2617	G2618	G2619	G2620	G2621	G2625	A2626	A2635	A2636	A2637	C2638	U2652	C2653	C2654	U2655	A2656	A2657	C2666	G2672	A2673	A2674	A2678																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
U2336	U2340	C2347	C2374	C2375	C2376	C2378	A2386	A2387	U2388	A2397	A2402	A2403	A2404	U2411	G2418	A2419	U2434	G2435	U2436	G2437	A2438	A2439	G2440	G2441	G2442	G2443	G2444	G2445	U2446	G2447	G2448	A2449	G2452	U2453	U2454	U2455	U2456	U2457	U2458	U2459	U2460	U2461	U2462	U2463	U2464	U2465	U2466	U2467	U2468	U2469	U2470	U2471	U2472	U2473	U2474	U2475	U2476	U2477	U2478	U2479	U2480	U2481	U2482	U2483	U2484	U2485	U2486	U2487	U2488	U2489	U2490	U2491	U2492	U2493	U2494	U2495	U2496	U2497	U2498	U2499	U2500	U2501	U2502	U2503	U2504	U2505	U2506	U2507	U2508	U2509	U2510	U2511	U2512	U2513	U2514	U2515	U2516	U2517	U2518	U2519	U2520	U2521	U2522	U2523	U2524	U2525	U2526	U2527	U2528	U2529	U2530	U2531	U2532	U2533	U2534	U2535	U2536	U2537	U2538	U2539	U2540	U2541	U2542	U2543	U2544	U2545	U2546	U2547	U2548	U2549	U2550	U2551	U2552	U2553	U2554	U2555	U2556	U2557	U2558	U2559	U2560	U2561	U2562	U2563	U2564	U2565	U2566	U2567	U2568	U2569	U2570	U2571	U2572	U2573	U2574	U2575	U2576	U2577	U2578	U2579	U2580	U2581	U2582	U2583	U2584	U2585	U2586	U2587	U2588	U2589	U2590	U2591	U2592	U2593	U2594	U2595	U2596	U2597	U2598	U2599	U2600	U2601	U2602	U2603	U2604	U2605	U2606	U2607	U2608	U2609	U2610	U2611	U2612	U2613	U2614	U2615	U2616	U2617	U2618	U2619	U2620	U2621	U2622	U2623	U2624	U2625	U2626	U2627	U2628	U2629	U2630	U2631	U2632	U2633	U2634	U2635	U2636	U2637	U2638	U2639	U2640	U2641	U2642	U2643	U2644	U2645	U2646	U2647	U2648	U2649	U2650	U2651	U2652	U2653	U2654	U2655	U2656	U2657	U2658	U2659	U2660	U2661	U2662	U2663	U2664	U2665	U2666	U2667	U2668	U2669	U2670	U2671	U2672	U2673	U2674	U2675	U2676	U2677	U2678	U2679	U2680	U2681	U2682	U2683	U2684	U2685	U2686	U2687	U2688	U2689	U2690	U2691	U2692	U2693	U2694	U2695	U2696	U2697	U2698	U2699	U2700	U2701	U2702	U2703	U2704	U2705	U2706	U2707	U2708	U2709	U2710	U2711	U2712	U2713	U2714	U2715	U2716	U2717	U2718	U2719	U2720	U2721	U2722	U2723	U2724	U2725	U2726	U2727	U2728	U2729	U2730	U2731	U2732	U2733	U2734	U2735	U2736	U2737	U2738	U2739	U2740	U2741	U2742	U2743	U2744	U2745	U2746	U2747	U2748	U2749	U2750	U2751	U2752	U2753	U2754	U2755	U2756	U2757	U2758	U2759	U2760	U2761	U2762	U2763	U2764	U2765	U2766	U2767	U2768	U2769	U2770	U2771	U2772	U2773	U2774	U2775	U2776	U2777	U2778	U2779	U2780	U2781	U2782	U2783	U2784	U2785	U2786	U2787	U2788	U2789	U2790	U2791	U2792	U2793	U2794	U2795	U2796	U2797	U2798	U2799	U2800	U2801	U2802	U2803	U2804	U2805	U2806	U2807	U2808	U2809	U2810	U2811	U2812	U2813	U2814	U2815	U2816	U2817	U2818	U2819	U2820	U2821	U2822	U2823	U2824	U2825	U2826	U2827	U2828	U2829	U2830	U2831	U2832	U2833	U2834	U2835	U2836	U2837	U2838	U2839	U2840	U2841	U2842	U2843	U2844	U2845	U2846	U2847	U2848	U2849	U2850	U2851	U2852	U2853	U2854	U2855	U2856	U2857	U2858	U2859	U2860	U2861	U2862	U2863	U2864	U2865	U2866	U2867	U2868	U2869	U2870	U2871	U2872	U2873	U2874	U2875	U2876	U2877	U2878	U2879	U2880	U2881	U2882	U2883	U2884	U2885	U2886	U2887	U2888	U2889	U2890	U2891	U2892	U2893	U2894	U2895	U2896	U2897	U2898	U2899	U2900	U2901	U2902	U2903	U2904	U2905	U2906	U2907	U2908	U2909	U2910	U2911	U2912	U2913	U2914	U2915	U2916	U2917	U2918	U2919	U2920	U2921	U2922	U2923	U2924	U2925	U2926	U2927	U2928	U2929	U2930	U2931	U2932	U2933	U2934	U2935	U2936	U2937	U2938	U2939	U2940	U2941	U2942	U2943	U2944	U2945	U2946	U2947	U2948	U2949	U2950	U2951	U2952	U2953	U2954	U2955	U2956	U2957	U2958	U2959	U2960	U2961	U2962	U2963	U2964	U2965	U2966	U2967	U2968	U2969	U2970	U2971	U2972	U2973	U2974	U2975	U2976	U2977	U2978	U2979	U2980	U2981	U2982	U2983	U2984	U2985	U2986	U2987	U2988	U2989	U2990	U2991	U2992	U2993	U2994	U2995	U2996	U2997	U2998	U2999	U3000	U3001	U3002	U3003	U3004	U3005	U3006	U3007	U3008	U3009	U3010	U3011	U3012	U3013	U3014	U3015	U3016	U3017	U3018	U3019	U3020	U3021	U3022	U3023	U3024	U3025	U3026	U3027	U3028	U3029	U3030	U3031	U3032	U3033	U3034	U3035	U3036	U3037	U3038	U3039	U3040	U3041	U3042	U3043	U3044	U3045	U3046	U3047	U3048	U3049	U3050	U3051	U3052	U3053	U3054	U3055	U3056	U3057	U3058	U3059	U3060	U3061	U3062	U3063	U3064	U3065	U3066	U3067	U3068	U3069	U3070	U3071	U3072	U3073	U3074	U3075	U3076	U3077	U3078	U3079	U3080	U3081	U3082	U3083	U3084	U3085	U3086	U3087	U3088	U3089	U3090	U3091	U3092	U3093	U3094	U3095	U3096	U3097	U3098	U3099	U3100	U3101	U3102	U3103	U3104	U3105	U3106	U3107	U3108	U3109	U3110	U3111	U3112	U3113	U3114	U3115	U3116	U3117	U3118	U3119	U3120	U3121	U3122	U3123	U3124	U3125	U3126	U3127	U3128	U3129	U3130	U3131	U3132	U3133	U3134	U3135	U3136	U3137	U3138	U3139	U3140	U3141	U3142	U3143	U3144	U3145	U3146	U3147	U3148	U3149	U3150	U3151	U3152	U3153	U3154	U3155	U3156	U3157	U3158	U3159	U3160	U3161	U3162	U3163	U3164	U3165	U3166	U3167	U3168	U3169	U3170	U3171	U3172	U3173	U3174	U3175	U3176	U3177	U3178	U3179	U3180	U3181	U3182	U3183	U3184	U3185	U3186	U3187	U3188	U3189	U3190	U3191	U3192	U3193	U3194	U3195	U3196	U3197	U3198	U3199	U3200	U3201	U3202	U3203	U3204	U3205	U3206	U3207	U3208	U3209	U3210	U3211	U3212	U3213	U3214	U3215	U3216	U3217	U3218	U3219	U3220	U3221	U3222	U3223	U3224	U3225	U3226	U3227	U3228	U3229	U3230	U3231	U3232	U3233	U3234	U3235	U3236	U3237	U3238	U3239	U3240	U3241	U3242	U3243	U3244	U3245	U3246	U3247	U3248	U3249	U3250	U3251	U3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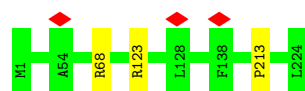
• Molecule 2: 5S ribosomal RNA



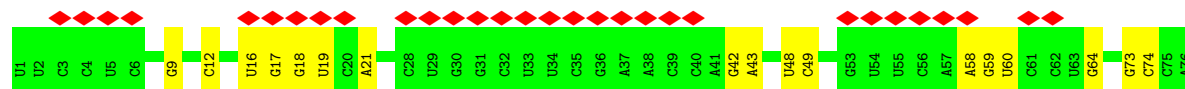
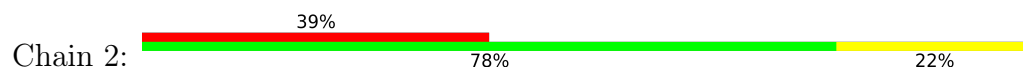
• Molecule 3: 5.8S ribosomal RNA



• Molecule 4: Eukaryotic translation initiation factor 6



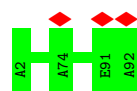
• Molecule 5: tRNA



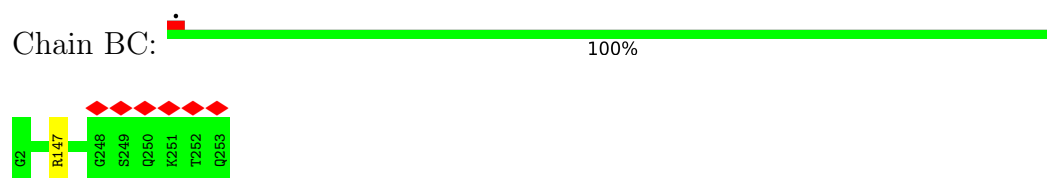
• Molecule 6: 60S ribosomal protein L42-A



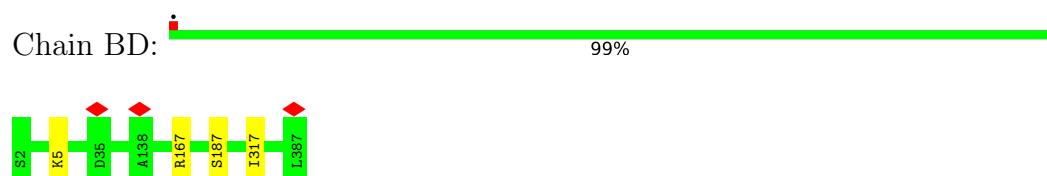
• Molecule 7: 60S ribosomal protein L43-A



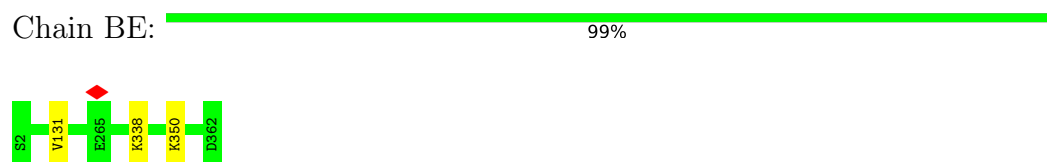
- Molecule 8: 60S ribosomal protein L2-A



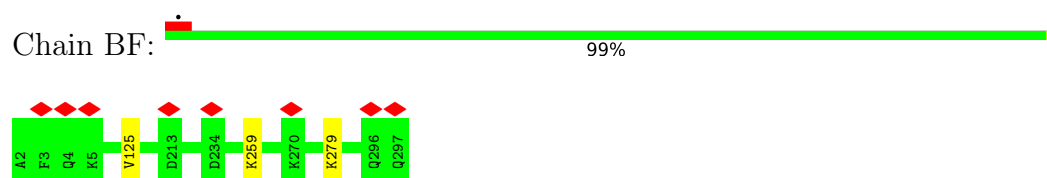
- Molecule 9: 60S ribosomal protein L3



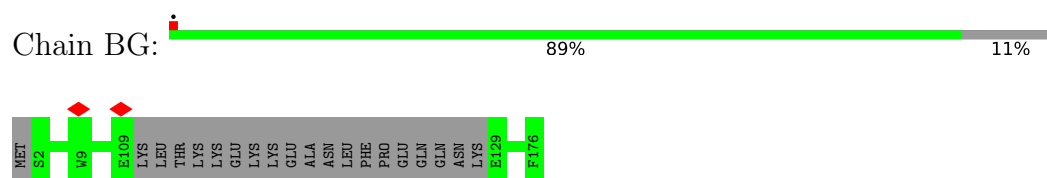
- Molecule 10: 60S ribosomal protein L4-A



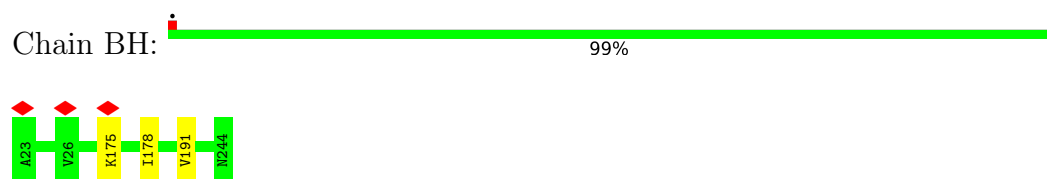
- Molecule 11: 60S ribosomal protein L5



- Molecule 12: 60S ribosomal protein L6-A

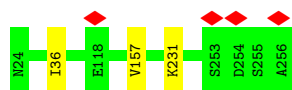


- Molecule 13: 60S ribosomal protein L7-A

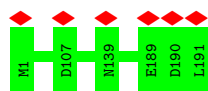


- Molecule 14: 60S ribosomal protein L8-A

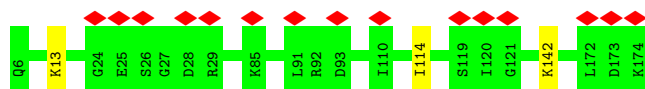




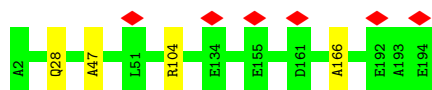
- Molecule 15: 60S ribosomal protein L9-A



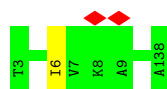
- Molecule 16: 60S ribosomal protein L11-B



- Molecule 17: 60S ribosomal protein L13-A



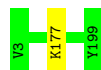
- Molecule 18: 60S ribosomal protein L14-A



- Molecule 19: 60S ribosomal protein L15-A



- Molecule 20: 60S ribosomal protein L16-A



- Molecule 21: 60S ribosomal protein L17-A

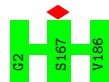


Chain BQ:  99%



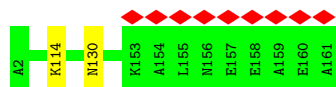
- Molecule 22: 60S ribosomal protein L18-A

Chain BR:  100%



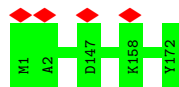
- Molecule 23: 60S ribosomal protein L19-A

Chain BS:  99%



- Molecule 24: 60S ribosomal protein L20-A

Chain BT:  100%



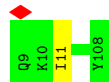
- Molecule 25: 60S ribosomal protein L21-A

Chain BU:  99%



- Molecule 26: 60S ribosomal protein L22-A

Chain BV:  99%

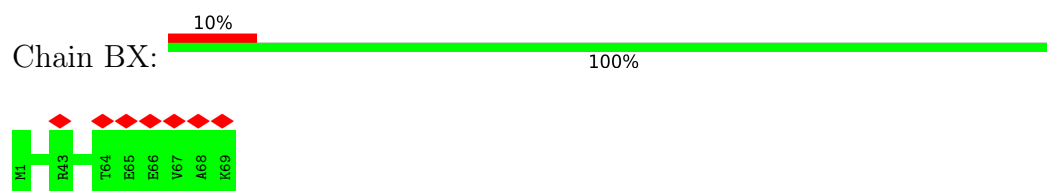


- Molecule 27: 60S ribosomal protein L23-A

Chain BW:  99%



- Molecule 28: 60S ribosomal protein L24-A

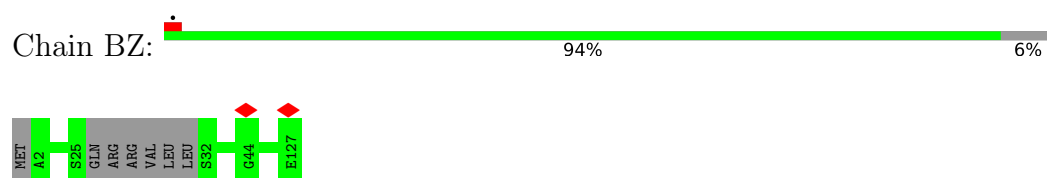


- Molecule 29: 60S ribosomal protein L25

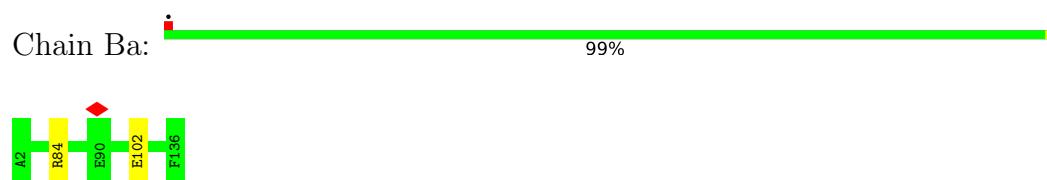


There are no outlier residues recorded for this chain.

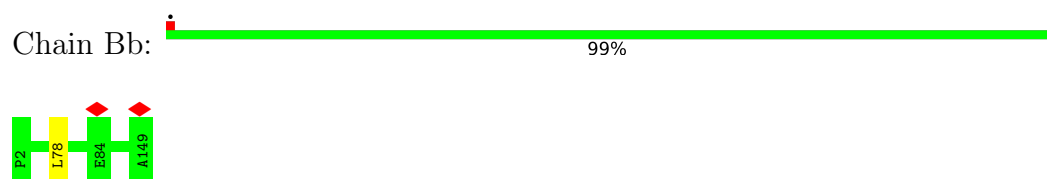
- Molecule 30: 60S ribosomal protein L26-A



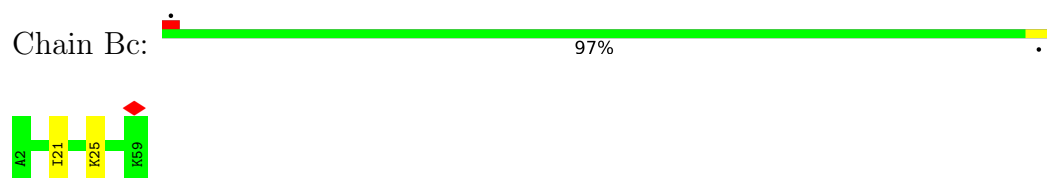
- Molecule 31: 60S ribosomal protein L27-A



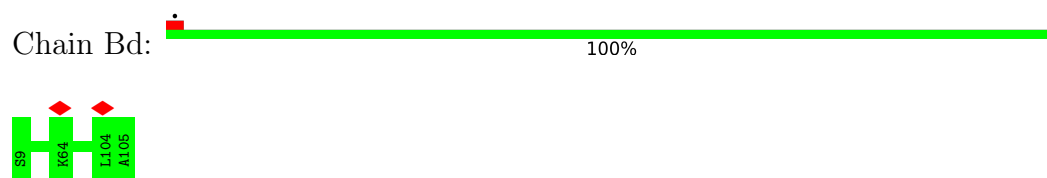
- Molecule 32: 60S ribosomal protein L28



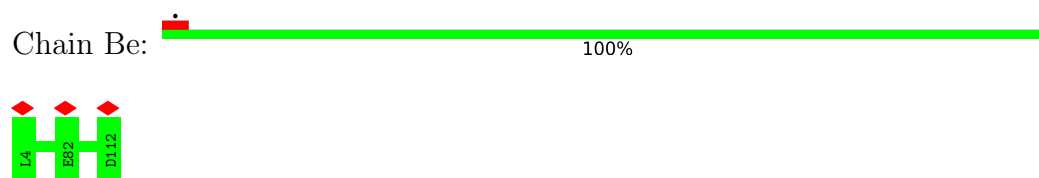
- Molecule 33: 60S ribosomal protein L29



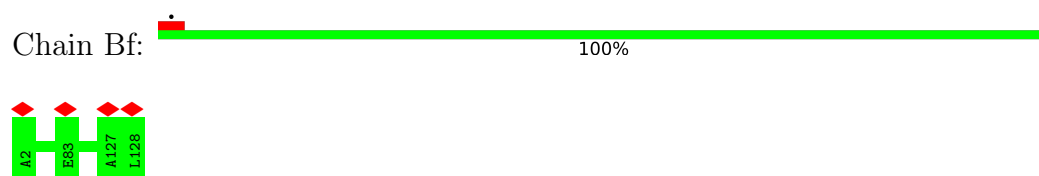
- Molecule 34: 60S ribosomal protein L30



- Molecule 35: 60S ribosomal protein L31-A



- Molecule 36: 60S ribosomal protein L32

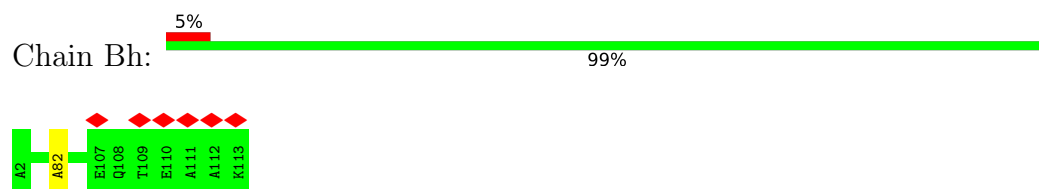


- Molecule 37: 60S ribosomal protein L33-A

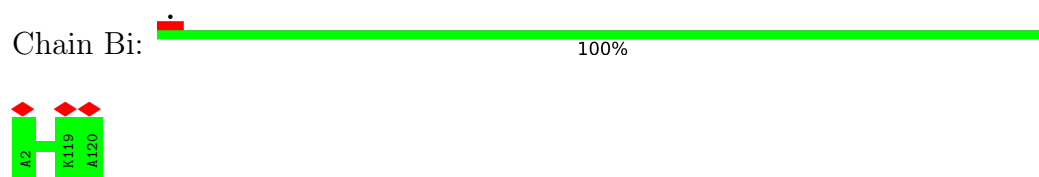


There are no outlier residues recorded for this chain.

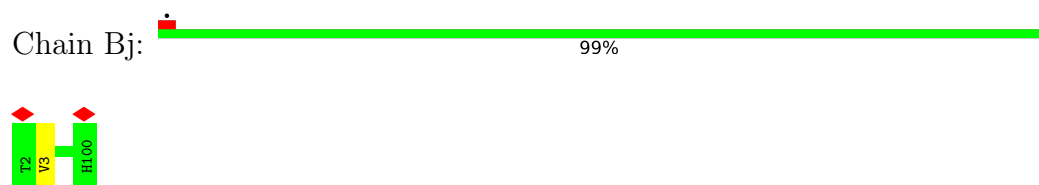
- Molecule 38: 60S ribosomal protein L34-A



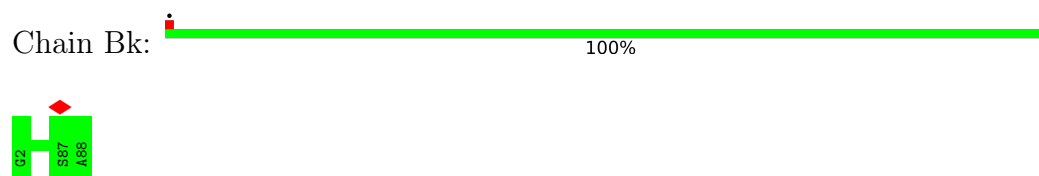
- Molecule 39: 60S ribosomal protein L35-A



- Molecule 40: 60S ribosomal protein L36-A

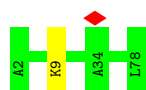


- Molecule 41: 60S ribosomal protein L37-A



- Molecule 42: 60S ribosomal protein L38

Chain Bl:  99%



- Molecule 43: 60S ribosomal protein L39

Chain Bm:  98%



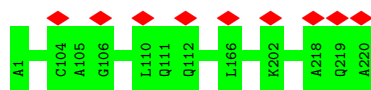
- Molecule 44: 60S ribosomal protein L40-A

Chain Bn:  100%



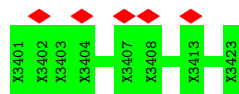
- Molecule 45: 60S ribosomal protein L10

Chain BK:  100%



- Molecule 46: Unknown chain

Chain B:  22%  
Chain B:  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	0.20	0/77733	0.79	25/121186 (0.0%)
2	3	0.18	0/2883	0.77	2/4491 (0.0%)
3	4	0.23	1/3746 (0.0%)	0.77	2/5832 (0.0%)
4	A	0.25	0/1653	0.56	1/2255 (0.0%)
5	2	0.19	0/1808	0.83	1/2816 (0.0%)
6	BA	0.26	0/860	0.55	0/1136
7	BB	0.24	0/701	0.59	0/934
8	BC	0.25	0/1948	0.55	0/2617
9	BD	0.24	0/3146	0.52	0/4228
10	BE	0.24	0/2800	0.52	0/3790
11	BF	0.24	0/2425	0.51	0/3271
12	BG	0.25	0/1260	0.50	0/1694
13	BH	0.25	0/1821	0.51	0/2451
14	BI	0.25	0/1836	0.50	0/2481
15	BJ	0.25	0/1539	0.52	0/2073
16	BL	0.27	0/1374	0.60	0/1842
17	BM	0.25	0/1568	0.57	0/2106
18	BN	0.24	0/1068	0.53	0/1438
19	BO	0.23	0/1757	0.57	0/2354
20	BP	0.25	0/1585	0.50	0/2128
21	BQ	0.25	0/1443	0.58	0/1944
22	BR	0.24	0/1465	0.55	0/1965
23	BS	0.24	0/1303	0.54	0/1740
24	BT	0.25	0/1481	0.54	0/1990
25	BU	0.24	0/1300	0.53	0/1743
26	BV	0.25	0/812	0.50	0/1099
27	BW	0.28	0/1018	0.57	0/1369
28	BX	0.27	0/565	0.58	0/752
29	BY	0.25	0/979	0.52	0/1321
30	BZ	0.24	0/949	0.55	0/1266
31	Ba	0.25	0/1118	0.49	0/1497
32	Bb	0.25	0/1204	0.58	0/1612

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Bc	0.26	0/473	0.56	0/629
34	Bd	0.27	0/751	0.50	0/1008
35	Be	0.24	0/890	0.54	0/1196
36	Bf	0.24	0/1041	0.53	0/1394
37	Bg	0.25	0/868	0.54	0/1168
38	Bh	0.24	0/890	0.55	0/1189
39	Bi	0.24	0/978	0.53	0/1301
40	Bj	0.24	0/778	0.56	0/1034
41	Bk	0.24	0/696	0.57	0/923
42	Bl	0.25	0/618	0.57	0/826
43	Bm	0.30	0/443	0.61	0/588
44	Bn	0.27	0/423	0.63	0/562
45	BK	0.25	0/1807	0.55	0/2425
All	All	0.22	1/137804 (0.0%)	0.71	31/203664 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	4	75	G	N7-C5	-6.73	1.35	1.39

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	213	PRO	CA-N-CD	-7.86	100.49	111.50
5	2	12	C	N3-C2-O2	-7.08	116.94	121.90
1	1	2708	C	N3-C2-O2	-6.72	117.19	121.90
1	1	2446	U	C2-N1-C1'	6.65	125.68	117.70
1	1	2507	C	C2-N1-C1'	6.45	125.89	118.80

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

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

## 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	
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	51
10	BE	359/361 (99%)	343 (96%)	14 (4%)	2 (1%)	22	57
11	BF	294/296 (99%)	288 (98%)	4 (1%)	2 (1%)	19	54
12	BG	152/176 (86%)	151 (99%)	1 (1%)	0	100	100
13	BH	220/222 (99%)	213 (97%)	5 (2%)	2 (1%)	14	49
14	BI	231/233 (99%)	225 (97%)	4 (2%)	2 (1%)	14	49
15	BJ	189/191 (99%)	186 (98%)	3 (2%)	0	100	100
16	BL	167/169 (99%)	154 (92%)	12 (7%)	1 (1%)	22	57
17	BM	191/193 (99%)	179 (94%)	9 (5%)	3 (2%)	8	37
18	BN	134/136 (98%)	130 (97%)	3 (2%)	1 (1%)	19	54
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%)	22	57
26	BV	98/100 (98%)	92 (94%)	5 (5%)	1 (1%)	13	47
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	BZ	116/127 (91%)	113 (97%)	3 (3%)	0	100	100
31	Ba	133/135 (98%)	128 (96%)	4 (3%)	1 (1%)	16	51
32	Bb	146/148 (99%)	140 (96%)	5 (3%)	1 (1%)	19	54
33	Bc	56/58 (97%)	55 (98%)	0	1 (2%)	7	35
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	49
39	Bi	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
40	Bj	97/99 (98%)	91 (94%)	5 (5%)	1 (1%)	13	47
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
45	BK	218/220 (99%)	209 (96%)	9 (4%)	0	100	100
All	All	6330/6443 (98%)	6148 (97%)	158 (2%)	24 (0%)	32	64

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%)	175 (99%)	2 (1%)	70	86
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%)	192 (100%)	1 (0%)	86	93
9	BD	320/322 (99%)	319 (100%)	1 (0%)	91	96
10	BE	288/288 (100%)	287 (100%)	1 (0%)	91	96
11	BF	244/244 (100%)	243 (100%)	1 (0%)	89	94
12	BG	134/153 (88%)	134 (100%)	0	100	100
13	BH	186/186 (100%)	185 (100%)	1 (0%)	86	93
14	BI	187/191 (98%)	186 (100%)	1 (0%)	86	93
15	BJ	171/171 (100%)	171 (100%)	0	100	100
16	BL	147/147 (100%)	145 (99%)	2 (1%)	62	82
17	BM	154/154 (100%)	153 (99%)	1 (1%)	84	92
18	BN	107/107 (100%)	107 (100%)	0	100	100
19	BO	175/175 (100%)	174 (99%)	1 (1%)	84	92
20	BP	160/160 (100%)	159 (99%)	1 (1%)	84	92
21	BQ	140/145 (97%)	139 (99%)	1 (1%)	81	92
22	BR	150/150 (100%)	150 (100%)	0	100	100
23	BS	131/131 (100%)	129 (98%)	2 (2%)	60	81
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%)	103 (99%)	1 (1%)	73	87
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%)	114 (99%)	1 (1%)	75	89
32	Bb	118/118 (100%)	118 (100%)	0	100	100
33	Bc	46/46 (100%)	45 (98%)	1 (2%)	47	73
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	Bg	90/90 (100%)	90 (100%)	0	100	100
38	Bh	95/95 (100%)	95 (100%)	0	100	100
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%)	67 (98%)	1 (2%)	60	81
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%)	5296 (100%)	20 (0%)	88	94

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	BS	114	LYS
31	Ba	84	ARG
42	Bl	9	LYS
33	Bc	25	LYS
13	BH	175	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
24	BT	46	GLN
27	BW	47	ASN
45	BK	208	ASN
28	BX	33	ASN
44	Bn	119	ASN

### 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 ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

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 ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

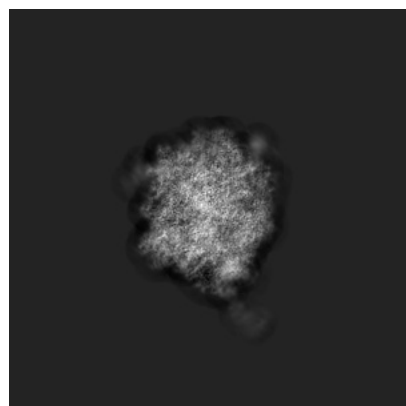
## 6 Map visualisation [i](#)

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.

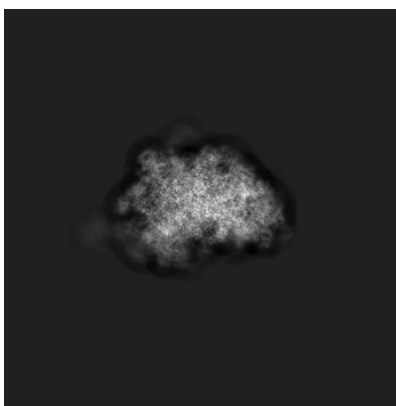
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

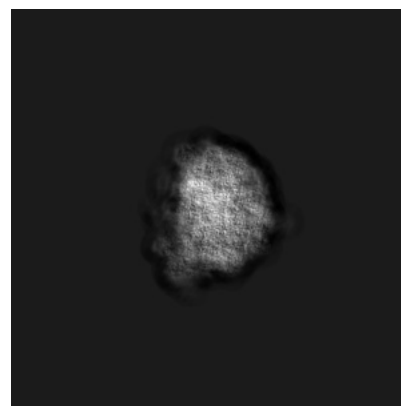
#### 6.1.1 Primary map



X

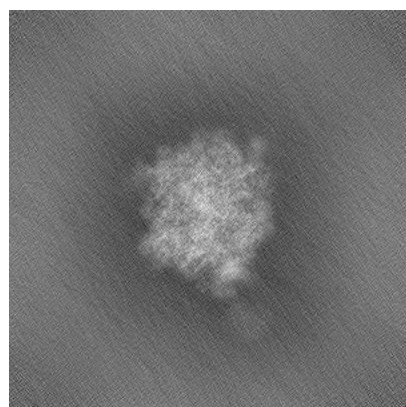


Y

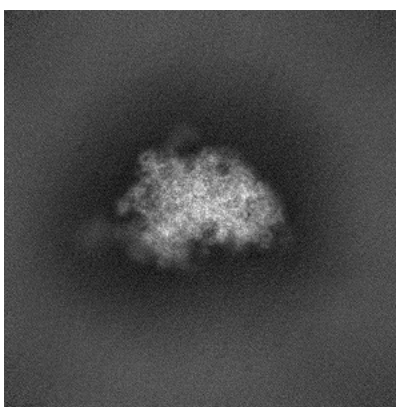


Z

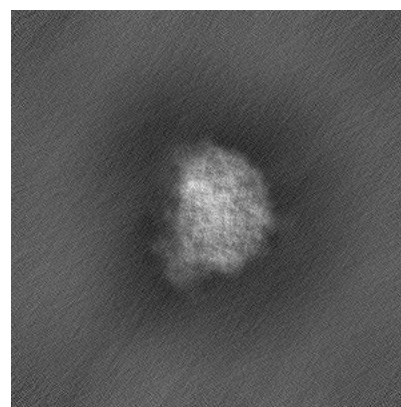
#### 6.1.2 Raw map



X



Y

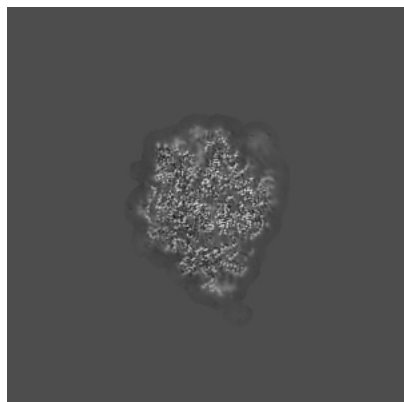


Z

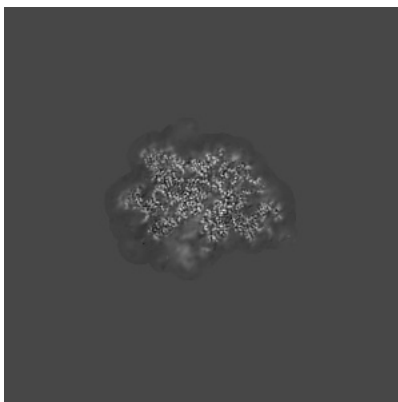
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

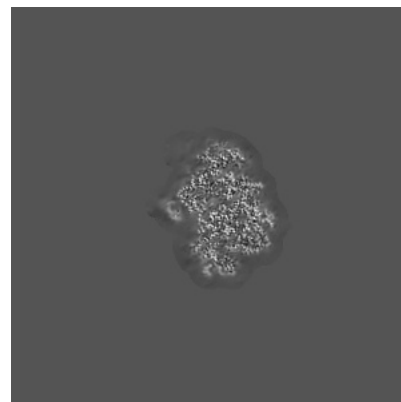
### 6.2.1 Primary map



X Index: 280

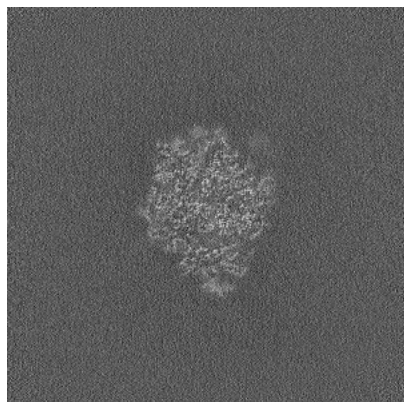


Y Index: 280

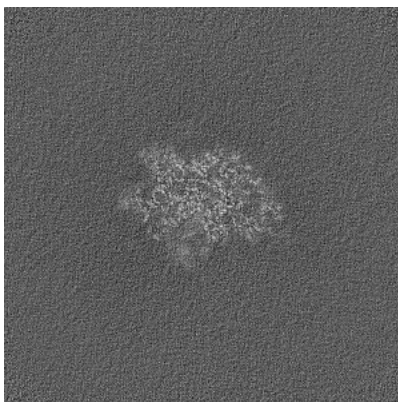


Z Index: 280

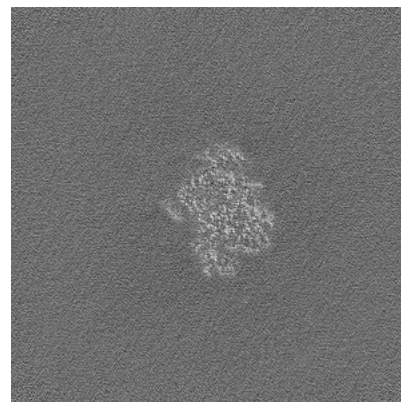
### 6.2.2 Raw map



X Index: 280



Y Index: 280



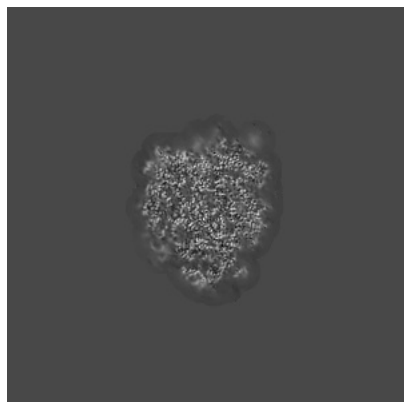
Z Index: 280

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

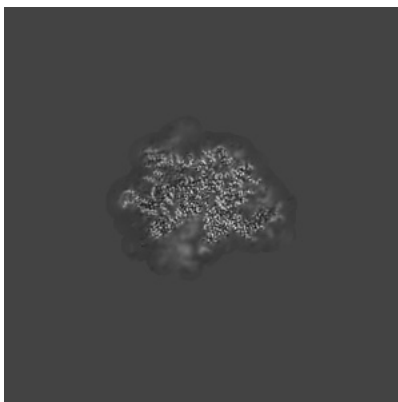


## 6.3 Largest variance slices [i](#)

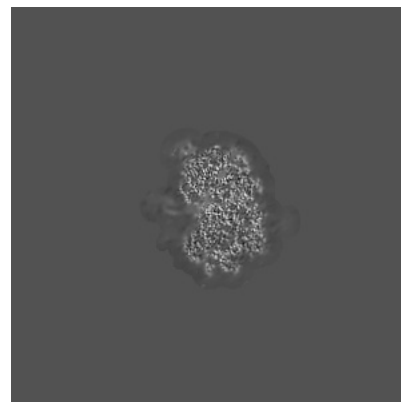
### 6.3.1 Primary map



X Index: 300

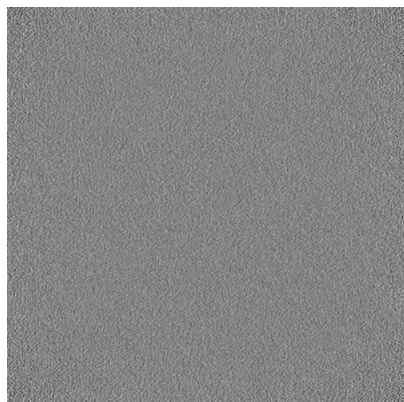


Y Index: 275

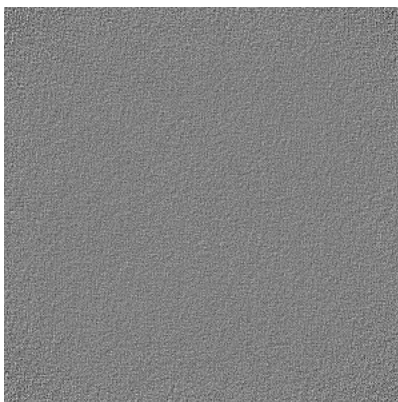


Z Index: 271

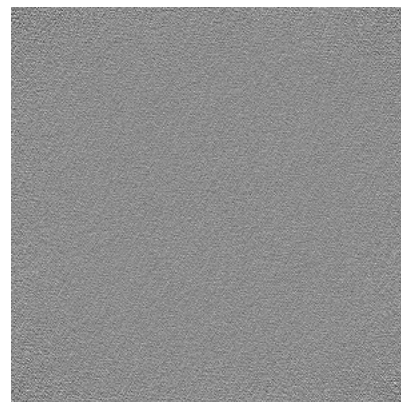
### 6.3.2 Raw map



X Index: 0



Y Index: 0



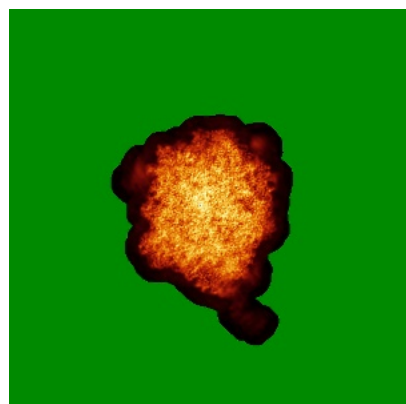
Z Index: 0

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

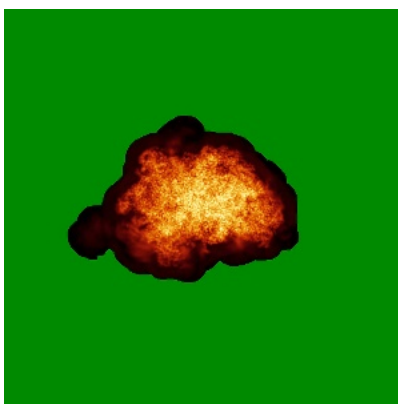


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

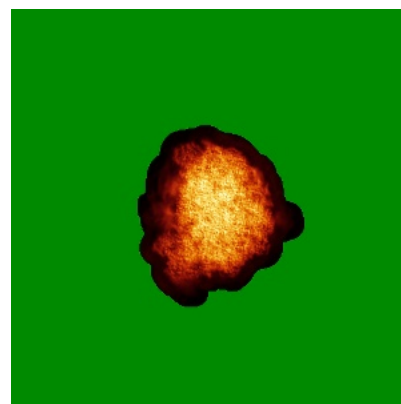
### 6.4.1 Primary map



X

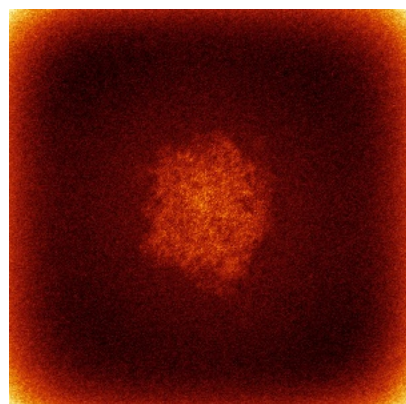


Y

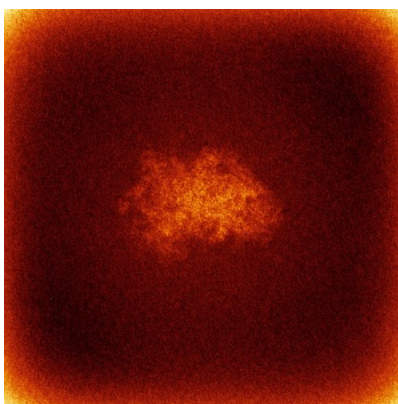


Z

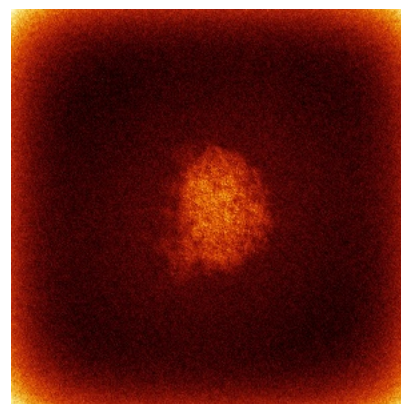
### 6.4.2 Raw map



X



Y



Z

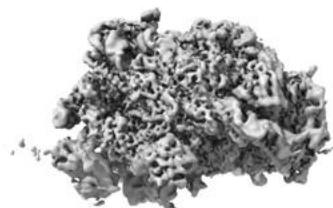
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



X



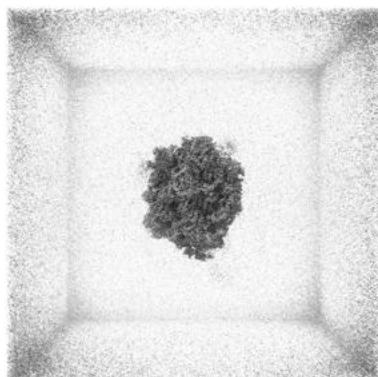
Y



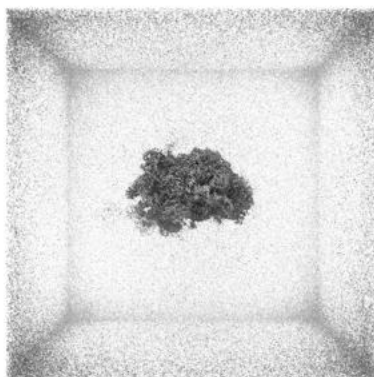
Z

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.

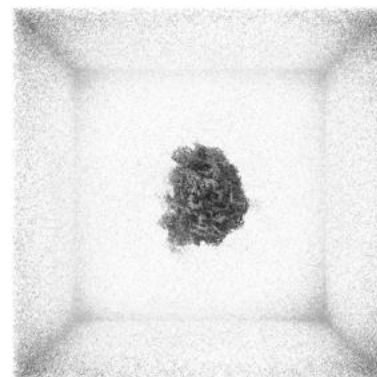
### 6.5.2 Raw map



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.

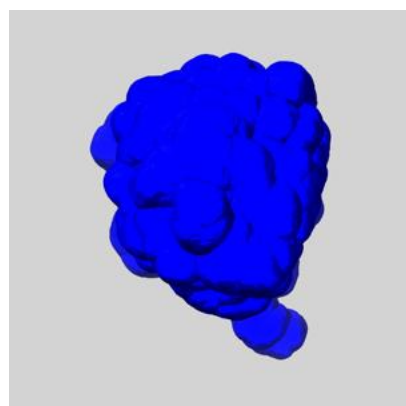
## 6.6 Mask visualisation [i](#)

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

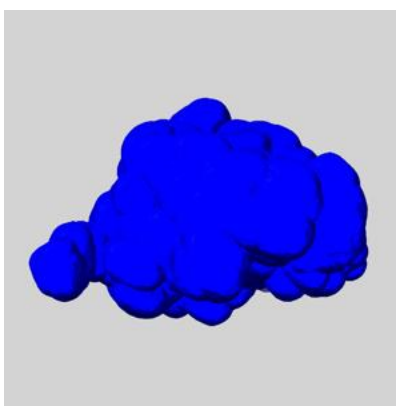
A mask typically either:

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

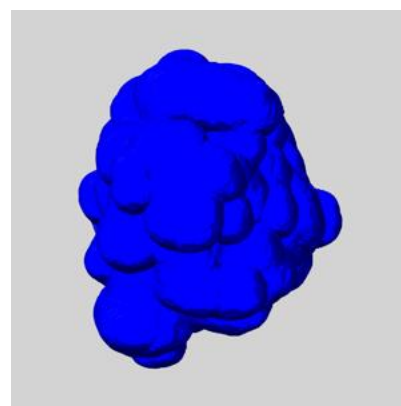
### 6.6.1 emd\_14926\_msk\_1.map [i](#)



X



Y

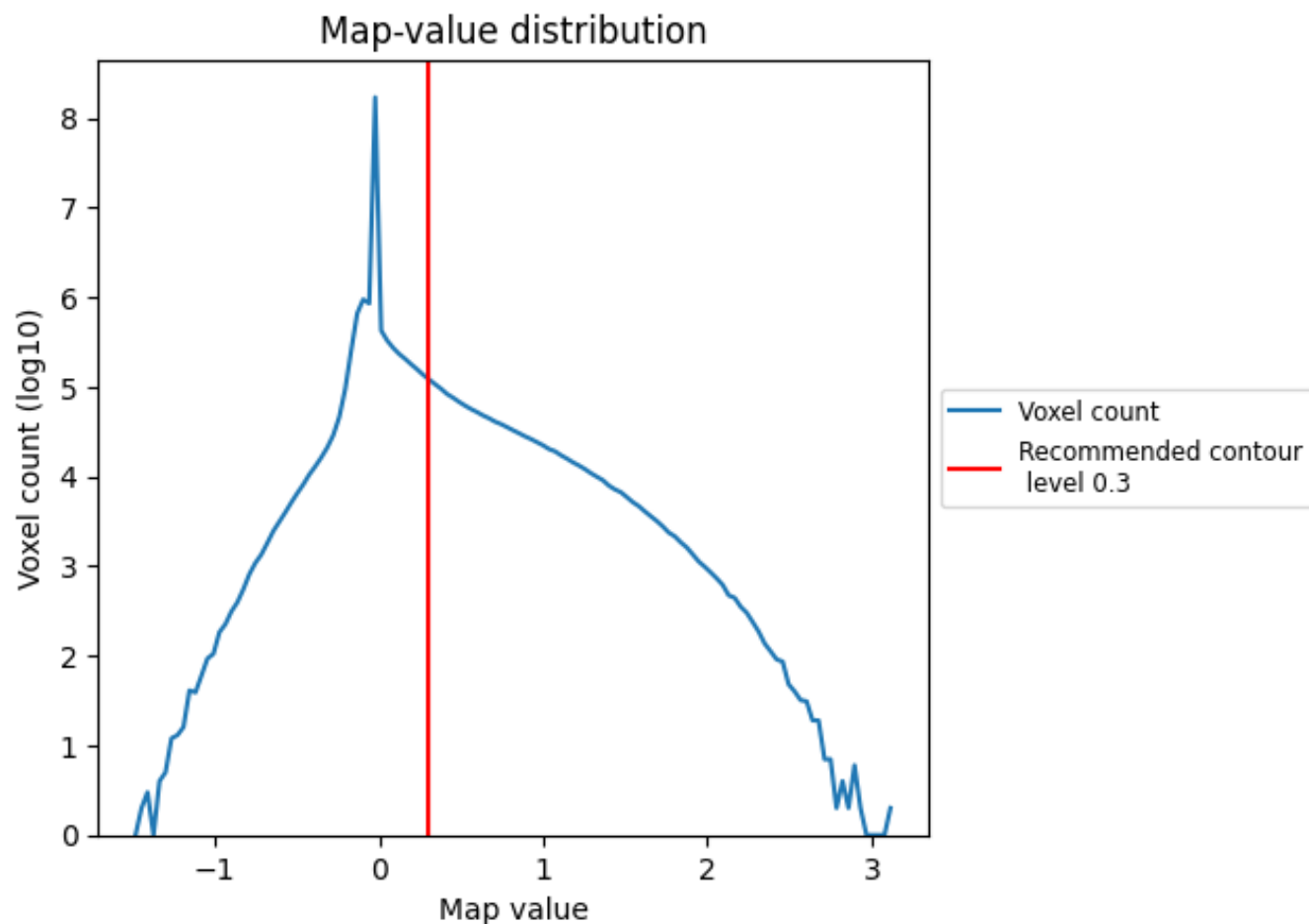


Z

## 7 Map analysis [i](#)

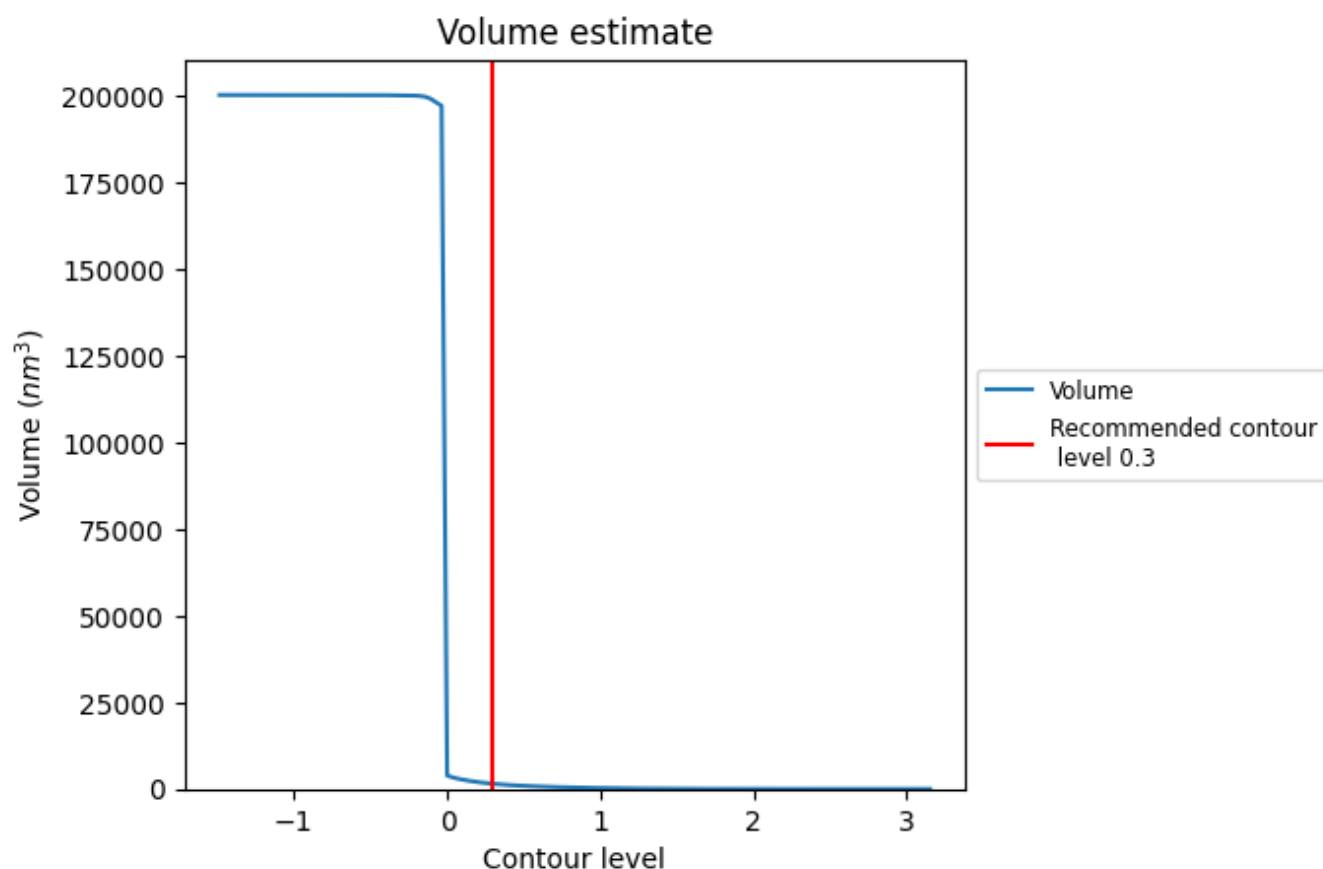
This section contains the results of statistical analysis of the map.

### 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.

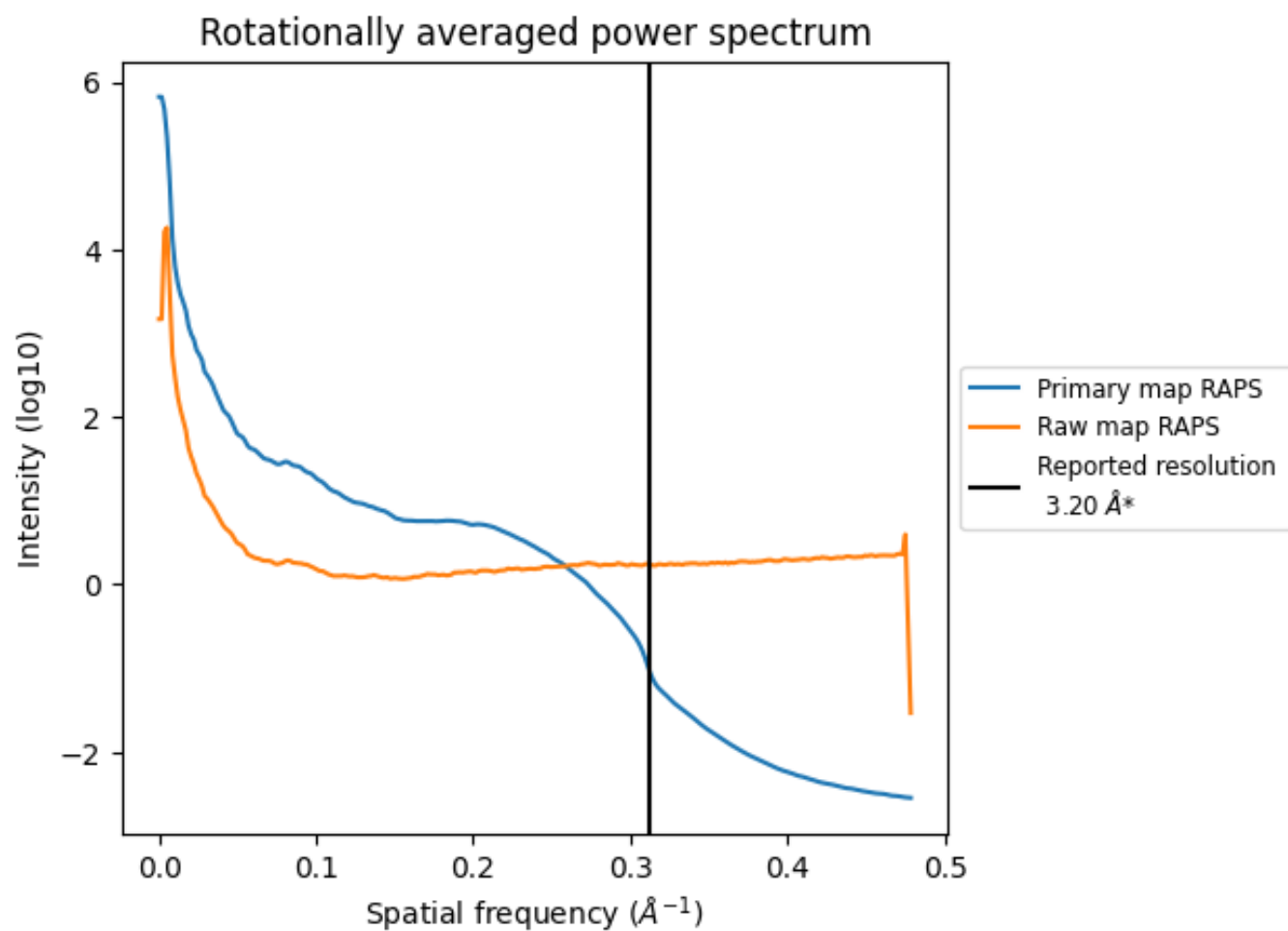
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1499 nm<sup>3</sup>; 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 ⓘ

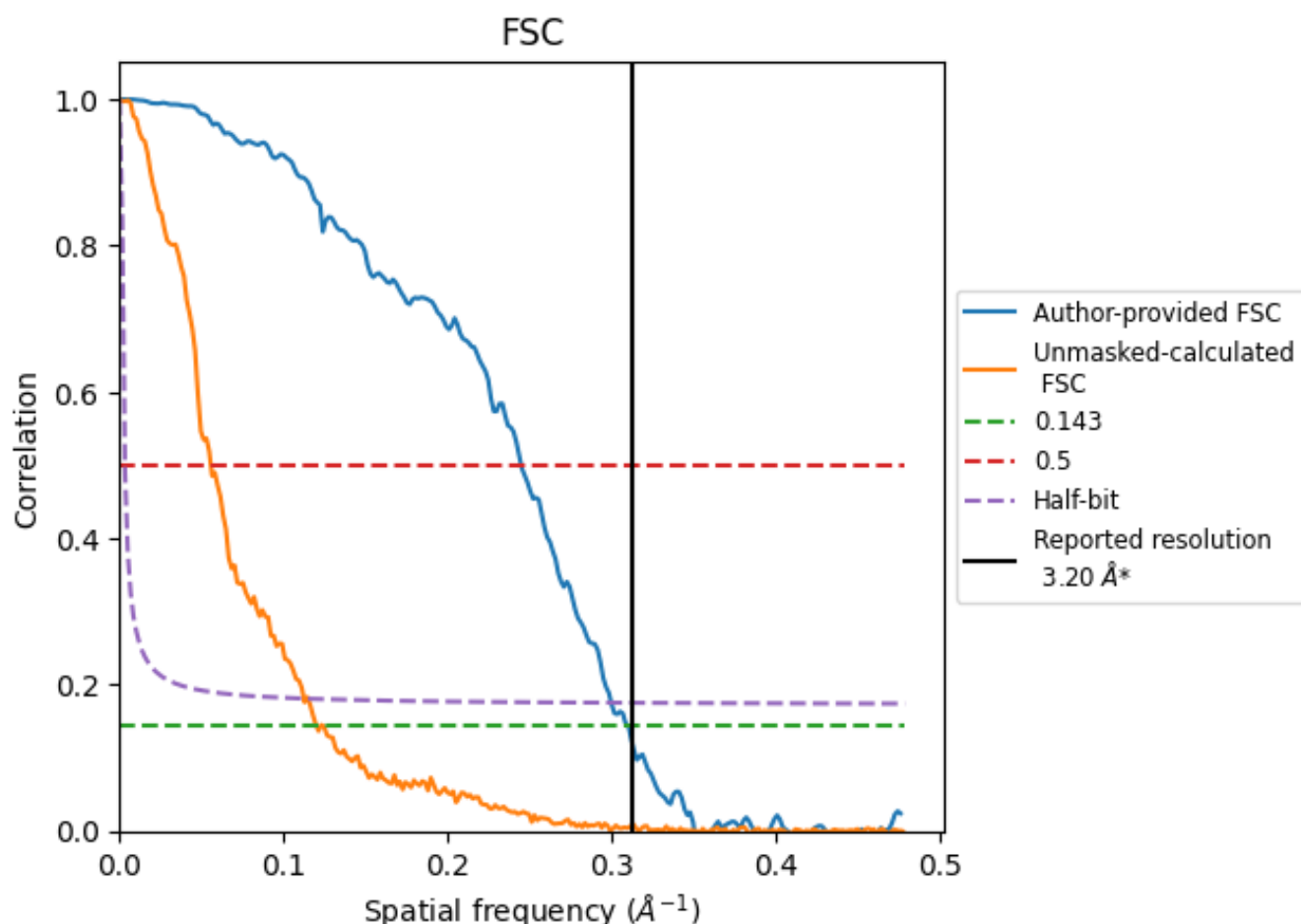


\*Reported resolution corresponds to spatial frequency of 0.312 Å<sup>-1</sup>

## 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

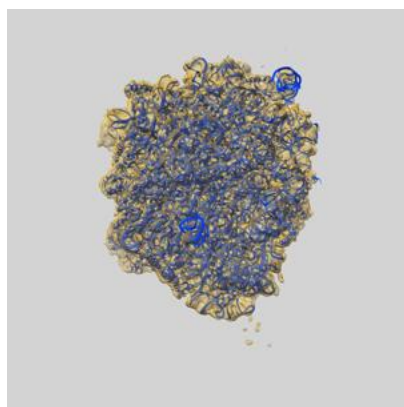
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.33 differs from the reported value 3.2 by more than 10 %



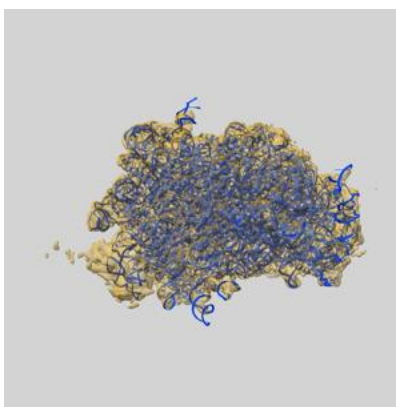
## 9 Map-model fit [i](#)

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.

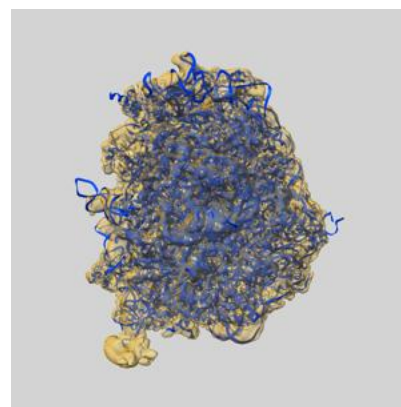
### 9.1 Map-model overlay [i](#)



X



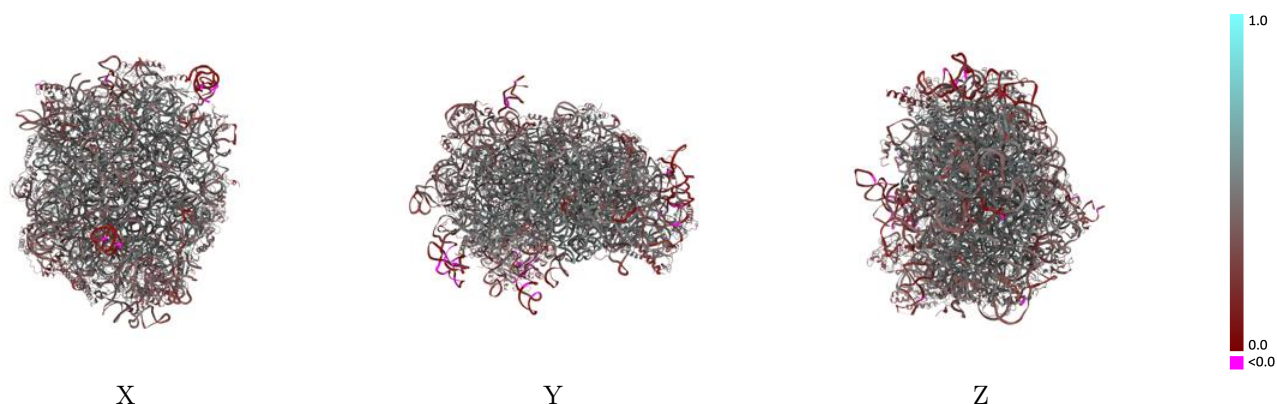
Y



Z

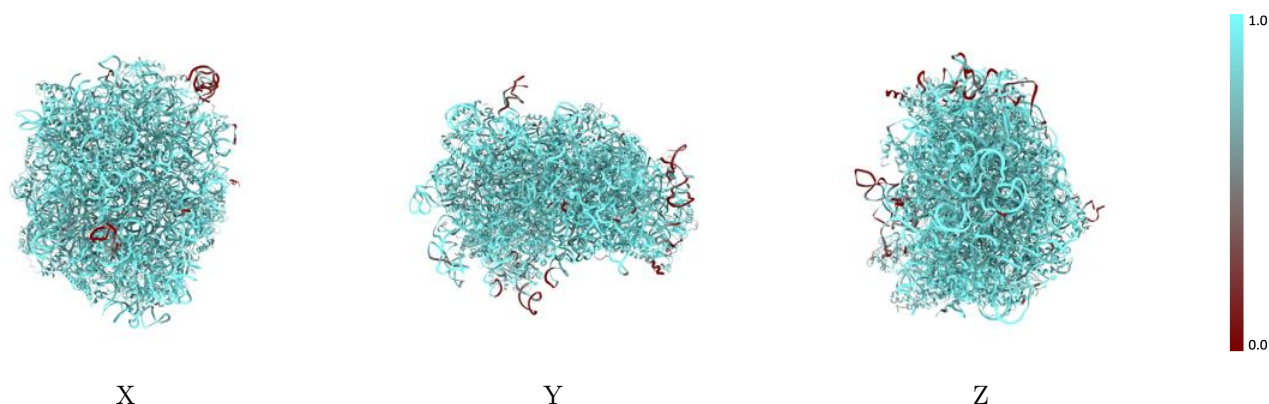
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



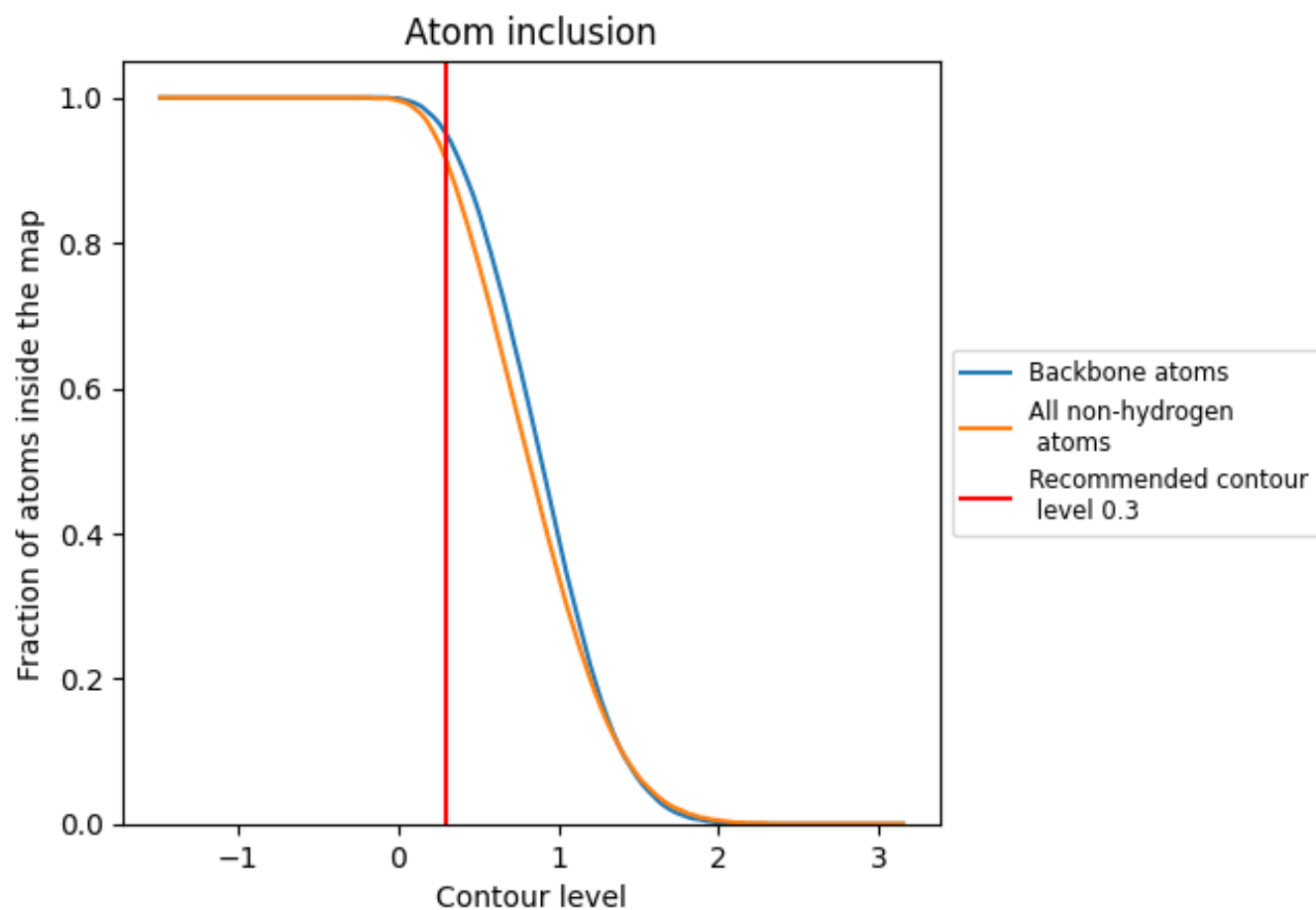
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



*Continued on next page...*

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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