



## wwPDB EM Validation Summary Report ⓘ

Feb 22, 2023 – 07:51 am 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 : 6SNT, 1G62, 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.dev43  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.32.1

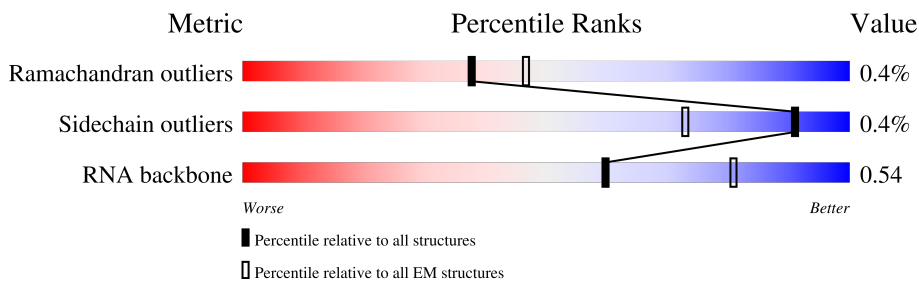
# 1 Overall quality at a glance i

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.



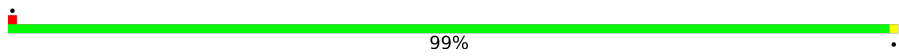
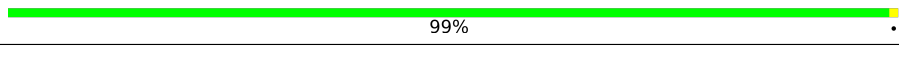
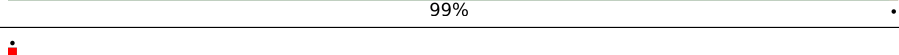
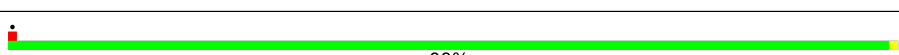
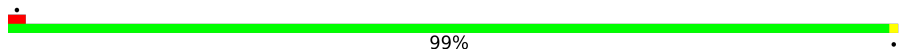
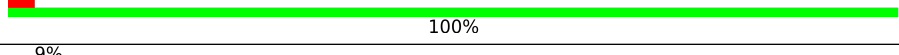
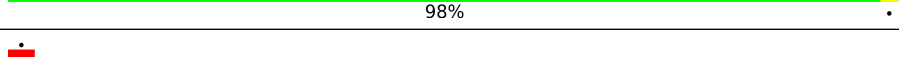
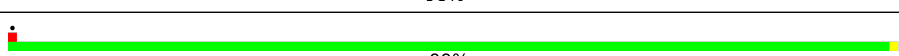
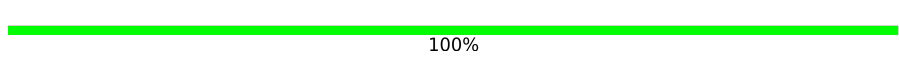
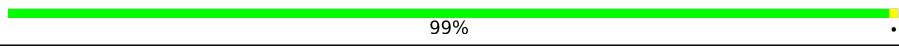
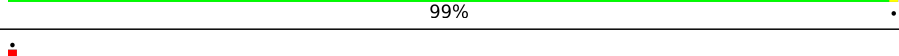
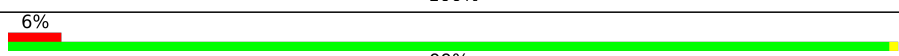
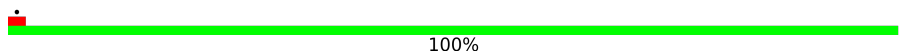
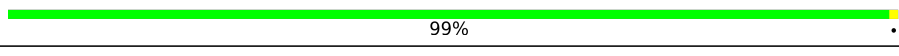
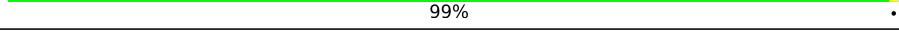
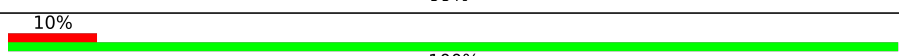
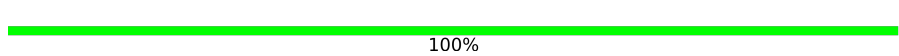
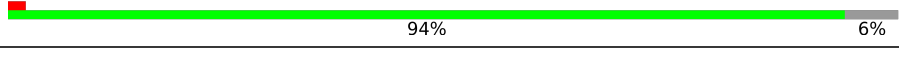
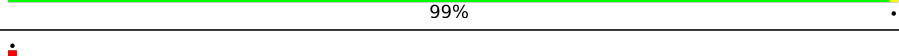
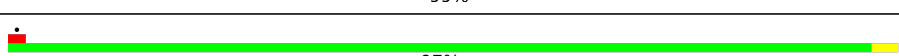



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	

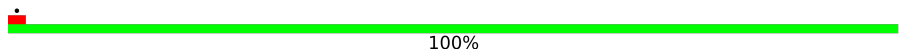
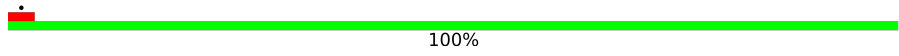
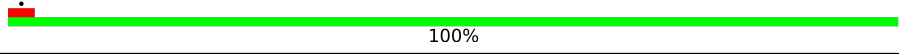
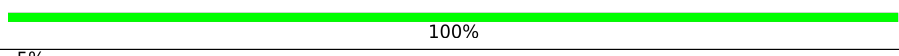
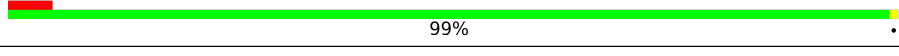
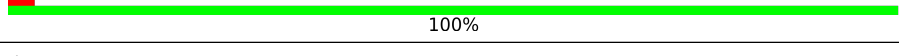
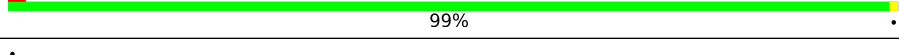
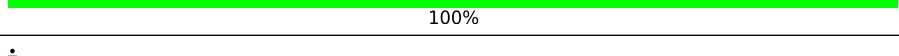
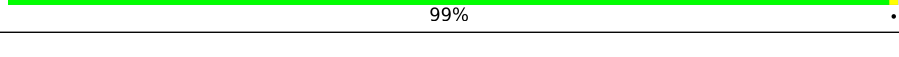
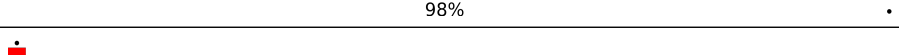
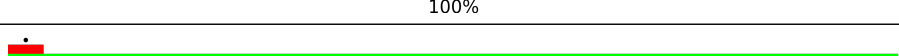
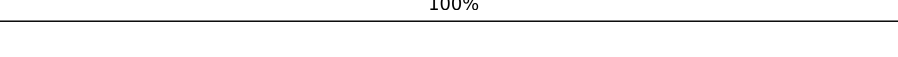
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Mol	Chain	Length	Quality of chain
9	BD	386	 99%
10	BE	361	 99%
11	BF	296	 99%
12	BG	176	 89% 11%
13	BH	222	 99%
14	BI	233	 99%
15	BJ	191	 100%
16	BL	169	 9% 98%
17	BM	193	 98%
18	BN	136	 99%
19	BO	203	 100%
20	BP	197	 99%
21	BQ	183	 99%
22	BR	185	 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%

## 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
			Total	C	N	O	P		
1	1	3248	69452	31022	12494	22688	3248	0	0

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

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

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

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

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

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

- Molecule 5 is a RNA chain called tRNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O		
21	BQ	183	1420	882	281	257	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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	B1	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 UNKNOWN (three-letter code: UNK) (formula: C<sub>4</sub>H<sub>9</sub>NO<sub>2</sub>).

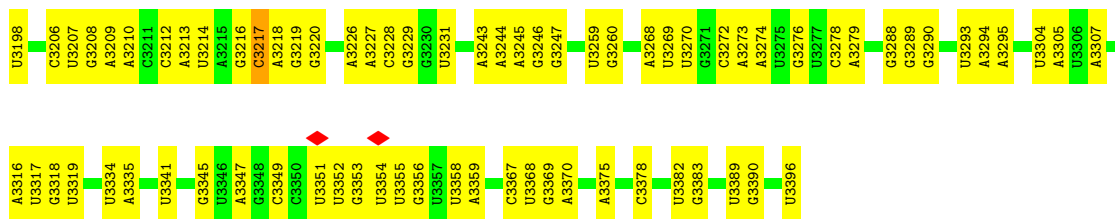
Mol	Chain	Residues	Atoms				AltConf
46	1	14	Total	C	N	O	0
			70	42	14	14	
46	BE	2	Total	C	N	O	0
			10	6	2	2	
46	BQ	4	Total	C	N	O	0
			20	12	4	4	
46	Bm	3	Total	C	N	O	0
			15	9	3	3	

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

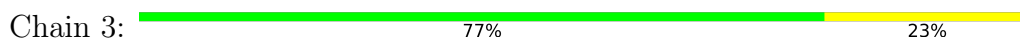
Mol	Chain	Residues	Atoms		AltConf
47	2	1	Total	Mg	0
			1	1	



A3048	A3049	U3056	U3057	U3058	G3059	U3078	G3079	G3080	A3086	C3092	A3113	C3117	U3121	A3122	A3130	U3131	A3141	A3142	C3143	G3144	U3151	U3152	C3153	C3154	U3155	U3156	U3157	G3158	A3170	U3171	A3172	G3173	A3174	U3175	G3176	U3179	A3180	C3181	G3182	U3185	A3186	A3187	U3189	U3196	G3197	A1408	A1580	C1581	C1582	A1583	C1432	A1433	A1434	A1435	U1436	C1437	A1446	G1447	U1448	U1620	A1621	U1629	U1630	A1643	C1644	U1645	U1688	U1695	A1696	U1715	U1716	U1717	G1718	G1719	U1724	G1730	U1731	U1739	U1740	A1741	A1749	A1750	G1751	G1561	C1562	C1563	U1567	U1568	U1569	U1570	A1571	U1572	C1578	C1579	A1580	C1581	C1582	A1583	A1588	A1589	U1595	U1596	A1602	A1605	U1620	A1621	U1629	U1630	A1643	C1644	U1645	U1688	U1695	A1696	U1715	U1716	U1717	G1718	G1719	U1724	G1730	U1731	U1739	U1740	A1741	A1749	A1750	G1751	A1760	C1761	C1762	U1763	U1764	U1765	G1769	U1770	C1577	C1773	C1774	G1775	G1780	C1793	G1794	U1795	G1796	A1797	A1798	A1813	A1814	U1815	A1816	G1817	U1818	U1819	U1820	U1821	C1822	A1835	U1839	U1840	A1841	A1842	C1843	U1844	C1845	C1846	A1847	G1848	C1849	A1850	G1851	A1858	C1866	A1867	G1878	A1879	U1880	U1885	A1886	A1893	G1902	G1906	C1907	A1908	A1909	C1977	A1913	G1914	C1926	U1931	A1932	G1952	G1953	G1954	U1955	A1956	G1959	A1960	G1961	G1962	G1963	C1964	C1965	U1966	U1967	G1968	G1969	A1972	G1973	A1974	C1975	G1976	C1977	U2040	U2041	G2042	U2043	U2044	G2045	U2046	A2047	G2048	A2049	C2050	C2054	U2055	U2056	G2057	G2058	U2059	A2081	U2082	A2086	C2087	A2088	A2089	A2093	U2101	U2102	G2111	U2112	A2113	C2114	G2121	G2122	A2125	A2126	A2131	A2138	A2142	A2143	A2144	A2145	U2148	G2157	A2158	U2159	G2160	A2166	G2169	U2176	C2177	A2178	C2179	U2186	U2187	A2188	G2189	C2190	C2191	C2192	C2193	C2194	C2195	C2196	C2197	C2198	C2199	C2200	C2201	C2202	C2203	C2204	C2205	C2206	C2207	C2208	C2209	C2210	A2243	A2244	G2248	G2249	G2250	A2252	A2256	C2257	U2258	A2259	U2260	U2269	A2270	A2271	G2272	A2280	A2281	U2282	C2287	U2297	U2298	A2299	G2306	G2307	C2308	A2309	U2310	A2313	U2314	U2315	U2318	U2319	U2334	G2335	U2336	U2340	C2374	C2375	C2376	A2386	A2387	U2388	A2397	A2402	G2403	A2404	U2411	G2418	A2419	U2434	G2435	U2436	A2438	A2439	G2440	A2441	G2442	A2443	C2444	A2445	U2446	A2447	G2448	A2449	G2452	U2544	A2547	C2548	G2549	U2550	C2552	G2555	U2558	U2559	C2560	C2568	U2571	C2572	C2582	G2585	A2593	C2600	G2606	G2607	G2614	G2618	G2619	G2620	G2621	C2625	A2626	A2635	A2636	A2637	C2638	U2652	C2653	C2654	U2655	A2656	A2657	C2666	G2672	A2673	A2674	A2678	A2679	A2680	A2801	A2802	A2803	C2810	G2814	G2815	G2816	A2817	U2818	U2842	U2843	C2844	A2845	U2846	A2847	A2848	A2849	A2850	A2851	A2852	A2853	A2854	A2855	A2856	A2857	A2858	A2859	A2860	A2861	A2862	A2863	A2864	A2865	A2866	A2867	A2868	A2869	A2870	A2871	A2872	A2873	A2874	A2875	A2876	A2877	A2878	A2879	A2880	A2881	A2882	A2883	A2884	A2885	A2886	A2887	A2888	A2889	A2890	A2891	A2892	A2893	A2894	A2895	A2896	A2897	A2898	A2899	A2900	A2901	A2902	A2903	A2904	A2905	A2906	A2907	A2908	A2909	A2910	A2911	A2912	A2913	A2914	A2915	A2916	A2917	A2918	A2919	A2920	A2921	A2922	A2923	A2924	A2925	A2926	A2927	A2928	A2929	A2930	A2931	A2932	A2933	A2934	A2935	A2936	A2937	A2938	A2939	A2940	A2941	A2942	A2943	A2944	A2945	A2946	A2947	A2948	A2949	A2950	A2951	A2952	A2953	A2954	A2955	A2956	A2957	A2958	A2959	A2960	A2961	A2962	A2963	A2964	A2965	A2966	A2967	A2968	A2969	A2970	A2971	A2972	A2973	A2974	A2975	A2976	A2977	A2978	A2979	A2980	A2981	A2982	A2983	A2984	A2985	A2986	A2987	A2988	A2989	A2990	A2991	A2992	A2993	A2994	A2995	A2996	A2997	A2998	A2999	A3000	A3001	A3002	A3003	A3004	A3005	A3006	A3007	A3008	A3009	A3010	A3011	A3012	A3013	A3014	A3015	A3016	A3017	A3018	A3019	A3020	A3021	A3022	A3023	A3024	A3025	A3026	A3027	A3028	A3029	A3030	A3031	A3032	A3033	A3034	A3035	A3036	A3037	A3038	A3039	A3040	A3041	A3042	A3043	A3044	A3045	A3046	A3047	A3048	A3049	A3050	A3051	A3052	A3053	A3054	A3055	A3056	A3057	A3058	A3059	A3060	A3061	A3062	A3063	A3064	A3065	A3066	A3067	A3068	A3069	A3070	A3071	A3072	A3073	A3074	A3075	A3076	A3077	A3078	A3079	A3080	A3081	A3082	A3083	A3084	A3085	A3086	A3087	A3088	A3089	A3090	A3091	A3092	A3093	A3094	A3095	A3096	A3097	A3098	A3099	A3100	A3101	A3102	A3103	A3104	A3105	A3106	A3107	A3108	A3109	A3110	A3111	A3112	A3113	A3114	A3115	A3116	A3117	A3118	A3119	A3120	A3121	A3122	A3123	A3124	A3125	A3126	A3127	A3128	A3129	A3130	A3131	A3132	A3133	A3134	A3135	A3136	A3137	A3138	A3139	A3140	A3141	A3142	A3143	A3144	A3145	A3146	A3147	A3148	A3149	A3150	A3151	A3152	A3153	A3154	A3155	A3156	A3157	A3158	A3159	A3160	A3161	A3162	A3163	A3164	A3165	A3166	A3167	A3168	A3169	A3170	A3171	A3172	A3173	A3174	A3175	A3176	A3177	A3178	A3179	A3180	A3181	A3182	A3183	A3184	A3185	A3186	A3187	A3188	A3189	A3190	A3191	A3192	A3193	A3194	A3195	A3196	A3197	A3198	A3199	A3200	A3201	A3202	A3203	A3204	A3205	A3206	A3207	A3208	A3209	A3210	A3211	A3212	A3213	A3214	A3215	A3216	A3217	A3218	A3219	A3220	A3221	A3222	A3223	A3224	A3225	A3226	A3227	A3228	A3229	A3230	A3231	A3232	A3233	A3234	A3235	A3236	A3237	A3238	A3239	A3240	A3241	A3242	A3243	A3244	A3245	A3246	A3247	A3248	A3249	A3250	A3251	A3252	A3253	A3254	A3255	A3256	A3257	A3258	A3259	A3260	A3261	A3262	A3263	A3264	A3265	A3266	A3267	A3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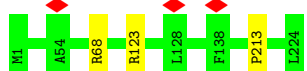
• Molecule 2: 5S ribosomal RNA



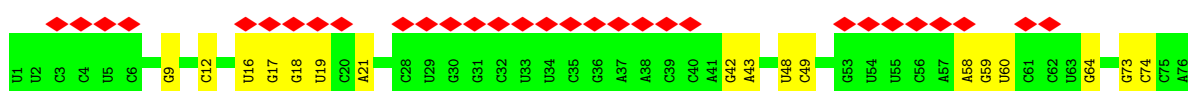
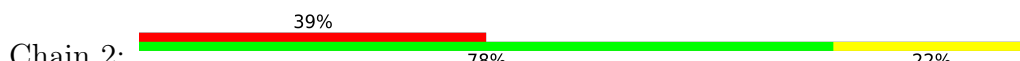
• Molecule 3: 5.8S ribosomal RNA



• Molecule 4: Eukaryotic translation initiation factor 6



• Molecule 5: tRNA



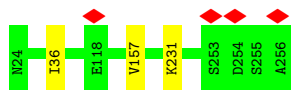
• Molecule 6: 60S ribosomal protein L42-A



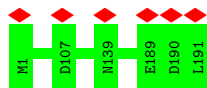
• Molecule 7: 60S ribosomal protein L43-A



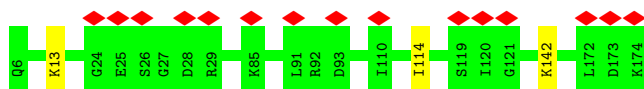




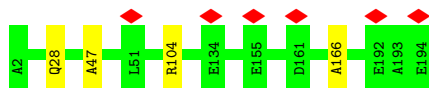
- Molecule 15: 60S ribosomal protein L9-A



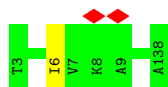
- Molecule 16: 60S ribosomal protein L11-B



- Molecule 17: 60S ribosomal protein L13-A



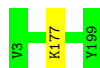
- Molecule 18: 60S ribosomal protein L14-A



- Molecule 19: 60S ribosomal protein L15-A



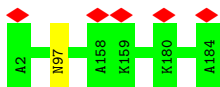
- Molecule 20: 60S ribosomal protein L16-A



- Molecule 21: 60S ribosomal protein L17-A

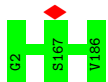


Chain BQ:  99%



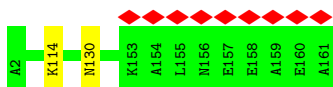
- Molecule 22: 60S ribosomal protein L18-A

Chain BR:  100%



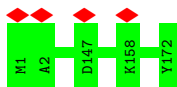
- Molecule 23: 60S ribosomal protein L19-A

Chain BS:  99%



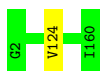
- Molecule 24: 60S ribosomal protein L20-A

Chain BT:  100%



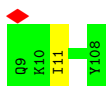
- Molecule 25: 60S ribosomal protein L21-A

Chain BU:  99%



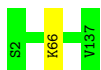
- Molecule 26: 60S ribosomal protein L22-A

Chain BV:  99%

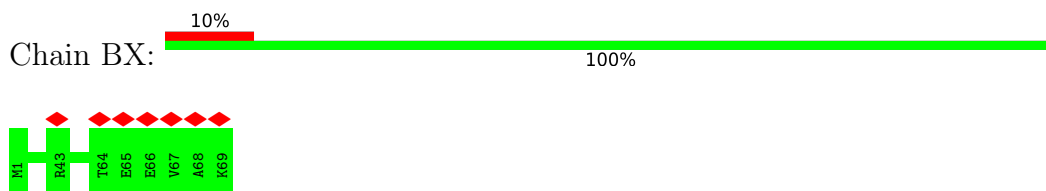


- Molecule 27: 60S ribosomal protein L23-A

Chain BW:  99%



- Molecule 28: 60S ribosomal protein L24-A

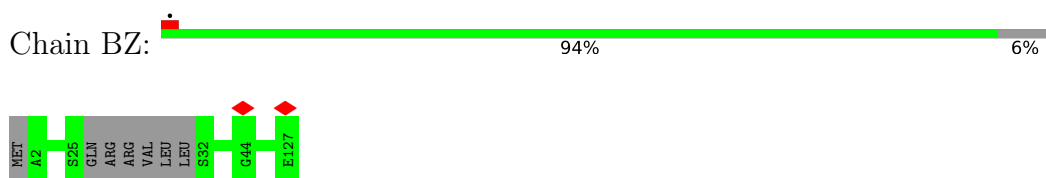


- Molecule 29: 60S ribosomal protein L25

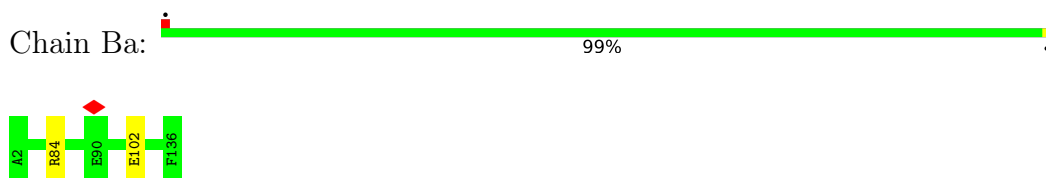


There are no outlier residues recorded for this chain.

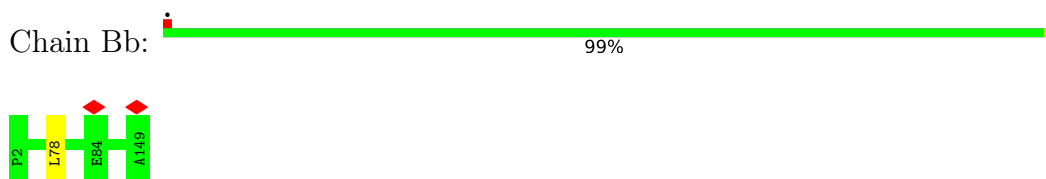
- Molecule 30: 60S ribosomal protein L26-A



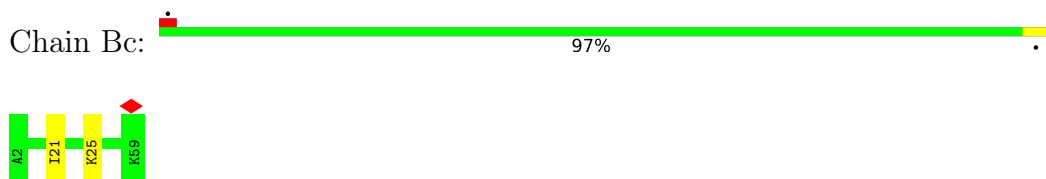
- Molecule 31: 60S ribosomal protein L27-A



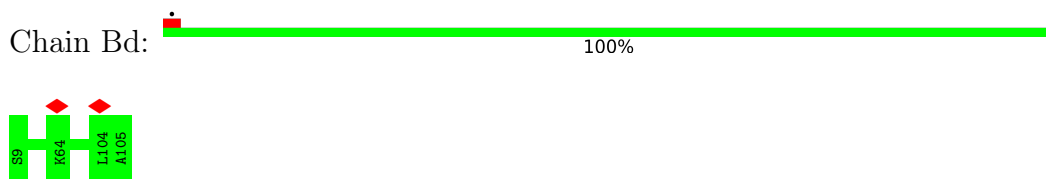
- Molecule 32: 60S ribosomal protein L28



- Molecule 33: 60S ribosomal protein L29

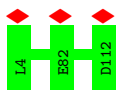


- Molecule 34: 60S ribosomal protein L30



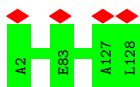
- Molecule 35: 60S ribosomal protein L31-A

Chain Be:  100%



- Molecule 36: 60S ribosomal protein L32

Chain Bf:  100%



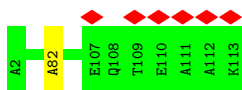
- Molecule 37: 60S ribosomal protein L33-A

Chain Bg:  100%

There are no outlier residues recorded for this chain.

- Molecule 38: 60S ribosomal protein L34-A

Chain Bh:  99%



- Molecule 39: 60S ribosomal protein L35-A

Chain Bi:  100%



- Molecule 40: 60S ribosomal protein L36-A

Chain Bj:  99%



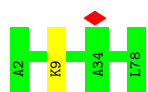
- Molecule 41: 60S ribosomal protein L37-A

Chain Bk:  100%



- Molecule 42: 60S ribosomal protein L38

Chain Bl:  99%



- Molecule 43: 60S ribosomal protein L39

Chain Bm:  98%



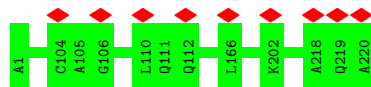
- Molecule 44: 60S ribosomal protein L40-A

Chain Bn:  100%



- Molecule 45: 60S ribosomal protein L10

Chain BK:  100%



## 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 [i](#)

### 5.1 Standard geometry [i](#)

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 [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	19	58
10	BE	359/361 (99%)	343 (96%)	14 (4%)	2 (1%)	25	64
11	BF	294/296 (99%)	288 (98%)	4 (1%)	2 (1%)	22	61
12	BG	152/176 (86%)	151 (99%)	1 (1%)	0	100	100
13	BH	220/222 (99%)	213 (97%)	5 (2%)	2 (1%)	17	56
14	BI	231/233 (99%)	225 (97%)	4 (2%)	2 (1%)	17	56
15	BJ	189/191 (99%)	186 (98%)	3 (2%)	0	100	100
16	BL	167/169 (99%)	154 (92%)	12 (7%)	1 (1%)	25	64
17	BM	191/193 (99%)	179 (94%)	9 (5%)	3 (2%)	9	43
18	BN	134/136 (98%)	130 (97%)	3 (2%)	1 (1%)	22	61
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%)	25	64
26	BV	98/100 (98%)	92 (94%)	5 (5%)	1 (1%)	15	54
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%)	19	58
32	Bb	146/148 (99%)	140 (96%)	5 (3%)	1 (1%)	22	61
33	Bc	56/58 (97%)	55 (98%)	0	1 (2%)	8	41
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%)	17	56
39	Bi	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
40	Bj	97/99 (98%)	91 (94%)	5 (5%)	1 (1%)	15	54
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%)	7	37
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%)	38	69

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 [i](#)

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%)	73	88
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%)	88	95
9	BD	320/322 (99%)	319 (100%)	1 (0%)	92	96
10	BE	288/288 (100%)	287 (100%)	1 (0%)	92	96
11	BF	244/244 (100%)	243 (100%)	1 (0%)	91	95
12	BG	134/153 (88%)	134 (100%)	0	100	100
13	BH	186/186 (100%)	185 (100%)	1 (0%)	88	95
14	BI	187/191 (98%)	186 (100%)	1 (0%)	88	95
15	BJ	171/171 (100%)	171 (100%)	0	100	100
16	BL	147/147 (100%)	145 (99%)	2 (1%)	67	86
17	BM	154/154 (100%)	153 (99%)	1 (1%)	86	94
18	BN	107/107 (100%)	107 (100%)	0	100	100
19	BO	175/175 (100%)	174 (99%)	1 (1%)	86	94
20	BP	160/160 (100%)	159 (99%)	1 (1%)	86	94
21	BQ	140/145 (97%)	139 (99%)	1 (1%)	84	94
22	BR	150/150 (100%)	150 (100%)	0	100	100
23	BS	131/131 (100%)	129 (98%)	2 (2%)	65	85
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%)	76	90
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%)	78	91
32	Bb	118/118 (100%)	118 (100%)	0	100	100
33	Bc	46/46 (100%)	45 (98%)	1 (2%)	52	79
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%)	65	85
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%)	91	95

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 [i](#)

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 [i](#)

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

#### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

#### 5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 23 are unknown and 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.

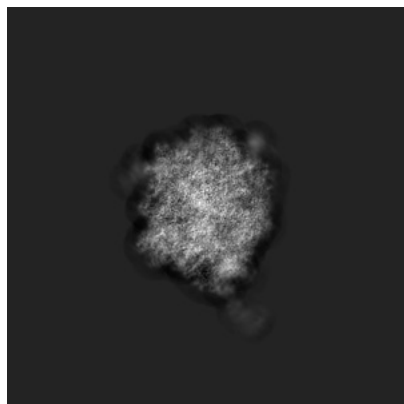
## 6 Map visualisation [i](#)

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.

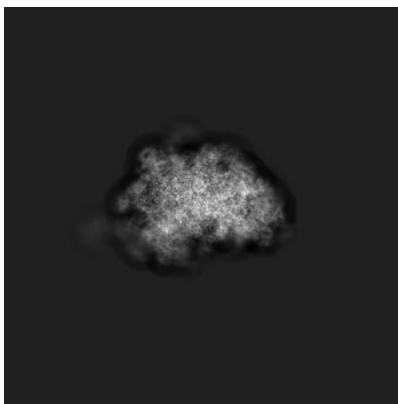
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

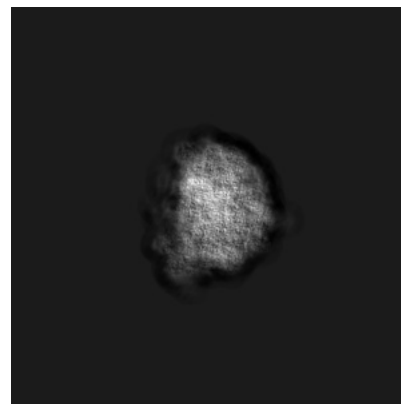
#### 6.1.1 Primary map



X

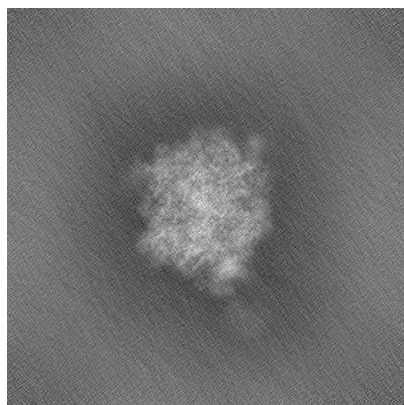


Y

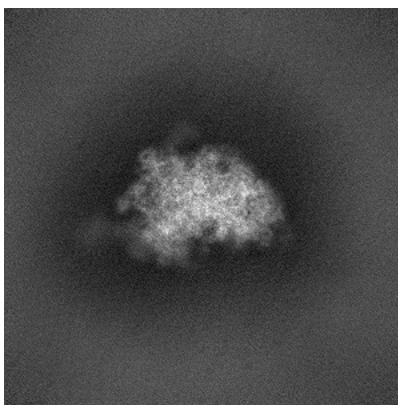


Z

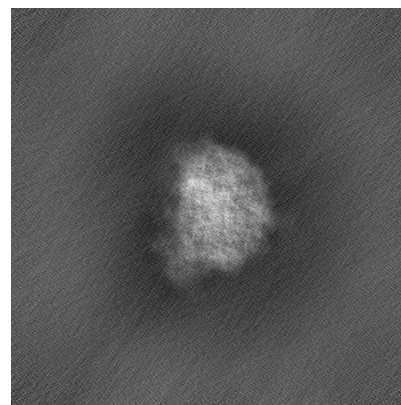
#### 6.1.2 Raw map



X



Y

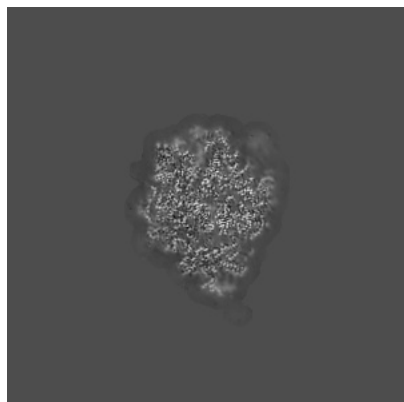


Z

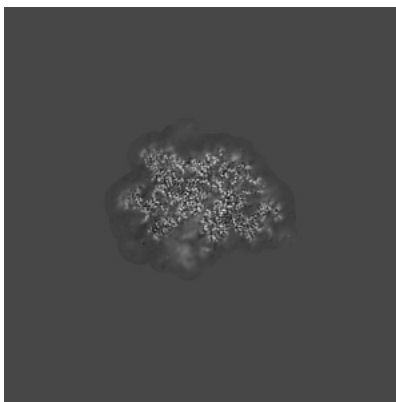
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

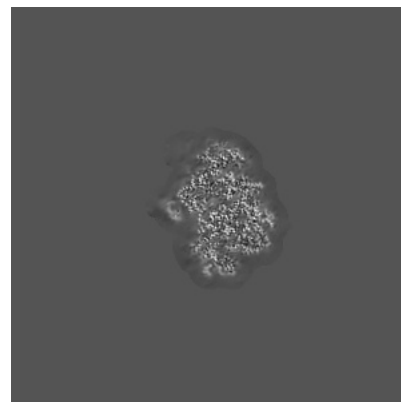
### 6.2.1 Primary map



X Index: 280

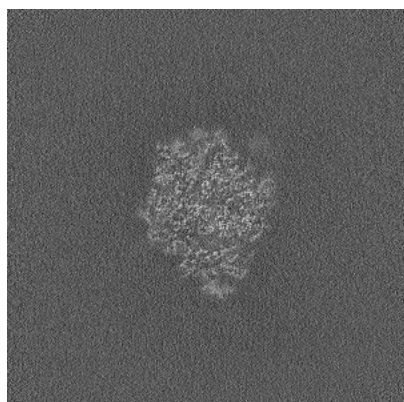


Y Index: 280

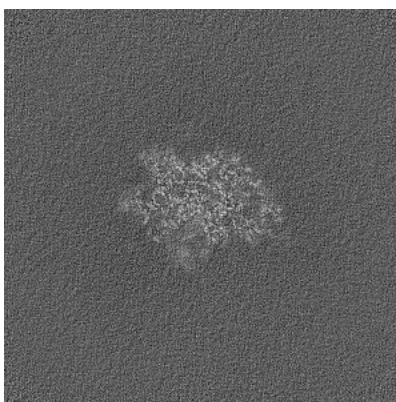


Z Index: 280

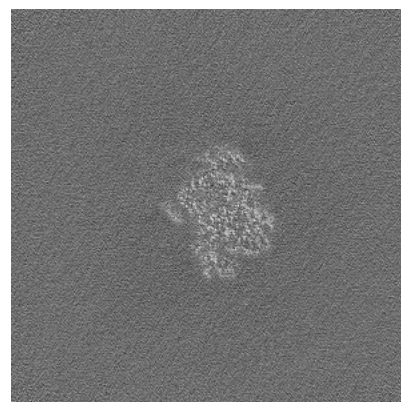
### 6.2.2 Raw map



X Index: 280



Y Index: 280

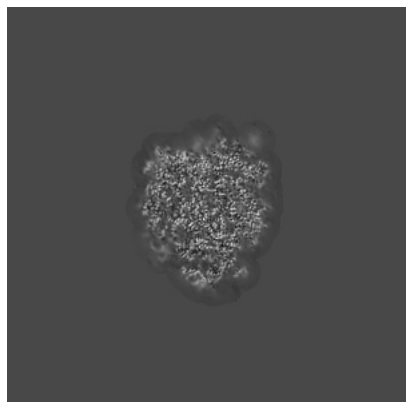


Z Index: 280

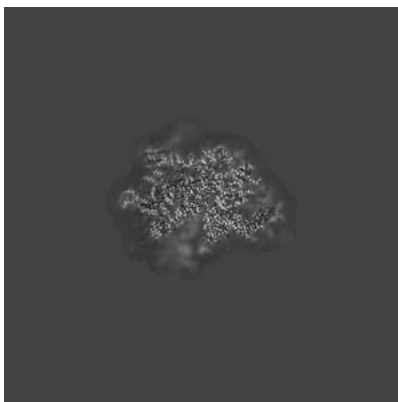
The images above show central slices of the map in three orthogonal directions.

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

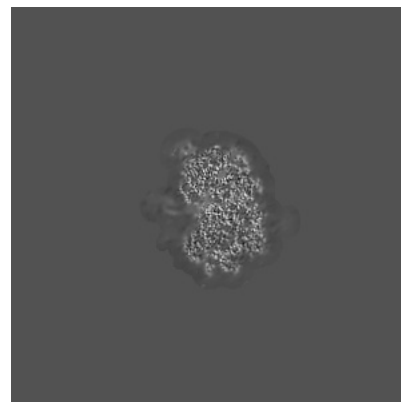
### 6.3.1 Primary map



X Index: 300

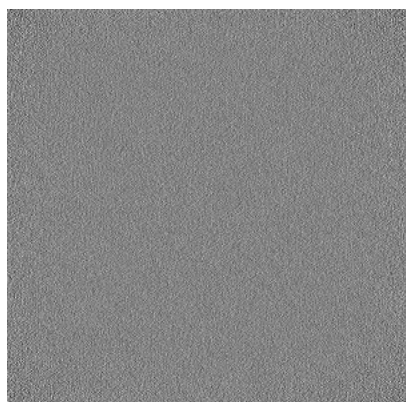


Y Index: 275

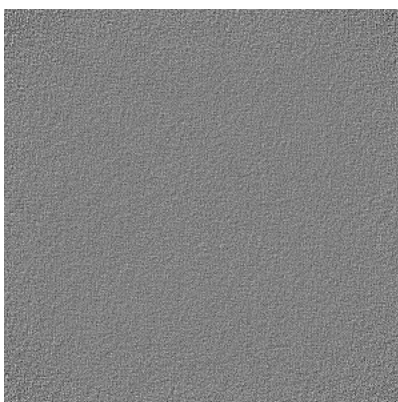


Z Index: 271

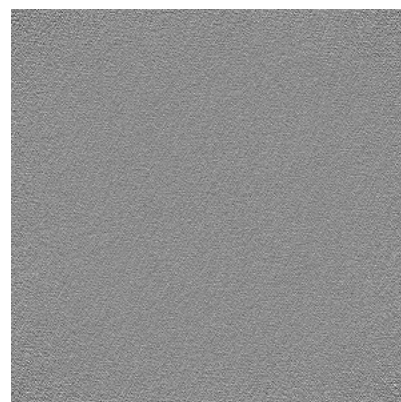
### 6.3.2 Raw map



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 surface views [i](#)

### 6.4.1 Primary map



X



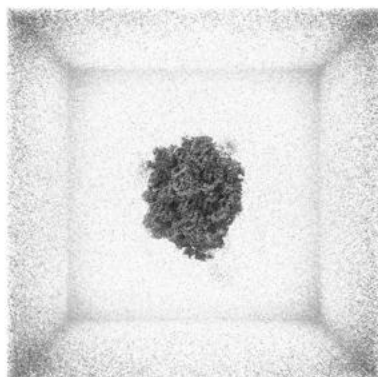
Y



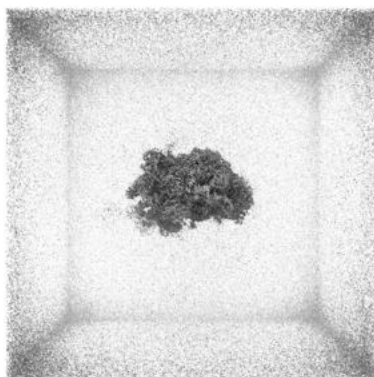
Z

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.

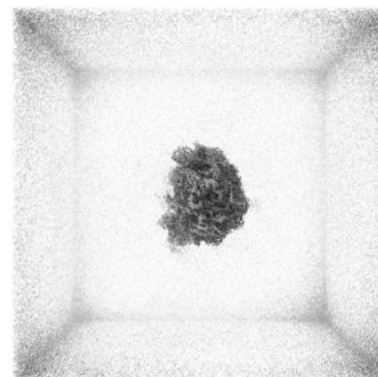
### 6.4.2 Raw map



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.

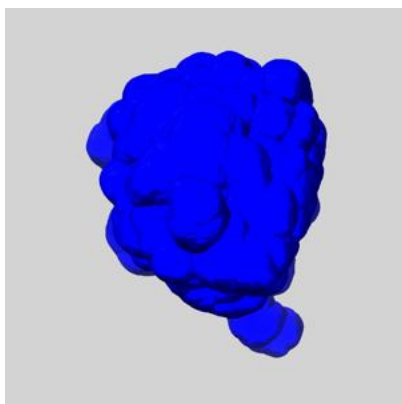
## 6.5 Mask visualisation [i](#)

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

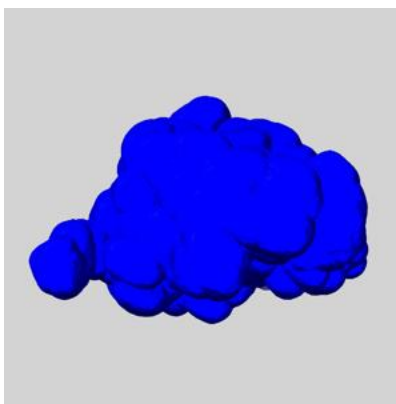
A mask typically either:

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

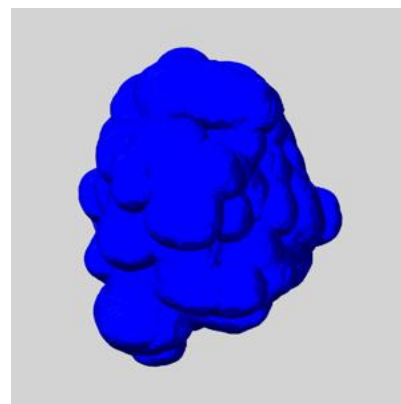
### 6.5.1 emd\_14926\_msk\_1.map [i](#)



X



Y

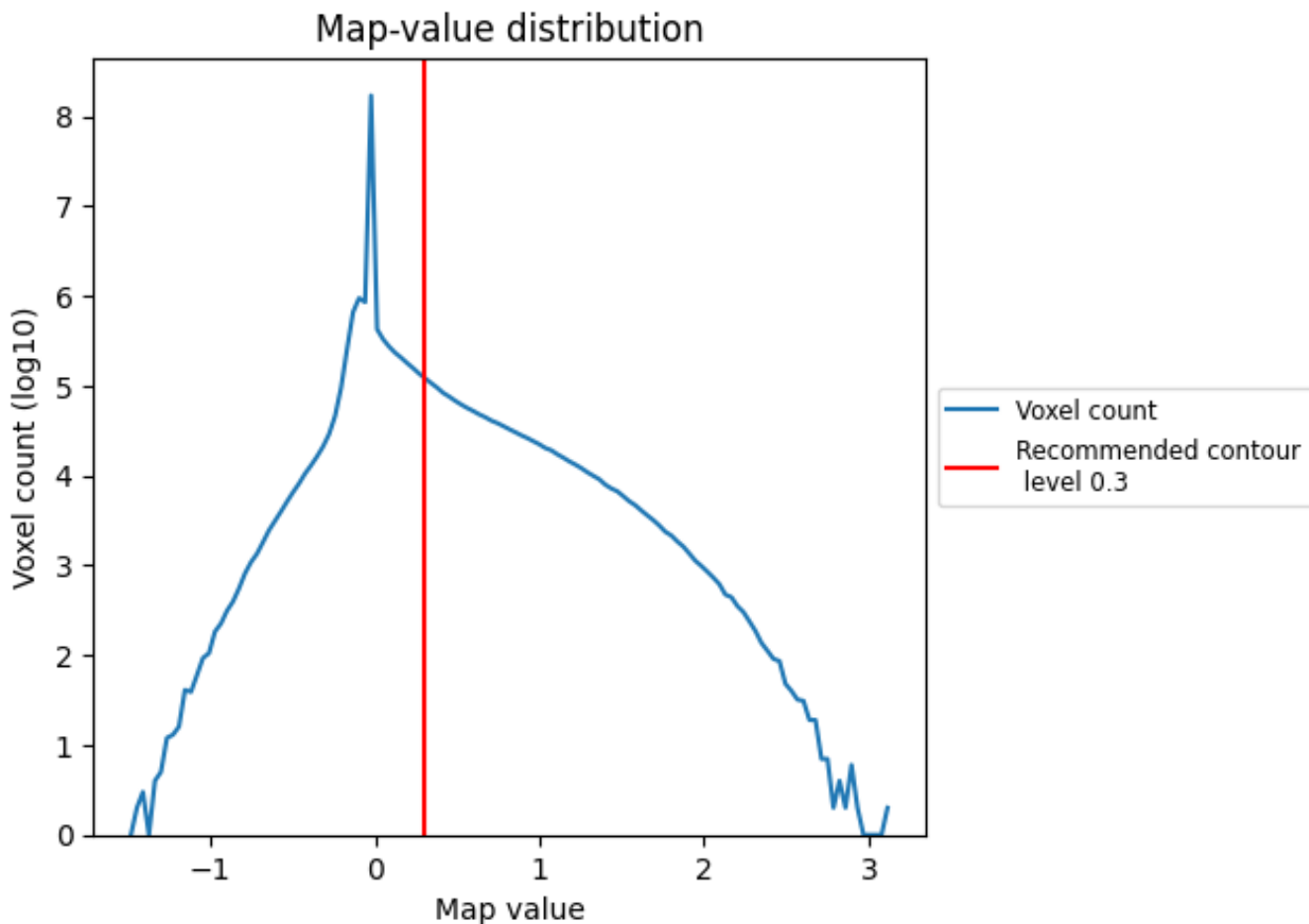


Z

## 7 Map analysis [i](#)

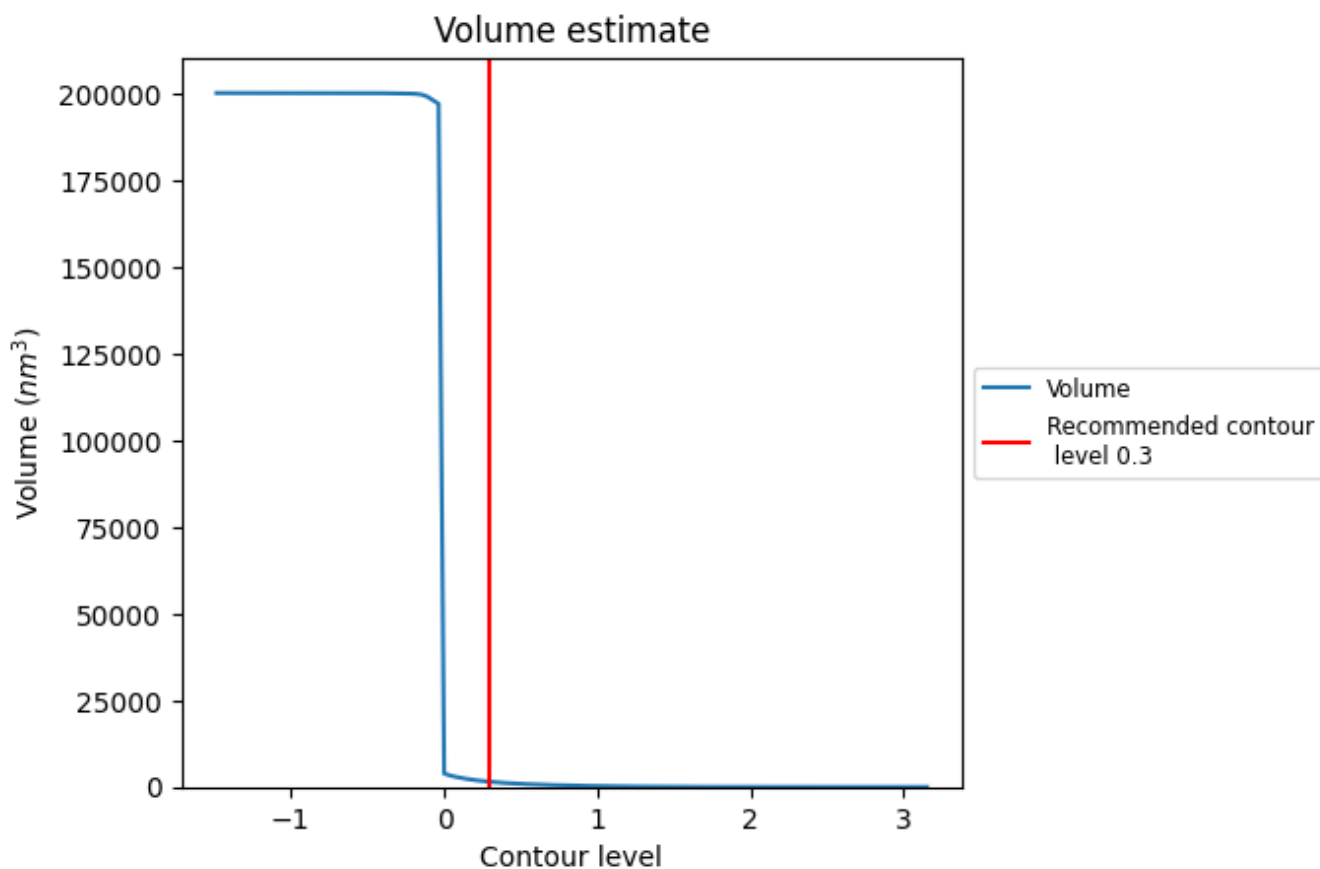
This section contains the results of statistical analysis of the map.

### 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.

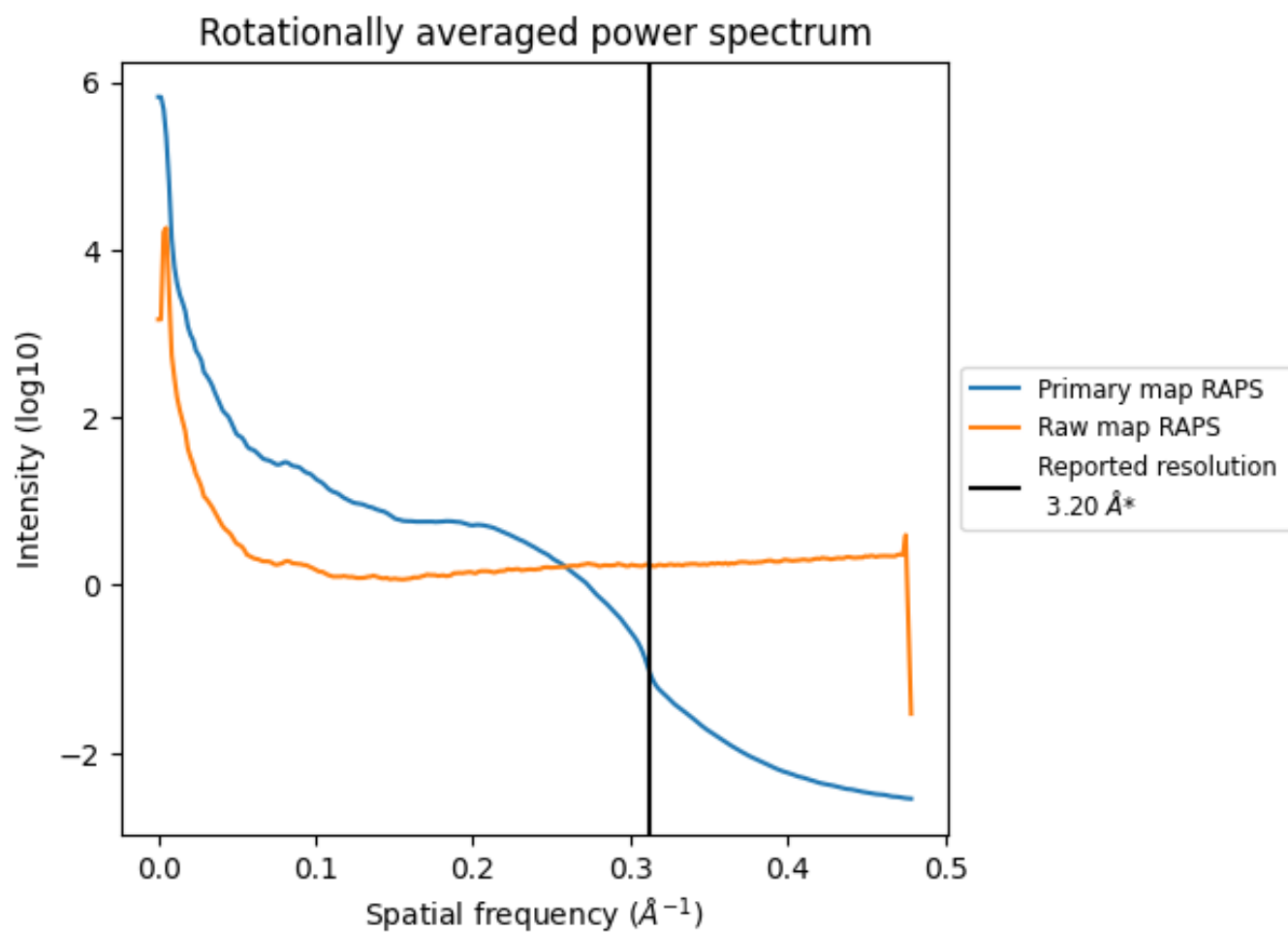
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is  $1499 \text{ nm}^3$ ; 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 i

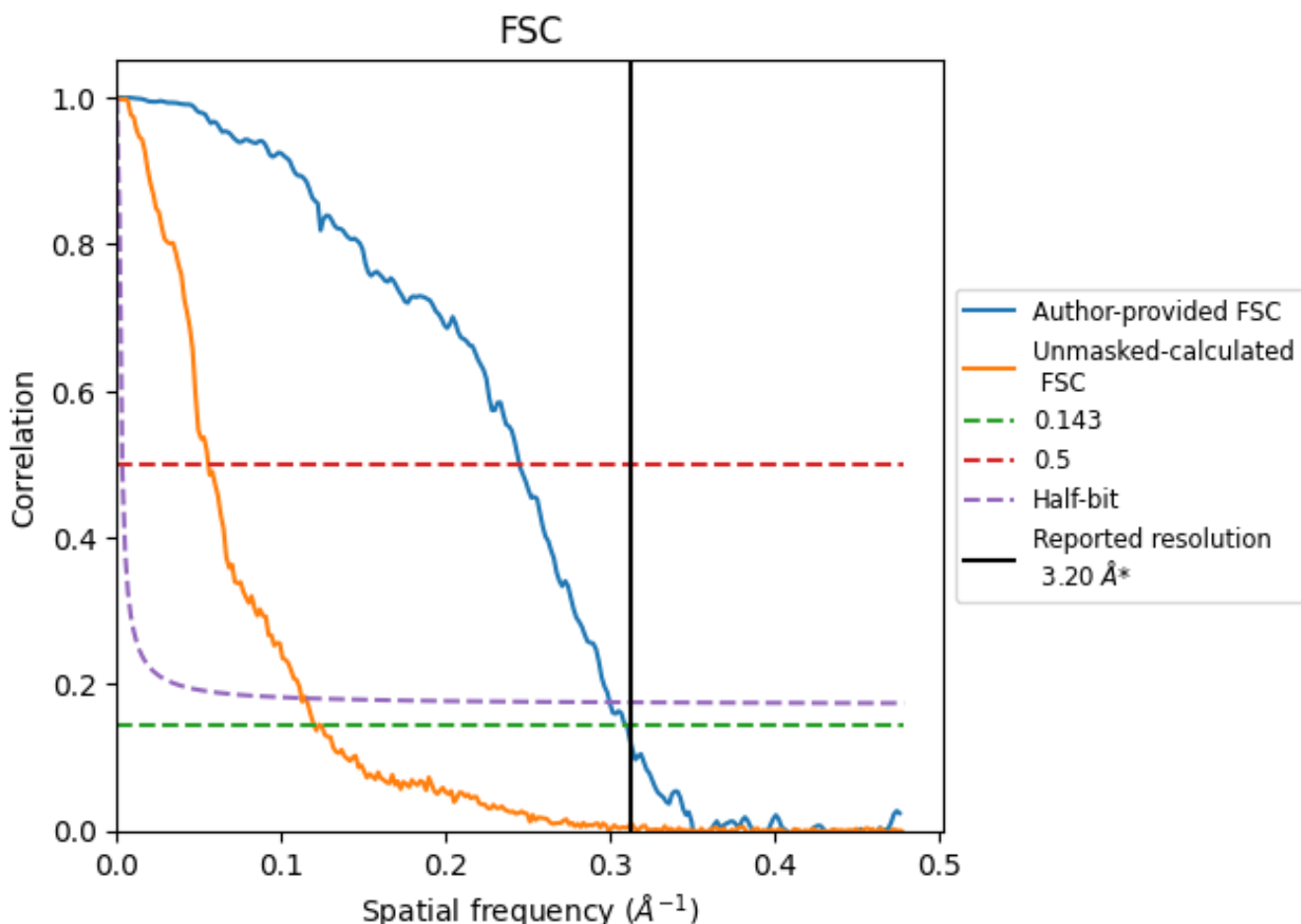


\*Reported resolution corresponds to spatial frequency of  $0.312 \text{ \AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



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

## 8.2 Resolution estimates [i](#)

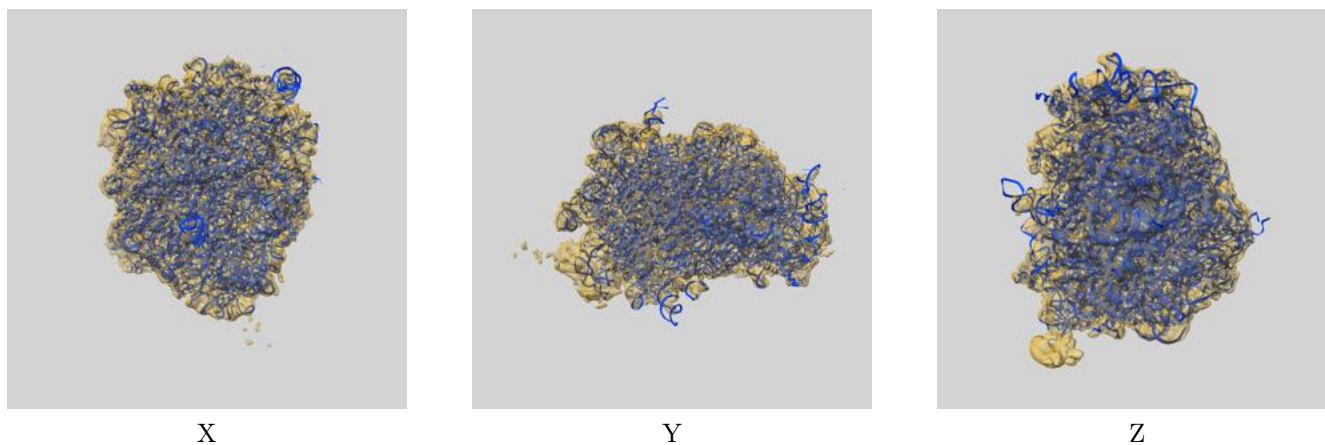
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.22	4.08	3.34
Unmasked-calculated*	8.33	17.99	8.90

\*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.

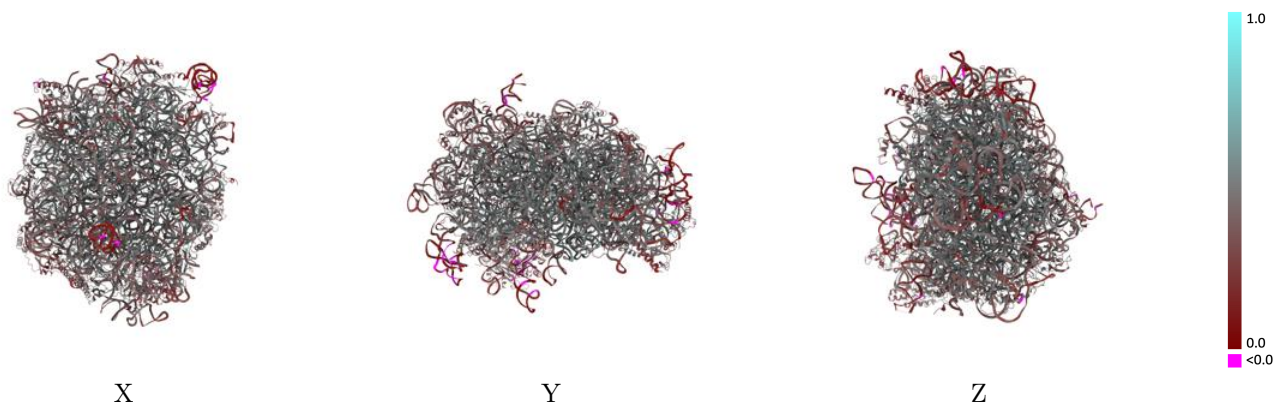
### 9.1 Map-model overlay [i](#)



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.

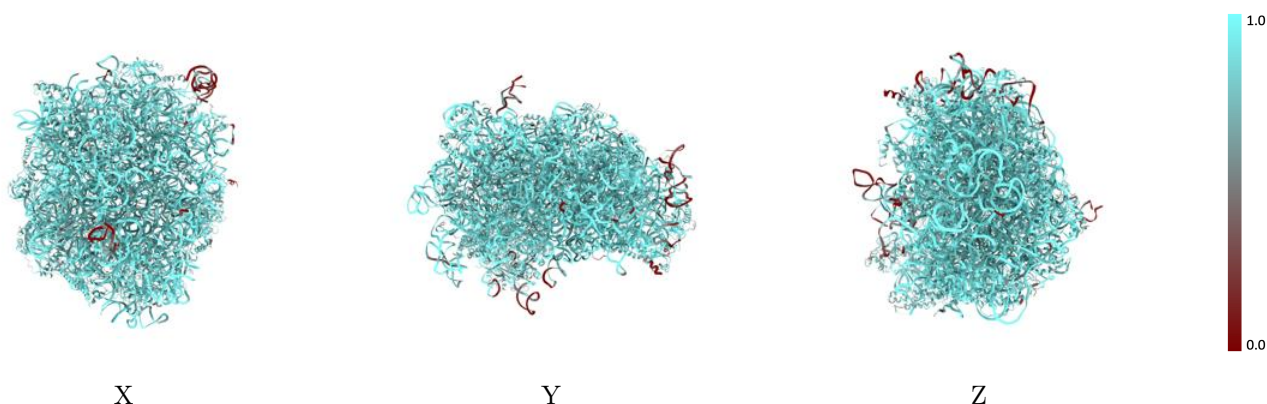


## 9.2 Q-score mapped to coordinate model [i](#)



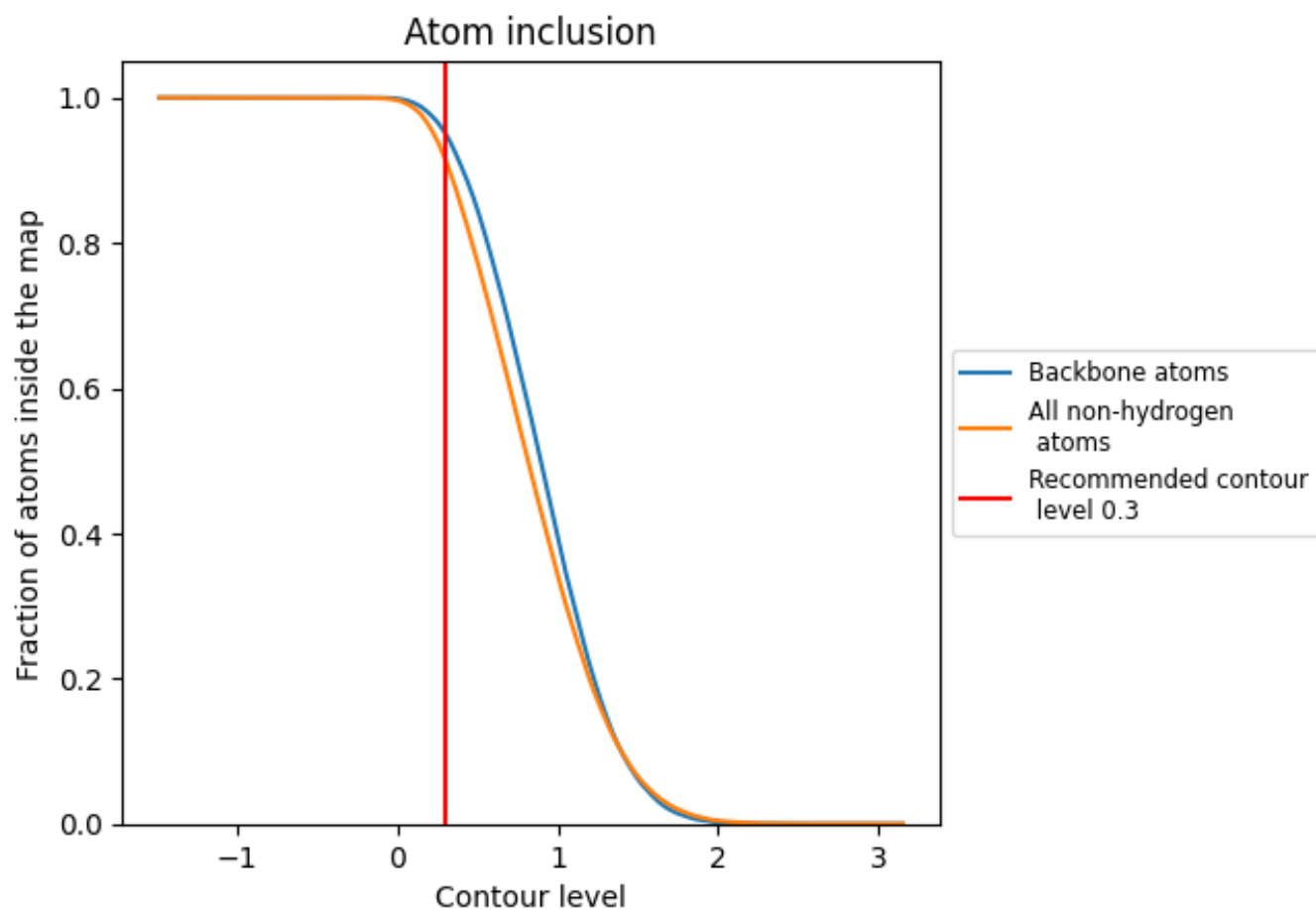
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.9138	 0.4210
1	 0.9385	 0.4160
2	 0.5327	 0.1110
3	 0.9624	 0.4120
4	 0.9776	 0.4490
A	 0.8318	 0.3510
BA	 0.8563	 0.4560
BB	 0.9193	 0.4630
BC	 0.9115	 0.4740
BD	 0.9184	 0.4570
BE	 0.9191	 0.4580
BF	 0.8490	 0.3730
BG	 0.8310	 0.3830
BH	 0.8886	 0.4470
BI	 0.8770	 0.3950
BJ	 0.8557	 0.4280
BK	 0.8612	 0.4220
BL	 0.8000	 0.3220
BM	 0.8716	 0.4410
BN	 0.8470	 0.3940
BO	 0.9444	 0.4970
BP	 0.9227	 0.4640
BQ	 0.9133	 0.4430
BR	 0.8932	 0.4620
BS	 0.8823	 0.4380
BT	 0.8730	 0.4500
BU	 0.8742	 0.4400
BV	 0.8824	 0.4000
BW	 0.9142	 0.4720
BX	 0.8547	 0.4210
BY	 0.9395	 0.4720
BZ	 0.8701	 0.4380
Ba	 0.8711	 0.4240
Bb	 0.9107	 0.4600
Bc	 0.8938	 0.4210



*Continued on next page...*

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Chain	Atom inclusion	Q-score
Bd	 0.8536	 0.4150
Be	 0.8812	 0.4630
Bf	 0.8883	 0.4570
Bg	 0.9026	 0.4710
Bh	 0.8719	 0.4410
Bi	 0.9120	 0.4320
Bj	 0.8725	 0.4210
Bk	 0.9450	 0.5100
Bl	 0.7913	 0.4030
Bm	 0.9116	 0.4690
Bn	 0.9132	 0.4600