



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:00 PM BST

PDB ID : 1C2W
EMDB ID: : unknown
Title : 23S RRNA STRUCTURE FITTED TO A CRYO-ELECTRON MICRO-
SCOPIE MAP AT 7.5 ANGSTROMS RESOLUTION
Authors : Brimacombe, R.; Mueller, F.
Deposited on : 1999-07-28
Resolution : 7.50 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

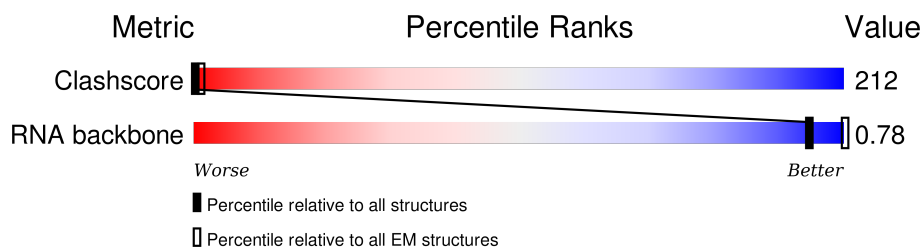
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY


The reported resolution of this entry is 7.50 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)
Clashescore	114402	924
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	B	2904	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	5MU	B	1915	-	-	X	-
1	5MU	B	1939	X	-	X	-
1	7MG	B	2069	-	-	X	-
1	5MU	B	2449	X	-	X	-
1	5MC	B	2498	X	-	X	-
1	7MG	B	745	-	-	X	-
1	PSU	B	746	-	-	X	-
1	5MU	B	747	-	-	X	-

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 62371 atoms, of which 23 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.

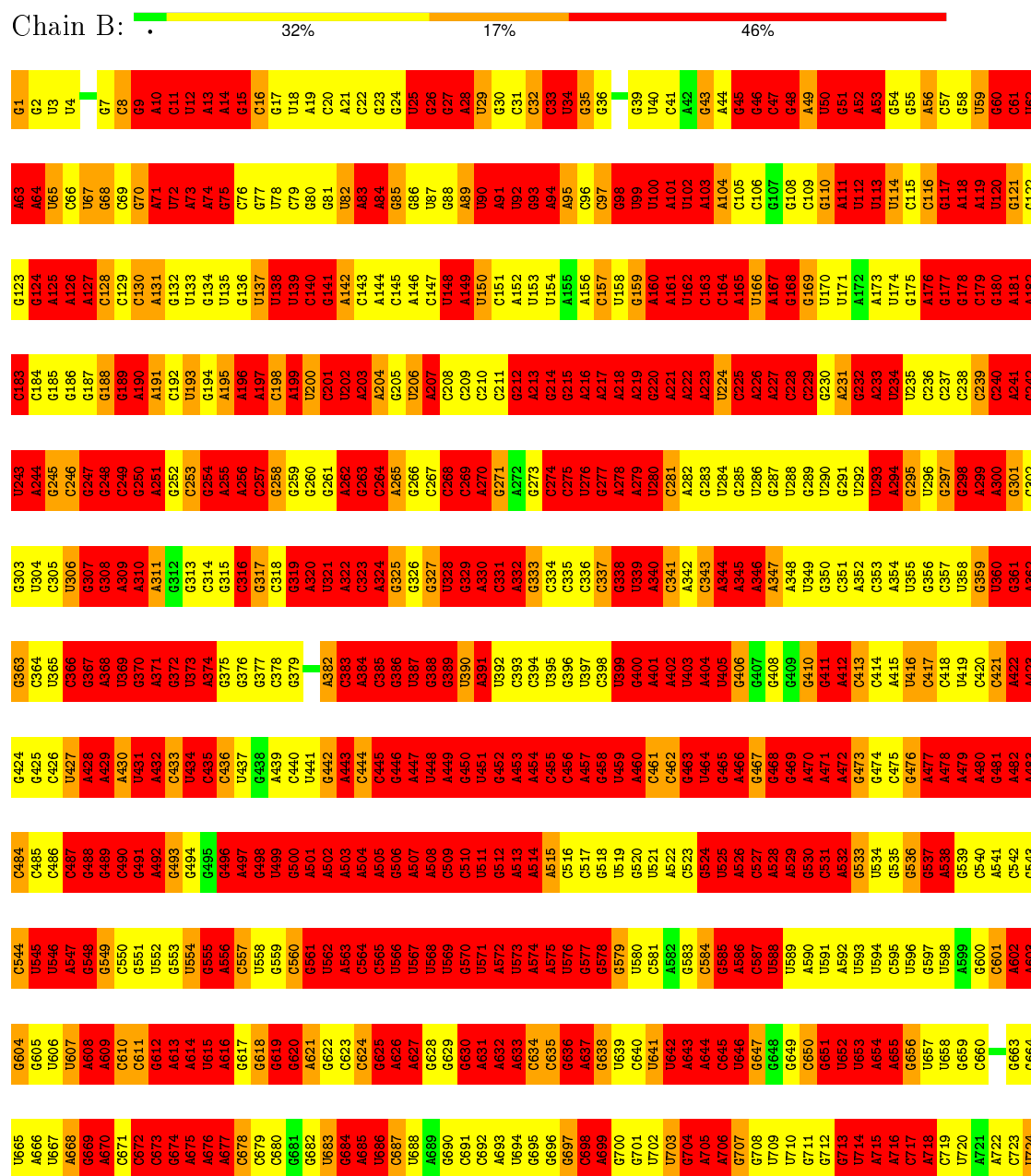
- Molecule 1 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	B	2904	Total	C	H	N	O	P	0	0
			62371	27819	23	11467	20158	2904		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: 23S RIBOSOMAL RNA






G2607	A2547	G2485	C2364	G2303	U2240	C2179	A2119	A2059	A1998	A1938	G1878	U1818	A1757	G1697
G2608	U2548	G2486	G2365	G2304	A2241	U2180	G2120	A2060	A1999	U1939	C1879	A1818	U1758	A1698
G2609	G2549	G2487	A2366	U2305	G2242	U2181	G2121	G2061	C2001	U1940	U1880	U1820	C1769	G1699
G2610	G2550	G2488	G2367	C2306	U2243	U2182	U2122	A2062		C1941	C1881	A1821	C1760	A1700
G2611	C2551	G2489	G2368	G2307	U2244	A2183	G2123	C2063		C1942	U1882	C1823	C1761	A1701
G2612	U2552	G2490	A2369	G2308	U2245	A2184	G2124	C2064	G2004	U1943	U1883	G1824	A1762	G1702
U2613	G2553	U2491	G2370	A2309	G2246	U2185	G2125	C2065	A2005	U1944	G1884	G1824	G1763	G1703
G2614	U2554	U2492	G2371	C2310	A2247	G2186	A2126	C2066	C2006	G1945	A1886	U1825	C1764	C1704
U2615	U2555	U2493	U2372	U2312	G2248	U2187	G2127	G2067	U2007	U1946	A1886	U1826	C1765	A1705
G2616	G2556	G2494	G2373	U2313	U2249	U2188	G2128	U2068	C2008	C1947	G1887	U1827	G1766	C1706
U2617	G2557	A2433	C2374	C2313	G2250	U2189	G2129	G2069	A2009	G1948	C1888	U1828	G1767	G1707
G2618	C2558	A2434	G2375		G2251	G2190	U2130	A2070	G2010	G1949	A1829	A1829	C1768	C1708
U2619	U2559	G2437	A2376	G2316	G2252	A2191	U2131	A2071	U2011	G1950	A1830	U1769	U1769	U1709
G2620	A2560	A2377	A2377	A2317	G2253	U2192	U2132	C2072	G2012	U1951	G1891	G1831	G1770	G1710
G2621	U2561	U2438	A2378	G2318	C2254	G2193	G2133	C2073	A2013	A1952	C1892	C1832	C1771	A1711
G2622	U2562	A2439	G2379	G2319	G2255	U2194	A2134	U2074	A2014	A1953	C1893	C1833	A1772	U1712
G2623	U2563	C2440	C2380	U2320	G2256	U2195	A2135	U2075	A2015	G1954	C1894	U1834	A1773	G1713
G2624	A2564	C2441	A2381	U2321	U2257	C2196	G2136	U2076	U2016	U1955	C1895	G1835	C1774	U1714
G2625	A2565	C2443	G2382	A2322	G2258	U2197	U2137	A2077	U2017	U1956	G1896	C1836	U1775	G1715
G2626	U2566	G2444	G2383	G2323	U2259	A2198	G2138	C2078	G2018	C1957	G1897	C1837	G1776	U1716
G2627	G2567	G2445	U2384	U2324	C2260	U2199	U2139	U2079	A2019	C1958	G1898	C1838	U1777	A1717
C2628	U2568	G2446	C2385	G2325	C2261	C2200	G2140	A2080	C2020	G1959	A1899	G1839	U1778	G1718
U2629	G2569	A2447	A2386	C2326	U2262	G2201	G2141	U2081	C2021	A1960	A1900	G1840	U1779	G1719
G2630	G2570	U2387	U2387	C2327	C2263	U2202	A2142	A2082	U2022	C1961	A1901	U1841	A1780	U1720
G2631	U2571	A2448	A2388	A2328	C2264	U2203	C2143	G2083	C2023	C1962	C1902	G1842	U1781	G1721
	A2572	A2450	G2388	U2329	U2265	G2204	G2144	C2084	G2024	U1963	G1903	C1843	U1782	A1722
G2635	C2573	A2451	U2390	G2330	A2266	A2205	C2145	U2085	C2025	G1964	G1904	C1844	A1783	G1723
G2636	G2574	C2452	G2391	G2331	A2267	C2206	C2146	U2086	U2026	C1965	G1905	G1845	G1724	G1724
U2637	C2575	A2453	A2392	C2332	A2268	C2207	A2147	A2087	G2027	A1966	G1906	G1846	U1725	U1725
G2638	G2576	G2454	U2393	A2333	G2269	C2208	G2148	A2088	U2028	C1967	G1907	A1847	C1726	G1726
A2639	G2577	G2455	C2394	U2334	A2270	G2209	U2149	C2089	G2029	G1968	C1908	A1848	C1788	C1727
G2640	U2578	C2456	C2395	A2335	G2271	U2210	C2150	A2090	A2030	A1969	C1909	G1849	A1789	C1728
G2641	C2579	U2457	G2396	A2336	U2272	A2211	U2151	C2091	A2031	A1970	G1910	G1850	C1790	U1729
G2642	U2580	G2458	G2397	G2337	A2273	A2212	C2152	U2092	G2032	A1971	U1911	U1851	A1791	G1730
G2643	G2581	A2459	U2398	C2338	A2274	U2213	C2153	G2093	A2033	G1972	C1912	U1852	G1792	G1731
G2644	U2582	U2460	G2399	C2339	C2275	C2214	A2154	A2094	U2034	G1973	A1913	A1853	C1793	G1732
G2645	G2583	A2461	G2400	A2340	U2276	C2215	U2155	A2095	G2035	C1974	C1914	A1854	A1794	G1733
C2646	U2584	C2462	U2401	G2341			G2156	C2096	C2036	U1976	U1916	U1855	C1795	G1734
U2647	U2585	C2463	U2402	C2342	A2281	G2218	G2157	A2097	A2037	A1977	U1917	U1856	U1796	G1735
G2648	U2586	G2464	C2403	U2343	G2282	U2219	A2158	U2098	G2038	C1977	U1917	G1857	G1797	U1736
G2649	A2587	C2465	U2404	U2344	C2283	U2220	C2159	U2099	U2039	A1978	A1918	A1858	U1798	G1737
U2650	G2588	C2466	G2405	G2345	A2284	G2221	C2160	G2100	G2040	U1979	A1919	U1859	G1799	G1738
C2651	A2589	C2467	A2406	C2346	C2285	G2222	C2161	A2101	U2041	G1980	C1920	G1860	A1800	A1739
C2652	G2590	A2468	U2407	C2347	G2286	G2223	G2162	G2102	A2042	A1981	G1921	G1861	A1801	G1740
	C2591	A2469	U2408	U2348	A2287	G2224	A2163	C2103	C2043	U1982	G1922	G1862	A1802	C1741
A2654	G2592	G2470	G2409	G2349	A2288	A2225	C2164	C2104	C2044	G1983	U1923	G1863	A1803	U1742
G2655	U2593	A2471	C2410	C2350	G2289	C2226	C2165	U2105	C2045	G1984	C1924	U1864	C1804	G1743
U2656	C2594	G2472	G2411	G2351	G2290	A2227	U2166	U2106	G2046	C1985	G1925	U1865	A1805	A1744
A2657	G2595	U2473	A2412	A2352	U2291	G2228	U2167	G2107	C2047	C1986	U1926	A1866	A1806	A1745
C2658	U2596	U2474	G2413	G2353	U2292	U2229	G2168	A2108	G2048	A1987	A1927	G1867	G1807	A1746
G2659	G2597	C2475	G2414	C2354	G2293	G2230	A2169	U2109	G2049	G1988	A1928	C1868	A1808	U1747
A2660	A2598	A2476	G2415	G2355	G2294	U2231	A2170	G2110	C2050	G1989	G1929	G1869	A1809	C1748
G2661	U2599	U2477	C2416	U2356	C2295	C2232	A2171	U2111	A2051	C1990	G1930	C1870	A1810	A1749
A2662	C2600	G2478	C2417	G2357	U2296	U2233	U2172	G2112	A2052	U1991	U1931	A1871	G1811	G1750
G2663	C2601	U2479	A2418	A2358	A2297	G2234	A2173	U2113	G2053	G1992	A1932	A1872	U1812	U1751
G2664	A2602	C2480	U2419	C2359	G2298	G2235	C2174	A2114	A2054	U1993	G1933	G1873	G1813	C1752
A2665	G2603	G2481	C2420	G2360	U2299	U2236	C2175	G2115	C2055	C1994	C1934	C1874	G1814	G1753
U2664	U2604	A2482	G2421	G2361	C2301	U2237	A2176	G2116	G2056	U1995	G1935	A1875	A1815	A1754
G2667	U2605	C2483	C2422	C2362	C2300	G2238	C2177	A2117	G2057	A1996	A1936	A1876	A1816	A1755
G2668	C2606	U2494	U2423	G2363	U2302	G2239	C2178	U2118	A2068	C1997	A1937	A1877	G1817	G1756

A2851	G2791	G2731	G2671
G2852	A2792	G2732	U2672
G2853	C2793	A2733	G2673
G2854	C2794	A2734	G2674
C2855	C2795	G2735	A2675
A2856	U2796	A2736	C2676
G2857	U2797	G2737	G2677
G2858	U2798	A2738	C2678
G2859	A2799	U2739	A2679
A2860	A2800	A2740	U2680
U2861	A2801	A2741	C2681
G2862	G2802	G2742	A2682
G2863	G2803	U2743	C2683
G2864	U2804	G2744	U2684
U2865	C2805	G2745	G2685
U2866	C2806	U2746	G2686
G2867	U2807	G2747	U2687
A2868	G2808	A2748	G2688
G2869	G2809	A2749	U2689
G2870	A2810	A2750	U2690
U2871	G2811	G2751	C2691
A2872	G2812	C2752	
A2873	A2813	A2753	G2694
C2874	A2814	U2754	U2695
C2875	G2815	G2755	U2696
G2876	G2816	U2756	G2697
G2877	U2817	A2757	U2698
U2878	U2818	A2758	C2699
A2879	G2819	G2759	A2700
C2880	A2820	C2760	U2701
U2881	A2821	A2761	G2702
A2882	G2822	C2762	C2703
A2883	A2823	G2763	C2704
U2884	C2824	A2764	A2705
G2885	G2825	A2765	A2706
A2886	A2826	A2766	U2707
G2887	C2827	C2767	G2708
C2888	G2828	U2768	G2709
C2889	A2829	U2769	C2710
G2890	C2830	G2770	A2711
U2891	G2831	C2771	C2712
G2892	U2832	C2772	U2713
A2893	U2833	C2773	G2714
G2894	G2834	G2774	C2715
G2895	A2835	G2775	C2716
C2896	U2836	A2776	C2717
U2897	A2837	G2777	G2718
U2898	G2838	A2778	G2719
A2899	G2839	U2779	U2720
A2900	C2840	G2780	A2721
C2901	C2841	A2781	G2722
C2902	G2842	G2782	C2723
U2903	G2843	U2783	U2724
U2904	G2844	U2784	A2725
	U2845	G2785	A2726
	G2846	U2786	A2727
	U2847	C2787	U2728
	G2848	C2788	G2729
	U2849	U2789	C2730

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	Not provided	Depositor
Voltage (kV)	Not provided	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, 1MA, 7MG, 5MC, PSU

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	B	5.79	6577/69489 (9.5%)	3.05	5861/108346 (5.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	466	117

The worst 5 of 6577 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	120	U	P-O5'	65.66	2.25	1.59
1	B	2848	G	C1'-N9	60.36	2.39	1.48
1	B	75	G	P-O5'	53.62	2.13	1.59
1	B	2322	A	P-O5'	53.13	2.12	1.59
1	B	429	A	C3'-O3'	52.73	2.15	1.42

The worst 5 of 5861 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	120	U	O5'-P-OP2	-42.40	59.83	110.70
1	B	1103	A	O5'-P-OP2	-38.71	64.25	110.70
1	B	239	C	P-O3'-C3'	-37.22	75.03	119.70
1	B	913	U	P-O5'-C5'	35.58	177.83	120.90
1	B	2849	U	P-O5'-C5'	35.58	177.83	120.90

5 of 466 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	10	A	C4'
1	B	12	U	C4'
1	B	15	G	C4'
1	B	27	G	C4',C3'
1	B	28	A	C4'

5 of 117 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	10	A	Sidechain
1	B	14	A	Sidechain
1	B	52	A	Sidechain
1	B	53	A	Sidechain
1	B	64	A	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	62348	23	31477	19819	0
All	All	62348	23	31477	19819	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 212.

The worst 5 of 19819 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:318:C:H5'	1:B:319:G:C8	1.24	1.68
1:B:69:C:H4'	1:B:85:G:C4'	1.23	1.68
1:B:1853:A:H4'	1:B:1853:A:C5'	1.23	1.68
1:B:1627:G:H1'	1:B:1641:A:C8	1.27	1.67
1:B:901:C:H5'	1:B:902:C:C5	1.19	1.66

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	2880/2904 (99%)	1502 (52%)	1148 (39%)

5 of 1502 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	9	G
1	B	10	A
1	B	11	C
1	B	12	U
1	B	13	A

5 of 1148 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	B	1326	U
1	B	1614	A
1	B	2713	U
1	B	1359	A
1	B	1495	A

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

13 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is

the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	1MA	B	1618	1	15,25,26	1.90	4 (26%)	15,37,40	1.78	5 (33%)
1	PSU	B	1911	1	15,21,22	1.66	3 (20%)	16,30,33	3.74	3 (18%)
1	5MU	B	1915	1	13,22,23	1.13	1 (7%)	16,32,35	5.04	4 (25%)
1	PSU	B	1917	1	15,21,22	1.39	2 (13%)	16,30,33	3.73	4 (25%)
1	5MU	B	1939	1	13,22,23	1.53	3 (23%)	16,32,35	5.14	5 (31%)
1	1MA	B	2030	1	15,25,26	1.78	4 (26%)	15,37,40	1.79	4 (26%)
1	7MG	B	2069	1	20,26,27	1.98	6 (30%)	23,39,42	2.44	5 (21%)
1	7MG	B	2251	1	20,26,27	6.93	8 (40%)	23,39,42	2.48	4 (17%)
1	5MU	B	2449	1	13,22,23	2.87	3 (23%)	16,32,35	5.43	6 (37%)
1	5MC	B	2498	1	14,22,23	2.17	2 (14%)	17,32,35	2.07	4 (23%)
1	7MG	B	745	1	20,26,27	6.83	8 (40%)	23,39,42	3.18	8 (34%)
1	PSU	B	746	1	15,21,22	1.50	3 (20%)	16,30,33	4.01	6 (37%)
1	5MU	B	747	1	13,22,23	1.27	2 (15%)	16,32,35	4.95	3 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	1MA	B	1618	1	-	0/3/25/26	0/3/3/3
1	PSU	B	1911	1	-	0/7/25/26	0/2/2/2
1	5MU	B	1915	1	-	0/3/25/26	0/2/2/2
1	PSU	B	1917	1	-	0/7/25/26	0/2/2/2
1	5MU	B	1939	1	2/2/5/5	0/3/25/26	0/2/2/2
1	1MA	B	2030	1	-	0/3/25/26	0/3/3/3
1	7MG	B	2069	1	-	0/7/37/38	0/3/3/3
1	7MG	B	2251	1	-	0/7/37/38	0/3/3/3
1	5MU	B	2449	1	1/1/5/5	1/3/25/26	0/2/2/2
1	5MC	B	2498	1	1/1/5/5	0/3/25/26	0/2/2/2
1	7MG	B	745	1	-	0/7/37/38	0/3/3/3
1	PSU	B	746	1	-	0/7/25/26	0/2/2/2
1	5MU	B	747	1	-	0/3/25/26	0/2/2/2

The worst 5 of 49 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	2251	7MG	C8-N9	-5.22	1.37	1.45
1	B	2069	7MG	C8-N9	-5.03	1.38	1.45
1	B	745	7MG	C8-N9	-4.83	1.38	1.45
1	B	1911	PSU	C5-C1'	-3.93	1.48	1.52
1	B	746	PSU	C6-C5	-3.09	1.34	1.38

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	747	5MU	C5-C4-N3	-13.64	113.90	125.35
1	B	2449	5MU	C5-C4-N3	-13.51	114.01	125.35
1	B	1915	5MU	C5-C4-N3	-13.44	114.07	125.35
1	B	1939	5MU	C5-C4-N3	-13.37	114.13	125.35
1	B	2069	7MG	C5-C6-N1	-8.14	111.27	123.39

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	2449	5MU	C4'
1	B	1939	5MU	C4'
1	B	1939	5MU	C3'
1	B	2498	5MC	C4'

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	2449	5MU	P-O5'-C5'-C4'

There are no ring outliers.

13 monomers are involved in 161 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	1618	1MA	1	0
1	B	1911	PSU	1	0
1	B	1915	5MU	10	0
1	B	1917	PSU	6	0
1	B	1939	5MU	41	0
1	B	2030	1MA	4	0
1	B	2069	7MG	14	0
1	B	2251	7MG	1	0
1	B	2449	5MU	14	0
1	B	2498	5MC	18	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	745	7MG	18	0
1	B	746	PSU	22	0
1	B	747	5MU	26	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.