



wwPDB EM Validation Summary Report ⓘ

Dec 17, 2023 – 08:22 PM EST

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

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

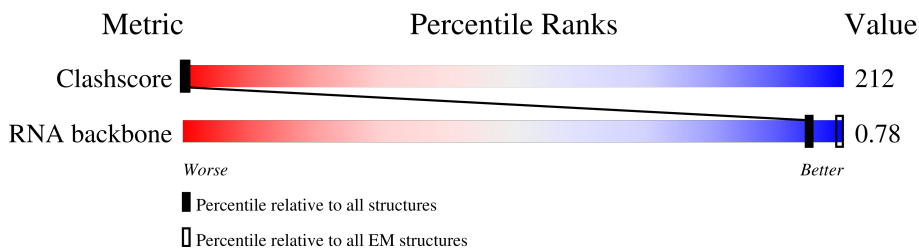
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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	158937	4297
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 ≥ 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 $\leq 5\%$

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

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.

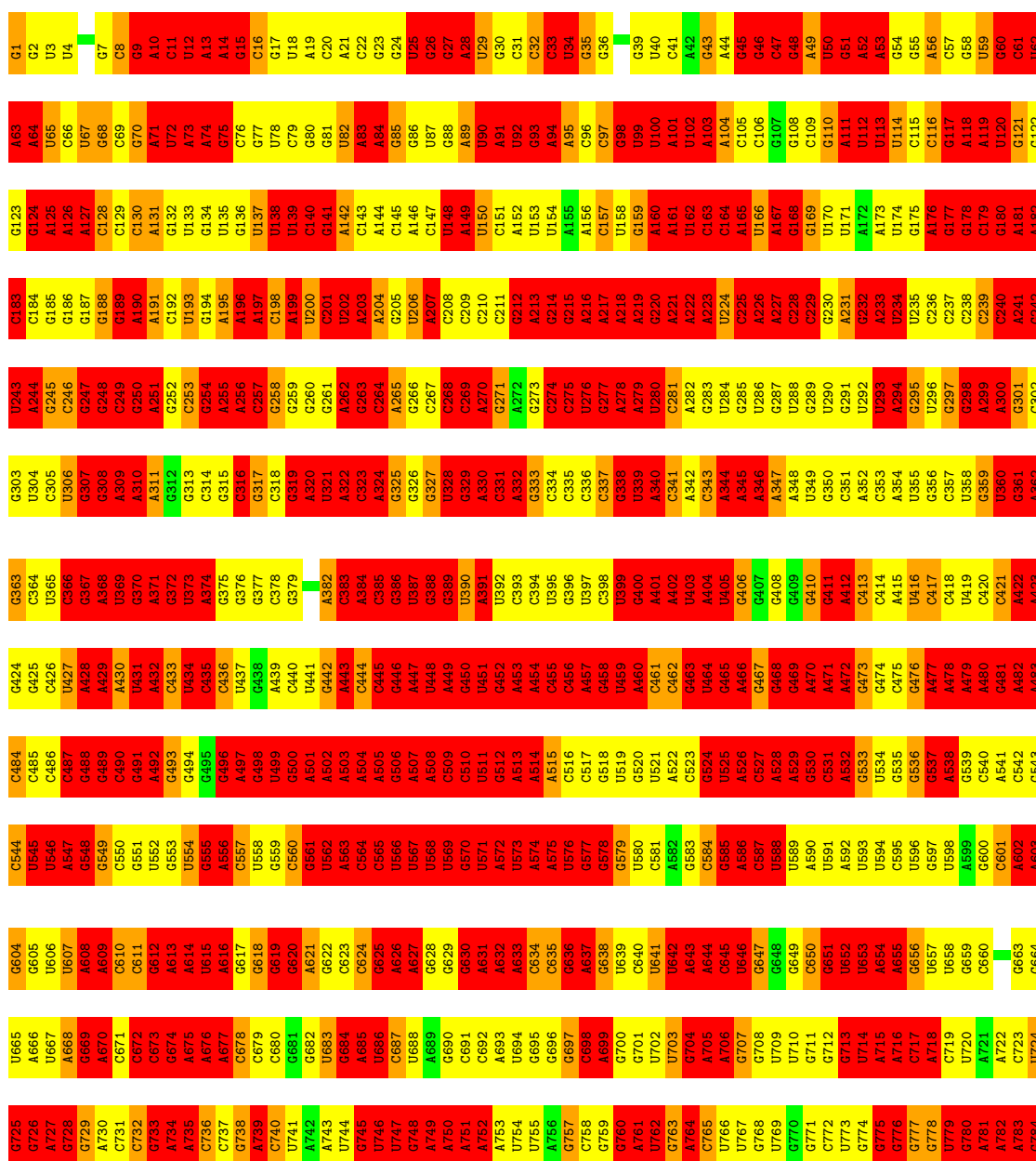
Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	B	2904	62371	27819	23	11467	20158	2904	0	0

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. 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

Chain B: 



G1697	U1636	A1453	A1593	C1330	U1209	U1148	A1088	A1028	C968	A905	U845	G785
A1698	A1637	C1454	U1594	G1331	G1210	G1149	A1089	A1029	G969	U906	U846	C786
G1699	C1638	G1455	U1395	G1332	G1271	C1150	A1090	C1030	G970	G907	U847	C787
A1700	A1640	G1456	U1396	G1333	G1212	C1151	A1091	G1031	C971	C908	U848	A788
G1701	A1641	U1457	U1397	G1334	A1213	C1152	A1092	U1032	A972	A910	U849	A789
G1702	G1642	U1458	C1398	C1335	A1214	C1153	G1093	U1033	A973	A911	U850	U790
G1703	G1643	G1459	C1399	G1339	G1215	C1154	U1094	G1034	G974	C912	C851	C791
G1704	C1644	U1460	U1400	G1339	G1216	A1155	A1095	U1035	A975	C915	U852	A792
G1706	G1645	C1461	U1401	U1340	U1217	A1156	A1096	G1036	G976	U913	C853	A793
G1707	A1646	A1462	U1402	G1341	G1218	C1157	A1097	G1037	G977	C914	U854	A794
G1708	C1647	C1463	A1403	A1342	U1219	C1158	A1098	U1038	G978	C915	G855	C795
G1709	U1648	G1464	C1404	G1343	G1220	U1159	G1099	A1039	A979	A916	G856	C796
G1710	G1648	G1465	U1405	U1344	C1221	C1160	C1100	A1040	A980	A917	G857	G797
G1711	A1650	U1466	U1406	C1345	U1222	G1161	U1101	G1041	A881	A918	C858	G798
G1712	G1651	U1467	G1407	G1346	G1223	G1162	A1102	G1042	C982	U919	G859	G799
G1713	A1652	C1468	U1408	A1347	U1224	G1163	A1103	G1043	C983	A920	U860	A800
G1714	C1653	A1469	U1409	C1348	G1225	C1164	U1104	C1044	A984	C921	A861	G801
G1715	A1654	A1470	U1410	C1349	A1226	A1165	U1105	G1045	C985	G922	G862	A802
G1716	A1655	G1471	U1411	C1350	G1227	G1166	G1106	A1046	C986	G926	A863	U803
G1717	A1596	C1472	U1412	C1351	G1228	C1167	G1107	G1047	C987	A927	A864	A804
G1718	G1597	G1473	A1413	U1352	C1229	G1168	U1108	A1048	A988	A928	C865	G805
G1719	A1598	U1474	C1414	A1353	A1230	A1169	C1109	C1049	G989	A929	A866	C806
G1720	U1599	G1475	U1415	A1354	U1231	C1170	G1110	A1050	A990	U929	C867	U807
G1721	C1600	U1476	G1416	G1355	C1232	G1171	A1111	G1051	C991	G930	U868	G808
G1722	U1601	A1477	C1417	G1356	G1233	C1172	U1112	C1052	C992	U931	G869	G809
G1723	G1663	G1478	G1418	C1357	U1234	U1173	U1113	C1053	G993	U932	U870	U810
G1724	A1664	C1479	A1419	G1358	G1235	U1174	C1114	A1054	C994	A933	U871	U811
G1725	A1665	U1480	A1420	A1359	G1236	A1175	G1115	U1055	C995	U934	U872	C812
G1726	C1666	U1481	G1421	G1360	A1237	U1176	U1116	G1056	A996	C935	C873	U813
G1727	G1667	G1482	G1422	G1361	G1238	G1177	C1117	A1057	A936	U936	G874	C814
G1728	A1668	G1483	G1423	C1362	G1239	C1178	U1118	U1058	C998	G937	G875	C815
G1729	C1670	U1484	G1424	C1363	U1240	G1179	U1119	G1059	U999	G938	C876	C816
G1730	C1671	U1485	G1425	G1364	A1241	U1180	G1120	U1060	A1000	G939	A877	C817
G1731	U1671	A1486	A1426	A1365	U1242	U1181	C1121	U1061	A1001	G940	G878	G818
G1732	A1672	U1487	G1427	A1366	A1304	U1182	A1122	G1062	G1002	A941	A879	A819
G1733	C1673	C1488	C1428	A1367	C1305	U1183	C1123	G1063	G1003	G942	G880	A820
G1734	G1674	A1489	G1429	G1368	G1245	U1184	G1124	C1064	U1004	A943	G881	A821
G1735	C1675	A1490	C1430	G1369	A1246	G1185	G1125	U1065	C1005	C944	G882	G822
G1736	A1676	G1491	A1431	C1370	A1247	U1186	A1126	U1066	C1006	A945	G883	C823
G1737	C1677	G1492	G1432	G1371	G1248	G1187	A1127	A1067	C1007	C946	U884	U824
G1738	A1678	C1493	A1433	U1372	U1249	U1188	G1128	G1068	A1008	A947	C885	A825
A1739	A1679	A1494	A1434	A1373	G1250	A1189	A1129	A1069	A1009	C948	U886	U826
G1740	U1680	A1495	G1435	G1374	C1251	G1190	U1130	A1070	A1010	G949	U887	U827
G1741	G1681	U1496	G1436	U1375	G1252	G1191	G1131	G1071	G1011	G950	C888	U828
G1742	G1682	U1497	C1437	C1376	A1253	G1193	U1132	C1072	U1012	C951	C869	A829
G1743	U1683	C1498	U1438	G1377	A1254	A1194	A1133	A1073	C1013	G954	G890	G830
A1744	C1684	A1500	A1439	A1378	U1255	G1195	A1134	G1074	A1014	G955	G891	G831
A1745	C1685	G1500	U1440	U1379	G1256	C1196	C1135	G1075	U1015	U956	A892	A832
A1746	C1686	A1505	G1441	G1380	C1257	G1197	G1136	C1076	G1016	C957	U894	G834
G1747	G1687	U1506	U1442	G1381	U1258	U1198	U1137	A1077	G1017	U958	U895	C835
G1748	U1688	U1507	U1443	G1382	G1259	U1199	G1138	U1078	U1018	A959	A896	C836
A1749	A1689	A1508	G1444	A1383	A1260	U1201	G1139	C1079	U1019	A960	C897	C837
G1750	C1690	A1509	C1445	A1384	C1261	U1202	A1140	A1080	A1020	C961	C898	C838
U1751	C1691	G1510	C1447	C1386	A1262	G1203	U1141	U1081	A1021	G962	A899	U839
G1752	G1692	G1511	G1448	G1387	G1324	U1204	A1142	U1082	G1022	U963	A900	C840
G1753	U1693	C1512	G1449	U1388	A1264	A1205	A1144	U1083	G1024	C964	C901	G841
A1754	C1694	U1513	G1450	G1389	A1265	G1206	C1145	A1085	G1025	C965	C902	U842
A1755	G1695	A1514	U1451	U1390	G1266	U1207	C1146	A1086	G1026	G966	C903	G843
G1756	C1696	A1515	G1452	A1392	U1329	C1208	A1147	G1087	A1027	U967	G904	A844

A2851	G2731	G2791	G2731
G2852	A2732	A2792	A2732
G2853	A2733	A2793	A2733
G2854	A2734	A2794	A2734
C2855	C2735	C2795	C2735
A2856	A2736	A2796	A2736
G2857	G2737	G2797	G2737
C2858	A2738	A2798	A2738
G2859	A2739	A2799	A2739
A2860	A2740	A2800	A2740
U2861	A2741	A2801	A2741
G2862	G2742	G2802	G2742
C2863	U2743	U2803	U2743
G2864	G2744	U2804	G2744
U2865	C2745	C2805	C2745
U2866	U2746	C2806	U2746
G2867	G2747	U2807	G2747
A2868	A2748	G2808	A2748
G2869	A2749	A2809	A2749
C2870	A2750	A2810	A2750
U2871	G2751	G2811	G2751
A2872	C2752	G2812	C2752
A2873	A2753	A2813	A2753
C2874	U2754	A2814	U2754
G2875	C2755	C2815	C2755
G2876	U2756	G2816	U2756
G2877	A2757	U2817	A2757
U2878	A2758	U2818	A2758
A2879	G2759	G2819	G2759
C2880	C2760	A2820	C2760
U2881	A2761	A2821	A2761
A2882	G2762	G2822	G2762
A2883	G2763	A2823	G2763
U2884	A2764	C2824	A2764
G2885	A2765	G2825	A2765
A2886	A2766	A2826	A2766
A2887	C2767	C2827	C2767
C2888	U2768	G2828	U2768
C2889	A2769	A2829	A2769
U2890	G2770	G2830	G2770
G2891	C2771	G2831	C2771
G2892	C2772	U2832	C2772
A2893	C2773	U2833	C2773
G2894	G2774	G2834	G2774
G2895	G2775	A2835	G2775
C2896	A2776	U2836	A2776
U2897	G2777	A2837	G2777
U2898	A2778	G2838	A2778
A2899	U2779	G2839	U2779
A2900	G2780	C2840	G2780
C2901	A2781	C2841	A2781
U2902	G2782	G2842	G2782
U2903	U2783	G2843	U2783
U2904	U2784	G2844	U2784
	C2785	U2845	C2785
	U2786	G2846	U2786
	C2787	U2847	C2787
	C2788	G2848	C2788
	U2789	U2849	U2789
	U2790	A2850	U2790

4 Data and refinement statistics

Xtrriage (Phenix) and EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	1.00Å 1.00Å 1.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 7.50	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-7.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	ERNA-3D	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	62371	wwPDB-VP
Average B, all atoms (Å ²)	0.0	wwPDB-VP

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: 5MC, PSU, 7MG, 5MU, 1MA

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	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	C3',C4'
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:69:C:H4'	1:B:85:G:C4'	1.23	1.68
1:B:318:C:H5'	1:B:319:G:C8	1.24	1.68
1:B:1853:A:C5'	1:B:1853:A:H4'	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	2326	C
1	B	2894	G
1	B	2394	C
1	B	2325	G
1	B	2639	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	5MC	B	2498	1	18,22,23	3.29	4 (22%)	26,32,35	2.68	7 (26%)
1	5MU	B	747	1	19,22,23	0.65	1 (5%)	28,32,35	1.14	4 (14%)
1	1MA	B	2030	1	16,25,26	1.97	6 (37%)	18,37,40	1.65	5 (27%)
1	PSU	B	1917	1	18,21,22	0.68	0	22,30,33	0.81	0
1	7MG	B	2251	1	22,26,27	7.73	5 (22%)	29,39,42	1.76	3 (10%)
1	7MG	B	745	1	22,26,27	7.53	6 (27%)	29,39,42	2.49	5 (17%)
1	PSU	B	1911	1	18,21,22	0.59	0	22,30,33	0.75	0
1	1MA	B	1618	1	16,25,26	2.09	6 (37%)	18,37,40	1.56	5 (27%)
1	5MU	B	1915	1	19,22,23	0.45	0	28,32,35	1.40	3 (10%)
1	PSU	B	746	1	18,21,22	0.89	0	22,30,33	1.37	2 (9%)
1	5MU	B	2449	1	19,22,23	2.53	3 (15%)	28,32,35	2.21	5 (17%)
1	5MU	B	1939	1	19,22,23	0.99	2 (10%)	28,32,35	1.77	5 (17%)
1	7MG	B	2069	1	22,26,27	3.17	2 (9%)	29,39,42	1.67	2 (6%)

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	5MC	B	2498	1	1/1/5/5	2/7/25/26	0/2/2/2
1	5MU	B	747	1	-	2/7/25/26	0/2/2/2
1	1MA	B	2030	1	-	3/3/25/26	0/3/3/3
1	PSU	B	1917	1	-	1/7/25/26	0/2/2/2
1	7MG	B	2251	1	-	2/7/37/38	0/3/3/3
1	7MG	B	745	1	-	2/7/37/38	0/3/3/3
1	PSU	B	1911	1	-	0/7/25/26	0/2/2/2
1	1MA	B	1618	1	-	2/3/25/26	0/3/3/3
1	5MU	B	1915	1	-	0/7/25/26	0/2/2/2
1	PSU	B	746	1	-	1/7/25/26	0/2/2/2
1	5MU	B	2449	1	1/1/5/5	6/7/25/26	0/2/2/2
1	5MU	B	1939	1	2/2/5/5	2/7/25/26	0/2/2/2
1	7MG	B	2069	1	-	0/7/37/38	0/3/3/3

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	2251	7MG	C1'-N9	32.23	2.06	1.46
1	B	745	7MG	C1'-N9	31.10	2.04	1.46
1	B	2251	7MG	C8-N9	-14.54	1.37	1.46
1	B	2069	7MG	C8-N9	-14.06	1.38	1.46
1	B	745	7MG	C8-N9	-13.55	1.38	1.46

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2449	5MU	O4'-C4'-C5'	-8.06	82.84	109.37
1	B	2498	5MC	C1'-N1-C6	7.80	134.11	121.12
1	B	2069	7MG	N9-C8-N7	7.43	114.01	103.38
1	B	745	7MG	N9-C8-N7	7.35	113.90	103.38
1	B	2251	7MG	N9-C8-N7	7.34	113.88	103.38

All (4) chirality outliers are listed below:

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

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	1939	5MU	C3'-C4'-C5'-O5'
1	B	2030	1MA	O4'-C4'-C5'-O5'
1	B	2030	1MA	C3'-C4'-C5'-O5'
1	B	2449	5MU	C3'-C4'-C5'-O5'
1	B	2449	5MU	O4'-C4'-C5'-O5'

There are no ring outliers.

13 monomers are involved in 161 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	2498	5MC	18	0
1	B	747	5MU	26	0
1	B	2030	1MA	4	0
1	B	1917	PSU	6	0
1	B	2251	7MG	1	0
1	B	745	7MG	18	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	1911	PSU	1	0
1	B	1618	1MA	1	0
1	B	1915	5MU	10	0
1	B	746	PSU	22	0
1	B	2449	5MU	14	0
1	B	1939	5MU	41	0
1	B	2069	7MG	14	0

5.5 Carbohydrates [i](#)

There are no monosaccharides 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1566

The worst 5 of 1566 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	75:G	O3'	76:C	P	2.66
1	B	2023:C	O3'	2024:G	P	2.65
1	B	87:U	O3'	88:G	P	2.57
1	B	1004:U	O3'	1005:C	P	2.55
1	B	2652:C	O3'	2653:U	P	2.55