



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:23 PM GMT

PDB ID : 1JZX  
Title : Structural Basis for the Interaction of Antibiotics with the Peptidyl Transferase Center in Eubacteria  
Authors : Schlutzen, F.; Zarivach, R.; Harms, J.; Bashan, A.; Tocilj, A.; Albrecht, R.; Yonath, A.; Franceschi, F.  
Deposited on : 2001-09-17  
Resolution : 3.10 Å(reported)

This is a wwPDB X-ray Structure 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
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) : trunk26865

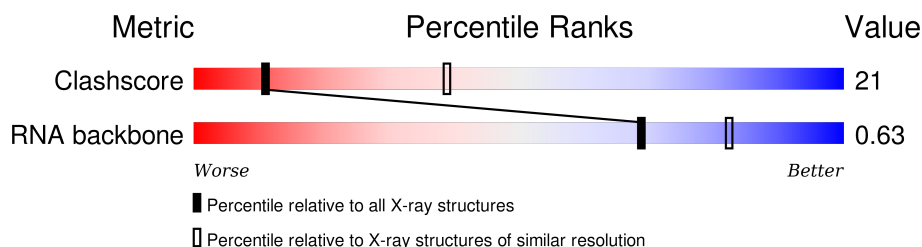
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 Å.

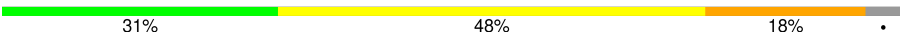

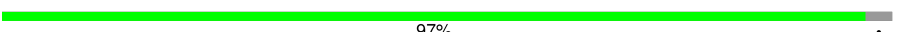
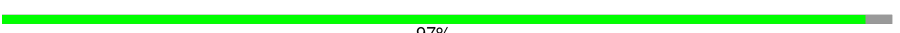
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1222 (3.14-3.06)
RNA backbone	2183	1010 (3.52-2.68)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	2880	 31%                      48%                      18%                      .
2	K	205	 96%                      .
3	L	134	 97%                      .
4	M	60	 97%                      .

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 59946 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	2774	Total	C	N	O	P	0	0	0
			59532	26556	10982	19221	2773			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1526	U	Y	SEE REMARK 999	GB 15805042

- Molecule 2 is a protein called Ribosomal Protein L4.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
2	K	197	Total	C	0	0	197
			197	197			

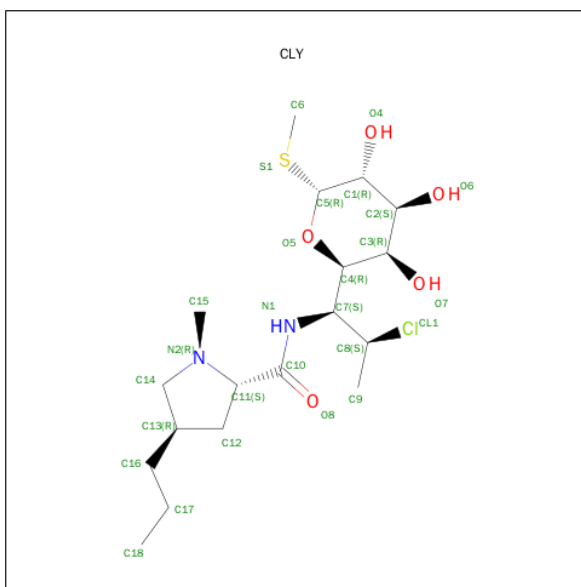
- Molecule 3 is a protein called Ribosomal Protein L22.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
3	L	130	Total	C	0	0	130
			130	130			

- Molecule 4 is a protein called Ribosomal Protein L32.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
4	M	58	Total	C	0	0	58
			58	58			

- Molecule 5 is CLINDAMYCIN (three-letter code: CLY) (formula: C<sub>18</sub>H<sub>33</sub>ClN<sub>2</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	Cl	N	O	S	0	0
			27	18	1	2	5	1		

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

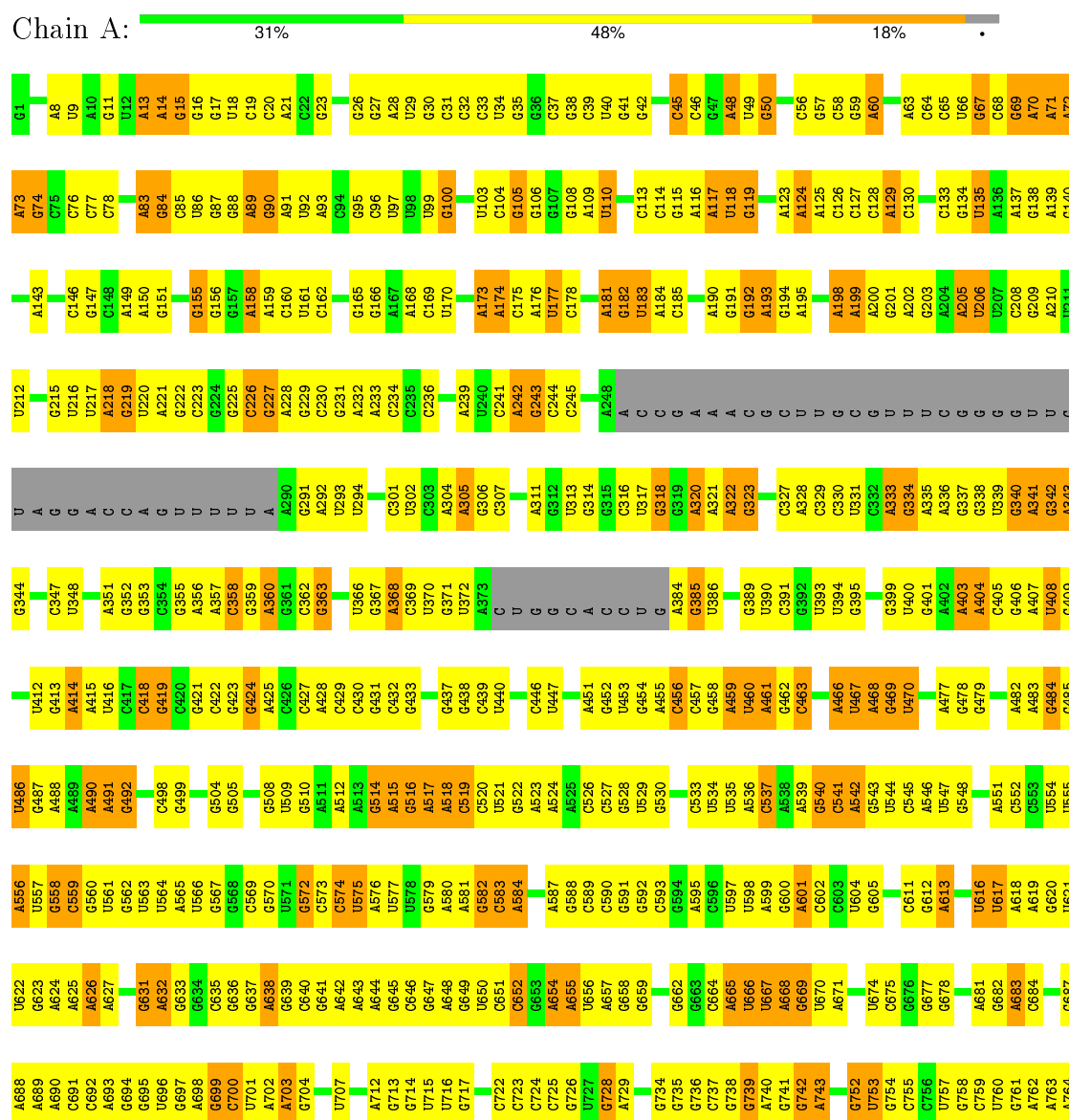
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Mg	0	0
			2	2		

### 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 and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

Note EDS was not executed.

#### • Molecule 1: 23S rRNA



U1826	A1753	G1683	U1611	U1539	A1474	U1403	G1333	G1265	G1189	G1047	U974	G	A833	C765
G1827	G1754	G1694	U1612	C1540	U1475	C1404	G1333	G1266	U1119	U1048	C975	C	A838	A766
C1828	G1755	A1685	G1613	G1541	G1476	A1405	A1334	A1267	G1120	C1049	C976	U	U839	G767
C1829	C1756	A1686	C1614	G1547	G1480	U1409	G1337	U1268	G1121	C1054	U978	A	U840	U768
C1830	C1757	U1687	G1617	U1548	U1481	U1410	G1338	G1269	A1122	C1054	A979	C909	G841	G773
C1831	C1758	U1688	U1618	C1549	U1482	U1411	U1339	C1271	G1123	A1055	A979	C910	G842	A774
C1834	C1762	U1689	A1619	U1551	G1483	C1412	C1340	G1272	G1125	A1057	C981	A911	G843	U775
C1835	G1763	G1691	C1623	C1552	G1484	C1415	U1342	G1273	A1126	G1058	C982	A912	G844	G776
C1836	G1764	A1692	A1624	G1553	U1485	A1416	U1343	C1274	C1127	A1059	G983	A913	A777	A777
C1840	U1765	A1693	A1625	G1554	A1486	A1416	U1344	C1275	G1128	C1060	A984	A913	C850	G778
C1841	G1766	A1694	A1626	A1555	C1487	C1417	G1345	U1276	A1129	A1061	G985	A918	C851	U784
C1851	U1768	U1697	C1627	U1556	C1488	C1417	C1346	G1277	U1130	U1061	G985	U919	U852	U785
C1854	U1769	C1698	C1631	G1557	C1489	A1420	C1347	A1278	U1202	A1065	A994	A922	C853	U786
C1855	U1770	A1699	A1632	C1558	U1490	U1421	C1348	G1279	U1203	G1066	A995	A922	G854	U787
C1856	C1771	C1703	A1632	C1559	U1493	U1424	G1349	U1280	G1204	G1067	A996	A923	G855	A787
C1857	C1772	G1703	C1633	A1560	G1494	G1425	G1350	A1281	G1205	A1068	C997	C924	A856	G788
C1857	C1773	G1704	A1634	A1561	G1495	U1426	G1351	C1283	A1137	G1069	C998	U925	U857	G789
C1867	A1774	A1707	G1635	G1562	G1496	U1427	G1352	C1284	A1138	G1070	A999	C926	G858	A790
C1871	U1775	U1563	C1640	U1564	C1497	G1428	A1353	G1285	A1139	U1071	G1000	C927	U859	G791
C1876	A1776	C1571	G1642	U1564	C1498	A1429	A1354	U1286	A1140	U1072	A1001	G928	U860	A794
C1877	A1777	G1710	U1645	U1572	A1498	G1430	A1355	A1287	G1142	G1073	C1003	A930	G861	A795
C1878	U1778	C1711	U1646	G1573	A1499	G1430	A1356	U1288	G1143	G1074	A1004	A931	G862	A796
C1879	U1787	G1712	U1647	G1574	U1500	U1431	G1356	A1288	U1443	C1075	U1005	G931	C863	A797
C1880	C1787	G1713	U1648	C1575	G1501	G1432	U1357	A1289	U1444	G1079	C1006	G932	C864	A798
C1881	C1788	A1714	U1649	G1576	G1502	A1433	G1358	U1290	G1145	A1080	A1007	G933	A865	G798
C1882	C1789	G1715	U1650	C1577	G1503	U1434	G1359	G1291	G1146	U1081	G1008	G934	U866	C799
C1883	C1790	U1717	U1651	G1578	U1504	G1435	C1364	C1218	A1081	A1080	A1007	G934	G867	U800
C1884	C1791	A1717	U1652	C1579	C1506	A1437	U1365	C1219	G1149	G1083	A1012	G938	U868	A801
C1885	C1792	G1722	C1653	C1580	U1507	G1438	A1366	G1220	C1150	C1084	G1013	G939	C869	A802
C1886	C1793	U1723	A1655	C1581	A1508	G1439	A1367	C1221	U1511	A1084	G1014	G940	C870	C803
C1887	A1794	G1724	U1656	A1582	A1509	G1440	G1368	G1222	C1152	G1085	G1014	G941	U871	C804
C1887	C1795	C1725	U1657	G1584	A1510	A1441	U1369	U1301	A1153	C1086	U1015	U941	G872	G805
C1888	G1798	G1726	U1657	G1585	A1511	C1442	U1370	C1302	G1155	A1088	C1016	U942	U873	A806
C1889	A1799	C1727	G1660	C1514	A1512	G1443	G1371	A1226	U1143	C1089	U1019	A944	A874	A807
C1890	C1800	A1728	C1661	U1515	C1514	A1445	G1373	U1307	C1160	C1090	A1020	G945	A876	C808
C1891	A1801	C1729	C1662	U1590	U1515	U1446	G1374	C1308	U1161	C1091	A1021	G948	G877	U810
C1892	C1802	G1730	C1663	C1591	G1519	U1447	G1377	G1310	C1162	U1092	A1022	C948	C878	G811
C1893	G1803	U1733	G1664	U1591	G1520	G1450	G1377	C1311	C1164	G1096	G1024	A951	C880	A813
C1894	A1807	C1734	C1665	U1592	U1521	C1451	C1380	G1312	G1165	A1097	G1028	A952	A886	G814
C1895	C1808	G1735	A1666	C1593	C1522	U1452	G1381	U1313	A1167	C1098	C1029	G953	G887	A815
C1896	C1809	C1736	A1667	U1594	A1523	A1453	G1382	A1314	G1168	A1099	U1030	G954	G888	A817
C1897	U1810	G1737	G1668	A1595	C1524	C1456	C1383	G1315	C1169	G1100	A1031	A955	C889	G818
C1898	A1811	U1738	G1670	A1596	A1525	C1457	G1384	G1316	U1170	U1101	G1032	A956	U890	C819
C1899	U1812	C1740	A1671	C1597	U1526	A1457	C1385	G1319	A1171	C1103	G1034	G957	A891	U820
C1900	A1813	C1742	A1672	U1598	G1527	U1458	A1386	C1320	U1172	C1103	G1034	G958	G892	A821
C1901	G1814	C1743	C1673	G1599	C1528	U1459	G1387	A1321	G1173	G1035	G1035	C959	G	G822
C1905	U1906	G1744	C1674	U1600	C1529	G1460	A1391	G1322	G1174	U1105	G1036	U960	G	U823
C1906	C1907	C1745	C1675	U1601	U1530	G1465	U1392	G1323	A1175	A1106	U1037	U961	G	U824
C1907	U1817	C1746	U1676	A1602	C1531	C1466	U1392	G1324	U1176	A1107	A1038	A964	G	C825
C1908	G1818	G1747	C1677	A1603	A1532	C1467	A1397	G1325	U1177	U1108	A1039	C968	C	U826
C1909	U1819	U1748	A1678	A1604	G1533	U1467	A1398	U1326	C1178	A1109	A1040	U969	C	C827
C1910	A1820	G1749	G1678	A1605	A1534	A1468	G1398	U1327	G1110	G1110	G1041	U970	U	C828
C1911	A1821	C1749	U1679	G1606	C1535	U1469	C1399	C1327	C1111	C1111	U1044	A971	A	C829
C1912	G1912	A1750	U1680	C1607	G1536	U1470	A1400	C1328	U1187	U1112	G1045	A971	C	C830
C1913	G1913	A1751	U1681	U1608	U1537	G1401	G1401	C1329	A1187	C1113	C972	C	C	C831
C1914	U1914	U1752	A1682	U1752	A1538	U1473	G1402	G1330	A1188	U1046	U1046	U973	A	A832

A2858	A2859	G2860	A2861	G2862	G2865	A2866	G2867	G2868	C2792	G2793	G2794	A2795	A2796	G2797	A2798	C2799	C2800	A2801	G2804	G2805	G2806	G2807	G2808	A2809	A2810	G2811	A2812	G2813	G2814	G2815	G2822	G2823	G2824	A2825	G2826	G2827	G2828	A2829	C2833	G2839	G2840	G2841	G2842	A2843	G2846	G2847	A2848	C2849	G2852	G2853	G2854	G2855																																																																																																																																																																																																																																	
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A2337	A2338	A2348	C2349	G2350	A2355	A2356	A2357	C2358	G2361	G2362	G2363	C2364	U2365	U2366	A2367	G2368	U2369	C2370	A2371	C2372	C2373	C2374	G2375	G2376	U2377	G2378	C2379	U2380	A2381	C2382	U2385	A2390	A2391	G2392	G2393	G2394	C2395	A2397	U2398	C2399	C2403	A2404	A2405	C2406	U2407	G2408	A2409	U2410	U2416	U2417																																																																																																																																																																																																																																			
U2185	G2186	A2189	A2190	C2191	U2192	C2193	A2194	C2195	U2197	U2198	C2199	G2200	C2201	G2202	G2203	A2204	C2205	C2206	G2207	U2208	G2209	C2210	U2211	U2212	G2213	G2217	A2218	U2219	G2225	A2226	C2227	U2228	G2229	G2234	G2235	U2236	G2237	G2238	C2239	C2240	U2241	C2242	C2243	C2244	A2245	A2246	A2247	A2248	U2251	A2252	A2253	G2254	G2255																																																																																																																																																																																																																																
G2256	G2261	C2262	C2263	C2264	A2265	A2266	A2267	G2268	G2269	U2270	C2271	A2272	C2273	C2274	C2275	G2276	G2282	G2283	U2284	U2285	G2286	G2287	U2291	C2292	G2293	C2294	C2295	U2296	A2299	G2300	A2301	A2306	A2307	A2308	A2312	G2313	A2314	A2315	G2317	U2318	G2319	G2320	C2321	U2322	U2323	U2324	U2325	U2326	U2327	U2328	U2329	U2330	U2331	U2332	U2333	U2334	U2335	U2336	U2337	U2338	U2339	U2340	U2341	U2342	U2343	U2344	U2345	U2346	U2347	U2348	U2349	U2350	U2351	U2352	U2353	U2354	U2355	U2356	U2357	U2358	U2359	U2360	U2361	U2362	U2363	U2364	U2365	U2366	U2367	U2368	U2369	U2370	U2371	U2372	U2373	U2374	U2375	U2376	U2377	U2378	U2379	U2380	U2381	U2382	U2383	U2384	U2385	U2386	U2387	U2388	U2389	U2390	U2391	U2392	U2393	U2394	U2395	U2396	U2397	U2398	U2399	U2400	U2401	U2402	U2403	U2404	U2405	U2406	U2407	U2408	U2409	U2410	U2411	U2412	U2413	U2414	U2415	U2416	U2417	U2418	U2419	U2420	U2421	U2422	U2423	U2424	U2425	U2426	U2427	U2428	U2429	U2430	U2431	U2432	U2433	U2434	U2435	U2436	U2437	U2438	U2439	U2440	U2441	U2442	U2443	U2444	U2445	U2446	U2447	U2448	U2449	U2450	U2451	U2452	U2453	U2454	U2455	U2456	U2457	U2458	U2459	U2460	U2461	U2462	U2463	U2464	U2465	U2466	U2467	U2468	U2469	U2470	U2471	U2472	U2473	U2474	U2475	U2476	U2477	U2478	U2479	U2480	U2481	U2482	U2483	U2484	U2485	U2486	U2487	U2488	U2489	U2490	U2491	U2492	U2493	U2494	U2495	U2496	U2497	U2498	U2499	U2500	U2501	U2502	U2503	U2504	U2505	U2506	U2507	U2508	U2509	U2510	U2511	U2512	U2513	U2514	U2515	U2516	U2517	U2518	U2519	U2520	U2521	U2522	U2523	U2524	U2525	U2526	U2527	U2528	U2529	U2530	U2531	U2532	U2533	U2534	U2535	U2536	U2537	U2538	U2539	U2540	U2541	U2542	U2543	U2544	U2545	U2546	U2547	U2548	U2549	U2550	U2551	U2552	U2553	U2554	U2555

• Molecule 2: Ribosomal Protein L4

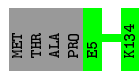
Chain K:

96%

MET	A2	E198	GLU	ALA	GLY	GLU	GLU	GLN	GLN
-----	----	------	-----	-----	-----	-----	-----	-----	-----

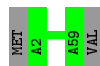
- Molecule 3: Ribosomal Protein L22

Chain L:  97% .



- Molecule 4: Ribosomal Protein L32

Chain M:  97% .





## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	170.30 Å   410.10 Å   697.20 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	35.00 – 3.10	Depositor
% Data completeness (in resolution range)	(Not available) (35.00-3.10)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS, REFMAC	Depositor
R, $R_{free}$	0.268 , 0.303	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	59946	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	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: MG, CLY

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	A	0.23	0/66661	0.66	2/103976 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	777	A	C2'-C3'-O3'	5.46	122.43	113.70
1	A	1746	A	C2'-C3'-O3'	5.25	122.09	113.70

There are no chirality outliers.

There are no planarity outliers.

### 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	A	59532	0	30004	1876	0
2	K	197	0	0	0	0
3	L	130	0	0	0	0
4	M	58	0	0	0	0
5	A	27	0	32	2	0
6	A	2	0	0	0	0
All	All	59946	0	30036	1876	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 21.

The worst 5 of 1876 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:A:1747:G:H4'	1:A:1749:G:H1'	1.29	1.14
1:A:2668:U:H4'	1:A:2669:C:H5'	1.32	1.12
1:A:940:G:H3'	1:A:941:U:H5''	1.34	1.09
1:A:367:G:H2'	1:A:368:A:H5''	1.34	1.08
1:A:1199:U:H3'	1:A:1200:G:H5''	1.35	1.07

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

There are no protein backbone outliers to report in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2765/2880 (96%)	556 (20%)	144 (5%)

5 of 556 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	13	A
1	A	14	A
1	A	15	G
1	A	23	G
1	A	45	C

5 of 144 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1279	G
1	A	1575	C
1	A	2633	A
1	A	1301	U
1	A	1355	A

## 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z  > 2$
5	CLY	A	2881	-	26,28,28	1.70	6 (23%)	30,40,40	1.29	4 (13%)

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
5	CLY	A	2881	-	-	0/19/53/53	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	2881	CLY	C12-C11	-2.76	1.48	1.53
5	A	2881	CLY	O5-C4	2.17	1.47	1.43
5	A	2881	CLY	C15-N2	2.30	1.51	1.46
5	A	2881	CLY	C4-C7	2.72	1.56	1.53
5	A	2881	CLY	C10-N1	2.77	1.40	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	2881	CLY	C11-C10-N1	-3.01	109.89	116.64
5	A	2881	CLY	C12-C11-C10	2.26	116.05	111.31
5	A	2881	CLY	O8-C10-N1	2.53	127.89	122.93
5	A	2881	CLY	C7-C8-CL1	2.68	113.50	108.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	2881	CLY	2	0

## 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 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.