



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:48 AM GMT

PDB ID : 3JQ4  
Title : The structure of the complex of the large ribosomal subunit from D. Radiodurans with the antibiotic lankacidin  
Authors : Auerbach-Nevo, T.; Mermershtain, I.; Davidovich, C.; Bashan, A.; Rozenberg, H.; Yonath, A.  
Deposited on : 2009-09-06  
Resolution : 3.52 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) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

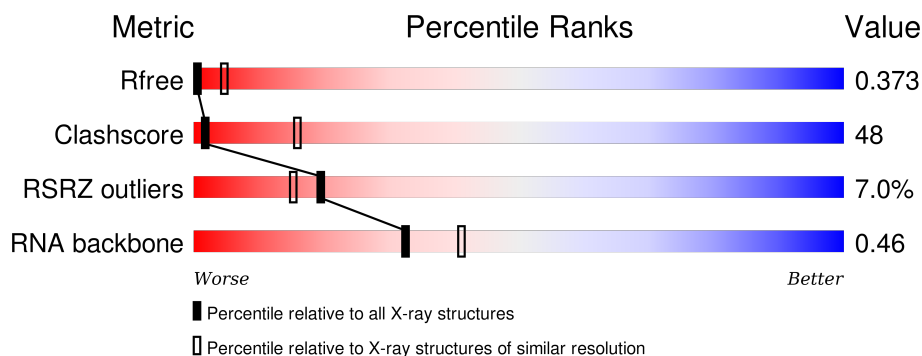
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.52 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))
$R_{free}$	91344	1089 (3.64-3.40)
Clashscore	102246	1197 (3.64-3.40)
RSRZ outliers	91569	1096 (3.64-3.40)
RNA backbone	2183	1051 (4.22-2.80)

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.

Mol	Chain	Length	Quality of chain
1	A	2880	<div> <div>7%</div> <div>13%</div> <div>56%</div> <div>23%</div> <div>• •</div> </div>
2	B	118	<div> <div>4%</div> <div>17%</div> <div>70%</div> <div>11%</div> <div>•</div> </div>

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
3	LC2	A	2881	-	-	-	X

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 61885 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.

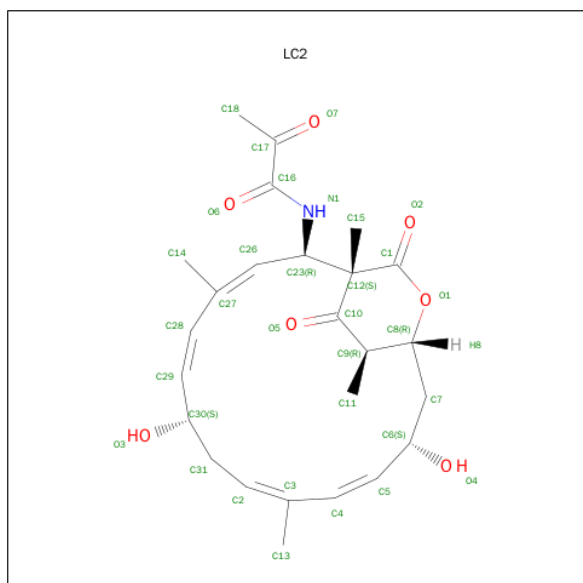
- Molecule 1 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	2765	Total	C	N	O	P	0	0	0
			59336	26469	10944	19159	2764			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	118	Total	C	N	O	P	0	0	0
			2516	1124	464	811	117			

- Molecule 3 is N-[(1S,2R,3E,5E,7S,9E,11E,13S,15R,19R)-7,13-DIHYDROXY-1,4,10,19-TETRAMETHYL-17,18-DIOXO-16-OXABICYCLO[13.2.2]NONADECA-3,5,9,11-TETRAEN-2-YL]-2-OXOPROPANAMIDE (three-letter code: LC2) (formula: C<sub>25</sub>H<sub>33</sub>NO<sub>7</sub>).

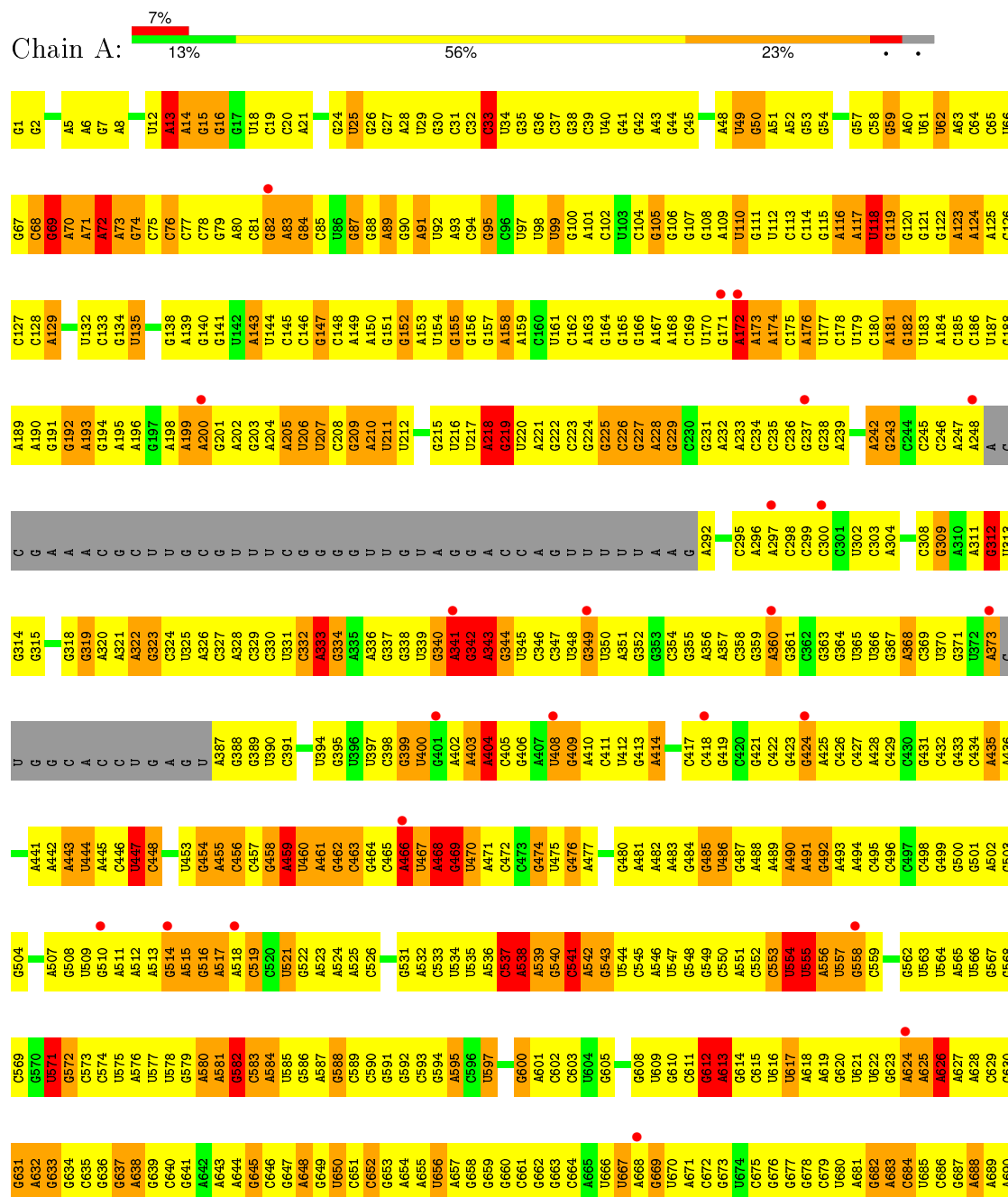


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			33	25	1	7		

### 3 Residue-property plots

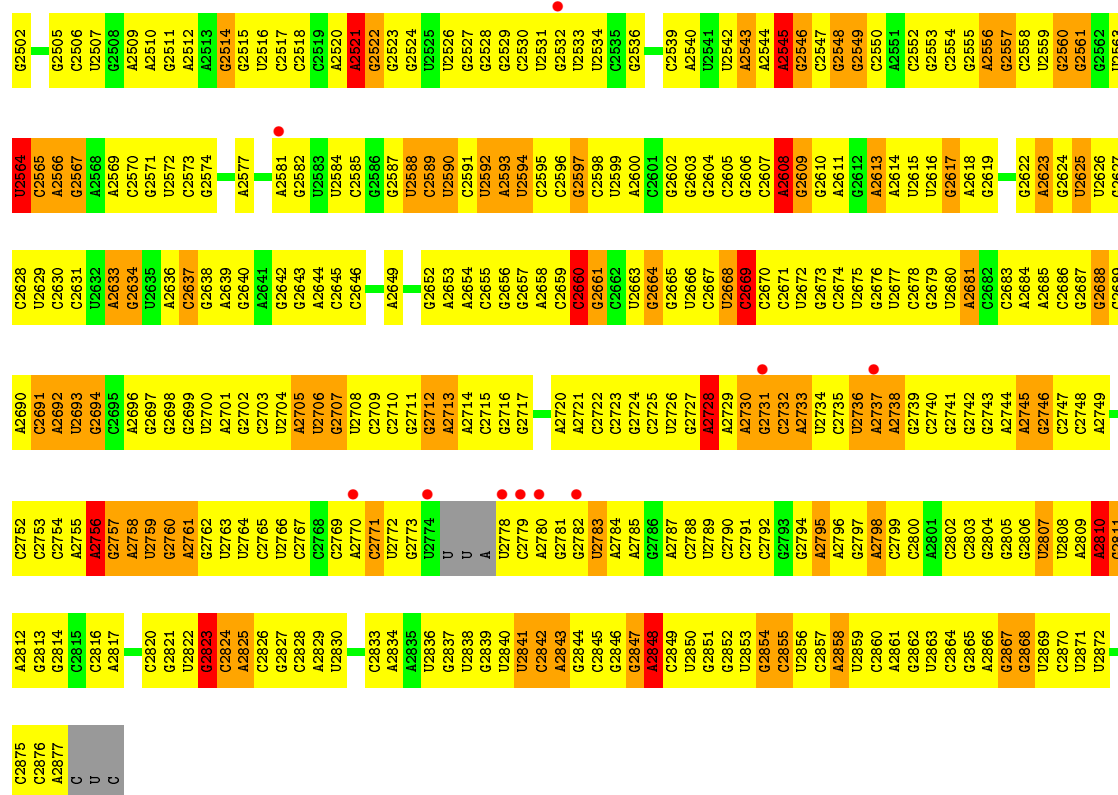
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ( $\text{RSRZ} > 2$ ). 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.

#### • Molecule 1: 23S ribosomal RNA

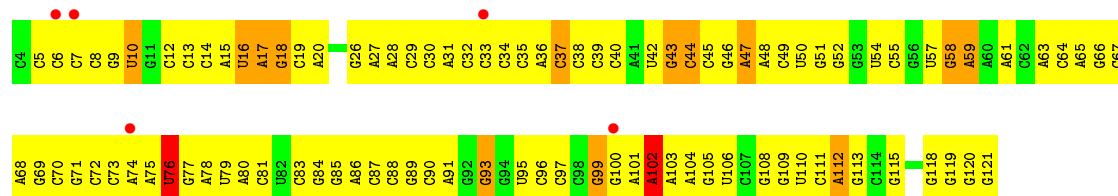


A1561	C1501	G1438	A1372	G1309	G1249	A1187	A1126	G1063	C998	C937	A875	G814	U753	C691
G1562	G1502	G1439	G1373	C1310	A1250	A1188	A1129	C1064	A999	G938	A876	A815	G754	C692
U1563	G1503	A1440	C1374	C1311	G1251	G1189	U1130	A1065	G1000	C939	C877	U816	C755	A693
U1564	G1504	A1441	C1375	G1312	C1252	C1190	U1131	A1066	A1001	G940	C878	G817	C756	G694
G1565	U1505	A1442	A1378	A1313	C1253	G1191	G1131	G1067	C1002	U941	A879	G818	U757	G695
G1566	C1506	G1443	A1379	A1314	G1254	A1192	G1132	A1068	C1003	U942	C880	C819	G758	U696
U1567	G1507	C1444	A1379	A1315	A1255	G1193	G1133	G1069	U1004	U943	U881	U820	C759	G697
A1568	A1508	A1445	C1380	G1316	C1256	U1194	C1134	U1072	U1005	U944	C882	A821	U760	A698
A1569	A1509	U1446	G1381	G1317	U1257	U1195	C1135	U1073	G945	A944	A883	G822	G761	A699
C1570	A1510	U1447	G1382	A1318	U1257	G1196	A1136	G1073	A1006	U946	C884	A823	A762	C700
A1571	A1511	G1383	C1383	A1318	A1259	U1197	A1137	G1074	G1008	C947	A885	U824	A763	U701
C1572	A1512	G1384	G1385	G1322	G1260	G1198	A1138	C1075	C1009	C948	A886	C825	A764	A702
G1573	U1513	C1385	A1386	G1323	U1261	U1199	A1139	U1076	U1010	G949	G887	U826	G765	A703
A1574	C1514	U1452	A1387	G1324	U1262	G1200	A1140	U1077	A1011	G950	G888	C827	A766	G704
C1575	U1515	A1453	G1387	G1325	G1263	G1201	U1141	A1078	A1012	G951	A891	C828	G767	C705
G1576	A1516	U1454	C1388	U1326	C1264	U1202	G1142	G1079	G1013	A952	G891	C829	A768	A706
G1577	C1517	C1455	G1389	C1327	G1265	A1203	A1143	A1080	G1014	G953	G	G830	U769	U707
C1578	G1518	G1390	G1390	C1328	G1266	G1204	U1144	A1081	U1015	U954	G	C831	U770	G708
U1579	G1519	A1457	A1391	U1329	A1267	G1205	G1145	A1082	C1016	G955	G	A832	C771	A709
G1580	G1520	A1458	U1392	G1330	U1268	G1206	G1146	G1083	C1017	A956	G	A833	G772	C710
A1581	U1521	U1459	G1393	G1331	G1269	G1209	G1147	A1084	C1018	G957	G	A834	G773	C711
A1582	C1522	G1460	G1394	G1332	C1270	C1210	G1148	G1085	U1019	G958	C	U835	A774	A712
A1583	A1523	C1461	A1395	G1333	C1271	G1211	G1149	G1086	C1020	C959	C	G836	U775	G713
G1584	C1524	C1462	C1396	A1334	G1272	U1212	C1150	C1087	U1021	U960	U	U837	G776	G714
A1585	A1525	A1463	A1397	A1335	G1273	U1213	G1151	A1088	A1022	U961	A	A838	A777	U715
A1586	U1526	A1464	G1398	G1336	C1274	U1213	G1152	C1089	U1023	C962	C	U839	G778	U716
A1587	G1527	G1465	C1399	G1337	A1275	C1214	A1153	C1090	A1024	G963	A	U840	U779	G717
A1588	C1528	C1466	A1400	G1338	U1276	A1215	A1154	A1096	A1025	A964	A	U841	U780	A718
A1589	C1529	U1467	G1401	U1339	G1277	G1216	G1155	U1092	U1026	G965	C	A842	G781	A719
G1590	U1530	A1468	G1402	C1340	A1278	U1217	A1156	U1093	C1027	A966	C	G843	U782	A720
U1591	C1531	U1469	U1403	G1341	G1279	C1218	G1157	C1094	G1028	G967	U	U844	G783	G721
U1592	A1532	G1470	A1404	U1342	U1280	C1219	A1158	A1095	C1029	C968	U	U845	C722	C722
C1593	G1533	G1471	A1405	C1343	A1281	G1220	U1159	A1096	U1030	U969	A	A846	C723	C723
U1594	A1534	C1472	A1406	G1344	A1282	U1221	G1160	A1097	C1031	A970	C	C947	C724	C725
A1595	U1535	U1473	G1407	C1345	C1283	G1222	U1161	G1098	A1032	A971	C	A848	G726	G726
G1596	G1536	A1474	A1408	C1346	G1284	G1223	A1162	A1099	G1033	C972	A911	G849	G789	G789
A1597	U1537	U1475	U1409	C1347	A1285	A1224	C1163	G1100	U1034	U973	A912	C850	A790	U727
C1598	U1537	G1476	U1410	C1348	U1286	G1225	C1164	U1101	G1035	U974	A913	C851	C791	G728
G1599	U1539	C1477	C1411	A1349	A1287	A1226	G1165	G1102	G1036	C975	C914	U852	U792	A729
C1600	C1540	G1480	A1416	G1352	A1288	G1229	A1166	C1103	U1037	C976	C915	C853	C730	C730
U1601	G1541	U1481	C1417	A1353	A1289	C1230	A1167	G1104	U1038	G977	U917	G854	A794	A731
G1602	G1542	U1482	C1418	A1354	G1290	A1231	G1168	U1105	A1039	U978	U918	G855	A795	A731
A1603	A1543	U1483	G1419	A1355	A1291	U1232	G1169	A1106	A1040	A979	A918	A856	A796	G734
A1604	G1544	G1483	A1420	G1356	A1292	A1233	U1170	U1108	G1041	G980	U919	U857	A797	G735
A1605	G1545	G1484	U1421	U1357	A1293	A1234	A1171	A1109	U1044	C981	G920	G858	G798	G736
C1606	C1546	C1487	C1422	C1358	U1294	C1235	U1172	G1110	G1045	C982	A921	U859	C799	C737
A1607	U1547	G1488	G1359	G1359	U1295	G1236	G1173	C1110	G983	U980	A922	U860	U800	G738
U1608	U1548	A1489	A1423	G1360	G1296	G1236	A1174	C1111	U1046	A801	A923	G861	A801	G739
G1609	C1549	C1489	G1427	G1361	A1297	G1237	A1175	U1112	G1047	G985	C924	A862	A802	A740
A1610	C1550	U1490	G1428	G1362	G1298	A1238	U1176	C1113	A986	A986	U925	C963	C803	G741
U1611	U1551	C1491	G1429	A1363	A1299	A1239	U1177	A1114	C926	G987	C926	C964	C804	G742
C1612	C1552	A1492	A1364	G1364	A1300	G1240	C1178	C1115	G1053	A865	C927	A866	G805	A743
G1613	G1553	A1493	G1430	C1365	U1301	G1241	A1179	U1119	G1054	G988	G928	U866	A806	A746
C1614	U1554	G1494	U1431	U1365	C1302	A1242	A1180	G1120	A1055	A950	A929	G867	A807	G746
G1615	A1555	G1495	G1432	A1366	U1303	G1243	C1181	U1056	U1056	A981	A930	C808	C808	A747
C1616	U1556	C1496	A1433	A1367	U1304	A1244	U1182	G1121	A1057	A982	G931	C870	C809	A748
G1617	G1557	C1497	U1434	G1368	C1305	G1245	C1183	A1122	G1058	C993	G932	C871	C809	C749
U1618	C1558	G1498	G1369	G1369	U1306	G1246	G1184	G1123	A994	A994	C935	U872	U810	G750
A1619	G1559	A1499	G1436	U1370	U1307	U1247	C1185	U1124	A1061	A995	G	U873	G812	G751
C1620	U1560	U1500	A1437	G1371	C1308	G1248	G1186	G1125	G1062	G	A936	A874	A813	G752





• Molecule 2: 5S ribosomal RNA



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	169.80 Å   410.30 Å   694.40 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	8.00 – 3.52 39.85 – 3.52	Depositor EDS
% Data completeness (in resolution range)	89.8 (8.00-3.52) 91.4 (39.85-3.52)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.16	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.87 (at 3.57 Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.268   ,   0.325 0.346   ,   0.373	Depositor DCC
$R_{free}$ test set	12315 reflections (5.21%)	DCC
Wilson B-factor (Å <sup>2</sup> )	106.6	Xtriage
Anisotropy	0.863	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.20 , 62.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 271261 reflections	Xtriage
$F_o, F_c$ correlation	0.82	EDS
Total number of atoms	61885	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	118.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.



## 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: LC2

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	0.57	3/66440 (0.0%)	0.82	93/103628 (0.1%)
2	B	0.39	0/2813	0.73	1/4384 (0.0%)
All	All	0.56	3/69253 (0.0%)	0.81	94/108012 (0.1%)

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	A	0	124
2	B	0	1
All	All	0	125

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	700	C	N1-C2	9.73	1.49	1.40
1	A	538	A	C5-C6	-5.98	1.35	1.41
1	A	462	G	C6-O6	5.16	1.28	1.24

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	985	G	N9-C1'-C2'	12.36	130.07	114.00
1	A	1337	G	N9-C1'-C2'	9.78	126.71	114.00
1	A	1279	G	N9-C1'-C2'	9.59	126.47	114.00
1	A	1474	A	N9-C1'-C2'	9.59	126.46	114.00
1	A	2608	A	N9-C1'-C2'	8.85	125.51	114.00

There are no chirality outliers.

5 of 125 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	15	G	Sidechain
1	A	16	G	Sidechain
1	A	172	A	Sidechain
1	A	25	U	Sidechain
1	A	33	C	Sidechain

## 5.2 Too-close contacts ⓘ

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	59336	0	29907	4296	0
2	B	2516	0	1286	150	0
3	A	33	0	33	1	0
All	All	61885	0	31226	4443	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 48.

The worst 5 of 4443 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:614:G:N2	1:A:634:G:H22	1.28	1.29
1:A:2194:A:H2'	1:A:2195:C:H5''	1.25	1.18
1:A:2691:C:C2'	1:A:2692:A:H5''	1.79	1.11
1:A:2198:U:H3'	1:A:2199:C:H4'	1.14	1.10
1:A:918:A:H2'	1:A:919:U:H5''	1.33	1.10

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	A	2756/2880 (95%)	675 (24%)	213 (7%)
2	B	117/118 (99%)	17 (14%)	2 (1%)
All	All	2873/2998 (95%)	692 (24%)	215 (7%)

5 of 692 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	13	A
1	A	14	A
1	A	45	C
1	A	49	U
1	A	50	G

5 of 215 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1315	A
1	A	1631	C
1	A	2660	C
1	A	1337	G
1	A	1473	U

## 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

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

1 ligand is 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	$\# Z  > 2$
3	LC2	A	2881	-	28,34,34	1.72	5 (17%)	20,49,49	1.44	3 (15%)

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
3	LC2	A	2881	-	-	0/31/61/61	0/0/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	2881	LC2	O7-C17	-2.23	1.18	1.23
3	A	2881	LC2	C2-C3	2.09	1.40	1.33
3	A	2881	LC2	C23-N1	3.08	1.52	1.46
3	A	2881	LC2	C12-C23	4.01	1.63	1.56
3	A	2881	LC2	C13-C3	4.56	1.60	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2881	LC2	O5-C10-C12	-2.19	117.75	121.72
3	A	2881	LC2	C6-C5-C4	-2.18	118.51	124.63
3	A	2881	LC2	O7-C17-C18	4.64	130.58	119.69

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2881	LC2	1	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](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	2765/2880 (96%)	0.45	196 (7%) 19 15	37, 107, 200, 200	0
2	B	118/118 (100%)	0.27	5 (4%) 40 31	100, 143, 183, 200	0
All	All	2883/2998 (96%)	0.44	201 (6%) 19 15	37, 108, 200, 200	0

The worst 5 of 201 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	558	G	11.1
1	A	1922	U	9.1
1	A	2125	C	8.9
1	A	1955	G	8.2
1	A	2174	G	8.2

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

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	LC2	A	2881	33/33	0.89	0.37	2.51	88,88,88,88	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.