



wwPDB X-ray Structure Validation Summary Report (i)

Feb 28, 2014 – 01:58 PM GMT

PDB ID : 2D3O
Title : Structure of Ribosome Binding Domain of the Trigger Factor on the 50S ribosomal subunit from *D. radiodurans*
Authors : Schlutzen, F.; Wilson, D.N.; Hansen, H.A.; Tian, P.; Harms, J.M.; McInnes, S.J.; Albrecht, R.; Buerger, J.; Wilbanks, S.M.; Fucini, P.
Deposited on : 2005-09-30
Resolution : 3.35 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

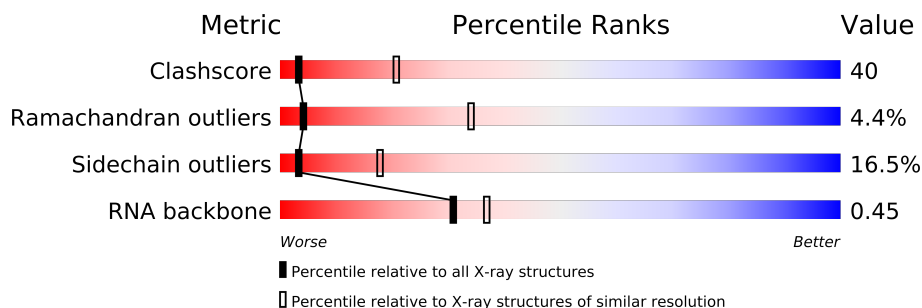
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.35 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	79885	1030 (3.48-3.24)
Ramachandran outliers	78287	1008 (3.48-3.24)
Sidechain outliers	78261	1007 (3.48-3.24)
RNA backbone	1838	1005 (4.00-2.72)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	0	2880	
2	R	95	
3	S	115	
4	W	67	
5	1	112	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 63004 atoms, of which 0 are hydrogen and 0 are deuterium.

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	0	2802	Total	C	N	O	P	0	0	0
			60132	26824	11089	19418	2801			

- Molecule 2 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	R	93	Total	C	N	O	S	0	0	0
			726	458	136	130	2			

- Molecule 3 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	S	110	Total	C	N	O	S	0	0	0
			825	513	160	151	1			

- Molecule 4 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	W	66	Total	C	N	O	S	0	0	0
			533	327	107	96	3			

- Molecule 5 is a protein called Trigger Factor.

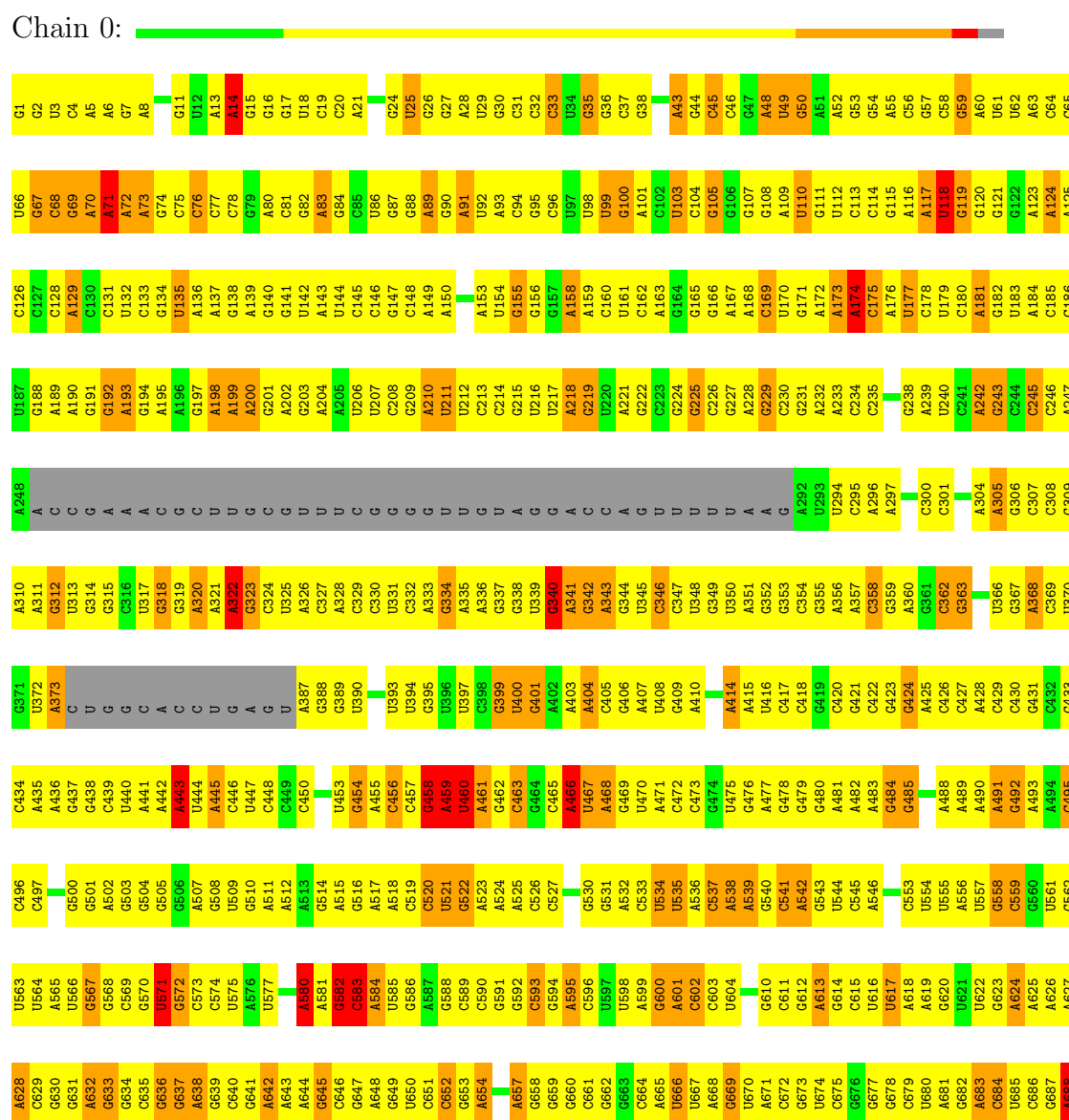
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	1	100	Total	C	N	O	0	0	0
			788	494	146	148			

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 RIBOSOMAL RNA



C1648	C1580	C1514	A1453	C1328	C1256	U1195	G1133	G1000	C935	U873	A813	G752	A689
A1581	U1515	G1393	U1454	U1329	U1257	G1196	C1134	A1001	A936	A874	G814	U752	A690
A1582	A1516	G1394	C1455	G1330	G1258	G1197	C1135	C1002	C937	G875	A815	U754	C691
G1652	C1517	A1395	C1456	G1331	A1259	C1198	C1136	C1003	G938	A876	U816	C755	C692
C1653	C1518	C1396	A1457	G1332	A1260	U1199	A1137	U1004	C939	G877	A817	C756	A693
A1654	G1519	C1397	A1458	G1333	G1261	G1200	A1138	U1005	G940	C878	G818	U757	G694
U1520	U1459	C1398	U1459	A1334	U1262	G1201	A1139	C1006	U941	A879	C819	G758	G695
U1521	G1460	A1399	C1460	A1335	G1263	U1202	A1140	C1007	U942	C880	U820	C759	U696
C1522	A1400	G1336	G1461	G1337	G1264	A1203	U1076	A1008	U943	U881	A821	U760	G697
A1523	G1401	G1337	C1462	G1338	G1265	G1204	A1077	C1009	A944	G882	A822	G761	A698
C1524	A1402	G1338	A1463	G1339	G1266	G1205	U1078	U1010	G945	A883	U823	A762	G699
U1525	U1403	U1339	A1464	C1340	G1269	G1206	A1080	A1011	U946	C884	U824	A763	C700
C1526	C1404	C1341	G1465	G1342	C1270	A1208	A1081	A1012	U947	A885	C825	A764	U701
A1661	A1405	G1341	C1466	G1342	C1271	G1209	G1082	G1013	C947	A886	U826	C765	A702
U1467	A1406	U1342	U1467	U1342	C1271	G1210	G1083	G1014	C948	G887	C827	A766	A703
A1468	G1407	C1343	A1468	C1344	C1274	C1211	U1076	U1015	U941	C888	C828	G767	G704
A1469	U1408	G1344	G1469	G1345	U1275	G1212	C1086	C1016	A952	U889	C829	U770	C705
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G1471	U1410	C1346	G1471	C1347	A1277	U1214	A1088	C1018	U954	A891	G831	C772	U707
C1472	C1411	C1347	U1472	C1348	G1279	U1215	C1089	U1019	G955	C	A832	C773	G708
U1473	C1412	C1348	U1473	C1349	G1280	G1216	C1090	A1020	A956	C	A833	G774	A709
U1474	A1413	A1349	A1474	A1350	A1281	U1217	C1091	A1021	G957	C	A834	A774	C710
U1475	G1414	G1350	U1475	G1351	U1282	C1218	U1092	A1022	G958	G	U835	U775	G711
G1476	C1415	G1351	G1476	G1352	U1283	C1219	U1093	U1023	C959	C	G836	G776	G712
C1477	A1416	G1352	C1477	G1353	A1284	G1220	C1094	G1024	U960	C	U837	A777	G713
U1478	C1417	A1353	U1478	A1354	A1285	C1221	A1095	A1025	G961	C	A838	G778	G714
U1479	G1418	A1354	G1479	A1355	A1286	G1222	A1096	U1026	C962	U	U839	U779	U715
G1480	C1419	A1355	U1480	A1356	A1287	G1223	A1097	C1027	U963	A	U840	U780	U716
A1481	A1420	G1356	U1481	G1357	A1288	A1224	C1098	G1028	C968	C	A841	G781	G717
U1482	U1421	U1357	U1482	U1358	A1289	G1225	A1099	C1029	U969	C	A842	U782	A718
G1483	C1422	C1358	G1483	C1359	A1290	C1226	G1100	U1030	A970	A	G843	G783	A719
U1484	A1423	G1359	U1484	G1360	G1291	A1227	U1101	C1031	A971	C	G844	U784	A720
U1485	U1424	C1363	U1485	C1364	U1292	G1228	G1102	A1032	C972	C	U845	U785	C721
A1486	G1425	A1364	A1486	A1365	G1293	C1229	C1103	G1033	U973	U	U846	C722	C722
G1487	U1426	G1365	G1487	G1366	A1294	C1230	G1104	U1034	U974	U	C847	A787	C723
C1488	G1427	U1366	G1488	U1367	A1295	A1231	U1105	G1035	C975	A	A848	G788	C724
G1489	G1428	A1366	C1489	A1367	A1299	U1232	A1106	G1036	C976	C	G849	G789	C725
U1490	A1429	A1367	U1490	G1368	A1300	A1233	A1107	U1037	G977	C	C850	A790	G726
C1491	G1430	G1369	C1491	G1370	U1301	C1234	U1108	U1038	U978	A911	U851	G791	G727
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G1493	A1432	U1371	U1493	G1372	U1303	G1236	C1113	A1040	C980	C913	G854	G793	G732
A1494	U1433	U1372	U1494	G1373	U1304	G1237	A1114	G1041	C981	C914	G855	A794	G733
G1495	G1434	A1372	G1495	G1374	C1305	U1175	C1115	U1042	C982	C915	A856	A795	G734
C1496	G1435	G1373	C1496	G1375	U1306	U1176	U1116	G1043	G983	C916	A857	A796	G735
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U1498	G1438	C1375	U1498	C1378	G1309	G1240	G1120	U1045	G985	U919	G858	G798	G737
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C1500	A1441	U1379	C1500	A1380	C1311	U1242	U1182	U1047	G987	A921	U860	U800	G739
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G1503	G1444	G1382	U1503	G1383	A1314	G1245	U1124	A1056	A990	C926	C863	C803	G742
U1504	A1445	C1383	U1504	G1384	G1315	U1246	G1125	U1057	A991	C927	C864	A743	A743
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A1511	U1512	G1326	A1511	U1327	U1326	A1192	U1194	C1064	C998	G934	U871	G812	G751
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A2314	A2315	G2319	G2320	G2321	G2322	G2323	G2324	G2325	G2326	G2327	G2328	G2329	G2330	G2331	G2332	G2333	G2334	G2335	G2336	G2337	G2338	G2339	G2340	G2341	G2342	G2343	G2344	A2345	G2346	G2347	G2348	G2349	A2352	G2353	G2354	A2355	A2356	A2357	G2358	U2359	G2360	G2361	G2362	G2363	G2364	G2365	G2366	A2367	G2368	G2369	G2370	A2371	A2372	G2373	G2374	G2375	G2376	U2377																																																															
U2251	A2252	A2253	G2254	G2255	G2256	A2257	G2258	G2259	G2260	G2261	G2262	G2263	G2264	G2265	G2266	G2267	G2268	G2269	G2270	G2271	G2272	G2273	G2274	G2275	G2276	A2277	A2278	G2279	A2280	G2281	U2284	U2285	G2286	G2287	A2288	A2289	A2290	U2291	G2292	G2293	G2294	G2295	U2296	G2297	U2298	G2299	A2300	A2301	G2302	A2306	A2307	A2308	G2309	G2310	U2311	A2312	G2313																																																																
U2251	A2252	A2253	G2254	G2255	G2256	A2257	G2258	G2259	G2260	G2261	G2262	G2263	G2264	G2265	G2266	G2267	G2268	G2269	G2270	G2271	G2272	G2273	G2274	G2275	G2276	A2277	A2278	G2279	A2280	G2281	U2284	U2285	G2286	G2287	A2288	A2289	A2290	U2291	G2292	G2293	G2294	G2295	U2296	G2297	U2298	G2299	A2300	A2301	G2302	A2306	A2307	A2308	G2309	G2310	U2311	A2312	G2313																																																																
A2187	A2188	A2189	A2190	A2191	A2192	G2193	A2194	A2195	U2196	U2197	U2198	G2199	G2200	G2201	G2202	G2203	A2204	G2205	G2206	G2209	G2210	G2211	U2212	G2213	G2214	G2215	G2216	G2217	G2218	U2219	A2220	G2221	G2222	U2223	U2224	G2225	A2226	G2227	U2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	U2237	G2238	G2239	G2240	U2241	G2242	A2245	A2246	A2247	G2248	G2249	G2250	G2251																																																													
A2187	A2188	A2189	A2190	A2191	A2192	G2193	A2194	A2195	U2196	U2197	U2198	G2199	G2200	G2201	G2202	G2203	A2204	G2205	G2206	G2209	G2210	G2211	U2212	G2213	G2214	G2215	G2216	G2217	G2218	U2219	A2220	G2221	G2222	U2223	U2224	G2225	A2226	G2227	U2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	U2237	G2238	G2239	G2240	U2241	G2242	A2245	A2246	A2247	G2248	G2249	G2250	G2251																																																													
G2039	A2040	A2041	A2042	A2043	G2044	A2045	G2046	G2047	G2048	G2049	G2050	U2051	G2052	G2053	A2054	G2055	G2056	U2057	G2058	U2059	A2060	G2061	U2062	A2063	U2064	A2065	G2066	U2067	G2068	G2069	G2070	G2071	A2072	A2073	U2074	G2075	G2076	G2077	G2078	A2079	U2080	U2081	G2082	G2083	G2084	G2085	U2086	U2087	G2089	G2090	U2096	A2097	G2098	G2099	A2100	U2105	G2106																																																																
G2039	A2040	A2041	A2042	A2043	G2044	A2045	G2046	G2047	G2048	G2049	G2050	U2051	G2052	G2053	A2054	G2055	G2056	U2057	G2058	U2059	A2060	G2061	U2062	A2063	U2064	A2065	G2066	U2067	G2068	G2069	G2070	G2071	A2072	A2073	U2074	G2075	G2076	G2077	G2078	A2079	U2080	U2081	G2082	G2083	G2084	G2085	U2086	U2087	G2089	G2090	U2096	A2097	G2098	G2099	A2100	U2105	G2106																																																																
G2107	G2108	A2109	G2110	G2111	G2112	G2115	G2116	A2117	G2123	G2124	G2125	U2126	U2127	U2128	U2129	G2133	U2134	G2140	A2141	G2142	G2143	G2144	A2145	A2146	G2147	G2148	G2149	U2150	G2151	A2152	A2153	A2154	U2155	A2156	A2165	G2166	G2170	U2171	U2172	G2173	G2174	A2175	U2176	G2177	U2178	G2179	U2180	G2181	A2182	G2183	U2184	U2185	G2186																																																																				
G2107	G2108	A2109	G2110	G2111	G2112	G2115	G2116	A2117	G2123	G2124	G2125	U2126	U2127	U2128	U2129	G2133	U2134	G2140	A2141	G2142	G2143	G2144	A2145	A2146	G2147	G2148	G2149	U2150	G2151	A2152	A2153	A2154	U2155	A2156	A2165	G2166	G2170	U2171	U2172	G2173	G2174	A2175	U2176	G2177	U2178	G2179	U2180	G2181	A2182	G2183	U2184	U2185	G2186																																																																				
U1976	G1977	A1978	A1979	A1980	A1981	U1982	G1983	G1986	U1987	A1988	G1989	G1993	U1994	G1995	A1996	A1997	A1998	U1999	U2000	G2001	A2002	A2003	U2004	U2005	G2006	G2007	G2008	U2009	G2010	U2011	A2012	A2013	A2014	G2015	A2016	U2017	G2018	G2019	G2020	G2021	G2022	G2023	U2024	A2025	G2026	G2027	G2028	G2029	U2030	A2031	G2032	G2033	G2034	G2035	A2037	G2038	U2039	G2040	G2041	G2042	G2043	G2044	G2045	G2046	G2047	G2048	G2049	G2050	G2051	G2052	G2053	G2054	G2055	G2056	G2057	G2058	G2059	G2060	G2061	G2062	G2063	G2064	G2065	G2066	G2067	G2068	G2069	G2070	G2071	G2072	G2073	G2074	G2075	G2076	G2077	G2078	G2079	G2080	G2081	G2082	G2083	G2084	G2085	G2086	G2087	G2088	G2089	G2090	G2091	G2092	G2093	G2094	G2095	G2096	G2097	G2098	G2099	G2100	G2101	G2102	G210

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, α , β , γ	169.50Å 410.50Å 695.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.84 – 3.35	Depositor
% Data completeness (in resolution range)	(Not available) (29.84-3.35)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.299 , 0.322	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	63004	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	0	0.67	3/67338 (0.0%)	0.82	72/105044 (0.1%)
2	R	0.48	0/737	0.80	0/988
3	S	0.42	0/835	0.73	1/1121 (0.1%)
4	W	0.44	0/537	0.58	0/714
5	1	0.48	0/802	0.68	0/1084
All	All	0.66	3/70249 (0.0%)	0.82	73/108951 (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	0	0	169
2	R	0	1
All	All	0	170

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	2776	U	C1'-N1	6.38	1.58	1.48
1	0	2775	U	C1'-N1	6.21	1.58	1.48
1	0	567	G	C5-C6	-5.13	1.37	1.42

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2034	A	N9-C1'-C2'	10.22	127.28	114.00
1	0	1342	U	N1-C1'-C2'	9.78	126.71	114.00
1	0	1467	U	N1-C1'-C2'	8.63	125.23	114.00
1	0	2775	U	C2-N1-C1'	-8.26	107.78	117.70
1	0	1631	C	N1-C1'-C2'	8.21	124.68	114.00

There are no chirality outliers.

5 of 170 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	118	U	Sidechain
1	0	14	A	Sidechain
1	0	25	U	Sidechain
1	0	43	A	Sidechain
1	0	71	A	Sidechain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	60132	0	30298	3519	0
2	R	726	0	753	126	0
3	S	825	0	881	117	0
4	W	533	0	558	81	0
5	1	788	0	784	74	0
All	All	63004	0	33274	3848	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 40.

The worst 5 of 3848 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:R:69:ILE:CG2	2:R:70:GLY:H	1.26	1.38
1:0:1325:U:H1'	1:0:1619:A:N1	1.50	1.25
2:R:69:ILE:HG22	2:R:70:GLY:N	1.30	1.19
3:S:92:THR:HB	3:S:95:ARG:HH22	1.05	1.18
1:0:67:G:H21	1:0:72:A:H2'	1.09	1.16

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. 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	
2	R	91/95 (96%)	70 (77%)	16 (18%)	5 (6%)	3	26
3	S	108/115 (94%)	79 (73%)	24 (22%)	5 (5%)	4	32
4	W	64/67 (96%)	54 (84%)	8 (12%)	2 (3%)	7	46
5	1	98/112 (88%)	81 (83%)	13 (13%)	4 (4%)	4	37
All	All	361/389 (93%)	284 (79%)	61 (17%)	16 (4%)	4	34

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	S	42	ARG
3	S	65	PRO
4	W	2	LYS
5	1	49	PRO
2	R	69	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. 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	
2	R	75/76 (99%)	61 (81%)	14 (19%)	2	11
3	S	91/96 (95%)	77 (85%)	14 (15%)	4	21
4	W	54/55 (98%)	43 (80%)	11 (20%)	2	8
5	1	83/93 (89%)	72 (87%)	11 (13%)	6	27
All	All	303/320 (95%)	253 (84%)	50 (16%)	3	18

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	S	40	LEU
3	S	112	LYS
5	1	88	ASP
3	S	43	ASP
3	S	80	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
3	S	64	ASN
3	S	71	GLN
5	1	55	ASN
3	S	57	ASN
5	1	24	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2798/2880 (97%)	580 (20%)	88 (3%)

5 of 580 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	14	A
1	0	25	U
1	0	33	C
1	0	35	G
1	0	45	C

5 of 88 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	1342	U
1	0	1664	G
1	0	2660	C
1	0	1355	A
1	0	1626	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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 ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

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

6.4 Ligands ⓘ

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

6.5 Other polymers ⓘ

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