



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2014 – 01:25 PM EDT

PDB ID : 4RB8
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome in complex with amicoumacin, mRNA and three deacylated tRNAs in the A, P and E sites
Authors : Polikanov, Y.S.; Osterman, I.A.; Szal, T.; Tashlitsky, V.N.; Serebryakova, M.V.; Kusochev, P.; Bulkley, D.; Malanicheva, I.A.; Efimenko, T.A.; Efremenkova, O.V.; Konevega, A.L.; Shaw, K.J.; Bogdanov, A.A.; Rodnina, M.V.; Dontsova, O.A.; Mankin, A.S.; Steitz, T.A.; Sergiev, P.V.
Deposited on : 2014-09-12
Resolution : 2.40 Å(reported)

This is a full wwPDB validation 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>

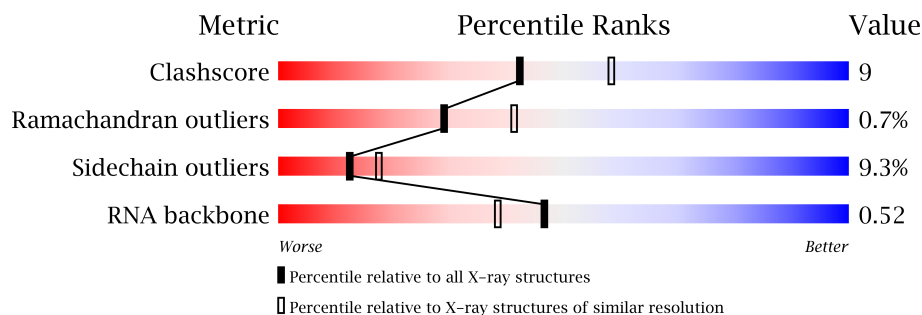
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 23426
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk24003

1 Overall quality at a glance

The reported resolution of this entry is 2.40 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	88313	3035 (2.40-2.40)
Ramachandran outliers	86584	2982 (2.40-2.40)
Cα geometry	86677	2981 (2.40-2.40)
Sidechain outliers	86556	2983 (2.40-2.40)
RNA backbone	2044	1127 (3.00-1.80)

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 ≥ 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	A	2915	
2	B	121	
3	D	276	
4	E	206	
5	F	210	
6	G	182	
7	H	180	
8	I	148	
9	N	140	
10	O	122	
11	P	150	
12	Q	141	
13	R	118	

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Mol	Chain	Length	Quality of chain
14	S	112	
15	T	146	
16	U	118	
17	V	101	
18	W	113	
19	X	96	
20	Y	110	
21	Z	206	
22	0	85	
23	1	98	
24	2	72	
25	3	60	
26	4	71	
27	5	60	
28	6	54	
29	7	49	
30	8	65	
31	9	37	

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 91678 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	A	2800	Total	C	N	O	P	0	0	0
			60314	26840	11284	19390	2800			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	120	Total	C	N	O	P	0	0	0
			2575	1146	476	833	120			

- Molecule 3 is a protein called 50S Ribosomal Protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

- Molecule 4 is a protein called 50S Ribosomal Protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 5 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 6 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	181	Total	C	N	O	S	0	0	0
			1428	913	258	253	4			

- Molecule 7 is a protein called 50S Ribosomal Protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 8 is a protein called 50S Ribosomal Protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	146	Total	C	N	O	S	0	0	0
			1064	681	186	196	1			

- Molecule 9 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	N	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 10 is a protein called 50S Ribosomal Protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	O	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 11 is a protein called 50S Ribosomal Protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	P	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 12 is a protein called 50S Ribosomal Protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	Q	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 13 is a protein called 50S Ribosomal Protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	R	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 14 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	S	110	Total	C	N	O			
			870	549	173	148	0	0	0

- Molecule 15 is a protein called 50S Ribosomal Protein L19.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	T	131	Total	C	N	O	S		
			1083	675	224	183	1	0	0

- Molecule 16 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
16	U	116	Total	C	N	O	S		
			959	608	201	149	1	0	0

- Molecule 17 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	V	101	Total	C	N	O	S		
			771	495	140	135	1	0	0

- Molecule 18 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	W	112	Total	C	N	O	S		
			886	557	174	153	2	0	0

- Molecule 19 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
19	X	95	Total	C	N	O	S		
			750	488	135	126	1	0	0

- Molecule 20 is a protein called 50S Ribosomal Protein L24.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
20	Y	107	Total	C	N	O	S		
			806	517	152	131	6	0	0

- Molecule 21 is a protein called 50S Ribosomal Protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	Z	160	Total	C	N	O	S	0	0	0
			1271	814	228	227	2			

- Molecule 22 is a protein called 50S Ribosomal Protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			

- Molecule 23 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

- Molecule 24 is a protein called 50S Ribosomal Protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

- Molecule 25 is a protein called 50S Ribosomal Protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	3	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 26 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	4	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

- Molecule 27 is a protein called 50S Ribosomal Protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 28 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	6	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 29 is a protein called 50S Ribosomal Protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 30 is a protein called 50S Ribosomal Protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 31 is a protein called 50S Ribosomal Protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 32 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	P	1	Total	Mg	0	0
			1	1		
32	B	21	Total	Mg	0	0
			21	21		
32	W	3	Total	Mg	0	0
			3	3		
32	X	1	Total	Mg	0	0
			1	1		
32	E	7	Total	Mg	0	0
			7	7		
32	V	2	Total	Mg	0	0
			2	2		
32	A	673	Total	Mg	0	0
			673	673		
32	5	2	Total	Mg	0	0
			2	2		
32	R	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	1	1	Total 1	Mg 1	0	0
32	D	6	Total 6	Mg 6	0	0
32	Z	1	Total 1	Mg 1	0	0
32	U	4	Total 4	Mg 4	0	0
32	0	1	Total 1	Mg 1	0	0
32	G	1	Total 1	Mg 1	0	0
32	Q	3	Total 3	Mg 3	0	0
32	T	1	Total 1	Mg 1	0	0
32	8	2	Total 2	Mg 2	0	0
32	O	1	Total 1	Mg 1	0	0
32	Y	1	Total 1	Mg 1	0	0
32	3	1	Total 1	Mg 1	0	0
32	F	7	Total 7	Mg 7	0	0

- Molecule 33 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	9	1	Total 1	Zn 1	0	0
33	Y	1	Total 1	Zn 1	0	0
33	4	1	Total 1	Zn 1	0	0
33	6	1	Total 1	Zn 1	0	0
33	5	1	Total 1	Zn 1	0	0

- Molecule 34 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	A	1039	Total 1039	O 1039	0	0
34	B	10	Total 10	O 10	0	0
34	D	17	Total 17	O 17	0	0
34	E	8	Total 8	O 8	0	0
34	F	6	Total 6	O 6	0	0
34	I	2	Total 2	O 2	0	0
34	N	1	Total 1	O 1	0	0
34	O	3	Total 3	O 3	0	0
34	P	12	Total 12	O 12	0	0
34	Q	1	Total 1	O 1	0	0
34	R	3	Total 3	O 3	0	0
34	T	3	Total 3	O 3	0	0
34	U	1	Total 1	O 1	0	0
34	V	1	Total 1	O 1	0	0
34	W	2	Total 2	O 2	0	0
34	X	2	Total 2	O 2	0	0
34	Y	1	Total 1	O 1	0	0
34	Z	2	Total 2	O 2	0	0
34	0	4	Total 4	O 4	0	0
34	1	4	Total 4	O 4	0	0
34	2	1	Total 1	O 1	0	0
34	3	1	Total 1	O 1	0	0

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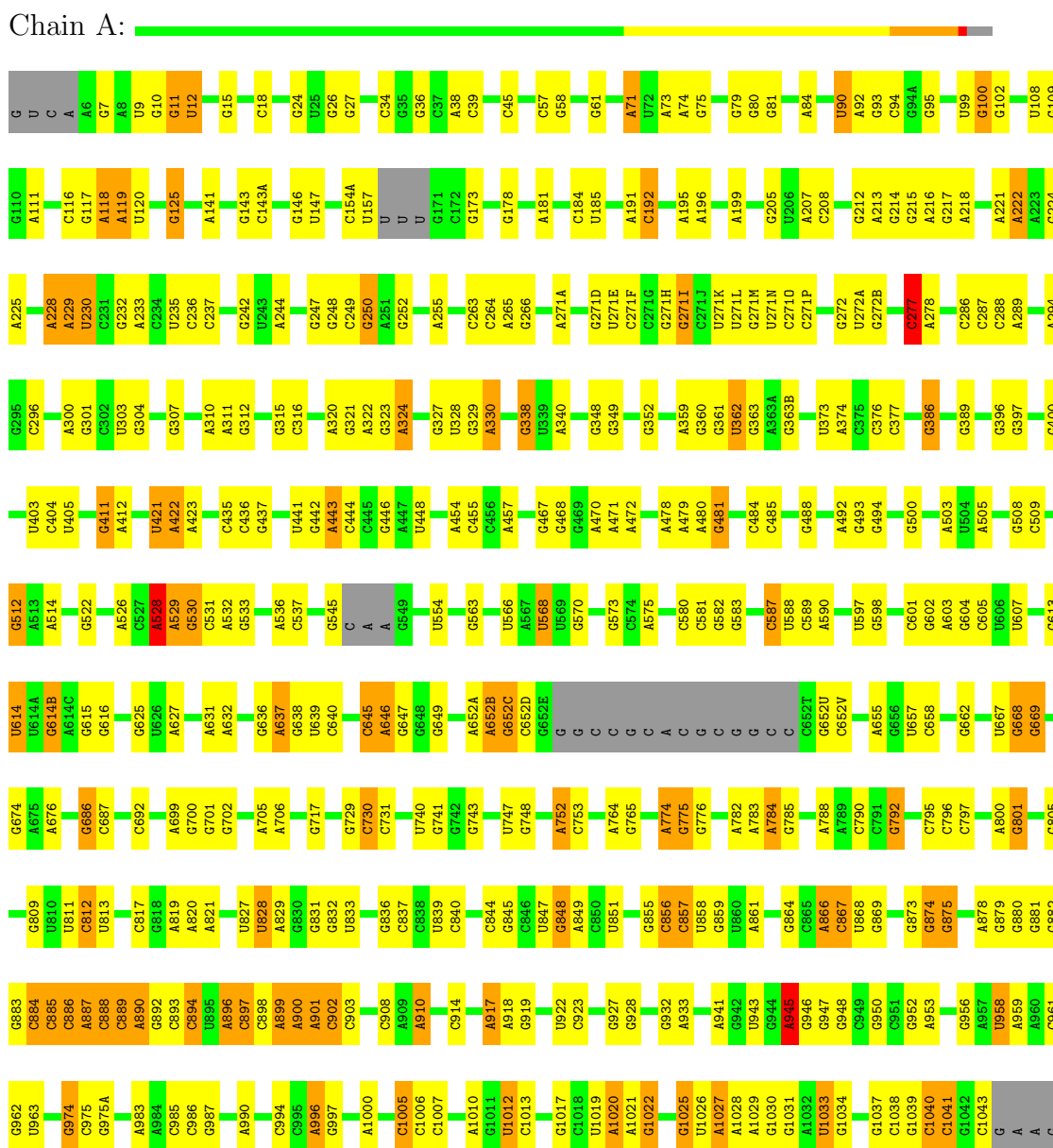
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	5	2	Total	O	0	0
			2	2		
34	7	5	Total	O	0	0
			5	5		
34	8	5	Total	O	0	0
			5	5		
34	9	1	Total	O	0	0
			1	1		

3 Residue-property plots

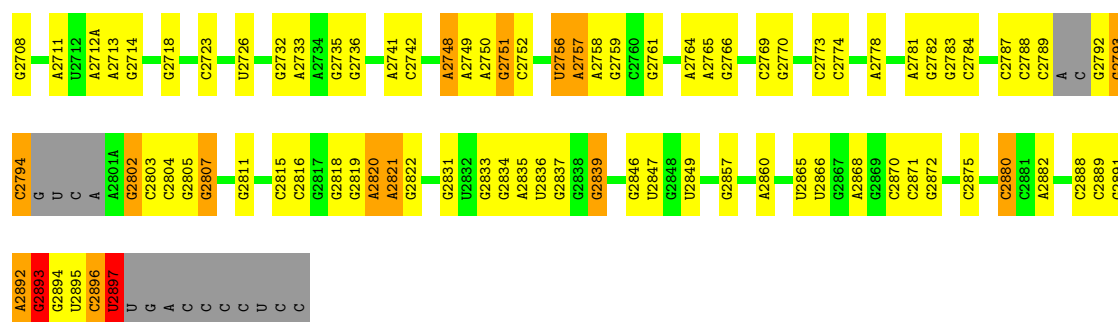
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

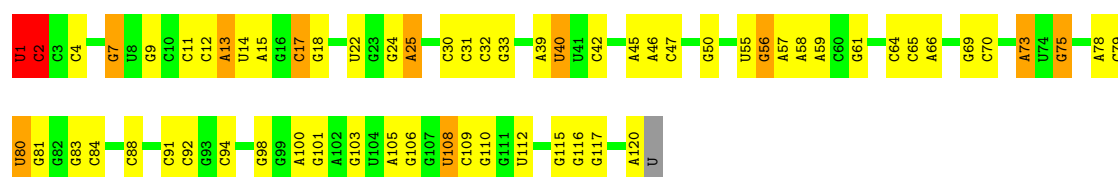


C2573	A2469	G2353	G2270	G2159	G2099	G1996	C1836	G1753	G1622	G1529	C1417	G1309	U1211	C
G2578	C2470	G2354	G2271	G2160	G2100	C1997	C1843	G1756	G1623	C1530	U1420	G1310	G1212	C
G2582	C2472	U2357	A2273	C2162	G2101	G1998	G1843	G1766	A1631A	C1532	C1421	U1313	C1218	A
G2589	U2473	C2364	A2274	C2163	G2102	G1999	A1847	A1759	G1636	C1533	A1427	C1314	A1220	C
U2593	C2474	G2365	G2275	C2164	G2103	G2000	A1848	A1762	A1637	U	C1428	C1315	G1112	C
G2602	C2475	G2366	G2277	G2165	G2104	G2010	G1856	G1763	G1638	A	G1434	U1335	G1114	A
U2611	A2476	G2367	A2278	G2166	G2105	A2013	G1857	G1764	C1639	G1539	A1435	A1336	G1115	G
C2612	C2477	G2368	G2279	U2167	G2106	A2014	G1858	G1769	C1640	U1540	G1436	G1337	G1116	A
U2615	A2376	C2380	C2283	A2170	G2107	G2018	A1877	G1770	A1641	G1541	C1437	U1339	G1117	G
C2617	A2377	C2381	C2284	A2171	G2110	A2019	A1878	G1771	G1642	A1542	U1445	U1340	U1130	U
G2629	G2379	C2382	C2285	U2172	G2111	G2018	C1879	G1772	G1647	A1543	A1445	U1341	G1230	U
G2632	C2380	C2383	A2286	A2173	G2112	A2019	C1879	G1772	C1648	C1543	C1445	A1342	G1231	U
U2634	G2381	G2384	C2287	C2174	U2113	U2022	A1885	A1773	G1648	C1548	C1446	G1336	G1232	G
G2639	G2382	G2385	C2288	A2175	G2115	G2023	C1886	U1777	G1651	C1549	G1447	U1352	C1135	C
U2647	U2291	C2386	C2289	C2176	G2116	G2024	C1886	U1778	A1652	G1458	G1438	G1137	G1138	U
G2652	C2387	C2389	C2290	C2177	G2117	C2025	G1891	U1779	G1653	A1554	A1449	G1139	G1139	U
U2653	U2303	G2390	C2291	C2178	U2118	U2028	G1899	C1781	A1654	C1557	G1450	G1355	C1140	A
G2655	G2304	G2391	G2292	C2182	A2119	G2029	A1900	G1782	A1665	G1558	A1452	U1357	U1141	G
A2657	A2305	C2392	C2293	C2183	G2120	A2030	G1906	A1783	G1666	G1559	G1453	G1358	U1142	A
G2659	G2306	G2393	C2294	C2184	U2122	A2031	A1912	A1784	G1667	G1560	G1455	A1359	A1142A	A
U2662	C2307	G2394	G2295	C2185	G2123	G2032	A1913	A1785	A1668	G1561	A1460	A1360	A1143	C
G2663	C2308	C2395	C2296	C2186	G2124	A2033	A1914	A1786	A1669	A1562	G1461	G1363	G1149	A
U2665	G2309	G2396	C2297	C2187	G2125	U2034	A1915	U1789	C1670	A1566	G1461	G1251	C1150	G
C2668	C2310	C2397	C2298	C2188	A2126	G2043	A1916	C1790	U1671	A1567	G1465	C1251	C1251	C
U2669	U2311	G2398	C2299	C2189	G2127	C2044	U1917	A1791	G1674	G1568	G1466	G1153	G1153	C
G2671	G2312	U2313	C2300	C2190	G2128	G2037	A1918	C1792	C1675	A1569	C1467	G1253	G1253	C
C2673	U2314	G2315	G2301	C2191	U2129	G2038	U1919	U1794	A1676	U1578	A1471	G1371	G1256	U
U2675	C2316	C2317	C2302	C2192	U2130	A2042	G1929	C1795	A1677	A1579	A1477	U1372	C1257	C
G2683	G2317	G2318	C2303	C2193	G2131	C2045	U1930	U1796	C1683	A1580	G1478	G1374	C1261	U
U2689	C2318	C2319	C2304	C2194	U2132	G2046	U1931	C1797	C1684	G1581	U1263	U1263	U1263	U
C2690	G2320	U2321	C2305	C2195	G2133	A2051	G1932	U1798	C1684	C1582	G1264	G1264	G1170	A
U2693	C2321	C2322	C2306	C2196	C2136	G2055	G1933	G1799	A1689	A1583	U1265	A1265	G1171	A
G2694	G2323	C2324	C2307	C2197	C2137	G2056	A1936	G1800	U1693	C1584	A1490	G1380	G	A
C2699	C2325	C2326	C2308	C2198	C2138	G2056	A1937	G1801	U1693	A1586	U1267	A1267	U1169	A
U2702	G2327	C2327	C2309	C2199	C2139	A2060	A1938	A1802	G1696	C1589	C1493	A1268	G1187	C
C2703	C2328	C2328	C2310	C2205	G2141	G2061	U1955	U1803	G1697	U1590	A1494	A1269	C1178	U
G2705	U2329	C2329	C2311	C2206	C2142	A2062	U1956	U1804	G1698	G1591	A1495	G1385	A	G
U2707	G2330	C2330	C2312	C2207	C2143	C2063	C1957	A1810	G1699	C1592	A1496	U1394	G1183	C
C2709	C2331	C2331	C2313	C2208	C2144	C2064	C1958	G1811	A1700	G1593	U1497	A1395	G1184	G
U2711	G2332	C2332	C2314	C2209	C2145	G2065	U1963	A1812	U1713	G1594	C1506	G1399	C1185	U
G2713	C2333	C2333	C2315	C2210	C2146	G2066	U1964	A1815	G1714	G1595	A1507	C1400	G1186	A
U2715	C2334	C2334	C2316	C2211	C2147	G2067	C1967	G1816	G1717	C1599	A1508	G1401	G1187	A
C2717	C2335	C2335	C2317	C2212	G2148	A2071	G1968	G1817	G1718	C1607	C1509	C1291	U1198	U
U2719	C2336	C2336	C2318	C2213	C2149	G2072	A1969	G1823	G1721	A1608	U1405	U1292	U1199	G
G2721	C2337	C2337	C2319	C2214	U2150	G2086	A1970	G1823	G1721	A1609B	U1406	U1292	U1199	G
U2723	U2344	C2344	C2320	U2244	G2151	G2087	A1971	A1829	A1722	G1615	U1407	C1298	C1201	C
C2725	C2345	C2345	C2321	C2248	G2152	G2087	A1972	C1830	G1740	A1610	C1408	G1298	C1201	C
U2727	G2346	C2346	C2322	C2249	G2153	G2094	G1973	C1833	G1746	A1614	A1412	U1300	A1204	A
G2729	C2347	C2347	C2323	C2250	G2154	C2095	U1991	U1833	G1746	C1615	G1413	U1301	U1205	C
U2731	C2348	C2348	C2324	C2251	C2155	U2096	U1992	U1834	C1752	A1616	G1413	A1301	U1205	C
C2733	U2349	C2349	C2325	C2252	G2156	C2097	U1993	U1835	C1752	A1616	G1416	C1306	G1206	U
U2735	C2350	C2350	C2326	C2253	G2157	C2097	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
G2737	C2351	C2351	C2327	C2254	G2158	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2739	C2352	C2352	C2328	C2255	G2159	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
C2741	C2353	C2353	C2329	C2256	G2160	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2743	C2354	C2354	C2330	C2257	G2161	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
G2745	C2355	C2355	C2331	C2258	G2162	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2747	C2356	C2356	C2332	C2259	G2163	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
C2749	C2357	C2357	C2333	C2260	G2164	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2751	C2358	C2358	C2334	C2261	G2165	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
G2753	C2359	C2359	C2335	C2262	G2166	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2755	C2360	C2360	C2336	C2263	G2167	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
C2757	C2361	C2361	C2337	C2264	G2168	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2759	C2362	C2362	C2338	C2265	G2169	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
G2761	C2363	C2363	C2339	C2266	G2170	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2763	C2364	C2364	C2340	C2267	G2171	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
C2765	C2365	C2365	C2341	C2268	G2172	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2767	C2366	C2366	C2342	C2269	G2173	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
G2769	C2367	C2367	C2343	C2270	G2174	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2771	C2368	C2368	C2344	C2271	G2175	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
C2773	C2369	C2369	C2345	C2272	G2176	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2775	C2370	C2370	C2346	C2273	G2177	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
G2777	C2371	C2371	C2347	C2274	G2178	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2779	C2372	C2372	C2348	C2275	G2179	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
C2781	C2373	C2373	C2349	C2276	G2180	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2783	C2374	C2374	C2350	C2277	G2181	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
G2785	C2375	C2375	C2351	C2278	G2182	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2787	C2376	C2376	C2352	C2279	G2183	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
C2789	C2377	C2377	C2353	C2280	G2184	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2791	C2378	C2378	C2354	C2281	G2185	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
G2793	C2379	C2379	C2355	C2282	G2186	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2795	C2380	C2380	C2356	C2283	G2187	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
C2797	C2381	C2381	C2357	C2284	G2188	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2799	C2382	C2382	C2358	C2285	G2189	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
G2801	C2383	C2383	C2359	C2286	G2190	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2803	C2384	C2384	C2360	C2287	G2191	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
C2805	C2385	C2385	C2361	C2288	G2192	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
U2807	C2386	C2386	C2362	C2289	G2193	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G
G2809	C2387	C2387	C2363	C2290	G2194	U2098	U1993	G1835	C1752	A1616	A1528A	C1306	G1206	G



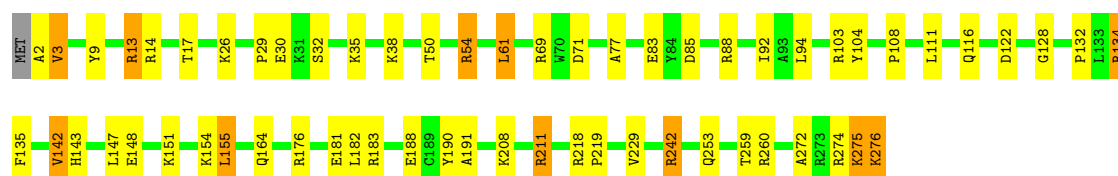
• Molecule 2: 5S Ribosomal RNA

Chain B:



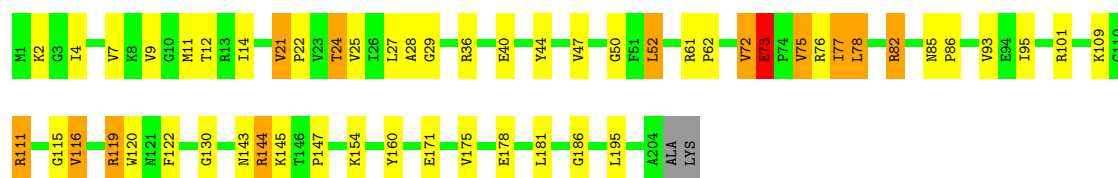
• Molecule 3: 50S Ribosomal Protein L2

Chain D:



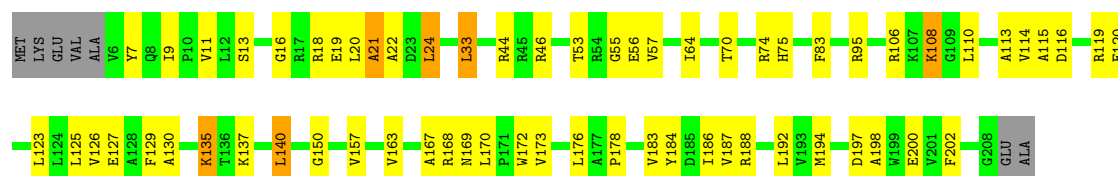
• Molecule 4: 50S Ribosomal Protein L3

Chain E:



• Molecule 5: 50S Ribosomal Protein L4

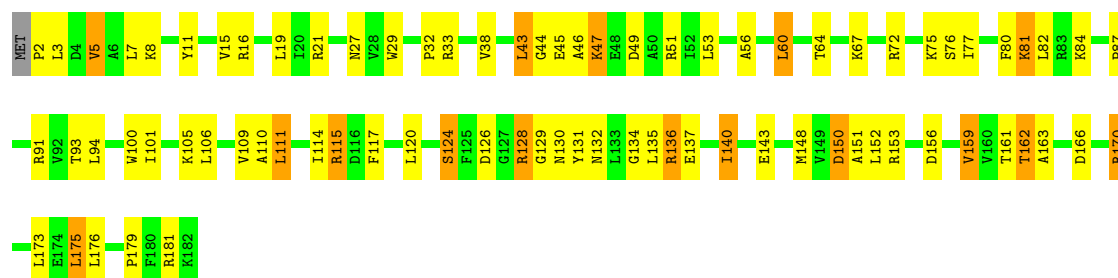
Chain F:



• Molecule 6: 50S Ribosomal Protein L5

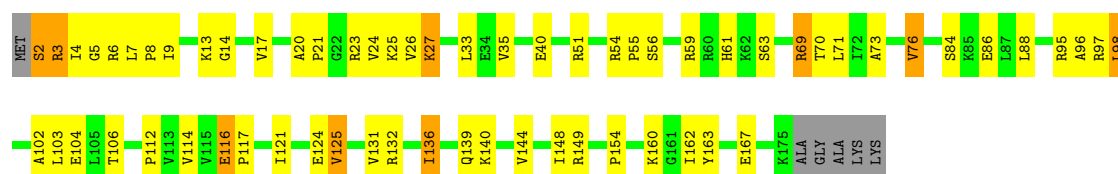
Chain G:





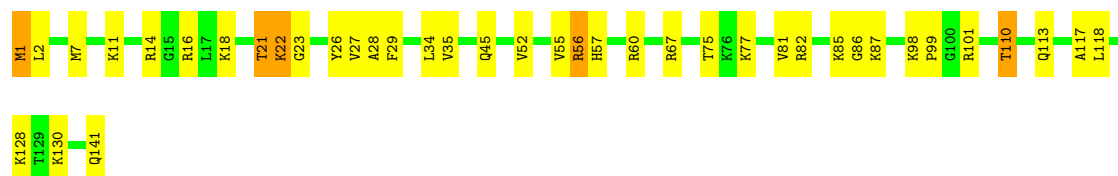
• Molecule 7: 50S Ribosomal Protein L6

Chain H:



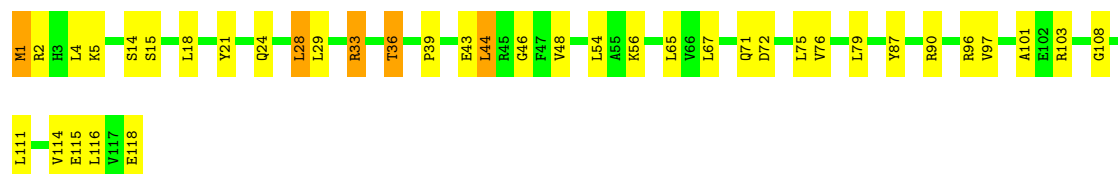
- Molecule 12: 50S Ribosomal Protein L16

Chain Q: 



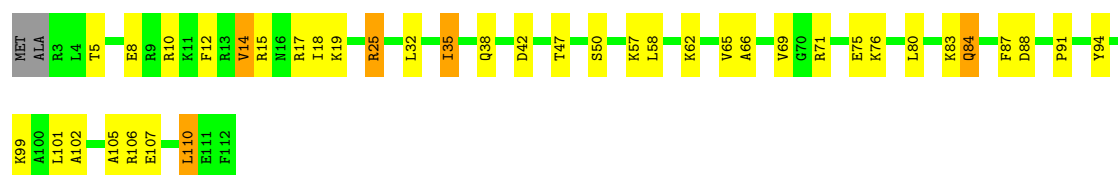
- Molecule 13: 50S Ribosomal Protein L17

Chain R: 



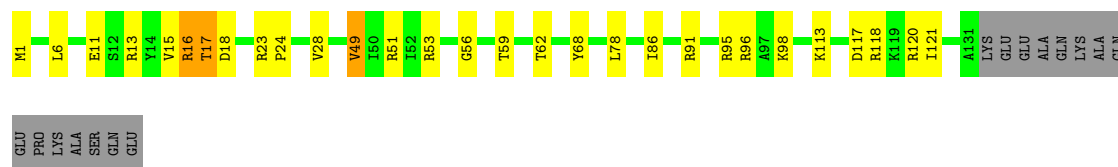
- Molecule 14: 50S Ribosomal Protein L18

Chain S: 



- Molecule 15: 50S Ribosomal Protein L19

Chain T: 



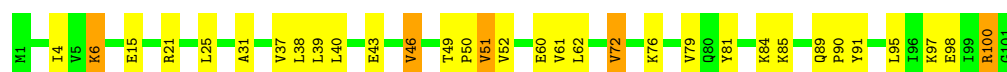
- Molecule 16: 50S Ribosomal Protein L20

Chain U: 



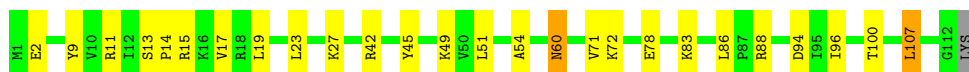
- Molecule 17: 50S Ribosomal Protein L21

Chain V: 



- Molecule 18: 50S Ribosomal Protein L22

Chain W:



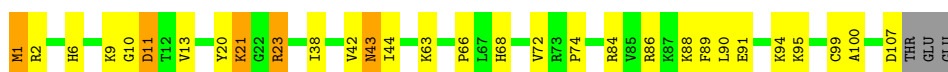
- Molecule 19: 50S Ribosomal Protein L23

Chain X:



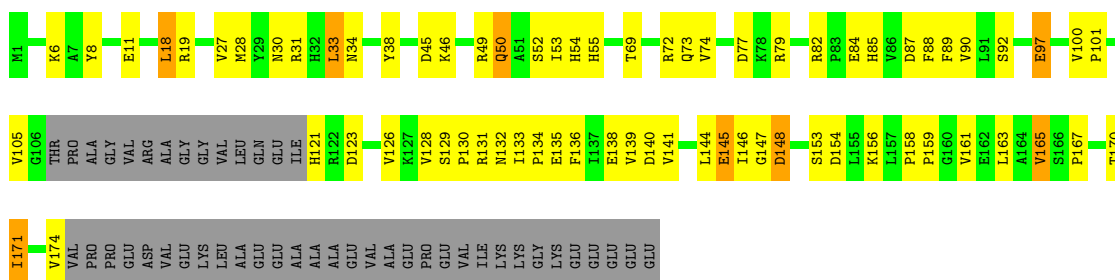
- Molecule 20: 50S Ribosomal Protein L24

Chain Y:



- Molecule 21: 50S Ribosomal Protein L25

Chain Z:



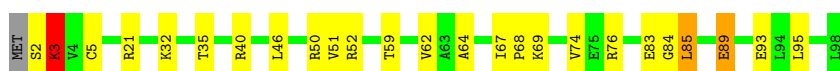
- Molecule 22: 50S Ribosomal Protein L27

Chain 0:



- Molecule 23: 50S Ribosomal Protein L28

Chain 1:



- Molecule 24: 50S Ribosomal Protein L29

Chain 2:



- Molecule 25: 50S Ribosomal Protein L30

Chain 3:



• Molecule 26: 50S Ribosomal Protein L31

Chain 4:



• Molecule 27: 50S Ribosomal Protein L32

Chain 5:



• Molecule 28: 50S Ribosomal Protein L33

Chain 6:



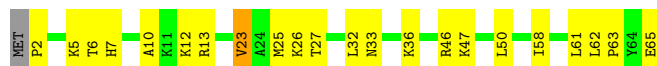
• Molecule 29: 50S Ribosomal Protein L34

Chain 7:



• Molecule 30: 50S Ribosomal Protein L35

Chain 8:



• Molecule 31: 50S Ribosomal Protein L36

Chain 9:



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.06Å 448.57Å 623.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	256.12 – 2.40	Depositor
% Data completeness (in resolution range)	99.7 (256.12-2.40)	Depositor
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.237 , 0.277	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	91678	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0.42	0/67545	0.92	63/105432 (0.1%)
2	B	0.47	1/2879 (0.0%)	0.91	2/4487 (0.0%)
3	D	0.34	0/2186	0.56	0/2944
4	E	0.34	0/1592	0.61	1/2149 (0.0%)
5	F	0.33	0/1615	0.55	0/2188
6	G	0.29	0/1453	0.52	0/1963
7	H	0.30	0/1356	0.54	0/1834
8	I	0.27	0/1079	0.55	1/1475 (0.1%)
9	N	0.32	0/1144	0.53	0/1543
10	O	0.32	0/943	0.56	1/1269 (0.1%)
11	P	0.32	0/1152	0.59	1/1533 (0.1%)
12	Q	0.32	0/1143	0.53	0/1527
13	R	0.34	0/982	0.55	0/1312
14	S	0.31	0/880	0.53	0/1172
15	T	0.30	0/1097	0.53	0/1468
16	U	0.34	0/977	0.53	0/1301
17	V	0.29	0/782	0.54	0/1049
18	W	0.33	0/897	0.55	0/1205
19	X	0.34	0/764	0.53	1/1025 (0.1%)
20	Y	0.33	0/819	0.54	0/1095
21	Z	0.30	0/1299	0.55	0/1763
22	0	0.30	0/662	0.49	0/881
23	1	0.33	0/762	0.52	0/1014
24	2	0.28	0/590	0.47	0/781
25	3	0.27	0/469	0.50	0/630
26	4	0.33	0/545	0.65	0/737
27	5	0.33	0/469	0.59	0/635
28	6	0.29	0/456	0.49	0/608
29	7	0.34	0/426	0.54	0/561
30	8	0.30	0/525	0.51	0/691
31	9	0.31	0/310	0.53	0/407
All	All	0.40	1/97798 (0.0%)	0.84	70/146679 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	U	OP3-P	-10.22	1.48	1.61

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1614	A	O5'-P-OP1	-8.54	98.02	105.70
1	A	2897	U	C2-N1-C1'	7.67	126.90	117.70
1	A	2139	C	N1-C2-O2	7.39	123.33	118.90
1	A	1298	C	O5'-P-OP2	-7.32	99.11	105.70
1	A	645	C	C2-N1-C1'	7.22	126.74	118.80
1	A	2167	U	C2-N1-C1'	7.19	126.33	117.70
1	A	2167	U	N1-C2-O2	7.08	127.76	122.80
1	A	277	C	N1-C2-O2	6.98	123.09	118.90
1	A	2893	G	C5-C6-O6	-6.74	124.56	128.60
1	A	512	G	O4'-C1'-N9	6.74	113.59	108.20
1	A	801	G	O5'-P-OP2	-6.61	99.75	105.70
1	A	2136	C	N1-C2-O2	6.23	122.64	118.90
8	I	75	LEU	CA-CB-CG	6.20	129.55	115.30
10	O	8	LEU	CA-CB-CG	6.20	129.55	115.30
1	A	1372	U	C5-C4-O4	-6.13	122.22	125.90
1	A	2473	U	C2-N1-C1'	6.13	125.06	117.70
4	E	72	VAL	C-N-CA	6.10	136.95	121.70
1	A	1992	G	P-O3'-C3'	6.07	126.98	119.70
1	A	2123	G	C5-C6-O6	-6.07	124.96	128.60
1	A	2893	G	N9-C4-C5	-6.06	102.97	105.40
1	A	2893	G	C4-C5-N7	6.03	113.21	110.80
1	A	2167	U	N3-C2-O2	-6.01	117.99	122.20
1	A	2175	C	C5-C6-N1	5.94	123.97	121.00
1	A	1372	U	N3-C4-O4	5.86	123.50	119.40
1	A	277	C	C2-N1-C1'	5.80	125.19	118.80
1	A	1698	A	O4'-C1'-N9	5.80	112.84	108.20
1	A	2155	G	N3-C2-N2	5.74	123.92	119.90
2	B	80	U	O4'-C1'-N1	5.72	112.78	108.20
1	A	2155	G	C6-N1-C2	5.70	128.52	125.10
1	A	528	A	C2-N3-C4	-5.69	107.76	110.60
1	A	2129	C	C2-N1-C1'	5.66	125.03	118.80
1	A	528	A	P-O3'-C3'	5.60	126.42	119.70
1	A	614	U	N3-C2-O2	-5.57	118.30	122.20
1	A	2175	C	C2-N1-C1'	5.57	124.93	118.80
1	A	2897	U	C5-C6-N1	5.57	125.48	122.70
1	A	2897	U	N1-C2-O2	5.55	126.69	122.80
1	A	2321	G	C4-N9-C1'	5.54	133.71	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	X	57	LEU	CA-CB-CG	5.52	128.00	115.30
1	A	1300	U	P-O3'-C3'	5.52	126.32	119.70
1	A	748	G	O4'-C1'-N9	5.47	112.58	108.20
1	A	2163	C	C6-N1-C2	-5.46	118.12	120.30
1	A	587	C	C2-N1-C1'	5.45	124.80	118.80
1	A	2447	G	N3-C4-N9	-5.45	122.73	126.00
1	A	277	C	N3-C2-O2	-5.42	118.11	121.90
1	A	2139	C	N3-C2-O2	-5.42	118.11	121.90
1	A	1647	G	O4'-C1'-N9	-5.40	103.88	108.20
1	A	1791	A	O5'-P-OP1	-5.38	100.86	105.70
1	A	192	C	O5'-P-OP1	-5.30	100.93	105.70
1	A	945	A	C2-N3-C4	-5.30	107.95	110.60
1	A	2140	C	C2-N1-C1'	5.29	124.62	118.80
2	B	2	C	C6-N1-C2	-5.27	118.19	120.30
1	A	645	C	C6-N1-C1'	-5.27	114.48	120.80
1	A	2689	U	P-O3'-C3'	5.25	126.00	119.70
1	A	2447	G	C6-C5-N7	5.25	133.55	130.40
1	A	488	G	N1-C6-O6	5.24	123.04	119.90
1	A	645	C	C5-C6-N1	5.23	123.62	121.00
1	A	917	A	O5'-P-OP2	-5.23	101.00	105.70
1	A	1352	U	O5'-P-OP1	-5.15	101.07	105.70
1	A	2893	G	N3-C4-N9	5.14	129.08	126.00
1	A	2447	G	C4-N9-C1'	-5.13	119.83	126.50
1	A	2139	C	C2-N1-C1'	5.13	124.44	118.80
1	A	192	C	OP1-P-OP2	5.12	127.28	119.60
1	A	2110	G	P-O3'-C3'	5.11	125.84	119.70
1	A	2163	C	C5-C6-N1	5.10	123.55	121.00
11	P	44	GLY	C-N-CA	5.06	134.36	121.70
1	A	2593	U	N3-C4-O4	-5.05	115.87	119.40
1	A	2130	U	C5-C6-N1	5.04	125.22	122.70
1	A	277	C	C6-N1-C2	-5.04	118.28	120.30
1	A	488	G	C5-C6-O6	-5.04	125.58	128.60
1	A	214	G	O4'-C1'-N9	5.03	112.22	108.20

There are no chirality outliers.

There are no planarity outliers.

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	A	60314	0	30412	730	0
2	B	2575	0	1303	51	0
3	D	2136	0	2218	53	0
4	E	1559	0	1617	38	0
5	F	1580	0	1619	42	0
6	G	1428	0	1438	55	0
7	H	1330	0	1407	41	0
8	I	1064	0	1082	29	0
9	N	1117	0	1184	21	0
10	O	933	0	996	14	0
11	P	1135	0	1212	47	0
12	Q	1122	0	1179	31	0
13	R	968	0	1033	32	0
14	S	870	0	923	23	0
15	T	1083	0	1136	18	0
16	U	959	0	1019	21	0
17	V	771	0	830	18	0
18	W	886	0	940	15	0
19	X	750	0	814	18	0
20	Y	806	0	881	18	0
21	Z	1271	0	1273	52	0
22	0	653	0	674	17	0
23	1	755	0	826	14	0
24	2	588	0	643	5	0
25	3	464	0	514	9	0
26	4	532	0	503	27	0
27	5	455	0	465	8	0
28	6	449	0	469	11	0
29	7	418	0	467	11	0
30	8	517	0	582	23	0
31	9	307	0	335	9	0
32	0	1	0	0	0	0
32	1	1	0	0	0	0
32	3	1	0	0	0	0
32	5	2	0	0	0	0
32	8	2	0	0	0	0
32	A	673	0	0	0	0
32	B	21	0	0	0	0
32	D	6	0	0	0	0
32	E	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	F	7	0	0	0	0
32	G	1	0	0	0	0
32	O	1	0	0	0	0
32	P	1	0	0	0	0
32	Q	3	0	0	0	0
32	R	1	0	0	0	0
32	T	1	0	0	0	0
32	U	4	0	0	0	0
32	V	2	0	0	0	0
32	W	3	0	0	0	0
32	X	1	0	0	0	0
32	Y	1	0	0	0	0
32	Z	1	0	0	0	0
33	4	1	0	0	0	0
33	5	1	0	0	0	0
33	6	1	0	0	0	0
33	9	1	0	0	0	0
33	Y	1	0	0	0	0
34	0	4	0	0	0	0
34	1	4	0	0	1	0
34	2	1	0	0	0	0
34	3	1	0	0	0	0
34	5	2	0	0	0	0
34	7	5	0	0	0	0
34	8	5	0	0	0	0
34	9	1	0	0	0	0
34	A	1039	0	0	58	0
34	B	10	0	0	1	0
34	D	17	0	0	0	0
34	E	8	0	0	1	0
34	F	6	0	0	0	0
34	I	2	0	0	0	0
34	N	1	0	0	0	0
34	O	3	0	0	0	0
34	P	12	0	0	3	0
34	Q	1	0	0	0	0
34	R	3	0	0	0	0
34	T	3	0	0	0	0
34	U	1	0	0	0	0
34	V	1	0	0	0	0
34	W	2	0	0	0	0
34	X	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	Y	1	0	0	1	0
34	Z	2	0	0	0	0
All	All	91678	0	59994	1308	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 9.

All (1308) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2124:G:H1	1:A:2174:C:H42	1.12	0.97
1:A:2121:G:H1	1:A:2177:C:H42	1.13	0.91
1:A:2807:G:N1	1:A:2893:G:O6	2.04	0.90
31:9:25:VAL:HB	31:9:34:GLN:HB2	1.55	0.89
2:B:7:G:H21	14:S:38:GLN:HE22	1.20	0.89
1:A:1689:A:H62	1:A:1698:A:H2	1.22	0.88
18:W:14:PRO:HG2	18:W:78:GLU:HG2	1.57	0.87
1:A:1315:C:OP2	34:A:4472:HOH:O	1.90	0.87
1:A:900:A:H2'	1:A:901:A:H8	1.39	0.86
1:A:2141:G:O6	1:A:2150:U:O2	1.95	0.85
1:A:2139:C:N4	1:A:2152:G:H1	1.75	0.85
1:A:948:G:OP1	34:A:4588:HOH:O	1.94	0.84
4:E:72:VAL:HG13	4:E:73:GLU:HG3	1.59	0.84
1:A:2139:C:N4	1:A:2152:G:N1	2.26	0.83
21:Z:46:LYS:O	21:Z:50:GLN:NE2	2.11	0.81
14:S:38:GLN:NE2	14:S:47:THR:OG1	2.13	0.81
1:A:1568:G:N7	34:A:5002:HOH:O	2.13	0.81
1:A:2139:C:N3	1:A:2152:G:N2	2.28	0.81
19:X:31:HIS:HD2	19:X:33:LYS:H	1.30	0.80
1:A:1973:G:OP1	34:A:4547:HOH:O	1.99	0.80
1:A:2287:A:H62	1:A:2344:U:H3	1.28	0.80
1:A:2206:G:H3'	1:A:2207:G:C8	2.17	0.80
1:A:1798:U:OP2	3:D:274:ARG:NH2	2.14	0.79
1:A:1648:C:OP1	34:A:4516:HOH:O	1.98	0.79
1:A:900:A:H2'	1:A:901:A:C8	2.18	0.79
1:A:2683:C:OP1	15:T:53:ARG:NH2	2.16	0.79
6:G:80:PHE:O	6:G:82:LEU:N	2.16	0.79
1:A:994:C:OP1	16:U:53:ARG:NH2	2.15	0.78
2:B:92:C:OP1	21:Z:79:ARG:NH1	2.16	0.78
1:A:1449:A:O2'	1:A:1529:G:N2	2.17	0.78
1:A:963:U:OP2	34:A:4588:HOH:O	2.02	0.78
12:Q:22:LYS:HD3	12:Q:23:GLY:N	1.98	0.78
1:A:1171:G:H1	1:A:1178:C:H42	1.29	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:Q:26:TYR:O	12:Q:67:ARG:NH1	2.16	0.77
1:A:301:G:OP2	20:Y:84:ARG:NH2	2.18	0.77
1:A:2121:G:H1	1:A:2177:C:N4	1.82	0.77
18:W:2:GLU:OE2	18:W:72:LYS:NZ	2.17	0.77
21:Z:72:ARG:NH2	21:Z:97:GLU:O	2.17	0.77
1:A:2124:G:H1	1:A:2174:C:N4	1.83	0.77
2:B:4:C:H42	2:B:117:G:H1	1.33	0.76
1:A:2122:U:O4	1:A:2176:A:N1	2.18	0.76
1:A:1798:U:H5'	3:D:259:THR:HG22	1.68	0.76
1:A:7:G:N2	1:A:2896:C:O2	2.14	0.76
1:A:2112:G:N7	1:A:2169:A:N6	2.33	0.76
1:A:990:A:OP2	34:A:4499:HOH:O	2.04	0.75
1:A:397:G:N7	34:A:4914:HOH:O	2.18	0.75
6:G:115:ARG:HD2	6:G:136:ARG:HH21	1.51	0.75
16:U:76:TYR:OH	16:U:92:ARG:NH1	2.19	0.74
19:X:11:PRO:HB3	19:X:92:LEU:HD11	1.69	0.74
1:A:2849:U:OP2	15:T:95:ARG:NH1	2.21	0.74
1:A:2646:C:OP2	1:A:2732:G:O2'	2.06	0.74
1:A:1019:U:H3	1:A:1142(A):A:H62	1.36	0.74
1:A:1800:C:OP2	3:D:183:ARG:NH2	2.20	0.73
9:N:128:HIS:O	9:N:131:GLN:NE2	2.21	0.73
12:Q:27:VAL:O	12:Q:29:PHE:N	2.19	0.73
1:A:2407:G:OP1	34:A:4203:HOH:O	2.07	0.73
23:1:50:ARG:HG2	23:1:59:THR:HG22	1.70	0.73
1:A:962:G:OP1	34:A:4588:HOH:O	2.06	0.73
21:Z:146:ILE:HG13	21:Z:174:VAL:HG12	1.70	0.73
1:A:467:G:OP1	29:7:33:ARG:NH1	2.22	0.72
1:A:2116:G:N2	1:A:2162:G:OP1	2.22	0.72
2:B:75:G:N2	21:Z:87:ASP:OD1	2.21	0.72
1:A:649:G:H4'	30:8:46:ARG:HH22	1.54	0.72
1:A:1314:C:OP1	34:A:4472:HOH:O	2.07	0.72
4:E:111:ARG:HB3	13:R:1:MET:HE1	1.70	0.72
1:A:2788:C:OP1	4:E:61:ARG:NH2	2.22	0.72
5:F:53:THR:HG23	5:F:55:GLY:H	1.55	0.72
10:O:35:VAL:HG11	10:O:103:ALA:HB3	1.70	0.72
11:P:96:THR:H	11:P:99:LEU:HD21	1.55	0.72
1:A:652(C):G:N2	1:A:652(V):C:O2	2.17	0.72
1:A:125:G:H5'	29:7:14:LYS:HD2	1.72	0.72
1:A:1171:G:N2	1:A:1178:C:N3	2.34	0.71
1:A:2033:A:OP1	34:A:4237:HOH:O	2.08	0.71
7:H:84:SER:HB3	7:H:132:ARG:HH11	1.55	0.71
11:P:44:GLY:O	34:P:301:HOH:O	2.07	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:4:44:THR:O	26:4:46:GLN:N	2.23	0.71
1:A:1968:G:OP1	34:A:4546:HOH:O	2.08	0.71
1:A:2135:A:H5'	1:A:2159:G:O2'	1.90	0.71
1:A:528:A:O2'	1:A:529:A:H5''	1.90	0.71
23:1:51:VAL:HG11	23:1:74:VAL:HG21	1.73	0.71
1:A:2135:A:H61	1:A:2157:G:N2	1.89	0.71
1:A:2805:G:H2'	1:A:2807:G:C8	2.25	0.71
6:G:161:THR:HG22	6:G:163:ALA:H	1.56	0.71
7:H:33:LEU:HD21	7:H:136:ILE:HB	1.73	0.71
1:A:2116:G:N7	1:A:2166:G:N2	2.39	0.70
1:A:2592:G:OP1	34:A:4546:HOH:O	2.09	0.70
1:A:775:G:O3'	34:A:4554:HOH:O	2.08	0.70
1:A:411:G:OP1	34:A:4203:HOH:O	2.08	0.70
1:A:1204:A:H2	1:A:1241:A:H62	1.38	0.70
1:A:958:U:OP2	12:Q:14:ARG:NH1	2.24	0.70
21:Z:92:SER:O	21:Z:130:PRO:HG3	1.91	0.70
1:A:1815:A:OP2	3:D:54:ARG:NH2	2.24	0.70
5:F:184:TYR:CE2	5:F:188:ARG:HD2	2.27	0.70
7:H:17:VAL:HG13	7:H:26:VAL:HG22	1.72	0.70
1:A:831:G:O2'	11:P:38:GLN:NE2	2.24	0.69
1:A:1342:A:OP2	34:A:4187:HOH:O	2.10	0.69
11:P:52:GLU:OE1	11:P:55:ARG:NH1	2.24	0.69
6:G:5:VAL:HG22	6:G:8:LYS:H	1.58	0.69
1:A:741:G:OP2	34:A:4523:HOH:O	2.11	0.69
1:A:1378:A:OP1	29:7:10:ARG:NH2	2.26	0.69
1:A:1310:G:OP2	29:7:9:ARG:NH1	2.25	0.69
3:D:71:ASP:HB3	3:D:103:ARG:HH22	1.57	0.69
1:A:2148:G:H2'	1:A:2149:G:C8	2.28	0.69
1:A:908:C:P	12:Q:22:LYS:HD2	2.32	0.68
1:A:1030:G:OP2	12:Q:128:LYS:NZ	2.26	0.68
1:A:2327:A:H2'	1:A:2328:A:C8	2.28	0.68
23:1:21:ARG:HD3	23:1:35:THR:HG21	1.74	0.68
12:Q:110:THR:HG23	12:Q:113:GLN:HB2	1.76	0.68
21:Z:27:VAL:HG12	21:Z:85:HIS:HE1	1.58	0.68
1:A:81:G:N7	34:A:4466:HOH:O	2.25	0.68
1:A:2447:G:OP2	34:A:4723:HOH:O	2.10	0.68
17:V:6:LYS:HB2	17:V:38:LEU:HD21	1.74	0.68
1:A:1452:A:OP2	34:A:4788:HOH:O	2.12	0.68
1:A:2028:U:O4	34:A:4237:HOH:O	2.10	0.67
7:H:104:GLU:HG3	7:H:114:VAL:HG22	1.75	0.67
11:P:100:LEU:HD12	11:P:112:LEU:HD11	1.75	0.67
1:A:1970:A:OP1	34:A:4259:HOH:O	2.12	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2379:G:O2'	14:S:17:ARG:NH2	2.25	0.67
1:A:2839:G:H5'	13:R:46:GLY:HA2	1.74	0.67
22:O:10:THR:HG22	22:O:12:ASN:H	1.60	0.67
1:A:249:C:O2	30:8:12:LYS:NZ	2.27	0.66
30:8:33:ASN:HA	30:8:36:LYS:HD2	1.77	0.66
1:A:2148:G:H2'	1:A:2149:G:H8	1.59	0.66
1:A:2880:C:O3'	13:R:90:ARG:NH1	2.27	0.66
1:A:307:G:N7	34:A:4267:HOH:O	2.27	0.66
7:H:7:LEU:HD12	7:H:8:PRO:HD2	1.75	0.66
1:A:1801:G:OP2	3:D:154:LYS:NZ	2.26	0.66
1:A:11:G:N7	34:A:4575:HOH:O	2.28	0.66
1:A:2118:U:C4	1:A:2149:G:H1'	2.30	0.66
8:I:93:THR:HG22	8:I:119:PRO:HB3	1.76	0.66
1:A:1783:A:OP1	34:A:4522:HOH:O	2.12	0.66
1:A:570:G:OP1	34:A:4397:HOH:O	2.12	0.66
2:B:13:A:N1	2:B:69:G:O2'	2.24	0.66
1:A:252:G:P	11:P:50:ARG:HH12	2.18	0.66
1:A:250:G:OP2	30:8:13:ARG:NH2	2.29	0.66
1:A:2819:G:N7	34:A:4380:HOH:O	2.29	0.66
1:A:1912:A:OP1	34:A:4643:HOH:O	2.13	0.65
26:4:59:PHE:H	26:4:59:PHE:HD1	1.45	0.65
1:A:1670:C:OP1	34:A:4063:HOH:O	2.13	0.65
1:A:1434:A:H61	1:A:1558:A:H62	1.43	0.65
1:A:2126:A:N6	1:A:2162:G:O2'	2.30	0.65
1:A:568:U:H5'	1:A:945:A:N1	2.12	0.65
26:4:24:THR:OG1	26:4:25:TYR:N	2.29	0.65
1:A:886:C:H1'	1:A:890:A:H61	1.62	0.65
4:E:47:VAL:HG11	4:E:86:PRO:HD2	1.79	0.65
1:A:1031:G:H5''	31:9:8:LYS:HE3	1.78	0.65
1:A:832:G:OP1	34:A:4580:HOH:O	2.13	0.65
1:A:1816:G:O6	3:D:35:LYS:NZ	2.20	0.65
1:A:1021:A:H62	1:A:1141:U:H3	1.42	0.65
1:A:1250:G:N7	11:P:18:ARG:NH2	2.45	0.65
1:A:2171:A:N3	1:A:2172:U:N3	2.45	0.65
1:A:300:A:OP1	20:Y:86:ARG:NH2	2.30	0.64
2:B:106:G:H5'	21:Z:31:ARG:HG2	1.79	0.64
5:F:21:ALA:HB3	5:F:22:ALA:HA	1.80	0.64
1:A:2291:U:OP1	1:A:2380:C:O2'	2.16	0.64
7:H:20:ALA:HB3	7:H:23:ARG:HG3	1.80	0.64
4:E:77:ILE:HD13	4:E:195:LEU:HD22	1.79	0.64
5:F:157:VAL:HB	5:F:194:MET:HG2	1.79	0.64
1:A:2632:A:HO2'	1:A:2811:G:HO2'	1.42	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:Q:1:MET:N	12:Q:1:MET:SD	2.65	0.63
13:R:21:TYR:CZ	13:R:43:GLU:HG2	2.33	0.63
4:E:72:VAL:HA	4:E:73:GLU:HB3	1.81	0.63
1:A:1420:U:O2'	1:A:1421:G:OP1	2.16	0.63
1:A:2807:G:H22	1:A:2892:A:H62	1.47	0.63
1:A:1266:G:O5'	18:W:15:ARG:NH2	2.31	0.63
5:F:24:LEU:HD23	5:F:115:ALA:HA	1.81	0.63
7:H:149:ARG:NH1	7:H:167:GLU:OE1	2.31	0.63
17:V:43:GLU:OE2	17:V:43:GLU:N	2.32	0.63
2:B:66:A:H61	2:B:109:C:H5'	1.64	0.63
3:D:132:PRO:HD3	3:D:190:TYR:CZ	2.34	0.63
5:F:24:LEU:HD21	5:F:114:VAL:HG12	1.80	0.63
21:Z:145:GLU:H	21:Z:148:ASP:HB2	1.62	0.63
8:I:31:LEU:HD21	8:I:38:LEU:HG	1.81	0.62
14:S:71:ARG:NH1	14:S:107:GLU:OE1	2.32	0.62
4:E:36:ARG:HG2	4:E:47:VAL:HG12	1.81	0.62
1:A:2308:G:O6	1:A:2311:A:N6	2.20	0.62
1:A:625:G:O6	11:P:107:LYS:NZ	2.30	0.62
1:A:2316:C:O2'	6:G:128:ARG:NH2	2.31	0.62
1:A:2870:C:H2'	1:A:2871:C:O4'	2.00	0.62
3:D:85:ASP:OD2	3:D:88:ARG:NH1	2.32	0.62
21:Z:156:LYS:HE3	21:Z:158:PRO:HD3	1.81	0.62
21:Z:159:PRO:HA	21:Z:161:VAL:H	1.63	0.62
11:P:50:ARG:HH21	30:8:7:HIS:HD2	1.45	0.62
1:A:692:C:O2'	3:D:38:LYS:NZ	2.31	0.62
1:A:1405:U:H2'	1:A:1406:U:C6	2.35	0.62
1:A:2151:G:H2'	1:A:2152:G:H8	1.65	0.62
2:B:24:G:N7	2:B:56:G:H2'	2.15	0.62
12:Q:35:VAL:HG13	12:Q:130:LYS:HB3	1.82	0.62
3:D:3:VAL:HG13	3:D:17:THR:HB	1.82	0.62
20:Y:23:ARG:HG2	20:Y:42:VAL:HG22	1.80	0.62
14:S:25:ARG:NH1	14:S:42:ASP:OD2	2.33	0.61
21:Z:153:SER:HB3	21:Z:167:PRO:HB3	1.81	0.61
1:A:2758:A:C2	1:A:2759:G:H1'	2.35	0.61
8:I:92:VAL:HG13	8:I:120:ILE:HB	1.82	0.61
19:X:57:LEU:HD21	19:X:78:LYS:HE2	1.81	0.61
1:A:1639:U:H2'	1:A:1640:C:H5''	1.80	0.61
20:Y:88:LYS:HZ3	20:Y:90:LEU:HA	1.64	0.61
13:R:101:ALA:HB3	27:5:47:PRO:HG3	1.83	0.61
3:D:132:PRO:HG2	3:D:135:PHE:CD2	2.35	0.61
1:A:2130:U:H4'	1:A:2133:G:H4'	1.81	0.61
13:R:2:ARG:NH1	13:R:5:LYS:O	2.33	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:Y:94:LYS:NZ	34:Y:601:HOH:O	2.32	0.61
24:2:35:LEU:HD12	24:2:53:LEU:HD12	1.82	0.61
5:F:167:ALA:HB1	5:F:173:VAL:HG11	1.81	0.61
12:Q:18:LYS:O	12:Q:98:LYS:NZ	2.28	0.61
1:A:1019:U:H2'	1:A:1020:A:H8	1.64	0.61
1:A:821:A:N1	34:A:4395:HOH:O	2.31	0.61
1:A:1218:C:OP2	16:U:15:LYS:NZ	2.32	0.61
17:V:4:ILE:HD12	17:V:39:LEU:HB3	1.83	0.61
22:0:11:ARG:O	22:0:14:ARG:NH2	2.34	0.60
1:A:1183:G:O3'	25:3:29:ARG:NH1	2.33	0.60
22:0:32:ARG:H	22:0:35:ASN:ND2	2.00	0.60
26:4:59:PHE:HA	26:4:61:ARG:N	2.16	0.60
1:A:2364:C:OP1	22:0:55:ARG:NH1	2.32	0.60
1:A:2615:U:OP1	34:A:4305:HOH:O	2.16	0.60
1:A:2655:G:O2'	1:A:2664:G:O6	2.15	0.60
2:B:14:U:OP2	2:B:70:C:O2'	2.17	0.60
6:G:150:ASP:N	6:G:150:ASP:OD1	2.25	0.60
1:A:974:G:OP1	1:A:1187:G:O2'	2.14	0.60
11:P:138:LEU:HD23	11:P:145:PRO:HB3	1.83	0.60
1:A:1891:G:O6	34:A:4758:HOH:O	2.16	0.59
1:A:2751:G:H8	7:H:2:SER:HA	1.66	0.59
1:A:848:G:N3	1:A:933:A:H1'	2.17	0.59
1:A:2183:C:H2'	1:A:2184:G:C8	2.37	0.59
1:A:2507:C:H5''	1:A:2573:C:N4	2.17	0.59
1:A:1033:U:OP1	31:9:9:ARG:NH2	2.36	0.59
1:A:1803:A:O2'	3:D:259:THR:HG21	2.02	0.59
1:A:2162:G:H4'	1:A:2172:U:H2'	1.83	0.59
1:A:2206:G:H8	1:A:2207:G:N7	1.99	0.59
1:A:322:A:OP2	5:F:169:ASN:HB2	2.02	0.59
15:T:117:ASP:OD2	15:T:120:ARG:NE	2.29	0.59
16:U:83:LEU:HD12	16:U:88:ILE:HB	1.83	0.59
1:A:2285:C:OP2	28:6:6:ARG:NH1	2.35	0.59
1:A:1159:U:H2'	1:A:1160:G:H8	1.67	0.59
1:A:1448:G:H4'	1:A:1542:A:OP1	2.03	0.59
13:R:67:LEU:HD13	13:R:76:VAL:HG21	1.83	0.59
1:A:1530:C:O2'	1:A:1531:C:O5'	2.15	0.59
1:A:1762:A:N1	34:A:4594:HOH:O	2.31	0.59
1:A:2447:G:N2	1:A:2450:A:OP2	2.35	0.59
1:A:1239:G:H2'	1:A:1240:U:O4'	2.02	0.59
1:A:1261:C:OP2	18:W:83:LYS:NZ	2.29	0.59
6:G:131:TYR:HB3	6:G:159:VAL:HG13	1.85	0.59
17:V:72:VAL:HG13	17:V:85:LYS:HB3	1.85	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:324:A:N6	1:A:338:G:O2'	2.36	0.59
2:B:101:G:OP2	34:B:3105:HOH:O	2.17	0.59
17:V:76:LYS:HB2	17:V:81:TYR:HB3	1.84	0.59
4:E:111:ARG:HG3	4:E:160:TYR:CD2	2.38	0.58
1:A:674:G:H1'	5:F:74:ARG:HD3	1.84	0.58
8:I:124:GLY:H	8:I:144:VAL:HG23	1.68	0.58
6:G:15:VAL:HG22	6:G:175:LEU:HB3	1.85	0.58
1:A:2176:A:H2'	1:A:2177:C:C6	2.38	0.58
1:A:2299:G:H2'	1:A:2300:G:H8	1.68	0.58
5:F:135:LYS:HG2	5:F:137:LYS:HZ3	1.68	0.58
1:A:631:A:OP1	11:P:65:ARG:NH1	2.37	0.58
14:S:15:ARG:O	14:S:19:LYS:HG2	2.02	0.58
4:E:116:VAL:HG13	4:E:122:PHE:HB2	1.85	0.58
8:I:4:ILE:HD11	8:I:44:LEU:HD13	1.84	0.58
20:Y:86:ARG:HD2	20:Y:100:ALA:HA	1.84	0.58
1:A:1012:U:H5	9:N:28:THR:HG21	1.67	0.58
1:A:1010:A:OP2	34:A:4488:HOH:O	2.17	0.58
1:A:1693:U:O2'	3:D:14:ARG:NH2	2.36	0.58
8:I:102:SER:O	8:I:106:GLY:N	2.36	0.58
23:1:32:LYS:O	34:1:202:HOH:O	2.16	0.58
1:A:1589:C:H2'	1:A:1590:U:H6	1.69	0.58
1:A:2693:A:H2'	1:A:2694:G:H8	1.68	0.58
1:A:526:A:OP1	34:A:4494:HOH:O	2.17	0.58
23:1:85:LEU:HB3	23:1:89:GLU:HB3	1.85	0.58
1:A:2136:C:HO2'	1:A:2137:C:H6	1.52	0.58
1:A:2836:U:H2'	1:A:2837:G:C8	2.39	0.58
10:O:8:LEU:HD12	10:O:84:ALA:HB2	1.84	0.58
15:T:17:THR:OG1	15:T:17:THR:O	2.21	0.58
18:W:60:ASN:HD22	18:W:60:ASN:N	2.02	0.58
1:A:880:G:H2'	1:A:881:G:H8	1.69	0.58
1:A:886:C:O2'	1:A:889:C:N4	2.37	0.58
1:A:1823:G:OP1	3:D:54:ARG:NH1	2.36	0.58
6:G:114:ILE:HA	6:G:140:ILE:HD11	1.86	0.58
1:A:2141:G:H2'	1:A:2142:C:O4'	2.03	0.57
1:A:2478:A:OP2	31:9:2:LYS:NZ	2.28	0.57
11:P:95:VAL:HA	11:P:99:LEU:HD21	1.85	0.57
21:Z:55:HIS:CE1	21:Z:135:GLU:HB2	2.39	0.57
1:A:2114:A:N6	1:A:2115:G:H21	2.02	0.57
6:G:137:GLU:HG2	6:G:152:LEU:HD13	1.86	0.57
16:U:49:HIS:HA	16:U:52:ARG:HB3	1.86	0.57
24:2:65:ASN:OD1	24:2:69:ARG:NH1	2.38	0.57
1:A:1037:G:H1	1:A:1118:C:H42	1.52	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:3:7:LYS:HG3	25:3:34:GLU:HG3	1.87	0.57
13:R:44:LEU:HD22	13:R:48:VAL:HG23	1.85	0.57
1:A:2128:C:H1'	1:A:2173:A:O2'	2.05	0.57
1:A:403:U:H4'	1:A:404:C:H5'	1.87	0.57
5:F:11:VAL:HG22	5:F:125:LEU:HD13	1.86	0.57
5:F:21:ALA:CB	5:F:22:ALA:HA	2.35	0.57
21:Z:19:ARG:NH1	21:Z:84:GLU:O	2.37	0.57
1:A:1364:G:N7	23:1:3:LYS:HE2	2.20	0.57
1:A:2103:C:H42	1:A:2186:G:H1	1.52	0.57
12:Q:34:LEU:HB2	12:Q:118:LEU:HD22	1.87	0.57
1:A:2023:G:H5'	1:A:2617:C:H4'	1.86	0.57
1:A:2122:U:H3	1:A:2176:A:H2	1.51	0.57
1:A:2693:A:H2'	1:A:2694:G:C8	2.40	0.57
21:Z:105:VAL:N	21:Z:139:VAL:O	2.37	0.57
5:F:135:LYS:HG2	5:F:137:LYS:NZ	2.20	0.57
9:N:20:GLY:HA2	9:N:61:ARG:HE	1.70	0.57
15:T:16:ARG:NH1	15:T:18:ASP:OD1	2.38	0.56
1:A:2892:A:H2'	1:A:2893:G:H5'	1.85	0.56
2:B:66:A:N6	2:B:108:U:H3'	2.20	0.56
2:B:57:A:H1'	6:G:29:TRP:HB2	1.87	0.56
7:H:56:SER:HB3	7:H:61:HIS:ND1	2.19	0.56
1:A:1019:U:H2'	1:A:1020:A:C8	2.40	0.56
15:T:24:PRO:HA	15:T:49:VAL:HG22	1.87	0.56
1:A:1220:A:OP2	16:U:19:LYS:NZ	2.33	0.56
1:A:2291:U:H2'	1:A:2292:C:C6	2.40	0.56
1:A:108:U:H2'	1:A:109:G:C8	2.40	0.56
1:A:1183:G:H5''	25:3:30:ARG:HH22	1.71	0.56
26:4:16:CYS:SG	26:4:17:GLY:N	2.79	0.56
1:A:400:G:N7	34:A:4696:HOH:O	2.32	0.56
3:D:17:THR:O	3:D:211:ARG:NH2	2.35	0.56
1:A:1005:C:H2'	1:A:1006:C:C6	2.40	0.56
14:S:87:PHE:CE1	14:S:102:ALA:HB2	2.41	0.56
1:A:2165:G:H2'	1:A:2166:G:H5''	1.88	0.56
2:B:103:G:N3	21:Z:73:GLN:NE2	2.43	0.56
6:G:32:PRO:HB3	6:G:163:ALA:HB2	1.88	0.56
17:V:40:LEU:HB2	17:V:46:VAL:HG13	1.88	0.56
1:A:1717:G:H2'	1:A:1718:G:H8	1.70	0.56
1:A:1799:G:O2'	3:D:181:GLU:OE2	2.20	0.56
28:6:6:ARG:NH1	28:6:26:ASN:HB2	2.20	0.56
1:A:1507:A:O2'	1:A:1508:A:O5'	2.24	0.56
1:A:2166:G:H3'	1:A:2167:U:H5''	1.88	0.55
1:A:2472:G:H2'	1:A:2475:C:H42	1.70	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:Z:52:SER:OG	21:Z:53:ILE:N	2.26	0.55
1:A:2815:C:H5'	27:5:29:THR:HG21	1.88	0.55
1:A:143:G:H4'	19:X:35:THR:HG21	1.88	0.55
1:A:307:G:N1	1:A:310:A:OP2	2.35	0.55
1:A:2376:A:N3	14:S:106:ARG:NH2	2.52	0.55
1:A:902:C:H2'	1:A:903:C:H6	1.71	0.55
14:S:15:ARG:NE	14:S:88:ASP:OD2	2.31	0.55
1:A:1012:U:C5	9:N:28:THR:HG21	2.40	0.55
1:A:108:U:H2'	1:A:109:G:H8	1.70	0.55
1:A:897:C:H3'	1:A:898:C:C6	2.41	0.55
7:H:6:ARG:HH21	7:H:54:ARG:HH12	1.54	0.55
1:A:1359:A:H61	1:A:1372:U:H3	1.55	0.55
1:A:1352:U:OP1	34:A:4122:HOH:O	2.18	0.55
1:A:2769:C:H2'	1:A:2770:G:O4'	2.07	0.55
1:A:1796:U:H2'	1:A:1797:C:C6	2.42	0.55
1:A:1778:U:H2'	1:A:1784:A:N6	2.22	0.55
1:A:1847:A:H3'	1:A:1848:A:H5'	1.88	0.55
1:A:271(H):G:O2'	1:A:271(I):G:OP2	2.25	0.55
17:V:60:GLU:HB2	17:V:97:LYS:HE2	1.87	0.55
19:X:31:HIS:CD2	19:X:33:LYS:H	2.16	0.55
1:A:330:A:H2	1:A:1210:A:HO2'	1.56	0.55
1:A:471:A:H2'	1:A:472:A:O4'	2.07	0.55
15:T:95:ARG:HG2	15:T:95:ARG:HH11	1.72	0.55
1:A:2357:U:OP1	22:0:20:ARG:NH1	2.35	0.54
1:A:2530:A:OP2	1:A:2535:G:N2	2.40	0.54
1:A:997:G:OP1	16:U:92:ARG:HG2	2.08	0.54
1:A:1116:C:H2'	1:A:1117:G:C8	2.42	0.54
1:A:885:C:H2'	1:A:886:C:H4'	1.89	0.54
11:P:59:LEU:HD21	30:8:10:ALA:HA	1.89	0.54
13:R:72:ASP:O	13:R:76:VAL:HG23	2.07	0.54
1:A:2167:U:H2'	1:A:2168:G:H21	1.71	0.54
1:A:323:G:O2'	1:A:1205:U:N3	2.37	0.54
1:A:861:A:N3	2:B:79:C:O2'	2.36	0.54
1:A:864:G:OP2	12:Q:22:LYS:HE3	2.08	0.54
11:P:121:LYS:O	11:P:123:LEU:N	2.40	0.54
1:A:2134:A:H2'	1:A:2134:A:N3	2.23	0.54
1:A:287:C:H2'	1:A:288:C:H6	1.73	0.54
11:P:63:PRO:HG2	30:8:25:MET:HB2	1.88	0.54
1:A:116:C:H2'	1:A:117:G:O4'	2.08	0.54
1:A:2118:U:N3	1:A:2149:G:H1'	2.22	0.54
1:A:2650:U:H2'	1:A:2651:C:C6	2.43	0.54
6:G:19:LEU:HD13	6:G:32:PRO:HG2	1.90	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:I:104:GLN:O	8:I:105:HIS:ND1	2.38	0.54
1:A:1971:A:OP1	34:A:4259:HOH:O	2.18	0.54
1:A:236:C:H2'	1:A:237:C:H6	1.72	0.54
1:A:687:C:OP2	34:A:4768:HOH:O	2.18	0.54
1:A:878:A:N6	1:A:899:A:O2'	2.41	0.54
8:I:71:ILE:O	8:I:75:LEU:HD13	2.08	0.54
1:A:1495:A:H2'	1:A:1496:A:C8	2.43	0.54
1:A:2630:G:H2'	1:A:2631:G:C8	2.43	0.54
1:A:296:C:O3'	20:Y:95:LYS:NZ	2.41	0.54
28:6:14:THR:OG1	28:6:48:VAL:O	2.26	0.54
31:9:10:ILE:HD12	31:9:32:HIS:HA	1.90	0.54
1:A:1300:U:H4'	1:A:1301:A:C5'	2.39	0.53
1:A:882:G:H2'	1:A:883:G:C8	2.43	0.53
2:B:9:G:H1	2:B:112:U:H3	1.54	0.53
15:T:59:THR:HG23	15:T:78:LEU:HB3	1.90	0.53
21:Z:159:PRO:HA	21:Z:161:VAL:N	2.23	0.53
3:D:164:GLN:NE2	3:D:176:ARG:HH22	2.05	0.53
1:A:952:G:OP1	12:Q:16:ARG:NH2	2.42	0.53
7:H:69:ARG:HG3	7:H:70:THR:N	2.23	0.53
19:X:43:VAL:HG21	19:X:81:VAL:HG11	1.91	0.53
1:A:1713:U:H2'	1:A:1714:G:H8	1.74	0.53
1:A:1957:C:OP1	34:A:4713:HOH:O	2.19	0.53
1:A:315:G:H2'	1:A:316:C:C6	2.44	0.53
1:A:922:U:H2'	1:A:923:C:C6	2.43	0.53
1:A:888:C:H5''	1:A:889:C:OP2	2.07	0.53
2:B:22:U:H3	2:B:61:G:H1	1.56	0.53
6:G:151:ALA:O	6:G:153:ARG:NH1	2.41	0.53
1:A:1817:G:OP1	3:D:88:ARG:NH2	2.42	0.53
1:A:2022:U:O2'	1:A:2617:C:H5'	2.09	0.53
2:B:1:U:O2'	2:B:2:C:O5'	2.20	0.53
3:D:132:PRO:HG2	3:D:135:PHE:HD2	1.72	0.53
6:G:46:ALA:HB2	6:G:53:LEU:HG	1.91	0.53
8:I:38:LEU:H	8:I:38:LEU:HD12	1.73	0.53
1:A:1579:A:H2'	1:A:1580:A:C8	2.43	0.53
1:A:2121:G:N2	1:A:2177:C:N3	2.46	0.53
1:A:1250:G:OP2	11:P:21:ARG:NH1	2.42	0.53
13:R:21:TYR:OH	13:R:43:GLU:HG2	2.09	0.53
1:A:2135:A:H61	1:A:2157:G:H21	1.56	0.53
1:A:2137:C:H2'	1:A:2138:C:H6	1.73	0.53
1:A:2144:U:O2	1:A:2148:G:N1	2.42	0.53
6:G:64:THR:HB	6:G:94:LEU:HD21	1.91	0.53
7:H:106:THR:HG22	7:H:112:PRO:HB3	1.91	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2144:U:O2'	1:A:2148:G:N2	2.42	0.53
4:E:9:VAL:HG22	4:E:25:VAL:HB	1.92	0.53
5:F:150:GLY:HA2	5:F:172:TRP:CE3	2.43	0.53
21:Z:121:HIS:N	21:Z:171:ILE:O	2.41	0.53
1:A:1769:G:O2'	1:A:1958:C:OP1	2.22	0.52
1:A:2303:G:O2'	6:G:132:ASN:ND2	2.39	0.52
21:Z:77:ASP:N	21:Z:82:ARG:O	2.36	0.52
1:A:1607:C:N4	1:A:1622:G:OP2	2.28	0.52
10:O:115:VAL:HG13	10:O:121:VAL:HG21	1.90	0.52
11:P:97:PRO:HD3	11:P:126:VAL:O	2.10	0.52
11:P:38:GLN:O	11:P:40:SER:N	2.38	0.52
1:A:1358:G:O2'	1:A:1359:A:H5''	2.10	0.52
1:A:2114:A:H62	1:A:2115:G:H21	1.58	0.52
1:A:2123:G:H1	1:A:2175:C:H42	1.57	0.52
1:A:2037:G:H2'	1:A:2038:G:C8	2.45	0.52
1:A:2133:G:N2	1:A:2157:G:H1'	2.23	0.52
1:A:2142:C:N3	1:A:2149:G:O6	2.42	0.52
1:A:2239:G:OP2	34:A:4263:HOH:O	2.19	0.52
1:A:855:G:H2'	1:A:856:C:C6	2.44	0.52
1:A:890:A:H2'	1:A:892:G:C8	2.44	0.52
1:A:93:G:H2'	1:A:94:C:C6	2.44	0.52
1:A:784:A:C6	3:D:229:VAL:HG11	2.45	0.52
11:P:44:GLY:CA	11:P:45:LEU:HB2	2.39	0.52
1:A:1771:C:OP1	34:A:4536:HOH:O	2.19	0.52
1:A:2469:A:H5'	1:A:2470:G:OP2	2.10	0.52
1:A:2144:U:H1'	1:A:2148:G:H22	1.75	0.52
1:A:2787:C:H1'	4:E:62:PRO:HG3	1.92	0.52
1:A:883:G:C6	1:A:884:C:C4	2.98	0.52
5:F:129:PHE:CD2	5:F:163:VAL:HG21	2.45	0.52
7:H:24:VAL:HG22	7:H:35:VAL:HB	1.91	0.52
11:P:96:THR:H	11:P:99:LEU:CD2	2.23	0.52
19:X:53:LYS:HB3	19:X:82:GLN:HB3	1.91	0.52
1:A:1584:C:O2'	1:A:1586:A:O5'	2.20	0.52
1:A:184:C:H2'	1:A:185:U:C6	2.45	0.52
1:A:71:A:N7	19:X:31:HIS:HE1	2.07	0.52
6:G:106:LEU:O	6:G:111:LEU:HD12	2.10	0.52
1:A:2815:C:H2'	1:A:2816:C:H6	1.74	0.52
1:A:668:G:H5'	1:A:669:G:OP2	2.10	0.52
3:D:142:VAL:HG13	3:D:191:ALA:HB1	1.92	0.52
6:G:115:ARG:CZ	6:G:115:ARG:HB3	2.40	0.52
1:A:1231:G:H2'	1:A:1232:G:C8	2.44	0.51
1:A:2507:C:H2'	1:A:2508:G:O4'	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:882:G:H2'	1:A:883:G:H8	1.75	0.51
1:A:887:A:H4'	1:A:888:C:H5	1.74	0.51
3:D:134:ARG:NH1	3:D:188:GLU:OE2	2.43	0.51
4:E:143:ASN:HD22	4:E:147:PRO:HD3	1.75	0.51
4:E:36:ARG:NH1	4:E:85:ASN:OD1	2.44	0.51
3:D:69:ARG:NH2	3:D:128:GLY:O	2.43	0.51
1:A:11:G:H2'	1:A:12:U:H5'	1.93	0.51
1:A:2183:C:H2'	1:A:2184:G:H8	1.75	0.51
1:A:947:G:H2'	1:A:948:G:C8	2.45	0.51
5:F:114:VAL:HG21	5:F:202:PHE:CE1	2.46	0.51
6:G:173:LEU:HD23	6:G:176:LEU:HD12	1.92	0.51
8:I:26:ALA:O	8:I:31:LEU:HB2	2.11	0.51
1:A:1025:G:C4	1:A:1135:C:H1'	2.45	0.51
1:A:2646:C:H2'	1:A:2647:U:O4'	2.10	0.51
1:A:602:G:O2'	1:A:655:A:N6	2.44	0.51
13:R:33:ARG:NH1	13:R:115:GLU:OE2	2.35	0.51
2:B:92:C:H5"	21:Z:79:ARG:NH1	2.25	0.51
13:R:87:TYR:OH	13:R:116:LEU:HB3	2.10	0.51
1:A:2110:G:H4'	1:A:2111:C:OP2	2.10	0.51
1:A:2031:A:N3	1:A:2455:G:O2'	2.34	0.51
1:A:2141:G:O6	1:A:2150:U:C2	2.62	0.51
3:D:108:PRO:HG2	3:D:111:LEU:HB2	1.92	0.51
26:4:61:ARG:NH1	26:4:62:ARG:O	2.44	0.51
1:A:2139:C:H2'	1:A:2140:C:O4'	2.11	0.51
1:A:2208:A:O2'	1:A:2218:U:OP2	2.28	0.51
6:G:56:ALA:O	6:G:60:LEU:HB2	2.11	0.51
12:Q:52:VAL:HA	12:Q:55:VAL:HG12	1.93	0.51
14:S:35:ILE:HD12	14:S:101:LEU:HD12	1.92	0.51
25:3:7:LYS:HE3	25:3:32:GLN:HG3	1.93	0.51
1:A:1355:G:O6	34:A:4423:HOH:O	2.18	0.51
1:A:528:A:C2	1:A:2042:A:H2'	2.45	0.51
1:A:2149:G:C5	1:A:2150:U:C2	2.99	0.51
1:A:247:G:H4'	1:A:386:G:C5	2.46	0.51
1:A:796:C:H2'	1:A:797:C:C6	2.46	0.51
14:S:10:ARG:NE	14:S:91:PRO:O	2.37	0.51
1:A:125:G:H1'	29:7:48:LYS:HE2	1.92	0.51
1:A:868:U:H2'	1:A:869:G:O4'	2.11	0.51
3:D:147:LEU:HD13	3:D:155:LEU:HD21	1.93	0.51
10:O:120:GLU:HB2	15:T:68:TYR:HE2	1.76	0.51
1:A:1580:A:H3'	1:A:1581:G:H8	1.76	0.50
1:A:866:A:H2	1:A:867:C:C5	2.29	0.50
1:A:1007:C:OP1	9:N:35:ARG:NH1	2.37	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:536:A:H2'	1:A:537:C:C6	2.46	0.50
1:A:994:C:O2'	1:A:996:A:OP1	2.17	0.50
20:Y:38:ILE:HD13	20:Y:66:PRO:HA	1.93	0.50
21:Z:28:MET:HA	21:Z:88:PHE:O	2.11	0.50
1:A:321:G:OP2	5:F:135:LYS:HG3	2.11	0.50
26:4:42:PHE:HA	26:4:48:ARG:HH22	1.75	0.50
1:A:141:A:C8	1:A:1408:C:O2'	2.65	0.50
1:A:2119:A:H62	1:A:2170:A:H62	1.59	0.50
9:N:15:LEU:HB2	9:N:135:PRO:HB2	1.92	0.50
1:A:566:U:H5''	11:P:29:LYS:HE3	1.92	0.50
1:A:422:A:H2'	1:A:423:A:C8	2.46	0.50
1:A:636:G:O2'	1:A:638:G:O2'	2.27	0.50
1:A:646:A:H2'	1:A:647:G:O4'	2.11	0.50
22:0:70:GLN:OE1	22:0:80:HIS:NE2	2.44	0.50
1:A:1270:C:H5''	1:A:1271:G:O5'	2.11	0.50
1:A:493:G:H2'	1:A:494:G:O4'	2.12	0.50
7:H:98:LEU:HD13	7:H:102:ALA:O	2.12	0.50
11:P:82:GLY:HA2	11:P:113:LYS:O	2.11	0.50
20:Y:44:ILE:HA	20:Y:63:LYS:O	2.11	0.50
27:5:16:ARG:HG3	27:5:17:ASP:N	2.26	0.50
11:P:86:LYS:HB3	11:P:118:GLY:HA3	1.93	0.50
1:A:1335:U:OP1	19:X:65:ARG:NH2	2.45	0.50
21:Z:6:LYS:HD2	21:Z:8:TYR:CE1	2.47	0.50
1:A:1341:U:OP2	1:A:1394:U:O2'	2.25	0.50
1:A:1354:A:H2'	1:A:1355:G:O4'	2.12	0.50
1:A:212:G:H2'	1:A:213:A:O4'	2.12	0.50
1:A:829:A:N7	1:A:2248:C:H5'	2.27	0.50
1:A:2352:A:N6	1:A:2365:G:O2'	2.44	0.50
11:P:3:LEU:HD13	11:P:6:LEU:HD12	1.93	0.50
1:A:855:G:O2'	22:0:27:GLU:OE2	2.30	0.49
23:1:5:CYS:SG	23:1:62:VAL:HG23	2.51	0.49
1:A:1683:C:H2'	1:A:1684:C:C6	2.47	0.49
1:A:1717:G:H2'	1:A:1718:G:C8	2.47	0.49
1:A:2117:A:O2'	1:A:2118:U:H5''	2.11	0.49
1:A:2149:G:H3'	1:A:2150:U:O4'	2.11	0.49
1:A:2206:G:H3'	1:A:2207:G:N7	2.27	0.49
1:A:2849:U:H4'	1:A:2868:A:C2	2.46	0.49
12:Q:56:ARG:HD3	12:Q:56:ARG:O	2.12	0.49
13:R:56:LYS:NZ	13:R:90:ARG:O	2.44	0.49
26:4:64:GLY:C	26:4:66:SER:H	2.15	0.49
1:A:729:G:H5'	1:A:730:C:H5''	1.94	0.49
3:D:108:PRO:HB3	3:D:143:HIS:CE1	2.47	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:G:11:TYR:CZ	6:G:16:ARG:HD3	2.47	0.49
1:A:1996:C:H4'	1:A:1997:G:OP1	2.12	0.49
6:G:126:ASP:OD1	6:G:130:ASN:ND2	2.39	0.49
8:I:133:HIS:HD2	8:I:134:PRO:HD2	1.77	0.49
16:U:86:ALA:O	17:V:49:THR:HG23	2.12	0.49
4:E:14:ILE:HG13	4:E:21:VAL:HG13	1.94	0.49
14:S:15:ARG:HE	14:S:88:ASP:CG	2.15	0.49
1:A:1359:A:N6	1:A:1372:U:H3	2.10	0.49
7:H:97:ARG:O	7:H:103:LEU:HD12	2.12	0.49
1:A:811:U:H2'	11:P:21:ARG:HA	1.94	0.49
11:P:42:SER:O	34:P:303:HOH:O	2.20	0.49
11:P:63:PRO:HD3	30:8:27:THR:HG22	1.94	0.49
1:A:1231:G:H2'	1:A:1232:G:H8	1.78	0.49
1:A:1263:U:C4	1:A:1264:G:C6	3.01	0.49
1:A:236:C:H2'	1:A:237:C:C6	2.48	0.49
3:D:108:PRO:HB3	3:D:143:HIS:HE1	1.78	0.49
5:F:7:TYR:O	5:F:22:ALA:N	2.44	0.49
19:X:84:ALA:HB3	19:X:87:GLN:NE2	2.28	0.49
1:A:441:U:H2'	1:A:442:G:C8	2.47	0.49
8:I:130:TYR:HB3	8:I:138:ILE:HB	1.95	0.49
15:T:51:ARG:HG3	15:T:98:LYS:HD2	1.94	0.49
18:W:71:VAL:HA	18:W:107:LEU:HD12	1.94	0.49
1:A:857:C:OP2	22:0:77:ARG:NH2	2.46	0.49
30:8:6:THR:HG22	30:8:63:PRO:HD2	1.95	0.49
2:B:58:A:H2'	2:B:59:A:O4'	2.13	0.49
12:Q:81:VAL:HG12	22:0:5:LYS:HD3	1.94	0.49
1:A:1784:A:O2'	34:A:4872:HOH:O	2.15	0.49
1:A:2099:U:H3	1:A:2190:G:H1	1.61	0.49
1:A:2124:G:N2	1:A:2174:C:N3	2.51	0.49
1:A:874:G:H5'	1:A:875:G:OP2	2.12	0.49
2:B:40:U:H1'	2:B:45:A:H61	1.78	0.49
5:F:113:ALA:HB1	5:F:186:ILE:HG21	1.94	0.49
12:Q:77:LYS:NZ	12:Q:86:GLY:O	2.46	0.49
26:4:15:ILE:HB	26:4:32:TYR:HD1	1.77	0.48
1:A:2137:C:H2'	1:A:2138:C:C6	2.48	0.48
2:B:55:U:H1'	6:G:29:TRP:HE1	1.77	0.48
6:G:115:ARG:HD2	6:G:136:ARG:NH2	2.24	0.48
4:E:24:THR:HG22	4:E:186:GLY:O	2.13	0.48
1:A:801:G:O6	5:F:53:THR:OG1	2.30	0.48
7:H:40:GLU:O	7:H:55:PRO:HG3	2.13	0.48
11:P:2:LYS:HG2	11:P:5:ASP:OD2	2.12	0.48
21:Z:130:PRO:HA	21:Z:133:ILE:HG13	1.96	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1833:U:O2'	1:A:1969:A:N1	2.38	0.48
1:A:2110:G:H5''	1:A:2111:C:H5	1.78	0.48
1:A:2116:G:O6	1:A:2165:G:N2	2.47	0.48
1:A:2149:G:C6	1:A:2150:U:C2	3.01	0.48
1:A:2151:G:H2'	1:A:2152:G:C8	2.46	0.48
1:A:2273:A:H2'	1:A:2274:A:C8	2.48	0.48
1:A:468:G:N7	29:7:39:ARG:NH2	2.56	0.48
1:A:597:U:H2'	1:A:598:G:C8	2.48	0.48
1:A:839:U:H2'	1:A:840:C:C6	2.48	0.48
1:A:1155:A:H5''	16:U:55:ARG:HD3	1.94	0.48
24:2:18:PRO:O	24:2:22:GLU:HG3	2.13	0.48
1:A:2320:A:N3	1:A:2320:A:H2'	2.28	0.48
2:B:66:A:N6	2:B:109:C:H5'	2.28	0.48
3:D:242:ARG:N	3:D:242:ARG:HD3	2.28	0.48
8:I:12:LEU:HD22	8:I:19:VAL:HG21	1.94	0.48
9:N:73:THR:HA	9:N:83:LYS:O	2.14	0.48
14:S:105:ALA:HB1	14:S:110:LEU:HD23	1.95	0.48
1:A:740:U:H2'	1:A:741:G:C8	2.49	0.48
2:B:31:C:H4'	6:G:29:TRP:CH2	2.48	0.48
8:I:66:GLU:OE1	8:I:69:LYS:HD3	2.13	0.48
15:T:51:ARG:HB3	15:T:62:THR:HB	1.96	0.48
20:Y:1:MET:HE3	20:Y:2:ARG:H	1.77	0.48
1:A:2507:C:H5''	1:A:2573:C:C4	2.49	0.48
1:A:303:U:H2'	1:A:304:G:C8	2.48	0.48
1:A:775:G:N3	34:A:4553:HOH:O	2.35	0.48
1:A:848:G:H2'	1:A:849:A:C8	2.48	0.48
1:A:99:U:H4'	1:A:100:G:H5''	1.94	0.48
4:E:4:ILE:HD11	4:E:29:GLY:HA2	1.94	0.48
16:U:61:TRP:CH2	16:U:93:LYS:HB2	2.48	0.48
21:Z:45:ASP:OD1	21:Z:49:ARG:HD2	2.12	0.48
6:G:67:LYS:HD3	26:4:5:ILE:HD12	1.96	0.48
1:A:1400:G:H2'	1:A:1401:G:C8	2.48	0.48
1:A:1548:C:H2'	1:A:1549:C:H6	1.77	0.48
1:A:2849:U:O4	15:T:23:ARG:NH2	2.32	0.48
1:A:24:G:O2'	18:W:78:GLU:O	2.27	0.48
28:6:13:CYS:SG	28:6:47:THR:HG21	2.54	0.48
1:A:1779:U:H2'	34:A:4825:HOH:O	2.13	0.48
1:A:2102:U:H2'	1:A:2103:C:C6	2.48	0.48
1:A:2103:C:N4	1:A:2186:G:H1	2.11	0.48
1:A:2893:G:H8	1:A:2893:G:OP2	1.97	0.48
12:Q:57:HIS:HD2	12:Q:117:ALA:HB2	1.79	0.48
1:A:2495:G:H5''	12:Q:82:ARG:HG2	1.95	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:X:4:ALA:HB1	19:X:42:ALA:HA	1.95	0.48
1:A:500:G:N1	1:A:503:A:OP2	2.46	0.48
1:A:910:A:N1	1:A:2277:G:H1'	2.29	0.48
17:V:37:VAL:HG11	17:V:40:LEU:HG	1.96	0.48
1:A:1218:C:H42	1:A:1231:G:H1	1.62	0.47
1:A:2127:G:H22	1:A:2161:C:H2'	1.78	0.47
1:A:597:U:H2'	1:A:598:G:H8	1.79	0.47
26:4:59:PHE:N	26:4:60:GLN:HB2	2.29	0.47
1:A:2136:C:O2'	1:A:2137:C:H6	1.97	0.47
1:A:589:C:H2'	1:A:590:A:C8	2.49	0.47
21:Z:144:LEU:HD22	21:Z:174:VAL:HG23	1.96	0.47
1:A:1040:C:H2'	1:A:1041:C:O4'	2.15	0.47
1:A:1857:G:C6	1:A:1858:G:C6	3.01	0.47
1:A:2029:G:H2'	1:A:2031:A:OP1	2.13	0.47
1:A:373:U:H2'	1:A:374:A:H8	1.78	0.47
7:H:20:ALA:HB1	7:H:21:PRO:HD2	1.96	0.47
8:I:61:ARG:HD3	8:I:61:ARG:HA	1.70	0.47
14:S:50:SER:O	14:S:76:LYS:NZ	2.30	0.47
21:Z:30:ASN:HA	21:Z:89:PHE:HE1	1.79	0.47
26:4:53:GLU:O	26:4:55:ARG:N	2.43	0.47
1:A:1548:C:H2'	1:A:1549:C:C6	2.49	0.47
1:A:2010:G:H5''	18:W:42:ARG:HB2	1.96	0.47
1:A:956:G:H5''	12:Q:77:LYS:HD2	1.97	0.47
19:X:35:THR:HG22	19:X:38:GLU:H	1.79	0.47
1:A:987:G:O2'	1:A:1000:A:N3	2.43	0.47
1:A:1506:C:H2'	1:A:1507:A:H5'	1.95	0.47
1:A:1518:U:H2'	1:A:1519:G:O4'	2.14	0.47
1:A:1721:G:N1	1:A:1739:U:OP2	2.47	0.47
1:A:2115:G:H4'	1:A:2167:U:O4	2.15	0.47
1:A:927:G:H2'	1:A:928:G:O4'	2.13	0.47
5:F:13:SER:OG	5:F:16:GLY:O	2.22	0.47
26:4:64:GLY:O	26:4:66:SER:N	2.37	0.47
1:A:1022:G:H22	1:A:1142(A):A:H2	1.61	0.47
1:A:1446:C:H42	1:A:1465:G:H1	1.62	0.47
1:A:747:U:O2	1:A:2014:A:H1'	2.14	0.47
8:I:4:ILE:HG12	8:I:18:VAL:HG22	1.97	0.47
8:I:40:THR:O	8:I:44:LEU:HB2	2.15	0.47
10:O:120:GLU:OE2	10:O:122:LEU:HD21	2.13	0.47
26:4:59:PHE:N	26:4:59:PHE:CD1	2.83	0.47
1:A:1539:G:H2'	1:A:1540:U:O4'	2.15	0.47
1:A:2243:U:H2'	1:A:2244:U:C6	2.49	0.47
1:A:2751:G:C8	7:H:2:SER:HA	2.47	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:322:A:OP1	5:F:168:ARG:HD2	2.15	0.47
1:A:631:A:H2'	1:A:632:A:O4'	2.15	0.47
7:H:86:GLU:OE2	7:H:132:ARG:NH2	2.47	0.47
13:R:44:LEU:HD23	13:R:44:LEU:HA	1.73	0.47
1:A:265:A:C8	1:A:266:G:H1'	2.49	0.47
16:U:85:LYS:HB3	16:U:116:ALA:HB1	1.97	0.47
13:R:33:ARG:NH2	27:5:57:VAL:O	2.35	0.47
1:A:1219:G:H1	1:A:1230:C:H42	1.62	0.47
1:A:2125:G:H21	1:A:2173:A:H62	1.62	0.47
1:A:2125:G:N2	1:A:2173:A:H62	2.13	0.47
1:A:2756:U:H1'	1:A:2757:A:H5''	1.97	0.47
1:A:2815:C:H2'	1:A:2816:C:C6	2.50	0.47
1:A:38:A:H2'	1:A:39:C:C6	2.50	0.47
1:A:866:A:H2	1:A:867:C:C4	2.32	0.47
1:A:985:C:H2'	1:A:986:C:H6	1.79	0.47
2:B:80:U:H2'	2:B:81:G:N7	2.29	0.47
4:E:28:ALA:HB3	4:E:93:VAL:HG12	1.96	0.47
6:G:109:VAL:HG21	26:4:14:ILE:HG21	1.97	0.47
26:4:46:GLN:C	26:4:48:ARG:H	2.17	0.47
1:A:117:G:OP2	1:A:119:A:O2'	2.22	0.47
1:A:1183:G:H2'	1:A:1184:G:C8	2.49	0.47
1:A:2469:A:H3'	1:A:2470:G:H8	1.79	0.47
1:A:250:G:P	30:8:13:ARG:HH22	2.38	0.47
1:A:27:G:N2	1:A:512:G:H1'	2.29	0.47
1:A:896:A:H5''	21:Z:147:GLY:HA3	1.96	0.47
2:B:91:C:OP2	12:Q:16:ARG:NH1	2.47	0.47
3:D:92:ILE:HD12	3:D:104:TYR:CE1	2.49	0.47
5:F:150:GLY:HA2	5:F:172:TRP:CD2	2.50	0.47
7:H:84:SER:HB3	7:H:132:ARG:NH1	2.27	0.47
20:Y:89:PHE:CZ	20:Y:95:LYS:HE2	2.50	0.47
1:A:851:U:H5'	25:3:49:LYS:HD2	1.97	0.47
1:A:514:A:N3	1:A:581:C:O2'	2.44	0.47
3:D:218:ARG:HB3	3:D:219:PRO:HD2	1.96	0.47
5:F:116:ASP:OD1	5:F:119:ARG:NH2	2.49	0.47
21:Z:6:LYS:HD2	21:Z:8:TYR:HE1	1.78	0.47
1:A:1021:A:H3'	1:A:1021:A:H8	1.80	0.46
1:A:1991:U:H2'	1:A:1992:G:H5''	1.96	0.46
1:A:2182:G:H2'	1:A:2183:C:C6	2.50	0.46
1:A:908:C:OP2	12:Q:22:LYS:NZ	2.33	0.46
2:B:4:C:N4	2:B:117:G:H1	2.06	0.46
3:D:164:GLN:HE21	3:D:176:ARG:HH22	1.63	0.46
3:D:276:LYS:HD3	3:D:276:LYS:H	1.79	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:P:50:ARG:HH21	30:8:7:HIS:CD2	2.29	0.46
12:Q:75:THR:HG21	12:Q:87:LYS:NZ	2.30	0.46
15:T:56:GLY:O	15:T:59:THR:HG22	2.15	0.46
1:A:1899:G:H2'	1:A:1899:G:N3	2.30	0.46
1:A:229:A:H5'	1:A:230:U:H5'	1.97	0.46
1:A:2663:G:H2'	1:A:2664:G:O4'	2.15	0.46
1:A:2820:A:C5	13:R:4:LEU:HD11	2.50	0.46
1:A:582:G:H2'	1:A:583:G:C8	2.49	0.46
1:A:2336:A:H61	22:O:43:THR:HG22	1.81	0.46
1:A:2756:U:H5''	31:9:19:ARG:HB3	1.96	0.46
1:A:2131:G:OP1	1:A:2132:U:O2'	2.18	0.46
1:A:868:U:C4	1:A:869:G:N7	2.83	0.46
2:B:105:A:OP1	21:Z:72:ARG:NH1	2.49	0.46
5:F:11:VAL:HB	5:F:18:ARG:HB3	1.97	0.46
6:G:33:ARG:NH2	6:G:162:THR:HG21	2.30	0.46
9:N:130:HIS:HB3	9:N:133:GLN:HG2	1.97	0.46
10:O:16:ALA:HB2	10:O:52:VAL:HG21	1.96	0.46
13:R:118:GLU:H	13:R:118:GLU:CD	2.18	0.46
4:E:111:ARG:HA	13:R:1:MET:SD	2.56	0.46
1:A:1339:G:H5''	19:X:16:LYS:HD3	1.98	0.46
1:A:2119:A:N6	1:A:2170:A:H62	2.13	0.46
1:A:2552:U:H2'	1:A:2554:U:OP2	2.15	0.46
13:R:24:GLN:HB3	13:R:44:LEU:HD11	1.98	0.46
1:A:1665:A:H2'	1:A:1666:G:O4'	2.15	0.46
1:A:2748:A:H5'	7:H:4:ILE:HD13	1.97	0.46
2:B:14:U:H1'	2:B:108:U:O2'	2.16	0.46
15:T:91:ARG:HB2	15:T:121:ILE:HG13	1.97	0.46
1:A:1830:C:OP2	34:A:4650:HOH:O	2.19	0.46
2:B:40:U:H2'	26:4:2:LYS:HE3	1.98	0.46
2:B:55:U:O2'	6:G:27:ASN:ND2	2.46	0.46
3:D:134:ARG:HD3	3:D:135:PHE:CE1	2.51	0.46
3:D:164:GLN:HE21	3:D:176:ARG:HH12	1.63	0.46
6:G:11:TYR:OH	6:G:33:ARG:HG2	2.16	0.46
7:H:154:PRO:HB3	7:H:163:TYR:CE2	2.50	0.46
27:5:16:ARG:HD2	27:5:17:ASP:OD1	2.15	0.46
1:A:1507:A:O2'	1:A:1508:A:O4'	2.32	0.46
1:A:889:C:O2'	1:A:890:A:OP2	2.30	0.46
4:E:101:ARG:CZ	4:E:171:GLU:HB2	2.45	0.46
1:A:1257:C:H4'	5:F:83:PHE:CD2	2.51	0.46
7:H:125:VAL:HG13	7:H:131:VAL:HG22	1.98	0.46
7:H:149:ARG:HA	7:H:162:ILE:HB	1.98	0.46
7:H:95:ARG:HG2	7:H:96:ALA:N	2.30	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:N:73:THR:OG1	9:N:82:LEU:HD11	2.15	0.46
14:S:65:VAL:O	14:S:69:VAL:HG12	2.16	0.46
1:A:1114:G:C2'	1:A:1115:G:H5'	2.45	0.46
1:A:2270:G:H2'	1:A:2271:G:O4'	2.15	0.46
1:A:2708:G:H1'	13:R:71:GLN:HE22	1.79	0.46
1:A:795:C:H2'	1:A:796:C:C6	2.51	0.46
11:P:111:ARG:HG2	11:P:128:HIS:CD2	2.51	0.46
1:A:2173:A:H2'	1:A:2174:C:O4'	2.16	0.46
1:A:287:C:H2'	1:A:288:C:C6	2.49	0.46
1:A:882:G:N2	1:A:894:C:N3	2.49	0.46
3:D:148:GLU:HB2	3:D:151:LYS:HD2	1.98	0.46
4:E:115:GLY:O	4:E:119:ARG:HB2	2.16	0.46
1:A:2136:C:N4	1:A:2155:G:H1	2.14	0.46
1:A:2882:A:H5'	13:R:96:ARG:HG3	1.96	0.46
2:B:78:A:C2	2:B:100:A:C4	3.04	0.46
3:D:2:ALA:O	3:D:3:VAL:HB	2.16	0.46
4:E:9:VAL:HG13	4:E:25:VAL:O	2.16	0.46
9:N:39:ARG:HA	9:N:40:PRO:HD3	1.79	0.46
14:S:83:LYS:HE3	14:S:84:GLN:HG3	1.98	0.46
17:V:98:GLU:CD	17:V:100:ARG:HH12	2.20	0.46
20:Y:13:VAL:HG12	20:Y:74:PRO:HA	1.98	0.46
1:A:1278:A:OP1	13:R:36:THR:HG23	2.16	0.45
1:A:2657:A:O2'	7:H:160:LYS:NZ	2.35	0.45
21:Z:128:VAL:HG22	21:Z:129:SER:O	2.15	0.45
23:1:67:ILE:N	23:1:68:PRO:HD2	2.32	0.45
1:A:2127:G:N1	1:A:2161:C:C2	2.84	0.45
1:A:2674:G:H2'	1:A:2675:A:C8	2.50	0.45
1:A:2888:C:H2'	1:A:2889:C:C6	2.51	0.45
1:A:918:A:C5	1:A:919:G:H1'	2.51	0.45
2:B:83:G:N2	2:B:94:C:O2	2.43	0.45
4:E:44:TYR:HB2	4:E:82:ARG:HH12	1.81	0.45
12:Q:85:LYS:HG2	22:O:7:LEU:HB3	1.97	0.45
1:A:2203:U:O2'	1:A:2205:C:H5'	2.16	0.45
1:A:265:A:H1'	1:A:266:G:O4'	2.16	0.45
1:A:484:C:H2'	1:A:485:C:C6	2.52	0.45
1:A:817:C:O2'	1:A:839:U:H5''	2.16	0.45
1:A:844:C:C5	1:A:845:G:C6	3.05	0.45
2:B:79:C:H2'	2:B:80:U:O4'	2.17	0.45
5:F:108:LYS:HB2	5:F:108:LYS:NZ	2.31	0.45
6:G:124:SER:OG	6:G:124:SER:O	2.32	0.45
6:G:75:LYS:HE3	6:G:77:ILE:HD11	1.98	0.45
11:P:65:ARG:HG3	30:8:25:MET:HG2	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:T:11:GLU:O	15:T:15:VAL:HG23	2.17	0.45
16:U:79:PHE:CZ	16:U:83:LEU:HD21	2.51	0.45
1:A:1721:G:H2'	1:A:1740:G:O6	2.17	0.45
1:A:1932:A:H2'	1:A:1933:G:O4'	2.17	0.45
1:A:2119:A:N6	1:A:2170:A:N7	2.64	0.45
1:A:2139:C:N4	1:A:2152:G:C6	2.82	0.45
4:E:2:LYS:NZ	4:E:95:ILE:O	2.32	0.45
6:G:111:LEU:HD23	6:G:117:PHE:HE2	1.81	0.45
6:G:72:ARG:NH1	6:G:87:PRO:HG3	2.31	0.45
13:R:97:VAL:HG22	13:R:114:VAL:HG22	1.98	0.45
1:A:1187:G:H5'	17:V:81:TYR:CE1	2.51	0.45
1:A:111:A:H4'	24:2:69:ARG:NH1	2.31	0.45
1:A:1149:G:H2'	1:A:1150:C:C6	2.51	0.45
1:A:1561:G:H2'	1:A:1562:A:C8	2.50	0.45
1:A:2331:G:O2'	22:0:43:THR:HG22	2.17	0.45
1:A:774:A:H2'	1:A:774:A:N3	2.31	0.45
1:A:800:A:H8	1:A:800:A:OP1	1.98	0.45
4:E:11:MET:HG2	4:E:24:THR:HB	1.98	0.45
5:F:53:THR:HG23	5:F:55:GLY:N	2.28	0.45
18:W:86:LEU:HD22	18:W:96:ILE:HD11	1.99	0.45
28:6:14:THR:OG1	28:6:48:VAL:HG13	2.17	0.45
1:A:2147:G:C2	1:A:2148:G:H1'	2.52	0.45
1:A:224:G:H2'	1:A:225:A:O4'	2.16	0.45
1:A:887:A:H4'	1:A:888:C:C5	2.50	0.45
1:A:1803:A:H4'	3:D:259:THR:HG23	1.98	0.45
4:E:27:LEU:HD22	15:T:1:MET:HE1	1.97	0.45
17:V:25:LEU:HA	17:V:25:LEU:HD23	1.77	0.45
19:X:50:LYS:O	19:X:84:ALA:N	2.49	0.45
19:X:25:LYS:HZ3	19:X:82:GLN:HE21	1.63	0.45
1:A:1810:A:H2'	1:A:1811:G:O4'	2.17	0.45
1:A:1999:C:H2'	1:A:2000:G:O4'	2.17	0.45
1:A:2723:C:OP2	4:E:109:LYS:NZ	2.45	0.45
5:F:20:LEU:HD13	5:F:21:ALA:N	2.32	0.45
23:1:2:SER:HB3	23:1:46:LEU:HD12	1.99	0.45
1:A:2133:G:O2'	1:A:2157:G:N2	2.50	0.45
1:A:304:G:O6	34:A:4492:HOH:O	2.19	0.45
1:A:492:A:H2'	1:A:493:G:O4'	2.17	0.45
6:G:11:TYR:OH	6:G:16:ARG:HD3	2.17	0.45
12:Q:21:THR:HG21	12:Q:101:ARG:HD3	1.99	0.45
23:1:89:GLU:O	23:1:93:GLU:HG2	2.17	0.45
26:4:15:ILE:HB	26:4:32:TYR:CD1	2.52	0.45
1:A:2096:U:H2'	1:A:2097:C:C6	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2483:C:H2'	1:A:2484:G:O4'	2.17	0.45
1:A:2543:G:H2'	1:A:2544:G:C8	2.52	0.45
1:A:448:U:H5''	34:A:4950:HOH:O	2.17	0.45
1:A:918:A:H5''	2:B:98:G:O2'	2.17	0.45
1:A:1140:C:O3'	9:N:25:ARG:NH1	2.50	0.45
9:N:67:LEU:HB3	9:N:88:GLU:HG3	1.99	0.45
25:3:18:ASP:N	25:3:18:ASP:OD1	2.45	0.45
1:A:1226:A:OP1	17:V:84:LYS:HE2	2.17	0.45
1:A:1247:A:OP1	5:F:95:ARG:NH2	2.45	0.45
1:A:1653:G:H3'	13:R:2:ARG:HD3	1.98	0.45
1:A:2035:G:OP1	34:A:4502:HOH:O	2.20	0.45
1:A:2064:C:H1'	1:A:2450:A:C2	2.52	0.45
1:A:443:A:H1'	1:A:1201:C:O4'	2.17	0.45
1:A:90:U:H1'	1:A:92:A:C8	2.51	0.45
7:H:25:LYS:HE2	7:H:27:LYS:HZ3	1.82	0.45
21:Z:105:VAL:O	21:Z:140:ASP:HA	2.17	0.45
29:7:9:ARG:CG	29:7:46:VAL:HG23	2.47	0.44
1:A:1453:U:O2'	1:A:1455:G:N7	2.44	0.44
1:A:1786:A:H1'	1:A:1938:A:N6	2.32	0.44
1:A:1915:U:H2'	1:A:1916:A:O4'	2.17	0.44
1:A:1999:C:H4'	1:A:2723:C:O2	2.17	0.44
3:D:71:ASP:HB3	3:D:103:ARG:NH2	2.30	0.44
19:X:12:VAL:HG22	19:X:29:TRP:CE2	2.52	0.44
30:8:58:ILE:HA	30:8:61:LEU:HD12	1.99	0.44
31:9:17:ILE:HA	31:9:17:ILE:HD12	1.78	0.44
1:A:1399:C:OP1	19:X:25:LYS:NZ	2.47	0.44
1:A:2167:U:H2'	1:A:2168:G:N3	2.32	0.44
1:A:2184:G:C2'	1:A:2185:C:H5'	2.47	0.44
1:A:2238:G:H2'	1:A:2238:G:N3	2.33	0.44
1:A:848:G:C2	1:A:933:A:H1'	2.51	0.44
8:I:29:TYR:O	8:I:32:PRO:HD2	2.17	0.44
10:O:4:PRO:O	10:O:5:GLN:HB2	2.18	0.44
25:3:3:ARG:HD3	25:3:60:GLU:CB	2.47	0.44
28:6:40:CYS:O	28:6:44:ARG:N	2.51	0.44
28:6:15:GLU:HG3	28:6:47:THR:CG2	2.48	0.44
1:A:1006:C:C2	1:A:1138:G:N2	2.85	0.44
1:A:1204:A:N6	1:A:1240:U:H2'	2.32	0.44
1:A:1336:A:H2'	1:A:1337:G:C8	2.53	0.44
1:A:143:G:H2'	1:A:143(A):C:C6	2.51	0.44
1:A:1557:C:OP2	1:A:1558:A:O2'	2.22	0.44
1:A:2114:A:O2'	1:A:2167:U:H1'	2.17	0.44
1:A:271(D):G:H2'	1:A:271(E):U:C6	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:601:C:O2	1:A:605:C:H4'	2.17	0.44
1:A:614(B):G:O2'	5:F:44:ARG:HD2	2.17	0.44
1:A:652(A):A:C3'	1:A:652(B):A:H5'	2.47	0.44
4:E:72:VAL:HA	4:E:73:GLU:CB	2.48	0.44
6:G:43:LEU:HA	6:G:43:LEU:HD12	1.80	0.44
9:N:30:ILE:O	9:N:34:LEU:HD22	2.17	0.44
12:Q:16:ARG:HG2	12:Q:18:LYS:HE2	1.98	0.44
14:S:94:TYR:CE1	14:S:99:LYS:HG3	2.53	0.44
21:Z:54:HIS:ND1	21:Z:101:PRO:HG3	2.32	0.44
1:A:1359:A:H2'	1:A:1360:A:H5'	2.00	0.44
1:A:1363:C:H2'	1:A:1364:G:H8	1.81	0.44
1:A:2024:G:H2'	1:A:2025:C:H6	1.81	0.44
1:A:667:U:O2	30:8:2:PRO:HD2	2.18	0.44
2:B:55:U:O3'	6:G:27:ASN:ND2	2.51	0.44
1:A:743:G:OP1	4:E:130:GLY:HA2	2.16	0.44
16:U:58:ARG:HA	16:U:61:TRP:CE3	2.53	0.44
18:W:9:TYR:HA	18:W:100:THR:CG2	2.47	0.44
1:A:2193:G:H2'	1:A:2194:G:H8	1.83	0.44
3:D:26:LYS:NZ	3:D:30:GLU:OE1	2.49	0.44
6:G:38:VAL:HG22	6:G:93:THR:HG23	2.00	0.44
5:F:187:VAL:HG12	11:P:3:LEU:HD22	1.98	0.44
16:U:61:TRP:CZ3	16:U:93:LYS:HB2	2.53	0.44
21:Z:126:VAL:CG1	21:Z:161:VAL:HG23	2.47	0.44
1:A:2150:U:H2'	1:A:2151:G:C8	2.53	0.44
1:A:613:G:H2'	1:A:614:U:O4'	2.16	0.44
3:D:134:ARG:HD3	3:D:135:PHE:CZ	2.52	0.44
3:D:182:LEU:HB2	3:D:272:ALA:HB3	1.99	0.44
1:A:1022:G:N7	9:N:66:LYS:HE2	2.32	0.44
20:Y:11:ASP:N	20:Y:11:ASP:OD2	2.50	0.44
21:Z:126:VAL:HG13	21:Z:161:VAL:HG23	1.99	0.44
1:A:686:G:C2	29:7:11:LYS:HE2	2.52	0.44
31:9:12:ASP:OD1	31:9:12:ASP:N	2.51	0.44
1:A:2650:U:H2'	1:A:2651:C:H6	1.82	0.44
1:A:2748:A:H2'	1:A:2749:A:O4'	2.17	0.44
1:A:348:G:H2'	1:A:349:G:C8	2.53	0.44
1:A:792:G:N3	1:A:2072:G:O2'	2.42	0.44
1:A:820:A:N3	1:A:943:U:H4'	2.33	0.44
1:A:975(A):G:C2	1:A:990:A:C8	3.05	0.44
3:D:274:ARG:O	3:D:275:LYS:HD3	2.17	0.44
5:F:53:THR:HG22	5:F:56:GLU:HG3	2.00	0.44
10:O:26:LYS:O	10:O:30:ALA:HB2	2.18	0.44
9:N:4:TYR:HB2	16:U:101:ARG:NH1	2.32	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:Z:148:ASP:N	21:Z:148:ASP:OD1	2.50	0.44
1:A:2357:U:OP1	22:0:20:ARG:HD3	2.18	0.44
1:A:1406:U:H2'	1:A:1407:C:C6	2.53	0.44
1:A:2156:G:O5'	1:A:2156:G:H8	2.01	0.44
1:A:2567:G:H2'	1:A:2568:C:C6	2.52	0.44
1:A:570:G:H2'	1:A:2030:A:C5	2.53	0.44
1:A:866:A:N6	1:A:914:C:C4	2.86	0.44
2:B:46:A:H2'	2:B:47:C:C6	2.53	0.44
5:F:178:PRO:HB3	5:F:198:ALA:HA	1.99	0.44
6:G:136:ARG:HD2	6:G:137:GLU:N	2.33	0.44
11:P:59:LEU:HD23	30:8:58:ILE:HD13	1.98	0.44
28:6:11:LEU:HB2	28:6:21:TYR:HB2	1.99	0.44
11:P:65:ARG:HG3	30:8:25:MET:CG	2.48	0.44
1:A:11:G:C2'	1:A:12:U:H5'	2.47	0.44
1:A:1420:U:HO2'	1:A:1421:G:P	2.40	0.44
1:A:1510:G:H2'	1:A:1511:C:O4'	2.18	0.44
1:A:1593:G:H2'	1:A:1594:G:C8	2.53	0.44
1:A:1835:G:H5'	1:A:1836:C:OP2	2.17	0.44
1:A:191:A:H2'	1:A:192:C:C6	2.52	0.44
1:A:2263:C:H2'	1:A:2264:C:O4'	2.18	0.44
1:A:2750:A:H8	1:A:2750:A:OP1	2.01	0.44
3:D:77:ALA:O	3:D:116:GLN:HG3	2.17	0.44
5:F:9:ILE:HD13	5:F:123:LEU:HD23	1.98	0.44
21:Z:133:ILE:HG22	21:Z:134:PRO:O	2.18	0.44
1:A:1313:U:OP1	34:A:4345:HOH:O	2.21	0.43
1:A:2119:A:N6	1:A:2171:A:C6	2.86	0.43
1:A:303:U:H2'	1:A:304:G:H8	1.83	0.43
6:G:129:GLY:O	6:G:161:THR:HB	2.18	0.43
8:I:131:LYS:HA	8:I:137:PRO:HA	1.99	0.43
8:I:54:GLN:HA	8:I:57:ARG:HE	1.82	0.43
8:I:57:ARG:O	8:I:61:ARG:HB2	2.17	0.43
1:A:1651:G:H5'	13:R:39:PRO:HG2	2.00	0.43
1:A:2354:G:H21	22:0:36:ILE:HD11	1.82	0.43
28:6:19:ARG:HD2	28:6:19:ARG:N	2.33	0.43
1:A:1291:C:H2'	1:A:1292:U:C6	2.53	0.43
1:A:1477:A:H2'	1:A:1478:G:O4'	2.18	0.43
1:A:1958:C:OP2	34:A:4710:HOH:O	2.20	0.43
1:A:2129:C:C2	1:A:2160:G:N1	2.84	0.43
1:A:307:G:H21	1:A:330:A:H62	1.65	0.43
1:A:359:A:H2'	1:A:360:G:O4'	2.18	0.43
1:A:376:C:H2'	1:A:377:C:C6	2.53	0.43
7:H:121:ILE:HD11	7:H:140:LYS:HG2	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:H:9:ILE:HG12	7:H:69:ARG:HD2	2.00	0.43
11:P:55:ARG:HG2	11:P:56:SER:N	2.33	0.43
11:P:83:VAL:HG12	11:P:112:LEU:HD21	1.99	0.43
1:A:1268:A:C2	1:A:2013:A:C4	3.06	0.43
1:A:2207:G:H3'	1:A:2208:A:H5''	2.00	0.43
1:A:2802:G:H2'	1:A:2803:C:O4'	2.19	0.43
1:A:866:A:C2	1:A:867:C:C5	3.06	0.43
10:O:64:ARG:HB2	10:O:83:ALA:HB3	1.99	0.43
13:R:103:ARG:HD3	13:R:108:GLY:O	2.17	0.43
21:Z:163:LEU:HA	21:Z:163:LEU:HD12	1.86	0.43
28:6:15:GLU:HG3	28:6:47:THR:HG23	1.99	0.43
1:A:1599:C:OP1	34:A:5027:HOH:O	2.20	0.43
1:A:2018:G:H2'	1:A:2019:A:O4'	2.19	0.43
1:A:2136:C:O2'	1:A:2137:C:O5'	2.36	0.43
1:A:2831:G:OP1	1:A:2834:G:H4'	2.19	0.43
1:A:348:G:H2'	1:A:349:G:H8	1.82	0.43
7:H:148:ILE:O	7:H:162:ILE:HD13	2.18	0.43
20:Y:21:LYS:HB3	20:Y:21:LYS:NZ	2.33	0.43
21:Z:8:TYR:HB2	21:Z:38:TYR:CE2	2.54	0.43
1:A:2612:C:OP2	27:5:2:ALA:N	2.51	0.43
1:A:2061:G:H5''	1:A:2503:A:C2	2.53	0.43
1:A:263:C:H2'	1:A:264:C:O4'	2.19	0.43
1:A:2735:G:H2'	1:A:2736:G:H8	1.83	0.43
1:A:2896:C:H2'	1:A:2897:U:C6	2.53	0.43
1:A:530:G:N3	1:A:530:G:O4'	2.50	0.43
2:B:80:U:H2'	2:B:81:G:C8	2.53	0.43
6:G:47:LYS:HD2	6:G:81:LYS:O	2.19	0.43
7:H:27:LYS:HB3	7:H:27:LYS:HE3	1.62	0.43
1:A:1021:A:H3'	1:A:1021:A:C8	2.53	0.43
1:A:2792:G:H2'	1:A:2792:G:N3	2.34	0.43
1:A:446:G:OP1	16:U:3:ARG:NH1	2.52	0.43
1:A:902:C:H2'	1:A:903:C:C6	2.51	0.43
10:O:98:VAL:HG22	10:O:118:ALA:HA	2.00	0.43
21:Z:73:GLN:O	21:Z:87:ASP:N	2.47	0.43
1:A:2128:C:N4	1:A:2161:C:N3	2.67	0.43
1:A:2376:A:H2'	1:A:2377:A:O4'	2.18	0.43
1:A:2526:G:H5'	1:A:2742:C:O2'	2.19	0.43
1:A:2659:G:N2	1:A:2662:A:OP2	2.51	0.43
1:A:2671:A:H2'	1:A:2672:G:O4'	2.19	0.43
1:A:2773:C:H2'	1:A:2774:C:H6	1.83	0.43
1:A:828:U:H4'	1:A:831:G:N1	2.33	0.43
1:A:880:G:N2	1:A:898:C:O2	2.52	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:E:144:ARG:HB3	4:E:145:LYS:H	1.45	0.43
5:F:126:VAL:HG21	5:F:129:PHE:CZ	2.53	0.43
14:S:62:LYS:O	14:S:66:ALA:N	2.44	0.43
16:U:49:HIS:O	16:U:53:ARG:N	2.51	0.43
1:A:2141:G:C6	1:A:2150:U:O2	2.71	0.43
1:A:2793:G:N2	1:A:2804:C:H1'	2.34	0.43
1:A:322:A:H5'	1:A:340:A:H1'	2.00	0.43
1:A:484:C:H2'	1:A:485:C:H6	1.84	0.43
2:B:39:A:O2'	2:B:40:U:H5'	2.19	0.43
4:E:178:GLU:OE2	4:E:178:GLU:N	2.29	0.43
8:I:12:LEU:HD23	8:I:12:LEU:HA	1.82	0.43
9:N:71:ILE:HG21	9:N:84:LYS:HB3	2.01	0.43
19:X:8:ILE:O	24:2:36:ARG:NH2	2.52	0.43
21:Z:33:LEU:HD21	21:Z:90:VAL:HG21	2.01	0.43
1:A:1029:A:N1	1:A:2465:C:O2'	2.39	0.43
1:A:118:A:N3	1:A:178:G:H1'	2.34	0.43
1:A:1805:U:O2	3:D:50:THR:HB	2.19	0.43
1:A:244:A:C2	1:A:255:A:C4	3.07	0.43
1:A:2741:A:H2'	1:A:2742:C:O4'	2.19	0.43
1:A:2811:G:N2	1:A:2891:G:H1'	2.34	0.43
4:E:7:VAL:HG12	4:E:27:LEU:HB3	2.00	0.43
10:O:7:TYR:HE1	10:O:20:MET:HE3	1.83	0.43
1:A:1374:G:H2'	1:A:1375:C:C6	2.54	0.43
1:A:2051:A:H5'	1:A:2578:G:O4'	2.19	0.43
1:A:286:C:H2'	1:A:287:C:C6	2.54	0.43
1:A:686:G:N2	1:A:788:A:H61	2.17	0.43
10:O:87:ILE:HD12	10:O:91:LEU:HA	2.01	0.43
18:W:88:ARG:NH1	18:W:94:ASP:OD2	2.51	0.43
1:A:1449:A:HO2'	1:A:1529:G:H21	1.60	0.42
1:A:1668:A:C8	1:A:1674:G:C6	3.07	0.42
1:A:1777:U:O2'	1:A:1778:U:H5'	2.19	0.42
1:A:2142:C:H2'	1:A:2143:C:C6	2.54	0.42
1:A:2277:G:OP2	22:O:10:THR:HG21	2.19	0.42
1:A:2474:C:H5''	1:A:2475:C:OP2	2.19	0.42
1:A:2611:U:H5'	1:A:2611:U:H6	1.84	0.42
1:A:271(E):U:H2'	1:A:271(F):C:C6	2.54	0.42
1:A:27:G:C2	1:A:512:G:N3	2.87	0.42
1:A:478:A:N1	1:A:500:G:H4'	2.34	0.42
1:A:858:U:O2	1:A:2268:A:H2'	2.19	0.42
11:P:63:PRO:O	30:8:13:ARG:HG2	2.19	0.42
13:R:97:VAL:HG22	13:R:114:VAL:HG13	2.00	0.42
23:1:64:ALA:HA	23:1:67:ILE:HG13	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1379:A:H4'	1:A:1380:G:OP2	2.19	0.42
1:A:1639:U:C2'	1:A:1640:C:H5''	2.46	0.42
1:A:361:G:O2'	1:A:362:U:H5'	2.18	0.42
1:A:652(A):A:O2'	1:A:652(B):A:H5'	2.19	0.42
10:O:68:GLU:HB3	10:O:78:ARG:HB2	2.00	0.42
17:V:21:ARG:HG2	17:V:91:TYR:CD2	2.54	0.42
25:3:6:VAL:HG13	25:3:56:VAL:HG22	2.01	0.42
1:A:1171:G:H1	1:A:1178:C:N4	2.05	0.42
1:A:1300:U:H4'	1:A:1301:A:H5'	2.01	0.42
1:A:1790:C:H5''	1:A:1791:A:OP1	2.19	0.42
1:A:1815:A:H8	1:A:1815:A:OP1	2.02	0.42
1:A:247:G:OP2	1:A:249:C:N4	2.46	0.42
1:A:2564:A:C2	1:A:2647:U:H4'	2.54	0.42
1:A:652(C):G:H2'	1:A:652(D):C:H6	1.85	0.42
1:A:952:G:P	12:Q:16:ARG:HH21	2.43	0.42
7:H:98:LEU:HB2	7:H:125:VAL:CG2	2.49	0.42
12:Q:21:THR:HG21	12:Q:101:ARG:HB2	2.02	0.42
1:A:2690:C:OP2	13:R:14:SER:HB3	2.19	0.42
14:S:14:VAL:O	14:S:18:ILE:HG12	2.20	0.42
21:Z:69:THR:HG22	21:Z:90:VAL:HA	2.00	0.42
1:A:2461:C:H2'	1:A:2462:U:C6	2.54	0.42
1:A:18:C:O2'	1:A:554:U:OP1	2.32	0.42
1:A:662:G:OP1	34:A:4487:HOH:O	2.21	0.42
2:B:11:C:OP2	2:B:12:C:H5	2.02	0.42
5:F:197:ASP:O	5:F:200:GLU:HB2	2.20	0.42
11:P:45:LEU:HD22	11:P:45:LEU:HA	1.61	0.42
1:A:1412:A:H2'	1:A:1413:G:C8	2.54	0.42
1:A:1641:A:H2'	1:A:1642:G:O4'	2.20	0.42
1:A:2110:G:H5''	1:A:2111:C:C5	2.53	0.42
1:A:2335:A:C8	1:A:2337:G:C5	3.07	0.42
1:A:218:A:C2	1:A:235:U:H4'	2.53	0.42
1:A:2516:G:H1	1:A:2568:C:H42	1.67	0.42
1:A:71:A:H5''	1:A:73:A:C8	2.55	0.42
6:G:106:LEU:HA	6:G:110:ALA:HB3	2.01	0.42
7:H:2:SER:O	7:H:3:ARG:HG2	2.19	0.42
1:A:117:G:C6	1:A:119:A:C6	3.08	0.42
1:A:184:C:H2'	1:A:185:U:H6	1.85	0.42
1:A:1877:A:H5'	1:A:1878:G:OP2	2.18	0.42
1:A:2224:G:H4'	1:A:2226:C:C2	2.55	0.42
1:A:2298:A:H2'	1:A:2299:G:O4'	2.19	0.42
16:U:27:LEU:HB3	16:U:31:SER:HB3	2.01	0.42
1:A:1184:G:C6	1:A:1185:C:C4	3.08	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2469:A:C6	1:A:2470:G:C4	3.07	0.42
1:A:277:C:O2	1:A:277:C:H2'	2.19	0.42
1:A:833:U:OP1	11:P:45:LEU:HD11	2.20	0.42
4:E:143:ASN:HD22	4:E:147:PRO:CD	2.32	0.42
4:E:78:LEU:HA	4:E:78:LEU:HD12	1.93	0.42
6:G:7:LEU:HD22	6:G:100:TRP:HE3	1.85	0.42
7:H:144:VAL:O	7:H:148:ILE:HG12	2.19	0.42
9:N:38:HIS:H	9:N:38:HIS:CD2	2.37	0.42
12:Q:99:PRO:HG2	21:Z:79:ARG:HH22	1.84	0.42
1:A:1478:G:O2'	1:A:1558:A:N1	2.52	0.42
1:A:1636:C:H2'	1:A:1637:A:C8	2.55	0.42
1:A:1676:A:H2'	1:A:1677:A:O4'	2.20	0.42
1:A:2140:C:O2	1:A:2140:C:H2'	2.19	0.42
1:A:2366:A:H2'	1:A:2367:G:O4'	2.19	0.42
1:A:2783:G:H2'	1:A:2784:C:C6	2.55	0.42
1:A:2865:U:C4	1:A:2866:U:C4	3.08	0.42
1:A:479:A:N3	1:A:481:G:H5''	2.34	0.42
1:A:652(C):G:H2'	1:A:652(D):C:C6	2.54	0.42
4:E:21:VAL:HA	4:E:22:PRO:HD3	1.88	0.42
7:H:3:ARG:NH2	7:H:5:GLY:H	2.18	0.42
9:N:67:LEU:C	9:N:88:GLU:HG3	2.40	0.42
18:W:23:LEU:O	18:W:27:LYS:NZ	2.53	0.42
21:Z:18:LEU:HD12	21:Z:18:LEU:HA	1.84	0.42
26:4:62:ARG:N	26:4:62:ARG:HE	2.18	0.42
1:A:373:U:H2'	1:A:374:A:C8	2.54	0.42
1:A:441:U:O2	5:F:46:ARG:NH2	2.44	0.42
1:A:79:G:H2'	1:A:80:G:O4'	2.20	0.42
8:I:124:GLY:N	8:I:144:VAL:HG23	2.35	0.42
8:I:70:GLU:O	8:I:74:ASN:HB2	2.19	0.42
9:N:15:LEU:HB3	9:N:137:LYS:HA	2.02	0.42
12:Q:18:LYS:HE3	12:Q:18:LYS:HB2	1.77	0.42
13:R:2:ARG:HG2	13:R:5:LYS:HB2	2.01	0.42
22:0:37:LEU:HG	22:0:60:PHE:HA	2.02	0.42
23:1:83:GLU:HA	23:1:84:GLY:HA2	1.72	0.42
1:A:1359:A:N1	1:A:1372:U:O4	2.53	0.42
1:A:1400:G:H2'	1:A:1401:G:H8	1.84	0.42
1:A:2114:A:N6	1:A:2119:A:H62	2.16	0.42
1:A:2122:U:C4	1:A:2176:A:N1	2.88	0.42
1:A:217:G:H2'	1:A:218:A:O4'	2.20	0.42
1:A:228:A:O2'	1:A:229:A:P	2.77	0.42
1:A:2781:A:H5''	1:A:2782:G:H5'	2.02	0.42
1:A:2896:C:H2'	1:A:2897:U:H6	1.85	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:33:LEU:HA	5:F:33:LEU:HD12	1.91	0.42
8:I:90:GLY:O	8:I:121:LYS:HE3	2.20	0.42
11:P:100:LEU:HD22	11:P:105:LEU:HD12	2.02	0.42
1:A:328:U:H4'	20:Y:68:HIS:CE1	2.55	0.42
1:A:1580:A:H8	1:A:1580:A:OP2	2.03	0.41
1:A:2391:G:O6	1:A:2425:A:H8	2.03	0.41
1:A:2648:C:H2'	1:A:2649:U:C6	2.54	0.41
1:A:436:C:H2'	1:A:437:G:C8	2.55	0.41
1:A:566:U:O2'	1:A:809:G:OP2	2.28	0.41
2:B:1:U:H2'	2:B:2:C:C6	2.55	0.41
4:E:50:GLY:HA3	4:E:75:VAL:HG11	2.02	0.41
4:E:76:ARG:NH1	34:E:405:HOH:O	2.53	0.41
6:G:76:SER:N	6:G:84:LYS:HB2	2.35	0.41
9:N:4:TYR:CD2	16:U:100:VAL:HG11	2.55	0.41
17:V:50:PRO:HG2	17:V:51:VAL:HG12	2.01	0.41
18:W:45:TYR:CZ	18:W:49:LYS:HE3	2.55	0.41
21:Z:138:GLU:H	21:Z:156:LYS:HE2	1.84	0.41
1:A:146:G:H2'	1:A:147:U:C6	2.56	0.41
1:A:1885:A:H2'	1:A:1886:C:O4'	2.20	0.41
1:A:676:A:H2	1:A:2069:G:N3	2.18	0.41
1:A:705:A:H2'	1:A:706:A:O4'	2.20	0.41
1:A:729:G:C6	3:D:208:LYS:HB2	2.55	0.41
7:H:73:ALA:O	7:H:76:VAL:HG22	2.19	0.41
7:H:98:LEU:HD23	7:H:125:VAL:HG22	2.02	0.41
21:Z:121:HIS:HB3	21:Z:123:ASP:O	2.19	0.41
1:A:2365:G:H4'	22:O:60:PHE:CZ	2.55	0.41
1:A:1027:A:O2'	1:A:1028:A:H5'	2.20	0.41
1:A:1198:U:H2'	1:A:1199:U:C6	2.55	0.41
1:A:1857:G:C6	1:A:1858:G:N1	2.88	0.41
1:A:2315:G:H2'	1:A:2316:C:C6	2.55	0.41
1:A:2749:A:H1'	7:H:63:SER:HA	2.02	0.41
1:A:657:U:H2'	1:A:658:C:C6	2.55	0.41
6:G:43:LEU:HB3	6:G:44:GLY:H	1.51	0.41
10:O:36:GLY:HA2	10:O:106:LEU:HD23	2.02	0.41
14:S:5:THR:OG1	14:S:8:GLU:HG3	2.20	0.41
16:U:108:GLU:O	16:U:112:ARG:HG2	2.20	0.41
25:3:4:LEU:O	25:3:36:VAL:HA	2.20	0.41
27:5:20:ARG:HG2	27:5:23:HIS:CE1	2.55	0.41
1:A:1357:U:H2'	1:A:1358:G:O4'	2.20	0.41
1:A:1589:C:H2'	1:A:1590:U:C6	2.52	0.41
2:B:24:G:H4'	2:B:25:A:C8	2.55	0.41
3:D:69:ARG:C	3:D:71:ASP:H	2.23	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:29:PRO:HA	3:D:83:GLU:OE1	2.21	0.41
13:R:67:LEU:CD1	13:R:76:VAL:HG21	2.48	0.41
15:T:59:THR:HG23	15:T:78:LEU:CB	2.50	0.41
18:W:13:SER:HA	18:W:14:PRO:HD3	1.91	0.41
20:Y:6:HIS:H	20:Y:6:HIS:CD2	2.38	0.41
1:A:1670:C:C5	1:A:1671:U:C4	3.09	0.41
1:A:2167:U:H2'	1:A:2168:G:N2	2.33	0.41
1:A:2273:A:O2'	1:A:2274:A:H5'	2.20	0.41
1:A:2506:U:OP1	4:E:144:ARG:NH2	2.54	0.41
1:A:26:G:C6	1:A:27:G:N1	2.88	0.41
1:A:2857:G:N2	1:A:2860:A:OP2	2.50	0.41
1:A:320:A:H4'	1:A:322:A:N7	2.35	0.41
1:A:702:G:C2	1:A:731:C:C2	3.08	0.41
2:B:30:C:OP2	14:S:32:LEU:HD11	2.20	0.41
8:I:117:GLU:HG3	8:I:118:LYS:H	1.86	0.41
11:P:95:VAL:HG13	11:P:125:VAL:HB	2.02	0.41
30:8:50:LEU:HA	30:8:50:LEU:HD23	1.93	0.41
1:A:2386:C:H2'	1:A:2387:U:C6	2.55	0.41
1:A:2393:A:H2'	1:A:2394:C:O4'	2.21	0.41
2:B:66:A:H61	2:B:108:U:H3'	1.84	0.41
7:H:116:GLU:HA	7:H:117:PRO:HD3	1.89	0.41
9:N:96:GLU:H	9:N:96:GLU:CD	2.23	0.41
11:P:36:LYS:O	34:P:304:HOH:O	2.22	0.41
1:A:1364:G:C5	23:1:3:LYS:HE2	2.55	0.41
30:8:26:LYS:HZ2	30:8:26:LYS:HB3	1.86	0.41
1:A:1219:G:H1	1:A:1230:C:N4	2.19	0.41
1:A:1272:A:H3'	1:A:1273:U:H5''	2.02	0.41
1:A:2347:C:H2'	1:A:2348:U:C6	2.55	0.41
1:A:2794:C:N4	1:A:2802:G:O6	2.53	0.41
1:A:811:U:C2	1:A:1251:C:C5	3.09	0.41
12:Q:141:GLN:NE2	21:Z:74:VAL:O	2.54	0.41
20:Y:9:LYS:HA	20:Y:10:GLY:HA2	1.58	0.41
21:Z:163:LEU:HG	21:Z:165:VAL:HG22	2.01	0.41
21:Z:97:GLU:HA	21:Z:126:VAL:O	2.20	0.41
26:4:61:ARG:NH1	26:4:61:ARG:O	2.49	0.41
1:A:1594:G:H2'	1:A:1595:G:O4'	2.21	0.41
1:A:1794:U:H2'	1:A:1795:C:C6	2.56	0.41
1:A:1916:A:H2'	1:A:1917:U:O4'	2.21	0.41
1:A:2000:G:N7	34:A:4385:HOH:O	2.37	0.41
1:A:2086:U:H2'	1:A:2087:G:C8	2.55	0.41
1:A:699:A:H2'	1:A:700:G:O4'	2.20	0.41
1:A:856:C:HO2'	1:A:857:C:P	2.43	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:73:A:N1	21:Z:34:ASN:ND2	2.68	0.41
6:G:166:ASP:O	6:G:170:ARG:HB2	2.21	0.41
6:G:16:ARG:HG3	6:G:16:ARG:HH11	1.85	0.41
8:I:123:LEU:HA	8:I:144:VAL:HG23	2.03	0.41
17:V:31:ALA:O	17:V:61:VAL:HG12	2.20	0.41
1:A:752:A:H3'	29:7:1:MET:SD	2.60	0.41
30:8:62:LEU:HB3	30:8:65:GLU:HG2	2.03	0.41
1:A:1306:C:H1'	1:A:1623:G:N2	2.36	0.41
1:A:1878:G:C2	1:A:1879:C:C2	3.08	0.41
1:A:2114:A:H2'	1:A:2114:A:N3	2.36	0.41
1:A:2168:G:C8	1:A:2170:A:N7	2.89	0.41
1:A:686:G:N3	29:7:11:LYS:HE2	2.36	0.41
2:B:105:A:H2'	2:B:106:G:O4'	2.21	0.41
2:B:33:G:C2	2:B:50:G:C2	3.09	0.41
2:B:33:G:H5'	6:G:2:PRO:HD3	2.01	0.41
2:B:55:U:H2'	2:B:56:G:O4'	2.21	0.41
3:D:9:TYR:CZ	3:D:13:ARG:HG2	2.56	0.41
3:D:61:LEU:HA	3:D:61:LEU:HD12	1.99	0.41
7:H:13:LYS:HA	7:H:14:GLY:HA2	1.57	0.41
11:P:107:LYS:O	11:P:110:TYR:HB2	2.20	0.41
26:4:20:ASN:OD1	26:4:21:VAL:N	2.54	0.41
29:7:9:ARG:HG3	29:7:46:VAL:HG23	2.02	0.41
1:A:1223:G:N2	1:A:1226:A:OP2	2.46	0.41
1:A:1752:C:H2'	1:A:1753:G:C8	2.55	0.41
1:A:271(O):C:H2'	1:A:271(P):C:C6	2.56	0.41
1:A:2846:G:H2'	1:A:2847:U:O4'	2.20	0.41
2:B:115:G:O4'	14:S:47:THR:HB	2.21	0.41
2:B:17:C:H2'	2:B:18:G:O4'	2.21	0.41
1:A:784:A:N6	3:D:229:VAL:HG11	2.36	0.41
5:F:176:LEU:HD23	5:F:176:LEU:HA	1.91	0.41
1:A:637:A:H8	11:P:117:GLU:HG3	1.86	0.41
18:W:54:ALA:HB1	18:W:107:LEU:HD22	2.02	0.41
23:1:85:LEU:HA	23:1:85:LEU:HD13	1.91	0.41
27:5:41:PRO:O	27:5:44:THR:OG1	2.36	0.41
1:A:2557:G:H2'	1:A:2558:C:H6	1.86	0.41
1:A:2888:C:H2'	1:A:2889:C:H6	1.86	0.41
1:A:867:C:N4	1:A:868:U:O4	2.54	0.41
5:F:137:LYS:HA	5:F:140:LEU:HB2	2.03	0.41
17:V:40:LEU:HB2	17:V:46:VAL:CG1	2.51	0.41
21:Z:171:ILE:HD13	21:Z:171:ILE:H	1.86	0.41
26:4:59:PHE:N	26:4:59:PHE:HD1	2.14	0.40
1:A:118:A:C8	1:A:119:A:C8	3.09	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1453:U:O4	13:R:67:LEU:HD21	2.21	0.40
1:A:1557:C:H5''	1:A:1558:A:OP2	2.21	0.40
1:A:222:A:H5''	1:A:421:U:OP1	2.21	0.40
1:A:839:U:H2'	1:A:840:C:H6	1.85	0.40
6:G:111:LEU:CD2	6:G:120:LEU:HD21	2.51	0.40
13:R:28:LEU:HA	13:R:28:LEU:HD23	1.91	0.40
16:U:106:PHE:HA	16:U:109:LEU:HD12	2.02	0.40
20:Y:20:TYR:CE1	20:Y:43:ASN:HA	2.56	0.40
1:A:1610:A:OP1	34:A:4119:HOH:O	2.21	0.40
1:A:1759:A:H1'	1:A:2711:A:C2	2.56	0.40
1:A:526:A:N3	1:A:2044:C:H1'	2.36	0.40
1:A:242:G:C8	30:8:5:LYS:HG2	2.56	0.40
1:A:2514:U:H2'	1:A:2515:C:C6	2.56	0.40
6:G:101:ILE:HG22	6:G:105:LYS:HE2	2.03	0.40
6:G:3:LEU:HD22	26:4:25:TYR:CE2	2.56	0.40
7:H:3:ARG:NH1	7:H:5:GLY:H	2.20	0.40
1:A:2404:C:O3'	11:P:77:ARG:NH2	2.53	0.40
6:G:179:PRO:HB2	26:4:42:PHE:HE1	1.85	0.40
6:G:179:PRO:HG3	26:4:43:TYR:CZ	2.56	0.40
11:P:62:LEU:O	30:8:13:ARG:HD3	2.22	0.40
1:A:1031:G:H21	31:9:36:GLN:HE22	1.69	0.40
1:A:1856:G:H2'	1:A:1857:G:O4'	2.21	0.40
1:A:330:A:H2	1:A:1210:A:H2'	1.85	0.40
3:D:92:ILE:HD12	3:D:104:TYR:CD1	2.56	0.40
5:F:64:ILE:HD11	5:F:75:HIS:HB2	2.03	0.40
1:A:2305:A:H5''	6:G:134:GLY:HA3	2.02	0.40
8:I:116:LEU:HD12	8:I:128:LEU:HD13	2.04	0.40
15:T:28:VAL:HG13	15:T:86:ILE:HG23	2.02	0.40
26:4:48:ARG:HD3	26:4:48:ARG:HA	1.69	0.40
1:A:2070:G:H2'	1:A:2071:A:O4'	2.21	0.40
1:A:2184:G:O2'	1:A:2185:C:H5'	2.21	0.40
1:A:2821:A:H2'	1:A:2822:G:C8	2.57	0.40
1:A:288:C:H2'	1:A:289:A:C8	2.57	0.40
1:A:57:C:H2'	1:A:58:G:O4'	2.21	0.40
1:A:918:A:N3	2:B:80:U:O2'	2.50	0.40
1:A:1843:C:H5'	3:D:253:GLN:NE2	2.36	0.40
11:P:126:VAL:HG12	11:P:148:LEU:HD23	2.03	0.40
17:V:89:GLN:HA	17:V:90:PRO:HD3	1.91	0.40
21:Z:100:VAL:HA	21:Z:101:PRO:HD3	1.91	0.40
26:4:62:ARG:HB3	26:4:63:TYR:CD2	2.56	0.40
28:6:18:ARG:HD2	28:6:42:TRP:CD1	2.57	0.40
30:8:23:VAL:CG1	30:8:47:LYS:HD3	2.52	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1789:A:H2'	1:A:1790:C:O4'	2.21	0.40
1:A:207:A:H2'	1:A:208:C:O4'	2.22	0.40
1:A:2107:C:H42	1:A:2182:G:H1	1.69	0.40
1:A:2143:C:C2	1:A:2144:U:H1'	2.57	0.40
1:A:2149:G:C6	1:A:2150:U:O2	2.74	0.40
1:A:2136:C:N4	1:A:2155:G:N1	2.69	0.40
1:A:2494:G:C4	1:A:2495:G:C8	3.10	0.40
1:A:271(H):G:O2'	1:A:271(I):G:C8	2.70	0.40
1:A:580:C:H2'	1:A:581:C:H6	1.87	0.40
1:A:812:C:H2'	1:A:813:U:H6	1.86	0.40
1:A:836:G:C5	1:A:837:C:C4	3.09	0.40
1:A:848:G:C4	1:A:933:A:H8	2.40	0.40
4:E:119:ARG:HB3	4:E:120:TRP:CD1	2.56	0.40
1:A:2094:G:P	8:I:22:LYS:HD2	2.61	0.40
14:S:38:GLN:HE21	14:S:47:THR:HG1	1.57	0.40

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	
3	D	273/276 (99%)	265 (97%)	7 (3%)	1 (0%)	42	59
4	E	202/206 (98%)	196 (97%)	4 (2%)	2 (1%)	21	30
5	F	201/210 (96%)	198 (98%)	1 (0%)	2 (1%)	21	30
6	G	179/182 (98%)	167 (93%)	10 (6%)	2 (1%)	20	27
7	H	172/180 (96%)	165 (96%)	7 (4%)	0	100	100
8	I	144/148 (97%)	133 (92%)	10 (7%)	1 (1%)	29	41
9	N	138/140 (99%)	136 (99%)	1 (1%)	1 (1%)	29	41
10	O	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
11	P	147/150 (98%)	138 (94%)	6 (4%)	3 (2%)	11	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	Q	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	29	41
13	R	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
14	S	108/112 (96%)	106 (98%)	1 (1%)	1 (1%)	23	33
15	T	129/146 (88%)	125 (97%)	4 (3%)	0	100	100
16	U	114/118 (97%)	114 (100%)	0	0	100	100
17	V	99/101 (98%)	97 (98%)	1 (1%)	1 (1%)	21	30
18	W	110/113 (97%)	110 (100%)	0	0	100	100
19	X	93/96 (97%)	91 (98%)	1 (1%)	1 (1%)	20	27
20	Y	105/110 (96%)	100 (95%)	5 (5%)	0	100	100
21	Z	156/206 (76%)	149 (96%)	6 (4%)	1 (1%)	32	46
22	0	81/85 (95%)	79 (98%)	2 (2%)	0	100	100
23	1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	20	27
24	2	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
25	3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
26	4	67/71 (94%)	55 (82%)	6 (9%)	6 (9%)	1	0
27	5	57/60 (95%)	57 (100%)	0	0	100	100
28	6	51/54 (94%)	50 (98%)	1 (2%)	0	100	100
29	7	46/49 (94%)	44 (96%)	1 (2%)	1 (2%)	10	10
30	8	62/65 (95%)	62 (100%)	0	0	100	100
31	9	35/37 (95%)	35 (100%)	0	0	100	100
All	All	3364/3526 (95%)	3248 (97%)	91 (3%)	25 (1%)	29	41

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	E	52	LEU
4	E	73	GLU
5	F	21	ALA
5	F	130	ALA
6	G	81	LYS
12	Q	28	ALA
26	4	45	GLY
26	4	49	PHE
26	4	60	GLN
29	7	46	VAL

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Mol	Chain	Res	Type
6	G	47	LYS
8	I	10	GLU
11	P	45	LEU
26	4	54	GLY
9	N	2	LYS
19	X	2	LYS
26	4	62	ARG
11	P	38	GLN
17	V	79	VAL
26	4	46	GLN
3	D	3	VAL
14	S	84	GLN
23	1	3	LYS
11	P	122	PRO
21	Z	165	VAL

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	
3	D	215/218 (99%)	201 (94%)	14 (6%)	23	35
4	E	164/166 (99%)	147 (90%)	17 (10%)	10	14
5	F	159/166 (96%)	144 (91%)	15 (9%)	12	17
6	G	143/156 (92%)	119 (83%)	24 (17%)	3	3
7	H	144/148 (97%)	129 (90%)	15 (10%)	10	14
8	I	105/124 (85%)	88 (84%)	17 (16%)	3	4
9	N	118/119 (99%)	106 (90%)	12 (10%)	10	14
10	O	100/100 (100%)	97 (97%)	3 (3%)	52	74
11	P	115/116 (99%)	106 (92%)	9 (8%)	17	26
12	Q	111/111 (100%)	101 (91%)	10 (9%)	13	19
13	R	101/101 (100%)	88 (87%)	13 (13%)	6	7
14	S	85/88 (97%)	76 (89%)	9 (11%)	9	13
15	T	113/127 (89%)	105 (93%)	8 (7%)	20	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	U	93/94 (99%)	88 (95%)	5 (5%)	30	46
17	V	80/82 (98%)	71 (89%)	9 (11%)	8	11
18	W	90/92 (98%)	84 (93%)	6 (7%)	22	33
19	X	77/78 (99%)	74 (96%)	3 (4%)	42	62
20	Y	85/91 (93%)	76 (89%)	9 (11%)	9	13
21	Z	137/179 (76%)	123 (90%)	14 (10%)	10	14
22	0	65/67 (97%)	62 (95%)	3 (5%)	36	54
23	1	80/83 (96%)	72 (90%)	8 (10%)	11	15
24	2	65/67 (97%)	60 (92%)	5 (8%)	18	26
25	3	50/52 (96%)	45 (90%)	5 (10%)	11	15
26	4	53/63 (84%)	39 (74%)	14 (26%)	1	0
27	5	50/52 (96%)	45 (90%)	5 (10%)	11	15
28	6	50/52 (96%)	49 (98%)	1 (2%)	66	85
29	7	41/42 (98%)	38 (93%)	3 (7%)	19	29
30	8	54/55 (98%)	52 (96%)	2 (4%)	44	65
31	9	34/34 (100%)	33 (97%)	1 (3%)	53	74
All	All	2777/2923 (95%)	2518 (91%)	259 (9%)	12	17

All (259) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	13	ARG
3	D	32	SER
3	D	54	ARG
3	D	61	LEU
3	D	94	LEU
3	D	122	ASP
3	D	134	ARG
3	D	142	VAL
3	D	155	LEU
3	D	211	ARG
3	D	242	ARG
3	D	260	ARG
3	D	275	LYS
3	D	276	LYS
4	E	12	THR

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Mol	Chain	Res	Type
4	E	21	VAL
4	E	24	THR
4	E	40	GLU
4	E	52	LEU
4	E	73	GLU
4	E	75	VAL
4	E	77	ILE
4	E	78	LEU
4	E	82	ARG
4	E	111	ARG
4	E	116	VAL
4	E	119	ARG
4	E	144	ARG
4	E	154	LYS
4	E	175	VAL
4	E	181	LEU
5	F	19	GLU
5	F	24	LEU
5	F	33	LEU
5	F	57	VAL
5	F	70	THR
5	F	106	ARG
5	F	108	LYS
5	F	110	LEU
5	F	120	GLU
5	F	127	GLU
5	F	135	LYS
5	F	140	LEU
5	F	170	LEU
5	F	183	VAL
5	F	192	LEU
6	G	5	VAL
6	G	21	ARG
6	G	43	LEU
6	G	45	GLU
6	G	49	ASP
6	G	51	ARG
6	G	60	LEU
6	G	91	ARG
6	G	111	LEU
6	G	115	ARG
6	G	124	SER

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Mol	Chain	Res	Type
6	G	128	ARG
6	G	135	LEU
6	G	136	ARG
6	G	140	ILE
6	G	143	GLU
6	G	148	MET
6	G	150	ASP
6	G	156	ASP
6	G	159	VAL
6	G	162	THR
6	G	170	ARG
6	G	175	LEU
6	G	181	ARG
7	H	2	SER
7	H	3	ARG
7	H	27	LYS
7	H	51	ARG
7	H	59	ARG
7	H	69	ARG
7	H	71	LEU
7	H	76	VAL
7	H	88	LEU
7	H	98	LEU
7	H	116	GLU
7	H	124	GLU
7	H	125	VAL
7	H	136	ILE
7	H	139	GLN
8	I	20	ASP
8	I	41	GLU
8	I	43	ASN
8	I	44	LEU
8	I	47	LEU
8	I	57	ARG
8	I	61	ARG
8	I	73	GLU
8	I	75	LEU
8	I	76	THR
8	I	77	LEU
8	I	104	GLN
8	I	108	THR
8	I	114	LEU

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Mol	Chain	Res	Type
8	I	121	LYS
8	I	123	LEU
8	I	140	LEU
9	N	28	THR
9	N	33	LEU
9	N	34	LEU
9	N	46	VAL
9	N	48	MET
9	N	62	VAL
9	N	87	LEU
9	N	99	LEU
9	N	104	LYS
9	N	120	LEU
9	N	137	LYS
9	N	139	GLU
10	O	8	LEU
10	O	69	ILE
10	O	108	GLU
11	P	15	ARG
11	P	45	LEU
11	P	55	ARG
11	P	65	ARG
11	P	95	VAL
11	P	99	LEU
11	P	112	LEU
11	P	125	VAL
11	P	149	GLU
12	Q	1	MET
12	Q	2	LEU
12	Q	7	MET
12	Q	11	LYS
12	Q	21	THR
12	Q	22	LYS
12	Q	45	GLN
12	Q	56	ARG
12	Q	60	ARG
12	Q	110	THR
13	R	1	MET
13	R	15	SER
13	R	18	LEU
13	R	28	LEU
13	R	29	LEU

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Mol	Chain	Res	Type
13	R	33	ARG
13	R	36	THR
13	R	44	LEU
13	R	54	LEU
13	R	65	LEU
13	R	75	LEU
13	R	79	LEU
13	R	111	LEU
14	S	12	PHE
14	S	14	VAL
14	S	25	ARG
14	S	35	ILE
14	S	57	LYS
14	S	58	LEU
14	S	75	GLU
14	S	80	LEU
14	S	110	LEU
15	T	6	LEU
15	T	13	ARG
15	T	16	ARG
15	T	17	THR
15	T	49	VAL
15	T	96	ARG
15	T	113	LYS
15	T	118	ARG
16	U	36	ARG
16	U	74	LEU
16	U	83	LEU
16	U	92	ARG
16	U	104	GLN
17	V	6	LYS
17	V	15	GLU
17	V	46	VAL
17	V	51	VAL
17	V	52	VAL
17	V	62	LEU
17	V	72	VAL
17	V	95	LEU
17	V	100	ARG
18	W	11	ARG
18	W	17	VAL
18	W	19	LEU

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Mol	Chain	Res	Type
18	W	51	LEU
18	W	60	ASN
18	W	107	LEU
19	X	23	GLU
19	X	57	LEU
19	X	90	GLU
20	Y	1	MET
20	Y	11	ASP
20	Y	21	LYS
20	Y	23	ARG
20	Y	43	ASN
20	Y	72	VAL
20	Y	91	GLU
20	Y	99	CYS
20	Y	107	ASP
21	Z	11	GLU
21	Z	18	LEU
21	Z	33	LEU
21	Z	50	GLN
21	Z	97	GLU
21	Z	131	ARG
21	Z	132	ASN
21	Z	136	PHE
21	Z	141	VAL
21	Z	145	GLU
21	Z	148	ASP
21	Z	154	ASP
21	Z	170	THR
21	Z	171	ILE
22	0	11	ARG
22	0	20	ARG
22	0	77	ARG
23	1	3	LYS
23	1	40	ARG
23	1	52	ARG
23	1	69	LYS
23	1	76	ARG
23	1	85	LEU
23	1	89	GLU
23	1	95	LEU
24	2	28	LYS
24	2	32	LEU

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Mol	Chain	Res	Type
24	2	44	LEU
24	2	53	LEU
24	2	70	GLN
25	3	3	ARG
25	3	23	LEU
25	3	30	ARG
25	3	32	GLN
25	3	54	VAL
26	4	1	MET
26	4	8	LYS
26	4	13	ARG
26	4	27	THR
26	4	34	GLU
26	4	37	SER
26	4	48	ARG
26	4	50	VAL
26	4	58	ARG
26	4	59	PHE
26	4	62	ARG
26	4	63	TYR
26	4	68	ARG
26	4	69	LYS
27	5	6	VAL
27	5	16	ARG
27	5	29	THR
27	5	40	LYS
27	5	48	GLU
28	6	14	THR
29	7	1	MET
29	7	14	LYS
29	7	41	ARG
30	8	23	VAL
30	8	32	LEU
31	9	17	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	87	ASN
3	D	164	GLN
3	D	253	GLN
4	E	143	ASN

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Mol	Chain	Res	Type
5	F	69	HIS
5	F	169	ASN
5	F	203	GLN
6	G	132	ASN
8	I	43	ASN
8	I	104	GLN
8	I	133	HIS
9	N	38	HIS
9	N	133	GLN
11	P	38	GLN
12	Q	13	GLN
12	Q	45	GLN
12	Q	57	HIS
12	Q	123	HIS
13	R	71	GLN
14	S	38	GLN
15	T	43	GLN
15	T	123	GLN
17	V	64	HIS
19	X	31	HIS
19	X	82	GLN
20	Y	43	ASN
21	Z	50	GLN
24	2	38	GLN
31	9	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2791/2915 (95%)	485 (17%)	29 (1%)
2	B	119/121 (98%)	20 (16%)	1 (0%)
All	All	2910/3036 (95%)	505 (17%)	30 (1%)

All (505) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	U
1	A	10	G
1	A	11	G
1	A	12	U
1	A	15	G

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Mol	Chain	Res	Type
1	A	34	C
1	A	36	G
1	A	45	C
1	A	61	G
1	A	71	A
1	A	74	A
1	A	75	G
1	A	84	A
1	A	90	U
1	A	95	G
1	A	100	G
1	A	102	G
1	A	118	A
1	A	119	A
1	A	120	U
1	A	125	G
1	A	154(A)	C
1	A	157	U
1	A	173	G
1	A	181	A
1	A	196	A
1	A	199	A
1	A	205	G
1	A	215	G
1	A	216	A
1	A	221	A
1	A	222	A
1	A	228	A
1	A	229	A
1	A	230	U
1	A	232	G
1	A	233	A
1	A	248	G
1	A	250	G
1	A	271(A)	A
1	A	271(I)	G
1	A	271(K)	U
1	A	271(L)	U
1	A	271(M)	G
1	A	271(N)	U
1	A	272	G
1	A	272(A)	U

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Mol	Chain	Res	Type
1	A	272(B)	G
1	A	277	C
1	A	278	A
1	A	294	A
1	A	311	A
1	A	312	G
1	A	324	A
1	A	327	G
1	A	329	G
1	A	330	A
1	A	338	G
1	A	352	G
1	A	362	U
1	A	363	G
1	A	363(B)	G
1	A	386	G
1	A	389	G
1	A	396	G
1	A	405	U
1	A	411	G
1	A	412	A
1	A	421	U
1	A	422	A
1	A	435	C
1	A	443	A
1	A	444	C
1	A	454	A
1	A	455	C
1	A	457	A
1	A	470	A
1	A	480	A
1	A	481	G
1	A	505	A
1	A	508	G
1	A	509	C
1	A	522	G
1	A	528	A
1	A	529	A
1	A	530	G
1	A	531	C
1	A	532	A
1	A	533	G

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Mol	Chain	Res	Type
1	A	545	G
1	A	563	G
1	A	568	U
1	A	573	G
1	A	575	A
1	A	587	C
1	A	588	U
1	A	603	A
1	A	604	G
1	A	607	U
1	A	614(B)	G
1	A	615	G
1	A	616	G
1	A	627	A
1	A	637	A
1	A	639	U
1	A	640	C
1	A	645	C
1	A	646	A
1	A	652(B)	A
1	A	652(C)	G
1	A	652(U)	G
1	A	668	G
1	A	669	G
1	A	686	G
1	A	701	G
1	A	717	G
1	A	730	C
1	A	752	A
1	A	753	C
1	A	765	G
1	A	775	G
1	A	776	G
1	A	782	A
1	A	783	A
1	A	784	A
1	A	785	G
1	A	790	C
1	A	792	G
1	A	805	G
1	A	812	C
1	A	819	A

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Mol	Chain	Res	Type
1	A	827	U
1	A	828	U
1	A	847	U
1	A	848	G
1	A	857	C
1	A	859	G
1	A	866	A
1	A	867	C
1	A	873	G
1	A	874	G
1	A	875	G
1	A	879	G
1	A	884	C
1	A	885	C
1	A	886	C
1	A	887	A
1	A	888	C
1	A	889	C
1	A	890	A
1	A	893	C
1	A	894	C
1	A	896	A
1	A	897	C
1	A	899	A
1	A	900	A
1	A	901	A
1	A	902	C
1	A	910	A
1	A	917	A
1	A	932	G
1	A	941	A
1	A	945	A
1	A	946	G
1	A	950	G
1	A	953	A
1	A	958	U
1	A	959	A
1	A	961	C
1	A	974	G
1	A	975	C
1	A	983	A
1	A	996	A

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Mol	Chain	Res	Type
1	A	1005	C
1	A	1012	U
1	A	1013	C
1	A	1017	G
1	A	1020	A
1	A	1022	G
1	A	1025	G
1	A	1026	U
1	A	1027	A
1	A	1033	U
1	A	1034	G
1	A	1038	C
1	A	1039	G
1	A	1040	C
1	A	1041	C
1	A	1043	C
1	A	1114	G
1	A	1115	G
1	A	1130	U
1	A	1135	C
1	A	1136	G
1	A	1139	G
1	A	1143	A
1	A	1153	C
1	A	1170	G
1	A	1171	G
1	A	1205	U
1	A	1206	G
1	A	1210	A
1	A	1211	U
1	A	1212	G
1	A	1219	G
1	A	1220	A
1	A	1229	G
1	A	1237	A
1	A	1244	G
1	A	1253	A
1	A	1256	G
1	A	1271	G
1	A	1272	A
1	A	1273	U
1	A	1300	U

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Mol	Chain	Res	Type
1	A	1301	A
1	A	1309	G
1	A	1314	C
1	A	1352	U
1	A	1359	A
1	A	1360	A
1	A	1365	A
1	A	1370	C
1	A	1384	A
1	A	1385	G
1	A	1395	A
1	A	1416	G
1	A	1417	C
1	A	1420	U
1	A	1421	G
1	A	1427	A
1	A	1428	C
1	A	1435	G
1	A	1437	C
1	A	1445	A
1	A	1449	A
1	A	1450	G
1	A	1455	G
1	A	1460	A
1	A	1461	G
1	A	1467	C
1	A	1471	A
1	A	1482	G
1	A	1490	A
1	A	1493	C
1	A	1494	A
1	A	1495	A
1	A	1496	A
1	A	1497	U
1	A	1508	A
1	A	1509	C
1	A	1509(A)	A
1	A	1528(A)	A
1	A	1531	C
1	A	1532	C
1	A	1533	G
1	A	1541	G

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Mol	Chain	Res	Type
1	A	1543	C
1	A	1554	A
1	A	1558	A
1	A	1559	G
1	A	1566	A
1	A	1569	A
1	A	1578	U
1	A	1582	C
1	A	1583	A
1	A	1584	C
1	A	1586	A
1	A	1591	G
1	A	1608	A
1	A	1610	A
1	A	1616	A
1	A	1631(A)	A
1	A	1640	C
1	A	1648	C
1	A	1654	A
1	A	1674	G
1	A	1696	G
1	A	1700	A
1	A	1721	G
1	A	1722	A
1	A	1746	G
1	A	1756	G
1	A	1762	A
1	A	1763	G
1	A	1764	G
1	A	1773	A
1	A	1780	A
1	A	1782	C
1	A	1791	A
1	A	1800	C
1	A	1801	G
1	A	1812	A
1	A	1816	G
1	A	1829	A
1	A	1847	A
1	A	1848	A
1	A	1877	A
1	A	1878	G

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Mol	Chain	Res	Type
1	A	1900	A
1	A	1906	G
1	A	1913	A
1	A	1914	C
1	A	1929	G
1	A	1930	G
1	A	1936	A
1	A	1938	A
1	A	1955	U
1	A	1963	U
1	A	1967	C
1	A	1970	A
1	A	1971	A
1	A	1972	A
1	A	1993	U
1	A	1997	G
1	A	2023	G
1	A	2031	A
1	A	2032	G
1	A	2033	A
1	A	2043	C
1	A	2055	C
1	A	2056	G
1	A	2060	A
1	A	2061	G
1	A	2062	A
1	A	2069	G
1	A	2099	U
1	A	2101	G
1	A	2104	G
1	A	2105	C
1	A	2107	C
1	A	2108	C
1	A	2110	G
1	A	2111	C
1	A	2116	G
1	A	2117	A
1	A	2119	A
1	A	2122	U
1	A	2126	A
1	A	2127	G
1	A	2130	U

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Mol	Chain	Res	Type
1	A	2131	G
1	A	2132	U
1	A	2133	G
1	A	2134	A
1	A	2135	A
1	A	2137	C
1	A	2138	C
1	A	2139	C
1	A	2144	U
1	A	2145	C
1	A	2146	C
1	A	2148	G
1	A	2149	G
1	A	2150	U
1	A	2151	G
1	A	2153	G
1	A	2154	G
1	A	2155	G
1	A	2156	G
1	A	2157	G
1	A	2158	A
1	A	2159	G
1	A	2160	G
1	A	2163	C
1	A	2166	G
1	A	2167	U
1	A	2168	G
1	A	2169	A
1	A	2172	U
1	A	2173	A
1	A	2175	C
1	A	2178	C
1	A	2184	G
1	A	2185	C
1	A	2186	G
1	A	2189	U
1	A	2192	G
1	A	2198	A
1	A	2206	G
1	A	2207	G
1	A	2208	A
1	A	2218	U

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Mol	Chain	Res	Type
1	A	2225	A
1	A	2238	G
1	A	2239	G
1	A	2268	A
1	A	2275	C
1	A	2279	G
1	A	2283	C
1	A	2287	A
1	A	2305	A
1	A	2308	G
1	A	2311	A
1	A	2312	U
1	A	2319	G
1	A	2320	A
1	A	2325	G
1	A	2334	G
1	A	2336	A
1	A	2347	C
1	A	2350	C
1	A	2376	A
1	A	2383	G
1	A	2385	C
1	A	2396	G
1	A	2406	U
1	A	2425	A
1	A	2428	G
1	A	2429	G
1	A	2430	A
1	A	2434	A
1	A	2435	A
1	A	2439	A
1	A	2441	C
1	A	2445	G
1	A	2448	A
1	A	2474	C
1	A	2476	A
1	A	2480	C
1	A	2487	G
1	A	2494	G
1	A	2502	G
1	A	2505	G
1	A	2506	U

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Mol	Chain	Res	Type
1	A	2507	C
1	A	2518	A
1	A	2520	C
1	A	2529	G
1	A	2554	U
1	A	2566	A
1	A	2567	G
1	A	2573	C
1	A	2578	G
1	A	2582	G
1	A	2602	A
1	A	2611	U
1	A	2612	C
1	A	2629	A
1	A	2630	G
1	A	2652	C
1	A	2654	A
1	A	2656	U
1	A	2663	G
1	A	2673	G
1	A	2689	U
1	A	2690	C
1	A	2694	G
1	A	2702	U
1	A	2703	C
1	A	2712(A)	A
1	A	2713	A
1	A	2714	G
1	A	2718	G
1	A	2726	U
1	A	2733	A
1	A	2748	A
1	A	2751	G
1	A	2752	C
1	A	2757	A
1	A	2761	G
1	A	2764	A
1	A	2765	A
1	A	2766	G
1	A	2778	A
1	A	2789	C
1	A	2793	G

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Mol	Chain	Res	Type
1	A	2794	C
1	A	2802	G
1	A	2807	G
1	A	2818	G
1	A	2820	A
1	A	2821	A
1	A	2833	G
1	A	2835	A
1	A	2839	G
1	A	2872	G
1	A	2875	C
1	A	2880	C
1	A	2892	A
1	A	2893	G
1	A	2894	G
1	A	2895	U
1	A	2896	C
1	A	2897	U
2	B	2	C
2	B	7	G
2	B	13	A
2	B	15	A
2	B	17	C
2	B	25	A
2	B	32	C
2	B	40	U
2	B	42	C
2	B	56	G
2	B	64	C
2	B	65	C
2	B	73	A
2	B	75	G
2	B	84	C
2	B	88	C
2	B	108	U
2	B	110	G
2	B	116	G
2	B	120	A

All (30) RNA pucker outliers are listed below:

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Mol	Chain	Res	Type
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Mol	Chain	Res	Type
1	A	195	A
1	A	196	A
1	A	228	A
1	A	271(K)	U
1	A	271(M)	G
1	A	277	C
1	A	528	A
1	A	529	A
1	A	587	C
1	A	752	A
1	A	764	A
1	A	774	A
1	A	827	U
1	A	856	C
1	A	900	A
1	A	1210	A
1	A	1300	U
1	A	1420	U
1	A	1493	C
1	A	1530	C
1	A	1653	G
1	A	1913	A
1	A	1992	G
1	A	2110	G
1	A	2119	A
1	A	2126	A
1	A	2406	U
1	A	2689	U
1	A	2756	U
2	B	1	U

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 ⓘ

Of 746 ligands modelled in this entry, 746 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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.