



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 11:36 AM UTC

PDB ID : 6DDD / pdb_00006ddd
EMDB ID : EMD-7867
Title : Structure of the 50S ribosomal subunit from Methicillin Resistant Staphylococcus aureus in complex with the oxazolidinone antibiotic LZD-5
Authors : Belousoff, M.J.; Venugopal, H.; Bamert, R.S.; Lithgow, T.
Deposited on : 2018-05-10
Resolution : 3.10 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

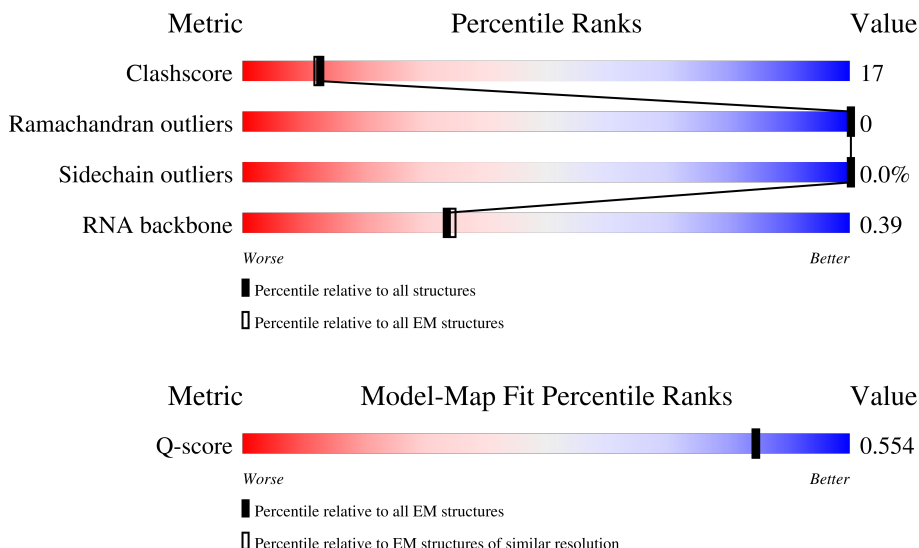
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	116	9% 54% 43% .
2	B	276	8% 63% 36% .
3	C	118	. 62% 36% .

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Mol	Chain	Length	Quality of chain
4	D	102	
5	E	116	
6	F	91	
7	G	105	
8	H	217	
9	I	85	
10	J	62	
11	K	69	
12	L	217	
13	M	59	
14	N	57	
15	O	49	
16	P	50	
17	Q	65	
18	R	37	
19	S	207	
20	V	145	
21	W	122	
22	X	146	
23	Y	144	
24	Z	122	
25	a	119	
26	1	2923	
27	2	115	

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 79136 atoms, of which 18 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	113	Total	C	N	O	0	0
			915	576	184	155		

- Molecule 2 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	274	Total	C	N	O	S	0	0
			2094	1303	415	371	5		

- Molecule 3 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	116	Total	C	N	O	S	0	0
			943	593	189	157	4		

- Molecule 4 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	100	Total	C	N	O	S	0	0
			785	499	139	146	1		

- Molecule 5 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	111	Total	C	N	O	S	0	0
			853	532	163	155	3		

- Molecule 6 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	87	Total	C	N	O	S	0	0
			711	449	128	130	4		

- Molecule 7 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	95	Total	C	N	O	S	0	0
			730	460	134	135	1		

- Molecule 8 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	93	Total	C	N	O	S	0	0
			727	465	129	132	1		

- Molecule 9 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	77	Total	C	N	O	0	0
			592	364	115	113		

- Molecule 10 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	59	Total	C	N	O	S	0	0
			463	287	99	76	1		

- Molecule 11 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	57	Total	C	N	O	0	0
			472	290	89	93		

- Molecule 12 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	215	Total	C	N	O	S	0	0
			1628	1018	299	306	5		

- Molecule 13 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	56	Total	C	N	O	0	0
			432	269	82	81		

- Molecule 14 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	50	Total	C	N	O	S	0	0
			397	241	83	68	5		

- Molecule 15 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	46	Total	C	N	O	S	0	0
			382	228	78	72	4		

- Molecule 16 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	44	Total	C	N	O	S	0	0
			372	228	90	53	1		

- Molecule 17 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

- Molecule 18 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	37	Total	C	N	O	S	0	0
			296	186	60	45	5		

- Molecule 19 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	171	Total	C	N	O	S	0	0
			1318	829	248	239	2		

- Molecule 20 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	143	Total	C	N	O	S	0	0
			1138	710	209	217	2		

- Molecule 21 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	112	Total	C	N	O	S	0	0
			850	526	163	158	3		

- Molecule 22 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	125	Total	C	N	O		0	0
			938	580	188	170			

- Molecule 23 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	136	Total	C	N	O	S	0	0
			1089	698	206	181	4		

- Molecule 24 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	114	Total	C	N	O	S	0	0
			902	556	175	170	1		

- Molecule 25 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	73	Total	C	N	O		0	0
			583	361	119	103			

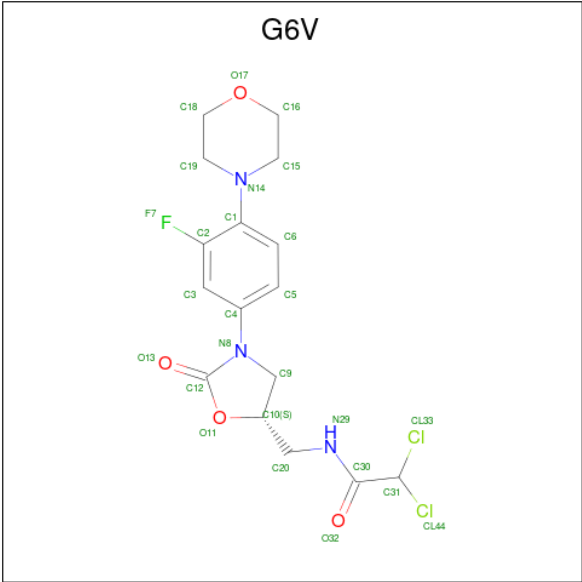
- Molecule 26 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1	2646	Total	C	N	O	P	0	0
			56747	25338	10405	18361	2643		

- Molecule 27 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	104	Total	C	N	O	P	0	0
			2214	990	395	725	104		

- Molecule 28 is 2,2-dichloro-N-((5S)-3-[3-fluoro-4-(morpholin-4-yl)phenyl]-2-oxo-1,3-oxazolidin-5-yl)methyl)acetamide (CCD ID: G6V) (formula: C₁₆H₁₈Cl₂FN₃O₄).

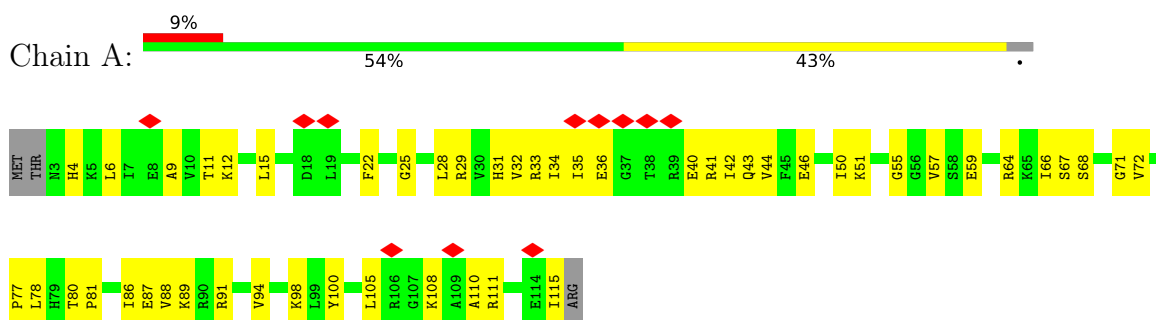


Mol	Chain	Residues	Atoms							AltConf
			Total	C	Cl	F	H	N	O	
28	1	1	44	16	2	1	18	3	4	0

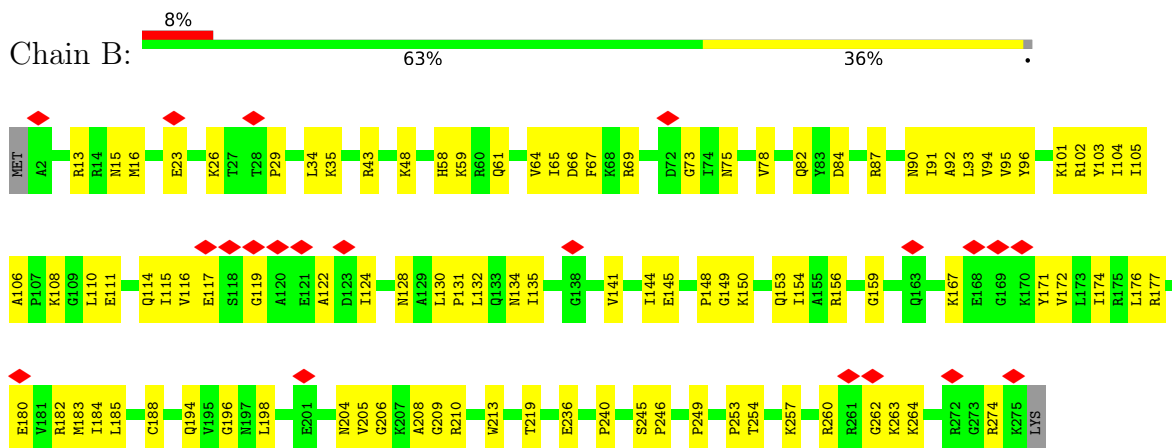
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

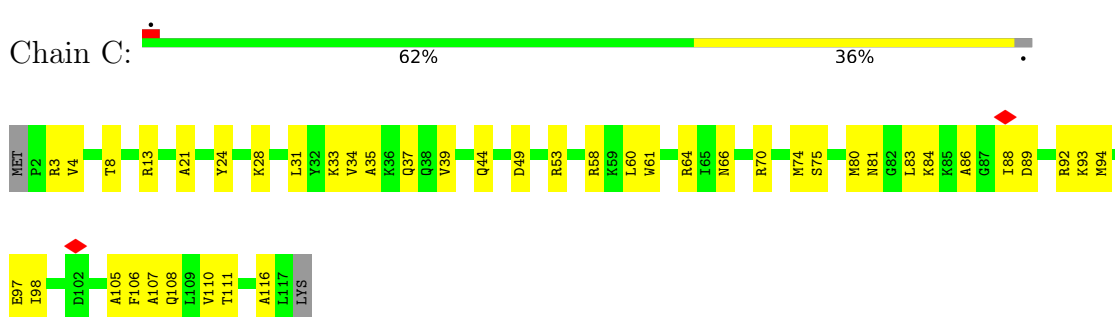
- Molecule 1: 50S ribosomal protein L19



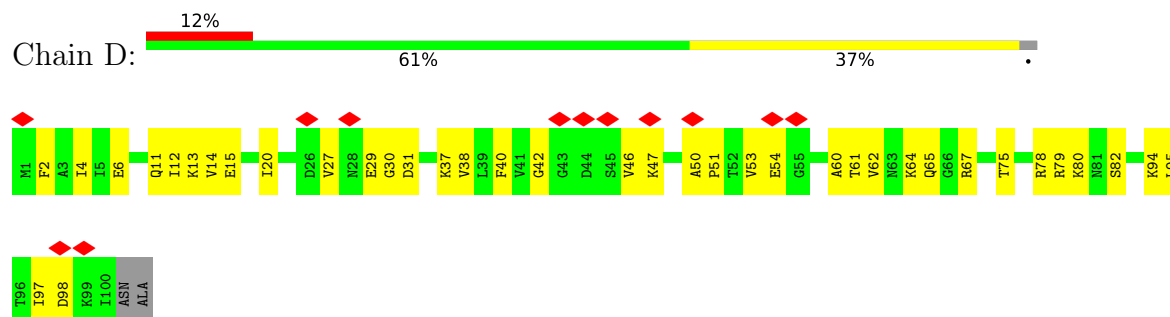
- Molecule 2: 50S ribosomal protein L2



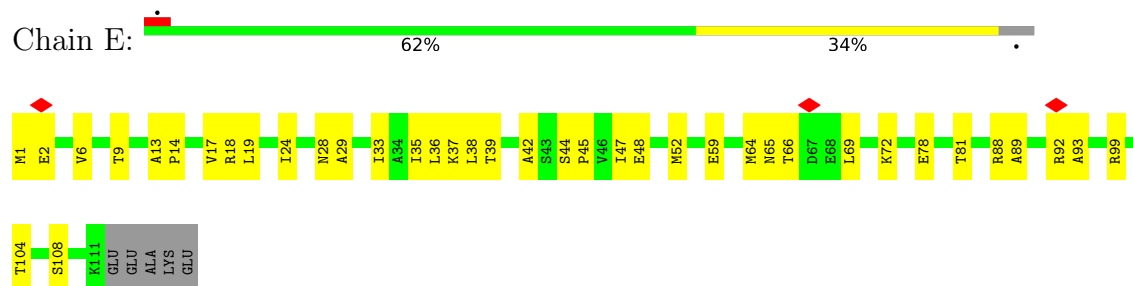
- Molecule 3: 50S ribosomal protein L20



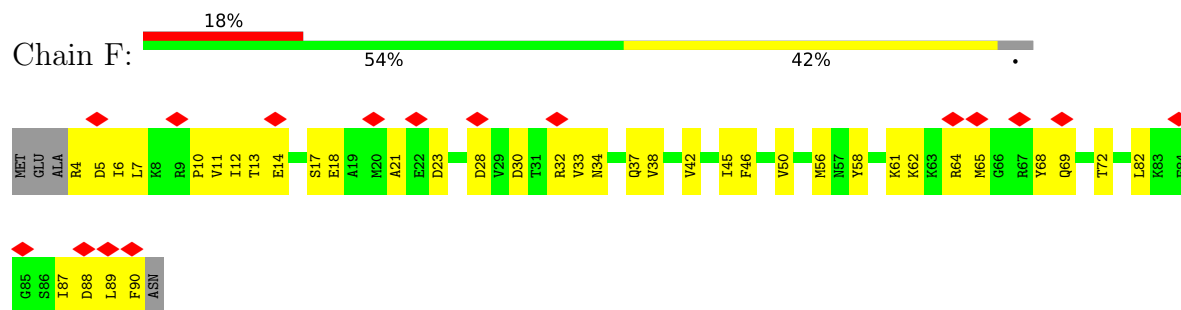
- Molecule 4: 50S ribosomal protein L21



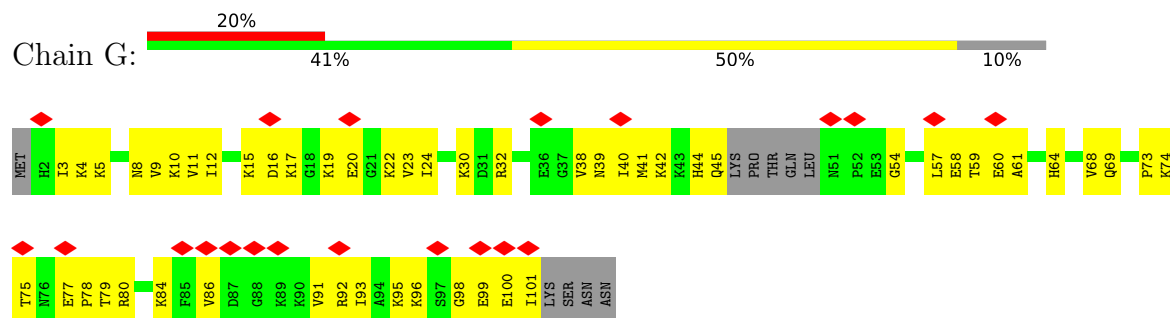
- Molecule 5: 50S ribosomal protein L22



- Molecule 6: 50S ribosomal protein L23

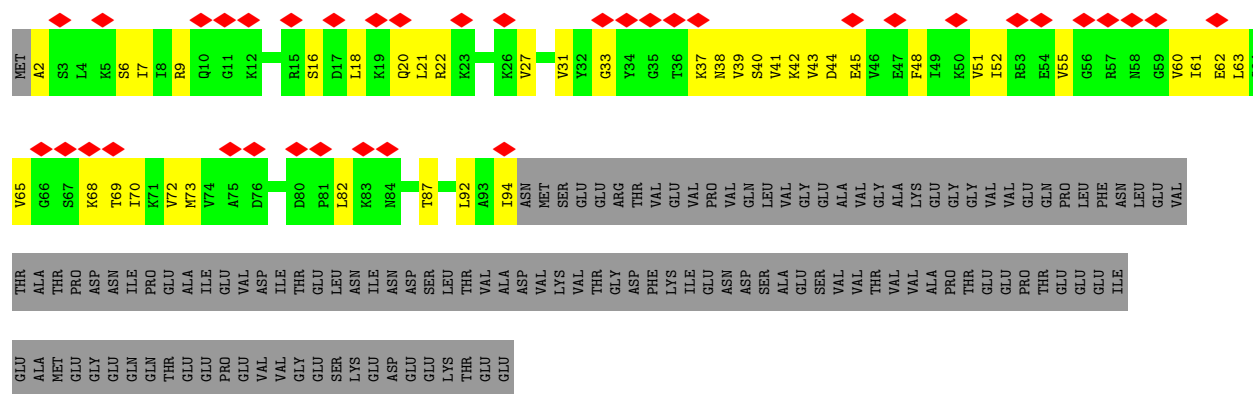


- Molecule 7: 50S ribosomal protein L24

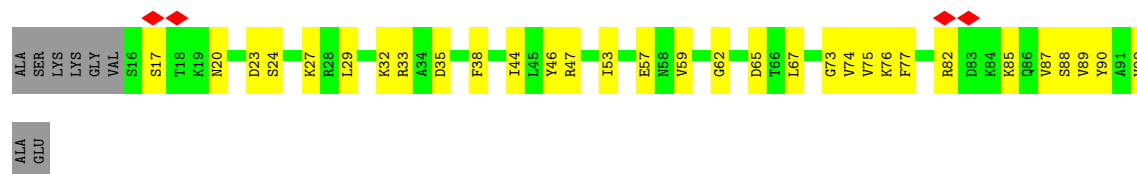


- Molecule 8: 50S ribosomal protein L25

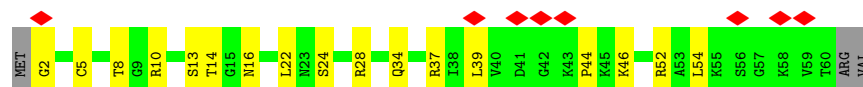




• Molecule 9: 50S ribosomal protein L27



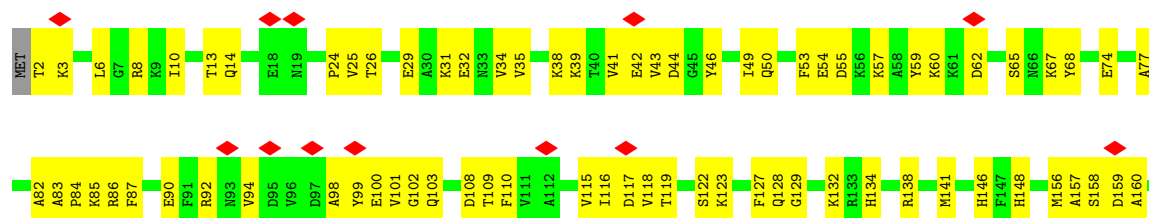
• Molecule 10: 50S ribosomal protein L28

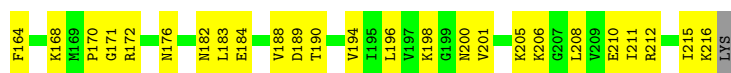


• Molecule 11: 50S ribosomal protein L29



• Molecule 12: 50S ribosomal protein L3





- Molecule 13: 50S ribosomal protein L30



- Molecule 14: 50S ribosomal protein L32



- Molecule 15: 50S ribosomal protein L33



- Molecule 16: 50S ribosomal protein L34



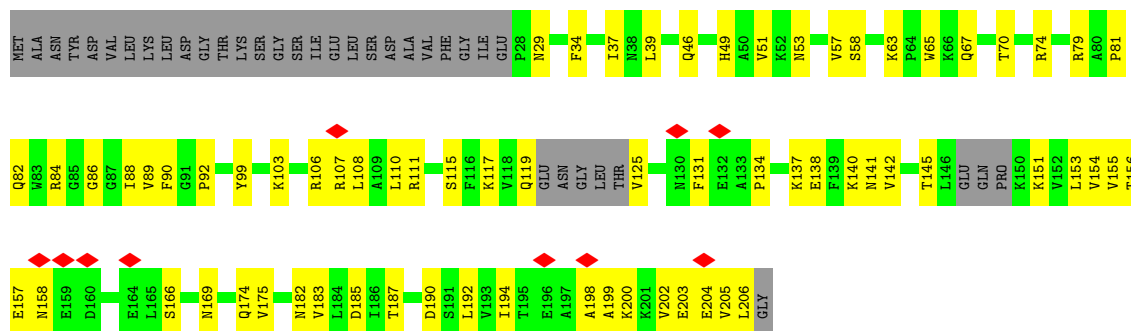
- Molecule 17: 50S ribosomal protein L35



- Molecule 18: 50S ribosomal protein L36



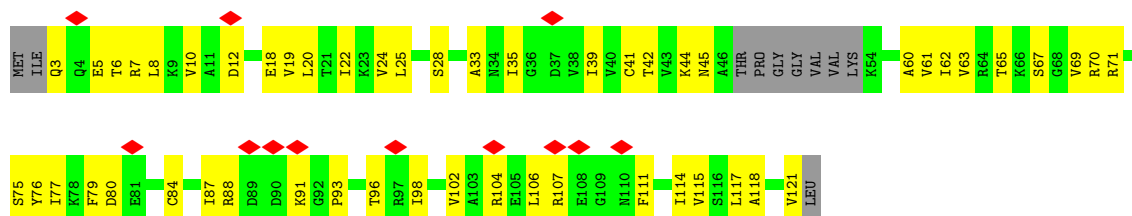
- Molecule 19: 50S ribosomal protein L4



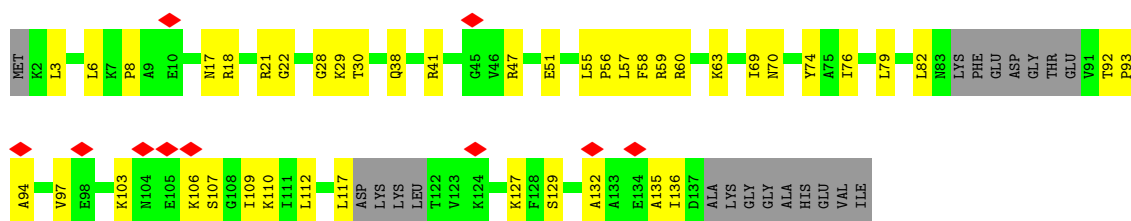
• Molecule 20: 50S ribosomal protein L13



• Molecule 21: 50S ribosomal protein L14

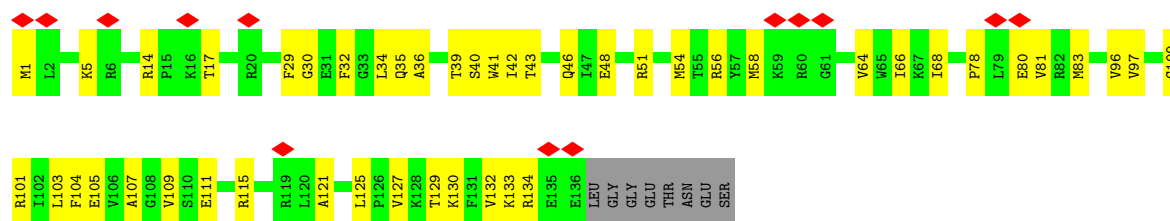


• Molecule 22: 50S ribosomal protein L15

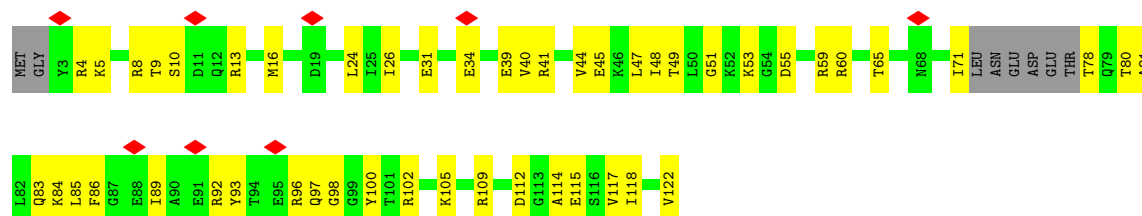


• Molecule 23: 50S ribosomal protein L16

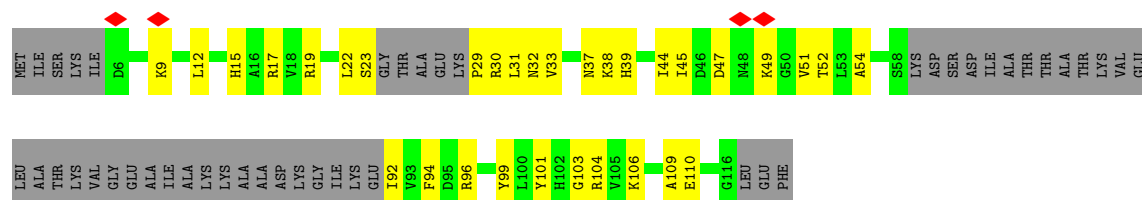




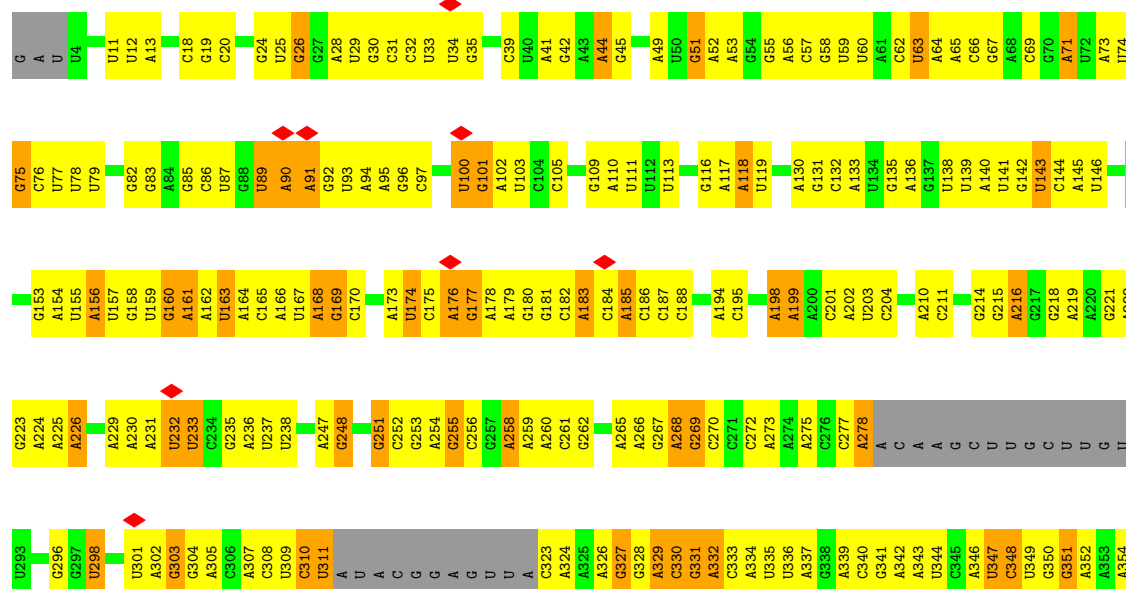
• Molecule 24: 50S ribosomal protein L17



• Molecule 25: 50S ribosomal protein L18

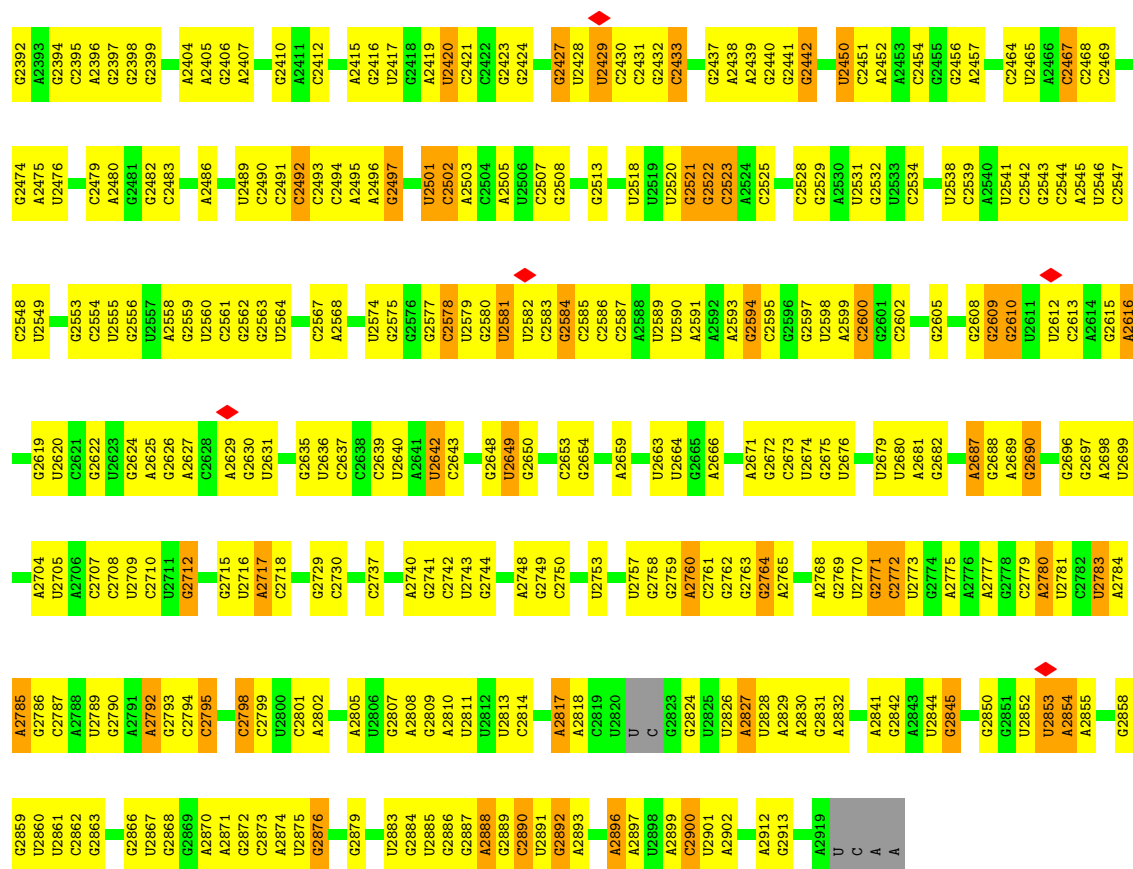


• Molecule 26: 23S rRNA

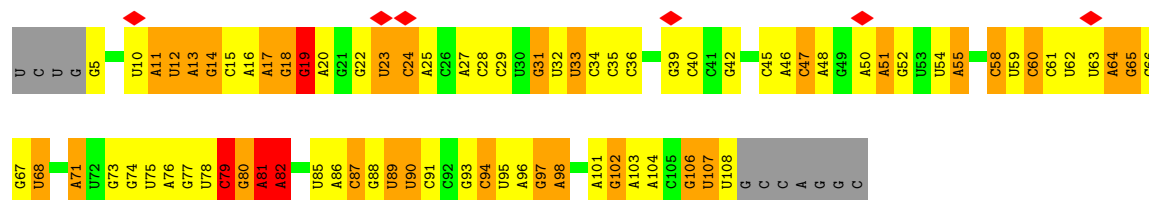
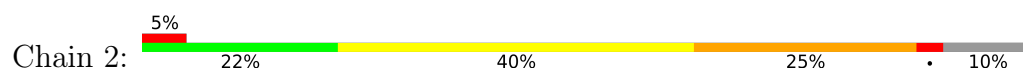


A1312	G1236	C	C1026	U	G876	U786	A713	G640	U569	U494	C421	G355
G1313	U1237	G	A1027	A	G877	U787	C717	A641	U570	A500	G422	A356
A1314	U1238	A	G1028	C	U878	A788	C718	U642	G575	C502	A423	A359
C1315	G1029	C	U1029	C	U879	C789	C719	C643	U576	A503	G428	A360
G1316	C1030	U	A1030	G	U884	U790	A720	C644	A577	C504	C429	U361
U1319	A1241	A	A1032	A	C885	U791	A721	A645	U578	G505	A430	C362
G1320	G1242	G	G1033	U947	A886	U792	A722	A646	U579	C506	C431	A363
A1321	G1243	G	A1034	U948	A887	G793	A723	G647	C580	A507	A432	A364
C1322	G1244	A	A1035	C949	A888	A794	G727	U648	U581	C508	G433	A365
G1323	G1245	U	G1036	A955	U889	A795	A727	U649	A583	C509	A434	G366
A1324	G1246	G	C1038	A956	U890	A796	A730	U650	C587	G509	A435	A367
U1325	G1247	U	U1039	U957	G891	A797	A731	G653	G588	A512	A436	A368
C1326	U1248	U	G1040	U958	A891	G798	C732	C654	U589	G513	A437	G369
G1327	G1250	G	G1041	A894	U892	U799	U733	A655	G590	G514	U438	A372
C1328	C1254	C	C1042	A895	U893	G800	C736	A656	U591	G515	C440	A373
U1329	U1257	U	U1043	U961	U896	A801	G745	U657	U592	A516	C441	U374
G1330	G1258	U	A1044	A962	A897	G802	U738	A658	A593	A517	G442	A378
C1334	U1259	A	G1046	A963	U898	G805	U739	A659	U594	A518	U443	C379
A1337	U1260	G	U1047	A969	U899	G808	C743	A660	G594	A519	G446	U380
U1338	G1261	A	U1048	U970	G900	A809	A744	U661	U597	G520	A447	G381
G1339	C1179	C	C1049	A971	G901	A810	G745	G662	G598	U521	A448	U382
U1340	G1182	G	A1053	A972	G902	C811	G746	G665	U600	G522	U451	A383
A1341	G1183	A	A1054	A973	G903	C812	U747	G666	G601	A523	C452	G384
C1342	G1184	C	A1055	U974	G904	U811	U748	G667	G604	A524	G457	A388
G1347	U1185	C	A1056	U975	U905	C813	U749	G668	U605	G525	A458	A389
U1348	U1186	U	C1057	U976	A906	A814	G749	C669	C607	A526	U462	A390
G1349	A1187	A	U1058	A977	G907	G907	G750	C670	U609	G527	C463	A391
C1350	U1188	C	U1059	U978	U908	A819	A751	G673	U610	A528	C466	U392
U1351	U1189	U	U1060	A979	C910	G820	G752	G674	G613	G529	U467	U393
C1352	G1196	U	U1063	U981	A911	A824	A756	G675	U611	C530	A468	U394
G1353	C1197	C	A1064	U982	U913	G825	G757	G676	G614	A536	C469	U395
A1354	G1198	A	A1065	G984	G914	A826	U	G677	U615	G537	U473	U396
C1355	U1199	A	U1066	A985	U915	U828	A	G678	A616	G538	G470	C398
U1356	G1207	A	U1067	A986	U916	U829	C	G679	G617	G539	U476	U399
G1357	A1208	C	G1068	A989	U917	A834	A763	U680	A621	U544	A477	U401
U1358	U1209	G	G1069	U990	G918	U835	A764	A691	A622	A545	U478	U402
A1359	U1210	A	A1070	G991	U919	C836	U765	A692	A623	G546	C479	A404
G1360	G1211	U	A1071	A992	A920	G837	U766	A693	G624	A547	U480	A405
U1361	U1212	C	U1072	G997	C921	U838	G767	A694	G625	A548	C481	U406
C1364	C1213	C	A1073	G1000	G	U848	A768	U695	G626	A549	U482	U408
G1365	U1214	G	G1074	G1001	A	A849	A769	A696	A627	U550	C483	G410
U1366	U1215	U	U1075	A1001	G	U850	G770	A697	A628	C554	U484	A411
C1367	U1216	A	U1076	A1004	G	C851	G771	G698	A629	C555	A485	U412
G1368	U1217	U	G1077	G1005	C	U852	A772	G699	G630	C556	G486	C413
U1369	G1218	U	U1078	G1009	C	U853	G773	G699	U631	U557	U487	C414
G1375	G1219	A	G1079	C1009	C	U854	G774	U697	U632	G558	C488	U415
U1376	U1220	C	C1080	U1010	C	C857	A775	U698	G633	A559	A489	G416
G1377	C1221	U	C1081	U1011	U	C862	G778	U699	A634	C562	C490	A417
U1378	U1224	C	G1086	U1012	C	C870	A779	A700	U637	G563	C491	G418
C1385	G1225	C	C	U1013	U	U871	A780	G701	U638	C567	C492	U419
U1386	U1226	U	C	U1014	C	U872	C781	U702	G639	U568	A493	A420
G1387	U1227	A	C	G1015	G	U873	C782	A703	U639	C569		
C1388	G1230	A	A	G1016	G	U874	C785	U704				
	A1233	U	A	A1017	G	A875		U709				

C2324	A2252	G	C2052	C1969	C1906	U1843	C1766	G1686	U1603	C	A1471	U1389
A2325	C2253	G	U2053	U1970	U1907	G1844	G1767	G1687	C1604	C	C1472	A1390
G2326	A2254	C	G2054	A1908	A1908	U1945	C1770	U1688	A1605	G	U1477	A1391
A2327	C2255	C	U2055	G1975	C1909	A1846	C1770	G1689	C1606	G	U1478	U1394
U2328	C2256	C	A2057	G1976	C1910	U1847	G1772	U1690	A1607	U	G1479	G1395
U2329	C2257	C	G2058	U1977	A1911	A1848	A1773	G1691	C1608	C	G1480	A1396
G2330	A2260	G	A2058	U1978	A1912	G1851	A1774	C1692	U1609	U	U1481	G1397
G2331	G2261	C	G2059	A1979	U1913	U1854	G1775	C1693	G1613	C	U1482	G1398
U	G2262	U	U2060	A1980	C1914	U1855	G1776	U1694	A1614	G	A1489	A1402
U	C2263	G	U2061	G1981	G1915	G1856	G1777	U1695	G1615	U	C1491	A1403
G	G2264	G	G2062	U1982	G1916	U1857	C1778	G1696	A1616	A	G1492	A1404
G	G2265	U	C2063	G1983	G1917	G1858	G1780	U1697	A1617	U	U1493	G1405
A	G2266	A	U2064	C1984	C1920	C1859	G1783	U1701	G1620	C	A1494	U1409
A	C2267	C	U2065	G1985	G1921	G1862	U1788	G1710	U1625	G	G1496	A1410
A	A2268	A	A2066	G1986	C1922	C1864	A1789	G1711	A1626	U	A1497	G1411
U	A2269	C	C2070	C1987	C1923	C1865	G1790	G1712	G1627	U	U1498	A1415
U2270	G2271	G	G2071	C1988	C1924	G1866	G1791	G1713	A1628	U	G1500	U1416
U2271	C2272	A	C2072	C1989	C1925	G1867	C1792	G1714	C1629	C	G1501	G1423
U2272	G2273	C	G2073	C1990	U1926	U1870	C1794	A1720	A1630	U	A1502	G1424
A2274	A2274	A	U2074	G1991	A1927	U1871	G1799	A1721	G1631	U	U1503	G1425
G2277	G2277	G	U2075	G1992	C1928	G1872	A1800	A1722	A1632	U	U1504	G1426
U2282	G2282	C	G2076	A1993	C1929	G1873	C1801	U1723	A1633	U	G1505	U1427
G2283	U2284	G	A2081	C1994	G1930	U1874	U1802	U1724	A1634	U	G1506	U1428
G2284	C2285	U	G2082	G1995	G1931	G1875	G1803	G1725	A1635	U	G1507	G1429
U2285	G2286	G	A1996	A1997	C1932	G1876	U1806	A1726	G1637	U	G1508	U1430
C2287	C2287	C	U2083	A1998	G1933	U1877	A1807	U1732	G1638	U	G1509	U1431
G2288	U2288	U	G2084	G1999	G1934	U1878	C1807	A1733	C1648	U	G1510	U1432
U2289	C2289	U	A2085	G2000	C1935	U1879	A1810	A1734	G1649	U	G1511	U1433
U2290	A2290	C	C2092	U2009	C1941	A1880	A1811	G1735	G1650	U	G1512	U1434
C2291	G2291	A	U2093	C2017	U1942	A1881	A1812	G1740	A1652	A	C1516	G1445
U2292	A2292	C	G2094	U2018	A1943	G1882	A1813	G1741	A1653	C	A1517	U1446
A2295	C2295	G	U2095	G2019	U1944	A1883	U1816	A1742	A1654	U	U1518	A1447
A2300	G2300	C	C2096	U2020	U1945	G1884	C1817	U1743	U1655	U	U1519	U1448
A2301	C2100	U	G2099	C2021	A1946	U1885	A1818	A1744	A1656	U	G1522	U1449
G2306	U2101	G	U2103	U2022	C1947	A1886	U1819	G1747	G1657	U	G1523	U1451
C2307	U2102	A	G2103	C2023	C1948	G1887	G1821	U1750	U1588	C	U1524	G1452
C2308	G2107	C	A2104	A2024	G1949	U1888	U1822	U1751	U1589	U	G	U1454
G2309	G2107	U	U2108	G2036	U1950	U1889	C1823	U1752	C1593	U	A	A1459
U2311	U2108	A	G2110	G2037	C1951	G1890	U1824	U1753	U1594	U	U	U1460
A2313	A2109	G	C2110	U2038	C1952	U1891	G1825	C1754	C1595	U	U	C1461
A2314	C2109	C	G2111	G2039	U1953	U1892	U1826	U1755	G1596	U	U	G1462
A2315	U2118	U	U2118	U2040	G1957	U1893	C1827	U1756	U1597	U	U	A1463
G2316	U2119	A	A2041	A2042	U1958	G1894	U1829	U1757	G1677	U	U	U1464
G2317	G2120	C	G2042	G2042	G1959	U1895	A1830	U1758	U1680	U	U	G1465
U2318	U2240	U	U2121	A2043	G1960	C1898	A1836	G1761	U1681	U	U	A1469
U2319	A2121	G	A2121	A2044	U1963	U1899	A1837	U1762	U1682	U	U	G1470
C2320	A2122	U	A2122	G2047	A1964	G1901	G1838	U1763	U1683	U	U	
C2321	U2242	G	A2123	G2048	A1965	U1902	U1841	A1764	U1684	U	U	
U2322	U2243	G	U2124	A2050	A1966	G1903	G1842	A1765	U1685	U	U	
C2323	U2244	A	U2125	A2051	U1967	G1904	A1842			U	U	
U2324	G2250	G	C		C1968	G1905				U	U	
A2361	G2218	U	G2218	G2218	U1938	G1877	U1806	U1732	C1648	U	U	
A2362	C2219	U	C2219	A2008	A1939	U1878	A1807	A1733	G1649	U	U	
A2363	G2220	C	U2018	U2009	A1940	U1879	C1807	A1734	G1650	U	U	
G2367	U2220	A	U2019	C1941	U1942	A1880	A1810	C1735	G1651	U	U	
C2368	U2221	G	G2018	A1943	U1943	A1881	A1811	G1740	A1652	U	U	
C2369	U2222	C	U2019	U1944	U1944	G1882	A1812	G1741	A1653	U	U	
U2370	C2223	U	U2020	U1945	A1945	A1883	U1813	A1742	A1654	U	U	
U2371	A2225	A	C2021	C1946	A1946	G1884	A1816	U1743	U1655	U	U	
A2305	U2224	C	U2022	C1947	C1947	U1885	C1817	A1744	A1656	U	U	
G2306	G2224	G	U2103	C1948	G1948	G1887	A1818	G1747	G1657	U	U	
G2307	C2225	U	G2104	U1949	U1949	U1888	U1821	U1750	U1588	U	U	
C2308	A2226	C	A2105	C1950	U1950	U1889	C1822	U1751	U1589	U	U	
G2309	G2226	A	C2106	C1951	C1951	G1890	U1823	U1752	C1593	U	U	
C2310	C2227	U	G2107	U1952	U1952	U1891	G1824	U1753	U1594	U	U	
U2311	C2228	U	U2108	U1953	U1953	U1892	U1825	U1754	C1595	U	U	
A2312	A2229	G	A2109	A1954	A1954	G1893	G1826	U1755	G1596	U	U	
A2313	G2230	C	C2110	A1955	A1955	G1894	U1827	U1756	U1597	U	U	
A2314	U2231	U	U2118	G1956	G1956	U1895	C1827	U1757	G1677	U	U	
A2315	C2232	U	A2041	U1957	U1957	U1896	U1828	U1758	U1680	U	U	
G2316	A2233	A	G2042	U1958	U1958	U1897	A1830	U1759	U1681	U	U	
G2317	U2234	C	U2043	G1959	G1959	C1898	A1836	G1761	U1682	U	U	
U2318	C2241	U	A2121	U1960	U1960	U1899	A1837	U1762	U1683	U	U	
A2385	U2242	G	A2122	A1963	A1963	G1901	G1838	U1763	U1684	U	U	
C2386	U2243	G	U2123	A1964	A1964	U1902	U1841	A1764	U1685	U	U	
G2387	G2244	A	U2124	A1965	A1965	G1903	G1842	A1765	U1686	U	U	
G2388	U2245	G	U2125	A2050	A2050	U1904	A1842		U1687	U	U	
G2389	G2246	G	C	A2051	C1968	G1905			U1688	U	U	
U2390	A2250	U							U1689	U	U	
U2391	G2251	G							U1690	U	U	



• Molecule 27: 5S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	49223	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.229	Depositor
Minimum map value	-0.118	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	385.83997, 385.83997, 385.83997	wwPDB
Map dimensions	364, 364, 364	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: G6V

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	0.37	0/927	0.53	0/1239
2	B	0.40	0/2129	0.53	0/2858
3	C	0.45	0/955	0.64	0/1265
4	D	0.36	0/795	0.55	0/1062
5	E	0.36	0/861	0.51	0/1159
6	F	0.37	0/719	0.70	1/959 (0.1%)
7	G	0.29	0/737	0.46	0/983
8	H	0.27	0/735	0.51	0/986
9	I	0.41	0/598	0.53	0/794
10	J	0.42	0/469	0.54	0/625
11	K	0.38	0/473	0.59	0/631
12	L	0.41	0/1652	0.58	0/2216
13	M	0.48	1/434 (0.2%)	0.83	5/585 (0.9%)
14	N	0.40	0/404	0.59	0/537
15	O	0.33	0/385	0.58	0/513
16	P	0.48	0/376	0.57	0/491
17	Q	0.44	0/526	0.52	0/690
18	R	0.34	0/299	0.56	0/393
19	S	0.37	0/1336	0.52	0/1799
20	V	0.40	0/1160	0.49	0/1563
21	W	0.35	0/855	0.46	0/1145
22	X	0.38	0/948	0.53	0/1262
23	Y	0.38	0/1113	0.52	0/1493
24	Z	0.37	0/905	0.53	0/1207
25	a	0.29	0/589	0.50	0/785
26	1	0.43	0/63551	0.41	9/99100 (0.0%)
27	2	0.33	1/2475 (0.0%)	0.83	22/3854 (0.6%)
All	All	0.41	2/86406 (0.0%)	0.46	37/130194 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	M	20	ARG	C-O	-5.32	1.17	1.24
27	2	68	U	C1'-N1	5.07	1.56	1.48

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	1	1931	G	C1'-C2'-O2'	-15.14	85.68	108.40
27	2	20	A	C4'-C3'-O3'	9.26	126.89	113.00
27	2	81	A	C1'-C2'-O2'	-9.18	94.63	108.40
27	2	80	G	C1'-C2'-O2'	-8.80	95.20	108.40
27	2	19	G	C1'-C2'-O2'	-8.77	95.24	108.40
27	2	82	A	C1'-C2'-O2'	-8.59	95.51	108.40
26	1	1954	A	C1'-C2'-O2'	-7.93	96.50	108.40
27	2	90	U	C1'-C2'-O2'	-7.88	96.58	108.40
27	2	20	A	C1'-C2'-O2'	-7.74	96.79	108.40
27	2	80	G	C4'-C3'-O3'	7.62	124.44	113.00
26	1	1868	U	C4'-C3'-O3'	7.24	123.86	113.00
27	2	20	A	N9-C1'-C2'	-7.13	101.30	112.00
27	2	90	U	C4'-C3'-O3'	7.00	123.51	113.00
26	1	1929	C	C4'-C3'-O3'	6.91	123.37	113.00
27	2	61	C	C4'-C3'-O3'	6.74	123.11	113.00
26	1	1955	A	C4'-C3'-O3'	6.67	123.00	113.00
27	2	79	C	C1'-C2'-O2'	-6.64	98.43	108.40
26	1	1931	G	C4'-C3'-O3'	6.42	122.64	113.00
27	2	60	C	C1'-C2'-O2'	-6.22	99.07	108.40
13	M	20	ARG	CA-C-N	6.15	128.43	120.44
13	M	20	ARG	C-N-CA	6.15	128.43	120.44
27	2	82	A	C3'-C2'-O2'	6.00	119.70	110.70
27	2	61	C	C2'-C3'-O3'	-5.78	105.03	113.70
6	F	28	ASP	N-CA-C	-5.71	100.68	109.76
13	M	18	THR	N-CA-C	-5.60	105.26	111.36
27	2	79	C	C4'-C3'-O3'	5.54	121.32	113.00
27	2	19	G	C4'-C3'-O3'	5.52	121.28	113.00
26	1	1955	A	N9-C1'-C2'	-5.48	103.77	112.00
27	2	91	C	C1'-C2'-O2'	-5.32	100.42	108.40
13	M	52	HIS	N-CA-C	5.27	117.11	111.36
27	2	61	C	C3'-C2'-O2'	5.22	118.53	110.70
13	M	51	LYS	N-CA-C	-5.20	106.62	113.12
27	2	19	G	C2'-C3'-O3'	-5.16	105.96	113.70
26	1	1927	A	C4'-C3'-O3'	-5.15	101.68	109.40
27	2	60	C	C4'-C3'-O3'	5.13	120.69	113.00
27	2	82	A	N9-C1'-C2'	-5.12	104.32	112.00
26	1	1863	C	C4'-C3'-O3'	5.10	120.65	113.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	915	0	987	55	0
2	B	2094	0	2205	99	0
3	C	943	0	1014	46	0
4	D	785	0	825	39	0
5	E	853	0	914	36	0
6	F	711	0	750	39	0
7	G	730	0	781	56	0
8	H	727	0	777	42	0
9	I	592	0	602	25	0
10	J	463	0	501	13	0
11	K	472	0	493	23	0
12	L	1628	0	1667	99	0
13	M	432	0	472	15	0
14	N	397	0	407	16	0
15	O	382	0	382	22	0
16	P	372	0	420	18	0
17	Q	521	0	586	32	0
18	R	296	0	340	13	0
19	S	1318	0	1377	67	0
20	V	1138	0	1130	43	0
21	W	850	0	895	46	0
22	X	938	0	977	40	0
23	Y	1089	0	1155	43	0
24	Z	902	0	958	42	0
25	a	583	0	598	29	0
26	1	56747	0	28540	1278	0
27	2	2214	0	1120	56	0
28	1	26	18	0	1	0
All	All	79118	18	50873	2107	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

All (2107) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:3:GLN:N	21:W:6:THR:HG1	1.37	1.20
26:1:1489:A:N6	26:1:1509:G:H21	1.45	1.15
26:1:1489:A:H62	26:1:1509:G:N2	1.44	1.14
26:1:275:A:H62	26:1:296:G:N2	1.52	1.06
24:Z:31:GLU:HG2	24:Z:118:ILE:HG12	1.45	0.99
19:S:155:VAL:HB	19:S:194:ILE:HG22	1.46	0.97
2:B:117:GLU:HB3	2:B:130:LEU:HB3	1.48	0.94
26:1:275:A:H62	26:1:296:G:H21	1.08	0.92
12:L:54:GLU:HB2	12:L:86:ARG:HB2	1.51	0.91
21:W:35:ILE:HD12	21:W:69:VAL:HG13	1.52	0.90
13:M:12:VAL:HG11	13:M:23:VAL:HG11	1.53	0.89
26:1:275:A:N6	26:1:296:G:H21	1.71	0.89
2:B:174:ILE:HG13	2:B:184:ILE:HD12	1.56	0.88
3:C:94:MET:HE1	20:V:3:GLN:HE21	1.39	0.86
8:H:18:LEU:HD23	8:H:21:LEU:HD12	1.56	0.86
12:L:38:LYS:HE2	12:L:100:GLU:HG3	1.56	0.85
3:C:4:VAL:HG22	26:1:1238:U:H1'	1.57	0.85
26:1:698:U:H2'	26:1:699:U:H5'	1.59	0.85
8:H:16:SER:HB3	27:2:89:U:H5'	1.57	0.84
26:1:231:A:H2'	26:1:232:U:H5''	1.60	0.84
7:G:41:MET:HG2	7:G:61:ALA:HB2	1.59	0.83
2:B:92:ALA:HB2	2:B:106:ALA:HB2	1.61	0.83
7:G:42:LYS:HG2	7:G:58:GLU:HG2	1.60	0.83
20:V:60:ALA:HB1	20:V:102:ILE:HD13	1.57	0.82
1:A:11:THR:HG21	12:L:13:THR:HG21	1.61	0.82
2:B:240:PRO:HB2	26:1:1930:G:OP1	1.78	0.82
26:1:905:U:H1'	26:1:2295:A:H5'	1.61	0.82
2:B:95:VAL:HG12	2:B:101:LYS:HD3	1.61	0.82
20:V:22:GLU:HG3	20:V:59:ASN:HB3	1.61	0.82
19:S:125:VAL:HG22	19:S:194:ILE:HD11	1.62	0.81
7:G:74:LYS:HG3	7:G:75:THR:HG23	1.62	0.81
12:L:215:ILE:HD12	12:L:216:LYS:HG3	1.62	0.81
8:H:6:SER:HB3	8:H:63:LEU:HD11	1.63	0.80
26:1:1521:A:H61	26:1:1559:G:H1	1.28	0.80
26:1:2340:C:H2'	26:1:2341:A:H8	1.46	0.80
23:Y:78:PRO:HG2	23:Y:81:VAL:HG11	1.62	0.80
2:B:117:GLU:HG3	2:B:122:ALA:H	1.46	0.80
20:V:7:ALA:H	20:V:46:THR:HG21	1.47	0.80
4:D:60:ALA:HB2	4:D:97:ILE:HD13	1.62	0.79
21:W:63:VAL:HG13	21:W:102:VAL:HG23	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:129:GLY:HA2	12:L:170:PRO:HB3	1.64	0.79
26:1:721:A:H8	26:1:2096:G:H21	1.28	0.79
26:1:1943:A:H5''	26:1:1944:U:H5	1.48	0.79
6:F:58:TYR:OH	26:1:1377:U:OP2	2.00	0.79
19:S:67:GLN:HE21	19:S:74:ARG:HD2	1.47	0.79
2:B:135:ILE:HD13	2:B:141:VAL:HG11	1.64	0.79
26:1:162:A:H8	26:1:2244:G:H21	1.30	0.79
5:E:6:VAL:HG22	5:E:104:THR:HG23	1.65	0.78
6:F:13:THR:H	6:F:17:SER:HB3	1.49	0.78
26:1:1063:U:OP1	26:1:1079:U:O2'	2.00	0.78
26:1:1451:U:H2'	26:1:1452:C:H4'	1.65	0.78
26:1:1523:G:H1	26:1:1557:C:H42	1.28	0.78
26:1:1070:A:OP2	26:1:1178:C:O2'	2.02	0.78
26:1:1320:G:N2	26:1:1323:A:OP2	2.15	0.78
26:1:1572:G:H22	26:1:1593:G:H1	1.30	0.78
2:B:176:LEU:HD12	2:B:180:GLU:HG2	1.65	0.78
12:L:3:LYS:HB2	12:L:109:THR:HG21	1.65	0.77
22:X:29:LYS:HD3	22:X:30:THR:HG23	1.67	0.77
24:Z:24:LEU:HD23	24:Z:44:VAL:HG21	1.67	0.77
26:1:1501:G:N2	26:1:2730:C:O2	2.16	0.77
26:1:2649:U:O2'	26:1:2845:G:N2	2.18	0.77
8:H:31:VAL:HB	8:H:39:VAL:HG22	1.65	0.77
4:D:14:VAL:HG21	4:D:97:ILE:HG13	1.67	0.76
27:2:45:C:H2'	27:2:46:A:H5'	1.68	0.76
19:S:194:ILE:HD13	19:S:199:ALA:HB2	1.66	0.76
26:1:2060:A:O2'	26:1:2062:G:OP2	2.03	0.76
19:S:110:LEU:HD23	19:S:206:LEU:HD11	1.67	0.76
25:a:96:ARG:NH1	25:a:99:TYR:O	2.19	0.76
26:1:1806:U:OP2	26:1:1811:A:N6	2.17	0.76
4:D:64:LYS:HB3	4:D:94:LYS:HG2	1.68	0.76
8:H:9:ARG:HE	8:H:40:SER:HB3	1.51	0.76
24:Z:112:ASP:OD1	26:1:1693:G:O2'	2.04	0.76
23:Y:36:ALA:HB2	23:Y:103:LEU:HD21	1.67	0.76
7:G:5:LYS:NZ	7:G:24:ILE:O	2.19	0.75
12:L:86:ARG:NH1	26:1:2850:G:OP2	2.19	0.75
2:B:69:ARG:HD3	2:B:104:ILE:HD12	1.68	0.75
15:O:2:ARG:NH1	26:1:2312:C:OP2	2.19	0.75
7:G:84:LYS:HB3	7:G:86:VAL:HG13	1.67	0.75
26:1:514:G:H2'	26:1:515:G:H5'	1.67	0.75
22:X:79:LEU:HD23	22:X:82:LEU:HD12	1.66	0.75
12:L:67:LYS:HB2	26:1:2850:G:H5'	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:107:ARG:HG3	19:S:206:LEU:HD22	1.68	0.75
4:D:61:THR:OG1	4:D:98:ASP:OD2	2.04	0.75
26:1:167:U:H2'	26:1:168:A:H5''	1.69	0.75
27:2:54:U:H4'	27:2:55:A:H5'	1.68	0.75
3:C:37:GLN:HE22	26:1:606:G:H21	1.33	0.75
26:1:410:G:H2'	26:1:411:A:H2	1.52	0.74
1:A:51:LYS:NZ	26:1:2712:G:OP2	2.21	0.74
4:D:27:VAL:HG21	4:D:62:VAL:HG21	1.69	0.74
26:1:656:G:O2'	26:1:659:A:N6	2.21	0.74
26:1:522:G:N1	26:1:525:A:OP2	2.21	0.74
26:1:1628:A:H3'	26:1:1629:U:H5''	1.68	0.74
21:W:71:ARG:HH12	21:W:104:ARG:HG3	1.52	0.74
12:L:184:GLU:HB2	12:L:198:LYS:HD2	1.70	0.74
24:Z:13:ARG:NH2	26:1:2717:A:OP2	2.21	0.74
6:F:64:ARG:HG3	6:F:69:GLN:HA	1.70	0.73
26:1:1219:G:O2'	26:1:1220:A:O4'	2.06	0.73
26:1:1453:G:H4'	26:1:1459:A:H1'	1.70	0.73
26:1:1423:C:O2'	26:1:1512:U:O2	2.03	0.73
26:1:2083:G:H1	26:1:2639:C:H5	1.37	0.73
3:C:37:GLN:HE21	26:1:1290:G:H1	1.33	0.73
13:M:15:ARG:HD2	13:M:53:LEU:HD21	1.70	0.73
19:S:157:GLU:HG3	19:S:158:ASN:H	1.53	0.73
21:W:3:GLN:N	21:W:6:THR:OG1	2.17	0.73
26:1:273:A:H62	26:1:298:U:H3	1.37	0.73
26:1:629:A:H62	26:1:1289:A:H2	1.34	0.73
26:1:1337:A:H4'	26:1:1338:U:H5''	1.71	0.73
2:B:274:ARG:NH2	26:1:1826:G:OP2	2.22	0.73
7:G:45:GLN:NE2	7:G:57:LEU:HB2	2.04	0.72
12:L:55:ASP:OD1	12:L:85:LYS:NZ	2.20	0.72
26:1:2497:G:O6	26:1:2503:A:O2'	2.07	0.72
5:E:88:ARG:NH2	26:1:793:G:OP2	2.22	0.72
26:1:2085:A:O2'	26:1:2086:A:O4'	2.07	0.72
7:G:16:ASP:HB2	7:G:38:VAL:HG13	1.69	0.72
26:1:328:G:H1	26:1:399:U:H3	1.37	0.72
26:1:1505:G:HO2'	26:1:2729:G:HO2'	1.34	0.72
16:P:38:LYS:HZ3	26:1:515:G:H1	1.35	0.72
22:X:38:GLN:HG3	26:1:850:G:H5'	1.72	0.72
24:Z:45:GLU:HG3	24:Z:100:TYR:HD2	1.55	0.72
25:a:106:LYS:NZ	25:a:110:GLU:OE1	2.22	0.72
27:2:97:G:H2'	27:2:98:A:C8	2.25	0.72
2:B:274:ARG:NH1	26:1:1825:U:OP2	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:53:ARG:NH2	26:1:1038:C:OP1	2.22	0.71
3:C:86:ALA:HB2	3:C:116:ALA:HB2	1.70	0.71
7:G:57:LEU:HD11	7:G:59:THR:HG23	1.71	0.71
8:H:62:GLU:HB3	8:H:69:THR:HB	1.72	0.71
23:Y:56:ARG:NH2	26:1:2496:A:O2'	2.22	0.71
26:1:2559:G:N2	26:1:2690:G:O2'	2.23	0.71
4:D:2:PHE:HB3	4:D:15:GLU:HG2	1.71	0.71
12:L:59:TYR:N	12:L:74:GLU:OE2	2.23	0.71
26:1:963:A:H62	26:1:2295:A:H2	1.37	0.71
26:1:902:A:C2'	26:1:903:G:H5'	2.20	0.71
3:C:49:ASP:OD2	26:1:579:U:O2'	2.05	0.71
23:Y:35:GLN:HE21	23:Y:100:GLY:HA2	1.55	0.71
2:B:171:TYR:HB3	2:B:183:MET:HB3	1.71	0.71
23:Y:80:GLU:OE2	26:1:2520:U:O2'	2.06	0.71
21:W:18:GLU:OE1	21:W:45:ASN:ND2	2.23	0.71
26:1:268:A:N6	26:1:473:U:O2'	2.24	0.71
5:E:24:ILE:HD13	5:E:36:LEU:HD11	1.72	0.71
14:N:16:ARG:NH2	26:1:1302:G:OP1	2.20	0.71
27:2:82:A:H61	27:2:87:C:H42	1.39	0.71
26:1:105:C:HO2'	26:1:337:A:HO2'	1.38	0.70
26:1:721:A:HO2'	26:1:2469:C:HO2'	1.35	0.70
8:H:48:PHE:HA	8:H:51:VAL:HG12	1.73	0.70
26:1:1914:C:H2'	26:1:1915:G:H5'	1.74	0.70
26:1:2318:U:H2'	26:1:2319:U:C6	2.27	0.70
8:H:7:ILE:HG23	8:H:42:LYS:HB2	1.72	0.70
21:W:71:ARG:HD2	21:W:75:SER:HB2	1.72	0.70
26:1:1220:A:H2'	26:1:1221:C:C6	2.26	0.70
26:1:1489:A:H62	26:1:1509:G:H21	0.74	0.70
12:L:108:ASP:OD1	12:L:190:THR:OG1	2.07	0.70
2:B:245:SER:OG	26:1:1869:G:O2'	2.10	0.70
12:L:25:VAL:HG21	12:L:196:LEU:HB3	1.72	0.70
26:1:1218:G:H2'	26:1:1219:G:O4'	1.92	0.70
26:1:409:G:H2'	26:1:410:G:H1'	1.72	0.69
26:1:405:G:H3'	26:1:406:A:H5''	1.74	0.69
26:1:2388:A:H2'	26:1:2389:G:H5'	1.74	0.69
1:A:35:ILE:HG22	1:A:40:GLU:HG2	1.72	0.69
26:1:2355:A:H2'	26:1:2356:A:C8	2.28	0.69
3:C:13:ARG:NH1	26:1:1290:G:OP2	2.20	0.69
13:M:40:ASN:OD1	26:1:973:A:O2'	2.08	0.69
21:W:28:SER:OG	26:1:2590:U:O2'	2.11	0.69
26:1:1628:A:H3'	26:1:1629:U:C5'	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1934:G:C2'	26:1:1935:C:H5'	2.22	0.69
26:1:2084:G:C2'	26:1:2085:A:H5'	2.22	0.69
27:2:13:A:O2'	27:2:14:G:O5'	2.09	0.69
21:W:61:VAL:HG13	21:W:87:ILE:HG13	1.73	0.69
26:1:697:U:O2'	26:1:699:U:O4	2.10	0.69
26:1:116:G:OP2	26:1:118:A:O2'	2.08	0.69
26:1:2740:A:O2'	26:1:2742:C:OP2	2.09	0.69
12:L:128:GLN:HE21	12:L:132:LYS:HG2	1.56	0.69
17:Q:14:VAL:HG21	17:Q:22:LEU:HB3	1.75	0.69
17:Q:58:VAL:HG13	17:Q:61:LEU:HD12	1.75	0.69
26:1:176:A:O2'	26:1:177:G:OP1	2.11	0.69
26:1:1452:C:H6	26:1:1453:G:H5''	1.58	0.69
4:D:14:VAL:CG2	4:D:97:ILE:HG13	2.22	0.69
17:Q:54:ASP:OD1	17:Q:57:ARG:NH1	2.26	0.69
26:1:889:U:H2'	26:1:890:G:O4'	1.93	0.69
22:X:47:ARG:NH1	26:1:199:A:OP2	2.26	0.69
26:1:688:A:N1	26:1:2396:A:O2'	2.24	0.68
26:1:1214:C:H1'	26:1:1217:U:C4	2.28	0.68
26:1:1772:G:H2'	26:1:1773:A:H5'	1.75	0.68
7:G:78:PRO:O	7:G:96:LYS:NZ	2.26	0.68
24:Z:41:ARG:HH12	26:1:2858:G:H1'	1.58	0.68
26:1:1207:G:C2'	26:1:1208:A:H5'	2.23	0.68
26:1:1945:A:O2'	26:1:1947:C:N4	2.26	0.68
10:J:2:GLY:N	26:1:1403:C:OP1	2.26	0.68
2:B:132:LEU:HB3	2:B:172:VAL:HG21	1.76	0.68
26:1:637:U:H2'	26:1:638:U:C6	2.29	0.68
7:G:15:LYS:NZ	26:1:546:A:OP1	2.26	0.68
26:1:92:G:H2'	26:1:93:U:C6	2.29	0.68
1:A:25:GLY:HA3	1:A:94:VAL:HG11	1.76	0.68
26:1:2125:U:O2	26:1:2218:G:O6	2.11	0.68
26:1:2608:G:N2	26:1:2608:G:OP2	2.26	0.68
17:Q:58:VAL:HG13	17:Q:61:LEU:HB2	1.77	0.67
19:S:67:GLN:HG3	19:S:74:ARG:HB2	1.76	0.67
26:1:1482:U:H3	26:1:1600:A:H2	1.41	0.67
26:1:2109:A:H2'	26:1:2110:G:O4'	1.94	0.67
5:E:89:ALA:HB2	26:1:793:G:H5'	1.75	0.67
26:1:350:G:H8	26:1:373:A:H61	1.40	0.67
26:1:1757:U:H2'	26:1:1758:A:H5''	1.74	0.67
26:1:1943:A:H5''	26:1:1944:U:C5	2.28	0.67
5:E:9:THR:OG1	26:1:553:A:N6	2.28	0.67
26:1:78:U:H2'	26:1:79:U:C6	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:3:VAL:HG12	26:1:2042:A:C2	2.29	0.66
17:Q:22:LEU:HB2	17:Q:50:VAL:HG22	1.77	0.66
17:Q:31:HIS:CD2	17:Q:32:LEU:HG	2.30	0.66
26:1:1313:G:OP2	26:1:1689:G:O2'	2.05	0.66
26:1:1985:C:C2'	26:1:1986:G:H5'	2.25	0.66
12:L:2:THR:HG22	12:L:94:VAL:HG12	1.76	0.66
26:1:1353:A:H2'	26:1:1354:G:H8	1.60	0.66
4:D:78:ARG:NH2	26:1:606:G:OP2	2.27	0.66
12:L:87:PHE:CD1	12:L:208:LEU:HD22	2.30	0.66
6:F:18:GLU:HA	6:F:21:ALA:HB2	1.78	0.66
12:L:98:ALA:HB1	12:L:103:GLN:HE22	1.61	0.66
26:1:505:U:H2'	26:1:506:A:H5''	1.76	0.66
2:B:59:LYS:HB2	26:1:1615:G:H4'	1.77	0.66
2:B:108:LYS:HE3	2:B:198:LEU:HD11	1.77	0.66
16:P:2:VAL:N	26:1:1663:G:HO2'	1.93	0.66
26:1:328:G:N2	26:1:399:U:O2	2.23	0.66
2:B:29:PRO:HB2	2:B:34:LEU:HD11	1.78	0.66
2:B:35:LYS:HE2	2:B:64:VAL:HG22	1.76	0.66
8:H:70:ILE:HG13	8:H:72:VAL:HG13	1.77	0.66
23:Y:30:GLY:O	23:Y:134:ARG:NH2	2.29	0.66
26:1:909:G:H2'	26:1:910:C:C6	2.30	0.66
13:M:52:HIS:CD2	13:M:52:HIS:H	2.14	0.66
26:1:1878:U:O2	26:1:1918:G:O6	2.13	0.66
23:Y:1:MET:HB3	23:Y:48:GLU:HG3	1.77	0.66
3:C:80:MET:HE2	3:C:92:ARG:HE	1.61	0.66
7:G:39:ASN:HB3	7:G:61:ALA:HB3	1.78	0.65
26:1:2650:G:O5'	26:1:2845:G:N2	2.29	0.65
27:2:29:C:O2'	27:2:51:A:N6	2.29	0.65
17:Q:14:VAL:CG2	17:Q:22:LEU:HB3	2.26	0.65
3:C:92:ARG:NH2	26:1:1197:C:OP1	2.28	0.65
7:G:11:VAL:HA	7:G:68:VAL:HG12	1.77	0.65
7:G:42:LYS:HA	7:G:57:LEU:O	1.96	0.65
12:L:157:ALA:HB2	26:1:2602:C:H5'	1.78	0.65
17:Q:15:LYS:NZ	26:1:676:A:OP2	2.20	0.65
26:1:44:A:H2	26:1:481:C:H41	1.44	0.65
26:1:1969:C:OP2	26:1:1970:U:O2'	2.10	0.65
27:2:96:A:H2'	27:2:97:G:H5'	1.78	0.65
26:1:100:U:H3'	26:1:101:G:H5'	1.78	0.65
26:1:1596:G:O2'	26:1:1767:G:N2	2.28	0.65
1:A:33:ARG:NH2	1:A:81:PRO:O	2.28	0.65
16:P:12:LYS:O	16:P:16:VAL:HG12	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:38:VAL:HG13	4:D:53:VAL:HG12	1.78	0.65
26:1:898:U:H2'	26:1:899:U:C6	2.31	0.65
26:1:1447:A:H2'	26:1:1448:U:H5''	1.78	0.65
26:1:1449:A:H8	26:1:1634:A:H62	1.45	0.65
1:A:34:ILE:O	1:A:40:GLU:HA	1.97	0.65
26:1:1460:U:H2'	26:1:1461:C:H5'	1.78	0.65
27:2:13:A:OP2	27:2:67:G:N2	2.30	0.65
26:1:2581:U:H2'	26:1:2582:U:C6	2.32	0.65
2:B:171:TYR:HB2	2:B:183:MET:HE2	1.80	0.64
3:C:44:GLN:OE1	4:D:75:THR:OG1	2.10	0.64
26:1:908:A:O2'	27:2:95:U:O2	2.09	0.64
26:1:1522:G:H1	26:1:1558:U:H3	1.45	0.64
26:1:1766:C:H2'	26:1:1767:G:H5'	1.79	0.64
26:1:1651:C:N4	26:1:1666:A:OP2	2.25	0.64
26:1:29:U:H3	26:1:556:U:H5	1.46	0.64
26:1:158:G:H2'	26:1:159:U:O4'	1.97	0.64
26:1:514:G:C2'	26:1:515:G:H5'	2.27	0.64
8:H:37:LYS:HB3	8:H:39:VAL:HG13	1.80	0.64
26:1:1053:A:N3	26:1:1197:C:O2'	2.30	0.64
26:1:1449:A:H2'	26:1:1634:A:N6	2.13	0.64
26:1:2687:A:H2'	26:1:2688:G:O4'	1.97	0.64
12:L:123:LYS:NZ	26:1:2708:C:OP2	2.30	0.64
26:1:397:U:H2'	26:1:398:C:C6	2.32	0.64
26:1:666:A:H2'	26:1:667:G:H5'	1.78	0.64
26:1:1942:U:H3'	26:1:1943:A:C2	2.32	0.64
26:1:2388:A:C2'	26:1:2389:G:H5'	2.28	0.64
25:a:44:ILE:HG12	25:a:54:ALA:HB3	1.79	0.64
19:S:182:ASN:ND2	19:S:185:ASP:OD2	2.25	0.64
26:1:1353:A:H2'	26:1:1354:G:C8	2.32	0.64
27:2:96:A:C2'	27:2:97:G:H5'	2.28	0.64
26:1:140:A:H2'	26:1:141:U:H6	1.60	0.64
26:1:414:C:C2'	26:1:415:U:H5'	2.28	0.64
27:2:71:A:H62	27:2:98:A:H2	1.44	0.64
7:G:11:VAL:HG22	7:G:68:VAL:HG12	1.79	0.63
12:L:46:TYR:OH	26:1:2663:U:O2'	2.15	0.63
21:W:91:LYS:HD2	21:W:111:PHE:CE1	2.32	0.63
26:1:142:G:C2'	26:1:143:U:H5'	2.28	0.63
26:1:159:U:H2'	26:1:160:G:H5''	1.78	0.63
26:1:410:G:H2'	26:1:411:A:C2	2.32	0.63
26:1:736:C:O2'	26:1:737:C:H5'	1.97	0.63
26:1:877:G:H2'	26:1:878:C:C6	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1823:U:H2'	26:1:1824:C:C6	2.32	0.63
27:2:31:G:H2'	27:2:32:U:C6	2.34	0.63
22:X:92:THR:HG22	22:X:94:ALA:H	1.63	0.63
26:1:142:G:H2'	26:1:143:U:H5'	1.79	0.63
26:1:395:U:H2'	26:1:396:G:H5'	1.79	0.63
26:1:1780:G:N2	26:1:1783:G:OP2	2.28	0.63
26:1:1979:A:N3	26:1:2587:C:O2'	2.32	0.63
2:B:150:LYS:HD3	26:1:2231:C:H4'	1.78	0.63
12:L:90:GLU:OE1	26:1:2663:U:H4'	1.99	0.63
26:1:156:A:H2'	26:1:157:U:O4'	1.98	0.63
26:1:409:G:H2'	26:1:410:G:C1'	2.28	0.63
6:F:64:ARG:CG	6:F:69:GLN:HA	2.29	0.63
17:Q:57:ARG:HD3	26:1:878:C:O2'	1.99	0.63
20:V:22:GLU:HG3	20:V:59:ASN:CB	2.29	0.63
26:1:1356:G:O2'	26:1:1357:G:H5'	1.98	0.63
26:1:2784:A:H2'	26:1:2785:A:H5'	1.80	0.63
1:A:34:ILE:HG22	1:A:36:GLU:H	1.63	0.63
26:1:2794:C:C2'	26:1:2795:C:H5'	2.29	0.63
26:1:1520:A:H2'	26:1:1521:A:O4'	1.98	0.63
11:K:48:LYS:HE3	26:1:75:G:O2'	1.98	0.63
11:K:58:ARG:NH2	26:1:111:U:OP1	2.27	0.63
12:L:31:LYS:HG3	12:L:32:GLU:OE1	1.99	0.63
26:1:2277:G:O2'	26:1:2523:C:OP1	2.14	0.63
26:1:2288:C:C2'	26:1:2289:U:H5'	2.29	0.63
6:F:11:VAL:O	6:F:17:SER:OG	2.16	0.63
12:L:3:LYS:HZ1	12:L:98:ALA:HB2	1.64	0.63
12:L:13:THR:HG22	12:L:14:GLN:H	1.62	0.62
26:1:2229:C:O2'	26:1:2231:C:OP1	2.11	0.62
27:2:15:C:H2'	27:2:16:A:O4'	1.97	0.62
24:Z:92:ARG:HG3	24:Z:93:TYR:CD1	2.34	0.62
26:1:2817:A:O2'	26:1:2818:A:H5''	1.98	0.62
22:X:41:ARG:NH2	26:1:852:U:OP2	2.32	0.62
26:1:1217:U:H1'	26:1:1218:G:N2	2.15	0.62
15:O:9:CYS:SG	15:O:10:THR:N	2.71	0.62
26:1:89:U:H3'	26:1:90:A:H3'	1.81	0.62
26:1:231:A:C2'	26:1:232:U:H5''	2.29	0.62
26:1:401:U:H2'	26:1:402:C:H5'	1.81	0.62
26:1:1800:A:H2'	26:1:1801:C:H5'	1.82	0.62
6:F:10:PRO:HD3	11:K:30:PHE:CD1	2.34	0.62
26:1:2052:C:H2'	26:1:2053:U:C6	2.35	0.62
7:G:79:THR:HG22	7:G:96:LYS:HD2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:55:LEU:HD12	22:X:56:PRO:HD2	1.80	0.62
26:1:215:G:H2'	26:1:216:A:O4'	2.00	0.62
26:1:645:A:O2'	26:1:700:A:N1	2.31	0.62
2:B:154:ILE:HG21	2:B:176:LEU:HD22	1.80	0.62
4:D:6:GLU:HB3	4:D:37:LYS:HB3	1.82	0.62
9:I:24:SER:OG	26:1:2289:U:OP2	2.08	0.62
12:L:32:GLU:HG2	12:L:55:ASP:OD2	1.99	0.62
12:L:38:LYS:HB3	12:L:100:GLU:HG2	1.82	0.62
26:1:1955:A:H2'	26:1:1955:A:N3	2.14	0.62
26:1:2583:C:H2'	26:1:2584:G:H5'	1.82	0.62
4:D:79:ARG:NH2	26:1:615:A:OP2	2.33	0.62
7:G:80:ARG:NH2	26:1:344:U:OP2	2.23	0.62
8:H:6:SER:HB3	8:H:63:LEU:CD1	2.29	0.62
19:S:137:LYS:NZ	26:1:362:C:OP2	2.33	0.62
26:1:140:A:H2'	26:1:141:U:C6	2.34	0.62
26:1:901:G:H2'	26:1:902:A:C8	2.34	0.62
26:1:1326:C:OP1	26:1:1691:G:N2	2.28	0.62
26:1:1449:A:H62	26:1:1632:A:H3'	1.64	0.62
12:L:118:VAL:HG22	12:L:211:ILE:HD12	1.81	0.62
15:O:7:LEU:HD21	15:O:32:MET:HG3	1.81	0.62
20:V:22:GLU:HG2	20:V:62:LYS:CB	2.29	0.62
20:V:109:MET:HE2	26:1:1182:G:N3	2.15	0.62
2:B:208:ALA:HB2	26:1:1817:C:O2'	2.00	0.61
12:L:189:ASP:HB3	12:L:194:VAL:HG22	1.82	0.61
26:1:1329:G:H2'	26:1:1330:U:C6	2.35	0.61
26:1:1637:A:H2'	26:1:1638:G:C8	2.36	0.61
26:1:2580:G:C8	26:1:2610:G:H1'	2.35	0.61
5:E:14:PRO:O	5:E:18:ARG:HG3	2.00	0.61
9:I:23:ASP:OD1	26:1:2290:C:N4	2.32	0.61
26:1:394:U:H2'	26:1:395:U:C6	2.36	0.61
26:1:884:U:H2'	26:1:885:C:C6	2.35	0.61
26:1:2326:G:H2'	26:1:2327:A:H8	1.65	0.61
26:1:2318:U:OP1	26:1:2407:A:O2'	2.18	0.61
12:L:138:ARG:HG2	26:1:2024:A:OP2	2.00	0.61
26:1:978:A:H2'	26:1:979:C:C6	2.36	0.61
26:1:1075:G:C2'	26:1:1076:A:H5'	2.30	0.61
26:1:2091:C:H2'	26:1:2092:C:C6	2.35	0.61
26:1:2347:A:H5''	26:1:2348:G:N7	2.15	0.61
18:R:1:MET:HB2	26:1:2553:G:O2'	2.01	0.61
22:X:22:GLY:O	22:X:28:GLY:HA3	2.00	0.61
26:1:787:U:H2'	26:1:788:A:C8	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1881:A:N6	26:1:1915:G:H1'	2.15	0.61
12:L:10:ILE:HD11	12:L:29:GLU:HG2	1.81	0.61
12:L:134:HIS:CD2	12:L:168:LYS:HD2	2.36	0.61
26:1:1453:G:C4'	26:1:1459:A:H1'	2.31	0.61
26:1:2875:U:C2'	26:1:2876:G:H5'	2.31	0.61
1:A:59:GLU:HG3	1:A:78:LEU:HD12	1.82	0.61
2:B:26:LYS:HB3	2:B:82:GLN:HG2	1.83	0.61
3:C:93:LYS:HE3	3:C:94:MET:HE2	1.81	0.61
26:1:414:C:H2'	26:1:415:U:H5'	1.82	0.61
26:1:83:G:H1	26:1:101:G:HO2'	1.47	0.61
26:1:1765:A:H2'	26:1:1766:C:C6	2.36	0.61
22:X:18:ARG:NH2	26:1:1288:G:N7	2.48	0.61
26:1:65:A:H1'	26:1:502:C:H41	1.66	0.61
26:1:2122:A:H2'	26:1:2123:A:C8	2.36	0.61
26:1:2221:U:H2'	26:1:2222:U:C6	2.36	0.61
12:L:53:PHE:CD2	12:L:54:GLU:HG2	2.35	0.60
26:1:1632:A:H4'	26:1:1633:A:C4	2.35	0.60
17:Q:22:LEU:HB2	17:Q:50:VAL:CG2	2.31	0.60
21:W:63:VAL:HG13	21:W:102:VAL:CG2	2.32	0.60
26:1:447:A:H2'	26:1:448:A:C8	2.35	0.60
26:1:1724:U:N3	26:1:1791:G:OP2	2.35	0.60
27:2:11:A:O2'	27:2:12:U:H3'	2.01	0.60
2:B:260:ARG:NH1	2:B:264:LYS:HD3	2.16	0.60
26:1:1756:U:H3	26:1:1773:A:H62	1.49	0.60
25:a:30:ARG:O	25:a:44:ILE:HA	2.01	0.60
26:1:975:U:O2'	26:1:976:U:H5'	2.01	0.60
26:1:1829:A:H2'	26:1:1830:A:C8	2.37	0.60
26:1:2875:U:H2'	26:1:2876:G:H5'	1.83	0.60
3:C:94:MET:O	3:C:98:ILE:HG12	2.02	0.60
4:D:53:VAL:O	4:D:54:GLU:HG2	2.02	0.60
6:F:64:ARG:HG3	6:F:68:TYR:O	2.01	0.60
26:1:1463:A:H2	26:1:1625:U:H3	1.49	0.60
26:1:2348:G:H5''	26:1:2349:A:OP2	2.01	0.60
5:E:36:LEU:O	5:E:44:SER:HB3	2.01	0.60
24:Z:4:ARG:HG2	24:Z:39:GLU:OE2	2.02	0.60
26:1:268:A:H2'	26:1:269:G:O4'	2.02	0.60
26:1:395:U:C2'	26:1:396:G:H5'	2.31	0.60
27:2:12:U:OP2	27:2:68:U:O2'	2.19	0.60
27:2:101:A:C2'	27:2:102:G:H5'	2.32	0.60
26:1:2698:A:H2'	26:1:2699:U:O4'	2.02	0.60
19:S:89:VAL:HG21	26:1:629:A:H5'	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:389:A:H2'	26:1:390:A:O4'	2.00	0.60
26:1:758:G:H1'	26:1:763:A:N6	2.16	0.60
26:1:1452:C:C6	26:1:1453:G:H5''	2.36	0.60
26:1:1920:C:H2'	26:1:1921:C:H5'	1.84	0.60
26:1:2084:G:H2'	26:1:2085:A:H5'	1.82	0.60
7:G:44:HIS:HB3	26:1:529:A:O4'	2.02	0.59
23:Y:17:THR:O	23:Y:39:THR:HG21	2.01	0.59
26:1:1220:A:H2'	26:1:1221:C:H6	1.66	0.59
26:1:1432:A:H4'	26:1:1434:U:C5	2.37	0.59
26:1:1510:U:H2'	26:1:1511:C:C6	2.37	0.59
27:2:62:U:H2'	27:2:63:U:C6	2.37	0.59
2:B:35:LYS:HE2	2:B:64:VAL:CG2	2.31	0.59
5:E:93:ALA:HB2	26:1:1658:A:N1	2.18	0.59
26:1:1514:A:O2'	26:1:1515:G:H5'	2.02	0.59
26:1:2419:A:H2	26:1:2451:C:H42	1.50	0.59
26:1:2808:A:H5''	26:1:2809:G:H5'	1.84	0.59
8:H:2:ALA:N	8:H:61:ILE:HG23	2.17	0.59
11:K:9:LEU:HB2	11:K:12:SER:HB3	1.84	0.59
27:2:27:A:H2'	27:2:28:C:C6	2.37	0.59
3:C:8:THR:OG1	26:1:1254:C:OP1	2.11	0.59
5:E:19:LEU:HD21	14:N:20:PHE:CE2	2.37	0.59
17:Q:40:GLN:NE2	26:1:2389:G:OP1	2.34	0.59
25:a:17:ARG:NH1	26:1:2362:A:O5'	2.36	0.59
7:G:54:GLY:HA2	26:1:529:A:O2'	2.02	0.59
21:W:96:THR:O	21:W:117:LEU:HD13	2.03	0.59
26:1:2672:G:H4'	26:1:2759:G:O2'	2.02	0.59
2:B:66:ASP:OD2	2:B:102:ARG:HD3	2.03	0.59
2:B:246:PRO:O	2:B:254:THR:HG22	2.03	0.59
7:G:10:LYS:HG3	7:G:19:LYS:O	2.03	0.59
15:O:32:MET:O	15:O:44:LEU:HA	2.03	0.59
16:P:10:LYS:NZ	26:1:1347:G:OP2	2.19	0.59
7:G:41:MET:CG	7:G:61:ALA:HB2	2.31	0.59
23:Y:54:MET:HE1	23:Y:104:PHE:CD1	2.37	0.59
26:1:2101:U:H2'	26:1:2102:U:C6	2.37	0.59
26:1:2122:A:H2'	26:1:2123:A:H8	1.68	0.59
23:Y:58:MET:SD	23:Y:109:VAL:HG21	2.43	0.59
26:1:1598:U:H2'	26:1:1599:G:O4'	2.03	0.59
4:D:64:LYS:HB3	4:D:94:LYS:CG	2.33	0.58
9:I:35:ASP:OD1	9:I:76:LYS:HA	2.02	0.58
26:1:309:U:O2'	26:1:310:C:H2'	2.03	0.58
26:1:2038:U:H2'	26:1:2039:G:O4'	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:16:MET:HG3	2:B:206:GLY:HA3	1.83	0.58
26:1:162:A:H2	26:1:166:A:H61	1.51	0.58
26:1:615:A:H61	26:1:2056:G:H8	1.48	0.58
19:S:115:SER:O	19:S:119:GLN:HG2	2.03	0.58
26:1:25:U:C2'	26:1:26:G:H5'	2.33	0.58
4:D:29:GLU:OE1	4:D:64:LYS:HA	2.03	0.58
23:Y:43:THR:H	23:Y:46:GLN:HE21	1.50	0.58
26:1:479:C:O2'	26:1:480:U:H5'	2.03	0.58
26:1:1906:C:H2'	26:1:1907:U:O4'	2.02	0.58
19:S:194:ILE:CD1	19:S:199:ALA:HB2	2.34	0.58
26:1:684:U:H2'	26:1:685:C:C6	2.39	0.58
26:1:1680:U:H2'	26:1:1681:U:C6	2.38	0.58
26:1:1816:A:H2'	26:1:1817:C:O4'	2.03	0.58
26:1:1821:U:H2'	26:1:1822:C:C6	2.38	0.58
26:1:2342:U:H2'	26:1:2343:U:C6	2.38	0.58
26:1:2852:U:H1'	26:1:2854:A:C5	2.39	0.58
7:G:3:ILE:HG23	7:G:23:VAL:HG21	1.85	0.58
26:1:2383:C:H2'	26:1:2384:U:O4'	2.02	0.58
5:E:39:THR:OG1	5:E:44:SER:OG	2.11	0.58
11:K:5:GLU:OE1	11:K:7:ARG:NH2	2.37	0.58
26:1:446:G:O2'	26:1:447:A:H5''	2.04	0.58
26:1:537:A:H2'	26:1:538:G:H5'	1.85	0.58
11:K:9:LEU:HD12	11:K:12:SER:HB2	1.85	0.58
12:L:189:ASP:HB3	12:L:194:VAL:CG2	2.34	0.58
26:1:1934:G:H2'	26:1:1935:C:H5'	1.86	0.58
2:B:117:GLU:CD	2:B:130:LEU:HD13	2.29	0.58
7:G:69:GLN:OE1	7:G:78:PRO:HB2	2.04	0.58
12:L:25:VAL:CG2	12:L:196:LEU:HB3	2.34	0.58
22:X:38:GLN:OE1	26:1:876:G:O2'	2.22	0.58
1:A:71:GLY:O	21:W:80:ASP:HB2	2.04	0.58
20:V:106:ILE:HD12	20:V:123:LEU:HD21	1.86	0.58
26:1:1636:U:H2'	26:1:1637:A:C8	2.39	0.58
26:1:1763:U:H2'	26:1:1765:A:OP2	2.03	0.58
1:A:46:GLU:OE2	1:A:89:LYS:NZ	2.19	0.57
20:V:8:ASN:OD1	26:1:583:A:H4'	2.04	0.57
24:Z:8:ARG:NE	24:Z:16:MET:HE1	2.19	0.57
26:1:90:A:H4'	26:1:91:A:OP1	2.03	0.57
26:1:1471:A:H4'	26:1:1472:C:O5'	2.03	0.57
12:L:38:LYS:HE2	12:L:100:GLU:CG	2.30	0.57
26:1:1357:G:OP2	26:1:1357:G:N2	2.28	0.57
26:1:1634:A:H3'	26:1:1635:A:H8	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:64:ARG:HD3	20:V:45:TYR:O	2.04	0.57
15:O:34:LYS:HB2	15:O:45:HIS:CD2	2.39	0.57
26:1:25:U:H2'	26:1:26:G:H5'	1.86	0.57
27:2:27:A:H2'	27:2:28:C:H6	1.68	0.57
19:S:34:PHE:CE2	22:X:8:PRO:HB3	2.39	0.57
23:Y:14:ARG:HD2	23:Y:41:TRP:HH2	1.69	0.57
26:1:262:G:H21	26:1:666:A:H8	1.52	0.57
27:2:101:A:H2'	27:2:102:G:O4'	2.04	0.57
10:J:10:ARG:NH2	10:J:52:ARG:HG2	2.20	0.57
15:O:31:GLU:HG2	15:O:46:ARG:CD	2.34	0.57
22:X:51:GLU:OE1	22:X:56:PRO:HA	2.04	0.57
22:X:93:PRO:O	22:X:97:VAL:HG23	2.04	0.57
23:Y:78:PRO:HG2	23:Y:81:VAL:CG1	2.34	0.57
26:1:277:C:H2'	26:1:278:A:H5'	1.86	0.57
26:1:1207:G:H2'	26:1:1208:A:H5'	1.85	0.57
26:1:2574:U:H2'	26:1:2575:G:C8	2.39	0.57
26:1:83:G:H21	26:1:102:A:H2	1.52	0.57
26:1:174:U:O2'	26:1:175:C:H5'	2.05	0.57
26:1:1757:U:C2'	26:1:1758:A:H5''	2.35	0.57
1:A:11:THR:HB	1:A:57:VAL:HG11	1.87	0.57
7:G:69:GLN:NE2	26:1:378:C:H5''	2.20	0.57
16:P:31:VAL:HG22	16:P:34:ARG:HH12	1.69	0.57
26:1:1904:A:H2'	26:1:1905:G:O4'	2.04	0.57
26:1:2288:C:H2'	26:1:2289:U:H5'	1.86	0.57
26:1:2501:U:OP2	26:1:2502:C:N4	2.31	0.57
5:E:19:LEU:HD21	14:N:20:PHE:CD2	2.40	0.57
15:O:9:CYS:HB3	15:O:12:CYS:O	2.04	0.57
19:S:29:ASN:HD22	19:S:108:LEU:HD21	1.70	0.57
20:V:70:GLU:OE2	20:V:91:GLY:HA3	2.05	0.57
20:V:113:THR:HG22	20:V:114:ARG:H	1.69	0.57
26:1:544:U:H2'	26:1:545:G:O4'	2.05	0.57
10:J:39:LEU:CD2	10:J:44:PRO:HG3	2.34	0.57
12:L:127:PHE:H	12:L:172:ARG:HA	1.69	0.57
12:L:215:ILE:HD13	26:1:2798:C:H4'	1.87	0.57
26:1:247:A:H2'	26:1:248:G:O4'	2.05	0.57
26:1:307:A:H2'	26:1:308:C:C6	2.40	0.57
26:1:769:U:O2'	26:1:770:G:H5'	2.05	0.57
26:1:1208:A:H2'	26:1:1209:U:H6	1.69	0.57
26:1:1298:G:H2'	26:1:1299:U:O4'	2.04	0.57
26:1:1510:U:H2'	26:1:1511:C:H6	1.68	0.57
13:M:40:ASN:HB2	13:M:43:ILE:H	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:4:ASN:HD21	17:Q:34:ALA:HB2	1.68	0.57
17:Q:18:ALA:HB2	26:1:673:G:H5''	1.87	0.57
19:S:57:VAL:HG11	19:S:79:ARG:HD2	1.87	0.57
19:S:151:LYS:HB2	19:S:190:ASP:HB2	1.86	0.57
22:X:21:ARG:HA	26:1:856:U:H2'	1.86	0.57
26:1:348:C:H2'	26:1:349:U:C6	2.40	0.57
26:1:1360:G:O2'	26:1:1361:G:H5'	2.05	0.57
26:1:1515:G:H22	26:1:1565:U:H3	1.51	0.57
26:1:2232:A:H2'	26:1:2233:C:C6	2.39	0.57
26:1:2439:A:H2'	26:1:2440:G:O4'	2.04	0.57
2:B:150:LYS:HE3	2:B:153:GLN:NE2	2.20	0.56
17:Q:15:LYS:HG2	17:Q:23:LYS:HB3	1.87	0.56
22:X:129:SER:OG	26:1:682:A:OP2	2.13	0.56
26:1:978:A:H2'	26:1:979:C:H6	1.70	0.56
26:1:2543:G:O2'	26:1:2544:C:H5'	2.05	0.56
26:1:2674:U:O2'	26:1:2675:G:H5'	2.05	0.56
9:I:27:LYS:O	9:I:29:LEU:HB2	2.05	0.56
26:1:422:G:H2'	26:1:423:A:C8	2.39	0.56
26:1:428:G:H22	26:1:438:U:H3	1.53	0.56
26:1:523:A:H2'	26:1:524:A:C8	2.41	0.56
26:1:2061:U:O2'	26:1:2062:G:H5'	2.05	0.56
26:1:2482:G:H2'	26:1:2483:C:C6	2.40	0.56
4:D:31:ASP:O	4:D:62:VAL:N	2.34	0.56
12:L:3:LYS:NZ	12:L:98:ALA:HB2	2.20	0.56
12:L:157:ALA:CB	26:1:2602:C:H5'	2.35	0.56
18:R:7:VAL:HG12	18:R:34:GLN:HB3	1.86	0.56
19:S:183:VAL:O	19:S:187:THR:HG22	2.05	0.56
23:Y:68:ILE:HG22	23:Y:101:ARG:HD3	1.88	0.56
26:1:422:G:H2'	26:1:423:A:H8	1.70	0.56
26:1:577:A:H4'	26:1:578:G:C8	2.40	0.56
26:1:905:U:C1'	26:1:2295:A:H5'	2.35	0.56
26:1:2679:U:H2'	26:1:2680:U:C6	2.40	0.56
2:B:95:VAL:HG12	2:B:101:LYS:CD	2.34	0.56
12:L:65:SER:CB	26:1:2850:G:H3'	2.34	0.56
22:X:69:ILE:HD13	26:1:2433:C:C2	2.41	0.56
26:1:2008:A:H5''	26:1:2009:U:OP2	2.05	0.56
1:A:28:LEU:CD2	1:A:88:VAL:HG22	2.35	0.56
26:1:326:A:H2'	26:1:327:G:H5''	1.87	0.56
26:1:1726:A:H61	26:1:1750:U:H3	1.54	0.56
26:1:2123:A:H2'	26:1:2124:U:C6	2.40	0.56
9:I:20:ASN:ND2	26:1:2305:A:OP2	2.26	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:24:VAL:CG1	21:W:33:ALA:HB2	2.35	0.56
26:1:82:G:O2'	26:1:83:G:H5'	2.06	0.56
26:1:2273:G:H2'	26:1:2274:A:C8	2.40	0.56
26:1:2781:U:O2'	26:1:2783:U:OP1	2.14	0.56
5:E:33:ILE:HG12	5:E:52:MET:SD	2.45	0.56
6:F:65:MET:HB2	26:1:64:A:N3	2.21	0.56
26:1:66:C:H2'	26:1:67:G:C8	2.40	0.56
26:1:406:A:O2'	26:1:407:G:OP1	2.21	0.56
26:1:589:U:O2'	26:1:590:U:H5''	2.06	0.56
26:1:1162:C:H2'	26:1:1163:U:O4'	2.06	0.56
26:1:1322:G:N2	26:1:1366:U:OP1	2.23	0.56
26:1:980:U:H2'	26:1:981:U:C6	2.41	0.56
26:1:2760:A:H2'	26:1:2761:C:O4'	2.06	0.56
2:B:171:TYR:CB	2:B:183:MET:HE2	2.36	0.56
26:1:44:A:H61	26:1:480:U:H3	1.53	0.56
26:1:556:U:C2'	26:1:557:G:H5'	2.35	0.56
26:1:2494:C:O2'	26:1:2495:A:H5'	2.06	0.56
27:2:64:A:H4'	27:2:65:G:OP1	2.04	0.56
4:D:50:ALA:HB1	4:D:51:PRO:HD2	1.88	0.56
5:E:89:ALA:CB	26:1:793:G:H5'	2.35	0.56
8:H:63:LEU:O	8:H:69:THR:HA	2.06	0.56
12:L:41:VAL:HA	12:L:44:ASP:O	2.06	0.56
26:1:900:G:H2'	26:1:901:G:O4'	2.06	0.56
26:1:2234:C:C2'	26:1:2235:A:H5'	2.36	0.56
26:1:2318:U:O2'	26:1:2319:U:H5'	2.06	0.56
8:H:65:VAL:O	8:H:68:LYS:HG2	2.06	0.55
25:a:32:ASN:HD22	25:a:33:VAL:H	1.53	0.55
20:V:32:GLU:OE2	20:V:144:ARG:HG2	2.06	0.55
26:1:1865:C:H4'	26:1:1866:G:H5''	1.86	0.55
26:1:2242:G:H2'	26:1:2243:U:C6	2.42	0.55
26:1:2688:G:H2'	26:1:2689:A:O4'	2.06	0.55
1:A:31:HIS:ND1	1:A:44:VAL:HG12	2.21	0.55
19:S:154:VAL:HB	19:S:175:VAL:HG22	1.87	0.55
23:Y:111:GLU:OE2	23:Y:133:LYS:NZ	2.22	0.55
26:1:79:U:O2'	26:1:389:A:H1'	2.06	0.55
26:1:1208:A:H2'	26:1:1209:U:C6	2.41	0.55
26:1:1423:C:H2'	26:1:1424:A:C8	2.41	0.55
26:1:1472:C:O2'	26:1:1616:A:OP2	2.17	0.55
26:1:1576:A:H2'	26:1:1577:G:C8	2.42	0.55
26:1:2768:A:H2'	26:1:2769:G:H5'	1.88	0.55
8:H:82:LEU:O	23:Y:130:LYS:NZ	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:16:ARG:HE	17:Q:22:LEU:HD21	1.72	0.55
24:Z:9:THR:HG22	24:Z:10:SER:H	1.72	0.55
25:a:103:GLY:HA3	27:2:47:C:OP1	2.07	0.55
26:1:457:G:OP2	26:1:2433:C:O2'	2.21	0.55
26:1:1409:U:HO2'	26:1:2239:A:H8	1.54	0.55
26:1:1617:A:H2'	26:1:1618:A:C8	2.42	0.55
26:1:2801:C:H2'	26:1:2802:A:O4'	2.06	0.55
2:B:117:GLU:HG2	2:B:119:GLY:O	2.07	0.55
8:H:33:GLY:HA3	8:H:92:LEU:HD12	1.88	0.55
12:L:39:LYS:HD2	12:L:44:ASP:OD2	2.06	0.55
12:L:138:ARG:HB2	12:L:148:HIS:O	2.07	0.55
14:N:24:VAL:HB	14:N:25:PRO:HD2	1.89	0.55
19:S:198:ALA:O	19:S:202:VAL:HG22	2.07	0.55
26:1:733:U:H5'	26:1:1807:A:C2	2.42	0.55
26:1:1480:G:O2'	26:1:1520:A:H1'	2.06	0.55
26:1:2007:G:O2'	26:1:2009:U:OP2	2.21	0.55
26:1:2681:A:H4'	26:1:2682:G:OP1	2.06	0.55
5:E:1:MET:O	5:E:108:SER:OG	2.13	0.55
9:I:44:ILE:HD13	9:I:47:ARG:HH11	1.72	0.55
12:L:42:GLU:CD	12:L:43:VAL:HG13	2.31	0.55
19:S:117:LYS:HE2	19:S:117:LYS:HA	1.87	0.55
23:Y:51:ARG:HD3	23:Y:66:ILE:HD11	1.89	0.55
26:1:177:G:O2'	26:1:178:A:H5'	2.06	0.55
26:1:1463:A:H5'	26:1:1465:G:O6	2.07	0.55
2:B:43:ARG:HA	2:B:48:LYS:O	2.07	0.55
25:a:38:LYS:HG3	25:a:39:HIS:CD2	2.41	0.55
26:1:744:A:H2	26:1:778:G:H21	1.55	0.55
26:1:751:A:H61	26:1:770:G:H1'	1.71	0.55
26:1:1567:A:OP2	26:1:1568:U:O2'	2.19	0.55
26:1:2582:U:H2'	26:1:2583:C:O4'	2.07	0.55
27:2:47:C:H2'	27:2:48:A:H8	1.70	0.55
2:B:13:ARG:CD	26:1:773:G:H4'	2.36	0.55
2:B:58:HIS:CD2	26:1:1614:A:H5'	2.42	0.55
5:E:2:GLU:OE2	5:E:72:LYS:HE2	2.06	0.55
7:G:57:LEU:CD1	7:G:59:THR:HG23	2.37	0.55
12:L:99:TYR:HB3	12:L:101:VAL:HG22	1.89	0.55
26:1:105:C:O2'	26:1:337:A:O2'	2.13	0.55
26:1:1044:A:H2'	26:1:1045:A:C8	2.41	0.55
26:1:1772:G:C2'	26:1:1773:A:H5'	2.37	0.55
6:F:82:LEU:HD11	6:F:87:ILE:HD11	1.89	0.55
24:Z:89:ILE:O	24:Z:92:ARG:HG2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1489:A:C2	26:1:1594:U:H1'	2.42	0.55
26:1:1514:A:H2	26:1:1566:G:H22	1.54	0.55
26:1:1817:C:H2'	26:1:1818:A:C5	2.42	0.55
26:1:1886:A:H62	26:1:1910:G:H8	1.55	0.55
26:1:2347:A:H5''	26:1:2348:G:C5	2.42	0.55
1:A:77:PRO:HD2	1:A:80:THR:HG21	1.89	0.55
6:F:89:LEU:HD23	11:K:30:PHE:HB3	1.89	0.55
13:M:17:GLU:OE1	13:M:21:LYS:HE2	2.07	0.55
26:1:392:U:H2'	26:1:393:G:C8	2.42	0.55
8:H:68:LYS:O	8:H:70:ILE:HG23	2.07	0.54
8:H:73:MET:CE	8:H:94:ILE:HD12	2.37	0.54
9:I:57:GLU:HG2	9:I:88:SER:HB2	1.88	0.54
20:V:22:GLU:HG2	20:V:62:LYS:HB2	1.87	0.54
23:Y:32:PHE:CZ	23:Y:111:GLU:HG2	2.42	0.54
26:1:348:C:O2'	26:1:349:U:H5'	2.07	0.54
26:1:791:U:H5''	26:1:792:U:OP1	2.07	0.54
26:1:1397:G:H2'	26:1:1398:G:H5'	1.88	0.54
26:1:1886:A:H2'	26:1:1887:G:H5'	1.87	0.54
5:E:37:LYS:HA	5:E:48:GLU:OE2	2.07	0.54
9:I:85:LYS:NZ	26:1:902:A:OP1	2.26	0.54
14:N:25:PRO:HB2	14:N:38:LEU:CD1	2.37	0.54
19:S:84:ARG:NH2	26:1:494:U:O4'	2.40	0.54
26:1:139:U:H2'	26:1:140:A:C8	2.42	0.54
26:1:418:G:O2'	26:1:446:G:O6	2.23	0.54
26:1:622:A:H2'	26:1:623:C:C6	2.43	0.54
26:1:696:G:C2'	26:1:697:U:H5'	2.37	0.54
22:X:74:TYR:CE2	22:X:127:LYS:HD3	2.42	0.54
26:1:698:U:C2'	26:1:699:U:H5'	2.35	0.54
26:1:794:A:H4'	26:1:1309:G:N3	2.22	0.54
26:1:948:U:H2'	26:1:949:C:C6	2.41	0.54
26:1:1515:G:H1	26:1:1565:U:H3	1.53	0.54
26:1:2350:G:H2'	26:1:2351:U:O4'	2.06	0.54
26:1:2707:C:O2'	26:1:2708:C:H5'	2.07	0.54
1:A:55:GLY:H	1:A:59:GLU:HB3	1.73	0.54
2:B:94:VAL:HG11	2:B:114:GLN:NE2	2.23	0.54
16:P:16:VAL:HG13	16:P:17:HIS:ND1	2.23	0.54
18:R:19:ARG:HD2	18:R:24:MET:SD	2.48	0.54
19:S:57:VAL:CG1	19:S:79:ARG:HD2	2.37	0.54
22:X:103:LYS:HD3	26:1:647:G:O6	2.07	0.54
26:1:160:G:H21	26:1:168:A:H2	1.55	0.54
26:1:360:A:H2'	26:1:361:U:H6	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:736:C:H2'	26:1:737:C:H6	1.71	0.54
26:1:1881:A:H62	26:1:1915:G:H1'	1.73	0.54
26:1:1883:A:C2'	26:1:1884:G:H5'	2.37	0.54
26:1:2308:C:C2'	26:1:2309:G:H5'	2.37	0.54
27:2:18:G:H2'	27:2:19:G:C8	2.42	0.54
26:1:93:U:O2'	26:1:94:A:H5'	2.07	0.54
26:1:763:A:H2'	26:1:764:C:O4'	2.08	0.54
26:1:1010:G:O4'	26:1:2294:A:N6	2.41	0.54
26:1:1449:A:N6	26:1:1632:A:H3'	2.22	0.54
26:1:1517:A:H2'	26:1:1518:G:H5'	1.90	0.54
26:1:1721:A:H2'	26:1:1722:A:H8	1.73	0.54
4:D:29:GLU:OE2	4:D:65:GLN:N	2.40	0.54
8:H:7:ILE:CG2	8:H:42:LYS:HB2	2.38	0.54
8:H:61:ILE:HB	8:H:72:VAL:HG23	1.88	0.54
12:L:159:ASP:HB2	26:1:2599:A:OP2	2.08	0.54
26:1:579:U:H2'	26:1:580:C:C6	2.43	0.54
26:1:1927:A:C2	26:1:1997:A:C5	2.96	0.54
26:1:2273:G:H2'	26:1:2274:A:H8	1.72	0.54
26:1:429:C:H5''	26:1:431:C:OP2	2.07	0.54
26:1:702:U:H2'	26:1:703:A:C8	2.43	0.54
26:1:991:A:H2'	26:1:992:A:C8	2.42	0.54
27:2:79:C:H42	27:2:90:U:H3	1.56	0.54
2:B:154:ILE:CG2	2:B:176:LEU:HD22	2.38	0.54
8:H:52:ILE:HA	8:H:55:VAL:HG22	1.90	0.54
8:H:60:VAL:HG12	8:H:73:MET:HE1	1.90	0.54
26:1:402:C:H2'	26:1:403:U:O4'	2.08	0.54
26:1:1821:U:H2'	26:1:1822:C:H6	1.71	0.54
26:1:2772:C:H2'	26:1:2773:U:C6	2.43	0.54
2:B:194:GLN:NE2	2:B:198:LEU:HD21	2.23	0.54
3:C:58:ARG:HH21	3:C:92:ARG:HH12	1.55	0.54
8:H:22:ARG:NH2	8:H:87:THR:O	2.31	0.54
19:S:138:GLU:O	19:S:142:VAL:HG23	2.08	0.54
21:W:24:VAL:HG13	21:W:33:ALA:HB2	1.90	0.54
25:a:29:PRO:HB2	25:a:92:ILE:HD12	1.90	0.54
26:1:2687:A:H3'	26:1:2688:G:C8	2.42	0.54
7:G:42:LYS:HG2	7:G:58:GLU:CG	2.34	0.54
12:L:29:GLU:OE2	12:L:31:LYS:NZ	2.41	0.54
26:1:210:A:H2'	26:1:211:C:O4'	2.08	0.54
26:1:1867:G:H2'	26:1:1868:U:C6	2.43	0.54
26:1:1930:G:H2'	26:1:1931:G:C8	2.43	0.54
26:1:1674:U:H2'	26:1:1675:G:O4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2261:G:O2'	26:1:2262:G:H5'	2.09	0.53
26:1:2300:A:H2'	26:1:2301:A:C8	2.43	0.53
1:A:25:GLY:CA	1:A:94:VAL:HG11	2.38	0.53
2:B:205:VAL:HG23	26:1:1818:A:H4'	1.90	0.53
4:D:80:LYS:O	4:D:82:SER:N	2.41	0.53
26:1:221:G:H22	26:1:238:U:H4'	1.73	0.53
26:1:360:A:H2'	26:1:361:U:C6	2.43	0.53
26:1:916:U:O2'	26:1:917:U:H5'	2.08	0.53
26:1:1602:U:H2'	26:1:1603:U:C6	2.42	0.53
26:1:1651:C:H5''	26:1:1652:A:H5'	1.89	0.53
26:1:2831:G:O2'	26:1:2832:A:H5'	2.08	0.53
6:F:37:GLN:HE21	26:1:144:C:H4'	1.73	0.53
9:I:75:VAL:HG12	9:I:89:VAL:HG22	1.90	0.53
22:X:74:TYR:CD1	22:X:107:SER:HB3	2.42	0.53
26:1:275:A:H1'	26:1:414:C:H1'	1.90	0.53
26:1:340:C:H2'	26:1:341:G:O4'	2.08	0.53
26:1:401:U:C2'	26:1:402:C:H5'	2.37	0.53
26:1:519:G:O2'	26:1:520:G:H5'	2.08	0.53
26:1:1232:G:O2'	26:1:1233:A:H5'	2.09	0.53
26:1:1880:A:H2'	26:1:1881:A:C8	2.44	0.53
26:1:1884:G:O2'	26:1:1885:G:H5'	2.08	0.53
2:B:94:VAL:HG11	2:B:114:GLN:HE21	1.74	0.53
26:1:92:G:H2'	26:1:93:U:H6	1.72	0.53
26:1:1569:G:O2'	26:1:1570:G:H5'	2.08	0.53
21:W:10:VAL:HG12	21:W:12:ASP:H	1.73	0.53
26:1:1597:U:OP1	26:1:1762:U:O2'	2.21	0.53
26:1:1884:G:H21	26:1:1912:A:H62	1.57	0.53
26:1:2262:G:H2'	26:1:2263:C:C6	2.43	0.53
4:D:6:GLU:O	4:D:37:LYS:HB2	2.09	0.53
7:G:9:VAL:O	7:G:20:GLU:HB2	2.09	0.53
7:G:57:LEU:HD13	7:G:58:GLU:N	2.24	0.53
19:S:74:ARG:HE	26:1:719:G:H1'	1.74	0.53
20:V:36:ILE:HD11	20:V:141:TYR:CE2	2.43	0.53
26:1:717:C:O2'	26:1:718:C:H5'	2.07	0.53
26:1:786:U:O2'	26:1:1720:A:OP1	2.26	0.53
26:1:955:A:H2'	26:1:956:A:C8	2.44	0.53
26:1:1016:G:OP2	26:1:1017:A:O2'	2.19	0.53
26:1:1241:A:H2'	26:1:1242:A:C8	2.44	0.53
26:1:1724:U:C2'	26:1:1725:G:H5'	2.39	0.53
19:S:182:ASN:HB2	19:S:185:ASP:HB2	1.89	0.53
21:W:87:ILE:HG22	21:W:88:ARG:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:109:ILE:HG13	22:X:109:ILE:O	2.09	0.53
24:Z:55:ASP:O	24:Z:59:ARG:HG3	2.09	0.53
26:1:100:U:H3'	26:1:101:G:C5'	2.38	0.53
26:1:506:A:H2'	26:1:507:C:C5'	2.39	0.53
26:1:878:C:H2'	26:1:879:U:C6	2.44	0.53
2:B:253:PRO:HG2	2:B:257:LYS:NZ	2.23	0.53
5:E:35:ILE:O	5:E:39:THR:HG23	2.08	0.53
21:W:65:THR:HG22	21:W:67:SER:H	1.74	0.53
26:1:884:U:H2'	26:1:885:C:H6	1.74	0.53
26:1:1522:G:H2'	26:1:1523:G:C8	2.44	0.53
26:1:1721:A:H2'	26:1:1722:A:C8	2.44	0.53
26:1:2340:C:H2'	26:1:2341:A:C8	2.35	0.53
26:1:2852:U:H1'	26:1:2854:A:C4	2.43	0.53
3:C:81:ASN:ND2	26:1:1195:A:H4'	2.24	0.53
18:R:17:ILE:HG13	18:R:18:LYS:H	1.74	0.53
19:S:63:LYS:CE	19:S:67:GLN:HB2	2.39	0.53
20:V:140:ASN:OD1	20:V:141:TYR:N	2.42	0.53
26:1:181:G:O2'	26:1:182:C:H5'	2.09	0.53
26:1:2346:U:H1'	26:1:2347:A:H2'	1.91	0.53
26:1:2405:A:C5	26:1:2406:G:H1'	2.44	0.53
4:D:46:VAL:C	4:D:47:LYS:HD3	2.33	0.53
7:G:41:MET:O	7:G:58:GLU:HA	2.08	0.53
15:O:2:ARG:HH12	26:1:2312:C:H6	1.56	0.53
19:S:200:LYS:O	19:S:204:GLU:HG3	2.08	0.53
26:1:131:G:O2'	26:1:132:C:H5'	2.09	0.53
26:1:641:A:O2'	26:1:642:U:H5'	2.09	0.53
8:H:60:VAL:HG12	8:H:73:MET:CE	2.39	0.52
10:J:16:ASN:HB3	10:J:24:SER:HB2	1.91	0.52
12:L:8:ARG:NH1	12:L:206:LYS:O	2.42	0.52
26:1:368:A:H2'	26:1:369:G:H8	1.74	0.52
26:1:897:A:O2'	26:1:898:U:H5'	2.09	0.52
26:1:2680:U:OP2	26:1:2681:A:O2'	2.21	0.52
22:X:103:LYS:HE2	26:1:648:G:O6	2.10	0.52
26:1:261:C:H2'	26:1:262:G:H5'	1.90	0.52
26:1:556:U:H2'	26:1:557:G:H5'	1.91	0.52
26:1:748:U:H2'	26:1:749:G:O4'	2.09	0.52
26:1:1878:U:H2'	26:1:1879:U:C6	2.44	0.52
2:B:145:GLU:HB2	2:B:188:CYS:HB3	1.90	0.52
2:B:167:LYS:HB2	2:B:172:VAL:HG12	1.91	0.52
7:G:77:GLU:O	7:G:79:THR:HG23	2.09	0.52
13:M:40:ASN:HB3	13:M:41:PRO:HD2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:491:C:O2'	26:1:492:G:H5'	2.09	0.52
26:1:1889:G:O2'	26:1:1890:G:H5'	2.09	0.52
26:1:1911:A:H2'	26:1:1912:A:H8	1.74	0.52
26:1:2648:G:H2'	26:1:2649:U:O4'	2.09	0.52
27:2:93:G:C2'	27:2:94:C:H5''	2.39	0.52
3:C:106:PHE:O	3:C:110:VAL:HG23	2.09	0.52
21:W:102:VAL:HG21	21:W:106:LEU:HD23	1.91	0.52
24:Z:102:ARG:HH21	24:Z:122:VAL:HG23	1.74	0.52
26:1:396:G:H2'	26:1:397:U:C6	2.44	0.52
26:1:1010:G:C2'	26:1:1011:U:H5'	2.38	0.52
26:1:1325:U:O2'	26:1:1326:C:OP1	2.21	0.52
26:1:2091:C:H2'	26:1:2092:C:H6	1.74	0.52
26:1:2748:A:H2'	26:1:2749:G:O4'	2.09	0.52
5:E:48:GLU:O	5:E:52:MET:HG2	2.09	0.52
7:G:32:ARG:HD3	7:G:64:HIS:HA	1.90	0.52
26:1:231:A:C2	26:1:233:U:H1'	2.44	0.52
26:1:1764:A:H3'	26:1:1765:A:C8	2.45	0.52
26:1:1865:C:O2	26:1:1865:C:H2'	2.08	0.52
26:1:1930:G:H2'	26:1:1931:G:H8	1.74	0.52
26:1:2101:U:O2'	26:1:2624:G:O2'	2.22	0.52
3:C:24:TYR:HB3	3:C:28:LYS:HB2	1.92	0.52
20:V:63:ILE:HD11	20:V:101:LEU:HD21	1.90	0.52
24:Z:4:ARG:HD3	26:1:1696:C:OP1	2.09	0.52
26:1:683:G:H2'	26:1:684:U:C6	2.45	0.52
26:1:902:A:O2'	26:1:903:G:H5'	2.09	0.52
26:1:1385:G:H2'	26:1:1386:U:H5'	1.92	0.52
26:1:1911:A:H2'	26:1:1912:A:C8	2.44	0.52
26:1:2547:C:O2'	26:1:2548:C:H5'	2.09	0.52
1:A:35:ILE:HG22	1:A:40:GLU:CG	2.38	0.52
25:a:104:ARG:HG3	27:2:47:C:P	2.50	0.52
26:1:575:G:N2	26:1:2050:A:OP1	2.42	0.52
26:1:666:A:H2'	26:1:667:G:C5'	2.39	0.52
26:1:1774:A:H2'	26:1:1775:G:C8	2.45	0.52
8:H:31:VAL:O	8:H:38:ASN:HA	2.10	0.52
12:L:183:LEU:HD22	12:L:198:LYS:O	2.10	0.52
16:P:31:VAL:HG22	16:P:34:ARG:NH1	2.25	0.52
19:S:151:LYS:HB2	19:S:190:ASP:H	1.75	0.52
20:V:54:TYR:CE1	20:V:122:LYS:HG2	2.45	0.52
26:1:131:G:H2'	26:1:132:C:C6	2.44	0.52
26:1:575:G:O2'	26:1:577:A:N7	2.41	0.52
26:1:787:U:H2'	26:1:788:A:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1160:C:H2'	26:1:1161:A:C8	2.45	0.52
26:1:1259:U:H2'	26:1:1260:C:C6	2.44	0.52
26:1:1648:C:O2'	26:1:1654:A:N1	2.37	0.52
26:1:2293:A:H4'	26:1:2294:A:O5'	2.10	0.52
26:1:2771:G:C2'	26:1:2772:C:H5'	2.40	0.52
26:1:2826:U:H2'	26:1:2827:A:N9	2.24	0.52
3:C:64:ARG:HD2	20:V:43:VAL:O	2.09	0.52
4:D:30:GLY:N	4:D:62:VAL:O	2.42	0.52
26:1:984:G:H2'	26:1:985:A:O4'	2.10	0.52
26:1:2084:G:O2'	26:1:2085:A:H5'	2.10	0.52
26:1:2322:C:O2'	26:1:2323:U:H5'	2.09	0.52
26:1:2394:G:O2'	26:1:2395:C:H5'	2.10	0.52
2:B:149:GLY:O	26:1:2232:A:H5'	2.10	0.52
3:C:21:ALA:HB1	3:C:24:TYR:CE2	2.45	0.52
3:C:33:LYS:HE2	26:1:624:C:OP2	2.10	0.52
7:G:11:VAL:HG22	7:G:68:VAL:CG1	2.40	0.52
7:G:69:GLN:HE21	26:1:378:C:H5''	1.75	0.52
12:L:83:ALA:O	12:L:85:LYS:HG3	2.10	0.52
17:Q:18:ALA:CB	26:1:673:G:H5''	2.39	0.52
19:S:140:LYS:HZ2	26:1:363:A:H61	1.56	0.52
26:1:383:A:H2'	26:1:384:G:O4'	2.09	0.52
26:1:1319:U:H2'	26:1:1320:G:O4'	2.10	0.52
26:1:1347:G:C2'	26:1:1348:U:H5'	2.40	0.52
7:G:30:LYS:HG3	7:G:32:ARG:HG2	1.91	0.51
26:1:89:U:H3'	26:1:90:A:C3'	2.40	0.51
26:1:163:U:O2'	26:1:166:A:N6	2.42	0.51
26:1:551:G:H4'	26:1:552:A:H5''	1.90	0.51
26:1:1837:A:H2'	26:1:1838:G:H5'	1.91	0.51
26:1:2581:U:H2'	26:1:2582:U:H6	1.74	0.51
1:A:98:LYS:HB3	1:A:100:TYR:CE2	2.45	0.51
3:C:107:ALA:O	3:C:111:THR:HG23	2.11	0.51
14:N:25:PRO:HB2	14:N:38:LEU:HD11	1.91	0.51
19:S:82:GLN:O	26:1:1294:G:N2	2.38	0.51
22:X:74:TYR:O	22:X:106:LYS:HE3	2.10	0.51
26:1:388:A:H1'	26:1:389:A:C2	2.45	0.51
26:1:1220:A:O2'	26:1:1221:C:H5'	2.10	0.51
26:1:1597:U:O2'	26:1:1598:U:H5'	2.11	0.51
2:B:132:LEU:HD23	2:B:135:ILE:HD12	1.93	0.51
12:L:8:ARG:HG2	12:L:206:LYS:HA	1.92	0.51
13:M:8:LEU:HB2	13:M:28:LEU:HD13	1.93	0.51
26:1:71:A:H5''	26:1:73:A:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1185:U:H4'	26:1:1186:A:O4'	2.10	0.51
26:1:1410:A:H5'	26:1:2239:A:H1'	1.93	0.51
26:1:2789:U:O2'	26:1:2790:G:H5'	2.11	0.51
26:1:2870:A:H2'	26:1:2871:A:C8	2.45	0.51
2:B:34:LEU:HD23	2:B:61:GLN:HB3	1.92	0.51
2:B:69:ARG:HE	2:B:116:VAL:HG22	1.76	0.51
3:C:92:ARG:HD3	26:1:1041:G:OP1	2.10	0.51
26:1:132:C:O2'	26:1:133:A:H5'	2.11	0.51
26:1:587:C:O2'	26:1:588:G:H5'	2.11	0.51
26:1:647:G:O2'	26:1:648:G:H5'	2.10	0.51
26:1:904:G:O2'	26:1:961:G:O6	2.28	0.51
26:1:1347:G:H2'	26:1:1348:U:H5'	1.93	0.51
26:1:1700:C:H2'	26:1:1701:U:H6	1.76	0.51
26:1:2883:U:O2'	26:1:2884:G:H5'	2.10	0.51
2:B:236:GLU:HG3	26:1:2627:A:H2	1.76	0.51
5:E:44:SER:HB2	5:E:45:PRO:HD3	1.93	0.51
12:L:60:LYS:NZ	12:L:62:ASP:HB2	2.25	0.51
26:1:277:C:C2'	26:1:278:A:H5'	2.41	0.51
26:1:556:U:C3'	26:1:557:G:H5'	2.41	0.51
26:1:1080:G:O2'	26:1:1081:G:H5'	2.10	0.51
26:1:1881:A:H62	26:1:1915:G:H8	1.59	0.51
1:A:4:HIS:HD2	1:A:6:LEU:HB3	1.75	0.51
2:B:257:LYS:O	26:1:1824:C:H4'	2.11	0.51
6:F:32:ARG:NH2	26:1:113:U:O2'	2.44	0.51
20:V:61:SER:OG	20:V:98:PRO:HG3	2.10	0.51
26:1:32:C:O2'	26:1:33:U:H5'	2.10	0.51
26:1:223:G:H5''	26:1:224:A:OP1	2.10	0.51
26:1:266:A:H2'	26:1:267:G:O4'	2.11	0.51
26:1:399:U:H2'	26:1:400:C:O4'	2.11	0.51
26:1:1214:C:O2'	26:1:1215:U:OP1	2.29	0.51
26:1:1762:U:H2'	26:1:1763:U:O4'	2.11	0.51
26:1:1992:C:H3'	26:1:1993:A:H2'	1.91	0.51
3:C:94:MET:HG3	4:D:11:GLN:HB3	1.91	0.51
17:Q:54:ASP:CG	22:X:57:LEU:HD22	2.35	0.51
19:S:53:ASN:O	19:S:57:VAL:HG23	2.10	0.51
19:S:84:ARG:O	19:S:84:ARG:HD3	2.10	0.51
26:1:482:U:H2'	26:1:483:C:C6	2.45	0.51
26:1:1872:G:O2'	26:1:1873:G:H5'	2.11	0.51
26:1:2344:C:H2'	26:1:2345:A:H5'	1.93	0.51
2:B:15:ASN:O	2:B:204:ASN:ND2	2.44	0.51
3:C:31:LEU:HB2	3:C:34:VAL:HG22	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:31:VAL:HB	8:H:39:VAL:CG2	2.37	0.51
20:V:18:VAL:HG12	20:V:139:GLU:O	2.10	0.51
26:1:1081:G:H2'	26:1:1082:C:C6	2.45	0.51
26:1:1877:G:O2'	26:1:1878:U:H5'	2.10	0.51
26:1:2507:C:O2'	26:1:2508:G:H5'	2.10	0.51
11:K:11:THR:O	11:K:15:GLU:HG3	2.11	0.51
15:O:26:ASN:ND2	26:1:2313:A:H2'	2.25	0.51
26:1:187:C:O2'	26:1:188:C:H5'	2.11	0.51
26:1:368:A:H2'	26:1:369:G:C8	2.46	0.51
26:1:1283:G:O2'	26:1:1284:A:H5'	2.11	0.51
26:1:1565:U:H2'	26:1:1566:G:C1'	2.41	0.51
26:1:1695:G:H2'	26:1:1696:C:O4'	2.10	0.51
26:1:1985:C:H2'	26:1:1986:G:H5'	1.92	0.51
26:1:2262:G:H2'	26:1:2263:C:H6	1.75	0.51
12:L:127:PHE:HA	12:L:171:GLY:O	2.11	0.51
15:O:2:ARG:HD3	26:1:2312:C:OP2	2.11	0.51
24:Z:97:GLN:O	26:1:2859:G:N2	2.30	0.51
26:1:1075:G:O2'	26:1:1076:A:H5'	2.10	0.51
26:1:1632:A:H4'	26:1:1633:A:C5	2.46	0.51
26:1:1901:C:H2'	26:1:1902:G:O4'	2.10	0.51
26:1:2792:A:H5'	26:1:2793:G:OP2	2.10	0.51
12:L:31:LYS:H	12:L:53:PHE:HE1	1.59	0.50
19:S:117:LYS:HG3	19:S:192:LEU:HD11	1.92	0.50
26:1:185:A:O2'	26:1:186:C:H5'	2.11	0.50
26:1:696:G:H2'	26:1:697:U:H5'	1.92	0.50
26:1:1627:G:H2'	26:1:1628:A:O4'	2.11	0.50
26:1:1987:A:H2'	26:1:1988:C:H5'	1.93	0.50
2:B:78:VAL:HG21	2:B:110:LEU:CD2	2.41	0.50
2:B:78:VAL:HG22	2:B:94:VAL:HG12	1.94	0.50
21:W:98:ILE:HB	21:W:118:ALA:HA	1.92	0.50
26:1:329:A:H2'	26:1:330:C:C6	2.46	0.50
26:1:349:U:H2'	26:1:350:G:O4'	2.11	0.50
26:1:481:C:O2	26:1:481:C:H2'	2.12	0.50
26:1:631:U:H2'	26:1:632:U:C6	2.45	0.50
26:1:667:G:O2'	26:1:668:C:H5'	2.11	0.50
26:1:902:A:H2'	26:1:903:G:H5'	1.92	0.50
1:A:11:THR:CB	1:A:57:VAL:HG11	2.40	0.50
2:B:78:VAL:HG21	2:B:110:LEU:HD21	1.94	0.50
2:B:108:LYS:HB3	2:B:196:GLY:HA2	1.93	0.50
12:L:117:ASP:OD1	12:L:212:ARG:HG3	2.10	0.50
19:S:65:TRP:HB2	19:S:70:THR:HG21	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:74:TYR:HE2	22:X:127:LYS:HD3	1.77	0.50
26:1:145:A:H2'	26:1:146:U:C6	2.47	0.50
26:1:222:A:N3	26:1:237:U:O2'	2.38	0.50
26:1:310:C:O2'	26:1:311:U:H5''	2.10	0.50
26:1:1896:U:O2'	26:1:1897:U:O4'	2.24	0.50
26:1:2429:U:C2'	26:1:2430:C:H5'	2.41	0.50
2:B:75:ASN:OD1	2:B:115:ILE:HG12	2.11	0.50
15:O:7:LEU:HB2	15:O:17:TYR:HB2	1.93	0.50
17:Q:9:GLY:O	17:Q:13:ARG:NH2	2.42	0.50
17:Q:15:LYS:CG	17:Q:23:LYS:HB3	2.40	0.50
17:Q:58:VAL:CG1	17:Q:61:LEU:HB2	2.41	0.50
26:1:267:G:C2'	26:1:268:A:H5''	2.42	0.50
26:1:346:A:H2'	26:1:347:U:C6	2.45	0.50
26:1:411:A:H2'	26:1:412:U:O4'	2.11	0.50
26:1:948:U:H2'	26:1:949:C:C5	2.47	0.50
26:1:1246:C:C2'	26:1:1247:G:H5'	2.41	0.50
26:1:1364:C:H2'	26:1:1365:G:C8	2.47	0.50
26:1:2055:U:O2'	26:1:2056:G:H5'	2.11	0.50
26:1:2794:C:O2'	26:1:2795:C:H5'	2.11	0.50
26:1:150:A:H61	26:1:179:A:H2	1.57	0.50
26:1:526:A:H3'	26:1:527:G:H5''	1.94	0.50
26:1:1072:A:N3	26:1:2513:G:O2'	2.37	0.50
26:1:1074:G:O2'	26:1:1075:G:H5'	2.12	0.50
26:1:1619:A:H2'	26:1:1620:G:H8	1.76	0.50
26:1:2317:G:H2'	26:1:2318:U:C6	2.47	0.50
26:1:2842:G:O2'	26:1:2844:U:OP2	2.19	0.50
1:A:6:LEU:HD23	12:L:10:ILE:HG13	1.94	0.50
4:D:4:ILE:HD12	4:D:40:PHE:HB3	1.92	0.50
6:F:42:VAL:CG2	6:F:50:VAL:HG21	2.42	0.50
11:K:6:ILE:O	11:K:6:ILE:HG22	2.12	0.50
21:W:60:ALA:HB1	21:W:84:CYS:HB2	1.94	0.50
24:Z:98:GLY:HA2	24:Z:100:TYR:CE2	2.47	0.50
26:1:155:U:C2'	26:1:156:A:H5'	2.42	0.50
26:1:335:U:O2'	26:1:336:U:H5'	2.12	0.50
26:1:1315:C:O2'	26:1:1316:G:H5'	2.11	0.50
26:1:1463:A:H2'	26:1:1464:U:H5''	1.93	0.50
26:1:1753:U:O2'	26:1:1754:C:H5'	2.11	0.50
26:1:2419:A:H2'	26:1:2420:U:O4'	2.11	0.50
26:1:2580:G:H2'	26:1:2581:U:O4'	2.11	0.50
26:1:2813:U:O2'	26:1:2814:C:H5'	2.12	0.50
1:A:29:ARG:HB2	1:A:87:GLU:CG	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:42:ALA:HB1	26:1:896:U:O2	2.12	0.50
19:S:58:SER:O	19:S:79:ARG:NE	2.44	0.50
19:S:205:VAL:HG12	19:S:206:LEU:HD23	1.94	0.50
26:1:308:C:O2'	26:1:309:U:H5'	2.12	0.50
26:1:525:A:N3	26:1:527:G:H5''	2.27	0.50
26:1:1563:U:H2'	26:1:1564:G:C8	2.46	0.50
1:A:33:ARG:HG2	1:A:42:ILE:CD1	2.42	0.50
5:E:42:ALA:HB2	26:1:2037:G:H5''	1.94	0.50
7:G:40:ILE:CD1	7:G:60:GLU:HG3	2.42	0.50
9:I:44:ILE:HD13	9:I:47:ARG:NH1	2.26	0.50
21:W:7:ARG:HD3	21:W:18:GLU:OE2	2.12	0.50
23:Y:17:THR:HG22	23:Y:96:VAL:HG23	1.94	0.50
26:1:82:G:H5''	26:1:339:A:H5'	1.94	0.50
26:1:402:C:O2'	26:1:403:U:H5'	2.12	0.50
26:1:642:U:O2'	26:1:643:G:H5'	2.12	0.50
26:1:1389:U:C2'	26:1:1390:A:H5''	2.40	0.50
26:1:1597:U:H5'	26:1:1767:G:H22	1.76	0.50
26:1:1858:G:O2'	26:1:1859:C:H5'	2.12	0.50
26:1:1865:C:N4	26:1:1925:U:H2'	2.27	0.50
26:1:2022:U:H3'	26:1:2023:C:H2'	1.92	0.50
26:1:2397:G:H2'	26:1:2398:G:H5'	1.94	0.50
26:1:2441:G:C2'	26:1:2442:G:H5'	2.42	0.50
26:1:2563:G:O2'	26:1:2564:U:H5'	2.12	0.50
6:F:56:MET:HE2	26:1:1378:U:O4'	2.12	0.50
26:1:265:A:N3	26:1:476:A:O2'	2.34	0.50
26:1:992:A:H1'	26:1:1028:G:C8	2.47	0.50
26:1:1469:G:H2'	26:1:1470:G:C8	2.47	0.50
26:1:1862:G:H1	26:1:1932:C:H5	1.58	0.50
8:H:27:VAL:HG23	8:H:45:GLU:HB2	1.94	0.49
11:K:8:ASP:OD1	11:K:9:LEU:N	2.44	0.49
17:Q:5:LYS:NZ	26:1:256:C:OP2	2.30	0.49
26:1:214:G:O2'	26:1:215:G:H5'	2.12	0.49
26:1:332:A:O2'	26:1:333:C:H5'	2.11	0.49
26:1:1914:C:C2'	26:1:1915:G:H5'	2.41	0.49
1:A:66:ILE:HD13	1:A:71:GLY:HA3	1.93	0.49
11:K:37:LEU:HD11	11:K:40:THR:HA	1.94	0.49
19:S:49:HIS:ND1	19:S:92:PRO:HB3	2.27	0.49
21:W:5:GLU:OE2	21:W:20:LEU:HD11	2.13	0.49
21:W:61:VAL:HG11	21:W:111:PHE:CE1	2.47	0.49
26:1:367:A:H2'	26:1:368:A:H5'	1.94	0.49
26:1:421:C:H2'	26:1:422:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:785:C:O2'	26:1:786:U:H5'	2.12	0.49
27:2:76:A:H2'	27:2:77:G:H5'	1.93	0.49
5:E:59:GLU:HB3	5:E:66:THR:CG2	2.42	0.49
16:P:41:LYS:HE3	26:1:505:U:H5''	1.95	0.49
17:Q:58:VAL:CG1	17:Q:61:LEU:HD12	2.41	0.49
18:R:2:LYS:NZ	18:R:31:LYS:O	2.45	0.49
26:1:1013:U:H2'	26:1:1014:U:C6	2.46	0.49
26:1:1894:G:O2'	26:1:1895:C:H5'	2.12	0.49
27:2:23:U:H5'	27:2:24:C:H5	1.77	0.49
26:1:102:A:H5'	26:1:103:U:OP2	2.12	0.49
26:1:1431:U:O2'	26:1:1432:A:H5'	2.13	0.49
26:1:1566:G:N3	26:1:1566:G:H2'	2.27	0.49
26:1:1773:A:H2'	26:1:1774:A:O4'	2.11	0.49
27:2:28:C:H2'	27:2:29:C:H5'	1.93	0.49
2:B:205:VAL:O	2:B:210:ARG:HD3	2.11	0.49
15:O:26:ASN:HD21	26:1:2313:A:H2'	1.77	0.49
26:1:226:A:O2'	26:1:466:C:O2	2.30	0.49
26:1:1368:C:O2'	26:1:1369:G:H5'	2.12	0.49
26:1:2226:A:N6	26:1:2251:G:O2'	2.39	0.49
26:1:2390:U:O2'	26:1:2391:C:H5'	2.13	0.49
26:1:2852:U:O2'	26:1:2853:U:OP2	2.25	0.49
1:A:66:ILE:HD13	1:A:71:GLY:CA	2.43	0.49
1:A:91:ARG:O	1:A:115:ILE:HG13	2.12	0.49
2:B:96:TYR:HE2	2:B:102:ARG:HD2	1.77	0.49
5:E:92:ARG:O	26:1:1658:A:N6	2.42	0.49
12:L:115:VAL:HG22	12:L:182:ASN:HA	1.94	0.49
26:1:83:G:N2	26:1:101:G:H1'	2.27	0.49
26:1:173:A:H2'	26:1:174:U:C6	2.48	0.49
26:1:800:G:O2'	26:1:801:A:H5'	2.13	0.49
26:1:1446:U:H2'	26:1:1447:A:C8	2.48	0.49
26:1:1501:G:O2'	26:1:1502:A:O4'	2.28	0.49
26:1:1522:G:H22	26:1:1558:U:H3	1.60	0.49
27:2:75:U:H3	27:2:94:C:H5	1.59	0.49
2:B:124:ILE:O	2:B:124:ILE:HG13	2.12	0.49
2:B:260:ARG:HB2	26:1:1825:U:OP1	2.12	0.49
4:D:42:GLY:HA3	4:D:46:VAL:O	2.13	0.49
5:E:2:GLU:HG2	5:E:108:SER:HB2	1.94	0.49
8:H:60:VAL:HG12	8:H:73:MET:SD	2.52	0.49
22:X:29:LYS:CD	22:X:30:THR:HG23	2.39	0.49
24:Z:26:ILE:CD1	24:Z:71:ILE:HD11	2.43	0.49
26:1:268:A:O2'	26:1:269:G:H4'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:653:G:H2'	26:1:654:C:C6	2.48	0.49
26:1:1445:C:H2'	26:1:1446:U:C6	2.48	0.49
26:1:1883:A:H2'	26:1:1884:G:H5'	1.95	0.49
2:B:177:ARG:HH22	26:1:1847:U:H5	1.61	0.49
9:I:38:PHE:HE1	9:I:92:VAL:HG11	1.78	0.49
10:J:37:ARG:HG2	10:J:46:LYS:HB3	1.94	0.49
23:Y:34:LEU:HD11	23:Y:129:THR:OG1	2.13	0.49
26:1:1041:G:O2'	26:1:1042:C:H5'	2.12	0.49
26:1:1217:U:H4'	26:1:1218:G:OP1	2.12	0.49
26:1:1505:G:O2'	26:1:2729:G:O2'	2.11	0.49
26:1:1732:U:O2'	26:1:1744:A:N7	2.35	0.49
26:1:1920:C:C2'	26:1:1921:C:H5'	2.43	0.49
26:1:2885:U:OP2	26:1:2886:G:O2'	2.12	0.49
7:G:91:VAL:HG12	7:G:92:ARG:O	2.13	0.49
11:K:9:LEU:HD12	11:K:12:SER:CB	2.42	0.49
21:W:8:LEU:HB2	21:W:19:VAL:CG2	2.42	0.49
25:a:23:SER:HB2	25:a:47:ASP:OD2	2.13	0.49
26:1:544:U:C2'	26:1:545:G:H5'	2.42	0.49
26:1:1869:G:H2'	26:1:1870:C:H6	1.78	0.49
26:1:2237:U:H4'	26:1:2238:U:O5'	2.12	0.49
1:A:41:ARG:HH12	21:W:104:ARG:HH12	1.59	0.49
2:B:182:ARG:NH1	26:1:1826:G:O2'	2.46	0.49
3:C:94:MET:HE3	4:D:11:GLN:C	2.38	0.49
9:I:77:PHE:CE1	9:I:87:VAL:HG22	2.48	0.49
26:1:373:A:H2	26:1:1248:U:H2'	1.78	0.49
26:1:398:C:O2'	26:1:399:U:H5'	2.13	0.49
26:1:674:C:H1'	26:1:684:U:O2'	2.12	0.49
26:1:1177:A:H4'	26:1:1178:C:H5''	1.95	0.49
26:1:1236:G:N2	26:1:1287:U:O2'	2.46	0.49
26:1:1385:G:C2'	26:1:1386:U:H5'	2.43	0.49
2:B:144:ILE:HG22	2:B:145:GLU:O	2.13	0.48
4:D:38:VAL:O	4:D:53:VAL:HG12	2.13	0.48
6:F:30:ASP:O	6:F:33:VAL:HG22	2.12	0.48
19:S:205:VAL:HG12	19:S:206:LEU:CD2	2.43	0.48
20:V:16:TRP:CE3	20:V:56:ILE:HD11	2.47	0.48
21:W:22:ILE:HD11	21:W:42:THR:HB	1.95	0.48
21:W:70:ARG:HG3	21:W:76:TYR:CE1	2.48	0.48
23:Y:1:MET:CB	23:Y:48:GLU:HG3	2.42	0.48
26:1:58:G:H2'	26:1:59:U:C6	2.48	0.48
26:1:505:U:C2'	26:1:506:A:H5''	2.42	0.48
26:1:969:A:H3'	26:1:970:U:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1389:U:H2'	26:1:1390:A:H5''	1.94	0.48
26:1:2715:G:OP1	26:1:2740:A:N6	2.45	0.48
2:B:210:ARG:HA	2:B:213:TRP:CE2	2.48	0.48
6:F:10:PRO:HD3	11:K:30:PHE:CE1	2.47	0.48
7:G:3:ILE:CD1	7:G:68:VAL:HG23	2.43	0.48
20:V:36:ILE:HD11	20:V:141:TYR:CZ	2.47	0.48
26:1:18:C:O2'	26:1:597:U:OP1	2.28	0.48
26:1:622:A:H2'	26:1:623:C:H6	1.77	0.48
26:1:813:G:O2'	26:1:814:A:H5'	2.13	0.48
26:1:2319:U:H2'	26:1:2320:C:C6	2.48	0.48
26:1:2326:G:H2'	26:1:2327:A:C8	2.46	0.48
1:A:28:LEU:HD22	1:A:86:ILE:CG2	2.44	0.48
3:C:24:TYR:CE1	26:1:578:G:H5'	2.47	0.48
7:G:8:ASN:ND2	7:G:22:LYS:HD2	2.28	0.48
11:K:6:ILE:HG21	11:K:53:LEU:HD23	1.95	0.48
12:L:26:THR:OG1	12:L:200:ASN:HA	2.13	0.48
15:O:9:CYS:HB2	15:O:45:HIS:CE1	2.48	0.48
21:W:12:ASP:OD1	21:W:98:ILE:HD13	2.14	0.48
23:Y:51:ARG:HA	23:Y:54:MET:HE3	1.96	0.48
26:1:537:A:C2'	26:1:538:G:H5'	2.42	0.48
26:1:837:G:N3	26:1:2099:G:O2'	2.46	0.48
26:1:1237:U:H2'	26:1:1238:U:C6	2.48	0.48
26:1:2377:C:O2'	26:1:2378:G:H5'	2.13	0.48
6:F:37:GLN:NE2	26:1:144:C:H4'	2.28	0.48
16:P:40:ARG:NH2	26:1:514:G:N7	2.59	0.48
22:X:132:ALA:O	22:X:136:ILE:HG13	2.13	0.48
24:Z:41:ARG:NH1	26:1:2858:G:H1'	2.27	0.48
26:1:138:U:H2'	26:1:140:A:OP2	2.14	0.48
26:1:307:A:H2'	26:1:308:C:H6	1.77	0.48
26:1:346:A:H2'	26:1:347:U:H6	1.79	0.48
26:1:597:U:O2'	26:1:598:G:H5'	2.14	0.48
26:1:1431:U:C2'	26:1:1432:A:H5'	2.43	0.48
26:1:1588:U:H2'	26:1:1589:U:O4'	2.14	0.48
26:1:1597:U:H5'	26:1:1767:G:N2	2.28	0.48
26:1:2121:A:O2'	26:1:2122:A:H5'	2.13	0.48
26:1:2697:G:O2'	26:1:2698:A:H5'	2.14	0.48
27:2:11:A:H2'	27:2:12:U:H5''	1.96	0.48
2:B:67:PHE:HE1	2:B:105:ILE:HD11	1.78	0.48
2:B:111:GLU:HG3	2:B:111:GLU:O	2.13	0.48
5:E:44:SER:O	5:E:48:GLU:HG3	2.13	0.48
7:G:15:LYS:HB3	26:1:352:A:H5'	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:22:ILE:O	14:N:22:ILE:HG13	2.12	0.48
16:P:38:LYS:NZ	26:1:515:G:H1	2.09	0.48
23:Y:29:PHE:HB2	23:Y:105:GLU:OE1	2.14	0.48
25:a:31:LEU:HD23	25:a:94:PHE:CD1	2.49	0.48
26:1:155:U:O2'	26:1:156:A:H5'	2.14	0.48
26:1:403:U:C2'	26:1:404:U:H5''	2.44	0.48
26:1:692:G:H2'	26:1:693:G:O4'	2.14	0.48
26:1:793:G:H22	26:1:796:A:C5'	2.26	0.48
26:1:1874:A:O2'	26:1:1875:A:OP2	2.26	0.48
26:1:2574:U:H2'	26:1:2575:G:H8	1.76	0.48
7:G:16:ASP:CB	7:G:38:VAL:HG13	2.43	0.48
13:M:38:GLU:O	13:M:43:ILE:HG21	2.14	0.48
23:Y:68:ILE:CG2	23:Y:101:ARG:HD3	2.43	0.48
26:1:873:U:H2'	26:1:874:A:C8	2.49	0.48
26:1:1895:C:H2'	26:1:1896:U:O4'	2.14	0.48
1:A:32:VAL:HG22	1:A:43:GLN:O	2.13	0.48
6:F:23:ASP:OD1	6:F:23:ASP:N	2.46	0.48
26:1:59:U:H2'	26:1:60:U:H5'	1.96	0.48
26:1:86:C:O2'	26:1:87:U:H5'	2.14	0.48
26:1:758:G:H1'	26:1:763:A:H61	1.78	0.48
26:1:886:A:O2'	26:1:887:A:H5'	2.13	0.48
26:1:1637:A:H2'	26:1:1638:G:H8	1.76	0.48
26:1:1700:C:H2'	26:1:1701:U:C6	2.49	0.48
26:1:2594:G:H2'	26:1:2595:C:C6	2.49	0.48
27:2:16:A:H5''	27:2:17:A:OP2	2.13	0.48
8:H:48:PHE:CA	8:H:51:VAL:HG12	2.43	0.48
8:H:61:ILE:O	8:H:72:VAL:N	2.47	0.48
15:O:7:LEU:CD2	15:O:32:MET:HG3	2.43	0.48
15:O:7:LEU:HA	15:O:46:ARG:O	2.12	0.48
26:1:2221:U:H2'	26:1:2222:U:H6	1.76	0.48
27:2:101:A:H2'	27:2:102:G:H5'	1.95	0.48
1:A:35:ILE:HA	1:A:40:GLU:HG2	1.94	0.48
6:F:6:ILE:HD11	6:F:37:GLN:O	2.14	0.48
12:L:24:PRO:HB3	26:1:2709:U:O2	2.14	0.48
20:V:70:GLU:HG2	20:V:91:GLY:CA	2.43	0.48
25:a:9:LYS:NZ	27:2:58:C:H5'	2.28	0.48
26:1:743:C:O2'	26:1:779:A:N6	2.44	0.48
26:1:1734:A:H2'	26:1:1735:C:O4'	2.13	0.48
26:1:1865:C:H5	26:1:1928:A:H62	1.60	0.48
26:1:2521:G:H2'	26:1:2522:G:H5'	1.96	0.48
26:1:2829:A:H2'	26:1:2830:A:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:ARG:HE	1:A:43:GLN:NE2	2.12	0.48
12:L:119:THR:HB	12:L:210:GLU:HG2	1.96	0.48
26:1:194:A:H2'	26:1:195:C:C6	2.49	0.48
26:1:396:G:H2'	26:1:397:U:H6	1.79	0.48
26:1:888:G:O2'	26:1:889:U:H5'	2.14	0.48
26:1:1325:U:HO2'	26:1:1326:C:P	2.36	0.48
26:1:1516:C:H2'	26:1:1517:A:O4'	2.13	0.48
26:1:1711:G:O2'	26:1:2018:U:O4	2.26	0.48
26:1:2884:G:O2'	26:1:2885:U:H5'	2.13	0.48
5:E:38:LEU:HD12	14:N:27:MET:SD	2.54	0.47
10:J:5:CYS:SG	10:J:8:THR:OG1	2.64	0.47
17:Q:7:HIS:HD2	17:Q:10:ALA:HB2	1.79	0.47
17:Q:26:ARG:NH2	17:Q:44:LEU:HD23	2.29	0.47
26:1:747:U:H2'	26:1:748:U:O4'	2.14	0.47
26:1:749:G:H1'	26:1:772:A:N6	2.29	0.47
26:1:1059:A:O2'	26:1:1060:U:H5'	2.13	0.47
26:1:1388:C:H2'	26:1:1389:U:O4'	2.13	0.47
26:1:2125:U:O2	26:1:2218:G:C6	2.67	0.47
26:1:2235:A:H2'	26:1:2236:C:C6	2.49	0.47
26:1:2870:A:N7	26:1:2888:A:O2'	2.35	0.47
1:A:35:ILE:HG22	1:A:40:GLU:CD	2.39	0.47
12:L:138:ARG:HD2	12:L:141:MET:HE2	1.96	0.47
14:N:9:SER:HB2	26:1:2047:A:H5'	1.95	0.47
22:X:117:LEU:HD12	22:X:135:ALA:O	2.14	0.47
26:1:159:U:H2'	26:1:160:G:C5'	2.42	0.47
26:1:509:G:N2	26:1:512:A:OP2	2.41	0.47
26:1:736:C:C2'	26:1:737:C:H5'	2.43	0.47
26:1:1352:C:H2'	26:1:1353:A:C8	2.48	0.47
26:1:2318:U:H2'	26:1:2319:U:H6	1.74	0.47
26:1:2464:C:O2'	26:1:2465:U:H5'	2.14	0.47
26:1:2642:U:H2'	26:1:2643:C:H6	1.78	0.47
26:1:2860:U:O2'	26:1:2861:U:H5'	2.13	0.47
2:B:87:ARG:NH2	26:1:1844:G:OP1	2.47	0.47
6:F:12:ILE:O	6:F:12:ILE:HG13	2.14	0.47
9:I:46:TYR:HB3	9:I:67:LEU:HD12	1.95	0.47
17:Q:53:SER:O	17:Q:56:LYS:HB2	2.14	0.47
25:a:94:PHE:CZ	25:a:109:ALA:HB2	2.49	0.47
26:1:569:U:H2'	26:1:570:U:C6	2.49	0.47
26:1:1175:G:O2'	26:1:2053:U:H5'	2.15	0.47
26:1:2423:G:O2'	26:1:2424:G:H5'	2.15	0.47
26:1:2583:C:H2'	26:1:2584:G:C5'	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:GLU:CG	1:A:78:LEU:HD12	2.43	0.47
12:L:42:GLU:OE2	12:L:43:VAL:HG13	2.13	0.47
12:L:57:LYS:HB2	12:L:68:TYR:CD1	2.49	0.47
26:1:613:G:H2'	26:1:2057:A:N7	2.30	0.47
26:1:738:U:H2'	26:1:739:U:C6	2.50	0.47
26:1:1576:A:O2'	26:1:1577:G:H5'	2.14	0.47
26:1:1955:A:N3	26:1:1955:A:C2'	2.77	0.47
26:1:2429:U:O2'	26:1:2430:C:H5'	2.14	0.47
26:1:2521:G:C2'	26:1:2522:G:H5'	2.44	0.47
1:A:108:LYS:HG3	1:A:111:ARG:CZ	2.44	0.47
7:G:3:ILE:HD13	7:G:68:VAL:HG23	1.96	0.47
14:N:3:VAL:HG12	26:1:2042:A:N3	2.28	0.47
16:P:4:ARG:NH1	26:1:797:A:OP1	2.48	0.47
23:Y:39:THR:O	23:Y:40:SER:OG	2.25	0.47
23:Y:58:MET:HE1	23:Y:64:VAL:HG23	1.94	0.47
26:1:1000:G:H2'	26:1:1001:A:H2'	1.96	0.47
26:1:1577:G:N2	26:1:1589:U:O2	2.47	0.47
26:1:1806:U:O2	26:1:1810:A:N6	2.48	0.47
26:1:1941:C:OP2	26:1:1941:C:H4'	2.13	0.47
26:1:2319:U:H2'	26:1:2320:C:H6	1.80	0.47
3:C:94:MET:HE1	20:V:3:GLN:NE2	2.18	0.47
6:F:10:PRO:HD2	11:K:33:ALA:CB	2.44	0.47
24:Z:49:THR:HG22	24:Z:53:LYS:HE3	1.95	0.47
24:Z:71:ILE:O	24:Z:78:THR:HA	2.14	0.47
26:1:799:U:O2'	26:1:800:G:H5'	2.14	0.47
26:1:907:G:H2'	26:1:908:A:O4'	2.15	0.47
26:1:1306:A:H2'	26:1:1307:G:O4'	2.14	0.47
26:1:2238:U:O2	26:1:2238:U:H2'	2.14	0.47
26:1:2671:A:O2'	26:1:2672:G:H5'	2.15	0.47
1:A:11:THR:HG21	12:L:13:THR:CG2	2.40	0.47
1:A:31:HIS:CE1	1:A:44:VAL:HG12	2.49	0.47
2:B:174:ILE:CG1	2:B:184:ILE:HD12	2.36	0.47
3:C:4:VAL:HG22	26:1:1238:U:C1'	2.37	0.47
4:D:27:VAL:CG2	4:D:62:VAL:HG21	2.41	0.47
7:G:79:THR:HG22	7:G:96:LYS:CD	2.45	0.47
8:H:48:PHE:HA	8:H:51:VAL:CG1	2.42	0.47
10:J:8:THR:OG1	10:J:10:ARG:HG2	2.15	0.47
10:J:34:GLN:OE1	26:1:2118:U:H1'	2.14	0.47
12:L:156:MET:O	26:1:2079:G:H4'	2.14	0.47
19:S:67:GLN:O	19:S:67:GLN:HG2	2.15	0.47
19:S:141:ASN:O	19:S:145:THR:HG23	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:79:LEU:CD2	22:X:82:LEU:HD12	2.42	0.47
24:Z:112:ASP:O	26:1:2036:G:H1'	2.15	0.47
26:1:66:C:H2'	26:1:67:G:H8	1.78	0.47
26:1:198:A:H61	26:1:201:C:H3'	1.78	0.47
26:1:275:A:N6	26:1:296:G:N2	2.33	0.47
26:1:849:A:H2'	26:1:851:C:C4	2.50	0.47
26:1:894:A:H2'	26:1:895:U:O2	2.15	0.47
26:1:1312:A:H4'	26:1:1313:G:OP1	2.15	0.47
26:1:1869:G:H2'	26:1:1870:C:C6	2.50	0.47
26:1:2591:A:OP1	26:1:2675:G:H4'	2.15	0.47
1:A:77:PRO:HB2	1:A:80:THR:HG23	1.96	0.47
2:B:93:LEU:HD23	2:B:103:TYR:CE1	2.50	0.47
2:B:176:LEU:HD12	2:B:180:GLU:CG	2.38	0.47
22:X:17:ASN:HD22	22:X:18:ARG:H	1.63	0.47
23:Y:83:MET:HE1	26:1:1000:G:O4'	2.15	0.47
23:Y:111:GLU:O	23:Y:115:ARG:HG3	2.14	0.47
25:a:17:ARG:NH2	26:1:2361:U:OP2	2.47	0.47
26:1:39:C:O2'	26:1:658:A:N1	2.41	0.47
26:1:447:A:H2'	26:1:448:A:H8	1.77	0.47
26:1:1823:U:H2'	26:1:1824:C:H6	1.78	0.47
27:2:47:C:H2'	27:2:48:A:C8	2.49	0.47
6:F:61:LYS:O	6:F:72:THR:HG23	2.15	0.47
19:S:37:ILE:HD11	19:S:187:THR:HG21	1.97	0.47
19:S:131:PHE:HZ	19:S:142:VAL:HG21	1.79	0.47
25:a:32:ASN:HD22	25:a:33:VAL:N	2.12	0.47
26:1:303:G:H2'	26:1:304:G:O4'	2.15	0.47
26:1:355:G:H2'	26:1:356:A:C8	2.50	0.47
26:1:872:U:O2'	26:1:2095:U:N3	2.48	0.47
4:D:60:ALA:CB	4:D:97:ILE:HD13	2.41	0.47
18:R:18:LYS:NZ	18:R:21:GLY:HA2	2.30	0.47
22:X:55:LEU:HD11	22:X:59:ARG:HH11	1.80	0.47
24:Z:59:ARG:HA	24:Z:86:PHE:CZ	2.50	0.47
25:a:49:LYS:HB2	25:a:51:VAL:HG23	1.97	0.47
26:1:525:A:H1'	26:1:526:A:H5''	1.97	0.47
26:1:661:U:H2'	26:1:662:G:H8	1.80	0.47
26:1:1774:A:H2'	26:1:1775:G:H8	1.80	0.47
26:1:2218:G:H2'	26:1:2219:C:C6	2.50	0.47
26:1:2354:A:H2'	26:1:2355:A:C8	2.50	0.47
1:A:22:PHE:HZ	1:A:78:LEU:HD21	1.80	0.46
3:C:105:ALA:O	3:C:108:GLN:HB2	2.15	0.46
12:L:8:ARG:CG	12:L:206:LYS:HA	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:39:LYS:O	17:Q:43:GLN:HG2	2.15	0.46
18:R:36:GLN:HE21	26:1:1169:G:C5'	2.28	0.46
26:1:1334:C:OP1	26:1:2737:C:H4'	2.14	0.46
26:1:1824:C:O2'	26:1:1825:U:H5'	2.15	0.46
26:1:2284:U:O2'	26:1:2285:C:H5'	2.15	0.46
26:1:2490:C:O2'	26:1:2491:C:H5'	2.14	0.46
26:1:2786:G:O2'	26:1:2787:C:H5'	2.14	0.46
1:A:29:ARG:HB2	1:A:87:GLU:HG2	1.97	0.46
25:a:103:GLY:N	25:a:106:LYS:HB3	2.29	0.46
26:1:11:U:O2'	26:1:12:U:H5'	2.16	0.46
26:1:57:C:H2'	26:1:58:G:O4'	2.15	0.46
26:1:203:U:H2'	26:1:204:C:H5'	1.96	0.46
26:1:486:G:H2'	26:1:487:U:C6	2.51	0.46
26:1:1078:G:H2'	26:1:1079:U:O4'	2.14	0.46
26:1:1793:C:O2'	26:1:1794:C:H5'	2.15	0.46
26:1:2341:A:H2'	26:1:2342:U:C6	2.50	0.46
1:A:105:LEU:CB	1:A:110:ALA:HB2	2.45	0.46
2:B:132:LEU:HG	2:B:188:CYS:O	2.15	0.46
4:D:2:PHE:HB3	4:D:15:GLU:CG	2.41	0.46
6:F:69:GLN:O	26:1:64:A:O2'	2.28	0.46
26:1:897:A:C2'	26:1:898:U:H5'	2.45	0.46
26:1:1949:G:H2'	26:1:1950:U:O4'	2.15	0.46
26:1:2397:G:C2'	26:1:2398:G:H5'	2.45	0.46
5:E:13:ALA:O	5:E:17:VAL:HG23	2.15	0.46
16:P:5:THR:O	26:1:731:U:O2'	2.27	0.46
26:1:109:G:O2'	26:1:110:A:H5'	2.16	0.46
26:1:765:U:H2'	26:1:766:G:C8	2.50	0.46
26:1:1197:C:H2'	26:1:1198:G:O4'	2.14	0.46
26:1:1398:G:H2'	26:1:1399:C:C6	2.50	0.46
26:1:1425:G:O2'	26:1:1426:G:H5'	2.16	0.46
26:1:2328:A:O2'	26:1:2329:U:H5'	2.14	0.46
8:H:51:VAL:O	8:H:55:VAL:HG22	2.14	0.46
11:K:15:GLU:O	11:K:19:LYS:HG3	2.16	0.46
17:Q:57:ARG:HG3	26:1:879:U:H5'	1.98	0.46
22:X:110:LYS:NZ	26:1:681:G:N7	2.45	0.46
26:1:94:A:H2'	26:1:95:A:O4'	2.15	0.46
26:1:609:U:O2'	26:1:610:U:H5'	2.16	0.46
26:1:1927:A:C2	26:1:1997:A:C6	3.04	0.46
26:1:2250:A:H2'	26:1:2251:G:O4'	2.15	0.46
26:1:2770:U:H2'	26:1:2771:G:O4'	2.15	0.46
1:A:34:ILE:HG23	1:A:36:GLU:HG3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:28:ASN:HD22	5:E:29:ALA:H	1.64	0.46
18:R:17:ILE:HG13	18:R:18:LYS:N	2.31	0.46
18:R:36:GLN:HE21	26:1:1169:G:H5'	1.80	0.46
26:1:183:A:O4'	26:1:481:C:H1'	2.16	0.46
26:1:590:U:OP1	26:1:1257:G:O2'	2.24	0.46
26:1:1250:G:H1'	26:1:1275:A:N6	2.30	0.46
26:1:2105:C:H2'	26:1:2106:U:C6	2.50	0.46
26:1:2615:G:C2'	26:1:2616:A:H5'	2.45	0.46
2:B:260:ARG:HH12	2:B:264:LYS:HD3	1.80	0.46
9:I:53:ILE:CG2	9:I:87:VAL:HG23	2.46	0.46
23:Y:83:MET:HE1	26:1:1000:G:C1'	2.45	0.46
26:1:342:A:H2'	26:1:343:A:C8	2.51	0.46
26:1:545:G:N1	26:1:548:A:OP2	2.26	0.46
26:1:1608:C:H2'	26:1:1609:U:C6	2.51	0.46
26:1:2866:G:H2'	26:1:2867:U:C6	2.50	0.46
27:2:62:U:H2'	27:2:63:U:H6	1.80	0.46
2:B:117:GLU:OE1	2:B:130:LEU:HD22	2.15	0.46
6:F:10:PRO:HD2	11:K:33:ALA:HB3	1.98	0.46
6:F:46:PHE:HZ	11:K:30:PHE:HE2	1.64	0.46
12:L:156:MET:HE2	12:L:160:ALA:HB2	1.96	0.46
15:O:32:MET:O	15:O:44:LEU:HD23	2.16	0.46
21:W:39:ILE:HD13	21:W:62:ILE:HD11	1.98	0.46
23:Y:17:THR:HG22	23:Y:96:VAL:CG2	2.45	0.46
24:Z:34:GLU:OE1	24:Z:115:GLU:HG2	2.14	0.46
26:1:273:A:N7	26:1:298:U:O4	2.49	0.46
26:1:1072:A:H2'	26:1:1073:A:C8	2.51	0.46
26:1:1350:U:O2'	26:1:1351:C:OP1	2.28	0.46
26:1:1686:G:H2'	26:1:1687:G:O4'	2.16	0.46
26:1:2325:A:N6	26:1:2345:A:O2'	2.49	0.46
12:L:39:LYS:NZ	12:L:90:GLU:OE2	2.30	0.46
13:M:8:LEU:HD12	13:M:53:LEU:O	2.15	0.46
20:V:22:GLU:CG	20:V:59:ASN:HB3	2.41	0.46
22:X:69:ILE:HG13	22:X:70:ASN:N	2.31	0.46
26:1:781:C:H2'	26:1:782:C:C6	2.51	0.46
26:1:862:C:O2'	26:1:884:U:OP1	2.28	0.46
26:1:1355:A:O2'	26:1:1356:G:H5'	2.15	0.46
26:1:2059:G:O6	26:1:2480:A:O2'	2.33	0.46
26:1:2465:U:O2'	26:1:2467:C:OP1	2.28	0.46
26:1:2531:U:H2'	28:1:3001:G6V:O13	2.15	0.46
1:A:59:GLU:CD	1:A:78:LEU:HD12	2.40	0.46
4:D:94:LYS:C	4:D:95:LEU:HD12	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:110:PHE:O	12:L:188:VAL:HG11	2.16	0.46
12:L:156:MET:HG2	26:1:2598:U:O2	2.16	0.46
24:Z:26:ILE:HD13	24:Z:71:ILE:HD11	1.97	0.46
26:1:181:G:C2'	26:1:182:C:H5'	2.46	0.46
26:1:811:C:H2'	26:1:812:U:O4'	2.17	0.46
26:1:1453:G:H4'	26:1:1459:A:C1'	2.44	0.46
26:1:2122:A:O2'	26:1:2123:A:H5'	2.15	0.46
26:1:2493:C:O2'	26:1:2494:C:H5'	2.15	0.46
26:1:2507:C:C2'	26:1:2508:G:H5'	2.46	0.46
26:1:2872:G:H2'	26:1:2873:C:O4'	2.15	0.46
2:B:156:ARG:N	26:1:1846:A:OP1	2.45	0.45
12:L:215:ILE:H	12:L:215:ILE:HG13	1.55	0.45
23:Y:35:GLN:OE1	23:Y:132:VAL:HG21	2.16	0.45
26:1:877:G:H2'	26:1:878:C:H6	1.77	0.45
26:1:1314:A:H2'	26:1:1315:C:C6	2.51	0.45
10:J:13:SER:HB3	26:1:441:C:O2'	2.16	0.45
20:V:54:TYR:HE1	20:V:122:LYS:HG2	1.80	0.45
25:a:106:LYS:O	25:a:110:GLU:HG2	2.15	0.45
26:1:955:A:H2	26:1:2291:C:O2	2.00	0.45
26:1:1596:G:O2'	26:1:1597:U:H5'	2.16	0.45
26:1:1619:A:H2'	26:1:1620:G:C8	2.51	0.45
26:1:1982:U:O2'	26:1:2579:U:H4'	2.16	0.45
26:1:2553:G:O2'	26:1:2554:C:H5'	2.15	0.45
5:E:78:GLU:OE2	26:1:562:C:O2'	2.23	0.45
16:P:4:ARG:HH12	26:1:797:A:P	2.39	0.45
26:1:686:U:H2'	26:1:687:G:O4'	2.17	0.45
26:1:1481:A:H1'	26:1:1561:G:H21	1.81	0.45
26:1:1806:U:H5	26:1:1811:A:N7	2.13	0.45
26:1:2810:A:H2'	26:1:2811:U:C6	2.50	0.45
2:B:159:GLY:O	2:B:177:ARG:NH1	2.49	0.45
9:I:24:SER:HB2	26:1:2289:U:H5	1.82	0.45
12:L:118:VAL:HG22	12:L:211:ILE:CD1	2.44	0.45
26:1:89:U:H3'	26:1:90:A:C2'	2.46	0.45
26:1:169:G:H2'	26:1:170:C:H5'	1.98	0.45
26:1:801:A:H2'	26:1:802:G:O4'	2.16	0.45
26:1:1398:G:H2'	26:1:1399:C:H6	1.81	0.45
26:1:1410:A:H2'	26:1:1411:G:H5'	1.98	0.45
26:1:1788:U:O2'	26:1:1789:A:H5'	2.16	0.45
26:1:1981:G:N3	26:1:2578:C:H5''	2.31	0.45
26:1:2482:G:H2'	26:1:2483:C:H6	1.80	0.45
26:1:2675:G:H2'	26:1:2676:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2704:A:H2'	26:1:2705:U:O4'	2.16	0.45
1:A:33:ARG:HG2	1:A:42:ILE:HD12	1.98	0.45
12:L:216:LYS:HE2	26:1:2759:G:OP1	2.16	0.45
16:P:3:LYS:HE2	26:1:732:C:H5''	1.97	0.45
21:W:107:ARG:HA	21:W:115:VAL:HG11	1.99	0.45
23:Y:32:PHE:HE1	23:Y:133:LYS:HE3	1.82	0.45
24:Z:8:ARG:CZ	24:Z:16:MET:HE1	2.47	0.45
24:Z:40:VAL:O	24:Z:44:VAL:HG12	2.16	0.45
24:Z:47:LEU:HD21	24:Z:65:THR:OG1	2.16	0.45
26:1:273:A:N6	26:1:298:U:H3	2.09	0.45
26:1:442:G:O2'	26:1:443:U:H5'	2.17	0.45
26:1:568:C:O2'	26:1:569:U:H5'	2.16	0.45
26:1:1921:C:O2'	26:1:1922:C:H5'	2.16	0.45
26:1:1991:G:O2'	26:1:1994:C:OP2	2.14	0.45
26:1:2325:A:N6	26:1:2345:A:H1'	2.31	0.45
26:1:2437:G:H2'	26:1:2438:A:O4'	2.17	0.45
26:1:2757:U:O2'	26:1:2758:G:H5'	2.16	0.45
26:1:2758:G:H2'	26:1:2759:G:C8	2.51	0.45
3:C:35:ALA:O	3:C:39:VAL:HG23	2.16	0.45
3:C:60:LEU:HD21	3:C:64:ARG:CZ	2.46	0.45
9:I:32:LYS:O	9:I:33:ARG:HD3	2.16	0.45
16:P:32:LEU:HD21	16:P:44:SER:OG	2.17	0.45
19:S:51:VAL:HG22	19:S:88:ILE:HG13	1.98	0.45
19:S:125:VAL:HA	19:S:194:ILE:O	2.17	0.45
23:Y:107:ALA:O	23:Y:109:VAL:HG23	2.17	0.45
26:1:19:G:H2'	26:1:20:C:O4'	2.17	0.45
26:1:173:A:O2'	26:1:174:U:H5'	2.16	0.45
26:1:920:A:C2'	26:1:921:C:H5'	2.47	0.45
26:1:1810:A:H5'	26:1:2635:G:H4'	1.97	0.45
26:1:2777:A:H1'	26:1:2779:C:N4	2.31	0.45
12:L:115:VAL:CG2	12:L:182:ASN:HA	2.47	0.45
21:W:65:THR:HG22	21:W:67:SER:N	2.30	0.45
21:W:111:PHE:HB3	21:W:114:ILE:HD12	1.98	0.45
26:1:154:A:H2'	26:1:155:U:O4'	2.16	0.45
26:1:331:G:O2'	26:1:332:A:OP2	2.28	0.45
26:1:1447:A:H2'	26:1:1448:U:O4'	2.16	0.45
26:1:1895:C:H2'	26:1:1896:U:C1'	2.47	0.45
7:G:4:LYS:HE2	7:G:4:LYS:HA	1.98	0.45
8:H:43:VAL:HG11	8:H:48:PHE:HB2	1.99	0.45
21:W:7:ARG:HA	21:W:19:VAL:O	2.17	0.45
23:Y:5:LYS:HG3	26:1:916:U:OP1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:909:G:H2'	26:1:910:C:H6	1.75	0.45
26:1:1996:A:O2'	26:1:1999:G:N3	2.42	0.45
26:1:2314:A:H62	26:1:2371:U:H3	1.65	0.45
26:1:2430:C:C2'	26:1:2431:C:H5'	2.47	0.45
27:2:76:A:C2'	27:2:77:G:H5'	2.47	0.45
7:G:3:ILE:CG2	7:G:23:VAL:HG21	2.46	0.45
8:H:48:PHE:O	8:H:51:VAL:HG12	2.17	0.45
12:L:127:PHE:CD1	26:1:1699:A:H1'	2.52	0.45
15:O:29:ARG:HE	15:O:47:GLU:H	1.65	0.45
15:O:29:ARG:HE	15:O:47:GLU:N	2.15	0.45
19:S:88:ILE:HG22	19:S:90:PHE:O	2.16	0.45
21:W:88:ARG:NH1	21:W:93:PRO:O	2.50	0.45
26:1:95:A:H2'	26:1:96:G:O4'	2.17	0.45
26:1:1452:C:H1'	26:1:1631:G:C6	2.52	0.45
26:1:1633:A:H3'	26:1:1634:A:C5'	2.47	0.45
5:E:65:ASN:O	5:E:69:LEU:HG	2.16	0.45
11:K:6:ILE:CG2	11:K:53:LEU:HD23	2.47	0.45
19:S:140:LYS:NZ	26:1:363:A:H61	2.15	0.45
26:1:89:U:C3'	26:1:90:A:H3'	2.46	0.45
26:1:388:A:H1'	26:1:389:A:H2	1.81	0.45
26:1:482:U:H2'	26:1:483:C:H6	1.82	0.45
26:1:625:G:H2'	26:1:626:G:C8	2.52	0.45
26:1:1497:A:H3'	26:1:1497:A:N3	2.31	0.45
26:1:1515:G:N2	26:1:1565:U:H3	2.13	0.45
26:1:1660:A:H4'	26:1:1661:C:OP2	2.17	0.45
26:1:1865:C:H4'	26:1:1866:G:C5'	2.47	0.45
26:1:2384:U:H2'	26:1:2385:A:H5''	1.99	0.45
26:1:2896:A:H5''	26:1:2897:A:OP2	2.17	0.45
3:C:66:ASN:O	3:C:70:ARG:HG2	2.17	0.44
7:G:15:LYS:HE3	26:1:372:A:N1	2.32	0.44
7:G:93:ILE:HG13	7:G:99:GLU:O	2.18	0.44
9:I:74:VAL:O	9:I:89:VAL:HA	2.16	0.44
19:S:51:VAL:CG2	19:S:88:ILE:HG13	2.46	0.44
19:S:103:LYS:HG2	19:S:106:ARG:HH21	1.82	0.44
26:1:77:U:O2'	26:1:78:U:H5'	2.16	0.44
26:1:432:G:OP2	26:1:434:G:N1	2.38	0.44
26:1:1212:U:H2'	26:1:1213:C:C6	2.52	0.44
26:1:1394:U:H2'	26:1:1395:G:O4'	2.17	0.44
26:1:1937:G:H2'	26:1:1938:U:O4'	2.16	0.44
26:1:1987:A:C2'	26:1:1988:C:H5'	2.47	0.44
26:1:2764:G:O2'	26:1:2765:A:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2826:U:H2'	26:1:2827:A:C8	2.52	0.44
26:1:2867:U:C2'	26:1:2868:G:H5'	2.47	0.44
27:2:28:C:H2'	27:2:29:C:C5'	2.47	0.44
2:B:148:PRO:HD3	2:B:185:LEU:HD23	1.99	0.44
5:E:64:MET:HG3	5:E:69:LEU:HD21	1.99	0.44
6:F:88:ASP:C	6:F:90:PHE:H	2.24	0.44
12:L:122:SER:N	12:L:176:ASN:O	2.38	0.44
12:L:215:ILE:CD1	12:L:216:LYS:HG3	2.41	0.44
21:W:61:VAL:HG13	21:W:87:ILE:CG1	2.45	0.44
26:1:597:U:C2'	26:1:598:G:H5'	2.46	0.44
26:1:983:G:C2'	26:1:984:G:H5'	2.47	0.44
26:1:1325:U:HO2'	26:1:1691:G:H22	1.65	0.44
26:1:1352:C:H2'	26:1:1353:A:H8	1.82	0.44
26:1:1480:G:H2'	26:1:1481:A:O4'	2.17	0.44
26:1:1766:C:C2'	26:1:1767:G:H5'	2.47	0.44
26:1:2050:A:H2'	26:1:2051:C:C6	2.52	0.44
26:1:2567:C:O2'	26:1:2568:A:H5'	2.17	0.44
4:D:20:ILE:HD11	4:D:97:ILE:HD11	1.99	0.44
7:G:12:ILE:O	7:G:17:LYS:HE2	2.17	0.44
12:L:118:VAL:HG13	12:L:211:ILE:HD13	2.00	0.44
18:R:7:VAL:HG22	18:R:37:GLY:HA2	2.00	0.44
20:V:113:THR:HG22	26:1:601:G:OP1	2.16	0.44
26:1:687:G:N2	26:1:689:A:H3'	2.33	0.44
26:1:2367:A:H2'	26:1:2368:G:H8	1.81	0.44
26:1:2709:U:O2'	26:1:2710:C:H5'	2.17	0.44
3:C:94:MET:HE3	4:D:12:ILE:HA	1.99	0.44
10:J:39:LEU:HD23	10:J:44:PRO:HG3	1.99	0.44
19:S:169:ASN:ND2	26:1:366:G:H2'	2.32	0.44
19:S:199:ALA:O	19:S:203:GLU:HG3	2.17	0.44
26:1:49:A:H5''	26:1:51:G:O4'	2.16	0.44
26:1:709:U:H4'	26:1:985:A:OP1	2.18	0.44
26:1:1864:C:H2'	26:1:1926:A:N6	2.33	0.44
26:1:2327:A:H2'	26:1:2328:A:C8	2.53	0.44
2:B:130:LEU:HD12	2:B:134:ASN:HB2	1.98	0.44
18:R:19:ARG:HG2	26:1:2783:U:OP2	2.18	0.44
19:S:74:ARG:NH1	26:1:2087:A:N7	2.65	0.44
26:1:367:A:C2'	26:1:368:A:H5'	2.48	0.44
26:1:2450:U:H6	26:1:2450:U:H5'	1.83	0.44
26:1:2912:A:H5'	26:1:2913:G:O5'	2.17	0.44
2:B:13:ARG:HG2	2:B:16:MET:CE	2.48	0.44
12:L:59:TYR:HB2	12:L:74:GLU:CD	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:138:ARG:HD2	12:L:141:MET:CE	2.48	0.44
22:X:55:LEU:O	22:X:60:ARG:NH1	2.51	0.44
23:Y:40:SER:HB2	23:Y:127:VAL:CG1	2.47	0.44
25:a:101:TYR:CE2	25:a:106:LYS:HD3	2.52	0.44
26:1:701:G:H2'	26:1:702:U:O4'	2.17	0.44
26:1:703:A:H2'	26:1:704:U:C6	2.53	0.44
26:1:757:G:H2'	26:1:758:G:H5'	2.00	0.44
26:1:1778:C:O2'	26:1:1779:C:H5'	2.18	0.44
26:1:1951:C:O2'	26:1:1952:C:H5'	2.17	0.44
26:1:2041:A:H2'	26:1:2042:A:C8	2.52	0.44
26:1:2048:G:H2'	26:1:2048:G:N3	2.32	0.44
7:G:79:THR:HG22	7:G:96:LYS:CG	2.48	0.44
8:H:27:VAL:CG2	8:H:45:GLU:HB2	2.47	0.44
9:I:62:GLY:O	9:I:65:ASP:N	2.45	0.44
26:1:59:U:C2'	26:1:60:U:H5'	2.48	0.44
26:1:100:U:H5'	26:1:101:G:C8	2.53	0.44
26:1:1320:G:O2'	26:1:1322:G:N7	2.45	0.44
2:B:67:PHE:CE1	2:B:156:ARG:HD2	2.53	0.44
2:B:154:ILE:HG21	2:B:176:LEU:CD2	2.47	0.44
5:E:35:ILE:HG13	14:N:27:MET:HE1	1.99	0.44
12:L:35:VAL:HG23	12:L:50:GLN:O	2.18	0.44
12:L:158:SER:HB3	26:1:2599:A:N7	2.33	0.44
14:N:38:LEU:O	14:N:41:ARG:HB2	2.18	0.44
19:S:39:LEU:HD11	19:S:99:TYR:O	2.18	0.44
19:S:46:GLN:NE2	26:1:487:U:O2	2.36	0.44
22:X:63:LYS:HE2	26:1:2421:C:H5''	2.00	0.44
26:1:757:G:C2'	26:1:758:G:H5'	2.47	0.44
26:1:852:U:O2'	26:1:2087:A:N1	2.47	0.44
26:1:1219:G:H2'	26:1:1220:A:H8	1.83	0.44
26:1:1799:G:N2	26:1:1801:C:H5''	2.32	0.44
26:1:1881:A:H3'	26:1:1882:G:H8	1.82	0.44
26:1:2489:U:H2'	26:1:2490:C:O4'	2.16	0.44
26:1:2888:A:H2'	26:1:2889:G:O4'	2.17	0.44
1:A:72:VAL:HG12	21:W:79:PHE:CD1	2.53	0.44
3:C:3:ARG:NH2	26:1:492:G:OP1	2.47	0.44
6:F:88:ASP:HB3	6:F:89:LEU:H	1.51	0.44
12:L:34:VAL:CG2	12:L:85:LYS:HE3	2.47	0.44
12:L:146:HIS:HE1	26:1:789:C:OP2	2.01	0.44
14:N:8:THR:HG22	14:N:9:SER:O	2.18	0.44
26:1:334:A:O2'	26:1:335:U:H5'	2.17	0.44
26:1:434:G:H2'	26:1:436:A:C2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:462:U:H2'	26:1:463:C:C6	2.53	0.44
26:1:1856:A:H2'	26:1:1857:C:H5'	1.99	0.44
26:1:2286:G:H1'	26:1:2454:C:C2	2.52	0.44
26:1:2798:C:H2'	26:1:2799:C:H6	1.82	0.44
27:2:80:G:H2'	27:2:81:A:C8	2.53	0.44
11:K:22:LYS:O	11:K:26:PHE:HB3	2.18	0.43
26:1:1207:G:O2'	26:1:1208:A:H5'	2.17	0.43
26:1:2125:U:C2	26:1:2218:G:O6	2.70	0.43
26:1:2258:U:O2'	26:1:2259:C:H5'	2.18	0.43
26:1:2622:G:N2	26:1:2625:A:OP2	2.42	0.43
27:2:80:G:H1	27:2:89:U:H3	1.66	0.43
3:C:84:LYS:O	3:C:84:LYS:HD2	2.18	0.43
6:F:14:GLU:OE1	26:1:1375:G:H4'	2.18	0.43
8:H:73:MET:HE3	8:H:94:ILE:HD12	1.99	0.43
9:I:73:GLY:HA3	9:I:90:TYR:O	2.17	0.43
22:X:76:ILE:HG23	22:X:112:LEU:CD1	2.49	0.43
26:1:178:A:H2'	26:1:179:A:C8	2.53	0.43
26:1:526:A:H2'	26:1:526:A:N3	2.32	0.43
26:1:736:C:H2'	26:1:737:C:C6	2.52	0.43
26:1:750:A:H2'	26:1:751:A:H8	1.84	0.43
26:1:1028:G:H2'	26:1:1028:G:N3	2.33	0.43
26:1:2017:C:H2'	26:1:2018:U:O4'	2.19	0.43
26:1:2339:U:H2'	26:1:2340:C:H5'	2.01	0.43
26:1:2577:G:C2'	26:1:2578:C:H5'	2.48	0.43
4:D:67:ARG:NH2	26:1:1261:G:OP1	2.52	0.43
5:E:78:GLU:OE1	5:E:78:GLU:N	2.50	0.43
7:G:73:PRO:HG2	7:G:101:ILE:HG22	2.00	0.43
23:Y:51:ARG:HA	23:Y:54:MET:CE	2.48	0.43
24:Z:34:GLU:OE2	24:Z:105:LYS:HE3	2.18	0.43
26:1:24:G:H2'	26:1:25:U:H6	1.83	0.43
26:1:694:G:H2'	26:1:695:C:O4'	2.18	0.43
26:1:848:U:O2'	26:1:849:A:H5'	2.18	0.43
26:1:1249:U:H4'	26:1:1250:G:OP2	2.19	0.43
26:1:1426:G:O2'	26:1:1427:U:H5'	2.18	0.43
26:1:2415:A:H5'	26:1:2416:G:OP2	2.18	0.43
26:1:2427:G:H2'	26:1:2428:U:H5'	2.00	0.43
5:E:59:GLU:HB3	5:E:66:THR:HG23	2.01	0.43
8:H:16:SER:O	8:H:20:GLN:HG2	2.18	0.43
16:P:13:HIS:NE2	16:P:45:ALA:HB1	2.33	0.43
19:S:155:VAL:CB	19:S:194:ILE:HG22	2.33	0.43
20:V:32:GLU:HG2	20:V:143:LEU:CD2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1161:A:O2'	26:1:1162:C:H5'	2.19	0.43
26:1:1387:C:O2'	26:1:1388:C:H5'	2.19	0.43
26:1:1854:U:O2'	26:1:1855:G:H5'	2.18	0.43
26:1:1908:A:H2'	26:1:1909:C:O4'	2.18	0.43
26:1:2538:U:H2'	26:1:2539:C:O4'	2.18	0.43
27:2:32:U:O5'	27:2:32:U:H6	2.02	0.43
27:2:93:G:H2'	27:2:94:C:H5''	2.01	0.43
3:C:83:LEU:HD22	3:C:89:ASP:OD2	2.19	0.43
10:J:14:THR:HG22	10:J:28:ARG:HG2	1.99	0.43
20:V:39:GLY:HA3	20:V:52:GLY:HA2	2.00	0.43
20:V:137:GLN:N	20:V:138:PRO:HD3	2.33	0.43
25:a:44:ILE:CG1	25:a:54:ALA:HB3	2.47	0.43
25:a:45:ILE:HA	25:a:52:THR:HA	2.00	0.43
26:1:1662:A:O2'	26:1:1663:G:H5'	2.18	0.43
26:1:2232:A:H2'	26:1:2233:C:H6	1.80	0.43
26:1:2626:G:O2'	26:1:2627:A:H5'	2.18	0.43
26:1:2901:U:H2'	26:1:2902:A:O4'	2.18	0.43
1:A:15:LEU:CD2	1:A:57:VAL:HG12	2.48	0.43
6:F:18:GLU:HA	6:F:21:ALA:CB	2.46	0.43
12:L:74:GLU:HG2	12:L:84:PRO:HG3	2.00	0.43
23:Y:14:ARG:HD2	23:Y:41:TRP:CH2	2.52	0.43
26:1:199:A:H2'	26:1:199:A:N3	2.34	0.43
26:1:577:A:H2'	26:1:577:A:N3	2.33	0.43
26:1:1066:G:H1'	26:1:1068:G:O6	2.18	0.43
26:1:1182:G:H2'	26:1:1183:G:O4'	2.19	0.43
26:1:1214:C:N4	26:1:1216:U:H5''	2.33	0.43
26:1:2619:G:O2'	26:1:2620:U:H5'	2.19	0.43
27:2:75:U:O2'	27:2:76:A:H5'	2.18	0.43
27:2:106:G:O2'	27:2:107:U:O4'	2.28	0.43
6:F:64:ARG:CD	6:F:69:GLN:HA	2.47	0.43
10:J:54:LEU:HD12	10:J:54:LEU:O	2.19	0.43
17:Q:32:LEU:O	17:Q:36:LYS:NZ	2.51	0.43
19:S:107:ARG:CG	19:S:206:LEU:HD22	2.43	0.43
24:Z:5:LYS:HD2	26:1:2029:G:OP1	2.18	0.43
24:Z:60:ARG:HG2	26:1:1498:U:H5	1.82	0.43
26:1:673:G:O2'	26:1:674:C:H5'	2.19	0.43
26:1:1563:U:H2'	26:1:1564:G:H8	1.83	0.43
26:1:2597:G:O2'	26:1:2598:U:H5'	2.19	0.43
26:1:2653:C:H2'	26:1:2654:G:O4'	2.19	0.43
26:1:2675:G:H2'	26:1:2676:U:O4'	2.19	0.43
26:1:2768:A:C2'	26:1:2769:G:H5'	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:70:ARG:HD3	3:C:74:MET:O	2.18	0.43
12:L:118:VAL:HG11	12:L:201:VAL:HG11	2.01	0.43
14:N:5:LYS:NZ	26:1:2082:C:OP1	2.44	0.43
18:R:25:VAL:O	18:R:33:LYS:HA	2.18	0.43
21:W:7:ARG:HH12	21:W:44:LYS:HE2	1.83	0.43
21:W:19:VAL:HB	21:W:41:CYS:SG	2.58	0.43
25:a:31:LEU:HD23	25:a:94:PHE:HD1	1.83	0.43
26:1:78:U:H2'	26:1:79:U:H6	1.78	0.43
26:1:258:A:H1'	26:1:430:A:C8	2.53	0.43
26:1:517:A:C2'	26:1:518:A:H5'	2.49	0.43
26:1:744:A:H62	26:1:1677:G:H21	1.65	0.43
26:1:1478:A:H2'	26:1:1479:G:O4'	2.19	0.43
26:1:1770:C:H2'	26:1:1771:A:H5''	2.01	0.43
26:1:2358:G:O2'	26:1:2359:C:H5'	2.18	0.43
26:1:2398:G:H2'	26:1:2399:G:O4'	2.18	0.43
26:1:2543:G:C2'	26:1:2544:C:H5'	2.49	0.43
26:1:2648:G:C2'	26:1:2649:U:H5'	2.49	0.43
7:G:40:ILE:HD13	7:G:60:GLU:HG3	2.00	0.43
9:I:17:SER:HB3	26:1:2282:G:H21	1.84	0.43
19:S:125:VAL:HG22	19:S:194:ILE:CD1	2.42	0.43
26:1:52:A:H2'	26:1:53:A:C8	2.53	0.43
26:1:340:C:C2'	26:1:341:G:H5'	2.49	0.43
26:1:390:A:H2'	26:1:391:A:C8	2.54	0.43
26:1:661:U:H2'	26:1:662:G:C8	2.54	0.43
26:1:1224:U:H5''	26:1:1225:G:OP1	2.18	0.43
26:1:1603:U:H2'	26:1:1604:C:C6	2.54	0.43
26:1:2344:C:C2'	26:1:2345:A:H5'	2.48	0.43
26:1:2389:G:O2'	26:1:2390:U:H5'	2.17	0.43
26:1:2505:A:H1'	26:1:2555:U:O2'	2.18	0.43
3:C:97:GLU:OE2	4:D:13:LYS:HD3	2.19	0.43
5:E:28:ASN:ND2	5:E:29:ALA:H	2.16	0.43
8:H:43:VAL:HG12	8:H:44:ASP:O	2.18	0.43
11:K:30:PHE:O	11:K:34:THR:HG23	2.19	0.43
19:S:134:PRO:HA	19:S:166:SER:OG	2.19	0.43
25:a:19:ARG:O	25:a:19:ARG:HG2	2.19	0.43
26:1:231:A:N1	26:1:233:U:H1'	2.34	0.43
26:1:326:A:C2'	26:1:327:G:H5''	2.47	0.43
26:1:793:G:N2	26:1:795:A:H3'	2.33	0.43
26:1:917:U:O2'	26:1:918:G:H5'	2.18	0.43
26:1:1269:A:H2'	26:1:1270:U:C6	2.54	0.43
26:1:2262:G:O2'	26:1:2263:C:H5'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2748:A:H1'	26:1:2893:A:O2'	2.18	0.43
26:1:2780:A:H2'	26:1:2781:U:O4'	2.19	0.43
27:2:33:U:H2'	27:2:34:C:C6	2.53	0.43
1:A:22:PHE:CZ	1:A:78:LEU:HD21	2.54	0.42
2:B:65:ILE:HD12	2:B:87:ARG:NH1	2.34	0.42
3:C:31:LEU:HD13	26:1:623:C:H4'	2.01	0.42
12:L:74:GLU:HG2	12:L:84:PRO:CG	2.48	0.42
20:V:26:LEU:HD21	20:V:105:SER:OG	2.19	0.42
21:W:77:ILE:HG23	21:W:77:ILE:O	2.19	0.42
21:W:104:ARG:HD3	21:W:121:VAL:HG11	2.01	0.42
22:X:3:LEU:HD12	22:X:6:LEU:HD11	2.01	0.42
25:a:37:ASN:HD21	27:2:27:A:H5''	1.84	0.42
26:1:24:G:H2'	26:1:25:U:C6	2.54	0.42
26:1:59:U:O5'	26:1:59:U:H6	2.02	0.42
26:1:142:G:C3'	26:1:143:U:H5'	2.49	0.42
26:1:556:U:H4'	26:1:1273:G:H4'	2.01	0.42
26:1:793:G:H22	26:1:796:A:H5''	1.82	0.42
26:1:870:C:H2'	26:1:871:U:O4'	2.19	0.42
26:1:1160:C:N3	26:1:1161:A:N6	2.67	0.42
26:1:1243:G:H2'	26:1:1244:G:O4'	2.19	0.42
26:1:1352:C:O2'	26:1:1429:G:H1'	2.19	0.42
26:1:2242:G:H2'	26:1:2243:U:H6	1.83	0.42
26:1:2597:G:C2'	26:1:2598:U:H5'	2.49	0.42
27:2:23:U:H4'	27:2:24:C:C5	2.53	0.42
27:2:66:C:C2'	27:2:67:G:H5'	2.49	0.42
1:A:11:THR:OG1	1:A:57:VAL:HG11	2.19	0.42
7:G:57:LEU:HD11	7:G:59:THR:CG2	2.45	0.42
9:I:53:ILE:HG22	9:I:87:VAL:HG23	2.00	0.42
9:I:76:LYS:HD3	9:I:90:TYR:CE2	2.54	0.42
17:Q:58:VAL:HG11	22:X:58:PHE:CE2	2.53	0.42
20:V:8:ASN:O	20:V:12:ILE:HG13	2.19	0.42
20:V:126:TYR:OH	20:V:133:HIS:NE2	2.43	0.42
23:Y:54:MET:HE1	23:Y:104:PHE:CE1	2.54	0.42
26:1:2100:C:O2'	26:1:2101:U:H5'	2.18	0.42
26:1:2240:U:H3'	26:1:2241:C:H5'	2.02	0.42
26:1:2642:U:H2'	26:1:2643:C:C6	2.54	0.42
26:1:2874:A:H2'	26:1:2875:U:O4'	2.19	0.42
27:2:5:G:H1	27:2:108:U:H3	1.66	0.42
1:A:67:SER:OG	1:A:68:SER:N	2.50	0.42
2:B:13:ARG:HD2	26:1:773:G:H4'	2.00	0.42
3:C:70:ARG:HE	3:C:75:SER:HA	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:80:ARG:HH22	26:1:344:U:P	2.40	0.42
19:S:79:ARG:HA	19:S:86:GLY:HA3	2.00	0.42
19:S:81:PRO:HD2	26:1:718:C:H5''	2.01	0.42
26:1:446:G:C2'	26:1:447:A:H5''	2.49	0.42
26:1:476:A:H5''	26:1:477:U:OP2	2.19	0.42
26:1:500:A:H4'	26:1:501:C:OP2	2.18	0.42
26:1:517:A:H2'	26:1:518:A:H5'	2.02	0.42
26:1:746:G:C2'	26:1:747:U:H5'	2.49	0.42
26:1:774:G:H5'	26:1:775:A:H5''	2.01	0.42
26:1:1065:A:H3'	26:1:1066:G:H5''	2.01	0.42
26:1:1842:A:H4'	26:1:1843:U:OP1	2.18	0.42
26:1:2058:A:C6	26:1:2525:C:H1'	2.54	0.42
2:B:117:GLU:O	2:B:131:PRO:HD3	2.20	0.42
5:E:81:THR:CG2	5:E:99:ARG:HG2	2.49	0.42
12:L:116:ILE:N	12:L:183:LEU:O	2.52	0.42
13:M:50:VAL:HG23	13:M:50:VAL:O	2.19	0.42
15:O:8:ALA:HA	15:O:14:ASP:O	2.20	0.42
19:S:51:VAL:HG21	19:S:88:ILE:HG21	2.01	0.42
26:1:89:U:O2'	26:1:90:A:OP1	2.25	0.42
26:1:1081:G:H2'	26:1:1082:C:H6	1.83	0.42
26:1:1246:C:H2'	26:1:1247:G:H5'	2.02	0.42
26:1:1757:U:O4	26:1:1772:G:O6	2.36	0.42
26:1:2080:G:H2'	26:1:2081:A:O4'	2.20	0.42
26:1:2268:A:H2'	26:1:2269:G:C8	2.54	0.42
26:1:2541:U:H2'	26:1:2542:C:H6	1.85	0.42
7:G:91:VAL:HG11	7:G:100:GLU:CG	2.49	0.42
16:P:38:LYS:HZ1	26:1:515:G:H22	1.66	0.42
23:Y:42:ILE:HD13	23:Y:97:VAL:HG21	2.01	0.42
25:a:22:LEU:CD2	25:a:30:ARG:HG2	2.49	0.42
26:1:481:C:H3'	26:1:482:U:C5'	2.49	0.42
26:1:872:U:H5'	26:1:873:U:C4	2.54	0.42
26:1:1017:A:H5'	26:1:1227:U:H1'	2.02	0.42
26:1:1326:C:H2'	26:1:1327:C:H6	1.84	0.42
26:1:1867:G:H2'	26:1:1868:U:H6	1.83	0.42
26:1:2343:U:O2'	26:1:2344:C:H5'	2.20	0.42
26:1:2743:U:O2'	26:1:2744:G:H5'	2.19	0.42
1:A:36:GLU:OE1	21:W:104:ARG:HD2	2.19	0.42
2:B:264:LYS:HE3	2:B:264:LYS:HB3	1.82	0.42
6:F:30:ASP:OD2	6:F:32:ARG:HG2	2.20	0.42
15:O:24:ARG:HG3	15:O:25:ASN:N	2.34	0.42
20:V:65:PHE:CZ	20:V:90:ALA:HB1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:9:THR:HG22	24:Z:10:SER:N	2.34	0.42
24:Z:112:ASP:HB3	24:Z:114:ALA:H	1.85	0.42
26:1:109:G:C2'	26:1:110:A:H5'	2.49	0.42
26:1:557:G:OP1	26:1:1272:U:O2'	2.37	0.42
26:1:1449:A:OP1	26:1:1449:A:H4'	2.20	0.42
26:1:1558:U:H2'	26:1:1559:G:C8	2.54	0.42
11:K:32:LEU:HD22	11:K:43:ILE:CD1	2.50	0.42
12:L:34:VAL:CG1	12:L:102:GLY:HA3	2.50	0.42
17:Q:23:LYS:NZ	26:1:675:G:OP1	2.52	0.42
19:S:134:PRO:HB2	26:1:364:A:H5'	2.02	0.42
23:Y:54:MET:HG3	23:Y:121:ALA:HB2	2.00	0.42
26:1:251:G:O5'	26:1:252:C:H5''	2.20	0.42
26:1:341:G:H5''	26:1:342:A:OP1	2.20	0.42
26:1:591:A:H4'	26:1:592:A:H5'	2.02	0.42
26:1:718:C:C2'	26:1:719:G:H5'	2.49	0.42
26:1:1214:C:H1'	26:1:1217:U:N3	2.35	0.42
26:1:1415:A:O2'	26:1:1416:U:OP2	2.37	0.42
26:1:1710:G:C2'	26:1:1711:G:H5'	2.49	0.42
26:1:2234:C:H2'	26:1:2235:A:H5'	2.01	0.42
2:B:253:PRO:HG2	2:B:257:LYS:HZ1	1.85	0.42
22:X:59:ARG:O	22:X:59:ARG:HG2	2.20	0.42
26:1:267:G:O2'	26:1:268:A:H5''	2.20	0.42
26:1:1364:C:H2'	26:1:1365:G:O4'	2.19	0.42
26:1:1800:A:C2'	26:1:1801:C:H5'	2.49	0.42
26:1:1847:U:H4'	26:1:1848:A:OP2	2.19	0.42
26:1:1951:C:C2'	26:1:1952:C:H5'	2.50	0.42
26:1:2687:A:H3'	26:1:2688:G:H8	1.84	0.42
1:A:50:ILE:HG13	1:A:64:ARG:HB2	2.00	0.42
2:B:205:VAL:CG2	26:1:1818:A:H5''	2.50	0.42
2:B:249:PRO:HD3	26:1:1851:G:O3'	2.20	0.42
6:F:42:VAL:HG23	6:F:50:VAL:HG21	2.01	0.42
6:F:89:LEU:HD12	6:F:89:LEU:O	2.20	0.42
7:G:93:ILE:HA	7:G:99:GLU:O	2.20	0.42
13:M:9:THR:HG21	13:M:55:THR:CG2	2.50	0.42
18:R:18:LYS:HZ1	18:R:21:GLY:HA2	1.85	0.42
23:Y:104:PHE:HE2	23:Y:125:LEU:HD11	1.84	0.42
26:1:33:U:O4	26:1:492:G:O2'	2.29	0.42
26:1:94:A:O2'	26:1:95:A:H5'	2.19	0.42
26:1:435:A:H2'	26:1:435:A:N3	2.34	0.42
1:A:9:ALA:HA	1:A:12:LYS:HG2	2.01	0.42
2:B:73:GLY:HA2	2:B:115:ILE:HG23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:209:GLY:CA	26:1:809:A:H5'	2.49	0.42
17:Q:27:ALA:O	17:Q:28:PHE:HB2	2.20	0.42
26:1:28:A:H1'	26:1:558:A:C2	2.55	0.42
26:1:351:G:C8	26:1:546:A:H1'	2.55	0.42
26:1:1310:A:H3'	26:1:1311:A:C8	2.55	0.42
26:1:1341:A:C2'	26:1:1342:C:H5'	2.50	0.42
26:1:1464:U:H5'	26:1:1465:G:OP2	2.20	0.42
26:1:1632:A:H4'	26:1:1633:A:C2	2.54	0.42
26:1:2431:C:H2'	26:1:2432:G:O4'	2.20	0.42
26:1:2541:U:H2'	26:1:2542:C:C6	2.55	0.42
26:1:2886:G:C2	26:1:2888:A:H1'	2.55	0.42
1:A:28:LEU:HD13	1:A:86:ILE:CG2	2.50	0.41
1:A:91:ARG:HB3	1:A:115:ILE:HD12	2.02	0.41
4:D:38:VAL:HG13	4:D:53:VAL:CG1	2.47	0.41
5:E:36:LEU:HD13	5:E:47:ILE:HG22	2.02	0.41
6:F:62:LYS:HG3	6:F:62:LYS:O	2.20	0.41
8:H:37:LYS:HB3	8:H:39:VAL:CG1	2.49	0.41
24:Z:51:GLY:HA2	24:Z:86:PHE:CE2	2.55	0.41
24:Z:105:LYS:HA	24:Z:117:VAL:HG12	2.02	0.41
26:1:131:G:H2'	26:1:132:C:H6	1.85	0.41
26:1:222:A:H2'	26:1:223:G:O4'	2.19	0.41
26:1:272:C:H1'	26:1:470:G:N2	2.35	0.41
26:1:633:A:H2'	26:1:634:C:O4'	2.20	0.41
26:1:825:G:H2'	26:1:827:A:N7	2.35	0.41
26:1:1326:C:H2'	26:1:1327:C:C6	2.55	0.41
26:1:2416:G:H5''	26:1:2417:U:O4'	2.20	0.41
27:2:35:C:H42	27:2:46:A:H2	1.68	0.41
27:2:73:G:H2'	27:2:74:G:O4'	2.20	0.41
1:A:29:ARG:NE	1:A:89:LYS:HD2	2.35	0.41
4:D:80:LYS:HE3	26:1:1017:A:OP2	2.21	0.41
6:F:4:ARG:HG2	6:F:5:ASP:H	1.85	0.41
6:F:7:LEU:HD12	6:F:45:ILE:HD12	2.02	0.41
19:S:108:LEU:HD13	19:S:111:ARG:NH2	2.35	0.41
26:1:153:G:H2'	26:1:154:A:C8	2.55	0.41
26:1:379:C:O2'	26:1:380:U:H5'	2.20	0.41
26:1:555:C:O2	26:1:555:C:H2'	2.20	0.41
26:1:898:U:H2'	26:1:899:U:H6	1.80	0.41
26:1:1167:C:O2'	26:1:1168:C:H5'	2.20	0.41
26:1:1315:C:H2'	26:1:1316:G:H8	1.84	0.41
26:1:1494:G:C2'	26:1:1495:C:H5'	2.50	0.41
26:1:1886:A:C2'	26:1:1887:G:H5'	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1975:G:O2'	26:1:1976:G:H5'	2.20	0.41
26:1:2036:G:C2'	26:1:2037:G:H5'	2.50	0.41
26:1:2548:C:O2'	26:1:2549:U:H5'	2.20	0.41
26:1:2675:G:H2'	26:1:2676:U:H6	1.85	0.41
26:1:2749:G:H2'	26:1:2750:C:C6	2.55	0.41
2:B:23:GLU:HG3	2:B:90:ASN:ND2	2.35	0.41
11:K:16:GLU:OE1	11:K:19:LYS:HD3	2.20	0.41
14:N:35:GLU:HB2	14:N:45:ASN:HD22	1.86	0.41
20:V:18:VAL:HA	20:V:56:ILE:O	2.21	0.41
20:V:32:GLU:HG2	20:V:143:LEU:HD22	2.03	0.41
20:V:33:VAL:HG11	20:V:106:ILE:HD13	2.01	0.41
24:Z:84:LYS:HG3	24:Z:89:ILE:HD12	2.01	0.41
24:Z:112:ASP:CB	24:Z:114:ALA:H	2.32	0.41
26:1:161:A:HO2'	26:1:162:A:P	2.42	0.41
26:1:341:G:N1	26:1:382:U:OP2	2.31	0.41
26:1:717:C:C2'	26:1:718:C:H5'	2.50	0.41
26:1:918:G:H2'	26:1:919:G:O4'	2.19	0.41
26:1:1891:U:OP1	26:1:2437:G:O2'	2.31	0.41
26:1:2051:C:H2'	26:1:2052:C:C6	2.56	0.41
26:1:2391:C:O2'	26:1:2392:G:H5'	2.20	0.41
26:1:2890:C:H2'	26:1:2891:U:O4'	2.21	0.41
13:M:17:GLU:O	13:M:21:LYS:HG3	2.20	0.41
19:S:153:LEU:HD23	19:S:192:LEU:CD2	2.51	0.41
26:1:615:A:H5''	26:1:616:G:OP2	2.20	0.41
26:1:794:A:O2'	26:1:1662:A:OP1	2.30	0.41
26:1:908:A:H2'	26:1:909:G:C8	2.56	0.41
26:1:1627:G:C2	26:1:1628:A:H1'	2.55	0.41
26:1:2000:G:H2'	26:1:2001:C:C6	2.55	0.41
26:1:2534:C:H5''	26:1:2600:C:N4	2.36	0.41
26:1:2560:U:H2'	26:1:2561:C:O4'	2.21	0.41
2:B:84:ASP:HB2	2:B:91:ILE:HG23	2.02	0.41
3:C:94:MET:HE3	4:D:11:GLN:O	2.20	0.41
10:J:22:LEU:HB2	26:1:203:U:H4'	2.02	0.41
12:L:92:ARG:NH2	26:1:2664:U:H5''	2.35	0.41
20:V:66:THR:OG1	26:1:1185:U:OP2	2.25	0.41
21:W:3:GLN:HG2	21:W:33:ALA:H	1.84	0.41
21:W:87:ILE:HD11	21:W:114:ILE:HD11	2.02	0.41
22:X:21:ARG:HH22	26:1:630:G:P	2.43	0.41
23:Y:101:ARG:O	23:Y:103:LEU:HD22	2.21	0.41
26:1:41:A:O2'	26:1:42:G:H5'	2.19	0.41
26:1:155:U:H2'	26:1:156:A:H5'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:323:C:C2'	26:1:324:A:H5'	2.50	0.41
26:1:409:G:H2'	26:1:410:G:O4'	2.19	0.41
26:1:1754:C:H2'	26:1:1755:U:C6	2.56	0.41
26:1:2347:A:H5''	26:1:2348:G:C8	2.56	0.41
26:1:2491:C:H2'	26:1:2492:C:O4'	2.19	0.41
26:1:2580:G:H8	26:1:2609:G:H21	1.67	0.41
26:1:2771:G:H2'	26:1:2772:C:H5'	2.02	0.41
26:1:2841:A:H2'	26:1:2842:G:O4'	2.21	0.41
26:1:2870:A:H2'	26:1:2871:A:H8	1.84	0.41
6:F:46:PHE:CD1	6:F:87:ILE:HG23	2.56	0.41
12:L:188:VAL:HG23	12:L:188:VAL:O	2.20	0.41
24:Z:48:ILE:HG21	24:Z:100:TYR:CD2	2.55	0.41
25:a:44:ILE:O	25:a:44:ILE:HG13	2.21	0.41
26:1:483:C:H2'	26:1:484:U:C6	2.55	0.41
26:1:1403:C:H2'	26:1:1404:A:O4'	2.20	0.41
26:1:1893:A:O2'	26:1:1894:G:OP1	2.34	0.41
26:1:2230:G:H5''	26:1:2231:C:O5'	2.20	0.41
26:1:2240:U:H3'	26:1:2241:C:C5'	2.50	0.41
26:1:2783:U:H4'	26:1:2784:A:OP1	2.20	0.41
2:B:262:GLY:O	2:B:263:LYS:HD2	2.20	0.41
3:C:74:MET:SD	3:C:110:VAL:HG13	2.61	0.41
8:H:9:ARG:HG2	8:H:40:SER:O	2.20	0.41
9:I:35:ASP:OD2	26:1:900:G:O2'	2.34	0.41
9:I:59:VAL:CG2	9:I:89:VAL:HG23	2.51	0.41
19:S:153:LEU:HA	19:S:174:GLN:O	2.20	0.41
20:V:39:GLY:O	20:V:45:TYR:HD1	2.04	0.41
24:Z:51:GLY:HA3	24:Z:85:LEU:CD2	2.50	0.41
26:1:344:U:OP1	26:1:344:U:H4'	2.21	0.41
26:1:405:G:C3'	26:1:406:A:H5''	2.49	0.41
26:1:545:G:N2	26:1:547:A:H3'	2.36	0.41
26:1:1214:C:OP2	26:1:1214:C:H4'	2.20	0.41
26:1:1297:G:O2'	26:1:1298:G:H5'	2.21	0.41
26:1:1875:A:H2'	26:1:1876:G:O4'	2.21	0.41
26:1:1978:U:H2'	26:1:1980:A:OP2	2.21	0.41
8:H:41:VAL:HG11	8:H:65:VAL:HG22	2.02	0.41
8:H:51:VAL:O	8:H:55:VAL:HG13	2.21	0.41
12:L:134:HIS:NE2	12:L:168:LYS:HD2	2.35	0.41
15:O:22:ASN:OD1	15:O:23:LYS:N	2.54	0.41
17:Q:58:VAL:HG13	17:Q:61:LEU:CD1	2.48	0.41
21:W:24:VAL:HG11	21:W:33:ALA:HB2	2.02	0.41
25:a:17:ARG:HB3	26:1:2362:A:OP2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:198:A:H5''	26:1:199:A:OP2	2.20	0.41
26:1:254:A:H2'	26:1:255:G:O4'	2.21	0.41
26:1:268:A:H2'	26:1:269:G:C4'	2.50	0.41
26:1:653:G:H2'	26:1:654:C:H6	1.85	0.41
26:1:683:G:H2'	26:1:684:U:O4'	2.21	0.41
26:1:980:U:H2'	26:1:981:U:H6	1.84	0.41
26:1:1453:G:N1	26:1:1631:G:OP2	2.54	0.41
26:1:1988:C:O2'	26:1:1989:C:H5'	2.21	0.41
26:1:2346:U:O3'	26:1:2347:A:H2'	2.20	0.41
27:2:35:C:H2'	27:2:36:C:O4'	2.20	0.41
2:B:219:THR:HG22	26:1:1817:C:OP1	2.21	0.41
3:C:61:TRP:CZ2	3:C:93:LYS:HD3	2.56	0.41
12:L:6:LEU:HD23	12:L:210:GLU:HB3	2.02	0.41
13:M:8:LEU:HD13	13:M:23:VAL:HG21	2.02	0.41
19:S:103:LYS:HG2	19:S:106:ARG:NH2	2.36	0.41
24:Z:96:ARG:HG3	24:Z:100:TYR:CE1	2.56	0.41
24:Z:109:ARG:NH1	24:Z:112:ASP:OD2	2.45	0.41
26:1:178:A:H2'	26:1:179:A:O4'	2.21	0.41
26:1:487:U:C2'	26:1:488:G:H5'	2.51	0.41
26:1:506:A:H2'	26:1:507:C:H5'	2.03	0.41
26:1:592:A:N3	26:1:592:A:O2'	2.53	0.41
26:1:592:A:O2'	26:1:593:U:O5'	2.38	0.41
26:1:786:U:H2'	26:1:787:U:O4'	2.21	0.41
26:1:1311:A:H3'	26:1:1312:A:H5''	2.02	0.41
26:1:1676:A:H3'	26:1:1677:G:C8	2.56	0.41
26:1:1910:G:H4'	26:1:1910:G:OP1	2.21	0.41
26:1:2308:C:O2'	26:1:2309:G:H5'	2.21	0.41
26:1:2369:C:H2'	26:1:2370:U:O4'	2.20	0.41
26:1:2584:G:H2'	26:1:2585:C:C6	2.56	0.41
6:F:34:ASN:O	6:F:38:VAL:HG23	2.20	0.41
12:L:77:ALA:HB1	12:L:82:ALA:O	2.21	0.41
16:P:43:LEU:HD23	16:P:43:LEU:HA	1.91	0.41
26:1:890:G:H21	26:1:977:A:N6	2.18	0.41
26:1:1010:G:H2'	26:1:1011:U:H5'	2.03	0.41
26:1:1757:U:C3'	26:1:1758:A:H5''	2.51	0.41
2:B:115:ILE:H	2:B:128:ASN:ND2	2.19	0.40
3:C:88:ILE:CG2	4:D:51:PRO:HB3	2.51	0.40
21:W:25:LEU:CD2	26:1:2589:U:H4'	2.52	0.40
22:X:76:ILE:HG23	22:X:112:LEU:HD12	2.03	0.40
26:1:25:U:C3'	26:1:26:G:H5'	2.50	0.40
26:1:96:G:H2'	26:1:97:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1026:C:O5'	26:1:1026:C:H6	2.04	0.40
26:1:1453:G:O6	26:1:1630:A:O2'	2.33	0.40
26:1:1651:C:H4'	26:1:1652:A:O5'	2.21	0.40
26:1:1837:A:C2'	26:1:1838:G:H5'	2.51	0.40
1:A:105:LEU:C	1:A:110:ALA:HB2	2.46	0.40
7:G:95:LYS:HA	7:G:95:LYS:HE2	2.03	0.40
20:V:3:GLN:O	20:V:3:GLN:HG2	2.21	0.40
20:V:39:GLY:HA3	20:V:52:GLY:CA	2.51	0.40
26:1:619:U:O2'	26:1:620:G:H5'	2.22	0.40
26:1:752:G:H2'	26:1:753:U:O4'	2.22	0.40
26:1:2892:G:O2'	26:1:2893:A:H5'	2.20	0.40
2:B:177:ARG:O	2:B:177:ARG:HG3	2.21	0.40
7:G:93:ILE:HD11	7:G:98:GLY:O	2.22	0.40
12:L:54:GLU:O	12:L:85:LYS:HA	2.20	0.40
20:V:113:THR:HG22	20:V:114:ARG:N	2.36	0.40
23:Y:39:THR:HA	23:Y:97:VAL:O	2.21	0.40
24:Z:81:ALA:O	24:Z:84:LYS:HB3	2.22	0.40
25:a:12:LEU:O	25:a:15:HIS:HB3	2.20	0.40
26:1:62:C:H5'	26:1:63:U:OP2	2.21	0.40
26:1:269:G:H2'	26:1:270:C:O4'	2.21	0.40
26:1:575:G:N3	26:1:575:G:H2'	2.37	0.40
26:1:576:U:OP1	26:1:604:G:N2	2.53	0.40
26:1:1080:G:H1	26:1:1163:U:H3	1.70	0.40
26:1:1291:A:H4'	26:1:1292:A:OP2	2.21	0.40
26:1:1398:G:O2'	26:1:1399:C:H5'	2.22	0.40
26:1:1618:A:H2'	26:1:1619:A:C8	2.57	0.40
26:1:2780:A:O2'	26:1:2781:U:H5'	2.21	0.40
27:2:54:U:C4'	27:2:55:A:H5'	2.46	0.40
2:B:59:LYS:CB	26:1:1615:G:H4'	2.49	0.40
2:B:159:GLY:HA3	2:B:198:LEU:HD23	2.03	0.40
2:B:171:TYR:OH	26:1:2250:A:OP1	2.33	0.40
7:G:84:LYS:CB	7:G:86:VAL:HG13	2.44	0.40
9:I:82:ARG:HG3	27:2:11:A:OP1	2.21	0.40
12:L:32:GLU:HB3	12:L:85:LYS:NZ	2.36	0.40
12:L:156:MET:HE1	12:L:164:PHE:CE2	2.56	0.40
19:S:156:THR:HG23	19:S:157:GLU:O	2.21	0.40
26:1:69:C:H4'	26:1:75:G:N7	2.37	0.40
26:1:253:G:H2'	26:1:254:A:C8	2.56	0.40
26:1:259:A:H2'	26:1:260:A:C8	2.56	0.40
26:1:416:G:H4'	26:1:417:A:OP2	2.22	0.40
26:1:920:A:H2'	26:1:921:C:H5'	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2327:A:H2'	26:1:2328:A:H8	1.86	0.40
26:1:2858:G:H1	26:1:2900:C:H5	1.67	0.40
2:B:96:TYR:CE2	2:B:102:ARG:HD2	2.56	0.40
12:L:3:LYS:HE3	12:L:49:ILE:CD1	2.52	0.40
12:L:205:LYS:O	12:L:206:LYS:HB2	2.22	0.40
24:Z:80:THR:HG1	24:Z:83:GLN:H	1.69	0.40
26:1:30:G:H2'	26:1:31:C:C6	2.57	0.40
26:1:162:A:H5''	26:1:163:U:H2'	2.04	0.40
26:1:420:A:H2'	26:1:421:C:O4'	2.22	0.40
26:1:640:G:O2'	26:1:641:A:H5'	2.21	0.40
26:1:1648:C:H2'	26:1:1649:C:C6	2.56	0.40
26:1:1733:A:OP2	26:1:1742:A:N6	2.55	0.40
26:1:1741:G:H3'	26:1:1742:A:H2'	2.03	0.40
26:1:1773:A:O2'	26:1:1774:A:H5'	2.22	0.40
26:1:1886:A:N6	26:1:1910:G:H8	2.18	0.40
26:1:1980:A:O2'	26:1:2586:C:O2	2.40	0.40
26:1:2088:G:H2'	26:1:2528:C:O2'	2.22	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 PDB entries followed by that with respect to all EM entries.

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	
1	A	111/116 (96%)	95 (86%)	16 (14%)	0	100	100
2	B	272/276 (99%)	236 (87%)	36 (13%)	0	100	100
3	C	114/118 (97%)	108 (95%)	6 (5%)	0	100	100
4	D	98/102 (96%)	87 (89%)	11 (11%)	0	100	100
5	E	109/116 (94%)	100 (92%)	9 (8%)	0	100	100
6	F	85/91 (93%)	72 (85%)	13 (15%)	0	100	100
7	G	91/105 (87%)	78 (86%)	13 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	91/217 (42%)	82 (90%)	9 (10%)	0	100	100
9	I	75/85 (88%)	64 (85%)	11 (15%)	0	100	100
10	J	57/62 (92%)	47 (82%)	10 (18%)	0	100	100
11	K	55/69 (80%)	50 (91%)	5 (9%)	0	100	100
12	L	213/217 (98%)	189 (89%)	24 (11%)	0	100	100
13	M	54/59 (92%)	47 (87%)	7 (13%)	0	100	100
14	N	48/57 (84%)	43 (90%)	5 (10%)	0	100	100
15	O	44/49 (90%)	41 (93%)	3 (7%)	0	100	100
16	P	42/50 (84%)	39 (93%)	3 (7%)	0	100	100
17	Q	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
18	R	35/37 (95%)	30 (86%)	5 (14%)	0	100	100
19	S	165/207 (80%)	146 (88%)	19 (12%)	0	100	100
20	V	141/145 (97%)	127 (90%)	14 (10%)	0	100	100
21	W	108/122 (88%)	99 (92%)	9 (8%)	0	100	100
22	X	119/146 (82%)	108 (91%)	11 (9%)	0	100	100
23	Y	134/144 (93%)	127 (95%)	7 (5%)	0	100	100
24	Z	110/122 (90%)	101 (92%)	9 (8%)	0	100	100
25	a	67/119 (56%)	61 (91%)	6 (9%)	0	100	100
All	All	2500/2896 (86%)	2234 (89%)	266 (11%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	
1	A	99/102 (97%)	99 (100%)	0	100	100
2	B	221/223 (99%)	221 (100%)	0	100	100
3	C	96/98 (98%)	96 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	85/86 (99%)	85 (100%)	0	100	100
5	E	90/94 (96%)	90 (100%)	0	100	100
6	F	79/82 (96%)	79 (100%)	0	100	100
7	G	80/90 (89%)	80 (100%)	0	100	100
8	H	81/190 (43%)	81 (100%)	0	100	100
9	I	61/66 (92%)	61 (100%)	0	100	100
10	J	49/52 (94%)	49 (100%)	0	100	100
11	K	52/62 (84%)	52 (100%)	0	100	100
12	L	173/175 (99%)	173 (100%)	0	100	100
13	M	50/53 (94%)	49 (98%)	1 (2%)	48	72
14	N	45/50 (90%)	45 (100%)	0	100	100
15	O	44/47 (94%)	44 (100%)	0	100	100
16	P	39/45 (87%)	39 (100%)	0	100	100
17	Q	55/56 (98%)	55 (100%)	0	100	100
18	R	35/35 (100%)	35 (100%)	0	100	100
19	S	141/170 (83%)	141 (100%)	0	100	100
20	V	122/123 (99%)	122 (100%)	0	100	100
21	W	92/100 (92%)	92 (100%)	0	100	100
22	X	96/112 (86%)	96 (100%)	0	100	100
23	Y	113/119 (95%)	113 (100%)	0	100	100
24	Z	95/102 (93%)	95 (100%)	0	100	100
25	a	60/95 (63%)	60 (100%)	0	100	100
All	All	2153/2427 (89%)	2152 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	M	18	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	HIS

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Mol	Chain	Res	Type
1	A	43	GLN
2	B	199	GLN
2	B	200	HIS
3	C	37	GLN
3	C	38	GLN
5	E	28	ASN
5	E	40	ASN
5	E	61	ASN
6	F	34	ASN
6	F	37	GLN
6	F	57	ASN
7	G	8	ASN
8	H	38	ASN
8	H	88	HIS
12	L	128	GLN
12	L	134	HIS
12	L	143	HIS
12	L	146	HIS
13	M	52	HIS
14	N	45	ASN
15	O	4	ASN
15	O	25	ASN
15	O	26	ASN
15	O	45	HIS
17	Q	7	HIS
17	Q	31	HIS
17	Q	35	ASN
18	R	36	GLN
19	S	29	ASN
19	S	38	ASN
19	S	67	GLN
19	S	169	ASN
19	S	188	ASN
20	V	24	GLN
20	V	59	ASN
22	X	17	ASN
23	Y	46	GLN
25	a	32	ASN
25	a	39	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	1	2634/2923 (90%)	628 (23%)	20 (0%)
27	2	103/115 (89%)	44 (42%)	3 (2%)
All	All	2737/3038 (90%)	672 (24%)	23 (0%)

All (672) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
26	1	13	A
26	1	26	G
26	1	34	U
26	1	35	G
26	1	44	A
26	1	45	G
26	1	51	G
26	1	55	G
26	1	56	A
26	1	63	U
26	1	71	A
26	1	74	U
26	1	75	G
26	1	76	C
26	1	85	G
26	1	90	A
26	1	91	A
26	1	100	U
26	1	101	G
26	1	117	A
26	1	118	A
26	1	119	U
26	1	130	A
26	1	135	G
26	1	136	A
26	1	143	U
26	1	150	A
26	1	156	A
26	1	160	G
26	1	161	A
26	1	163	U
26	1	164	A
26	1	165	C
26	1	168	A
26	1	169	G
26	1	174	U

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Mol	Chain	Res	Type
26	1	176	A
26	1	177	G
26	1	180	G
26	1	183	A
26	1	184	C
26	1	185	A
26	1	198	A
26	1	199	A
26	1	202	A
26	1	216	A
26	1	218	G
26	1	219	A
26	1	225	A
26	1	226	A
26	1	230	A
26	1	232	U
26	1	233	U
26	1	235	G
26	1	236	A
26	1	248	G
26	1	251	G
26	1	255	G
26	1	258	A
26	1	268	A
26	1	269	G
26	1	278	A
26	1	298	U
26	1	301	U
26	1	302	A
26	1	303	G
26	1	305	A
26	1	310	C
26	1	311	U
26	1	327	G
26	1	329	A
26	1	330	C
26	1	331	G
26	1	332	A
26	1	347	U
26	1	348	C
26	1	351	G
26	1	354	A

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Mol	Chain	Res	Type
26	1	359	A
26	1	366	G
26	1	372	A
26	1	373	A
26	1	374	U
26	1	378	C
26	1	381	G
26	1	389	A
26	1	395	U
26	1	396	G
26	1	398	C
26	1	401	U
26	1	402	C
26	1	404	U
26	1	405	G
26	1	406	A
26	1	407	G
26	1	408	U
26	1	410	G
26	1	411	A
26	1	415	U
26	1	432	G
26	1	434	G
26	1	437	A
26	1	440	C
26	1	447	A
26	1	448	A
26	1	452	G
26	1	457	G
26	1	458	A
26	1	463	C
26	1	466	C
26	1	468	A
26	1	481	C
26	1	482	U
26	1	486	G
26	1	489	A
26	1	502	C
26	1	503	A
26	1	506	A
26	1	507	C
26	1	521	U

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Mol	Chain	Res	Type
26	1	522	G
26	1	523	A
26	1	526	A
26	1	527	G
26	1	530	C
26	1	536	A
26	1	537	A
26	1	540	G
26	1	547	A
26	1	548	A
26	1	549	U
26	1	550	A
26	1	552	A
26	1	553	A
26	1	554	C
26	1	557	G
26	1	562	C
26	1	563	G
26	1	567	G
26	1	568	C
26	1	570	U
26	1	575	G
26	1	576	U
26	1	577	A
26	1	578	G
26	1	583	A
26	1	590	U
26	1	592	A
26	1	593	U
26	1	594	G
26	1	599	A
26	1	606	G
26	1	608	C
26	1	616	G
26	1	618	A
26	1	620	G
26	1	646	A
26	1	647	G
26	1	650	U
26	1	658	A
26	1	660	A
26	1	665	G

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Mol	Chain	Res	Type
26	1	666	A
26	1	667	G
26	1	682	A
26	1	683	G
26	1	689	A
26	1	690	U
26	1	691	A
26	1	698	U
26	1	699	U
26	1	713	A
26	1	727	G
26	1	730	A
26	1	731	U
26	1	737	C
26	1	744	A
26	1	745	G
26	1	756	A
26	1	757	G
26	1	768	A
26	1	771	G
26	1	775	A
26	1	780	A
26	1	792	U
26	1	793	G
26	1	802	G
26	1	805	G
26	1	808	G
26	1	809	A
26	1	810	A
26	1	819	A
26	1	820	G
26	1	824	A
26	1	827	A
26	1	829	U
26	1	834	A
26	1	835	U
26	1	837	G
26	1	850	G
26	1	852	U
26	1	857	C
26	1	872	U
26	1	873	U

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Mol	Chain	Res	Type
26	1	874	A
26	1	875	G
26	1	891	A
26	1	903	G
26	1	904	G
26	1	912	C
26	1	914	G
26	1	917	U
26	1	919	G
26	1	955	A
26	1	960	C
26	1	970	U
26	1	971	U
26	1	972	A
26	1	974	U
26	1	977	A
26	1	985	A
26	1	989	A
26	1	990	G
26	1	997	G
26	1	1001	A
26	1	1004	A
26	1	1005	G
26	1	1009	C
26	1	1011	U
26	1	1018	A
26	1	1027	A
26	1	1029	C
26	1	1032	A
26	1	1034	A
26	1	1040	A
26	1	1043	U
26	1	1045	A
26	1	1047	G
26	1	1049	C
26	1	1054	A
26	1	1055	A
26	1	1056	U
26	1	1057	A
26	1	1066	G
26	1	1068	G
26	1	1069	G

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Mol	Chain	Res	Type
26	1	1070	A
26	1	1072	A
26	1	1076	A
26	1	1077	U
26	1	1161	A
26	1	1163	U
26	1	1173	A
26	1	1174	U
26	1	1176	U
26	1	1177	A
26	1	1178	C
26	1	1179	C
26	1	1186	A
26	1	1187	A
26	1	1194	U
26	1	1195	A
26	1	1208	A
26	1	1211	G
26	1	1213	C
26	1	1214	C
26	1	1215	U
26	1	1217	U
26	1	1218	G
26	1	1220	A
26	1	1227	U
26	1	1249	U
26	1	1265	G
26	1	1275	A
26	1	1277	C
26	1	1291	A
26	1	1293	U
26	1	1294	G
26	1	1295	C
26	1	1309	G
26	1	1310	A
26	1	1311	A
26	1	1312	A
26	1	1313	G
26	1	1321	A
26	1	1323	A
26	1	1326	C
26	1	1337	A

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Mol	Chain	Res	Type
26	1	1338	U
26	1	1339	U
26	1	1350	U
26	1	1351	C
26	1	1357	G
26	1	1358	A
26	1	1366	U
26	1	1367	C
26	1	1378	U
26	1	1386	U
26	1	1389	U
26	1	1390	A
26	1	1391	A
26	1	1402	A
26	1	1405	G
26	1	1415	A
26	1	1416	U
26	1	1433	U
26	1	1447	A
26	1	1448	U
26	1	1449	A
26	1	1451	U
26	1	1452	C
26	1	1453	G
26	1	1454	U
26	1	1460	U
26	1	1461	C
26	1	1462	G
26	1	1463	A
26	1	1464	U
26	1	1465	G
26	1	1471	A
26	1	1472	C
26	1	1477	U
26	1	1491	C
26	1	1493	U
26	1	1497	A
26	1	1498	U
26	1	1499	U
26	1	1500	G
26	1	1502	A
26	1	1504	U

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Mol	Chain	Res	Type
26	1	1509	G
26	1	1510	U
26	1	1511	C
26	1	1516	C
26	1	1517	A
26	1	1519	U
26	1	1524	C
26	1	1557	C
26	1	1559	G
26	1	1561	G
26	1	1566	G
26	1	1570	G
26	1	1571	G
26	1	1575	A
26	1	1590	C
26	1	1595	C
26	1	1602	U
26	1	1606	C
26	1	1607	A
26	1	1613	G
26	1	1616	A
26	1	1625	U
26	1	1628	A
26	1	1629	U
26	1	1631	G
26	1	1632	A
26	1	1634	A
26	1	1635	A
26	1	1636	U
26	1	1650	G
26	1	1652	A
26	1	1653	A
26	1	1654	A
26	1	1663	G
26	1	1671	A
26	1	1675	G
26	1	1676	A
26	1	1677	G
26	1	1683	U
26	1	1690	A
26	1	1691	G
26	1	1692	C

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Mol	Chain	Res	Type
26	1	1693	G
26	1	1698	A
26	1	1717	G
26	1	1718	G
26	1	1719	C
26	1	1720	A
26	1	1722	A
26	1	1740	G
26	1	1747	G
26	1	1756	U
26	1	1758	A
26	1	1759	G
26	1	1760	G
26	1	1764	A
26	1	1771	A
26	1	1772	G
26	1	1777	G
26	1	1789	A
26	1	1790	G
26	1	1791	G
26	1	1800	A
26	1	1803	G
26	1	1811	A
26	1	1813	A
26	1	1818	A
26	1	1826	G
26	1	1827	C
26	1	1829	A
26	1	1836	A
26	1	1841	G
26	1	1842	A
26	1	1843	U
26	1	1856	A
26	1	1862	G
26	1	1863	C
26	1	1865	C
26	1	1866	G
26	1	1876	G
26	1	1888	U
26	1	1893	A
26	1	1894	G
26	1	1897	U

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Mol	Chain	Res	Type
26	1	1898	C
26	1	1899	U
26	1	1900	G
26	1	1910	G
26	1	1913	U
26	1	1918	G
26	1	1926	A
26	1	1927	A
26	1	1928	A
26	1	1929	C
26	1	1930	G
26	1	1933	G
26	1	1935	C
26	1	1939	A
26	1	1940	A
26	1	1941	C
26	1	1942	U
26	1	1943	A
26	1	1944	U
26	1	1946	A
26	1	1949	G
26	1	1953	U
26	1	1954	A
26	1	1955	A
26	1	1956	G
26	1	1957	G
26	1	1959	A
26	1	1960	G
26	1	1963	A
26	1	1965	A
26	1	1967	U
26	1	1982	U
26	1	1986	G
26	1	1988	C
26	1	1989	C
26	1	1990	C
26	1	1993	A
26	1	1994	C
26	1	1997	A
26	1	1998	A
26	1	1999	G
26	1	2008	A

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Mol	Chain	Res	Type
26	1	2009	U
26	1	2018	U
26	1	2020	U
26	1	2033	C
26	1	2048	G
26	1	2049	U
26	1	2050	A
26	1	2051	C
26	1	2052	C
26	1	2058	A
26	1	2059	G
26	1	2060	A
26	1	2063	C
26	1	2068	U
26	1	2070	C
26	1	2072	C
26	1	2073	G
26	1	2079	G
26	1	2082	C
26	1	2083	G
26	1	2086	A
26	1	2087	A
26	1	2088	G
26	1	2089	A
26	1	2095	U
26	1	2096	G
26	1	2104	A
26	1	2107	G
26	1	2118	U
26	1	2119	U
26	1	2125	U
26	1	2220	U
26	1	2224	U
26	1	2226	A
26	1	2231	C
26	1	2235	A
26	1	2237	U
26	1	2238	U
26	1	2239	A
26	1	2240	U
26	1	2241	C
26	1	2252	A

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Mol	Chain	Res	Type
26	1	2254	A
26	1	2265	G
26	1	2266	G
26	1	2270	U
26	1	2289	U
26	1	2295	A
26	1	2306	G
26	1	2307	G
26	1	2309	G
26	1	2310	C
26	1	2313	A
26	1	2314	A
26	1	2315	A
26	1	2319	U
26	1	2324	C
26	1	2328	A
26	1	2330	G
26	1	2346	U
26	1	2347	A
26	1	2348	G
26	1	2349	A
26	1	2353	U
26	1	2360	A
26	1	2362	A
26	1	2363	A
26	1	2371	U
26	1	2374	C
26	1	2377	C
26	1	2385	A
26	1	2389	G
26	1	2404	A
26	1	2410	G
26	1	2412	C
26	1	2420	U
26	1	2427	G
26	1	2429	U
26	1	2433	C
26	1	2442	G
26	1	2450	U
26	1	2452	A
26	1	2456	G
26	1	2457	A

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Mol	Chain	Res	Type
26	1	2467	C
26	1	2468	C
26	1	2474	G
26	1	2475	A
26	1	2476	U
26	1	2479	C
26	1	2486	A
26	1	2492	C
26	1	2497	G
26	1	2501	U
26	1	2502	C
26	1	2518	U
26	1	2521	G
26	1	2522	G
26	1	2523	C
26	1	2529	G
26	1	2532	G
26	1	2545	A
26	1	2546	U
26	1	2556	G
26	1	2558	A
26	1	2562	G
26	1	2578	C
26	1	2581	U
26	1	2584	G
26	1	2593	A
26	1	2594	G
26	1	2600	C
26	1	2605	G
26	1	2609	G
26	1	2610	G
26	1	2612	U
26	1	2613	C
26	1	2616	A
26	1	2629	A
26	1	2630	G
26	1	2631	U
26	1	2636	U
26	1	2637	C
26	1	2640	U
26	1	2642	U
26	1	2649	U

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Mol	Chain	Res	Type
26	1	2659	A
26	1	2666	A
26	1	2673	C
26	1	2687	A
26	1	2690	G
26	1	2696	G
26	1	2712	G
26	1	2716	U
26	1	2717	A
26	1	2718	C
26	1	2741	G
26	1	2753	U
26	1	2760	A
26	1	2762	G
26	1	2763	G
26	1	2764	G
26	1	2771	G
26	1	2772	C
26	1	2775	A
26	1	2780	A
26	1	2783	U
26	1	2785	A
26	1	2792	A
26	1	2795	C
26	1	2798	C
26	1	2805	A
26	1	2807	G
26	1	2817	A
26	1	2824	G
26	1	2827	A
26	1	2828	U
26	1	2845	G
26	1	2853	U
26	1	2854	A
26	1	2855	A
26	1	2862	C
26	1	2863	G
26	1	2876	G
26	1	2879	G
26	1	2887	G
26	1	2888	A
26	1	2890	C

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Mol	Chain	Res	Type
26	1	2892	G
26	1	2896	A
26	1	2899	A
26	1	2900	C
27	2	10	U
27	2	11	A
27	2	12	U
27	2	13	A
27	2	14	G
27	2	17	A
27	2	18	G
27	2	19	G
27	2	22	G
27	2	23	U
27	2	24	C
27	2	25	A
27	2	31	G
27	2	33	U
27	2	39	G
27	2	40	C
27	2	42	G
27	2	47	C
27	2	50	A
27	2	51	A
27	2	52	G
27	2	55	A
27	2	58	C
27	2	59	U
27	2	60	C
27	2	64	A
27	2	65	G
27	2	71	A
27	2	79	C
27	2	81	A
27	2	82	A
27	2	85	U
27	2	86	A
27	2	87	C
27	2	88	G
27	2	89	U
27	2	94	C
27	2	97	G

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Mol	Chain	Res	Type
27	2	98	A
27	2	102	G
27	2	103	A
27	2	104	A
27	2	106	G
27	2	107	U

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	1	44	A
26	1	89	U
26	1	90	A
26	1	183	A
26	1	229	A
26	1	406	A
26	1	433	U
26	1	525	A
26	1	1214	C
26	1	1350	U
26	1	1510	U
26	1	1631	G
26	1	1865	C
26	1	1893	A
26	1	1926	A
26	1	1927	A
26	1	1953	U
26	1	1988	C
26	1	2827	A
26	1	2887	G
27	2	59	U
27	2	78	U
27	2	88	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
28	G6V	1	3001	-	28,28,28	2.11	8 (28%)	39,39,39	2.63	15 (38%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	G6V	1	3001	-	-	4/17/37/37	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	1	3001	G6V	C20-C10	6.26	1.60	1.51
28	1	3001	G6V	C30-N29	3.76	1.42	1.33
28	1	3001	G6V	O11-C12	3.37	1.40	1.35
28	1	3001	G6V	C12-N8	2.80	1.39	1.36
28	1	3001	G6V	C6-C5	2.79	1.43	1.38
28	1	3001	G6V	C31-CL33	2.54	1.84	1.76
28	1	3001	G6V	C31-CL44	2.49	1.84	1.76
28	1	3001	G6V	C1-N14	2.48	1.46	1.41

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	3001	G6V	C9-N8-C12	-9.70	104.00	111.17
28	1	3001	G6V	C10-C9-N8	4.89	106.47	101.85
28	1	3001	G6V	C4-N8-C12	4.64	130.85	125.98
28	1	3001	G6V	C19-N14-C1	3.97	125.61	116.19
28	1	3001	G6V	C31-C30-N29	3.94	123.19	114.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	3001	G6V	C3-C2-C1	3.47	126.42	123.35
28	1	3001	G6V	O11-C10-C9	-3.47	101.14	104.50
28	1	3001	G6V	O11-C10-C20	3.24	112.80	109.13
28	1	3001	G6V	C2-C1-N14	3.07	124.00	120.42
28	1	3001	G6V	C10-C20-N29	2.64	117.24	111.98
28	1	3001	G6V	C15-N14-C1	2.38	121.84	116.19
28	1	3001	G6V	O32-C30-C31	-2.35	116.68	121.19
28	1	3001	G6V	O11-C12-N8	2.19	111.77	109.92
28	1	3001	G6V	C9-N8-C4	2.16	125.10	121.36
28	1	3001	G6V	C6-C1-C2	-2.05	113.26	117.31

There are no chirality outliers.

All (4) torsion outliers are listed below:

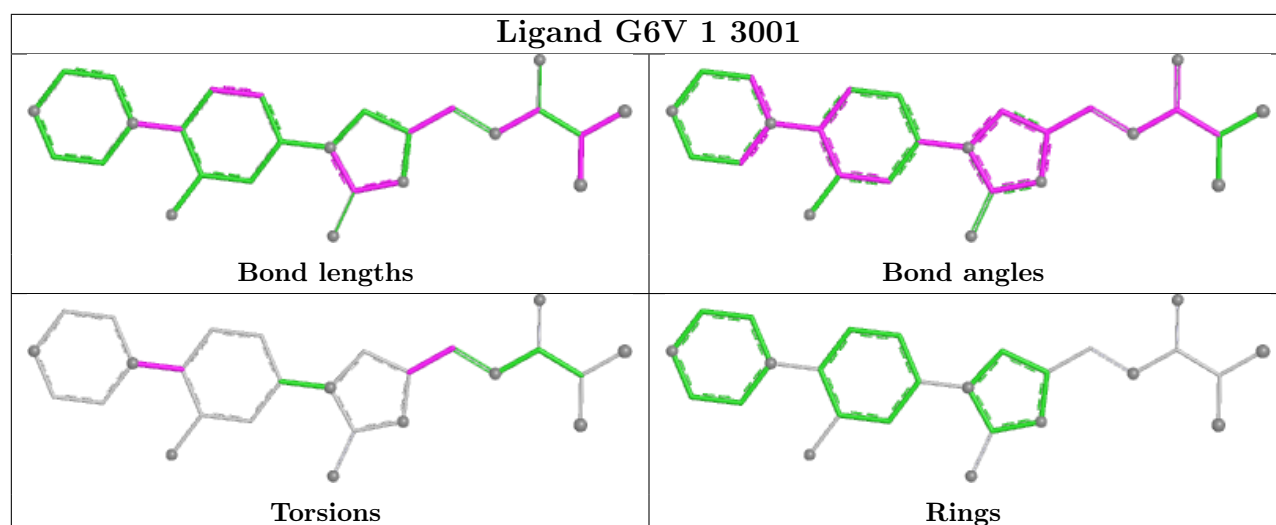
Mol	Chain	Res	Type	Atoms
28	1	3001	G6V	C9-C10-C20-N29
28	1	3001	G6V	C2-C1-N14-C19
28	1	3001	G6V	C6-C1-N14-C19
28	1	3001	G6V	O11-C10-C20-N29

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	1	3001	G6V	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

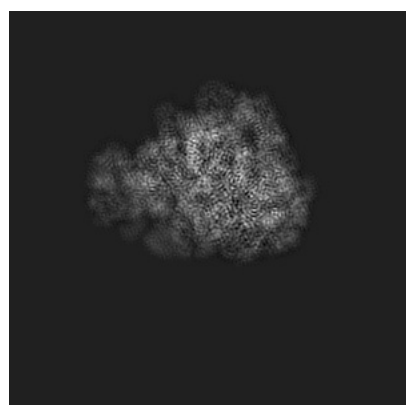
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7867. These allow visual inspection of the internal detail of the map and identification of artifacts.

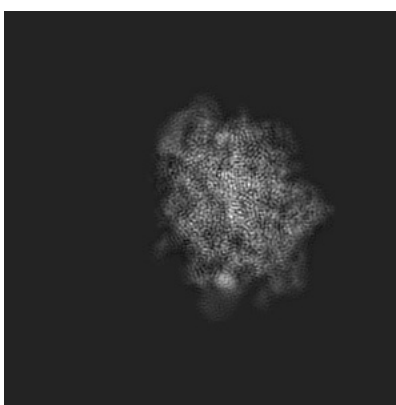
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

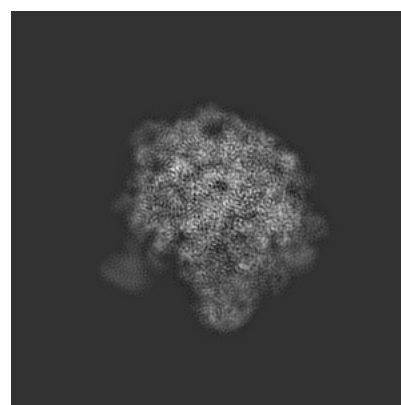
6.1.1 Primary map



X



Y

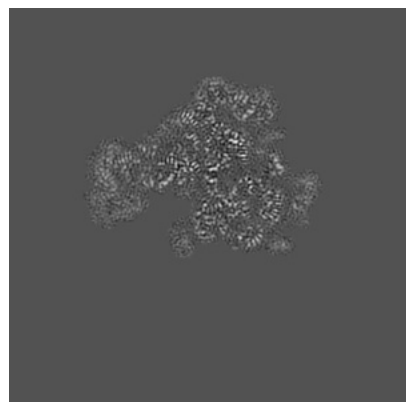


Z

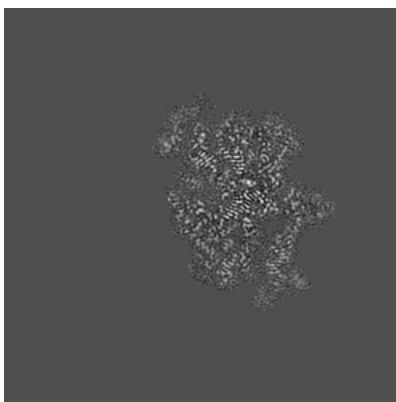
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

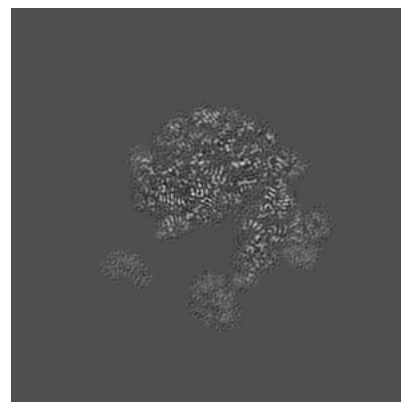
6.2.1 Primary map



X Index: 182



Y Index: 182

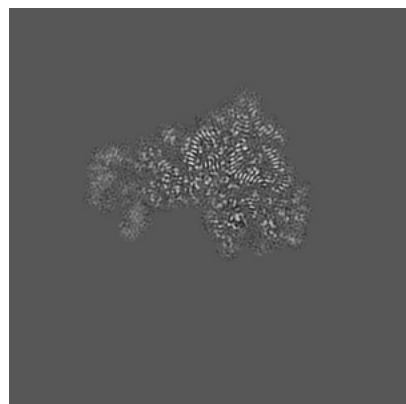


Z Index: 182

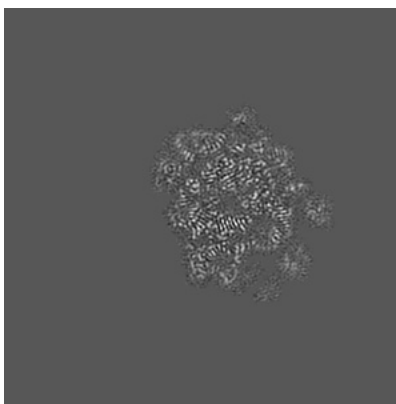
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

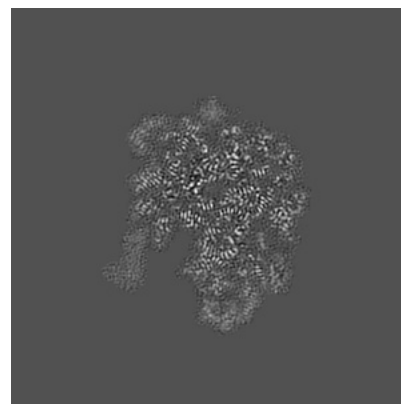
6.3.1 Primary map



X Index: 204



Y Index: 199

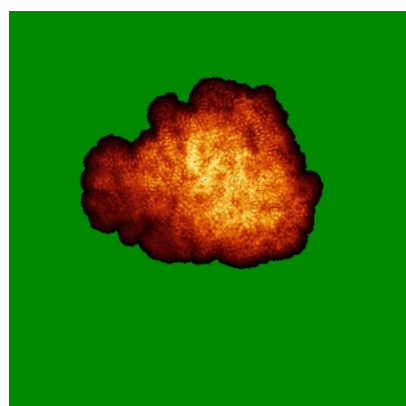


Z Index: 206

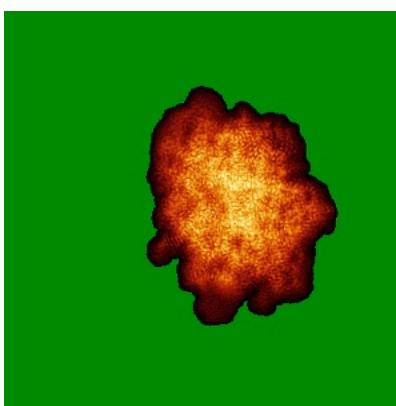
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

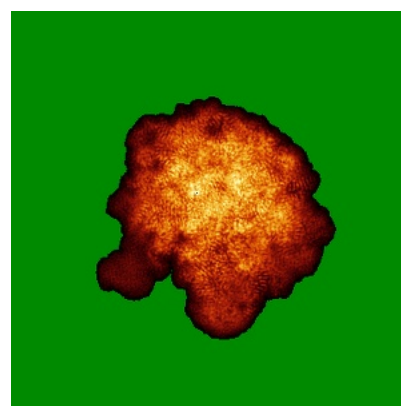
6.4.1 Primary map



X



Y

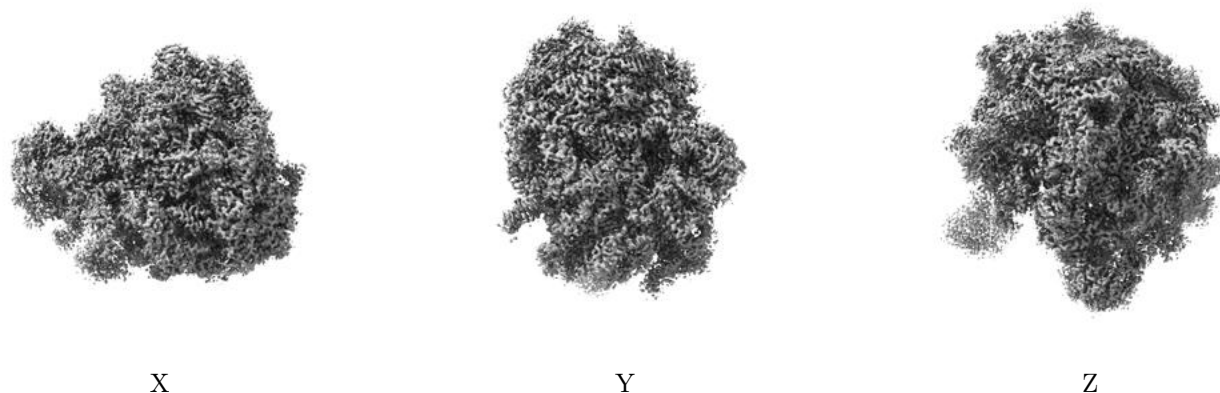


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

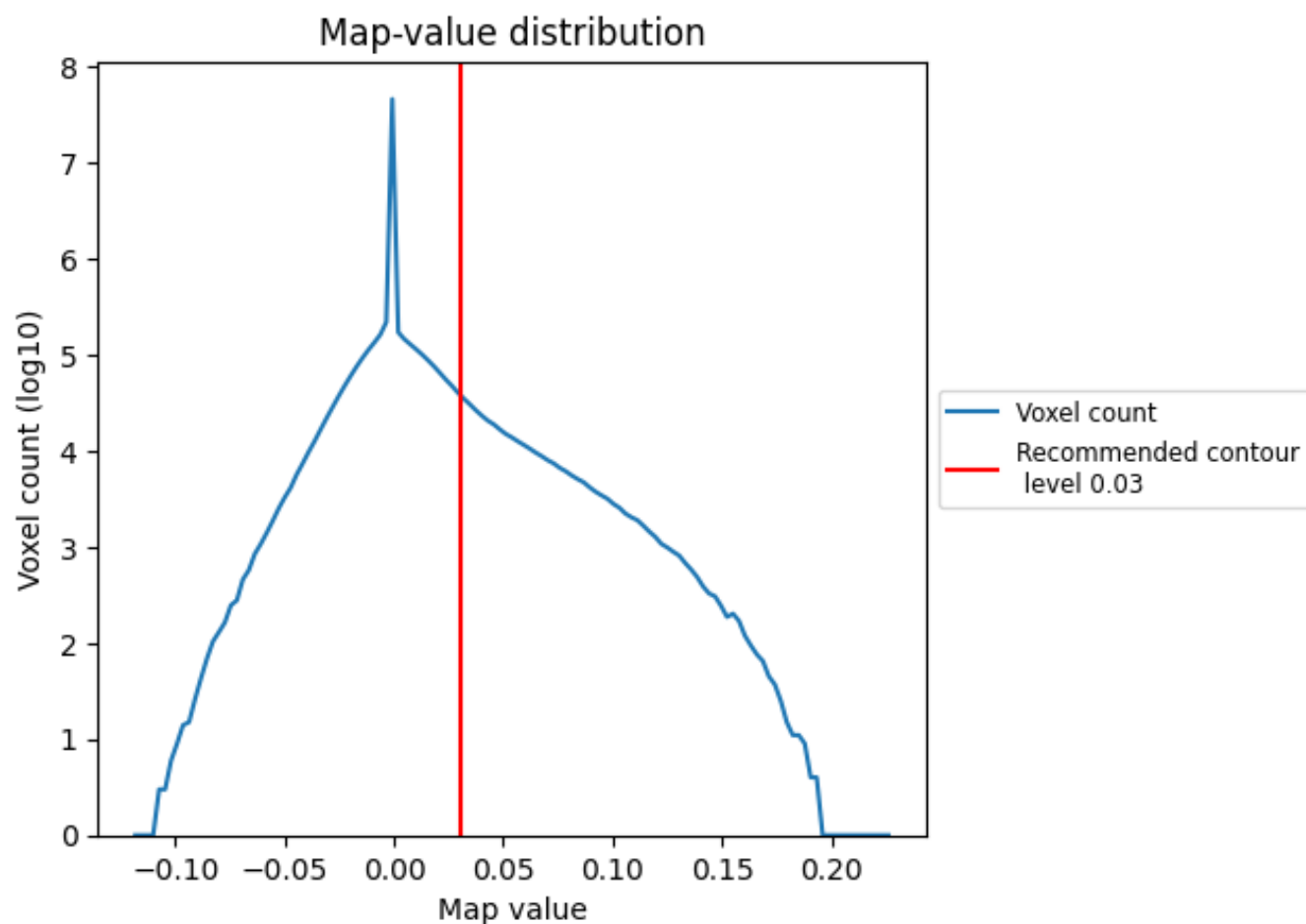
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

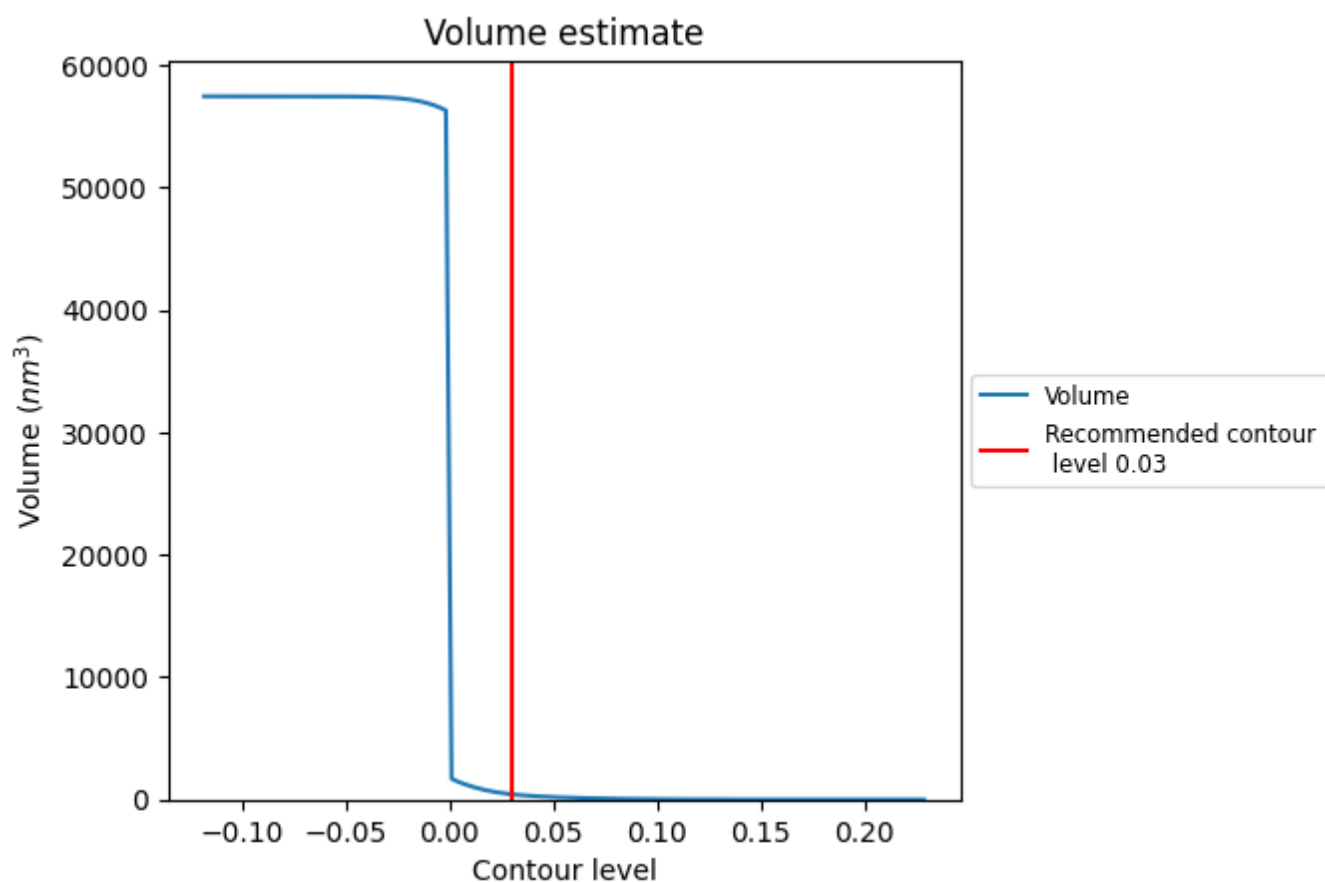
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

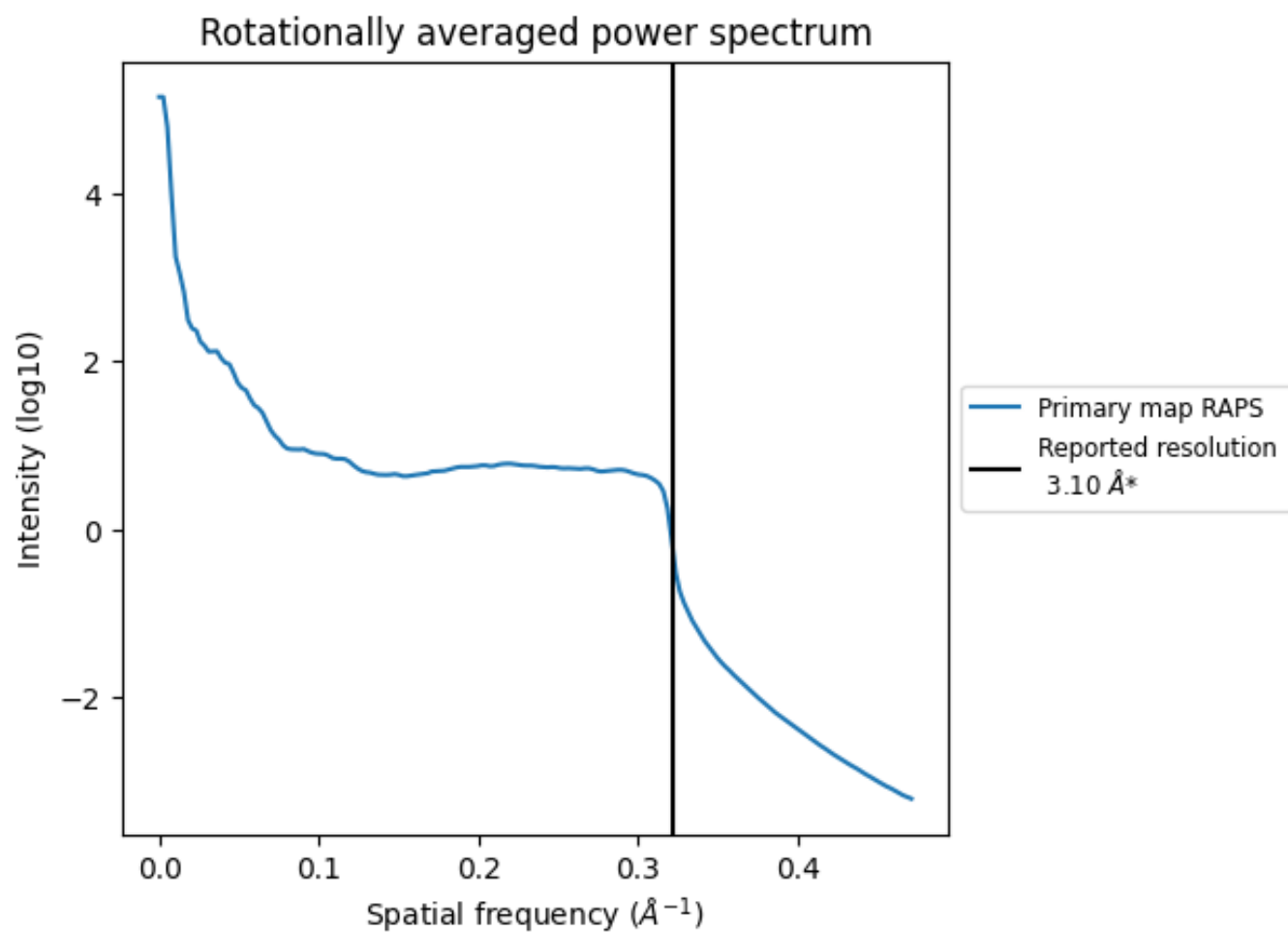
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 434 nm³; this corresponds to an approximate mass of 392 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

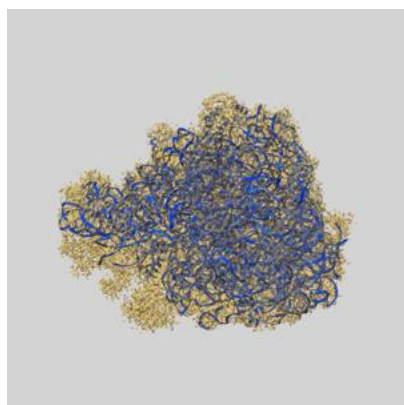
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

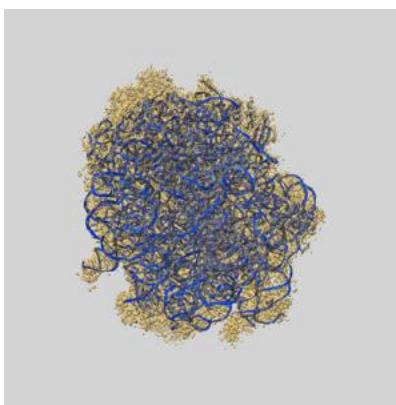
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7867 and PDB model 6DDD. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

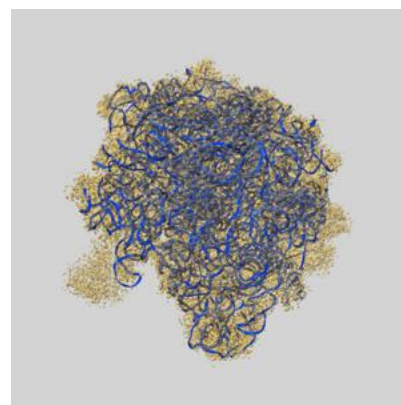
9.1 Map-model overlay [i](#)



X



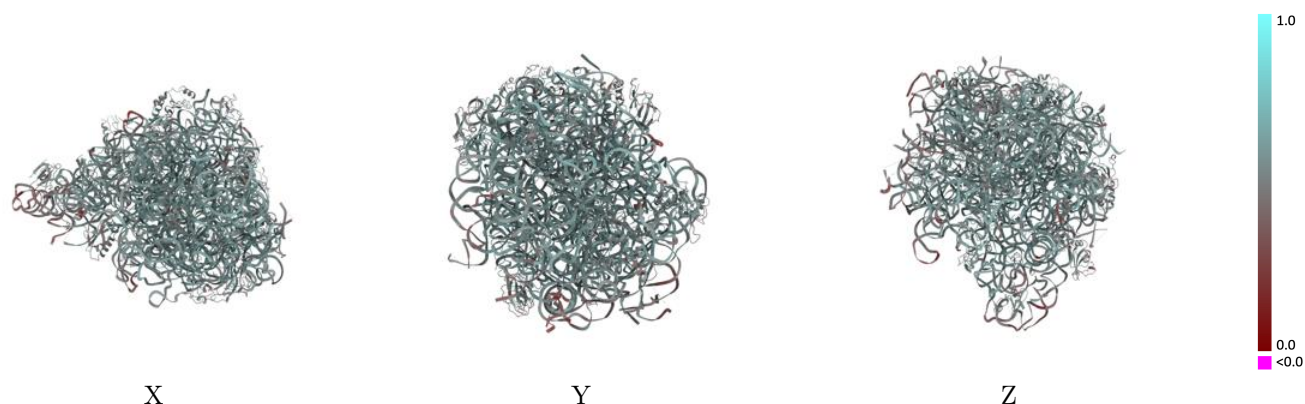
Y



Z

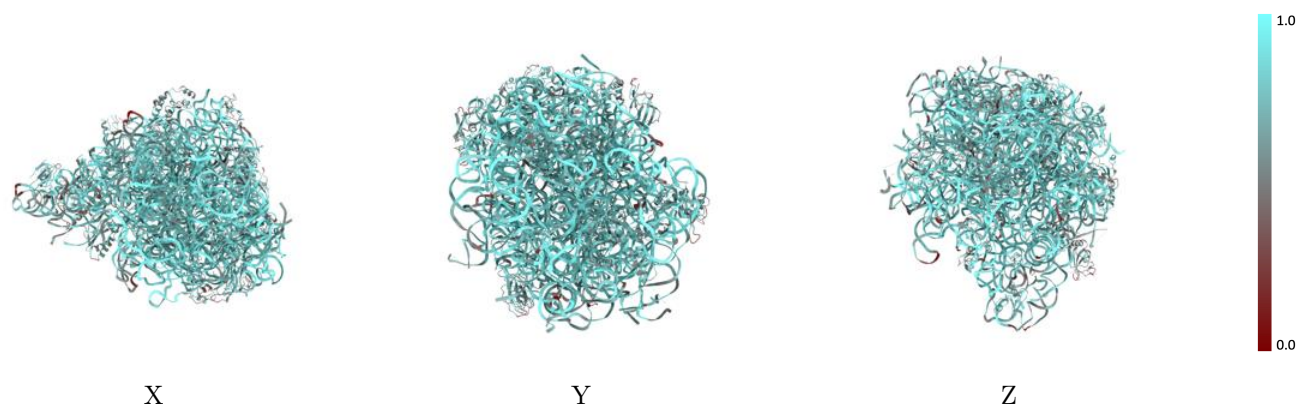
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



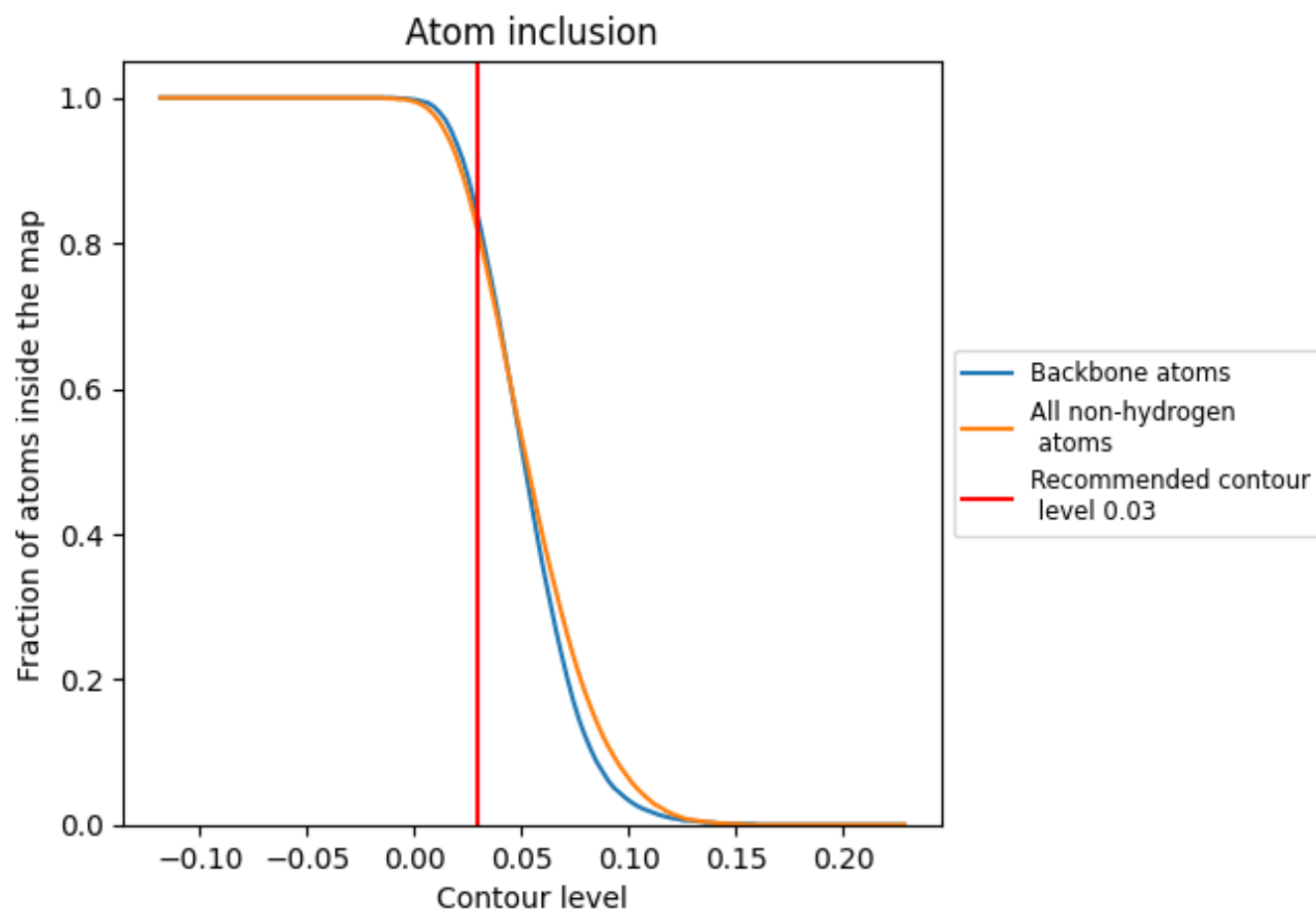
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8140	 0.5540
1	 0.8570	 0.5650
2	 0.7130	 0.4680
A	 0.6560	 0.5120
B	 0.7100	 0.5480
C	 0.7630	 0.5550
D	 0.6870	 0.5120
E	 0.7470	 0.5460
F	 0.6540	 0.5160
G	 0.5780	 0.4820
H	 0.4800	 0.4690
I	 0.7210	 0.5460
J	 0.6420	 0.5230
K	 0.6860	 0.4900
L	 0.7580	 0.5490
M	 0.6980	 0.5380
N	 0.7940	 0.5580
O	 0.6400	 0.5170
P	 0.8010	 0.6000
Q	 0.7790	 0.5820
R	 0.6760	 0.5370
S	 0.7100	 0.5400
V	 0.7500	 0.5430
W	 0.6660	 0.5280
X	 0.7220	 0.5440
Y	 0.7070	 0.5450
Z	 0.7260	 0.5470
a	 0.6650	 0.4990

