



Full wwPDB EM Validation Report ⓘ

Oct 5, 2024 – 07:44 PM EDT

PDB ID : 6DDD
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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

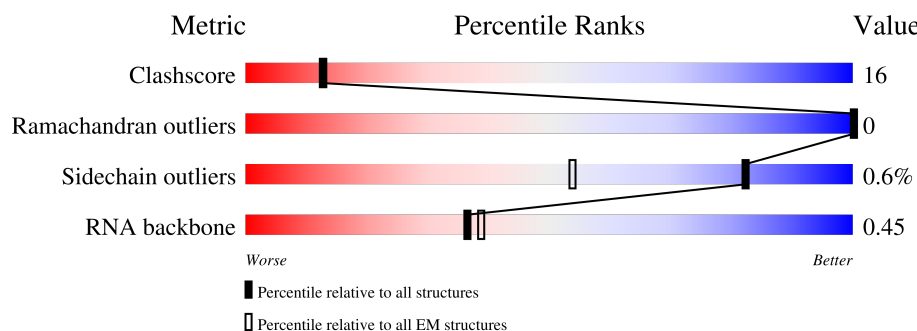
1 Overall quality at a glance

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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	<div> <div>9%</div> <div>54%</div> <div>43%</div> <div>.</div> </div>
2	B	276	<div> <div>8%</div> <div>63%</div> <div>36%</div> <div>.</div> </div>
3	C	118	<div> <div>63%</div> <div>36%</div> <div>.</div> </div>
4	D	102	<div> <div>12%</div> <div>61%</div> <div>37%</div> <div>.</div> </div>
5	E	116	<div> <div>62%</div> <div>33%</div> <div>.</div> </div>
6	F	91	<div> <div>18%</div> <div>57%</div> <div>38%</div> <div>.</div> </div>
7	G	105	<div> <div>20%</div> <div>41%</div> <div>49%</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
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			

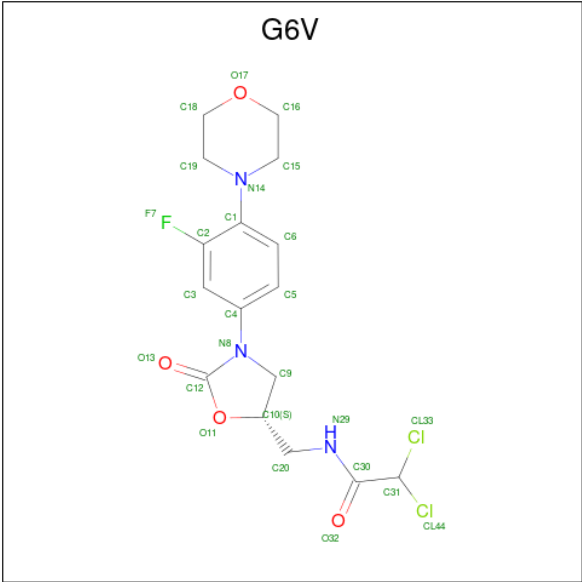
- Molecule 26 is a RNA chain called 23S rRNA.

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 (three-letter code: G6V) (formula: C₁₆H₁₈Cl₂FN₃O₄).

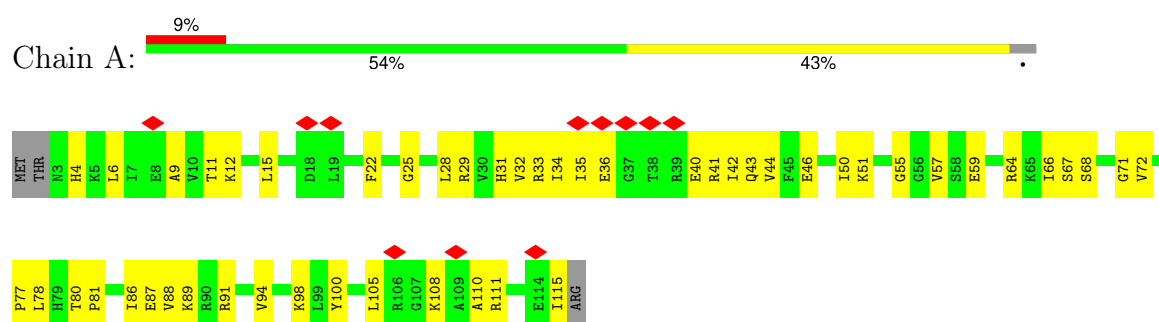


Mol	Chain	Residues	Atoms							AltConf
			Total	C	Cl	F	H	N	O	
28	1	1	44	16	2	1	18	3	4	0

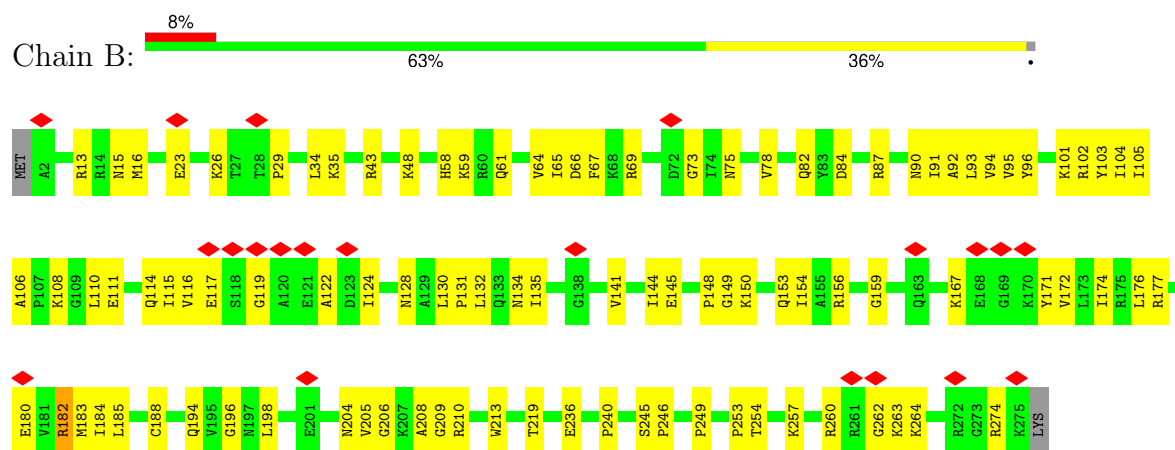
3 Residue-property plots [i](#)

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.

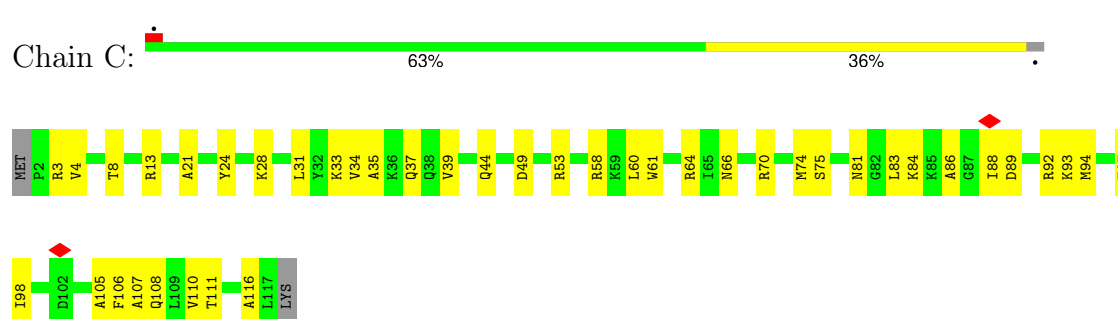
- Molecule 1: 50S ribosomal protein L19



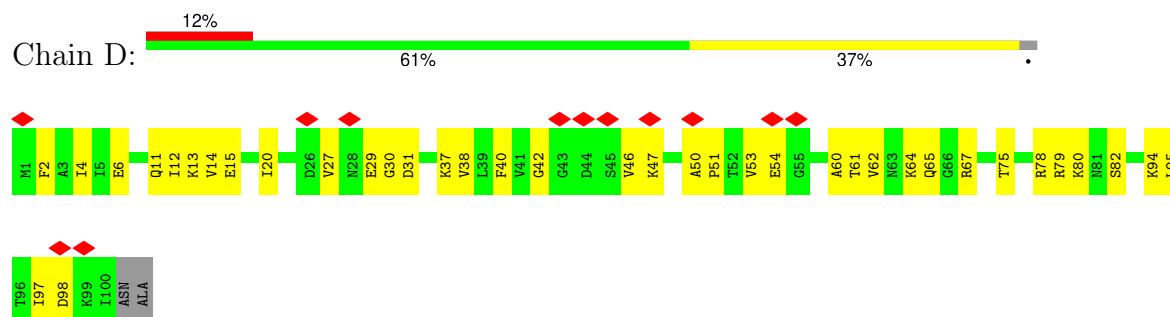
- Molecule 2: 50S ribosomal protein L2



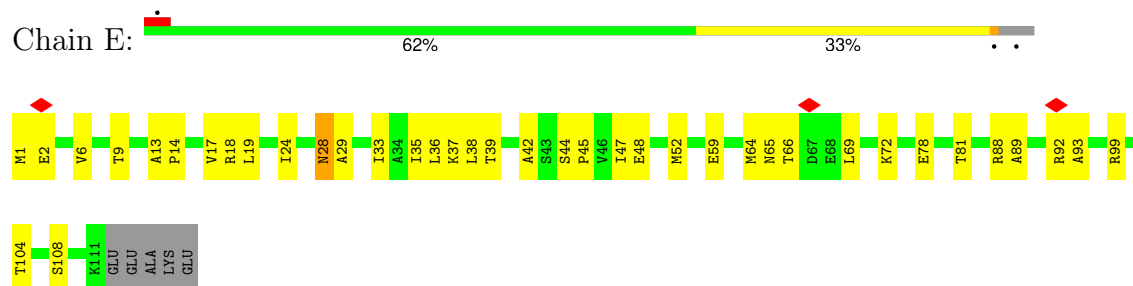
- Molecule 3: 50S ribosomal protein L20



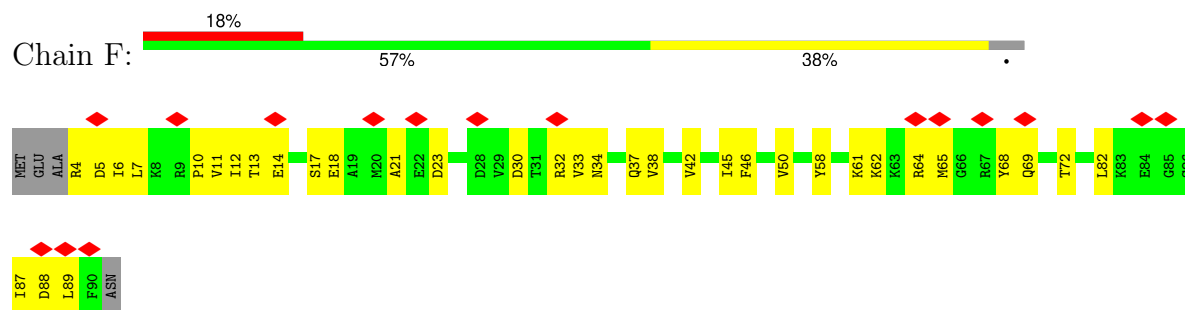
- Molecule 4: 50S ribosomal protein L21



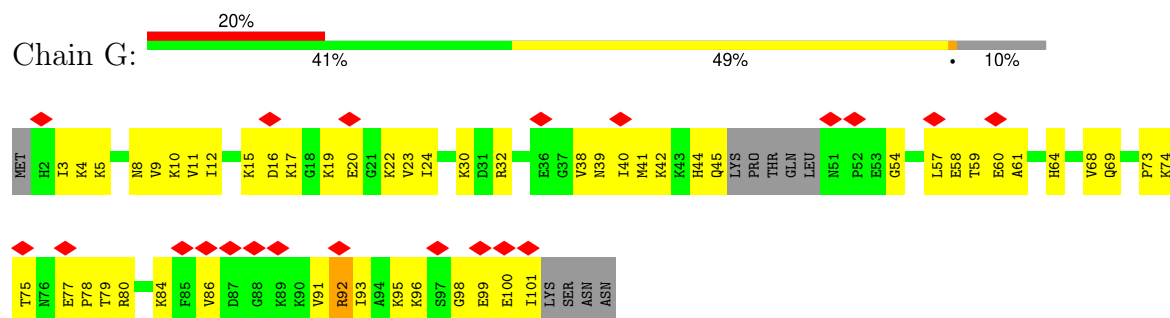
- Molecule 5: 50S ribosomal protein L22



- Molecule 6: 50S ribosomal protein L23

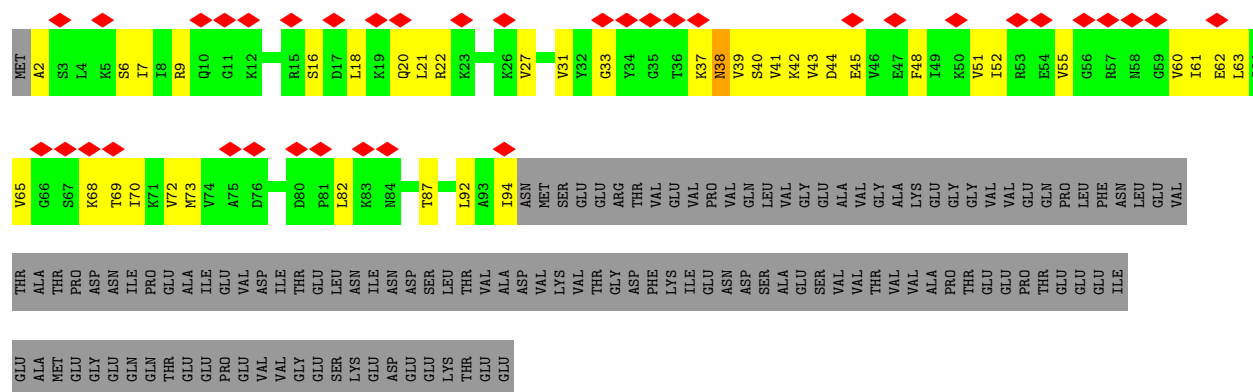


- Molecule 7: 50S ribosomal protein L24

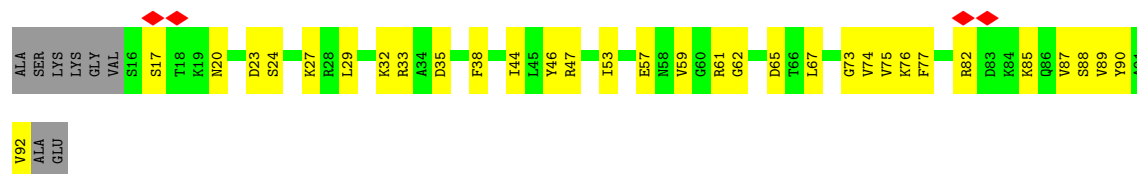


- Molecule 8: 50S ribosomal protein L25

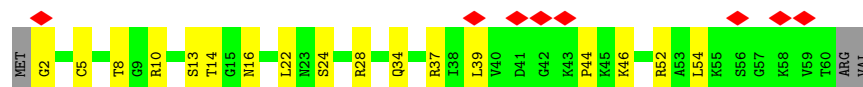




• Molecule 9: 50S ribosomal protein L27



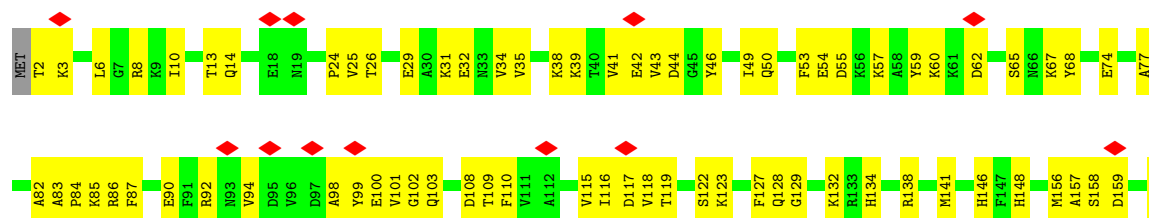
• Molecule 10: 50S ribosomal protein L28



• Molecule 11: 50S ribosomal protein L29

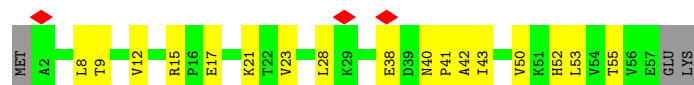


• Molecule 12: 50S ribosomal protein L3

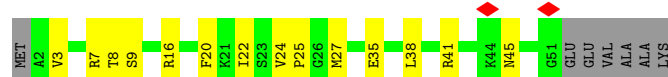




- Molecule 13: 50S ribosomal protein L30



- Molecule 14: 50S ribosomal protein L32



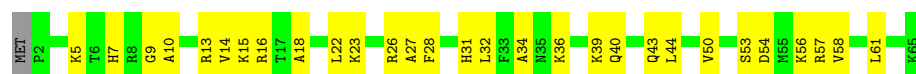
- Molecule 15: 50S ribosomal protein L33



- Molecule 16: 50S ribosomal protein L34



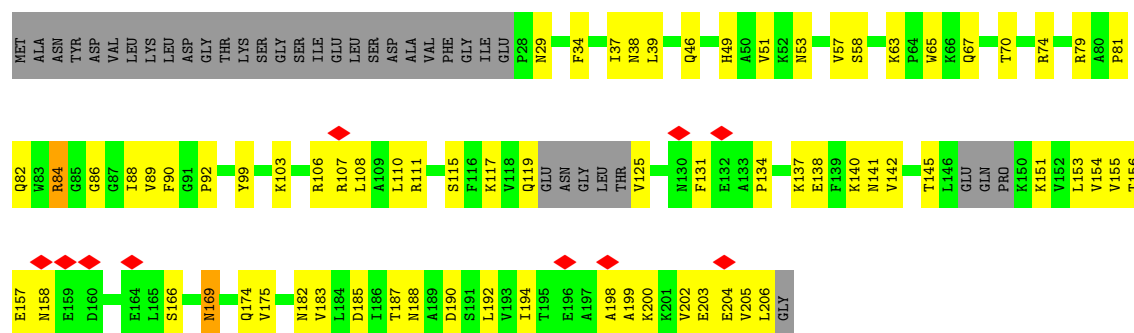
- Molecule 17: 50S ribosomal protein L35



- Molecule 18: 50S ribosomal protein L36



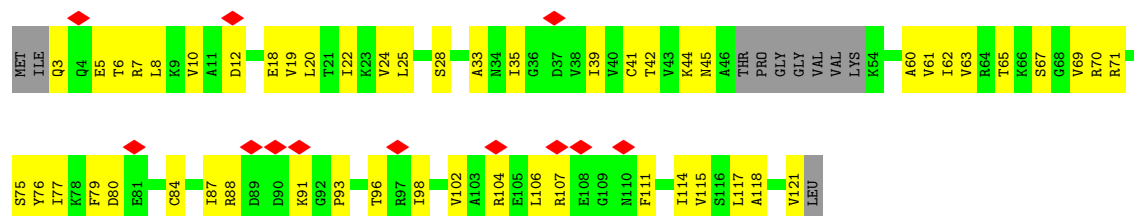
- Molecule 19: 50S ribosomal protein L4



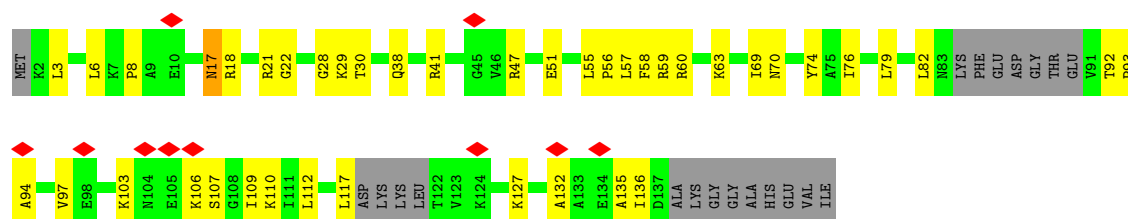
- Molecule 20: 50S ribosomal protein L13



- Molecule 21: 50S ribosomal protein L14

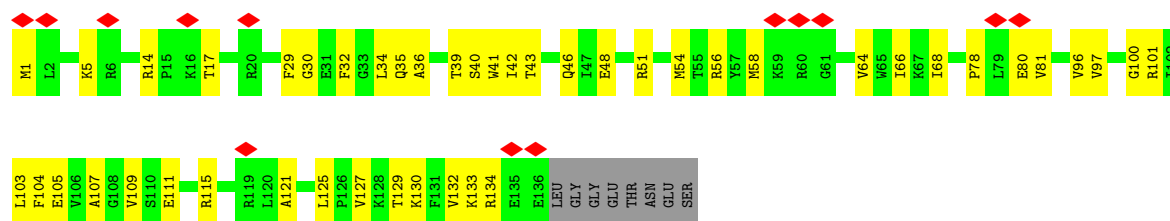


- Molecule 22: 50S ribosomal protein L15

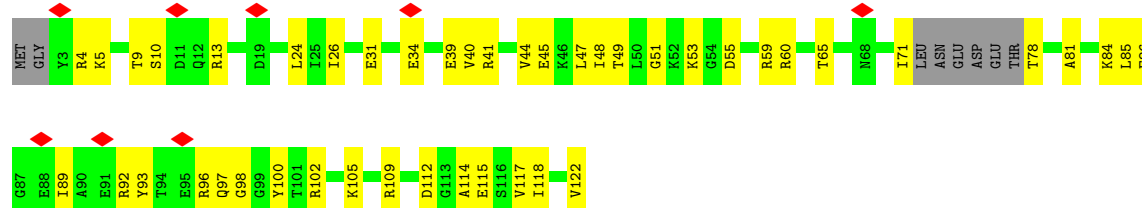


- Molecule 23: 50S ribosomal protein L16

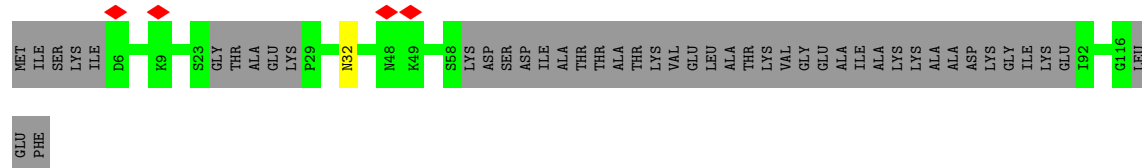




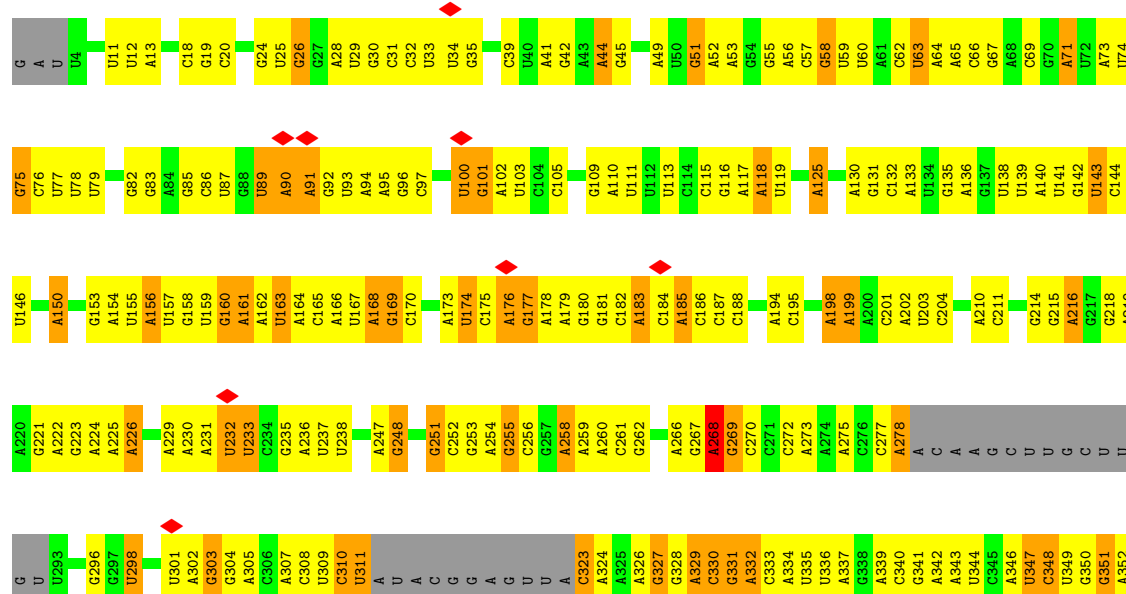
• Molecule 24: 50S ribosomal protein L17



• Molecule 25: 50S ribosomal protein L18

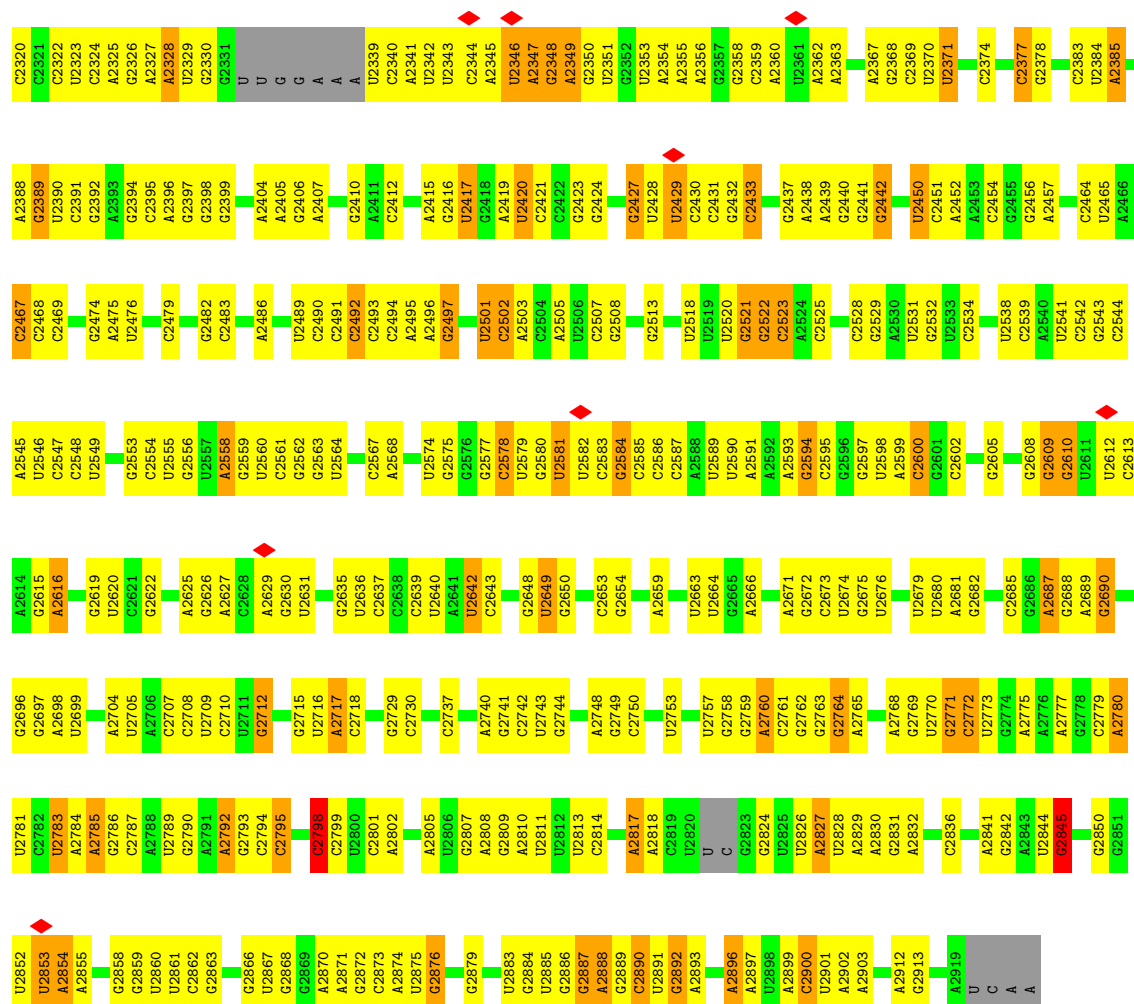


• Molecule 26: 23S rRNA

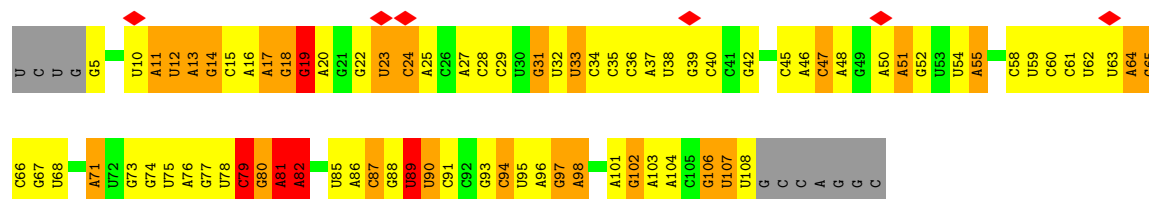
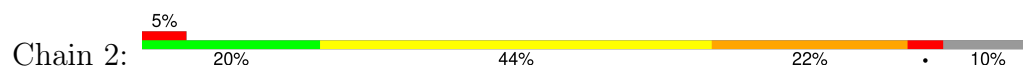




G2244	A1965	G1902	A1764	G1882	U1601	U1386
A2250	U1966	A1903	A1765	U1883	U1602	C1387
G2251	C1967	A1904	C1766	U1883	U1603	U1388
A2252	U1968	G1905	G1767	G1686	C1604	U1389
G2253	C1969	C1906	C1768	G1687	A1605	A1390
A2254	U1970	U1907	G1769	U1688	G1606	A1391
U2255	G1976	A1908	C1770	G1689	A1607	U1394
C2256	U1976	C1909	A1771	A1690	U1608	U1395
A2257	U1976	G1910	G1772	G1691	U1609	G1396
G2258	U1977	A1911	A1773	U1692	C1692	A1397
A2259	U1978	A1912	A1774	G1693	U1693	G1480
G2260	U1979	C1913	G1775	A1694	C1694	A1481
G2261	A1980	U1914	A1776	G1695	G1615	G1398
G2262	U1981	G1915	G1777	C1696	A1616	C1399
C2263	U1982	U1918	C1778	G1697	U1617	U1402
A2264	C1985	G1919	A1779	A1698	A1618	A1403
U2265	U1986	C1920	C1780	A1699	A1619	G1404
G2266	A1987	C1921	A1782	U1701	G1620	G1405
A2267	U1988	C1922	G1783	G1710	U1625	U1409
G2268	C1990	U1925	U1788	G1711	A1626	A1410
U2269	G1991	A1926	G1789	G1717	G1627	G1411
A2270	C1992	A1927	G1790	G1718	A1628	U1415
G2271	U1993	C1928	G1791	G1719	U1629	U1416
C2272	C1994	G1930	C1792	A1720	G1631	C1423
U2273	U1995	G1931	G1793	A1721	U1632	A1424
A2274	G1996	C1932	C1794	U1722	U1633	G1425
G2275	A1997	G1933	G1799	A1723	G1634	G1426
C2276	U1998	C1934	U1800	U1724	A1635	U1427
A2277	A1999	G1935	C1801	G1725	U1636	U1428
U2278	C2000	C1936	U1802	A1726	G1637	G1429
G2279	C2001	G1937	G1803	U1732	U1638	A1511
C2280	G2007	U1938	U1806	U1733	C1648	U1430
A2281	A2008	A1939	A1807	G1734	C1649	U1431
U2282	U2009	C1940	A1807	A1734	U1650	U1432
G2283	C2017	U1942	A1810	G1740	C1651	U1434
A2284	U2018	A1943	A1811	G1741	A1652	C1445
C2285	G2019	C1944	A1812	A1742	A1653	U1446
U2286	U2020	U1945	A1813	G1743	U1654	U1447
G2287	C2021	A1946	A1816	A1744	G1658	U1448
C2288	U2022	C1947	C1817	U1747	C1659	A1449
U2289	C2023	G1948	A1818	U1750	A1660	U1450
A2290	A2024	U1949	U1821	U1753	C1661	C1452
C2291	G2028	U1950	C1822	C1754	A1662	G1453
U2292	C2033	C1951	U1823	U1755	G1663	U1454
G2293	U2036	C1952	C1824	C1756	A1666	U1588
A2294	G2037	U1953	U1825	U1757	U1671	U1589
C2295	U2038	C1954	U1826	U1757	A1674	C1590
U2296	G2039	A1955	C1827	A1758	G1675	A1459
G2297	U2040	G1956	U1828	G1759	C1595	U1460
A2298	A2041	U1957	A1829	U1760	U1596	C1461
C2299	C2042	U1958	A1830	G1761	U1597	G1462
U2300	A2047	C1959	A1836	U1762	G1599	U1463
G2301	U2118	U1997	U1837	U1763	A1600	U1464
A2302	U2119	C1999	U1837	U1763		G1465
C2303	A2122	C1901				
U2304						
G2305						
A2306						
C2307						
U2308						
G2309						
A2310						
C2311						
U2312						
G2313						
A2314						
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U2335						
G2336						
A2337						
C2338						
U2339						
G2340						
A2341						
C2342						
U2343						



• 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

5.1 Standard geometry

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	0.44	0/927	0.57	0/1239
2	B	0.44	0/2129	0.56	0/2858
3	C	0.51	0/955	0.57	0/1265
4	D	0.43	0/795	0.57	0/1062
5	E	0.39	0/861	0.55	0/1159
6	F	0.42	0/719	0.59	0/959
7	G	0.35	0/737	0.55	0/983
8	H	0.36	0/735	0.55	0/986
9	I	0.47	0/598	0.59	0/794
10	J	0.44	0/469	0.59	0/625
11	K	0.41	0/473	0.55	0/631
12	L	0.48	0/1652	0.58	0/2216
13	M	0.44	0/434	0.61	0/585
14	N	0.48	0/404	0.57	0/537
15	O	0.39	0/385	0.59	0/513
16	P	0.52	0/376	0.56	0/491
17	Q	0.47	0/526	0.54	0/690
18	R	0.40	0/299	0.54	0/393
19	S	0.42	0/1336	0.55	0/1799
20	V	0.49	0/1160	0.55	0/1563
21	W	0.42	0/855	0.53	0/1145
22	X	0.44	0/948	0.56	0/1262
23	Y	0.47	0/1113	0.56	0/1493
24	Z	0.42	0/905	0.54	0/1207
25	a	0.38	0/589	0.54	0/785
26	1	0.93	0/63551	0.94	65/99100 (0.1%)
27	2	0.58	0/2475	1.08	17/3854 (0.4%)
All	All	0.83	0/86406	0.88	82/130194 (0.1%)

There are no bond length outliers.

All (82) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	2	20	A	N9-C1'-C2'	-9.73	101.30	112.00
26	1	1931	G	C1'-C2'-O2'	-8.31	85.68	110.60
26	1	1501	G	N3-C4-N9	-8.14	121.12	126.00
26	1	557	G	O4'-C1'-N9	7.58	114.27	108.20
26	1	481	C	N1-C2-O2	7.52	123.41	118.90
26	1	1955	A	N9-C1'-C2'	-7.48	103.77	112.00
26	1	556	U	N3-C2-O2	-7.18	117.18	122.20
27	2	82	A	N9-C1'-C2'	-6.98	104.32	112.00
26	1	2238	U	N1-C2-O2	6.97	127.68	122.80
27	2	20	A	C4'-C3'-O3'	6.94	126.89	113.00
26	1	1501	G	N3-C4-C5	6.83	132.01	128.60
26	1	1390	A	N7-C8-N9	6.81	117.21	113.80
26	1	1395	G	C4-C5-N7	6.80	113.52	110.80
26	1	1868	U	N1-C1'-C2'	-6.77	104.56	112.00
26	1	2238	U	C2-N1-C1'	6.77	125.82	117.70
26	1	1559	G	N3-C4-N9	-6.62	122.03	126.00
26	1	1395	G	C4-N9-C1'	6.49	134.93	126.50
27	2	80	G	N9-C1'-C2'	-6.47	104.88	112.00
27	2	89	U	N1-C1'-C2'	-6.43	104.93	112.00
26	1	2238	U	N3-C2-O2	-6.29	117.79	122.20
26	1	1501	G	C4-N9-C1'	-6.25	118.38	126.50
26	1	1390	A	C8-N9-C4	-6.18	103.33	105.80
26	1	125	A	C5-N7-C8	-6.16	100.82	103.90
26	1	793	G	C6-C5-N7	-6.10	126.74	130.40
26	1	592	A	N1-C6-N6	-6.09	114.94	118.60
26	1	1929	C	N1-C1'-C2'	-6.01	105.39	112.00
26	1	1395	G	C6-C5-N7	-6.00	126.80	130.40
26	1	481	C	N3-C2-O2	-5.99	117.71	121.90
26	1	268	A	O4'-C1'-N9	5.95	112.96	108.20
26	1	1501	G	C8-N9-C1'	5.94	134.72	127.00
26	1	125	A	N7-C8-N9	5.92	116.76	113.80
26	1	323	C	C2-N1-C1'	5.85	125.23	118.80
26	1	2845	G	N3-C4-C5	5.83	131.51	128.60
27	2	90	U	N1-C1'-C2'	-5.82	105.60	112.00
26	1	2845	G	C2-N3-C4	-5.80	109.00	111.90
26	1	721	A	C5-N7-C8	-5.76	101.02	103.90
27	2	80	G	C4'-C3'-O3'	5.72	124.44	113.00
26	1	2845	G	N3-C4-N9	-5.72	122.57	126.00
27	2	91	C	N1-C1'-C2'	-5.69	105.74	112.00
26	1	1395	G	N7-C8-N9	5.68	115.94	113.10
26	1	793	G	N1-C6-O6	5.65	123.29	119.90
26	1	58	G	N1-C6-O6	-5.64	116.52	119.90
26	1	323	C	C6-N1-C2	-5.62	118.05	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	1	2417	U	C2-N1-C1'	5.60	124.42	117.70
26	1	2056	G	C5-N7-C8	-5.59	101.51	104.30
26	1	1395	G	C5-N7-C8	-5.56	101.52	104.30
27	2	79	C	N1-C1'-C2'	-5.45	106.01	112.00
26	1	1868	U	C4'-C3'-O3'	5.43	123.86	113.00
26	1	555	C	N1-C2-O2	5.42	122.15	118.90
26	1	125	A	C8-N9-C4	-5.39	103.64	105.80
26	1	1395	G	C8-N9-C1'	-5.39	120.00	127.00
27	2	61	C	N1-C1'-C2'	-5.38	106.09	112.00
26	1	1806	U	C5-C6-N1	-5.35	120.02	122.70
27	2	81	A	N9-C1'-C2'	-5.34	106.12	112.00
27	2	81	A	C1'-C2'-O2'	-5.32	94.63	110.60
26	1	1390	A	C5-N7-C8	-5.31	101.25	103.90
26	1	1559	G	N3-C2-N2	-5.30	116.19	119.90
26	1	793	G	N7-C8-N9	5.28	115.74	113.10
26	1	1395	G	O4'-C1'-N9	5.27	112.42	108.20
26	1	515	G	C5-N7-C8	-5.26	101.67	104.30
26	1	556	U	N1-C2-O2	5.26	126.48	122.80
26	1	1201	G	C4-N9-C1'	5.26	133.34	126.50
27	2	90	U	C4'-C3'-O3'	5.25	123.51	113.00
26	1	666	A	C5-N7-C8	-5.20	101.30	103.90
26	1	1929	C	C4'-C3'-O3'	5.18	123.37	113.00
26	1	721	A	C2-N3-C4	-5.18	108.01	110.60
26	1	1453	G	O4'-C1'-N9	5.18	112.34	108.20
26	1	1501	G	N3-C2-N2	-5.16	116.29	119.90
26	1	721	A	N7-C8-N9	5.14	116.37	113.80
27	2	80	G	C1'-C2'-O2'	-5.13	95.20	110.60
27	2	19	G	C1'-C2'-O2'	-5.12	95.24	110.60
26	1	1781	C	C2-N1-C1'	5.10	124.41	118.80
26	1	1221	C	C2-N1-C1'	5.08	124.38	118.80
26	1	2239	A	N7-C8-N9	5.06	116.33	113.80
26	1	1559	G	N3-C4-C5	5.06	131.13	128.60
27	2	61	C	C4'-C3'-O3'	5.05	123.11	113.00
26	1	481	C	C2-N1-C1'	5.05	124.36	118.80
26	1	1768	C	C2-N1-C1'	5.05	124.36	118.80
26	1	2887	G	P-O3'-C3'	5.04	125.75	119.70
27	2	82	A	C1'-C2'-O2'	-5.03	95.51	110.60
26	1	2798	C	N1-C2-O2	5.02	121.91	118.90
26	1	1955	A	C4'-C3'-O3'	5.00	123.00	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	54	0
2	B	2094	0	2205	97	0
3	C	943	0	1014	42	0
4	D	785	0	825	38	0
5	E	853	0	914	35	0
6	F	711	0	750	36	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	98	0
13	M	432	0	472	15	0
14	N	397	0	407	14	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	66	0
20	V	1138	0	1129	40	0
21	W	850	0	895	46	0
22	X	938	0	977	39	0
23	Y	1089	0	1155	39	0
24	Z	902	0	958	39	0
25	a	583	0	598	0	0
26	1	56747	0	28540	1263	0
27	2	2214	0	1120	53	0
28	1	26	18	0	1	0
All	All	79118	18	50872	2052	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 16.

All (2052) 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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:37:GLN:HE22	26:1:606:G:H21	1.33	0.75
3:C:94:MET:HE3	4:D:12:ILE:HA	1.68	0.74
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
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
26:1:1505:G:HO2'	26:1:2729:G:HO2'	1.34	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
12:L:55:ASP:OD1	12:L:85:LYS:NZ	2.20	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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
26:1:105:C:HO2'	26:1:337:A:HO2'	1.37	0.71
27:2:82:A:H61	27:2:87:C:H42	1.39	0.71
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
16:P:2:VAL:N	26:1:1663:G:HO2'	1.89	0.70
13:M:40:ASN:OD1	26:1:973:A:O2'	2.08	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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
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
7:G:78:PRO:O	7:G:96:LYS:NZ	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
5:E:39:THR:OG1	5:E:44:SER:OG	2.11	0.62
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
12:L:123:LYS:NZ	26:1:2708:C:OP2	2.30	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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
26:1:1991:G:O2'	26:1:1994:C:OP2	2.14	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
26:1:115:C:HO2'	26:1:125:A:H8	1.50	0.59
7:G:41:MET:CG	7:G:61:ALA:HB2	2.31	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
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
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
23:Y:51:ARG:HA	23:Y:54:MET:HE3	1.86	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
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
3:C:93:LYS:HE3	3:C:94:MET:HE1	1.87	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
26:1:738:U:HO2'	26:1:1390:A:H8	1.53	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
26:1:1325:U:O2'	26:1:1326:C:OP1	2.21	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
22:X:38:GLN:OE1	26:1:876:G:O2'	2.22	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2760:A:H2'	26:1:2761:C:O4'	2.06	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
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
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
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
26:1:457:G:OP2	26:1:2433:C:O2'	2.21	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:44:ILE:HD13	9:I:47:ARG:HH11	1.72	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
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
26:1:2582: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
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
16:P:10:LYS:NZ	26:1:1347:G:OP2	2.19	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
26:1:622: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
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
3:C:94:MET:HE3	4:D:12:ILE:CA	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:117:GLU:CD	2:B:130:LEU:HD13	2.29	0.53
21:W:10:VAL:HG12	21:W:12:ASP:H	1.73	0.53
26:1:1409:U:HO2'	26:1:2239:A:H8	1.56	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
26:1:2558:A:HO2'	26:1:2685:C:HO2'	1.56	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2405:A:C5	26:1:2406:G:H1'	2.44	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
12:L:39:LYS:NZ	12:L:90:GLU:OE2	2.30	0.52
26:1:368:A:H2'	26:1:369:G:H8	1.74	0.52
26:1:575:G:O2'	26:1:577:A:N7	2.41	0.52
26:1:897:A:O2'	26:1:898:U:H5'	2.09	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
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
26:1:2091: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
3:C:24:TYR:HB3	3:C:28:LYS:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
26:1:787:U:H2'	26:1:788:A:H8	1.75	0.52
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
26:1:2293: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
23:Y:111:GLU:OE2	23:Y:133:LYS:NZ	2.22	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
26:1:222:A:N3	26:1:237:U:O2'	2.38	0.51
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
26:1:1347: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
8:H:31:VAL:HB	8:H:39:VAL:CG2	2.37	0.51
8:H:60:VAL:HG12	8:H:73:MET:HE1	1.93	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
26:1:1648:C:O2'	26:1:1654:A:N1	2.37	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
12:L:42:GLU:CD	12:L:43:VAL:HG13	2.31	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
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
26:1:310: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
12:L:60:LYS:HZ2	12:L:62:ASP:HB2	1.77	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2563:G:O2'	26:1:2564:U:H5'	2.12	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
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
23:Y:39:THR:O	23:Y:40:SER:OG	2.25	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
14:N:22:ILE:O	14:N:22:ILE:HG13	2.12	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
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
9:I:77:PHE:CE1	9:I:87:VAL:HG22	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
26:1:537:A:C2'	26:1:538:G:H5'	2.42	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
4:D:46:VAL:C	4:D:47:LYS:HD3	2.33	0.48
6:F:23:ASP:N	6:F:23:ASP:OD1	2.46	0.48
8:H:73:MET:HE3	8:H:94:ILE:HD12	1.94	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
26:1:862:C:O2'	26:1:884:U:OP1	2.28	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
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
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
26:1:1516: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
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
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
26:1:418:G:O2'	26:1:446:G:O6	2.23	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
17:Q:54:ASP:CG	22:X:57:LEU:HD22	2.35	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
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
26:1:1325:U:HO2'	26:1:1691:G:H22	1.63	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:111:GLU:O	23:Y:115:ARG:HG3	2.14	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
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
26:1:525:A:H1'	26:1:526:A:H5''	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
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
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
26:1:1355:A:O2'	26:1:1356:G:H5'	2.15	0.46
26:1:1515:G:HO2'	26:1:1516:C:H6	1.63	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
12:L:110:PHE:O	12:L:188:VAL:HG11	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
23:Y:58:MET:HE1	23:Y:64:VAL:HG23	1.97	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
26:1:2704:A:H2'	26:1:2705:U:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
26:1:2325: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
26:1:837:G:N3	26:1:2099:G:O2'	2.46	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
26:1:1352: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
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: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
12:L:3:LYS:HZ1	12:L:98:ALA:HB2	1.81	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
1:A:67:SER:OG	1:A:68:SER:N	2.50	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
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
26:1:1219: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
26:1:33:U:O4	26:1:492:G:O2'	2.29	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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:35:ILE:HG22	1:A:40:GLU:CD	2.39	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
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
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
26:1:24:G:H2'	26:1:25:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
27:2:37:A:HO2'	27:2:38:U:C5'	2.32	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
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
26:1:2836:C:O2	26:1:2903:A:O2'	2.29	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
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
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
23:Y:51:ARG:HA	23:Y:54:MET:CE	2.48	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
26:1:672:A:N1	26:1:681:G:O2'	2.42	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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
23:Y:104:PHE:HE2	23:Y:125:LEU:HD11	1.84	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
26:1:1325:U:HO2'	26:1:1326:C:P	2.42	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
26:1:161:A:HO2'	26:1:162:A:P	2.42	0.41
26:1:615:A:H5''	26:1:616:G:OP2	2.20	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
5:E:1:MET:O	5:E:108:SER:OG	2.13	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
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
26:1:483:C:H2'	26:1:484:U:C6	2.55	0.41
26:1:852:U:O2'	26:1:2087:A:N1	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1403:C:H2'	26:1:1404:A:O4'	2.20	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
1:A:59:GLU:CD	1:A:78:LEU:HD12	2.40	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
12:L:138:ARG:HD2	12:L:141:MET:HE2	2.03	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
2:B:177:ARG:HG3	2:B:177:ARG:O	2.21	0.41
4:D:94:LYS:C	4:D:95:LEU:HD12	2.41	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
18:R:18:LYS:HZ1	18:R:21:GLY:HA2	1.86	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: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
26:1:1026:C:O5'	26:1:1026:C:H6	2.04	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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:3:LYS:HZ2	12:L:98:ALA:HB2	1.86	0.40
12:L:32:GLU:HB3	12:L:85:LYS:NZ	2.36	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
26:1:404:U:HO2'	26:1:405:G:H8	1.69	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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	220 (100%)	1 (0%)	86	92
3	C	96/98 (98%)	96 (100%)	0	100	100
4	D	85/86 (99%)	85 (100%)	0	100	100
5	E	90/94 (96%)	89 (99%)	1 (1%)	70	84
6	F	79/82 (96%)	79 (100%)	0	100	100
7	G	80/90 (89%)	79 (99%)	1 (1%)	65	82
8	H	81/190 (43%)	80 (99%)	1 (1%)	67	83
9	I	61/66 (92%)	60 (98%)	1 (2%)	58	79
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%)	172 (99%)	1 (1%)	84	91
13	M	50/53 (94%)	50 (100%)	0	100	100
14	N	45/50 (90%)	44 (98%)	1 (2%)	47	71
15	O	44/47 (94%)	44 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	137 (97%)	4 (3%)	38	66
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%)	95 (99%)	1 (1%)	73	86
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%)	59 (98%)	1 (2%)	56	78
All	All	2153/2427 (89%)	2140 (99%)	13 (1%)	82	91

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	182	ARG
5	E	28	ASN
7	G	92	ARG
8	H	38	ASN
9	I	61	ARG
12	L	162	ARG
14	N	7	ARG
19	S	38	ASN
19	S	84	ARG
19	S	169	ASN
19	S	188	ASN
22	X	17	ASN
25	a	32	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	HIS
1	A	43	GLN
2	B	61	GLN
2	B	134	ASN
2	B	199	GLN

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Mol	Chain	Res	Type
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	54	ASN
6	F	57	ASN
7	G	8	ASN
8	H	13	GLN
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
19	S	29	ASN
19	S	38	ASN
19	S	67	GLN
19	S	169	ASN
19	S	188	ASN
20	V	3	GLN
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%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	2	103/115 (89%)	43 (41%)	3 (2%)
All	All	2737/3038 (90%)	671 (24%)	23 (0%)

All (671) 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	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
27	2	98	A

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Mol	Chain	Res	Type
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:

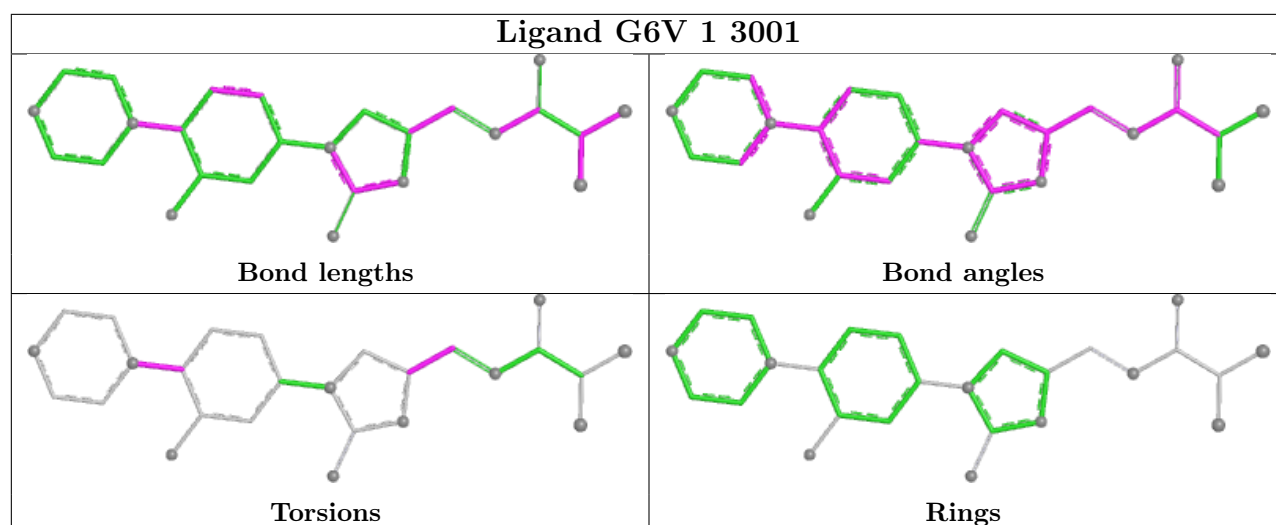
Mol	Chain	Res	Type	Atoms
28	1	3001	G6V	C9-C10-C20-N29
28	1	3001	G6V	C2-C1-N14-C19
28	1	3001	G6V	C6-C1-N14-C19
28	1	3001	G6V	O11-C10-C20-N29

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.

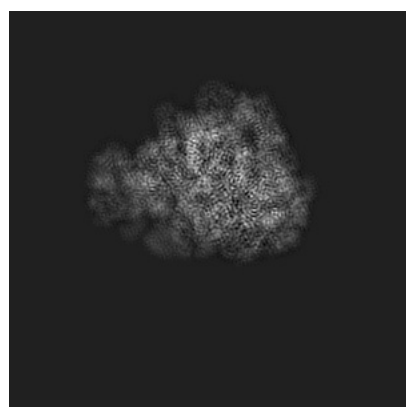
6 Map visualisation [i](#)

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.

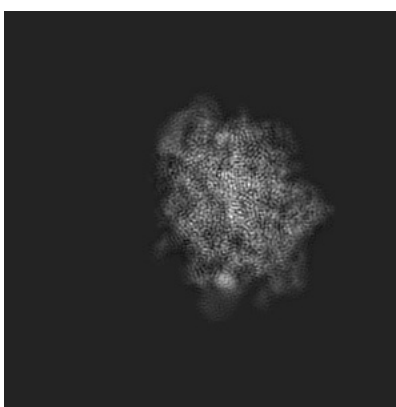
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

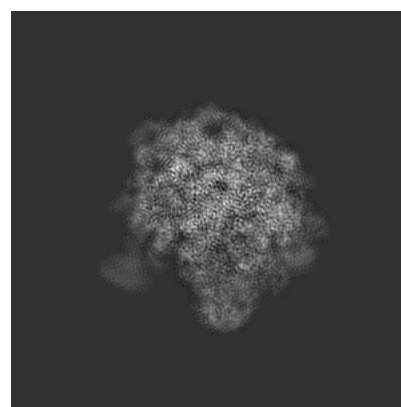
6.1.1 Primary map



X



Y

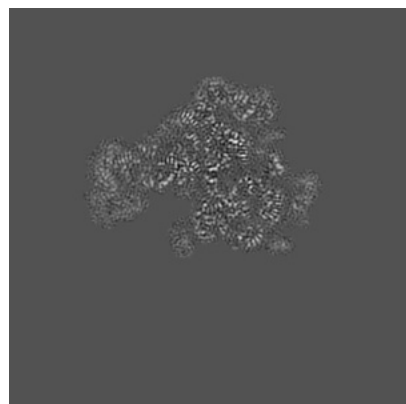


Z

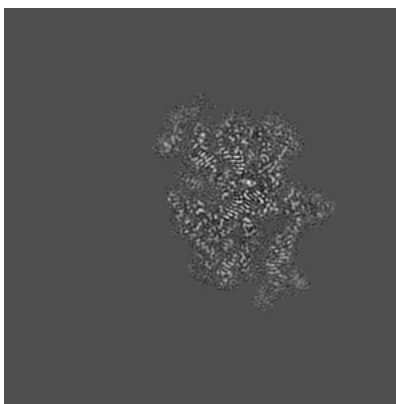
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

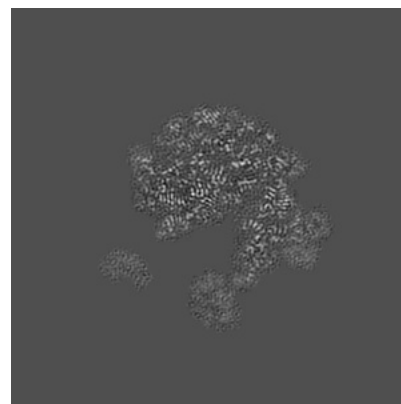
6.2.1 Primary map



X Index: 182



Y Index: 182

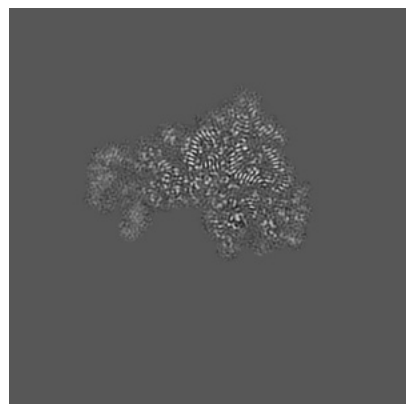


Z Index: 182

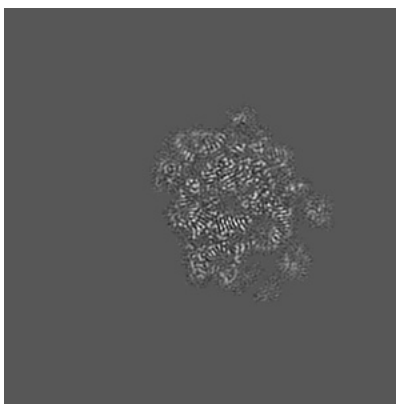
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

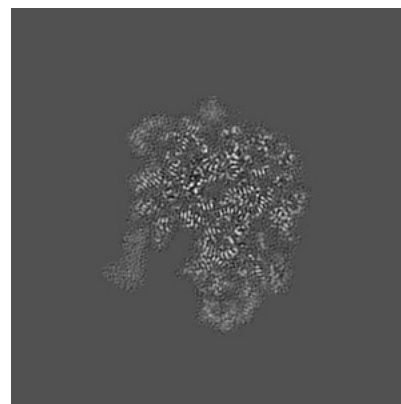
6.3.1 Primary map



X Index: 204



Y Index: 199

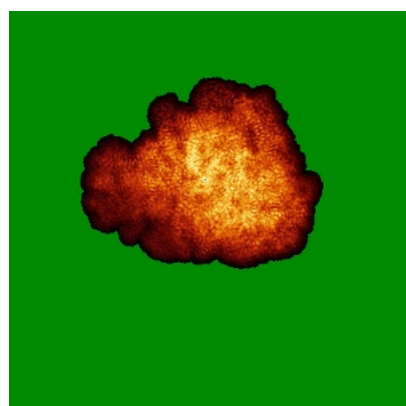


Z Index: 206

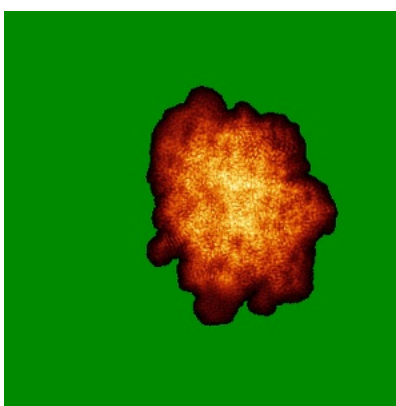
The images above show the largest variance slices of the map in three orthogonal directions.

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

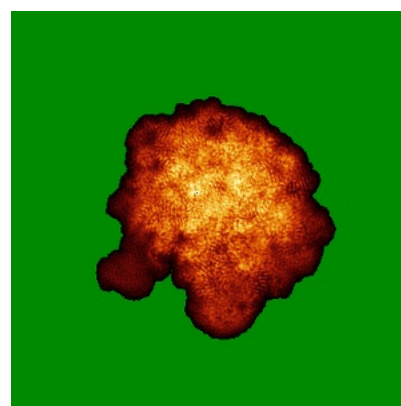
6.4.1 Primary map



X



Y

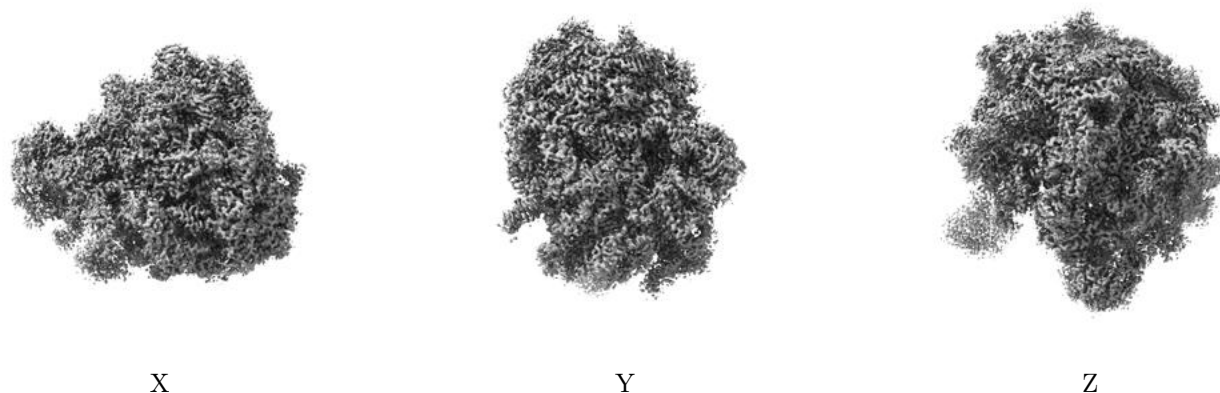


Z

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.

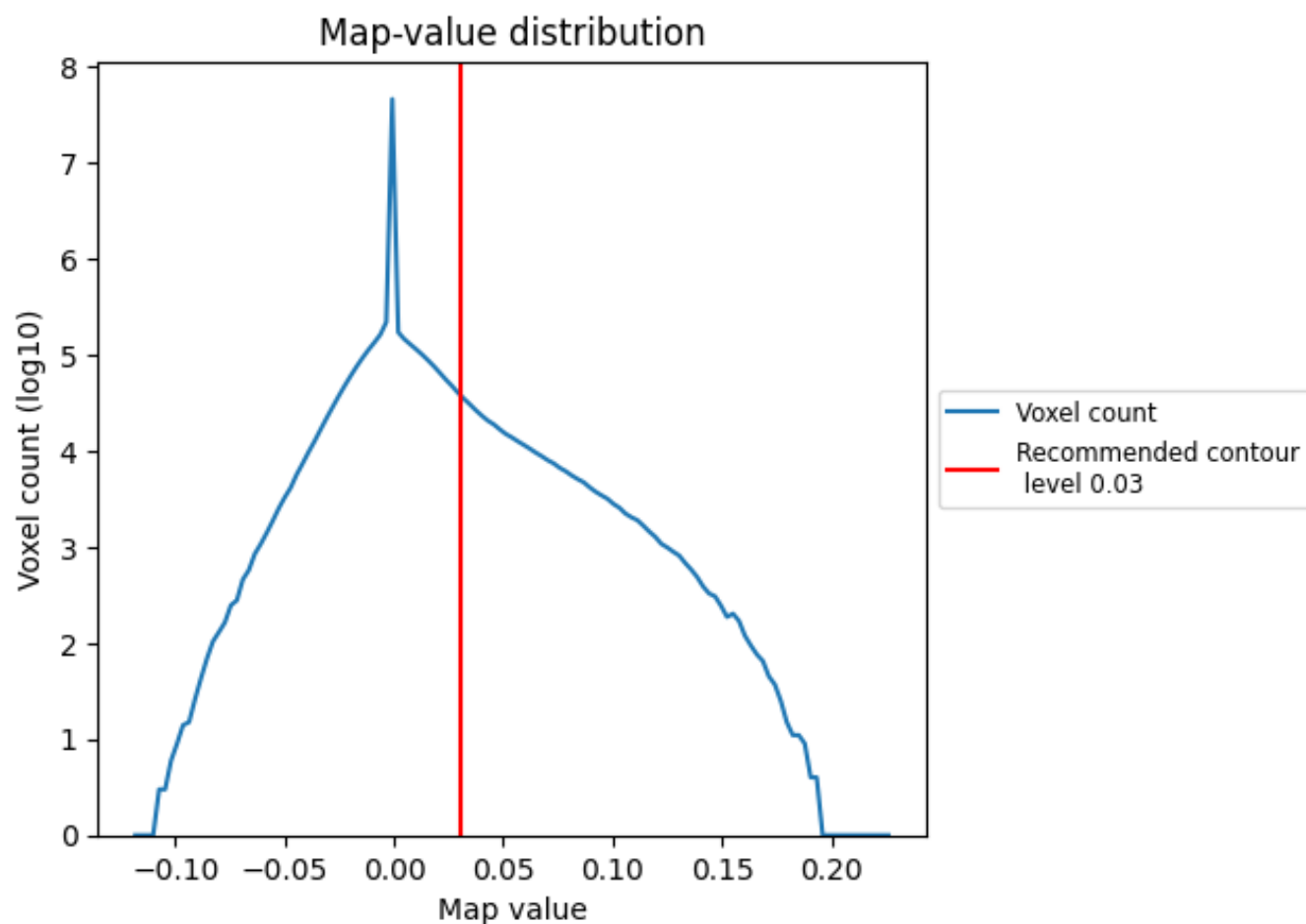
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

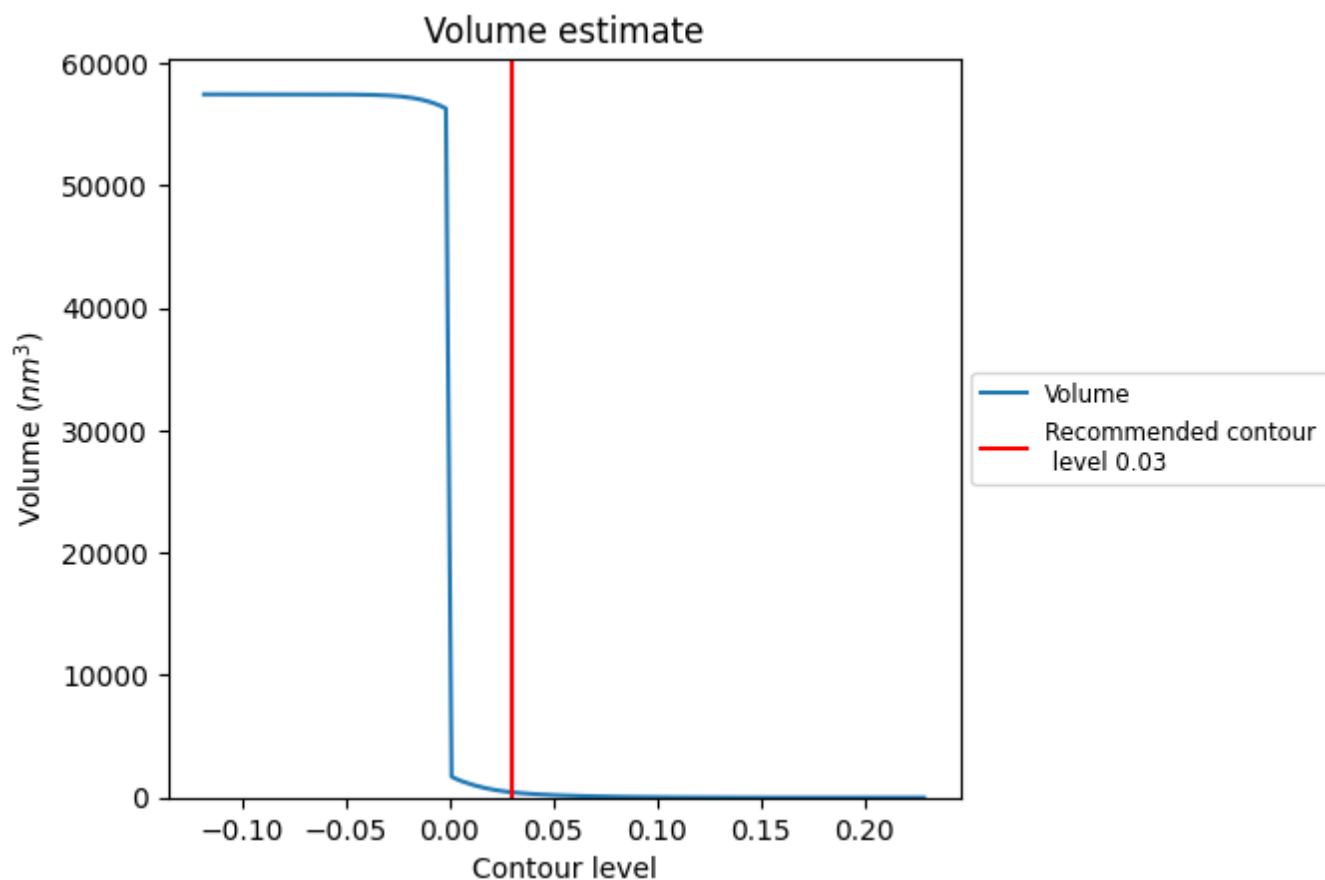
This section contains the results of statistical analysis of the map.

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.

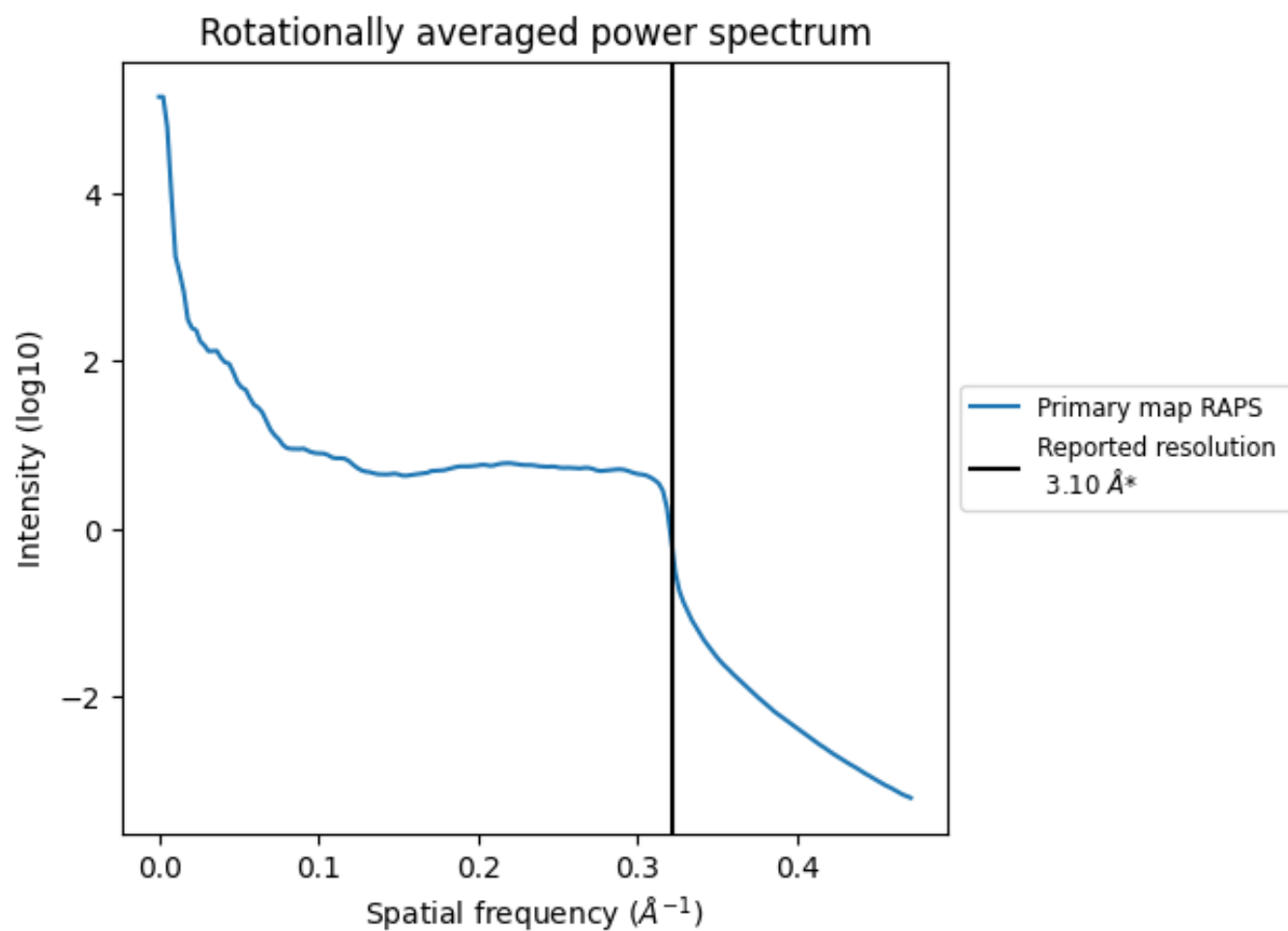
7.2 Volume estimate [i](#)



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

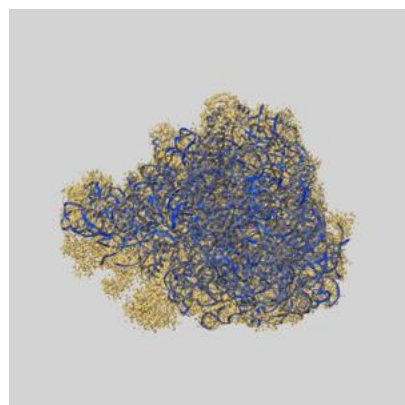
8 Fourier-Shell correlation

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

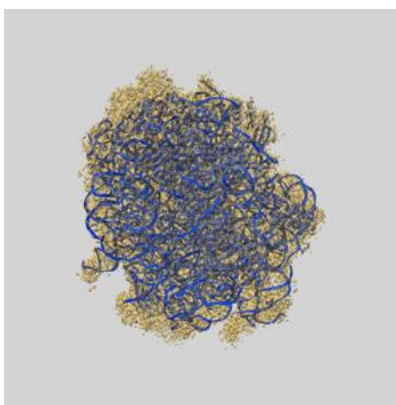
9 Map-model fit [i](#)

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](#).

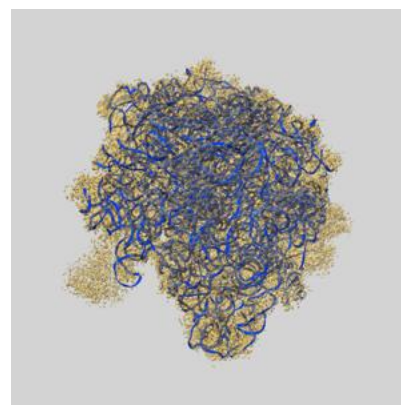
9.1 Map-model overlay [i](#)



X



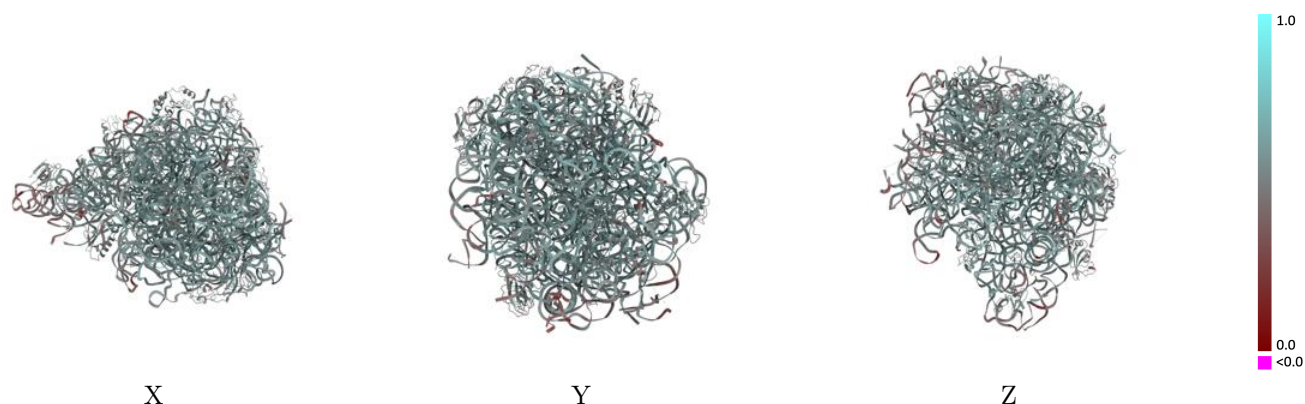
Y



Z

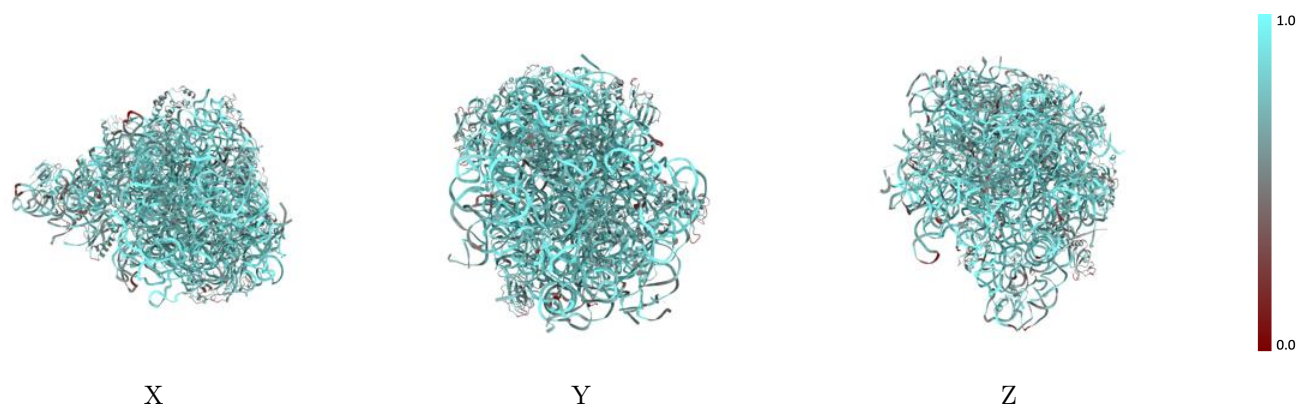
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



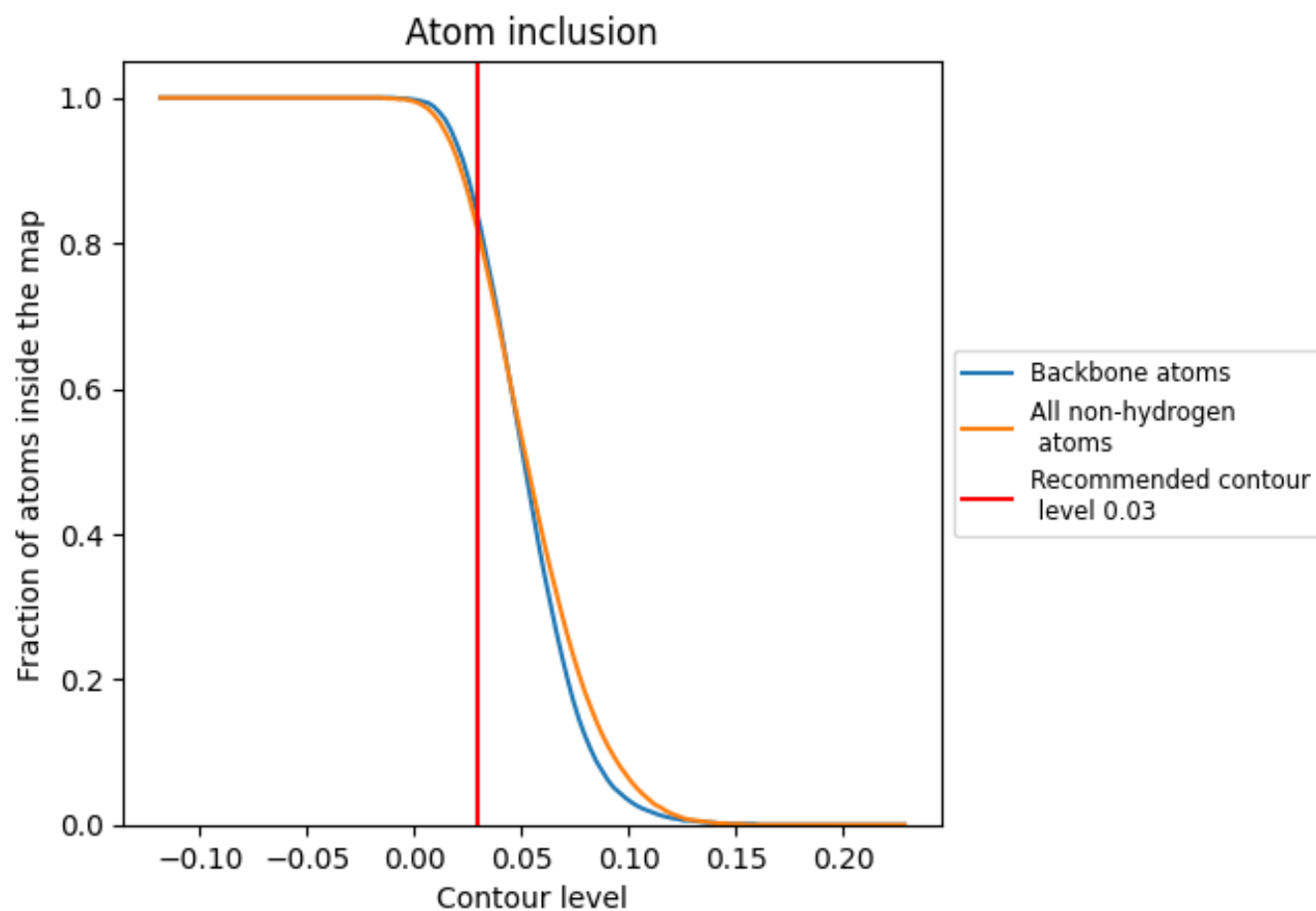
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

