Full wwPDB X-ray Structure Validation Report ⓘ

Feb 11, 2024 – 03:14 PM EST

PDB ID	:	3CCR
Title	:	Structure of Anisomycin resistant 50S Ribosomal Subunit: 23S rRNA mutation A2488C. Density for anisomycin is visible but not included in the model.
Authors	:	Blaha, G.; Gurel, G.
Deposited on	:	2008-02-26
Resolution	:	3.00 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp
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:

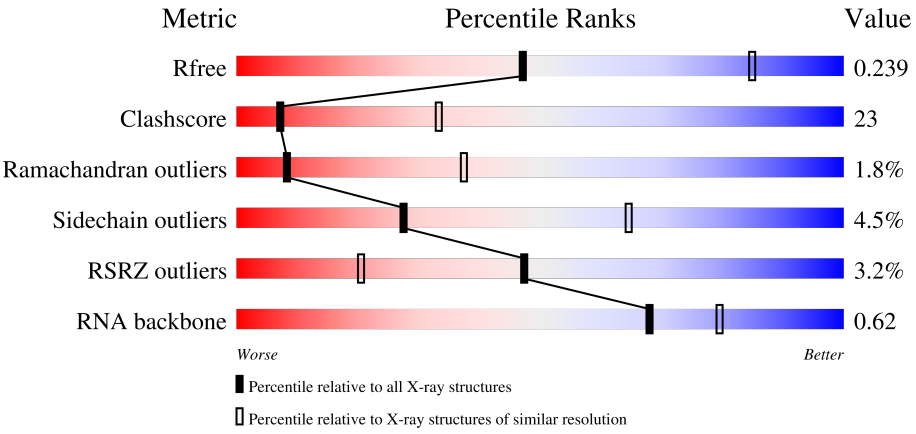
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)
RNA backbone	3102	1173 (3.30-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	240	62% 33%
2	B	338	58% 37%
3	C	246	68% 27% 5%
4	D	177	8% 42% 35% 21%

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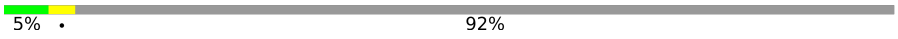
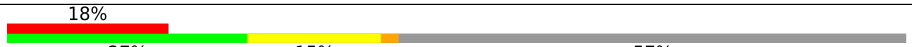
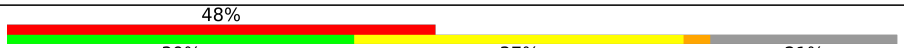
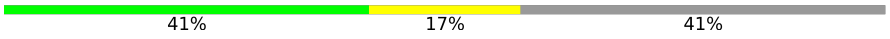
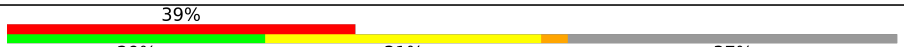
Mol	Chain	Length	Quality of chain
5	E	178	
6	F	120	
7	G	348	
8	H	177	
9	I	162	
10	J	145	
11	K	132	
12	L	165	
13	M	196	
14	N	187	
15	O	116	
16	P	149	
17	Q	96	
18	R	155	
19	S	85	
20	T	120	
21	U	67	
22	V	71	
23	W	154	
24	X	92	
25	Y	241	
26	Z	116	
27	1	57	
28	2	50	
29	3	92	

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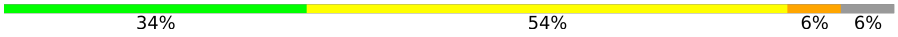
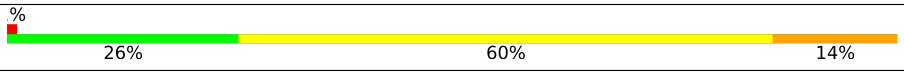
Mol	Chain	Length	Quality of chain
30	0	2923	
31	9	122	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
33	CL	3	8804	-	-	X	-
33	CL	B	8819	-	-	X	-
33	CL	M	8818	-	-	X	-
34	SR	0	8957	-	-	-	X
34	SR	0	8982	-	-	-	X
34	SR	0	8986	-	-	-	X
34	SR	0	8997	-	-	-	X
34	SR	0	9004	-	-	-	X
34	SR	0	9006	-	-	-	X
35	NA	0	8528	-	-	-	X
35	NA	0	8559	-	-	-	X
35	NA	0	8563	-	-	-	X

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 99120 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L2P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	S	0	0	0
			1753	1072	352	324	5			

- Molecule 2 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	337	Total	C	N	O	S	0	0	0
			2625	1616	493	511	5			

- Molecule 3 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	246	Total	C	N	O	S	0	0	0
			1860	1130	345	384	1			

- Molecule 4 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	140	Total	C	N	O	S	0	0	0
			1094	685	195	210	4			

- Molecule 5 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	172	Total	C	N	O	S	0	0	0
			1357	840	224	289	4			

- Molecule 6 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	119	Total	C	N	O	S	0	0	0
			890	551	141	197	1			

- Molecule 7 is a protein called 50S ribosomal protein L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	29	Total	C	N	O	S	0	0	0
			240	149	39	51	1			

- Molecule 8 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	160	Total	C	N	O	S	0	0	0
			1282	798	240	238	6			

- Molecule 9 is a protein called 50S ribosomal protein L11P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	70	Total	C	N	O	S	0	0	0
			519	323	81	114	1			

- Molecule 10 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	142	Total	C	N	O	S	0	0	0
			1120	696	199	222	3			

- Molecule 11 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	132	Total	C	N	O	S	0	0	0
			994	609	189	192	4			

- Molecule 12 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
12	L	145	Total	C	N	O	0	0	0
			1118	670	222	226			

- Molecule 13 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	194	Total	C	N	O	S	0	0	0
			1558	943	333	281	1			

- Molecule 14 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	186	Total	C	N	O	S	0	0	0
			1445	895	262	286	2			

- Molecule 15 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	O	115	Total	C	N	O	0	0	0
			865	529	161	175			

- Molecule 16 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
16	P	143	Total	C	N	O	0	0	0
			1136	683	229	224			

- Molecule 17 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	Q	95	Total	C	N	O	0	0	0
			735	450	141	144			

- Molecule 18 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	R	150	Total	C	N	O	S	0	0	0
			1149	713	209	223	4			

- Molecule 19 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	81	Total	C	N	O	S	0	0	0
			641	389	111	138	3			

- Molecule 20 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
20	T	119	Total	C	N	O	0	0	0
			950	568	180	202			

- Molecule 21 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	U	53	Total	C	N	O	S	0	0	0
			410	244	75	86	5			

- Molecule 22 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	V	65	Total	C	N	O	S	0	0	0
			499	304	94	100	1			

- Molecule 23 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	W	154	Total	C	N	O	S	0	0	0
			1196	737	209	244	6			

- Molecule 24 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	X	82	Total	C	N	O	S	0	0	0
			654	402	129	122	1			

- Molecule 25 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	Y	142	Total	C	N	O	0	0	0
			1130	686	228	216			

- Molecule 26 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	Z	73	Total	C	N	O	S	0	0	0
			573	343	113	112	5			

- Molecule 27 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 28 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

- Molecule 29 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 30 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	0	2754	Total	C	N	O	P	0	0	0
			59018	26348	10871	19054	2745			

- Molecule 31 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	9	122	Total	C	N	O	P	0	0	0
			2599	1160	471	847	121			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	A	1	Total	Mg	0	0
			1	1		
32	B	2	Total	Mg	0	0
			2	2		
32	K	1	Total	Mg	0	0
			1	1		
32	T	1	Total	Mg	0	0
			1	1		
32	Y	1	Total	Mg	0	0
			1	1		
32	2	1	Total	Mg	0	0
			1	1		
32	3	1	Total	Mg	0	0
			1	1		
32	0	84	Total	Mg	0	0
			84	84		
32	9	1	Total	Mg	0	0
			1	1		

- Molecule 33 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
33	A	1	Total Cl 1 1	0	0
33	B	1	Total Cl 1 1	0	0
33	J	3	Total Cl 3 3	0	0
33	K	1	Total Cl 1 1	0	0
33	L	1	Total Cl 1 1	0	0
33	M	1	Total Cl 1 1	0	0
33	N	1	Total Cl 1 1	0	0
33	O	1	Total Cl 1 1	0	0
33	R	1	Total Cl 1 1	0	0
33	Y	1	Total Cl 1 1	0	0
33	3	1	Total Cl 1 1	0	0
33	0	9	Total Cl 9 9	0	0

- Molecule 34 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
34	A	3	Total Sr 3 3	0	0
34	B	2	Total Sr 2 2	0	0
34	F	1	Total Sr 1 1	0	0
34	R	1	Total Sr 1 1	0	0
34	S	1	Total Sr 1 1	0	0
34	1	2	Total Sr 2 2	0	0
34	3	2	Total Sr 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
34	0	93	Total Sr 93 93	0	0
34	9	3	Total Sr 3 3	0	0

- Molecule 35 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
35	C	1	Total Na 1 1	0	0
35	J	1	Total Na 1 1	0	0
35	M	1	Total Na 1 1	0	0
35	Q	1	Total Na 1 1	0	0
35	R	2	Total Na 2 2	0	0
35	S	1	Total Na 1 1	0	0
35	0	66	Total Na 66 66	0	0
35	9	2	Total Na 2 2	0	0

- Molecule 36 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
36	M	1	Total K 1 1	0	0
36	0	1	Total K 1 1	0	0

- Molecule 37 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
37	O	1	Total Cd 1 1	0	0
37	U	1	Total Cd 1 1	0	0
37	Z	1	Total Cd 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
37	1	1	Total Cd 1 1	0	0
37	3	1	Total Cd 1 1	0	0

- Molecule 38 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
38	A	121	Total O 121 121	0	0
38	B	145	Total O 145 145	0	0
38	C	166	Total O 166 166	0	0
38	D	46	Total O 46 46	0	0
38	E	43	Total O 43 43	0	0
38	F	31	Total O 31 31	0	0
38	G	17	Total O 17 17	0	0
38	H	72	Total O 72 72	0	0
38	I	5	Total O 5 5	0	0
38	J	52	Total O 52 52	0	0
38	K	52	Total O 52 52	0	0
38	L	81	Total O 81 81	0	0
38	M	133	Total O 133 133	0	0
38	N	56	Total O 56 56	0	0
38	O	41	Total O 41 41	0	0
38	P	63	Total O 63 63	0	0
38	Q	52	Total O 52 52	0	0

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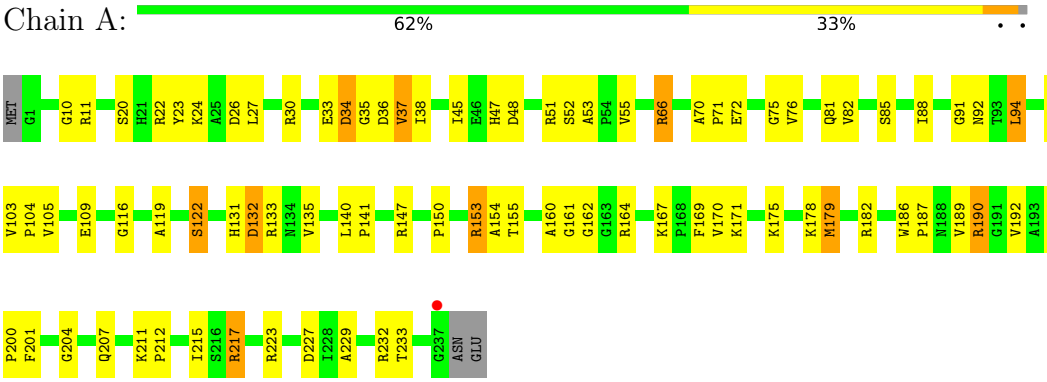
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
38	R	75	Total O 75 75	0	0
38	S	37	Total O 37 37	0	0
38	T	40	Total O 40 40	0	0
38	U	28	Total O 28 28	0	0
38	V	15	Total O 15 15	0	0
38	W	69	Total O 69 69	0	0
38	X	22	Total O 22 22	0	0
38	Y	100	Total O 100 100	0	0
38	Z	28	Total O 28 28	0	0
38	1	61	Total O 61 61	0	0
38	2	45	Total O 45 45	0	0
38	3	76	Total O 76 76	0	0
38	0	5897	Total O 5897 5897	0	0
38	9	154	Total O 154 154	0	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 electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

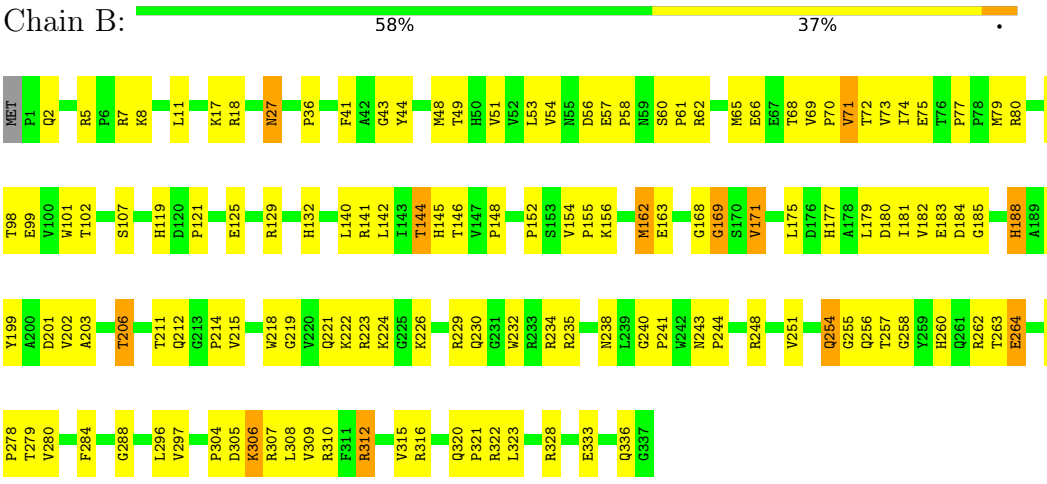
• Molecule 1: 50S ribosomal protein L2P

Chain A:



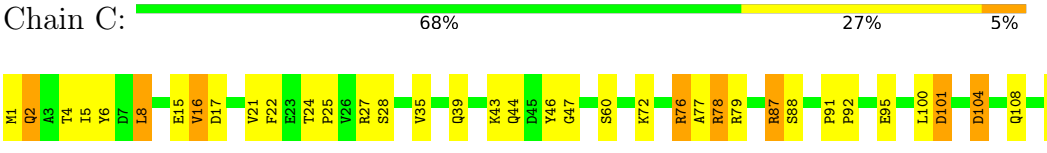
• Molecule 2: 50S ribosomal protein L3P

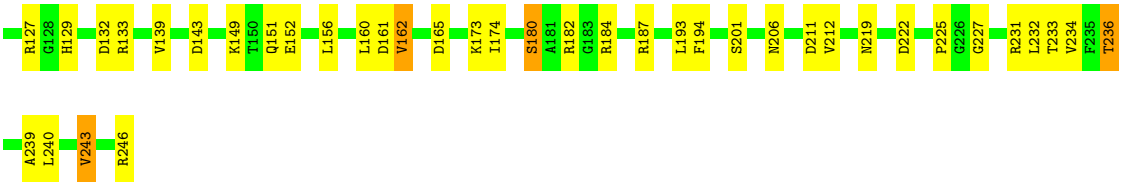
Chain B:



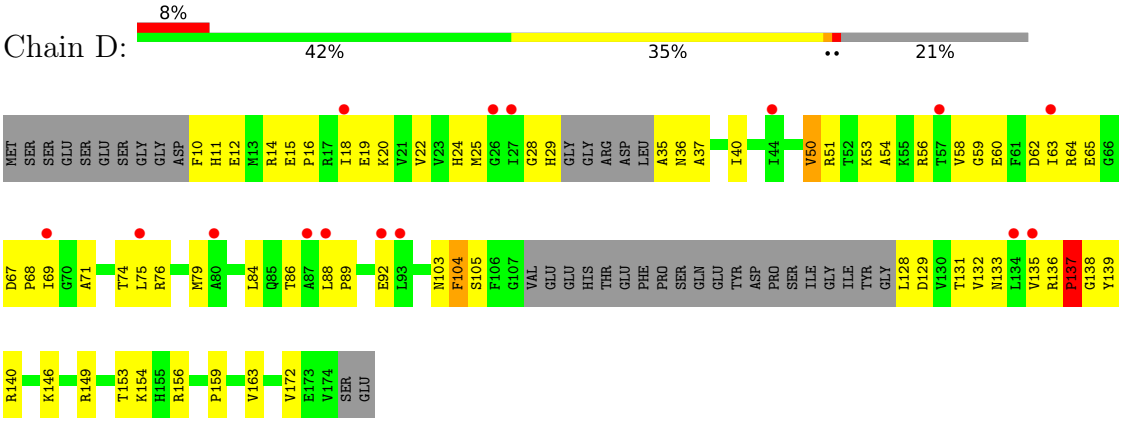
• Molecule 3: 50S ribosomal protein L4P

Chain C:

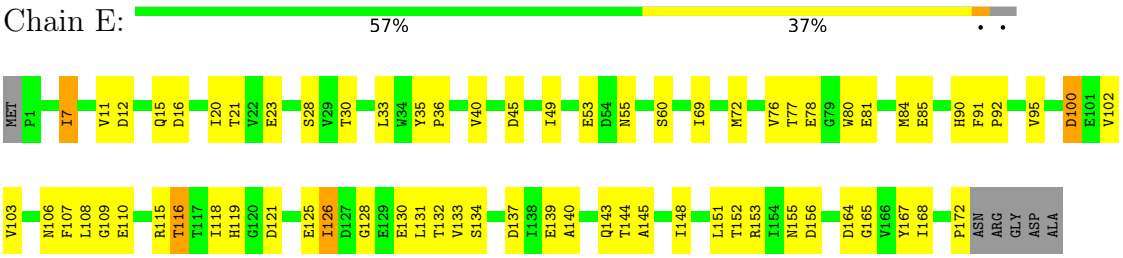




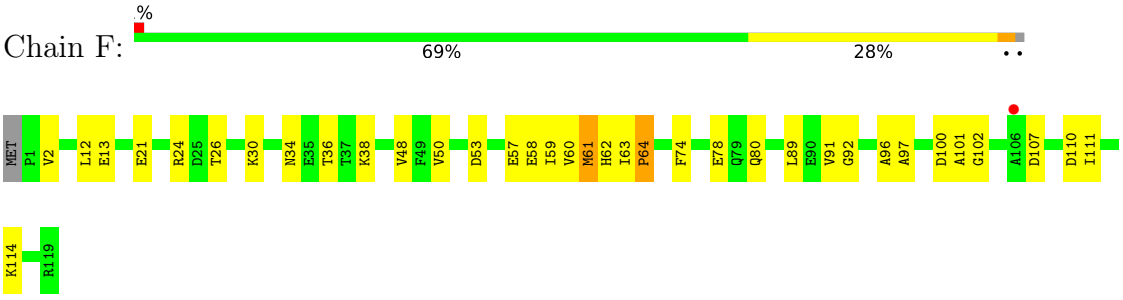
• Molecule 4: 50S ribosomal protein L5P



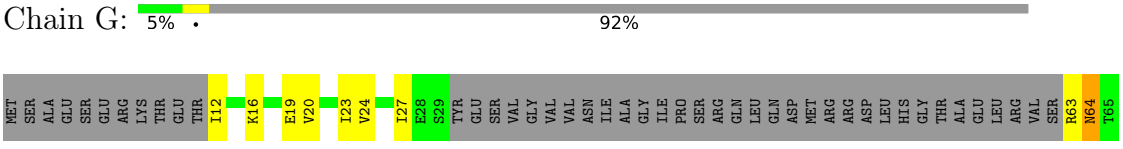
• Molecule 5: 50S ribosomal protein L6P

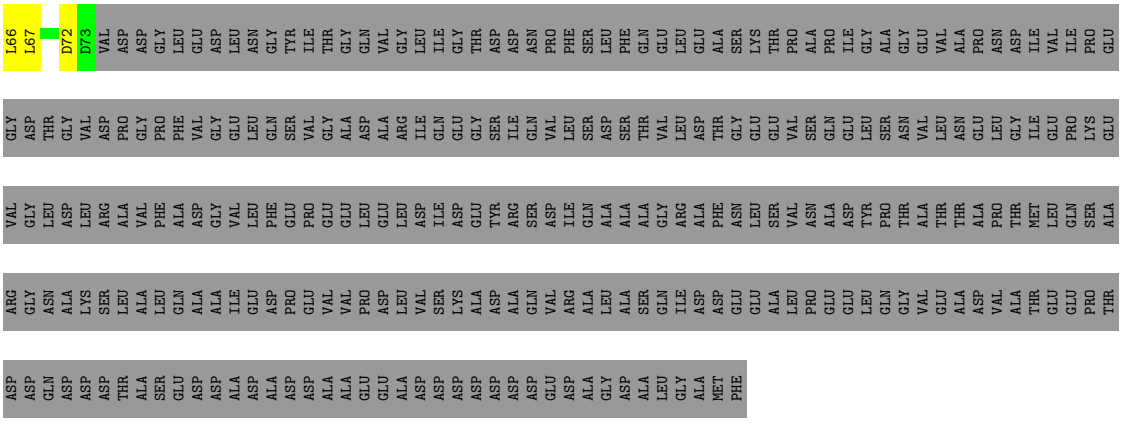


• Molecule 6: 50S ribosomal protein L7Ae



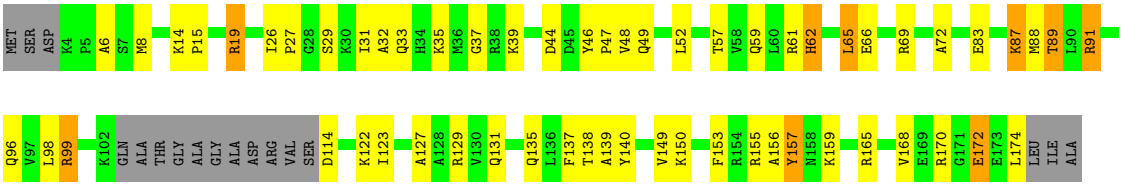
• Molecule 7: 50S ribosomal protein L10E





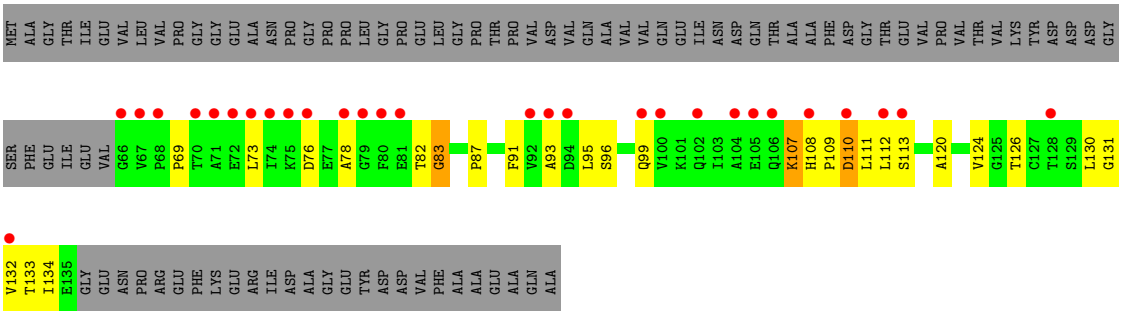
• Molecule 8: 50S ribosomal protein L10e

Chain H:



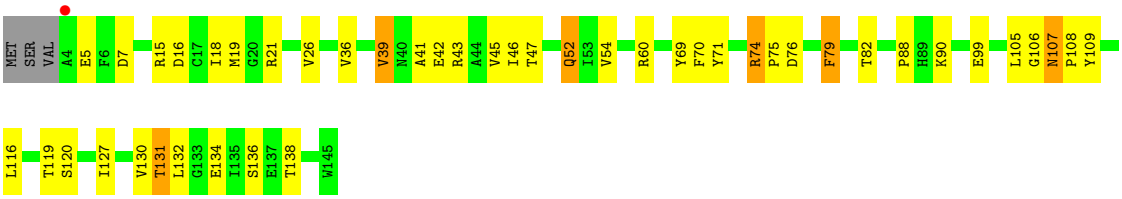
• Molecule 9: 50S ribosomal protein L11P

Chain I:



• Molecule 10: 50S ribosomal protein L13P

Chain J:

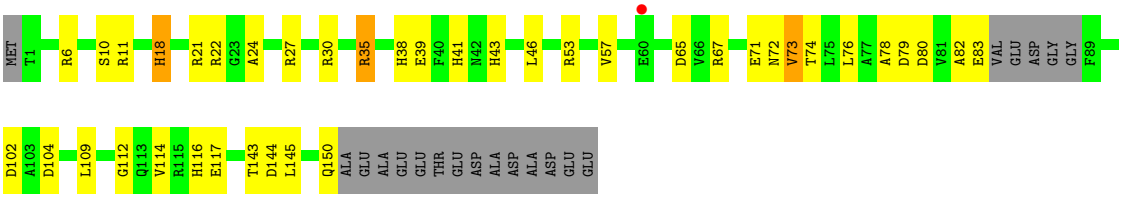


• Molecule 11: 50S ribosomal protein L14P

Chain K:

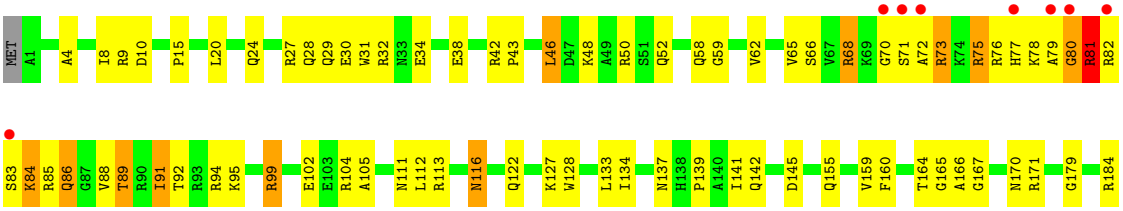
• Molecule 12: 50S ribosomal protein L15P

Chain L:



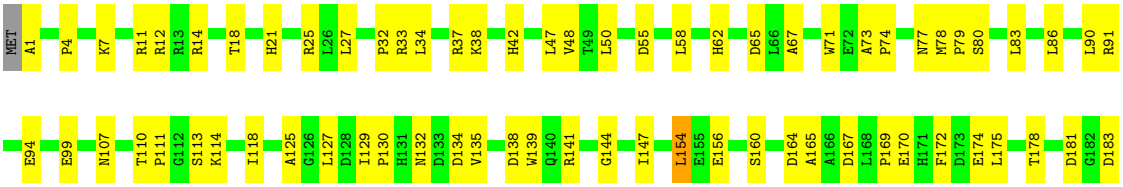
• Molecule 13: 50S ribosomal protein L15e

Chain M:



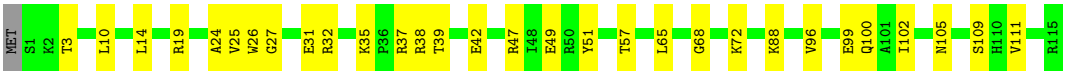
• Molecule 14: 50S ribosomal protein L18P

Chain N:



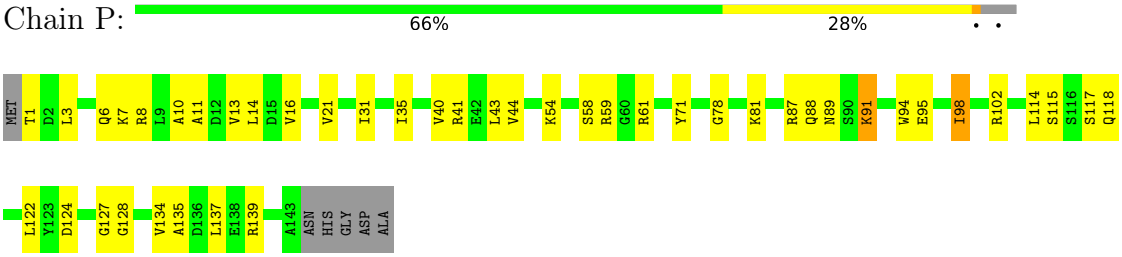
• Molecule 15: 50S ribosomal protein L18e

Chain O:



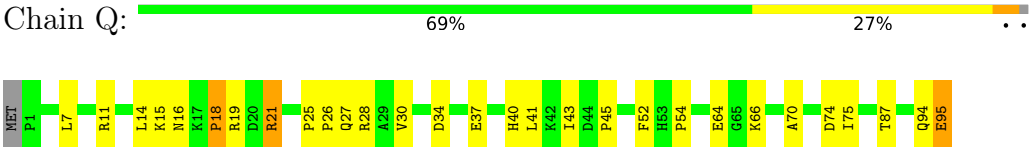
• Molecule 16: 50S ribosomal protein L19e

Chain P:



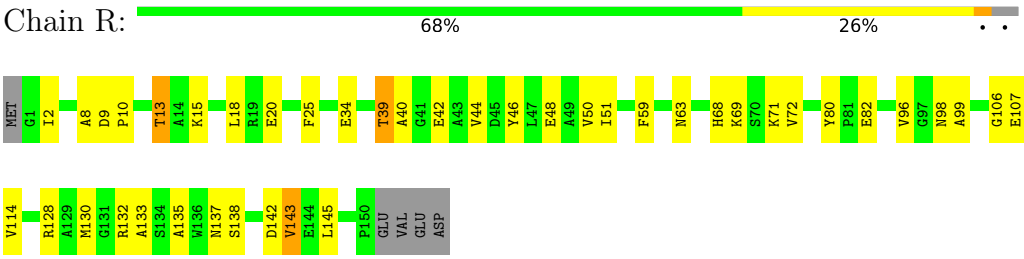
• Molecule 17: 50S ribosomal protein L21e

Chain Q:



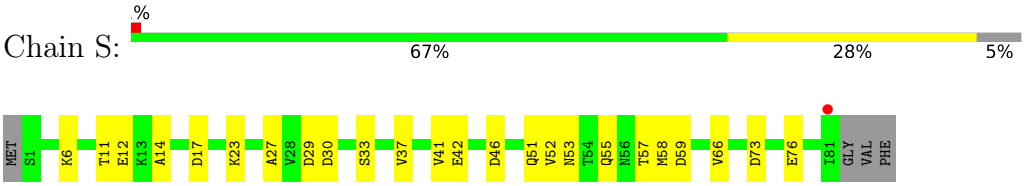
• Molecule 18: 50S ribosomal protein L22P

Chain R:



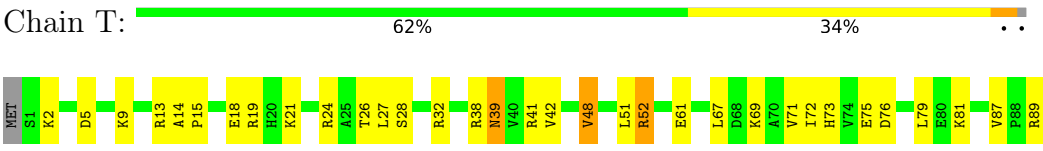
• Molecule 19: 50S ribosomal protein L23P

Chain S:



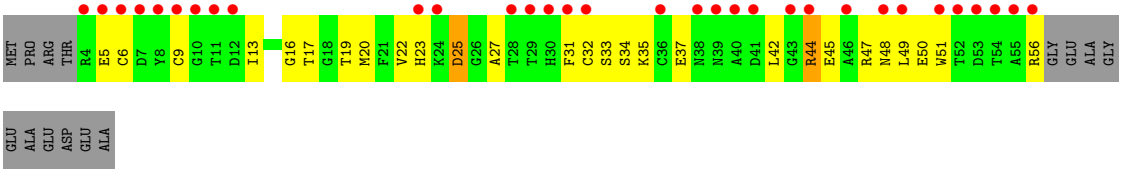
• Molecule 20: 50S ribosomal protein L24P

Chain T:



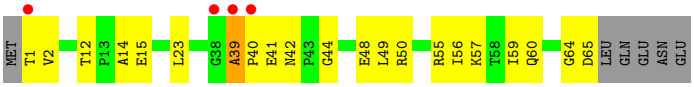
• Molecule 21: 50S ribosomal protein L24e

Chain U:



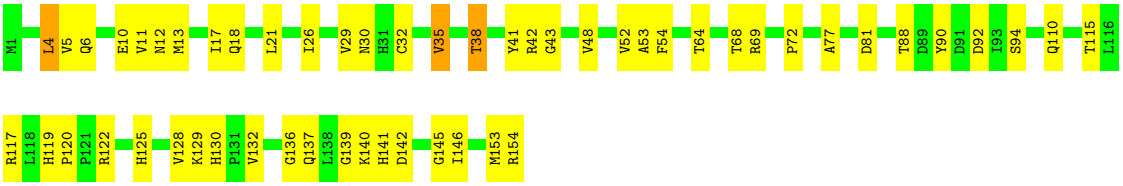
• Molecule 22: 50S ribosomal protein L29P

Chain V:



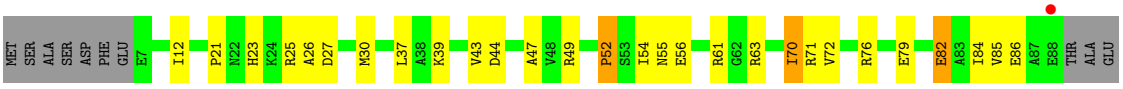
• Molecule 23: 50S ribosomal protein L30P

Chain W:



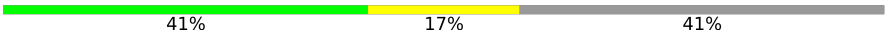
• Molecule 24: 50S ribosomal protein L31e

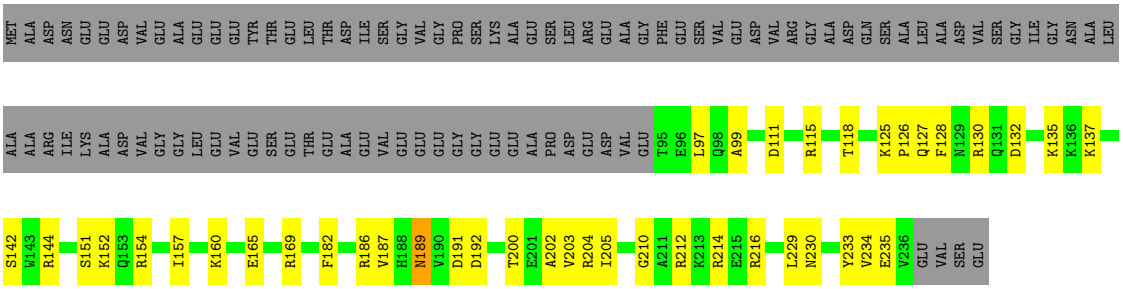
Chain X:



• Molecule 25: 50S ribosomal protein L32e

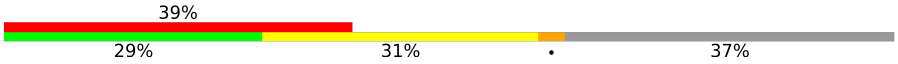
Chain Y:

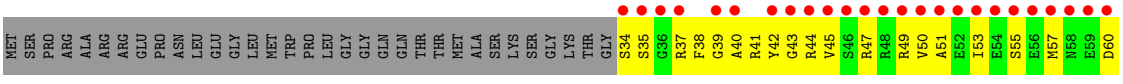


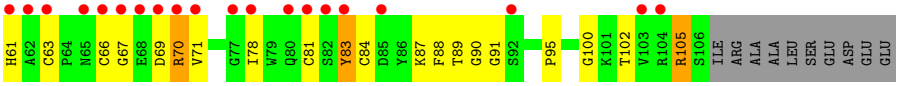


• Molecule 26: 50S ribosomal protein L37Ae

Chain Z:

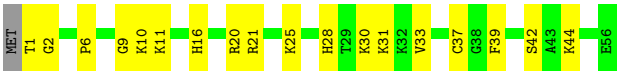






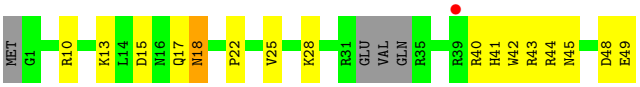
• Molecule 27: 50S ribosomal protein L37e

Chain 1:



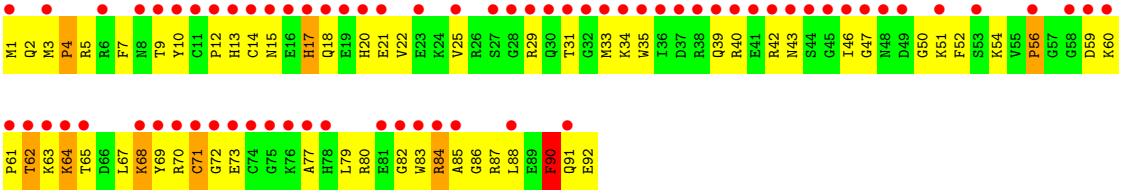
• Molecule 28: 50S ribosomal protein L39e

Chain 2:



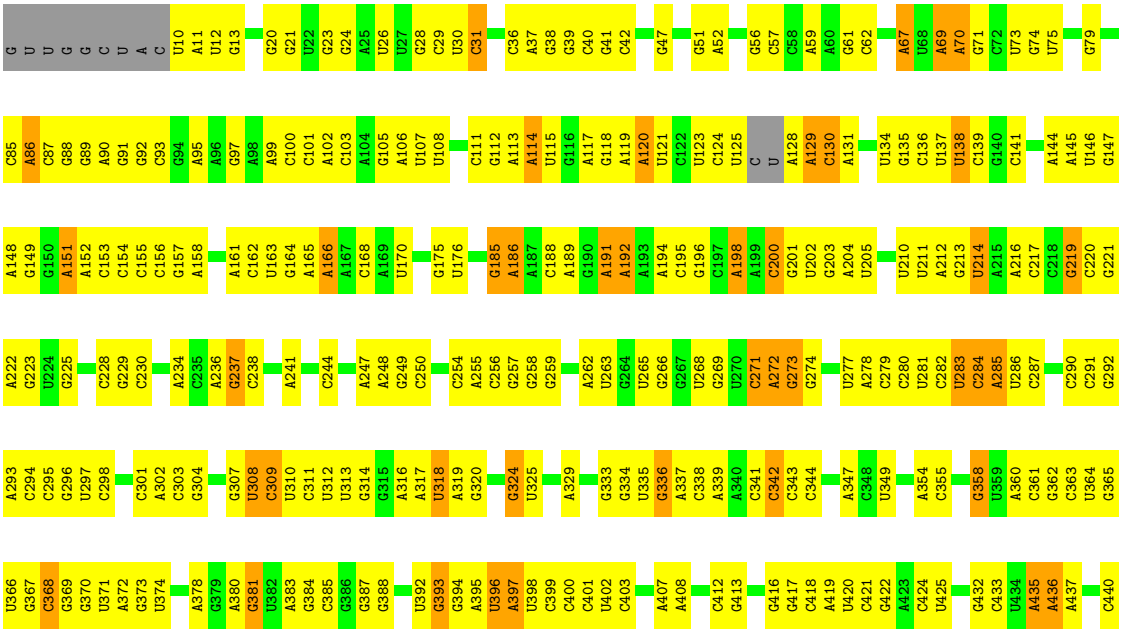
• Molecule 29: 50S ribosomal protein L44E

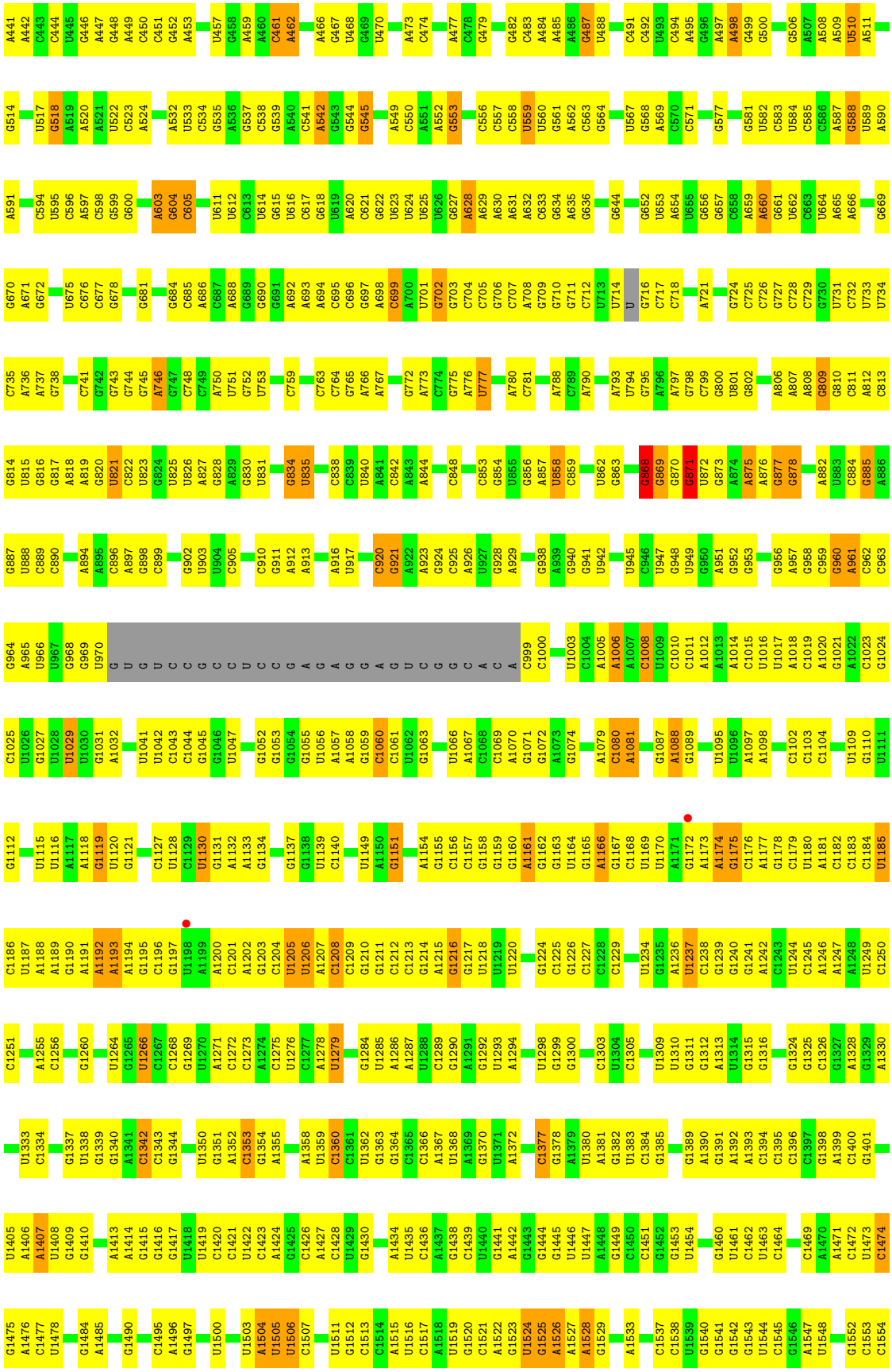
Chain 3:

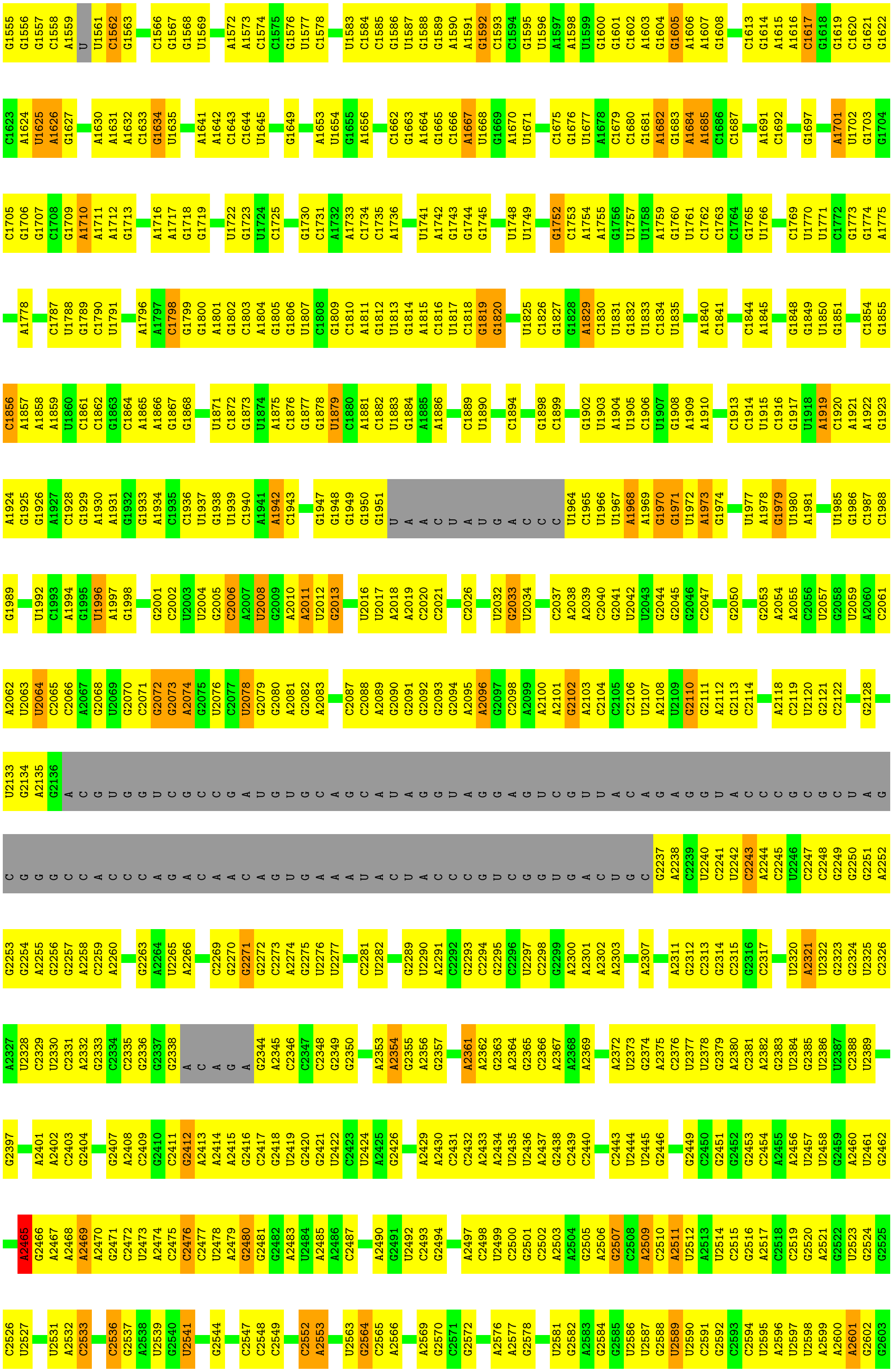


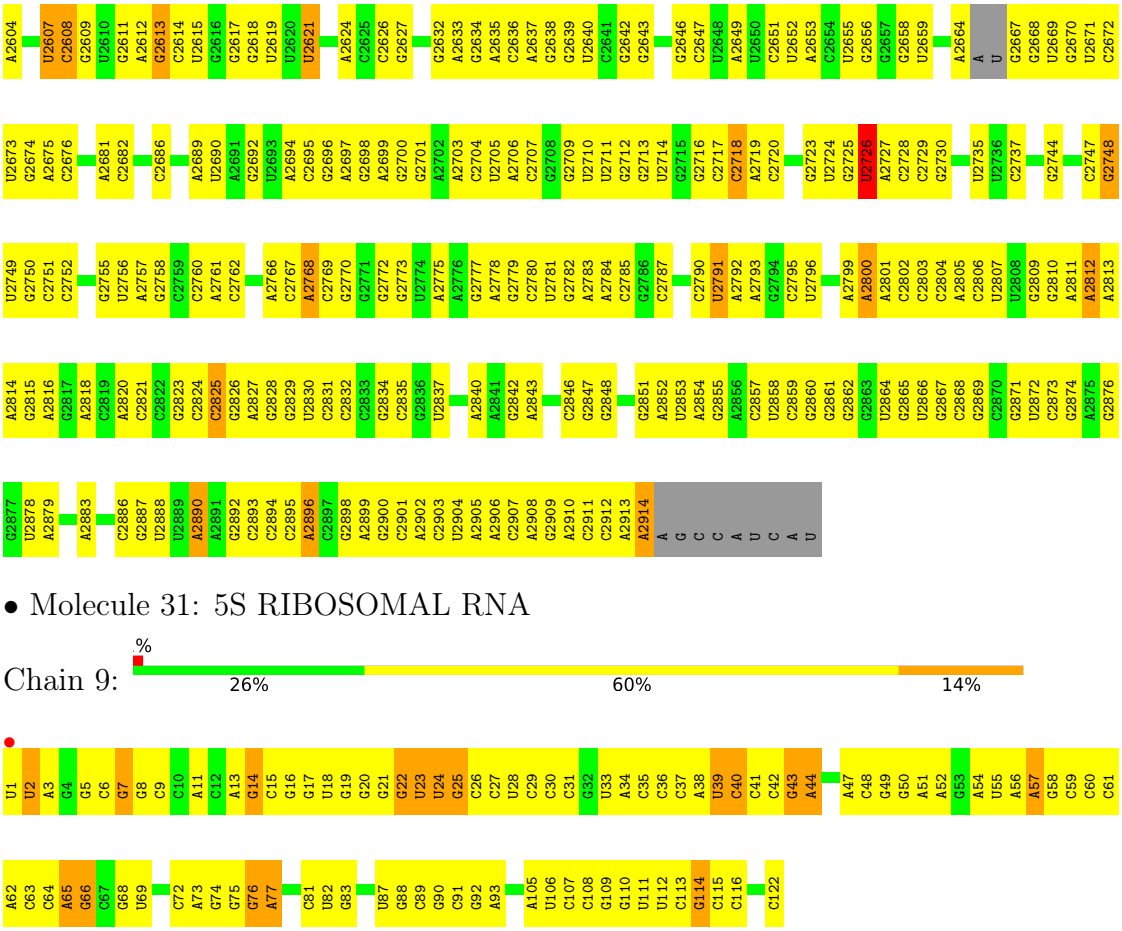
• Molecule 30: 23S RIBOSOMAL RNA

Chain 0:






G1555 G1556 G1557 C1558 A1559 U U1561 C1562 G1563 C1566 G1567 G1568 U1569 A1572 A1573 C1574 C1575 G1576 U1577 C1578 U1583 C1584 C1585 G1586 U1587 G1588 G1589 A1590 A1591 G1592 C1593 C1594 G1595 U1596 A1597 A1598 U1599 G1600 G1601 C1602 A1603 G1604 G1605 A1606 A1607 G1608 C1613 G1614 A1615 A1616 C1617 G1618 G1619 C1620 G1621 G1622
C1623 A1624 U1625 A1626 G1627 A1630 A1631 A1632 C1633 G1634 U1635 A1641 A1642 C1643 C1644 U1645 G1649 A1653 U1654 G1655 A1656 C1662 G1663 A1664 G1665 C1666 A1667 U1668 G1669 A1670 U1671 C1675 G1676 U1677 A1678 C1679 C1680 G1681 A1682 G1683 A1684 A1685 C1686 C1687 A1691 C1692 G1697 A1701 U1702 G1703 G1704
C1705 G1706 G1707 C1708 G1709 A1710 A1711 A1712 G1713 A1716 A1717 G1718 G1719 U1722 G1723 U1724 C1725 G1730 C1731 A1732 A1733 C1734 C1735 A1736 U1741 A1742 G1743 G1744 G1745 U1748 U1749 G1752 C1753 A1754 A1755 G1756 U1757 U1758 A1759 G1760 U1761 C1762 C1763 C1764 G1765 U1766 C1769 U1770 U1771 C1772 G1773 G1774 A1775
A1778 C1787 U1788 G1789 C1790 U1791 A1796 A1797 C1798 G1799 G1800 A1801 G1802 C1803 A1804 G1805 G1806 U1807 C1808 G1809 C1810 A1811 G1812 U1813 G1814 A1815 C1816 U1817 C1818 G1819 G1820 U1825 C1826 G1827 G1828 A1829 C1830 U1831 G1832 U1833 C1834 U1835 A1840 C1841 C1844 A1845 G1848 G1849 U1850 G1851 C1854 G1855
C1856 A1857 A1858 A1859 U1860 C1861 C1862 G1863 C1864 A1865 A1866 G1867 G1868 U1871 C1872 G1873 U1874 A1875 C1876 G1877 G1878 U1879 C1880 A1881 C1882 U1883 G1884 A1885 A1886 C1889 U1890 C1894 G1898 C1899 G1902 U1903 A1904 U1905 C1906 U1907 G1908 A1909 A1910 C1913 G1914 U1915 C1916 G1917 U1918 A1919 C1920 A1921 A1922 G1923
A1924 G1925 G1926 A1927 C1928 G1929 A1930 A1931 G1932 G1933 A1934 C1935 C1936 U1937 G1938 U1939 C1940 A1941 A1942 C1943 G1947 G1948 G1949 G1950 G1951 U A A C U A U G A C C C U1964 C1965 U1966 U1967 A1968 A1969 G1970 G1971 U1972 A1973 G1974 U1977 A1978 G1979 U1980 A1981 U1985 G1986 C1987 C1988
G1989 U1992 C1993 A1994 G1995 U1996 A1997 G1998 G2001 C2002 U2003 U2004 G2005 C2006 A2007 U2008 G2009 A2010 A2011 U2012 G2013 U2016 U2017 A2018 A2019 C2020 C2021 C2026 U2032 G2033 U2034 C2037 A2038 A2039 C2040 G2041 U2042 U2043 G2044 G2045 G2046 C2047 G2050 G2053 A2054 A2055 C2056 U2057 G2058 U2059 A2060 C2061
A2062 U2063 U2064 C2065 C2066 A2067 G2068 U2069 G2070 C2071 G2072 G2073 A2074 G2075 U2076 C2077 U2078 G2079 G2080 A2081 G2082 A2083 C2087 C2088 A2089 G2090 G2091 G2092 G2093 G2094 A2095 A2096 G2097 C2098 A2099 A2100 A2101 G2102 A2103 C2104 C2105 C2106 U2107 A2108 U2109 G2110 G2111 A2112 G2113 C2114 A2118 C2119 U2120 G2121 C2122 G2128
U2133 G2134 A2135 G2136 A C G U G G U C G C C G A U G U G C A G C A U A G G U A G G A G U C G U U A C A G A G G U A C C C G C G C U A G
C G G G C C A C C C A G A C A A C A G U G A A A U A C U A C C C G U C G G U G A C U G C G2237 A2238 C2239 U2240 C2241 U2242 C2243 A2244 C2245 U2246 C2247 G2248 G2249 G2250 G2251 A2252
G2253 G2254 A2255 G2256 G2257 A2258 C2259 A2260 G2263 A2264 U2265 A2266 C2269 G2270 G2271 G2272 C2273 A2274 G2275 U2276 U2277 C2281 U2282 G2289 U2290 A2291 C2292 G2293 C2294 G2295 C2296 U2297 C2298 G2299 A2300 A2301 A2302 A2303 A2307 A2311 G2312 C2313 G2314 C2315 G2316 C2317 U2320 A2321 U2322 G2323 G2324 U2325 C2326
A2327 U2328 C2329 U2330 C2331 A2332 G2333 C2334 C2335 G2336 G2337 G2338 A C A G A G2344 A2345 C2346 C2347 C2348 G2349 G2350 A2353 A2354 G2355 A2356 G2357 A2361 A2362 G2363 A2364 G2365 C2366 A2367 A2368 A2369 A2372 U2373 G2374 A2375 C2376 U2377 U2378 G2379 A2380 C2381 G2382 G2383 U2384 G2385 U2386 U2387 C2388 U2389
G2397 A2401 A2402 C2403 G2404 G2407 A2408 C2409 G2410 C2411 G2412 A2413 A2414 A2415 G2416 C2417 G2418 U2419 G2420 G2421 U2422 C2423 U2424 A2425 G2426 A2429 A2430 C2431 C2432 A2433 A2434 U2435 U2436 A2437 G2438 C2439 C2440 C2443 U2444 U2445 G2446 G2449 C2450 G2451 G2452 G2453 C2454 A2455 A2456 U2457 U2458 G2459 A2460 U2461 G2462
A2465 G2466 A2467 A2468 A2469 A2470 G2471 C2472 U2473 A2474 C2475 C2476 C2477 U2478 A2479 G2480 G2481 G2482 A2483 U2484 A2485 A2486 C2487 A2490 G2491 U2492 C2493 G2494 A2497 C2498 U2499 C2500 G2501 C2502 A2503 A2504 G2505 A2506 G2507 C2508 A2509 C2510 A2511 U2512 A2513 U2514 C2515 G2516 A2517 C2518 C2519 G2520 A2521 G2522 U2523 G2524 G2525
C2526 U2527 U2531 A2532 C2533 C2536 G2537 A2538 U2539 G2540 U2541 G2544 C2547 C2548 C2549 C2552 A2553 U2563 G2564 C2565 A2566 A2569 G2570 C2571 G2572 A2576 A2577 G2578 U2581 G2582 A2583 G2584 G2585 U2586 U2587 G2588 U2589 U2590 C2591 G2592 C2593 C2594 U2595 A2596 U2597 U2598 A2599 A2600 A2601 G2602 G2603



• Molecule 31: 5S RIBOSOMAL RNA

Chain 9:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	212.41Å 299.52Å 574.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.81 – 3.00 85.66 – 2.40	Depositor EDS
% Data completeness (in resolution range)	77.8 (49.81-3.00) 77.4 (85.66-2.40)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.00 (at 2.40Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.180 , 0.247 0.177 , 0.239	Depositor DCC
R_{free} test set	6547 reflections (0.98%)	wwPDB-VP
Wilson B-factor (Å^2)	52.9	Xtriage
Anisotropy	0.446	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 82.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	99120	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.09% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CD, UR3, PSU, NA, OMG, CL, MG, SR, 1MA, OMU, K

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	0.34	0/1786	0.65	0/2408
2	B	0.34	0/2690	0.64	0/3652
3	C	0.38	0/1885	0.65	0/2552
4	D	0.32	0/1111	0.56	0/1498
5	E	0.34	0/1382	0.59	0/1880
6	F	0.34	0/901	0.58	0/1224
7	G	0.33	0/241	0.48	0/324
8	H	0.34	0/1302	0.65	0/1743
9	I	0.31	0/526	0.51	0/716
10	J	0.38	0/1136	0.62	0/1530
11	K	0.36	0/1004	0.67	0/1351
12	L	0.33	0/1130	0.62	0/1509
13	M	0.38	0/1582	0.63	0/2116
14	N	0.32	0/1474	0.63	0/1999
15	O	0.37	0/874	0.60	0/1181
16	P	0.34	0/1147	0.53	0/1528
17	Q	0.33	0/749	0.69	0/1005
18	R	0.37	0/1172	0.63	0/1578
19	S	0.38	0/648	0.60	0/875
20	T	0.34	0/958	0.66	1/1289 (0.1%)
21	U	0.45	0/417	0.67	0/562
22	V	0.32	0/502	0.55	0/675
23	W	0.36	0/1219	0.64	0/1655
24	X	0.35	0/664	0.61	0/895
25	Y	0.36	0/1146	0.62	0/1536
26	Z	0.45	0/584	0.63	0/781
27	1	0.43	0/438	0.57	0/578
28	2	0.35	0/401	0.60	0/529
29	3	0.48	0/771	0.66	0/1024
30	0	0.41	0/65954	0.68	4/102862 (0.0%)
31	9	0.35	0/2904	0.68	0/4526
All	All	0.39	0/98698	0.67	5/147581 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
23	W	0	1
30	0	0	18
31	9	0	1
All	All	0	20

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
30	0	1819	G	C5'-C4'-C3'	5.99	125.59	116.00
30	0	871	G	C5'-C4'-O4'	-5.85	102.08	109.10
30	0	1504	A	C1'-O4'-C4'	-5.36	105.62	109.90
20	T	52	ARG	N-CA-C	5.08	124.73	111.00
30	0	2726	U	N1-C1'-C2'	5.01	120.52	114.00

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
30	0	1266	U	Sidechain
30	0	1430	G	Sidechain
30	0	2076	U	Sidechain
30	0	2078	U	Sidechain
30	0	214	U	Sidechain
30	0	2412	G	Sidechain
30	0	2465	A	Sidechain
30	0	2552	C	Sidechain
30	0	2607	U	Sidechain
30	0	2726	U	Sidechain
30	0	324	G	Sidechain
30	0	393	G	Sidechain
30	0	435	A	Sidechain
30	0	436	A	Sidechain
30	0	462	A	Sidechain
30	0	518	G	Sidechain
30	0	664	U	Sidechain
30	0	868	G	Sidechain

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Mol	Chain	Res	Type	Group
31	9	76	G	Sidechain
23	W	90	TYR	Sidechain

5.2 Too-close contacts (i)

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	1753	0	1766	97	0
2	B	2625	0	2532	127	0
3	C	1860	0	1813	70	0
4	D	1094	0	1085	50	0
5	E	1357	0	1266	55	0
6	F	890	0	843	27	0
7	G	240	0	231	11	0
8	H	1282	0	1292	55	0
9	I	519	0	500	26	0
10	J	1120	0	1098	44	0
11	K	994	0	1027	39	0
12	L	1118	0	1076	29	0
13	M	1558	0	1573	98	0
14	N	1445	0	1401	59	0
15	O	865	0	873	32	0
16	P	1136	0	1123	44	0
17	Q	735	0	729	21	0
18	R	1149	0	1122	37	0
19	S	641	0	605	16	0
20	T	950	0	924	33	0
21	U	410	0	368	38	0
22	V	499	0	511	19	0
23	W	1196	0	1137	52	0
24	X	654	0	653	24	0
25	Y	1130	0	1133	44	0
26	Z	573	0	535	64	0
27	1	431	0	426	20	0
28	2	396	0	413	21	0
29	3	755	0	732	90	0
30	0	59018	0	29810	2239	0
31	9	2599	0	1325	161	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	0	84	0	0	0	0
32	2	1	0	0	0	0
32	3	1	0	0	0	0
32	9	1	0	0	0	0
32	A	1	0	0	0	0
32	B	2	0	0	0	0
32	K	1	0	0	0	0
32	T	1	0	0	0	0
32	Y	1	0	0	0	0
33	0	9	0	0	2	0
33	3	1	0	0	3	0
33	A	1	0	0	1	0
33	B	1	0	0	2	0
33	J	3	0	0	2	0
33	K	1	0	0	0	0
33	L	1	0	0	1	0
33	M	1	0	0	2	0
33	N	1	0	0	0	0
33	O	1	0	0	0	0
33	R	1	0	0	0	0
33	Y	1	0	0	0	0
34	0	93	0	0	0	0
34	1	2	0	0	0	0
34	3	2	0	0	0	0
34	9	3	0	0	0	0
34	A	3	0	0	0	0
34	B	2	0	0	0	0
34	F	1	0	0	0	0
34	R	1	0	0	0	0
34	S	1	0	0	0	0
35	0	66	0	0	0	0
35	9	2	0	0	0	0
35	C	1	0	0	0	0
35	J	1	0	0	0	0
35	M	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	2	0	0	0	0
35	S	1	0	0	0	0
36	0	1	0	0	0	0
36	M	1	0	0	0	0
37	1	1	0	0	0	0
37	3	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	O	1	0	0	0	0
37	U	1	0	0	0	0
37	Z	1	0	0	0	0
38	0	5897	0	0	323	0
38	1	61	0	0	3	0
38	2	45	0	0	1	0
38	3	76	0	0	7	0
38	9	154	0	0	11	0
38	A	121	0	0	3	0
38	B	145	0	0	20	0
38	C	166	0	0	13	0
38	D	46	0	0	7	0
38	E	43	0	0	4	0
38	F	31	0	0	1	0
38	G	17	0	0	0	0
38	H	72	0	0	10	0
38	I	5	0	0	2	0
38	J	52	0	0	4	0
38	K	52	0	0	3	0
38	L	81	0	0	4	0
38	M	133	0	0	12	0
38	N	56	0	0	6	0
38	O	41	0	0	2	0
38	P	63	0	0	5	0
38	Q	52	0	0	1	0
38	R	75	0	0	2	0
38	S	37	0	0	0	0
38	T	40	0	0	3	0
38	U	28	0	0	5	0
38	V	15	0	0	1	0
38	W	69	0	0	7	0
38	X	22	0	0	4	0
38	Y	100	0	0	5	0
38	Z	28	0	0	5	0
All	All	99120	0	59922	3377	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 23.

All (3377) 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)
30:0:871:G:C8	30:0:871:G:H5'	1.74	1.22
30:0:1160:G:H5'	30:0:1161:A:C5'	1.70	1.20
30:0:1160:G:C5'	30:0:1161:A:H5'	1.73	1.18
30:0:1278:A:H4'	30:0:1279:U:C4	1.81	1.16
13:M:171:ARG:HD3	30:0:156:C:H5"	1.15	1.13
14:N:37:ARG:NH1	31:9:6:C:H5"	1.65	1.12
30:0:1559:A:H1'	38:0:5836:HOH:O	1.48	1.11
10:J:82:THR:HG23	30:0:1242:A:H5'	1.30	1.10
30:0:236:A:H4'	30:0:237:G:H5'	1.26	1.09
14:N:37:ARG:HH12	31:9:6:C:H5"	1.04	1.08
30:0:1205:U:H2'	30:0:1206:U:C5'	1.83	1.07
30:0:1205:U:H2'	30:0:1206:U:H5'	1.32	1.06
2:B:264:GLU:HG2	2:B:267:LYS:HE2	1.35	1.06
30:0:545:G:H5'	30:0:545:G:H8	1.18	1.05
29:3:88:LEU:HD22	33:3:8804:CL:CL	1.95	1.03
30:0:871:G:H5'	30:0:871:G:H8	0.89	1.02
31:9:54:A:O2'	31:9:55:U:H5'	1.58	1.02
30:0:2506:A:HO2'	30:0:2507:G:H8	1.04	1.01
30:0:1118:A:H8	30:0:1118:A:H3'	1.24	1.01
22:V:50:ARG:HH12	30:0:56:G:H5"	1.25	1.01
31:9:14:G:H5'	31:9:14:G:H8	1.25	1.01
30:0:960:G:H4'	38:0:7414:HOH:O	1.61	0.99
30:0:558:C:C2'	30:0:559:U:H5"	1.92	0.99
29:3:68:LYS:HD3	29:3:70:ARG:HH21	1.28	0.99
30:0:2372:A:H2'	30:0:2373:U:H6	1.28	0.99
30:0:1603:A:H5'	30:0:1605:G:O4'	1.61	0.98
30:0:1834:C:H2'	30:0:1840:A:N6	1.78	0.98
31:9:76:G:H3'	31:9:77:A:H5"	1.44	0.98
29:3:47:GLY:HA2	30:0:2121:G:H4'	1.43	0.98
30:0:1666:C:O2'	30:0:1667:A:H5"	1.62	0.98
18:R:8:ALA:HB1	18:R:13:THR:HG21	1.46	0.97
30:0:694:A:H2'	30:0:695:C:H5'	1.44	0.97
30:0:877:G:H5'	30:0:878:G:OP1	1.65	0.97
2:B:238:ASN:HD22	2:B:240:GLY:H	1.09	0.97
21:U:51:TRP:HD1	30:0:2865:G:HO2'	1.07	0.96
30:0:2717:C:C2'	30:0:2718:C:H5"	1.95	0.96
30:0:1118:A:H3'	30:0:1118:A:C8	1.99	0.96
30:0:1305:C:H5'	38:0:9833:HOH:O	1.66	0.96
30:0:1209:C:H2'	30:0:1210:G:H8	1.31	0.95
31:9:29:C:H2'	31:9:30:C:H5'	1.49	0.95
30:0:363:C:H1'	38:0:5247:HOH:O	1.67	0.95
30:0:2717:C:O2'	30:0:2718:C:H5"	1.65	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:3:THR:HG22	30:0:656:G:H5'	1.46	0.95
30:0:545:G:H5'	30:0:545:G:C8	2.01	0.95
38:M:8869:HOH:O	30:0:381:G:H5"	1.67	0.95
26:Z:44:ARG:HH21	30:0:1771:U:H5'	1.31	0.95
30:0:2420:G:O2'	30:0:2421:G:H5'	1.64	0.94
31:9:59:C:H2'	31:9:60:C:H6	1.33	0.94
30:0:1118:A:H62	30:0:1244:U:H3	1.14	0.93
30:0:871:G:H8	30:0:871:G:C5'	1.81	0.93
30:0:2321:A:H2	30:0:2378:U:H3	1.12	0.93
3:C:127:ARG:NH2	3:C:225:PRO:HG2	1.82	0.93
30:0:2748:G:H2'	38:0:7523:HOH:O	1.68	0.93
30:0:559:U:H6	30:0:559:U:H5'	1.34	0.92
31:9:54:A:C2'	31:9:55:U:H5'	1.99	0.92
30:0:1116:U:H3	30:0:1246:A:H62	1.17	0.92
30:0:2586:U:H3	30:0:2592:G:H22	1.18	0.91
30:0:2710:U:H1'	38:0:7601:HOH:O	1.69	0.91
30:0:2649:A:H3'	38:0:9829:HOH:O	1.70	0.91
30:0:1856:C:H1'	38:0:5846:HOH:O	1.70	0.91
30:0:1170:U:H2'	30:0:1172:G:OP2	1.71	0.91
30:0:1835:U:H5	30:0:1840:A:N7	1.68	0.91
30:0:1595:G:O2'	30:0:1596:U:H5'	1.71	0.91
30:0:2769:C:C2'	30:0:2770:G:H5'	2.01	0.90
8:H:49:GLN:HE21	8:H:140:TYR:HE2	1.18	0.90
30:0:870:G:H2'	30:0:871:G:H5"	1.51	0.90
13:M:58:GLN:HE22	30:0:259:G:H21	1.13	0.90
10:J:52:GLN:HE22	30:0:1119:G:H2'	1.37	0.90
30:0:963:C:H2'	30:0:964:G:C8	2.05	0.90
23:W:4:LEU:HD13	23:W:52:VAL:HG21	1.51	0.90
30:0:615:G:H1'	38:0:5221:HOH:O	1.72	0.90
30:0:1835:U:H2'	38:0:3618:HOH:O	1.72	0.90
30:0:625:U:H5"	30:0:1044:C:N4	1.87	0.89
30:0:969:G:H1	30:0:999:C:N4	1.71	0.89
30:0:1701:A:H4'	30:0:1702:U:H5"	1.55	0.89
16:P:115:SER:H	16:P:118:GLN:HE21	0.89	0.89
10:J:52:GLN:NE2	30:0:1119:G:H2'	1.88	0.88
13:M:73:ARG:NH2	30:0:2263:G:H5"	1.87	0.88
1:A:199:HIS:HD2	1:A:201:PHE:H	1.21	0.88
28:2:43:ARG:HH22	30:0:1684:A:H1'	1.37	0.87
30:0:542:A:H5'	30:0:542:A:H8	1.39	0.87
30:0:814:G:H4'	38:0:3128:HOH:O	1.73	0.87
30:0:2502:C:H2'	30:0:2503:A:H5'	1.57	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1666:C:H2'	30:0:1667:A:H5'	1.55	0.87
30:0:2005:G:H3'	30:0:2005:G:OP2	1.75	0.87
25:Y:187:VAL:HG23	25:Y:192:ASP:HB2	1.57	0.87
30:0:506:G:H22	30:0:509:A:C5'	1.87	0.86
31:9:56:A:H2'	31:9:57:A:H5"	1.57	0.86
30:0:2637:A:H4'	38:0:6039:HOH:O	1.75	0.86
30:0:506:G:H22	30:0:509:A:H5"	1.40	0.86
30:0:2908:A:H2'	30:0:2909:G:O4'	1.75	0.86
30:0:2248:C:H3'	38:0:5403:HOH:O	1.76	0.86
13:M:71:SER:HB2	13:M:92:THR:HG22	1.56	0.86
30:0:2372:A:H2'	30:0:2373:U:C6	2.09	0.86
11:K:10:GLN:HE21	11:K:10:GLN:H	1.18	0.86
30:0:553:G:H3'	38:0:4066:HOH:O	1.76	0.86
30:0:969:G:H1	30:0:999:C:H42	1.24	0.86
16:P:115:SER:H	16:P:118:GLN:NE2	1.73	0.86
6:F:63:ILE:HB	6:F:64:PRO:HD3	1.57	0.86
30:0:1183:C:H2'	38:0:6223:HOH:O	1.75	0.85
13:M:99:ARG:HE	13:M:170:ASN:HD22	1.19	0.85
30:0:558:C:H2'	30:0:559:U:H5"	1.57	0.85
30:0:2419:U:H5"	30:0:2420:G:H5'	1.57	0.85
29:3:20:HIS:CD2	29:3:69:TYR:HB3	2.12	0.85
30:0:2421:G:H1'	38:0:7004:HOH:O	1.75	0.85
30:0:2505:G:O2'	30:0:2506:A:H5'	1.76	0.85
30:0:308:U:H5'	30:0:309:C:OP1	1.75	0.85
30:0:1474:C:H6	30:0:1474:C:H5'	1.40	0.85
30:0:200:C:H2'	38:0:3433:HOH:O	1.75	0.84
30:0:2345:A:H3'	30:0:2346:C:H6	1.43	0.84
30:0:1474:C:H5'	30:0:1474:C:C6	2.13	0.84
30:0:870:G:C2'	30:0:871:G:H5"	2.07	0.84
31:9:13:A:O2'	31:9:14:G:H5"	1.77	0.84
11:K:39:GLY:HA2	38:0:5187:HOH:O	1.75	0.84
30:0:1080:C:H4'	30:0:1081:A:OP1	1.76	0.84
23:W:137:GLN:HE21	23:W:141:HIS:HE1	1.23	0.83
16:P:115:SER:N	16:P:118:GLN:HE21	1.74	0.83
31:9:73:A:H2'	31:9:74:G:H8	1.43	0.83
30:0:12:U:H2'	30:0:13:G:H5'	1.57	0.83
30:0:2717:C:H2'	30:0:2718:C:H5"	1.59	0.83
30:0:558:C:H2'	30:0:559:U:C5'	2.08	0.83
31:9:92:G:H2'	31:9:93:A:C8	2.14	0.83
30:0:2570:G:H5"	38:0:4880:HOH:O	1.78	0.83
13:M:68:ARG:NH2	13:M:73:ARG:HD3	1.94	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2896:A:H5”	38:0:6075:HOH:O	1.77	0.83
31:9:14:G:H5’	31:9:14:G:C8	2.14	0.83
30:0:271:C:H41	30:0:378:A:H2	1.22	0.82
30:0:1644:C:H2’	30:0:1645:U:H6	1.44	0.82
30:0:810:G:H2’	30:0:811:C:C6	2.13	0.82
30:0:2437:A:H2’	30:0:2438:G:C8	2.14	0.82
22:V:12:THR:HG22	22:V:15:GLU:HG3	1.60	0.82
30:0:236:A:C4’	30:0:237:G:H5’	2.09	0.82
30:0:1205:U:C2’	30:0:1206:U:C5’	2.57	0.82
30:0:1206:U:H5’	30:0:1206:U:H6	1.43	0.82
4:D:25:MET:SD	4:D:40:ILE:HD11	2.19	0.82
3:C:236:THR:HG22	3:C:239:ALA:H	1.44	0.82
15:O:3:THR:CG2	30:0:656:G:H5’	2.09	0.82
30:0:2345:A:H3’	30:0:2346:C:C6	2.15	0.82
30:0:2426:G:H1’	38:0:6068:HOH:O	1.79	0.82
30:0:2502:C:C2’	30:0:2503:A:H5’	2.10	0.82
13:M:134:ILE:HG23	13:M:141:ILE:HD13	1.62	0.81
30:0:1116:U:O2’	30:0:1118:A:H2	1.62	0.81
30:0:1191:A:H2’	30:0:1193:A:H5’	1.62	0.81
30:0:1278:A:H4’	30:0:1279:U:C5	2.15	0.81
30:0:614:U:O2’	30:0:615:G:H5’	1.80	0.81
30:0:2604:A:H5’	38:0:5760:HOH:O	1.79	0.81
26:Z:42:TYR:HA	30:0:1829:A:H61	1.45	0.81
30:0:185:G:H4’	30:0:186:A:OP1	1.78	0.81
14:N:67:ALA:HA	14:N:71:TRP:HB3	1.62	0.81
30:0:282:C:O2’	30:0:283:U:H5’	1.79	0.81
18:R:39:THR:HG22	18:R:42:GLU:H	1.44	0.80
13:M:171:ARG:CD	30:0:156:C:H5”	2.06	0.80
31:9:56:A:C2’	31:9:57:A:H5”	2.11	0.80
30:0:1632:A:H2’	30:0:1633:C:H5’	1.61	0.80
29:3:2:GLN:O	30:0:2320:U:H2’	1.80	0.80
6:F:91:VAL:HG12	6:F:92:GLY:H	1.47	0.80
30:0:1119:G:N2	30:0:1246:A:C2	2.48	0.80
30:0:2467:A:H3’	38:0:5416:HOH:O	1.82	0.80
31:9:59:C:H2’	31:9:60:C:C6	2.16	0.80
30:0:558:C:O2’	30:0:559:U:H5”	1.81	0.80
22:V:50:ARG:NH1	30:0:56:G:H5”	1.95	0.80
30:0:1185:U:H2’	30:0:1186:C:H6	1.46	0.80
11:K:14:LYS:HB2	11:K:45:PRO:HG2	1.63	0.80
31:9:29:C:C2’	31:9:30:C:H5’	2.12	0.79
1:A:167:LYS:HE2	26:Z:50:VAL:HG13	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:55:GLN:NE2	30:0:1446:U:H2'	1.97	0.79
21:U:56:ARG:HD2	30:0:2890:A:N9	1.97	0.79
28:2:41:HIS:H	28:2:45:ASN:HD22	1.31	0.79
30:0:1116:U:HO2'	30:0:1118:A:H2	0.80	0.79
30:0:1603:A:H5"	30:0:1605:G:H5'	1.65	0.79
13:M:58:GLN:NE2	30:0:259:G:H21	1.81	0.79
1:A:199:HIS:CD2	1:A:201:PHE:H	2.00	0.79
13:M:159:VAL:HG12	33:M:8818:CL:CL	2.20	0.79
30:0:2506:A:O2'	30:0:2507:G:H8	1.66	0.79
30:0:2717:C:H2'	30:0:2718:C:C5'	2.13	0.79
31:9:73:A:H2'	31:9:74:G:C8	2.17	0.79
30:0:282:C:H1'	30:0:368:C:H41	1.46	0.79
30:0:282:C:H1'	30:0:368:C:N4	1.98	0.79
30:0:2604:A:H4'	38:0:7586:HOH:O	1.83	0.79
30:0:2783:A:H3'	38:0:5197:HOH:O	1.82	0.78
30:0:2769:C:O2'	30:0:2770:G:H5'	1.84	0.78
30:0:1829:A:H2'	30:0:1830:C:H5'	1.65	0.78
30:0:2533:C:H5'	30:0:2533:C:H6	1.47	0.78
30:0:2906:A:H5'	30:0:2907:C:O4'	1.83	0.78
31:9:55:U:H5"	38:9:9146:HOH:O	1.82	0.78
30:0:541:C:C2'	30:0:542:A:H5"	2.13	0.78
30:0:853:C:H3'	38:0:4528:HOH:O	1.83	0.78
2:B:221:GLN:HE22	11:K:42:ASN:HD22	1.32	0.78
10:J:74:ARG:HB3	10:J:74:ARG:HH11	1.48	0.78
13:M:70:GLY:HA3	13:M:73:ARG:NH2	1.99	0.78
30:0:2416:G:H2'	30:0:2417:C:H6	1.49	0.78
30:0:2237:G:H1'	38:0:4824:HOH:O	1.83	0.78
30:0:297:U:H2'	30:0:298:C:H6	1.49	0.78
31:9:56:A:C3'	31:9:57:A:H5"	2.12	0.78
13:M:171:ARG:HD3	30:0:156:C:C5'	2.07	0.77
30:0:1189:A:H1'	30:0:1209:C:O4'	1.84	0.77
30:0:1426:C:H2'	38:0:9600:HOH:O	1.83	0.77
30:0:1617:C:C4	30:0:1643:C:H4'	2.19	0.77
30:0:1741:U:H5'	30:0:1742:A:OP1	1.83	0.77
30:0:603:A:H1'	30:0:605:C:C2	2.19	0.77
30:0:1942:A:H5'	38:0:7329:HOH:O	1.84	0.77
30:0:2440:C:H5"	38:0:3808:HOH:O	1.83	0.77
30:0:1118:A:C8	30:0:1118:A:C3'	2.66	0.77
4:D:105:SER:OG	30:0:2338:G:H1'	1.83	0.77
30:0:2769:C:H2'	30:0:2770:G:O4'	1.82	0.77
10:J:70:PHE:CE1	30:0:2676:C:H4'	2.19	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2578:G:H5'	30:0:2578:G:H8	1.49	0.77
8:H:91:ARG:O	30:0:1003:U:H4'	1.84	0.77
11:K:10:GLN:H	11:K:10:GLN:NE2	1.83	0.76
29:3:64:LYS:HA	29:3:84:ARG:HA	1.67	0.76
30:0:247:A:H2'	38:0:3913:HOH:O	1.85	0.76
30:0:2335:C:H2'	30:0:2336:G:C8	2.20	0.76
30:0:2469:A:H1'	38:0:3231:HOH:O	1.85	0.76
20:T:71:VAL:HG11	20:T:90:PRO:HB3	1.65	0.76
30:0:1205:U:H2'	30:0:1206:U:H5"	1.66	0.76
30:0:1834:C:H2'	30:0:1840:A:H62	1.48	0.76
30:0:1249:U:H2'	30:0:1250:C:H6	1.51	0.76
30:0:136:C:H2'	30:0:137:U:O4'	1.86	0.76
30:0:960:G:H3'	30:0:960:G:N3	2.00	0.76
30:0:1170:U:H1'	30:0:1172:G:N7	2.00	0.76
31:9:36:C:H4'	38:9:9029:HOH:O	1.85	0.76
30:0:1634:G:H3'	38:0:3885:HOH:O	1.85	0.76
30:0:146:U:O2'	30:0:147:G:H5'	1.86	0.76
30:0:541:C:H2'	30:0:542:A:C5'	2.15	0.75
31:9:75:G:H1	31:9:106:U:H3	1.33	0.75
2:B:18:ARG:HE	2:B:256:GLN:HE21	1.31	0.75
13:M:88:VAL:HG21	30:0:2122:C:O2'	1.86	0.75
26:Z:63:CYS:SG	26:Z:81:CYS:HB2	2.26	0.75
30:0:564:G:H1'	38:0:6290:HOH:O	1.85	0.75
30:0:2083:A:H3'	38:0:7559:HOH:O	1.86	0.75
30:0:1434:A:HO2'	30:0:1435:U:H6	1.32	0.75
30:0:297:U:H2'	30:0:298:C:C6	2.21	0.75
30:0:1189:A:H3'	38:0:7661:HOH:O	1.86	0.75
30:0:281:U:O2'	30:0:282:C:H5'	1.85	0.75
30:0:1524:U:OP1	30:0:1524:U:H4'	1.87	0.75
30:0:40:C:H4'	38:0:6986:HOH:O	1.86	0.75
30:0:1184:C:H1'	38:0:7447:HOH:O	1.86	0.75
30:0:1377:C:H5'	30:0:1377:C:H6	1.52	0.74
30:0:69:A:H5'	30:0:69:A:C8	2.22	0.74
30:0:718:C:O2	30:0:718:C:H2'	1.87	0.74
8:H:44:ASP:HA	8:H:170:ARG:HH12	1.50	0.74
30:0:279:C:O2'	30:0:280:C:H5'	1.87	0.74
30:0:635:A:H2'	30:0:636:G:H5"	1.68	0.74
30:0:1279:U:O2	30:0:1279:U:H2'	1.85	0.74
30:0:1787:C:O2'	30:0:1788:U:H5'	1.87	0.74
1:A:223:ARG:NH2	30:0:2271:G:H5'	2.02	0.74
30:0:1972:U:H2'	30:0:1973:A:C5'	2.18	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:26:VAL:HG13	10:J:36:VAL:HG11	1.69	0.74
30:0:848:C:H5'	38:0:7257:HOH:O	1.87	0.74
30:0:1589:G:N2	30:0:1605:G:H1'	2.02	0.74
30:0:1165:G:O3'	30:0:1174:A:H4'	1.88	0.74
1:A:47:HIS:CD2	30:0:1654:U:H2'	2.22	0.74
30:0:629:A:H4'	38:0:4498:HOH:O	1.88	0.74
30:0:694:A:C2'	30:0:695:C:H5'	2.18	0.74
30:0:2831:C:C2'	30:0:2832:C:H5'	2.18	0.74
30:0:1185:U:H5'	38:0:7447:HOH:O	1.88	0.73
21:U:44:ARG:HD3	21:U:49:LEU:HD11	1.70	0.73
30:0:2100:A:H5'	38:0:7373:HOH:O	1.88	0.73
30:0:2703:A:H2'	30:0:2704:C:H6	1.52	0.73
29:3:68:LYS:CD	29:3:70:ARG:HH21	2.01	0.73
30:0:2011:A:H5"	38:0:4388:HOH:O	1.87	0.73
30:0:254:C:O2	30:0:254:C:H2'	1.88	0.73
30:0:1603:A:C5'	30:0:1605:G:H5'	2.19	0.73
2:B:18:ARG:HE	2:B:256:GLN:NE2	1.86	0.73
30:0:1855:G:H4'	30:0:1856:C:O5'	1.88	0.73
30:0:2769:C:H2'	30:0:2770:G:H5'	1.69	0.73
31:9:1:U:H4'	31:9:3:A:OP1	1.88	0.73
30:0:137:U:H2'	30:0:139:C:C5	2.23	0.73
2:B:201:ASP:HB2	2:B:312:ARG:HD2	1.70	0.73
30:0:69:A:H5'	30:0:69:A:H8	1.54	0.73
30:0:1589:G:H22	30:0:1605:G:H1'	1.53	0.73
30:0:1835:U:C5	30:0:1840:A:N7	2.53	0.73
30:0:2505:G:C2'	30:0:2506:A:H5'	2.19	0.73
31:9:3:A:N6	31:9:22:G:H1'	2.03	0.73
10:J:47:THR:HG21	30:0:1244:U:H2'	1.69	0.73
30:0:871:G:C8	30:0:871:G:C5'	2.63	0.73
30:0:2064:U:H5'	30:0:2652:U:O3'	1.89	0.73
30:0:2472:C:O2'	30:0:2634:G:H4'	1.89	0.73
38:B:9106:HOH:O	30:0:2672:C:H1'	1.87	0.72
30:0:2635:A:O2'	30:0:2636:C:H5'	1.88	0.72
1:A:109:GLU:HG2	1:A:116:GLY:H	1.53	0.72
30:0:283:U:H5	30:0:284:C:N3	1.87	0.72
30:0:1625:U:H6	30:0:1625:U:H3'	1.54	0.72
30:0:1666:C:H2'	30:0:1667:A:C5'	2.19	0.72
13:M:99:ARG:HD2	13:M:167:GLY:HA2	1.71	0.72
30:0:1733:A:C6	30:0:1734:C:C2	2.77	0.72
1:A:48:ASP:HB3	38:A:9085:HOH:O	1.90	0.72
13:M:79:ALA:HB1	38:0:4442:HOH:O	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:58:VAL:HB	4:D:62:ASP:HB3	1.72	0.72
13:M:76:ARG:HB2	13:M:88:VAL:HG13	1.72	0.72
18:R:132:ARG:NH2	30:0:2055:A:H4'	2.05	0.72
30:0:1372:A:H3'	38:0:7172:HOH:O	1.88	0.72
30:0:2467:A:H1'	38:0:9049:HOH:O	1.89	0.72
30:0:2898:G:O2'	30:0:2899:A:H5'	1.89	0.72
30:0:1316:G:H5"	38:0:5285:HOH:O	1.88	0.72
30:0:2831:C:O2'	30:0:2832:C:H5'	1.88	0.72
30:0:272:A:H5'	30:0:273:G:OP2	1.90	0.72
30:0:1178:G:H2'	30:0:1179:C:C6	2.25	0.72
30:0:1713:G:H1'	38:0:5039:HOH:O	1.89	0.72
30:0:2297:U:H1'	38:0:5144:HOH:O	1.88	0.72
30:0:2253:G:H2'	30:0:2254:G:H8	1.55	0.72
30:0:595:U:O2'	30:0:596:C:H5'	1.90	0.71
30:0:603:A:H5"	30:0:604:G:OP1	1.89	0.71
31:9:26:C:O2'	31:9:27:C:H5'	1.91	0.71
30:0:958:G:H2'	30:0:959:C:C6	2.24	0.71
30:0:1979:G:H3'	38:0:3283:HOH:O	1.88	0.71
18:R:2:ILE:HG22	30:0:21:G:H4'	1.71	0.71
30:0:1477:C:H5'	30:0:1868:G:H5'	1.72	0.71
23:W:125:HIS:CE1	30:0:1097:A:H5"	2.25	0.71
25:Y:187:VAL:HG23	25:Y:192:ASP:CB	2.21	0.71
27:1:25:LYS:HD2	28:2:49:GLU:H	1.55	0.71
30:0:1801:A:H3'	38:0:7596:HOH:O	1.90	0.71
30:0:2321:A:H2	30:0:2378:U:N3	1.88	0.71
30:0:1197:G:H1'	30:0:1203:G:N2	2.06	0.71
30:0:1398:G:H2'	30:0:1399:A:C8	2.25	0.71
30:0:2769:C:H2'	30:0:2770:G:C5'	2.20	0.71
5:E:143:GLN:NE2	30:0:2779:G:H21	1.89	0.71
14:N:33:ARG:HH21	14:N:48:VAL:HG11	1.55	0.71
26:Z:84:CYS:HB3	30:0:1604:G:H22	1.56	0.71
30:0:920:C:H4'	30:0:921:G:C2	2.26	0.71
30:0:2780:C:H2'	30:0:2781:U:C6	2.26	0.71
21:U:56:ARG:HH11	21:U:56:ARG:HG3	1.56	0.71
31:9:55:U:H4'	31:9:56:A:C8	2.25	0.71
30:0:1666:C:C2'	30:0:1667:A:C5'	2.69	0.71
3:C:139:VAL:HG13	38:C:8645:HOH:O	1.91	0.70
30:0:1185:U:H2'	30:0:1186:C:C6	2.25	0.70
30:0:2321:A:C2	30:0:2378:U:N3	2.55	0.70
30:0:2524:G:H21	30:0:2526:C:N4	1.88	0.70
3:C:78:ARG:HH11	3:C:78:ARG:HG3	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1118:A:N6	30:0:1244:U:H3	1.89	0.70
30:0:2416:G:H2'	30:0:2417:C:C6	2.26	0.70
22:V:57:LYS:HA	22:V:60:GLN:HE21	1.57	0.70
30:0:1972:U:H2'	30:0:1973:A:H5'	1.73	0.70
30:0:2312:G:H2'	30:0:2313:C:H5'	1.72	0.70
30:0:2717:C:C2'	30:0:2718:C:C5'	2.68	0.70
14:N:4:PRO:HB2	30:0:1010:C:H4'	1.73	0.70
26:Z:43:GLY:O	26:Z:47:ARG:HG2	1.91	0.70
30:0:1596:U:H2'	30:0:1598:A:OP2	1.90	0.70
30:0:2565:C:H4'	38:0:4806:HOH:O	1.91	0.70
13:M:164:THR:HG22	13:M:166:ALA:H	1.57	0.70
30:0:1829:A:C2'	30:0:1830:C:H5'	2.21	0.70
30:0:2539:U:H1'	38:0:7770:HOH:O	1.90	0.70
1:A:223:ARG:HH12	30:0:2270:G:H4'	1.55	0.70
38:C:8565:HOH:O	20:T:2:LYS:HE3	1.92	0.70
14:N:11:ARG:HD3	31:9:114:G:O6	1.90	0.70
29:3:40:ARG:HA	29:3:52:PHE:CE1	2.26	0.70
30:0:1226:G:H2'	30:0:1227:C:H6	1.57	0.70
31:9:59:C:O5'	31:9:59:C:H6	1.74	0.69
30:0:522:U:O2'	30:0:1366:C:H5'	1.92	0.69
30:0:1589:G:H5'	38:0:6843:HOH:O	1.91	0.69
30:0:2415:A:H2'	30:0:2416:G:H5'	1.74	0.69
1:A:135:VAL:HG11	1:A:147:ARG:NH2	2.07	0.69
7:G:64:ASN:HD22	7:G:64:ASN:N	1.90	0.69
10:J:70:PHE:CD1	30:0:2676:C:H4'	2.27	0.69
30:0:714:U:H4'	38:0:5705:HOH:O	1.93	0.69
30:0:1181:A:C2'	30:0:1182:C:H5'	2.22	0.69
30:0:2404:G:H5"	38:0:5177:HOH:O	1.91	0.69
8:H:168:VAL:HG13	38:H:218:HOH:O	1.91	0.69
30:0:2667:G:H1'	30:0:2914:A:N3	2.08	0.69
26:Z:37:ARG:HB3	38:0:4665:HOH:O	1.91	0.69
29:3:20:HIS:HD2	29:3:69:TYR:HB3	1.56	0.69
14:N:37:ARG:NH1	31:9:6:C:C5'	2.50	0.69
30:0:545:G:H8	30:0:545:G:C5'	1.99	0.69
30:0:1205:U:C2'	30:0:1206:U:H5"	2.23	0.69
2:B:258:GLY:H	2:B:260:HIS:CE1	2.10	0.69
3:C:76:ARG:HB3	3:C:76:ARG:HH11	1.57	0.69
30:0:735:C:H2'	30:0:736:A:O4'	1.93	0.69
15:O:32:ARG:HE	15:O:35:LYS:HD2	1.58	0.69
30:0:1741:U:O2'	30:0:2723:G:H4'	1.91	0.69
30:0:2705:U:H2'	30:0:2706:A:C8	2.28	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:81:ARG:HD2	13:M:85:ARG:HG3	1.74	0.69
18:R:128:ARG:NH2	30:0:2054:A:N3	2.41	0.69
30:0:2827:A:H2'	30:0:2828:G:O4'	1.92	0.69
30:0:596:C:H2'	30:0:597:A:H8	1.58	0.69
21:U:56:ARG:HB2	30:0:2890:A:C8	2.27	0.68
30:0:1632:A:C2'	30:0:1633:C:H5'	2.22	0.68
30:0:2795:C:O2'	30:0:2796:U:H5'	1.93	0.68
11:K:74:VAL:HG21	11:K:96:VAL:HG23	1.75	0.68
18:R:138:SER:HB3	30:0:2053:G:OP1	1.94	0.68
16:P:117:SER:HB3	30:0:1593:C:OP1	1.92	0.68
30:0:1702:U:H5'	38:0:3414:HOH:O	1.92	0.68
26:Z:47:ARG:NH2	30:0:1771:U:H1'	2.08	0.68
30:0:2111:G:H1'	38:0:9052:HOH:O	1.94	0.68
30:0:2635:A:C2'	30:0:2636:C:H5'	2.23	0.68
23:W:137:GLN:HE21	23:W:141:HIS:CE1	2.10	0.68
2:B:264:GLU:HG2	2:B:267:LYS:CE	2.19	0.68
30:0:333:G:O2'	30:0:334:G:H5'	1.94	0.68
30:0:2637:A:H5'	38:0:4897:HOH:O	1.94	0.68
23:W:125:HIS:NE2	30:0:1097:A:H5"	2.09	0.68
29:3:50:GLY:HA3	30:0:170:U:H1'	1.75	0.68
30:0:585:C:H5"	38:0:4840:HOH:O	1.94	0.68
30:0:1197:G:H1'	30:0:1203:G:C2	2.28	0.68
2:B:267:LYS:HD3	38:B:8996:HOH:O	1.93	0.68
26:Z:42:TYR:CA	30:0:1829:A:H61	2.07	0.68
30:0:685:C:O2	30:0:748:C:H4'	1.94	0.68
30:0:1209:C:H2'	30:0:1210:G:C8	2.23	0.68
2:B:206:THR:HG21	30:0:2716:G:H5"	1.76	0.68
10:J:18:ILE:HD13	30:0:1244:U:OP1	1.94	0.68
10:J:74:ARG:HH11	10:J:74:ARG:CB	2.07	0.68
30:0:1151:G:H2'	38:0:5713:HOH:O	1.92	0.68
30:0:2840:A:H3'	38:0:7629:HOH:O	1.94	0.68
3:C:76:ARG:HB3	3:C:76:ARG:NH1	2.09	0.67
10:J:39:VAL:HG22	10:J:106:GLY:O	1.94	0.67
13:M:95:LYS:HE2	30:0:157:G:H4'	1.76	0.67
18:R:98:ASN:HD21	30:0:500:G:H21	1.40	0.67
29:3:90:PHE:HD1	29:3:90:PHE:H	1.42	0.67
30:0:1625:U:H3'	30:0:1625:U:C6	2.29	0.67
13:M:70:GLY:HA2	30:0:2263:G:H4'	1.76	0.67
21:U:42:LEU:HD22	30:0:1810:C:H1'	1.76	0.67
30:0:1118:A:C8	30:0:1119:G:H5"	2.29	0.67
30:0:1813:U:H2'	38:0:6701:HOH:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:57:THR:HG23	8:H:131:GLN:HA	1.76	0.67
30:0:541:C:H2'	30:0:542:A:H5"	1.74	0.67
30:0:1528:A:H2'	30:0:1529:G:O4'	1.95	0.67
30:0:2524:G:H5"	38:0:4698:HOH:O	1.94	0.67
13:M:91:ILE:HG23	38:0:7530:HOH:O	1.94	0.67
30:0:1787:C:H4'	30:0:2883:A:O4'	1.94	0.67
13:M:73:ARG:HH22	30:0:2263:G:H5"	1.58	0.67
21:U:19:THR:HG22	21:U:20:MET:H	1.59	0.67
28:2:28:LYS:HE2	30:0:86:A:H1'	1.77	0.67
30:0:2894:C:O2'	30:0:2895:C:H5'	1.95	0.67
30:0:119:A:H2'	30:0:120:A:H5"	1.77	0.67
30:0:370:G:O2'	30:0:371:U:H5'	1.93	0.67
31:9:76:G:C3'	31:9:77:A:H5"	2.23	0.67
12:L:46:LEU:O	30:0:2430:A:H4'	1.95	0.67
30:0:2780:C:H2'	30:0:2781:U:H6	1.59	0.67
30:0:2829:G:N2	30:0:2912:C:C2	2.63	0.67
30:0:1641:A:H2'	30:0:1642:A:H5'	1.77	0.67
4:D:154:LYS:H	4:D:154:LYS:HD2	1.60	0.67
5:E:91:PHE:HE1	30:0:2694:A:H4'	1.58	0.67
10:J:75:PRO:HG2	10:J:105:LEU:HD21	1.77	0.67
11:K:20:CYS:HB2	11:K:29:LEU:HG	1.77	0.67
29:3:60:LYS:HG3	29:3:61:PRO:HD2	1.77	0.67
30:0:256:C:H2'	30:0:257:G:O4'	1.95	0.67
30:0:810:G:H2'	30:0:811:C:H6	1.56	0.67
16:P:59:ARG:HD3	38:0:6249:HOH:O	1.95	0.66
1:A:135:VAL:HG21	1:A:147:ARG:HB3	1.77	0.66
30:0:596:C:H2'	30:0:597:A:C8	2.29	0.66
30:0:2785:C:H5'	38:0:7694:HOH:O	1.95	0.66
14:N:33:ARG:NH2	14:N:48:VAL:HG11	2.10	0.66
15:O:14:LEU:HD23	15:O:102:ILE:HD11	1.77	0.66
29:3:68:LYS:HD3	29:3:70:ARG:NH2	2.07	0.66
30:0:468:U:H3'	38:0:7549:HOH:O	1.93	0.66
13:M:48:LYS:HE3	13:M:52:GLN:HE21	1.60	0.66
30:0:869:G:H1'	38:0:3302:HOH:O	1.95	0.66
30:0:1041:U:H2'	30:0:1042:U:H5'	1.78	0.66
11:K:12:LEU:HB2	11:K:47:ALA:HB3	1.77	0.66
30:0:1120:U:H5'	30:0:1121:G:OP2	1.95	0.66
14:N:113:SER:HB2	38:N:8852:HOH:O	1.94	0.66
30:0:123:U:H5'	38:0:6635:HOH:O	1.96	0.66
30:0:1205:U:C2'	30:0:1206:U:H5'	2.18	0.66
30:0:1942:A:H3'	38:0:7329:HOH:O	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2329:C:O2'	30:0:2330:U:H5'	1.95	0.66
2:B:27:ASN:HD22	2:B:27:ASN:H	1.44	0.66
28:2:43:ARG:NH2	30:0:1684:A:H1'	2.10	0.66
30:0:318:U:H5'	30:0:339:A:C2	2.31	0.66
30:0:704:C:H2'	30:0:705:C:H6	1.60	0.66
30:0:1063:G:H5"	38:0:9856:HOH:O	1.94	0.66
30:0:1167:G:H2'	30:0:1168:C:C6	2.31	0.66
30:0:2032:U:H2'	30:0:2033:G:C5'	2.26	0.66
30:0:2760:C:H5"	38:0:5294:HOH:O	1.95	0.66
31:9:7:G:H5'	38:9:9102:HOH:O	1.95	0.66
3:C:184:ARG:NH2	30:0:450:C:OP1	2.29	0.66
30:0:559:U:H5'	30:0:559:U:C6	2.23	0.66
30:0:921:G:H4'	30:0:924:G:N1	2.11	0.66
30:0:2533:C:H5'	30:0:2533:C:C6	2.31	0.66
30:0:449:A:H3'	38:0:6214:HOH:O	1.95	0.65
30:0:1249:U:H2'	30:0:1250:C:C6	2.30	0.65
30:0:1603:A:H5'	30:0:1605:G:C4'	2.26	0.65
2:B:179:LEU:O	2:B:183:GLU:HG2	1.96	0.65
12:L:143:THR:HG22	12:L:144:ASP:H	1.61	0.65
14:N:80:SER:HB2	38:N:8833:HOH:O	1.95	0.65
20:T:9:LYS:HE3	20:T:13:ARG:NH1	2.12	0.65
26:Z:44:ARG:NH2	30:0:1771:U:H5'	2.09	0.65
30:0:559:U:H6	30:0:559:U:C5'	2.09	0.65
30:0:2851:G:H2'	30:0:2902:A:H61	1.60	0.65
30:0:368:C:H2'	30:0:369:G:H5'	1.77	0.65
26:Z:78:ILE:HG21	26:Z:87:LYS:HE2	1.78	0.65
31:9:29:C:C5	31:9:30:C:C6	2.84	0.65
38:D:7597:HOH:O	31:9:56:A:H2	1.79	0.65
30:0:2707:C:O2	30:0:2707:C:H2'	1.96	0.65
1:A:122:SER:HB2	1:A:164:ARG:NH1	2.11	0.65
16:P:88:GLN:NE2	30:0:1800:G:H1'	2.10	0.65
21:U:56:ARG:HD2	30:0:2890:A:C1'	2.25	0.65
5:E:91:PHE:CE1	30:0:2694:A:H4'	2.32	0.65
9:I:110:ASP:O	30:0:1163:G:H5'	1.95	0.65
25:Y:115:ARG:HH21	30:0:1266:U:H4'	1.60	0.65
30:0:213:G:N2	30:0:225:G:H2'	2.11	0.65
30:0:416:G:H5"	38:0:7402:HOH:O	1.96	0.65
30:0:696:C:H4'	38:0:7263:HOH:O	1.96	0.65
30:0:1061:C:H3'	38:0:5051:HOH:O	1.97	0.65
30:0:1132:A:N6	30:0:1229:C:H2'	2.12	0.65
30:0:1666:C:C2'	30:0:1667:A:H5"	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2597:U:H2'	30:0:2598:U:H5'	1.77	0.65
30:0:1385:G:H1'	38:0:4024:HOH:O	1.97	0.65
2:B:238:ASN:HD22	2:B:240:GLY:N	1.90	0.65
38:O:1484:HOH:O	30:0:710:G:H1'	1.97	0.65
30:0:42:C:H1'	38:0:4645:HOH:O	1.97	0.65
30:0:290:C:O2'	30:0:291:C:H5'	1.96	0.65
30:0:812:A:H2'	30:0:813:C:C6	2.31	0.65
16:P:81:LYS:O	30:0:1761:U:H5'	1.97	0.65
30:0:2119:C:O2'	30:0:2120:U:H5'	1.97	0.65
30:0:696:C:O2'	30:0:697:G:H5'	1.97	0.64
30:0:1586:G:O2'	30:0:1587:U:H5'	1.97	0.64
30:0:2892:G:C6	30:0:2893:C:C4	2.85	0.64
31:9:61:C:H2'	31:9:62:A:H8	1.62	0.64
30:0:1377:C:H5'	30:0:1377:C:C6	2.33	0.64
30:0:1422:U:H2'	30:0:1423:C:C6	2.32	0.64
30:0:1735:C:O2'	30:0:1736:A:H5'	1.97	0.64
30:0:1862:C:H1'	38:0:7203:HOH:O	1.96	0.64
1:A:47:HIS:HD2	30:0:1654:U:H2'	1.61	0.64
38:B:8996:HOH:O	30:0:2766:A:H5'	1.97	0.64
30:0:441:A:H1'	30:0:442:A:N7	2.13	0.64
2:B:36:PRO:HA	2:B:168:GLY:HA3	1.78	0.64
21:U:56:ARG:HD2	30:0:2890:A:C8	2.33	0.64
30:0:671:A:O2'	30:0:672:G:H2'	1.97	0.64
30:0:1819:G:H5'	38:0:4680:HOH:O	1.96	0.64
30:0:1972:U:C2'	30:0:1973:A:H5"	2.27	0.64
2:B:312:ARG:HD3	2:B:315:VAL:HG13	1.80	0.64
27:1:9:GLY:HA2	30:0:1687:C:O2	1.98	0.64
30:0:281:U:H2'	30:0:282:C:O4'	1.98	0.64
30:0:693:A:H2'	30:0:694:A:C8	2.33	0.64
5:E:20:ILE:HD11	5:E:40:VAL:HG11	1.79	0.64
5:E:143:GLN:HE22	30:0:2779:G:H21	1.44	0.64
23:W:6:GLN:HB2	23:W:26:ILE:HD11	1.79	0.64
26:Z:70:ARG:HH11	26:Z:83:TYR:HD1	1.46	0.64
27:1:21:ARG:HD2	27:1:37:CYS:SG	2.38	0.64
30:0:1706:G:H1'	30:0:1712:A:H61	1.61	0.64
30:0:2768:A:O2'	30:0:2769:C:H5'	1.97	0.64
3:C:78:ARG:HG3	3:C:78:ARG:NH1	2.13	0.64
30:0:1181:A:H2'	30:0:1182:C:H5'	1.80	0.64
30:0:1973:A:H2'	30:0:1974:G:O4'	1.96	0.64
30:0:2088:C:H2'	30:0:2089:A:H8	1.62	0.64
25:Y:154:ARG:HH22	30:0:1071:G:H4'	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:169:ARG:HD2	30:0:1328:A:OP1	1.98	0.64
3:C:16:VAL:HG12	3:C:17:ASP:H	1.62	0.64
14:N:86:LEU:HD12	14:N:125:ALA:HB2	1.78	0.64
30:0:459:A:H5"	38:0:9055:HOH:O	1.96	0.64
8:H:27:PRO:HD3	8:H:123:ILE:HG22	1.79	0.63
11:K:66:ARG:HH22	30:0:1994:A:P	2.21	0.63
21:U:23:HIS:HD2	21:U:27:ALA:HB3	1.63	0.63
30:0:1748:U:C5	30:0:1749:U:C5	2.85	0.63
3:C:132:ASP:O	3:C:133:ARG:HG3	1.98	0.63
3:C:236:THR:HG21	38:C:8571:HOH:O	1.97	0.63
11:K:98:VAL:CG1	11:K:102:GLU:HA	2.28	0.63
18:R:40:ALA:O	18:R:44:VAL:HG23	1.99	0.63
30:0:541:C:H2'	30:0:542:A:H5'	1.77	0.63
30:0:2867:G:H2'	30:0:2868:C:C6	2.33	0.63
8:H:19:ARG:HH12	30:0:1008:C:H5"	1.63	0.63
17:Q:26:PRO:O	17:Q:30:VAL:HG23	1.97	0.63
30:0:541:C:O2'	30:0:542:A:H5"	1.97	0.63
30:0:1116:U:O2'	30:0:1118:A:C2	2.40	0.63
30:0:2727:A:H2'	30:0:2728:C:H5'	1.80	0.63
31:9:17:G:O2'	31:9:18:U:H5'	1.97	0.63
13:M:66:SER:HB3	13:M:128:TRP:CD1	2.33	0.63
13:M:164:THR:HG22	13:M:166:ALA:N	2.13	0.63
30:0:1835:U:H3'	38:0:5539:HOH:O	1.97	0.63
30:0:2032:U:O2'	30:0:2033:G:H5"	1.98	0.63
23:W:88:THR:HG22	23:W:110:GLN:HB3	1.81	0.63
30:0:506:G:H22	30:0:509:A:H5'	1.63	0.63
30:0:2659:U:H5"	38:0:4112:HOH:O	1.98	0.63
1:A:211:LYS:HB3	1:A:212:PRO:HD2	1.79	0.63
26:Z:38:PHE:HB3	26:Z:42:TYR:CD1	2.33	0.63
29:3:65:THR:O	29:3:82:GLY:HA3	1.99	0.63
30:0:90:A:H2'	30:0:91:G:O4'	1.98	0.63
30:0:1985:U:H1'	38:0:4497:HOH:O	1.98	0.63
31:9:91:C:H2'	31:9:92:G:O4'	1.99	0.63
14:N:37:ARG:HH12	31:9:6:C:C5'	1.95	0.63
14:N:164:ASP:OD1	14:N:167:ASP:HA	1.98	0.63
30:0:1149:U:H5"	30:0:1151:G:O4'	1.98	0.63
30:0:1644:C:H2'	30:0:1645:U:C6	2.31	0.63
30:0:2291:A:H8	38:0:6453:HOH:O	1.81	0.63
30:0:2675:A:H1'	30:0:2813:A:C2	2.34	0.63
30:0:2824:C:H5"	30:0:2825:C:H5'	1.80	0.63
2:B:280:VAL:HG13	2:B:333:GLU:O	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:131:THR:HG21	30:0:2348:C:H1'	1.79	0.63
22:V:42:ASN:HB3	38:V:7247:HOH:O	1.98	0.63
29:3:2:GLN:HB3	29:3:91:GLN:CD	2.19	0.63
29:3:59:ASP:HB3	29:3:63:LYS:NZ	2.13	0.63
30:0:2250:G:H2'	30:0:2251:G:O4'	1.99	0.63
30:0:2766:A:O2'	30:0:2767:C:H5'	1.99	0.63
5:E:60:SER:OG	30:0:2784:A:H1'	1.98	0.63
11:K:74:VAL:CG1	11:K:113:ILE:HG12	2.29	0.63
28:2:41:HIS:HB3	28:2:44:ARG:HB2	1.80	0.63
30:0:279:C:C2'	30:0:280:C:H5'	2.29	0.63
30:0:630:A:H5"	38:0:4722:HOH:O	1.99	0.63
30:0:956:G:C8	38:0:9387:HOH:O	2.50	0.63
30:0:2782:G:H3'	38:0:5004:HOH:O	1.98	0.63
12:L:57:VAL:HG21	30:0:2443:C:H5'	1.80	0.62
20:T:72:ILE:HD13	20:T:93:THR:HG22	1.81	0.62
26:Z:34:SER:HB2	38:0:7481:HOH:O	1.99	0.62
26:Z:41:ARG:HD2	30:0:1830:C:O2	1.98	0.62
27:1:2:GLY:O	27:1:6:PRO:HG2	1.99	0.62
30:0:1165:G:H21	30:0:1173:A:C5'	2.12	0.62
30:0:2349:G:H2'	30:0:2350:G:H8	1.62	0.62
29:3:54:LYS:HE2	30:0:2468:A:N7	2.14	0.62
30:0:1921:A:O2'	30:0:1922:A:H5'	1.98	0.62
30:0:1527:A:H1'	30:0:1528:A:C8	2.34	0.62
4:D:54:ALA:HB2	4:D:69:ILE:HD12	1.80	0.62
14:N:160:SER:HB3	31:9:51:A:H5'	1.82	0.62
21:U:49:LEU:HD12	38:U:3805:HOH:O	1.99	0.62
30:0:1351:G:H5'	38:0:3619:HOH:O	1.99	0.62
30:0:1878:G:H1'	38:0:6097:HOH:O	2.00	0.62
30:0:1889:C:H2'	30:0:1890:U:O4'	2.00	0.62
30:0:1477:C:H5'	30:0:1868:G:C5'	2.29	0.62
5:E:153:ARG:HH12	30:0:2778:A:H1'	1.65	0.62
8:H:15:PRO:HG3	30:0:1053:G:OP1	2.00	0.62
20:T:61:GLU:HG2	38:T:3851:HOH:O	1.99	0.62
30:0:229:G:O2'	30:0:230:C:H5'	2.00	0.62
30:0:790:A:H1'	30:0:1710:A:O2'	1.99	0.62
3:C:246:ARG:NH2	30:0:677:C:H4'	2.14	0.62
29:3:68:LYS:NZ	30:0:2436:U:H5'	2.14	0.62
30:0:1226:G:H5'	38:0:4509:HOH:O	1.98	0.62
15:O:51:TYR:CE2	30:0:721:A:H5"	2.35	0.62
22:V:39:ALA:H	22:V:40:PRO:HD2	1.65	0.62
26:Z:53:ILE:O	26:Z:57:MET:HB2	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:2:22:PRO:HG2	28:2:25:VAL:HG23	1.82	0.62
30:0:920:C:H4'	30:0:921:G:N2	2.14	0.62
30:0:2510:C:H5'	30:0:2511:A:OP2	1.99	0.62
17:Q:14:LEU:HD21	17:Q:43:ILE:HD12	1.82	0.62
30:0:303:C:O2'	30:0:304:G:H5'	2.00	0.62
30:0:630:A:H5'	38:0:9372:HOH:O	1.98	0.62
30:0:1752:G:H2'	38:0:7531:HOH:O	2.00	0.62
3:C:129:HIS:CE1	3:C:231:ARG:HA	2.35	0.61
23:W:64:THR:O	23:W:68:THR:HG22	2.00	0.61
30:0:236:A:H4'	30:0:237:G:C5'	2.17	0.61
30:0:1131:G:H1'	38:0:3907:HOH:O	1.99	0.61
30:0:1279:U:O2	30:0:1279:U:C2'	2.48	0.61
30:0:2251:G:H2'	30:0:2252:A:C8	2.35	0.61
30:0:2300:A:H4'	30:0:2301:A:O5'	2.00	0.61
30:0:2439:C:H5'	38:0:5449:HOH:O	1.99	0.61
30:0:2775:A:C6	30:0:2799:A:C8	2.88	0.61
31:9:91:C:H1'	38:9:9149:HOH:O	1.98	0.61
9:I:130:LEU:CD2	30:0:1167:G:H4'	2.29	0.61
22:V:55:ARG:O	22:V:59:ILE:HG12	2.01	0.61
30:0:825:U:H5"	30:0:826:U:OP1	2.00	0.61
30:0:1477:C:O2'	30:0:1478:U:H5'	1.99	0.61
30:0:2576:A:H2'	38:0:7732:HOH:O	2.00	0.61
25:Y:186:ARG:HG2	25:Y:186:ARG:HH11	1.65	0.61
30:0:2314:G:C2'	30:0:2315:C:H5'	2.30	0.61
2:B:262:ARG:HG3	30:0:2716:G:H5'	1.83	0.61
7:G:12:ILE:HG23	38:0:5418:HOH:O	1.98	0.61
13:M:75:ARG:NH2	13:M:78:LYS:HE2	2.16	0.61
23:W:52:VAL:HG22	23:W:53:ALA:H	1.63	0.61
24:X:71:ARG:HD2	38:X:7542:HOH:O	1.99	0.61
30:0:301:C:O2'	30:0:302:A:H5'	2.00	0.61
30:0:1711:A:O2'	30:0:1712:A:H5'	2.00	0.61
30:0:2912:C:O5'	30:0:2912:C:H6	1.83	0.61
1:A:20:SER:HB3	30:0:1872:C:H5	1.65	0.61
2:B:320:GLN:HE21	2:B:321:PRO:HD2	1.65	0.61
2:B:336:GLN:O	30:0:2862:G:H4'	2.00	0.61
9:I:91:PHE:HD2	9:I:131:GLY:HA2	1.66	0.61
12:L:67:ARG:HB2	12:L:112:GLY:HA3	1.83	0.61
30:0:39:G:N2	30:0:444:C:C2	2.68	0.61
30:0:1118:A:H8	30:0:1119:G:H5"	1.64	0.61
9:I:130:LEU:HD21	30:0:1167:G:H4'	1.81	0.61
23:W:13:MET:HE1	23:W:18:GLN:HA	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:705:C:O2	30:0:705:C:H2'	1.99	0.61
30:0:2526:C:H3'	30:0:2526:C:H6	1.65	0.61
22:V:12:THR:HG22	22:V:15:GLU:CG	2.31	0.61
30:0:228:C:H2'	30:0:229:G:H5'	1.80	0.61
30:0:877:G:C5'	30:0:878:G:OP1	2.46	0.61
30:0:1774:G:O2'	30:0:1775:A:H5'	2.01	0.61
31:9:20:G:H3'	38:9:9057:HOH:O	2.00	0.61
23:W:145:GLY:HA3	38:W:6373:HOH:O	2.00	0.61
30:0:282:C:O2	30:0:282:C:H2'	2.00	0.61
30:0:1676:G:O2'	30:0:1677:U:H5'	2.01	0.61
30:0:1856:C:H5'	30:0:1858:A:O4'	2.01	0.61
30:0:2834:G:C2	30:0:2835:C:H1'	2.35	0.61
30:0:283:U:C5	30:0:284:C:C4	2.88	0.61
30:0:807:A:H2'	30:0:808:A:C8	2.36	0.61
30:0:1398:G:H2'	30:0:1399:A:H8	1.64	0.61
31:9:39:U:HO2'	31:9:42:C:H5	1.48	0.61
8:H:174:LEU:HD21	30:0:1220:U:H4'	1.82	0.61
11:K:10:GLN:HE21	11:K:10:GLN:N	1.96	0.61
30:0:558:C:H2'	30:0:559:U:H5'	1.81	0.61
30:0:1701:A:H4'	30:0:1702:U:C5'	2.30	0.61
1:A:140:LEU:HB3	1:A:141:PRO:HD2	1.83	0.60
10:J:47:THR:HB	38:0:4807:HOH:O	2.01	0.60
38:3:9025:HOH:O	30:0:2468:A:H5'	2.00	0.60
30:0:31:C:H4'	38:0:7408:HOH:O	2.00	0.60
30:0:1878:G:HO2'	30:0:1879:U:H6	1.42	0.60
2:B:102:THR:HG23	2:B:182:VAL:HG12	1.81	0.60
2:B:320:GLN:HE21	2:B:321:PRO:CD	2.14	0.60
3:C:27:ARG:NH2	30:0:657:G:OP1	2.34	0.60
29:3:9:THR:HG23	29:3:20:HIS:ND1	2.15	0.60
30:0:1175:G:H1'	30:0:1193:A:C2'	2.31	0.60
30:0:1697:G:H4'	38:0:9347:HOH:O	2.02	0.60
30:0:2281:C:H2'	30:0:2282:U:H5'	1.82	0.60
11:K:74:VAL:HG12	11:K:75:ARG:HG3	1.83	0.60
30:0:282:C:O2'	30:0:283:U:C5'	2.49	0.60
30:0:2071:C:H5'	38:0:9540:HOH:O	2.00	0.60
30:0:2312:G:C2'	30:0:2313:C:H5'	2.30	0.60
30:0:2872:U:H2'	30:0:2873:C:O4'	2.02	0.60
25:Y:126:PRO:HG2	25:Y:128:PHE:CE1	2.36	0.60
26:Z:84:CYS:HB3	30:0:1604:G:N2	2.15	0.60
30:0:38:G:O2'	30:0:39:G:H5'	2.02	0.60
30:0:407:A:H3'	38:0:4438:HOH:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1201:C:H5”	38:0:6211:HOH:O	2.00	0.60
30:0:1495:C:H1’	30:0:1573:A:H1’	1.83	0.60
2:B:72:THR:HB	38:B:9076:HOH:O	2.02	0.60
11:K:74:VAL:HG13	11:K:113:ILE:HG12	1.82	0.60
20:T:48:VAL:HG22	20:T:97:ARG:O	2.01	0.60
30:0:51:G:H1’	38:0:9033:HOH:O	2.01	0.60
30:0:947:U:H2’	30:0:948:G:C8	2.36	0.60
30:0:1205:U:O2’	30:0:1206:U:H5”	2.01	0.60
30:0:1398:G:O2’	30:0:1399:A:H5’	2.02	0.60
30:0:1407:A:O2’	30:0:1408:U:H3’	2.01	0.60
30:0:1972:U:C2’	30:0:1973:A:C5’	2.80	0.60
30:0:2420:G:C2’	30:0:2421:G:H5’	2.30	0.60
7:G:16:LYS:HE2	7:G:63:ARG:HH12	1.67	0.60
13:M:102:GLU:OE1	13:M:164:THR:HG21	2.01	0.60
16:P:41:ARG:HH22	30:0:1500:U:P	2.24	0.60
30:0:146:U:C2’	30:0:147:G:H5’	2.31	0.60
30:0:2893:C:O2’	30:0:2894:C:H5’	2.01	0.60
31:9:18:U:H2’	31:9:19:G:C8	2.37	0.60
31:9:23:U:O2’	31:9:24:U:H4’	2.01	0.60
8:H:72:ALA:HB2	8:H:156:ALA:HB2	1.81	0.60
15:O:14:LEU:CD2	15:O:102:ILE:HD11	2.32	0.60
18:R:135:ALA:HB1	18:R:137:ASN:HD21	1.67	0.60
29:3:31:THR:OG1	29:3:34:LYS:HD3	2.01	0.60
30:0:2353:A:H4’	30:0:2354:A:O5’	2.01	0.60
33:B:8819:CL:CL	38:B:8997:HOH:O	2.54	0.60
13:M:188:ARG:HD3	30:0:155:C:OP2	2.02	0.60
30:0:1844:C:O5’	30:0:1844:C:H6	1.84	0.60
30:0:2608:C:H3’	38:0:7790:HOH:O	2.02	0.60
31:9:3:A:C6	31:9:22:G:H1’	2.36	0.60
31:9:26:C:H2’	31:9:27:C:C6	2.36	0.60
31:9:29:C:H2’	31:9:30:C:C5’	2.28	0.60
2:B:79:MET:HB2	2:B:188:HIS:CE1	2.36	0.60
10:J:82:THR:CG2	30:0:1242:A:H5’	2.20	0.60
18:R:46:TYR:O	18:R:50:VAL:HG23	2.00	0.60
30:0:307:G:H3’	38:0:6667:HOH:O	2.01	0.60
30:0:567:U:H5”	38:0:5254:HOH:O	2.02	0.60
6:F:58:GLU:CD	13:M:27:ARG:HH22	2.05	0.60
29:3:43:ASN:HB2	29:3:52:PHE:CE1	2.36	0.60
30:0:74:G:H2’	30:0:75:U:C6	2.37	0.60
30:0:947:U:H2’	30:0:948:G:H8	1.65	0.60
2:B:235:ARG:HD3	30:0:2091:G:H5”	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:91:LYS:O	16:P:95:GLU:HG3	2.02	0.59
30:0:319:A:H4'	30:0:338:C:C4	2.37	0.59
30:0:324:G:O2'	30:0:325:U:H5'	2.02	0.59
30:0:1878:G:O2'	30:0:1879:U:C6	2.50	0.59
31:9:63:C:O2'	31:9:64:C:H5'	2.01	0.59
11:K:130:MET:SD	21:U:25:ASP:O	2.60	0.59
13:M:82:ARG:HH22	13:M:85:ARG:HH21	1.49	0.59
27:1:20:ARG:HG2	30:0:111:C:O2'	2.01	0.59
30:0:1590:A:H1'	30:0:1606:A:C2	2.36	0.59
30:0:2686:C:C2	30:0:2709:G:N2	2.70	0.59
31:9:65:A:N6	31:9:112:U:C6	2.71	0.59
1:A:94:LEU:HG	1:A:99:ILE:HD11	1.84	0.59
3:C:236:THR:HA	38:C:8648:HOH:O	2.01	0.59
5:E:145:ALA:HB1	5:E:168:ILE:HD11	1.85	0.59
30:0:2403:C:H5'	38:0:6001:HOH:O	2.01	0.59
30:0:2718:C:H6	30:0:2718:C:H5'	1.67	0.59
30:0:2820:A:H2'	30:0:2821:C:C6	2.36	0.59
2:B:101:TRP:HB2	2:B:119:HIS:CD2	2.38	0.59
2:B:156:LYS:HB3	30:0:2846:C:H4'	1.84	0.59
12:L:79:ASP:HB3	38:L:8859:HOH:O	2.03	0.59
14:N:86:LEU:O	14:N:90:LEU:HG	2.02	0.59
30:0:653:U:H2'	30:0:654:A:C8	2.37	0.59
30:0:834:G:H4'	30:0:835:U:OP2	2.02	0.59
30:0:2867:G:H2'	30:0:2868:C:H6	1.67	0.59
1:A:33:GLU:H	1:A:33:GLU:CD	2.06	0.59
1:A:179:MET:HG2	1:A:186:TRP:CB	2.32	0.59
2:B:62:ARG:HG2	2:B:65:MET:HE3	1.85	0.59
6:F:13:GLU:OE2	6:F:78:GLU:HG2	2.01	0.59
30:0:652:G:C2	30:0:653:U:H1'	2.37	0.59
30:0:1585:C:H2'	30:0:1586:G:C8	2.37	0.59
30:0:2809:G:H2'	30:0:2810:G:C8	2.37	0.59
30:0:2831:C:H2'	30:0:2832:C:H5'	1.82	0.59
30:0:2874:G:H3'	38:0:9586:HOH:O	2.02	0.59
38:B:8993:HOH:O	30:0:2549:C:H1'	2.03	0.59
4:D:58:VAL:HG12	4:D:60:GLU:HG2	1.83	0.59
8:H:37:GLY:HA3	8:H:87:LYS:HA	1.85	0.59
30:0:812:A:H2'	30:0:813:C:H6	1.68	0.59
30:0:1702:U:H5"	38:0:7201:HOH:O	2.01	0.59
30:0:2846:C:H4'	38:0:5047:HOH:O	2.03	0.59
2:B:215:VAL:HB	38:B:9089:HOH:O	2.02	0.59
8:H:155:ARG:NH1	30:0:2503:A:H5"	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:542:A:H5'	30:0:542:A:C8	2.29	0.59
30:0:590:A:H2'	30:0:591:A:H5'	1.83	0.59
30:0:1380:U:C4	30:0:2748:G:C4	2.91	0.59
30:0:2065:C:O2'	30:0:2066:C:H5'	2.02	0.59
2:B:145:HIS:HD2	2:B:146:THR:O	1.85	0.59
4:D:159:PRO:O	4:D:163:VAL:HG23	2.02	0.59
11:K:41:LYS:HA	30:0:2582:G:O3'	2.03	0.59
16:P:7:LYS:HD3	16:P:21:VAL:HG22	1.85	0.59
18:R:39:THR:HG23	18:R:107:GLU:O	2.03	0.59
24:X:37:LEU:HD13	24:X:85:VAL:HG21	1.84	0.59
30:0:499:G:O2'	30:0:500:G:H5'	2.02	0.59
30:0:702:G:O2'	30:0:703:G:H5'	2.02	0.59
30:0:921:G:H4'	30:0:924:G:C6	2.37	0.59
30:0:1563:G:H4'	38:0:4215:HOH:O	2.01	0.59
30:0:1566:C:O2'	30:0:1567:G:H5'	2.03	0.59
30:0:1972:U:H2'	30:0:1973:A:H5"	1.83	0.59
31:9:54:A:C2	31:9:55:U:C2	2.91	0.59
6:F:30:LYS:HB2	6:F:97:ALA:HB3	1.84	0.59
10:J:69:TYR:CE1	30:0:2081:A:H4'	2.38	0.59
10:J:88:PRO:HD3	30:0:1104:C:H4'	1.85	0.59
13:M:137:ASN:ND2	30:0:145:A:H4'	2.18	0.59
30:0:255:A:H2'	30:0:256:C:H6	1.67	0.59
30:0:281:U:C2'	30:0:282:C:H5'	2.33	0.59
26:Z:40:ALA:HA	30:0:1773:G:C8	2.38	0.58
30:0:925:C:H3'	38:0:3826:HOH:O	2.02	0.58
30:0:1568:G:O2'	30:0:1569:U:H5'	2.03	0.58
30:0:2563:U:H2'	30:0:2565:C:O5'	2.02	0.58
30:0:2724:U:H2'	30:0:2725:G:O4'	2.03	0.58
30:0:2826:G:C6	30:0:2913:A:C6	2.90	0.58
2:B:243:ASN:HB3	38:0:6624:HOH:O	2.02	0.58
2:B:297:VAL:HB	38:B:9076:HOH:O	2.03	0.58
8:H:98:LEU:HD11	8:H:127:ALA:HB2	1.85	0.58
25:Y:169:ARG:HD3	30:0:1328:A:C8	2.38	0.58
29:3:47:GLY:HA2	30:0:2121:G:C4'	2.25	0.58
30:0:28:G:H1'	38:0:4650:HOH:O	2.03	0.58
30:0:1245:C:O5'	30:0:1245:C:H6	1.85	0.58
30:0:2825:C:H4'	30:0:2826:G:O5'	2.03	0.58
3:C:79:ARG:O	3:C:87:ARG:HG2	2.04	0.58
4:D:28:GLY:HA2	4:D:69:ILE:HG23	1.85	0.58
9:I:83:GLY:H	30:0:1168:C:H5"	1.68	0.58
12:L:145:LEU:HB2	38:L:8836:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:28:GLN:HA	13:M:31:TRP:HB2	1.85	0.58
26:Z:34:SER:HA	30:0:797:A:H4'	1.83	0.58
30:0:951:A:C2'	30:0:952:G:H5'	2.33	0.58
30:0:1158:G:O2'	30:0:1159:G:H5'	2.03	0.58
30:0:1187:U:H2'	38:0:6880:HOH:O	2.01	0.58
30:0:1290:G:H4'	38:0:7465:HOH:O	2.02	0.58
30:0:2467:A:H5"	38:0:4285:HOH:O	2.03	0.58
20:T:52:ARG:HD2	30:0:317:A:H5"	1.85	0.58
30:0:293:A:C4	30:0:360:A:C2	2.91	0.58
30:0:1186:C:H42	30:0:1190:G:H22	1.48	0.58
30:0:2590:U:H2'	30:0:2591:C:H5'	1.85	0.58
3:C:182:ARG:HH12	30:0:450:C:H3'	1.67	0.58
12:L:18:HIS:HD2	30:0:902:G:N7	2.01	0.58
25:Y:234:VAL:HG12	25:Y:235:GLU:H	1.66	0.58
30:0:204:A:H2'	30:0:205:U:H5'	1.85	0.58
30:0:1711:A:C2'	30:0:1712:A:H5'	2.33	0.58
30:0:2784:A:O5'	30:0:2784:A:H8	1.87	0.58
10:J:127:ILE:HG22	33:J:8801:CL:CL	2.40	0.58
26:Z:70:ARG:HB2	26:Z:81:CYS:SG	2.44	0.58
30:0:1520:G:C6	30:0:1521:C:C4	2.92	0.58
2:B:162:MET:HG3	2:B:310:ARG:HD3	1.84	0.58
5:E:100:ASP:HB3	38:E:2789:HOH:O	2.02	0.58
30:0:164:G:H3'	38:0:3636:HOH:O	2.03	0.58
30:0:271:C:N4	30:0:378:A:C2	2.66	0.58
30:0:368:C:C2'	30:0:369:G:H5'	2.34	0.58
30:0:1503:U:C2'	30:0:1504:A:H5'	2.34	0.58
31:9:39:U:H1'	31:9:44:A:N6	2.19	0.58
2:B:267:LYS:HA	38:B:8996:HOH:O	2.04	0.58
17:Q:11:ARG:NH2	30:0:2363:G:H5"	2.19	0.58
26:Z:42:TYR:HA	30:0:1829:A:N6	2.16	0.58
30:0:482:G:H4'	30:0:508:A:N1	2.19	0.58
30:0:951:A:O2'	30:0:952:G:H5'	2.03	0.58
30:0:1662:C:H2'	30:0:1663:G:O4'	2.03	0.58
30:0:2073:G:OP2	30:0:2490:A:H5'	2.03	0.58
30:0:2493:C:O2	30:0:2493:C:H2'	2.02	0.58
30:0:2505:G:H2'	30:0:2506:A:H5'	1.86	0.58
30:0:2624:A:H1'	38:0:9769:HOH:O	2.04	0.58
31:9:54:A:C2	31:9:55:U:N3	2.72	0.58
8:H:172:GLU:HB2	38:H:248:HOH:O	2.04	0.58
22:V:1:THR:HG23	22:V:2:VAL:H	1.69	0.58
30:0:412:C:O2'	30:0:413:G:H5'	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:544:G:H2'	30:0:545:G:H5"	1.85	0.58
30:0:625:U:H3'	38:0:3244:HOH:O	2.03	0.58
30:0:1585:C:H2'	30:0:1586:G:H8	1.68	0.58
30:0:1634:G:H2'	30:0:1635:U:C6	2.38	0.58
30:0:1973:A:H5'	30:0:1973:A:H8	1.69	0.58
30:0:2511:A:H2'	30:0:2512:U:O4'	2.03	0.58
30:0:2581:U:H1'	38:0:4452:HOH:O	2.03	0.58
30:0:51:G:O2'	30:0:52:A:H5'	2.03	0.58
30:0:1041:U:C2'	30:0:1042:U:H5'	2.34	0.58
30:0:1160:G:H5'	30:0:1161:A:H5'	0.78	0.58
30:0:1300:G:H1'	38:0:4652:HOH:O	2.03	0.58
30:0:2812:A:N7	38:0:7497:HOH:O	2.32	0.58
1:A:75:GLY:HA2	26:Z:88:PHE:HA	1.86	0.57
2:B:125:GLU:O	2:B:129:ARG:HG3	2.03	0.57
3:C:236:THR:CG2	3:C:239:ALA:H	2.16	0.57
4:D:76:ARG:CZ	31:9:44:A:H1'	2.34	0.57
11:K:20:CYS:SG	11:K:22:ASP:OD1	2.62	0.57
15:O:10:LEU:HD13	15:O:99:GLU:HG3	1.84	0.57
30:0:12:U:C2'	30:0:13:G:H5'	2.32	0.57
30:0:1057:A:H1'	30:0:2492:U:O2'	2.03	0.57
10:J:70:PHE:HE1	30:0:2676:C:H4'	1.68	0.57
20:T:111:ARG:HB3	20:T:119:ALA:HB2	1.85	0.57
30:0:820:G:H5'	30:0:821:U:H5'	1.86	0.57
30:0:2705:U:H2'	30:0:2706:A:H8	1.68	0.57
30:0:2748:G:H5'	38:0:7523:HOH:O	2.04	0.57
30:0:1166:A:H61	30:0:1180:U:H3	1.51	0.57
1:A:53:ALA:HB2	1:A:122:SER:OG	2.05	0.57
14:N:48:VAL:HG13	14:N:55:ASP:HB3	1.86	0.57
26:Z:90:GLY:HA3	26:Z:95:PRO:O	2.04	0.57
30:0:590:A:C2'	30:0:591:A:H5'	2.33	0.57
30:0:821:U:H3'	38:0:3764:HOH:O	2.03	0.57
30:0:1216:G:H2'	30:0:1217:G:O4'	2.03	0.57
30:0:1256:C:H6	38:0:7140:HOH:O	1.87	0.57
30:0:1342:C:C2'	30:0:1343:C:H5'	2.34	0.57
3:C:236:THR:HG22	3:C:239:ALA:N	2.15	0.57
20:T:18:GLU:O	20:T:21:LYS:HG2	2.03	0.57
30:0:283:U:H5	30:0:284:C:C4	2.22	0.57
30:0:916:A:C2	30:0:928:G:C4	2.93	0.57
30:0:1503:U:O2'	30:0:1504:A:H5'	2.04	0.57
30:0:2712:G:H5'	38:0:5187:HOH:O	2.02	0.57
11:K:14:LYS:CB	11:K:45:PRO:HG2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:51:LYS:HG3	29:3:52:PHE:CD2	2.40	0.57
30:0:694:A:H2'	30:0:695:C:C5'	2.27	0.57
30:0:727:G:H3'	30:0:728:C:H6	1.68	0.57
30:0:1552:G:H2'	30:0:1553:C:C6	2.40	0.57
30:0:1555:G:H4'	30:0:1630:A:H2	1.69	0.57
30:0:1883:U:C2'	30:0:1884:G:H5'	2.34	0.57
3:C:8:LEU:HD11	3:C:143:ASP:O	2.04	0.57
5:E:125:GLU:HB2	5:E:132:THR:HG23	1.86	0.57
30:0:544:G:C2'	30:0:545:G:H5"	2.35	0.57
30:0:1754:A:H5"	38:0:9757:HOH:O	2.04	0.57
30:0:1819:G:H2'	30:0:1820:G:H4'	1.85	0.57
30:0:2078:U:O2'	30:0:2079:G:H5'	2.05	0.57
30:0:2240:U:O2'	30:0:2241:C:H5'	2.04	0.57
30:0:2335:C:H2'	30:0:2336:G:H8	1.67	0.57
30:0:2828:G:O5'	30:0:2828:G:H8	1.87	0.57
3:C:127:ARG:HD3	3:C:129:HIS:HE1	1.70	0.57
21:U:56:ARG:HG3	21:U:56:ARG:NH1	2.19	0.57
24:X:43:VAL:HG22	24:X:76:ARG:NH1	2.20	0.57
30:0:1189:A:H1'	30:0:1209:C:C1'	2.35	0.57
30:0:1577:U:O2'	30:0:1578:C:H5'	2.05	0.57
30:0:2001:G:O2'	30:0:2002:C:H5'	2.04	0.57
1:A:153:ARG:HD3	38:A:9011:HOH:O	2.04	0.57
2:B:214:PRO:HD2	38:B:8989:HOH:O	2.05	0.57
5:E:153:ARG:NH1	30:0:2778:A:H1'	2.19	0.57
14:N:160:SER:CB	31:9:51:A:H5'	2.34	0.57
15:O:19:ARG:NH1	30:0:1276:U:H3'	2.19	0.57
18:R:68:HIS:O	30:0:2842:G:H5'	2.05	0.57
21:U:13:ILE:HG12	21:U:32:CYS:HB3	1.86	0.57
21:U:33:SER:O	21:U:37:GLU:HG3	2.04	0.57
25:Y:216:ARG:HD2	38:Y:8871:HOH:O	2.03	0.57
26:Z:45:VAL:HG13	26:Z:49:ARG:HE	1.70	0.57
30:0:138:U:OP2	30:0:139:C:C5	2.58	0.57
30:0:371:U:O2'	30:0:372:A:H5'	2.05	0.57
30:0:403:C:H3'	38:0:6286:HOH:O	2.05	0.57
30:0:1718:G:O2'	30:0:1719:G:H5'	2.04	0.57
30:0:2010:A:H2'	38:0:5933:HOH:O	2.03	0.57
1:A:190:ARG:HD2	30:0:1884:G:O6	2.03	0.57
2:B:41:PHE:CZ	2:B:79:MET:HG3	2.40	0.57
13:M:68:ARG:O	13:M:68:ARG:HD3	2.05	0.57
20:T:24:ARG:HH21	20:T:39:ASN:HD22	1.53	0.57
24:X:30:MET:HE1	24:X:55:ASN:HA	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1182:C:H1'	30:0:1192:A:H8	1.69	0.57
30:0:1971:G:H5'	38:0:7053:HOH:O	2.05	0.57
30:0:2407:G:O2'	30:0:2408:A:H5'	2.05	0.57
31:9:23:U:H2'	31:9:24:U:H4'	1.87	0.57
31:9:64:C:C2'	31:9:65:A:H5'	2.35	0.57
10:J:116:LEU:HB2	10:J:119:THR:HG21	1.87	0.56
30:0:10:U:C4	30:0:532:A:C8	2.94	0.56
30:0:312:U:O2'	30:0:313:U:H5'	2.05	0.56
30:0:407:A:H2'	30:0:408:A:C8	2.40	0.56
30:0:1079:A:OP2	30:0:1080:C:N4	2.36	0.56
30:0:2251:G:H2'	30:0:2252:A:H8	1.70	0.56
30:0:2769:C:C2'	30:0:2770:G:C5'	2.78	0.56
11:K:32:ILE:HD11	11:K:56:SER:HB2	1.86	0.56
13:M:82:ARG:HD2	30:0:170:U:OP2	2.05	0.56
30:0:1020:A:H2'	30:0:1021:G:C8	2.40	0.56
30:0:1173:A:H4'	30:0:1174:A:C8	2.40	0.56
30:0:2110:G:O2'	30:0:2111:G:H5'	2.05	0.56
30:0:2265:U:H2'	30:0:2266:A:C8	2.40	0.56
30:0:2698:G:H2'	30:0:2699:A:O4'	2.05	0.56
30:0:2700:G:H3'	38:0:3575:HOH:O	2.05	0.56
31:9:54:A:HO2'	31:9:55:U:H5'	1.67	0.56
11:K:98:VAL:HG13	11:K:102:GLU:HA	1.85	0.56
14:N:48:VAL:CG1	14:N:55:ASP:HB3	2.35	0.56
14:N:141:ARG:NH2	31:9:48:C:H4'	2.21	0.56
23:W:38:THR:O	23:W:42:ARG:HB2	2.04	0.56
28:2:40:ARG:HG3	28:2:45:ASN:HB2	1.85	0.56
29:3:34:LYS:HB3	38:3:9001:HOH:O	2.05	0.56
30:0:280:C:H2'	30:0:281:U:O4'	2.06	0.56
30:0:695:C:O2'	30:0:696:C:H5'	2.04	0.56
30:0:947:U:O2'	30:0:948:G:H5'	2.05	0.56
30:0:1183:C:N4	30:0:1184:C:H41	2.03	0.56
30:0:1616:A:H5"	30:0:1617:C:OP1	2.05	0.56
30:0:1928:C:H2'	30:0:1929:G:O4'	2.05	0.56
30:0:1948:G:O2'	30:0:1949:G:H5'	2.05	0.56
30:0:2011:A:H5'	30:0:2013:G:H1'	1.87	0.56
2:B:17:LYS:O	2:B:260:HIS:HD2	1.88	0.56
8:H:49:GLN:NE2	8:H:140:TYR:HE2	1.95	0.56
13:M:171:ARG:NH2	30:0:189:A:OP1	2.38	0.56
15:O:24:ALA:HB3	30:0:710:G:OP1	2.05	0.56
17:Q:45:PRO:O	30:0:2365:G:H4'	2.06	0.56
30:0:162:C:H2'	30:0:163:U:H5'	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1735:C:H2'	30:0:1736:A:C8	2.40	0.56
30:0:2659:U:H3'	38:0:4379:HOH:O	2.05	0.56
31:9:33:U:H2'	38:9:9068:HOH:O	2.04	0.56
13:M:68:ARG:HG3	30:0:1469:C:OP1	2.05	0.56
30:0:26:U:H5	38:0:3099:HOH:O	1.89	0.56
30:0:1904:A:H2'	30:0:1905:U:O4'	2.05	0.56
30:0:2064:U:H4'	30:0:2653:A:OP1	2.05	0.56
30:0:2289:G:O2'	30:0:2290:U:H5'	2.06	0.56
30:0:2349:G:H2'	30:0:2350:G:C8	2.38	0.56
2:B:223:ARG:HD3	33:B:8819:CL:CL	2.43	0.56
29:3:65:THR:HG23	33:3:8804:CL:CL	2.43	0.56
30:0:113:A:OP2	30:0:114:A:H2'	2.06	0.56
30:0:473:A:O2'	30:0:474:C:H5'	2.06	0.56
30:0:799:C:O2'	30:0:800:G:H5'	2.05	0.56
30:0:1042:U:O2'	30:0:1043:C:H5'	2.05	0.56
30:0:1434:A:O2'	30:0:1435:U:H2'	2.05	0.56
30:0:2502:C:H2'	30:0:2503:A:C5'	2.34	0.56
2:B:199:TYR:HE2	2:B:268:ARG:HB2	1.71	0.56
12:L:27:ARG:NH2	12:L:30:ARG:HD3	2.21	0.56
16:P:127:GLY:HA3	38:P:152:HOH:O	2.05	0.56
25:Y:165:GLU:HB3	38:0:6689:HOH:O	2.05	0.56
26:Z:34:SER:HA	30:0:797:A:C4'	2.36	0.56
29:3:18:GLN:HB3	38:3:9013:HOH:O	2.06	0.56
30:0:138:U:OP2	30:0:139:C:H5	1.88	0.56
30:0:1127:C:C5	30:0:1128:U:C4	2.94	0.56
30:0:2595:U:O2'	30:0:2596:A:H5'	2.05	0.56
31:9:54:A:H2'	31:9:55:U:H5'	1.82	0.56
1:A:27:LEU:HD21	1:A:55:VAL:HG21	1.88	0.56
3:C:4:THR:HA	3:C:15:GLU:HB3	1.88	0.56
13:M:24:GLN:HE22	13:M:27:ARG:HH11	1.53	0.56
13:M:94:ARG:HD2	30:0:158:A:OP2	2.06	0.56
21:U:44:ARG:HD3	21:U:49:LEU:CD1	2.35	0.56
21:U:56:ARG:HD2	30:0:2890:A:H1'	1.87	0.56
27:1:28:HIS:HE1	30:0:776:A:OP1	1.88	0.56
30:0:473:A:O2'	30:0:890:C:H5'	2.05	0.56
30:0:1292:G:HO2'	30:0:1293:U:H6	1.52	0.56
30:0:2241:C:O2'	30:0:2242:U:H5'	2.05	0.56
30:0:2514:U:OP1	30:0:2572:G:H1'	2.04	0.56
15:O:47:ARG:HH11	15:O:47:ARG:HG3	1.71	0.56
30:0:1679:C:H5'	38:0:9332:HOH:O	2.06	0.56
30:0:1788:U:C2	30:0:1805:G:N2	2.73	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2673:U:C4	30:0:2674:G:C6	2.94	0.56
31:9:18:U:H2'	31:9:19:G:H8	1.71	0.56
2:B:68:THR:HG21	21:U:16:GLY:HA3	1.87	0.56
3:C:174:ILE:HD11	30:0:338:C:H4'	1.89	0.56
12:L:41:HIS:HD2	30:0:926:A:O2'	1.89	0.56
21:U:23:HIS:CD2	21:U:27:ALA:HB3	2.40	0.56
25:Y:142:SER:HB2	38:Y:8902:HOH:O	2.05	0.56
30:0:660:A:H4'	30:0:661:G:O5'	2.06	0.56
30:0:1020:A:H2'	30:0:1021:G:H8	1.71	0.56
30:0:1181:A:H2'	30:0:1182:C:O4'	2.06	0.56
30:0:2314:G:H2'	30:0:2315:C:H5'	1.87	0.56
30:0:2578:G:H5'	30:0:2578:G:C8	2.36	0.56
30:0:2911:C:H2'	30:0:2912:C:C6	2.42	0.56
31:9:49:G:H2'	31:9:50:G:O4'	2.06	0.56
1:A:47:HIS:HD2	30:0:1654:U:C2'	2.18	0.55
30:0:558:C:C2'	30:0:559:U:C5'	2.68	0.55
30:0:1116:U:H3	30:0:1246:A:N6	1.96	0.55
30:0:1878:G:C1'	38:0:6097:HOH:O	2.53	0.55
5:E:49:ILE:HD11	5:E:69:ILE:HD12	1.88	0.55
25:Y:99:ALA:HB2	25:Y:233:TYR:CZ	2.42	0.55
29:3:33:MET:HG2	30:0:1922:A:H2'	1.88	0.55
30:0:339:A:H2'	38:0:4203:HOH:O	2.06	0.55
30:0:684:G:H5"	38:0:4053:HOH:O	2.06	0.55
30:0:858:U:H2'	30:0:859:C:H6	1.71	0.55
30:0:1613:C:H2'	30:0:1614:G:O4'	2.06	0.55
30:0:2271:G:N3	30:0:2271:G:H2'	2.20	0.55
30:0:2325:U:O2'	30:0:2411:C:H1'	2.06	0.55
30:0:2852:A:H5"	38:0:5199:HOH:O	2.05	0.55
3:C:115:LEU:HD21	3:C:243:VAL:HG13	1.86	0.55
23:W:52:VAL:HG22	23:W:53:ALA:N	2.20	0.55
30:0:735:C:C6	30:0:736:A:C8	2.94	0.55
30:0:1165:G:H21	30:0:1173:A:H5"	1.72	0.55
30:0:1172:G:H1'	38:0:4940:HOH:O	2.05	0.55
30:0:1183:C:H41	30:0:1192:A:H5'	1.72	0.55
30:0:1512:G:O2'	30:0:1513:C:H5'	2.05	0.55
30:0:2113:G:C6	30:0:2114:C:C4	2.94	0.55
3:C:1:MET:HG2	3:C:2:GLN:H	1.72	0.55
25:Y:210:GLY:HA2	38:0:5285:HOH:O	2.06	0.55
26:Z:44:ARG:HB2	30:0:1886:A:O2'	2.05	0.55
30:0:913:A:H8	30:0:913:A:O5'	1.90	0.55
30:0:920:C:H5'	30:0:921:G:C4	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2668:G:H2'	30:0:2669:U:C6	2.42	0.55
2:B:229:ARG:NH2	30:0:1753:C:O2	2.39	0.55
3:C:21:VAL:HG13	38:C:8594:HOH:O	2.05	0.55
7:G:16:LYS:HE2	7:G:63:ARG:NH1	2.21	0.55
24:X:76:ARG:HH11	24:X:76:ARG:HG3	1.72	0.55
29:3:59:ASP:HB3	29:3:63:LYS:HZ3	1.72	0.55
30:0:310:U:H2'	30:0:311:C:C6	2.41	0.55
30:0:1625:U:C6	30:0:1625:U:C3'	2.85	0.55
30:0:2250:G:N2	30:0:2251:G:H1'	2.21	0.55
3:C:149:LYS:HB2	3:C:152:GLU:HG3	1.89	0.55
3:C:162:VAL:HG22	3:C:232:LEU:HD21	1.87	0.55
10:J:19:MET:HE1	10:J:132:LEU:HD21	1.87	0.55
38:Y:8879:HOH:O	30:0:1355:A:H5"	2.06	0.55
26:Z:63:CYS:SG	26:Z:81:CYS:CB	2.94	0.55
29:3:47:GLY:CA	30:0:2121:G:H4'	2.29	0.55
30:0:956:G:H3'	38:0:9387:HOH:O	2.06	0.55
30:0:1562:C:N4	38:0:5836:HOH:O	2.38	0.55
30:0:1909:A:H2'	30:0:1910:A:C8	2.42	0.55
2:B:36:PRO:HA	2:B:168:GLY:CA	2.36	0.55
23:W:119:HIS:HD2	23:W:120:PRO:O	1.89	0.55
30:0:212:A:O4'	30:0:214:U:C6	2.59	0.55
30:0:545:G:C8	30:0:545:G:C5'	2.81	0.55
30:0:571:C:O5'	30:0:571:C:H6	1.90	0.55
30:0:822:C:C2	30:0:823:U:C5	2.94	0.55
30:0:835:U:H3'	38:0:9381:HOH:O	2.06	0.55
30:0:1691:A:H5"	38:0:3140:HOH:O	2.06	0.55
30:0:1736:A:H1'	38:0:7566:HOH:O	2.07	0.55
2:B:102:THR:HG21	2:B:182:VAL:O	2.07	0.55
4:D:140:ARG:HH11	4:D:140:ARG:HG3	1.72	0.55
13:M:111:ASN:HB2	38:M:8852:HOH:O	2.07	0.55
29:3:90:PHE:N	29:3:90:PHE:CD1	2.75	0.55
30:0:401:C:H2'	30:0:402:U:H6	1.72	0.55
30:0:696:C:HO2'	30:0:697:G:H5'	1.71	0.55
30:0:2274:A:H2'	30:0:2275:G:C8	2.42	0.55
30:0:2868:C:H1'	38:0:7107:HOH:O	2.07	0.55
31:9:59:C:C2	31:9:60:C:C5	2.94	0.55
5:E:132:THR:HB	38:E:2227:HOH:O	2.06	0.55
13:M:70:GLY:CA	30:0:2263:G:H4'	2.37	0.55
19:S:37:VAL:O	19:S:41:VAL:HG23	2.05	0.55
28:2:43:ARG:HH22	30:0:1684:A:C1'	2.16	0.55
30:0:130:C:O2'	30:0:131:A:N7	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:291:C:H2'	30:0:292:G:O4'	2.07	0.55
30:0:1156:C:O2'	30:0:1157:C:H5'	2.07	0.55
30:0:1166:A:C6	30:0:1181:A:C2	2.95	0.55
30:0:1175:G:H2'	30:0:1176:C:C6	2.42	0.55
30:0:1200:A:N1	30:0:1201:C:C2	2.75	0.55
5:E:53:GLU:HB3	5:E:55:ASN:ND2	2.21	0.55
5:E:118:ILE:HG23	5:E:144:THR:HG21	1.89	0.55
30:0:777:U:OP2	30:0:777:U:H4'	2.07	0.55
30:0:1849:G:H1'	30:0:2011:A:N1	2.22	0.55
30:0:1905:U:H2'	30:0:1906:C:H6	1.72	0.55
30:0:2584:G:H4'	38:0:7102:HOH:O	2.07	0.55
30:0:2689:A:C2'	30:0:2690:U:H5'	2.37	0.55
30:0:2790:C:HO2'	30:0:2791:U:H6	1.55	0.55
1:A:76:VAL:HG23	26:Z:87:LYS:HB3	1.88	0.54
3:C:2:GLN:HB3	38:C:8581:HOH:O	2.07	0.54
3:C:132:ASP:HB2	3:C:161:ASP:HB3	1.89	0.54
14:N:110:THR:HB	14:N:113:SER:OG	2.07	0.54
30:0:690:G:H4'	30:0:741:C:O2	2.06	0.54
30:0:820:G:H5'	30:0:821:U:C5'	2.37	0.54
30:0:941:G:C5	30:0:942:U:C4	2.95	0.54
30:0:1377:C:H6	30:0:1377:C:C5'	2.20	0.54
30:0:1903:U:O2'	30:0:1904:A:N7	2.40	0.54
30:0:1909:A:N1	30:0:2128:G:H1'	2.22	0.54
30:0:2782:G:N2	30:0:2783:A:N6	2.55	0.54
2:B:232:TRP:CZ3	30:0:2614:C:H5"	2.41	0.54
4:D:146:LYS:NZ	14:N:107:ASN:HD21	2.05	0.54
5:E:108:LEU:HD11	5:E:164:ASP:HB2	1.88	0.54
29:3:12:PRO:HG2	29:3:13:HIS:HD2	1.71	0.54
30:0:363:C:O2'	30:0:364:U:H5'	2.07	0.54
30:0:814:G:H2'	30:0:815:U:O4'	2.07	0.54
30:0:960:G:H8	38:0:5945:HOH:O	1.89	0.54
30:0:1593:C:H1'	38:0:6083:HOH:O	2.06	0.54
31:9:58:G:N7	31:9:59:C:C4	2.75	0.54
2:B:41:PHE:CE1	2:B:79:MET:HG3	2.43	0.54
2:B:140:LEU:HA	38:B:9051:HOH:O	2.05	0.54
9:I:78:ALA:HB2	9:I:95:LEU:HD21	1.89	0.54
14:N:114:LYS:O	14:N:118:ILE:HG13	2.07	0.54
14:N:130:PRO:HA	38:N:8837:HOH:O	2.06	0.54
27:1:28:HIS:HD2	27:1:30:LYS:H	1.53	0.54
30:0:1015:C:H4'	38:0:6566:HOH:O	2.06	0.54
30:0:1175:G:H4'	38:0:6842:HOH:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2032:U:C2'	30:0:2033:G:C5'	2.86	0.54
30:0:2032:U:C2'	30:0:2033:G:H5"	2.38	0.54
30:0:2524:G:H21	30:0:2526:C:H41	1.55	0.54
30:0:2869:G:H5'	38:0:5457:HOH:O	2.07	0.54
5:E:85:GLU:HG2	5:E:130:GLU:HG2	1.89	0.54
6:F:2:VAL:HG22	6:F:57:GLU:OE1	2.08	0.54
13:M:59:GLY:HA3	13:M:141:ILE:HD12	1.90	0.54
30:0:1447:U:OP1	30:0:1506:U:N3	2.39	0.54
30:0:1876:C:H4'	30:0:1877:G:OP2	2.08	0.54
30:0:2281:C:C2'	30:0:2282:U:H5'	2.38	0.54
31:9:27:C:H2'	31:9:28:U:O4'	2.08	0.54
1:A:192:VAL:CG1	1:A:207:GLN:HB3	2.38	0.54
1:A:223:ARG:NH1	30:0:2270:G:H4'	2.22	0.54
9:I:87:PRO:HD2	30:0:1180:U:H1'	1.89	0.54
9:I:91:PHE:CD2	9:I:131:GLY:HA2	2.42	0.54
12:L:143:THR:HG22	12:L:144:ASP:N	2.22	0.54
13:M:99:ARG:HE	13:M:170:ASN:ND2	1.96	0.54
15:O:19:ARG:HH22	30:0:1278:A:P	2.31	0.54
30:0:1139:U:H2'	30:0:1140:C:H6	1.72	0.54
30:0:2477:C:O2'	30:0:2478:U:H5'	2.07	0.54
31:9:36:C:C5	31:9:37:C:C5	2.96	0.54
1:A:195:ASN:ND2	30:0:877:G:C8	2.76	0.54
12:L:67:ARG:O	12:L:71:GLU:HG3	2.08	0.54
29:3:60:LYS:HB3	29:3:62:THR:O	2.07	0.54
30:0:236:A:H4'	30:0:237:G:OP1	2.08	0.54
30:0:312:U:C2	30:0:320:G:N2	2.76	0.54
30:0:710:G:O2'	30:0:711:G:H5'	2.08	0.54
30:0:963:C:O2	30:0:1005:A:N1	2.40	0.54
30:0:1697:G:H5'	38:0:5475:HOH:O	2.08	0.54
30:0:2081:A:H2'	30:0:2082:G:O4'	2.08	0.54
30:0:2107:U:O2'	30:0:2108:A:H5'	2.07	0.54
30:0:2321:A:C4	30:0:2323:G:C8	2.95	0.54
30:0:2831:C:H3'	38:0:7197:HOH:O	2.07	0.54
16:P:35:ILE:HD13	38:P:171:HOH:O	2.08	0.54
17:Q:19:ARG:HH21	31:9:11:A:P	2.30	0.54
30:0:461:C:N3	30:0:479:G:H5'	2.22	0.54
30:0:623:U:O2'	30:0:624:U:H5'	2.08	0.54
30:0:661:G:C5	30:0:686:A:C2	2.96	0.54
30:0:706:G:HO2'	30:0:707:C:H6	1.53	0.54
30:0:960:G:N3	30:0:960:G:C3'	2.71	0.54
30:0:1617:C:C5	30:0:1643:C:H4'	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2078:U:H2'	30:0:2079:G:C8	2.42	0.54
30:0:2892:G:C5	30:0:2893:C:C5	2.95	0.54
2:B:62:ARG:HA	2:B:65:MET:HE3	1.88	0.54
4:D:135:VAL:HG21	4:D:139:TYR:CD1	2.43	0.54
5:E:116:THR:HG22	5:E:151:LEU:HD22	1.90	0.54
18:R:99:ALA:HB1	18:R:109:MET:CE	2.37	0.54
27:1:16:HIS:HD2	30:0:470:U:O2'	1.91	0.54
30:0:1175:G:H1'	30:0:1193:A:H2'	1.89	0.54
30:0:1676:G:H1'	38:0:9441:HOH:O	2.08	0.54
30:0:1850:U:H2'	30:0:1851:G:H8	1.73	0.54
30:0:2045:G:H5"	38:0:7204:HOH:O	2.06	0.54
30:0:2256:G:O2'	30:0:2257:G:H5'	2.08	0.54
30:0:2670:G:O2'	30:0:2671:U:H5'	2.08	0.54
31:9:30:C:O2	31:9:30:C:H2'	2.08	0.54
13:M:164:THR:CG2	13:M:165:GLY:N	2.70	0.54
15:O:19:ARG:HH11	30:0:1276:U:H3'	1.73	0.54
30:0:334:G:C4	30:0:335:U:C6	2.96	0.54
30:0:1625:U:H5"	38:0:5995:HOH:O	2.07	0.54
30:0:2487:C:H5	38:0:4858:HOH:O	1.91	0.54
30:0:2787:C:H5	38:0:4605:HOH:O	1.90	0.54
30:0:2908:A:O5'	30:0:2908:A:H8	1.91	0.54
28:2:13:LYS:O	28:2:17:GLN:HG3	2.07	0.54
30:0:541:C:C2'	30:0:542:A:C5'	2.78	0.54
30:0:853:C:H2'	30:0:854:G:O4'	2.08	0.54
30:0:2831:C:H2'	30:0:2832:C:C5'	2.38	0.54
31:9:23:U:C2'	31:9:24:U:H4'	2.38	0.54
1:A:179:MET:HG2	1:A:186:TRP:HB2	1.91	0.53
2:B:238:ASN:ND2	2:B:240:GLY:H	1.92	0.53
8:H:99:ARG:NH1	30:0:1055:G:OP2	2.41	0.53
14:N:132:ASN:HD22	30:0:2413:A:H4'	1.72	0.53
25:Y:97:LEU:HA	25:Y:234:VAL:O	2.08	0.53
30:0:30:U:H5"	38:0:5777:HOH:O	2.08	0.53
30:0:338:C:H5"	38:0:3793:HOH:O	2.07	0.53
30:0:354:A:H2'	30:0:355:C:H6	1.73	0.53
30:0:1453:G:H2'	30:0:1454:U:O4'	2.07	0.53
30:0:1525:G:H5'	30:0:1526:A:OP2	2.08	0.53
30:0:2106:C:H2'	30:0:2107:U:C6	2.43	0.53
30:0:2599:A:H5"	38:0:3367:HOH:O	2.08	0.53
9:I:111:LEU:HD23	30:0:1163:G:H4'	1.90	0.53
15:O:105:ASN:HD21	15:O:109:SER:H	1.56	0.53
16:P:7:LYS:HD3	16:P:21:VAL:CG2	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1268:C:H2'	30:0:1269:G:H8	1.73	0.53
30:0:2321:A:C5	30:0:2323:G:C8	2.96	0.53
30:0:2379:G:N3	30:0:2418:G:H2'	2.22	0.53
30:0:2553:A:H2'	30:0:2553:A:N3	2.23	0.53
30:0:2563:U:O2'	30:0:2564:G:H3'	2.08	0.53
30:0:2769:C:H2'	30:0:2770:G:C4'	2.37	0.53
1:A:33:GLU:O	1:A:34:ASP:HB2	2.08	0.53
2:B:212:GLN:HA	30:0:1733:A:H4'	1.89	0.53
18:R:25:PHE:HB3	38:R:8914:HOH:O	2.07	0.53
23:W:35:VAL:HG23	23:W:41:TYR:CD2	2.43	0.53
30:0:421:C:H2'	30:0:422:G:H8	1.74	0.53
30:0:1226:G:C4	30:0:1227:C:C5	2.96	0.53
30:0:1311:G:C2	30:0:1312:G:C8	2.97	0.53
30:0:2465:A:H5'	38:0:6910:HOH:O	2.07	0.53
31:9:73:A:H61	31:9:108:C:H42	1.57	0.53
1:A:20:SER:HB3	30:0:1872:C:C5	2.44	0.53
12:L:11:ARG:O	30:0:903:U:C2	2.61	0.53
23:W:5:VAL:HG22	23:W:32:CYS:HB2	1.91	0.53
30:0:491:C:O2'	30:0:492:C:H5'	2.09	0.53
30:0:869:G:C8	30:0:869:G:OP2	2.62	0.53
30:0:1754:A:H2'	30:0:1755:A:O4'	2.09	0.53
30:0:2703:A:H2'	30:0:2704:C:C6	2.40	0.53
31:9:114:G:H2'	31:9:115:C:C6	2.43	0.53
8:H:49:GLN:HG3	8:H:140:TYR:CE2	2.43	0.53
16:P:71:TYR:CE2	30:0:1790:C:H5	2.26	0.53
30:0:213:G:H22	30:0:225:G:H2'	1.72	0.53
30:0:549:A:C2	30:0:550:C:C2	2.97	0.53
30:0:597:A:O2'	30:0:598:C:H5'	2.08	0.53
30:0:718:C:O2	30:0:718:C:C2'	2.55	0.53
30:0:1271:A:H2'	30:0:1272:C:C6	2.43	0.53
30:0:1741:U:C4	30:0:2033:G:C8	2.96	0.53
30:0:1762:C:O2'	30:0:1763:C:H5'	2.08	0.53
30:0:2119:C:C2'	30:0:2120:U:H5'	2.38	0.53
30:0:2831:C:C2	30:0:2910:A:C2	2.96	0.53
30:0:2895:C:H2'	38:0:9579:HOH:O	2.08	0.53
8:H:69:ARG:HD3	38:H:239:HOH:O	2.08	0.53
11:K:89:LYS:HA	38:K:7064:HOH:O	2.08	0.53
21:U:56:ARG:CD	30:0:2890:A:H1'	2.38	0.53
29:3:68:LYS:HZ1	30:0:2436:U:H5'	1.73	0.53
30:0:466:A:H2'	30:0:467:G:O4'	2.08	0.53
30:0:535:G:C5	30:0:2063:U:C4	2.96	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1278:A:C4'	30:0:1279:U:C4	2.74	0.53
30:0:2078:U:H2'	30:0:2079:G:H8	1.74	0.53
30:0:2321:A:H2'	30:0:2321:A:N3	2.24	0.53
30:0:2501:G:H1	30:0:2519:C:H42	1.56	0.53
31:9:58:G:C8	31:9:59:C:C5	2.97	0.53
2:B:305:ASP:O	2:B:306:LYS:HB2	2.09	0.53
14:N:11:ARG:HG3	14:N:14:ARG:NH1	2.23	0.53
29:3:31:THR:O	30:0:1923:G:H4'	2.09	0.53
30:0:195:C:H2'	30:0:196:G:H5'	1.91	0.53
30:0:398:U:H2'	30:0:399:C:C6	2.44	0.53
30:0:561:G:N3	30:0:562:A:C8	2.77	0.53
30:0:1706:G:C6	30:0:1707:G:C6	2.97	0.53
30:0:1806:G:C5	30:0:1807:U:C5	2.97	0.53
30:0:1819:G:H5'	38:0:5785:HOH:O	2.07	0.53
30:0:1972:U:O2'	30:0:1973:A:H5"	2.09	0.53
30:0:2321:A:H4'	30:0:2322:U:OP1	2.08	0.53
1:A:164:ARG:HB3	1:A:164:ARG:HH11	1.73	0.53
1:A:199:HIS:HD2	1:A:201:PHE:N	2.00	0.53
2:B:141:ARG:HD2	2:B:163:GLU:OE2	2.08	0.53
10:J:39:VAL:HG22	10:J:107:ASN:HA	1.91	0.53
11:K:41:LYS:O	11:K:42:ASN:HB2	2.09	0.53
13:M:179:GLY:O	30:0:399:C:H5'	2.08	0.53
13:M:187:LEU:CD2	13:M:194:GLY:HA3	2.38	0.53
14:N:154:LEU:C	14:N:156:GLU:H	2.11	0.53
22:V:44:GLY:O	22:V:48:GLU:HG2	2.08	0.53
23:W:154:ARG:NH1	30:0:588:G:O6	2.40	0.53
25:Y:154:ARG:NH2	30:0:1071:G:H4'	2.23	0.53
30:0:69:A:H2'	30:0:70:A:OP2	2.09	0.53
30:0:191:A:H61	30:0:435:A:N6	2.06	0.53
30:0:424:C:H2'	30:0:425:U:C6	2.44	0.53
30:0:735:C:C5	30:0:736:A:C5	2.97	0.53
30:0:1167:G:H2'	30:0:1168:C:H6	1.71	0.53
30:0:1769:C:O2'	30:0:1770:U:H5'	2.09	0.53
30:0:2250:G:C2	30:0:2251:G:H1'	2.44	0.53
30:0:2613:G:O2'	30:0:2614:C:H5'	2.09	0.53
30:0:2864:U:C2'	30:0:2865:G:H5'	2.38	0.53
2:B:62:ARG:HA	2:B:65:MET:CE	2.38	0.53
8:H:6:ALA:HA	8:H:61:ARG:HH12	1.74	0.53
10:J:41:ALA:HB3	38:J:8863:HOH:O	2.09	0.53
16:P:115:SER:OG	16:P:118:GLN:HG3	2.08	0.53
30:0:334:G:H2'	30:0:335:U:O4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1158:G:C2'	30:0:1159:G:H5'	2.39	0.53
30:0:1913:C:H2'	30:0:1914:C:H6	1.73	0.53
30:0:1922:A:N1	30:0:2449:G:O2'	2.38	0.53
30:0:1968:A:H2'	30:0:1969:A:C8	2.44	0.53
30:0:2336:G:H2'	38:0:6275:HOH:O	2.09	0.53
9:I:108:HIS:H	9:I:109:PRO:HD2	1.74	0.53
14:N:38:LYS:HE2	14:N:107:ASN:ND2	2.24	0.53
30:0:74:G:H1	30:0:103:C:H42	1.55	0.53
30:0:1844:C:O2'	30:0:1845:A:H5'	2.08	0.53
30:0:2642:G:H2'	30:0:2643:G:O4'	2.09	0.53
1:A:45:ILE:HG22	26:Z:78:ILE:HG12	1.89	0.52
1:A:105:VAL:HG13	1:A:155:THR:O	2.09	0.52
8:H:26:ILE:HA	8:H:123:ILE:HG21	1.91	0.52
8:H:159:LYS:HG2	30:0:2519:C:O2	2.09	0.52
30:0:216:A:O2'	30:0:217:C:H5'	2.09	0.52
30:0:488:U:H2'	38:0:3993:HOH:O	2.08	0.52
30:0:1014:A:H2'	30:0:1015:C:H5'	1.90	0.52
30:0:1188:A:C6	30:0:1189:A:C6	2.97	0.52
30:0:1244:U:H4'	30:0:1246:A:O4'	2.09	0.52
30:0:1451:C:H5'	30:0:1505:U:C5	2.44	0.52
30:0:2037:C:H3'	38:0:6684:HOH:O	2.09	0.52
30:0:2719:A:H2'	30:0:2720:C:H5'	1.90	0.52
31:9:20:G:O2'	31:9:21:G:H5'	2.09	0.52
31:9:37:C:O2	31:9:47:A:H1'	2.09	0.52
31:9:58:G:C6	31:9:59:C:C2	2.97	0.52
15:O:25:VAL:HG13	30:0:709:G:O3'	2.10	0.52
23:W:4:LEU:HD22	23:W:54:PHE:HB3	1.90	0.52
30:0:675:U:H2'	30:0:676:C:H5'	1.90	0.52
30:0:1164:U:H5	38:0:6024:HOH:O	1.91	0.52
3:C:43:LYS:HG2	30:0:449:A:N7	2.24	0.52
5:E:126:ILE:HA	5:E:131:LEU:HD23	1.91	0.52
13:M:24:GLN:NE2	13:M:27:ARG:HH11	2.07	0.52
13:M:73:ARG:HH21	30:0:2263:G:H5"	1.70	0.52
19:S:33:SER:O	19:S:37:VAL:HG23	2.10	0.52
30:0:125:U:H2'	38:0:3760:HOH:O	2.10	0.52
30:0:271:C:C2	30:0:273:G:O4'	2.61	0.52
30:0:622:G:O2'	30:0:623:U:H5'	2.10	0.52
30:0:1515:A:H2'	30:0:1516:U:C6	2.44	0.52
30:0:1557:G:O2'	30:0:1558:C:H5'	2.09	0.52
30:0:1684:A:O2'	30:0:1685:A:H5"	2.10	0.52
30:0:2901:C:H6	30:0:2901:C:O5'	1.93	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:1:U:C4'	31:9:3:A:OP1	2.58	0.52
11:K:66:ARG:HH12	30:0:1992:U:H3'	1.75	0.52
20:T:26:THR:HG23	20:T:97:ARG:HG3	1.90	0.52
23:W:130:HIS:NE2	31:9:88:G:OP1	2.42	0.52
28:2:49:GLU:HB2	38:2:131:HOH:O	2.08	0.52
30:0:24:G:N2	30:0:518:G:H1'	2.24	0.52
30:0:40:C:O5'	30:0:40:C:H6	1.93	0.52
30:0:249:G:N2	30:0:250:C:C2	2.77	0.52
30:0:1359:U:O5'	30:0:1360:C:H5"	2.10	0.52
30:0:1664:A:H8	30:0:1664:A:OP1	1.92	0.52
30:0:1865:A:H2'	30:0:1866:A:C8	2.44	0.52
30:0:2320:U:H4'	30:0:2321:A:O4'	2.09	0.52
30:0:2407:G:H2'	30:0:2408:A:O4'	2.09	0.52
30:0:2783:A:O2'	30:0:2784:A:H5'	2.09	0.52
31:9:38:A:C2	31:9:39:U:C4	2.97	0.52
2:B:226:LYS:HG2	2:B:230:GLN:NE2	2.25	0.52
6:F:53:ASP:OD1	6:F:80:GLN:HB2	2.10	0.52
13:M:81:ARG:HB3	13:M:86:GLN:HG2	1.91	0.52
14:N:55:ASP:OD2	31:9:7:G:H4'	2.09	0.52
29:3:68:LYS:HG2	29:3:77:ALA:HB3	1.91	0.52
30:0:204:A:C2'	30:0:205:U:H5'	2.39	0.52
30:0:916:A:C2	30:0:928:G:N3	2.78	0.52
30:0:1590:A:C2	30:0:1606:A:H1'	2.44	0.52
1:A:66:ARG:HH11	1:A:66:ARG:HB2	1.74	0.52
4:D:18:ILE:HD13	4:D:84:LEU:HD12	1.91	0.52
5:E:153:ARG:HH12	30:0:2778:A:C1'	2.22	0.52
18:R:111:ILE:HG23	18:R:145:LEU:HD11	1.90	0.52
18:R:132:ARG:HH22	30:0:2055:A:H4'	1.74	0.52
20:T:106:GLU:HG3	38:T:4913:HOH:O	2.09	0.52
30:0:1087:G:O2'	33:0:8822:CL:CL	2.55	0.52
30:0:1139:U:H2'	30:0:1140:C:C6	2.45	0.52
30:0:1180:U:O2'	30:0:1181:A:H5'	2.10	0.52
30:0:1641:A:C2'	30:0:1642:A:H5'	2.40	0.52
30:0:1649:G:H1'	38:0:5498:HOH:O	2.09	0.52
31:9:49:G:O2'	31:9:50:G:H5'	2.08	0.52
2:B:223:ARG:HG3	2:B:232:TRP:O	2.10	0.52
25:Y:132:ASP:OD2	30:0:621:C:H5'	2.10	0.52
28:2:18:ASN:HD21	28:2:40:ARG:HB3	1.74	0.52
30:0:228:C:C2'	30:0:229:G:H5'	2.40	0.52
30:0:1052:G:H2'	30:0:1052:G:N3	2.24	0.52
30:0:1886:A:H4'	38:0:9333:HOH:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1890:U:H4'	30:0:2010:A:C6	2.44	0.52
30:0:1930:A:H2'	30:0:1931:A:C8	2.44	0.52
30:0:2041:G:O2'	30:0:2042:U:H5'	2.10	0.52
30:0:2526:C:C3'	30:0:2526:C:C6	2.93	0.52
31:9:58:G:C5	31:9:59:C:C2	2.98	0.52
38:I:1549:HOH:O	30:0:1180:U:H1'	2.10	0.52
18:R:18:LEU:HB2	18:R:143:VAL:HG13	1.91	0.52
27:1:11:LYS:HG2	30:0:777:U:O2'	2.10	0.52
30:0:506:G:N2	30:0:509:A:H5"	2.18	0.52
30:0:595:U:H3'	38:0:6474:HOH:O	2.09	0.52
30:0:734:U:O2'	30:0:736:A:N7	2.33	0.52
30:0:800:G:H2'	30:0:801:U:C6	2.45	0.52
30:0:2637:A:C5'	38:0:4897:HOH:O	2.55	0.52
30:0:2651:C:H2'	30:0:2652:U:O4'	2.10	0.52
31:9:34:A:H2'	31:9:35:C:O4'	2.10	0.52
2:B:243:ASN:HB2	30:0:2607:U:OP2	2.10	0.52
6:F:91:VAL:HG12	6:F:92:GLY:N	2.20	0.52
7:G:63:ARG:O	7:G:67:LEU:HG	2.10	0.52
12:L:73:VAL:HG23	12:L:74:THR:H	1.75	0.52
30:0:599:G:H2'	30:0:600:G:H8	1.74	0.52
30:0:615:G:H2'	30:0:616:U:C6	2.44	0.52
30:0:793:A:C5	30:0:794:U:C5	2.98	0.52
30:0:1183:C:C4	30:0:1184:C:N4	2.78	0.52
30:0:1522:A:C2'	30:0:1523:G:H5'	2.40	0.52
30:0:2672:C:H2'	30:0:2673:U:H6	1.74	0.52
13:M:73:ARG:HD2	13:M:73:ARG:N	2.25	0.52
29:3:4:PRO:HA	29:3:91:GLN:O	2.09	0.52
30:0:308:U:C4	30:0:342:C:H1'	2.45	0.52
30:0:818:A:C6	30:0:819:A:N1	2.78	0.52
30:0:1154:A:H2'	30:0:1155:G:C8	2.44	0.52
30:0:1422:U:H2'	30:0:1423:C:H6	1.72	0.52
30:0:1504:A:H5'	38:0:4396:HOH:O	2.10	0.52
30:0:2088:C:H2'	30:0:2089:A:C8	2.44	0.52
12:L:78:ALA:HB3	38:L:8860:HOH:O	2.11	0.51
13:M:43:PRO:HG3	13:M:62:VAL:HG21	1.91	0.51
24:X:49:ARG:HD3	24:X:84:ILE:HG12	1.92	0.51
30:0:818:A:C6	30:0:819:A:C2	2.98	0.51
30:0:1175:G:N7	30:0:1176:C:C4	2.78	0.51
30:0:1191:A:C2'	30:0:1193:A:H5'	2.38	0.51
30:0:1309:U:O2'	30:0:1310:U:H5'	2.10	0.51
30:0:1743:G:H2'	30:0:1744:G:O4'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2872:U:H2'	30:0:2873:C:H6	1.76	0.51
2:B:144:THR:HB	38:B:9096:HOH:O	2.10	0.51
14:N:7:LYS:HE3	17:Q:21:ARG:O	2.09	0.51
17:Q:87:THR:HB	38:Q:1295:HOH:O	2.10	0.51
20:T:52:ARG:HH12	30:0:308:U:H2'	1.75	0.51
26:Z:38:PHE:HB3	26:Z:42:TYR:CE1	2.46	0.51
30:0:395:A:H2'	30:0:397:A:H62	1.74	0.51
30:0:1395:C:H2'	30:0:1396:C:C6	2.46	0.51
30:0:2498:C:O2'	30:0:2499:U:H5'	2.10	0.51
30:0:2900:G:H2'	30:0:2901:C:O4'	2.10	0.51
25:Y:205:ILE:HB	25:Y:230:ASN:HD21	1.75	0.51
30:0:20:G:H5"	30:0:510:U:O4	2.09	0.51
30:0:1667:A:H5'	30:0:1667:A:H8	1.75	0.51
30:0:1992:U:H2'	30:0:1994:A:OP2	2.10	0.51
30:0:2544:G:H5'	38:0:3418:HOH:O	2.10	0.51
9:I:120:ALA:O	9:I:124:VAL:HG23	2.09	0.51
29:3:54:LYS:HE2	30:0:2468:A:C8	2.45	0.51
30:0:1641:A:H2'	30:0:1642:A:C5'	2.40	0.51
30:0:2032:U:H2'	30:0:2033:G:H5"	1.92	0.51
30:0:2614:C:O2'	30:0:2615:U:H5'	2.10	0.51
1:A:175:LYS:HE2	33:A:8809:CL:CL	2.48	0.51
15:O:65:LEU:HD13	30:0:746:A:C6	2.45	0.51
30:0:1160:G:H2'	38:0:5597:HOH:O	2.11	0.51
30:0:1167:G:H2'	30:0:1168:C:O4'	2.11	0.51
30:0:1395:C:H2'	30:0:1396:C:H6	1.76	0.51
31:9:56:A:H3'	31:9:57:A:H5"	1.89	0.51
3:C:127:ARG:HD3	3:C:129:HIS:CE1	2.45	0.51
10:J:21:ARG:HH21	30:0:1244:U:H5"	1.76	0.51
11:K:91:GLU:HG3	38:U:151:HOH:O	2.11	0.51
17:Q:7:LEU:HD12	30:0:2424:U:H1'	1.93	0.51
30:0:254:C:O2	30:0:254:C:C2'	2.57	0.51
30:0:660:A:N6	30:0:746:A:O4'	2.43	0.51
30:0:702:G:C2	30:0:703:G:C8	2.98	0.51
30:0:2700:G:O2'	30:0:2701:G:H5'	2.09	0.51
30:0:2846:C:H3'	38:0:7070:HOH:O	2.11	0.51
30:0:2851:G:H2'	30:0:2902:A:N6	2.26	0.51
31:9:58:G:H3'	31:9:59:C:C5	2.45	0.51
2:B:234:ARG:HG3	30:0:1735:C:OP2	2.11	0.51
5:E:137:ASP:OD1	5:E:139:GLU:HB2	2.11	0.51
8:H:114:ASP:HA	38:H:204:HOH:O	2.11	0.51
17:Q:94:GLN:O	17:Q:95:GLU:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:56:GLU:HG2	30:0:1400:C:H4'	1.92	0.51
29:3:40:ARG:HA	29:3:52:PHE:HE1	1.73	0.51
29:3:83:TRP:NE1	30:0:2380:A:H2	2.09	0.51
30:0:37:A:H2'	30:0:38:G:C8	2.46	0.51
30:0:128:A:O2'	30:0:129:A:H5'	2.10	0.51
30:0:633:C:O2'	30:0:634:G:H5'	2.10	0.51
30:0:1019:C:O2'	30:0:1020:A:H5'	2.11	0.51
30:0:1947:G:N2	30:0:1966:U:C2	2.79	0.51
30:0:2032:U:H2'	30:0:2033:G:H5'	1.93	0.51
30:0:2719:A:C2'	30:0:2720:C:H5'	2.41	0.51
3:C:149:LYS:HE3	38:0:4023:HOH:O	2.10	0.51
3:C:219:ASN:O	3:C:222:ASP:HB2	2.11	0.51
6:F:36:THR:HG23	6:F:97:ALA:HB2	1.93	0.51
6:F:91:VAL:HG11	30:0:262:A:OP2	2.10	0.51
7:G:64:ASN:HD22	7:G:64:ASN:H	1.58	0.51
13:M:28:GLN:O	13:M:32:ARG:HG3	2.10	0.51
15:O:37:ARG:HD2	30:0:656:G:OP2	2.11	0.51
20:T:32:ARG:NH1	20:T:38:ARG:NH1	2.58	0.51
26:Z:53:ILE:HG23	38:Z:8719:HOH:O	2.10	0.51
26:Z:78:ILE:HD12	38:Z:8715:HOH:O	2.11	0.51
30:0:210:U:O2'	30:0:211:U:H5'	2.11	0.51
30:0:727:G:H3'	30:0:728:C:C6	2.45	0.51
30:0:822:C:N3	30:0:823:U:C5	2.79	0.51
30:0:1236:A:O2'	30:0:1237:U:H5'	2.11	0.51
30:0:2047:C:H5'	38:0:9814:HOH:O	2.10	0.51
30:0:2456:A:O2'	30:0:2457:U:H5'	2.10	0.51
30:0:2689:A:H2'	30:0:2690:U:H5'	1.92	0.51
8:H:61:ARG:HH11	8:H:61:ARG:HG3	1.75	0.51
11:K:66:ARG:NH2	30:0:1994:A:OP1	2.44	0.51
16:P:128:GLY:HA3	30:0:801:U:O4'	2.11	0.51
24:X:61:ARG:O	30:0:2744:G:H5"	2.11	0.51
25:Y:127:GLN:HA	38:Y:8909:HOH:O	2.11	0.51
30:0:523:C:H2'	30:0:524:A:C8	2.46	0.51
30:0:1890:U:H1'	30:0:2013:G:N2	2.26	0.51
30:0:2589:U:H2'	30:0:2590:U:C6	2.46	0.51
30:0:2712:G:C5'	38:0:5187:HOH:O	2.58	0.51
2:B:80:ARG:HB2	2:B:145:HIS:CE1	2.45	0.51
8:H:31:ILE:HD11	8:H:65:LEU:HB3	1.93	0.51
16:P:118:GLN:O	16:P:122:LEU:HG	2.11	0.51
29:3:22:VAL:HG12	29:3:90:PHE:CE2	2.46	0.51
30:0:39:G:C2	30:0:444:C:C2	2.99	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:255:A:H2'	30:0:256:C:C6	2.46	0.51
30:0:617:C:H2'	30:0:618:G:O4'	2.11	0.51
30:0:1186:C:N4	30:0:1187:U:C4	2.79	0.51
30:0:1568:G:H2'	30:0:1569:U:O4'	2.10	0.51
30:0:1819:G:H2'	30:0:1820:G:C5'	2.41	0.51
30:0:2526:C:O2'	30:0:2527:U:H5'	2.10	0.51
2:B:71:VAL:HG21	2:B:296:LEU:HB3	1.92	0.50
7:G:20:VAL:O	7:G:24:VAL:HG23	2.11	0.50
9:I:83:GLY:HA3	30:0:1168:C:H5'	1.93	0.50
11:K:97:ILE:HG22	11:K:98:VAL:N	2.25	0.50
22:V:12:THR:HG23	22:V:14:ALA:H	1.76	0.50
26:Z:102:THR:HG23	26:Z:105:ARG:HD2	1.93	0.50
30:0:553:G:O4'	30:0:1325:G:H5'	2.10	0.50
30:0:560:U:H2'	30:0:561:G:H8	1.75	0.50
30:0:1226:G:C5	30:0:1227:C:C5	2.99	0.50
30:0:1441:G:O2'	30:0:1442:A:H5'	2.11	0.50
30:0:1511:U:O2'	30:0:1512:G:H5'	2.11	0.50
30:0:1642:A:C8	30:0:1643:C:C5	2.99	0.50
30:0:1796:A:H8	30:0:1796:A:O5'	1.94	0.50
30:0:1805:G:O2'	30:0:1806:G:H5'	2.11	0.50
30:0:2587:OMU:H2'	30:0:2589:U:H5"	1.93	0.50
3:C:127:ARG:HH21	3:C:225:PRO:HG2	1.71	0.50
25:Y:210:GLY:N	30:0:1313:A:H5"	2.27	0.50
30:0:134:U:O2	30:0:145:A:C2	2.63	0.50
30:0:1167:G:N2	30:0:1180:U:C2	2.79	0.50
30:0:2087:C:O2'	30:0:2088:C:H5'	2.11	0.50
30:0:2672:C:C2	30:0:2673:U:C6	3.00	0.50
30:0:2847:G:O2'	30:0:2848:G:H5'	2.11	0.50
2:B:248:ARG:O	2:B:251:VAL:HG22	2.11	0.50
3:C:193:LEU:HA	3:C:211:ASP:O	2.10	0.50
3:C:236:THR:HG22	3:C:239:ALA:CB	2.41	0.50
5:E:7:ILE:HG13	5:E:11:VAL:HB	1.93	0.50
21:U:35:LYS:HA	30:0:2755:G:OP1	2.11	0.50
27:1:16:HIS:CD2	30:0:470:U:O2'	2.64	0.50
29:3:29:ARG:HA	38:3:9012:HOH:O	2.11	0.50
30:0:523:C:H2'	30:0:524:A:H8	1.76	0.50
30:0:876:A:H2'	30:0:876:A:N3	2.26	0.50
30:0:1087:G:H4'	30:0:1088:A:OP1	2.12	0.50
30:0:1216:G:N2	30:0:1217:G:H1'	2.26	0.50
30:0:1461:U:H2'	30:0:1462:C:C6	2.46	0.50
30:0:1735:C:H2'	30:0:1736:A:H8	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2899:A:O2'	30:0:2900:G:H5'	2.12	0.50
10:J:107:ASN:C	10:J:107:ASN:HD22	2.15	0.50
12:L:65:ASP:HA	12:L:109:LEU:O	2.11	0.50
29:3:10:TYR:CE1	30:0:2408:A:H1'	2.46	0.50
29:3:10:TYR:HB2	29:3:17:HIS:HE1	1.76	0.50
30:0:40:C:H2'	30:0:41:G:C8	2.46	0.50
30:0:1181:A:H2'	30:0:1182:C:C5'	2.41	0.50
30:0:1463:U:H2'	30:0:1464:C:C6	2.47	0.50
30:0:1474:C:H6	30:0:1474:C:C5'	2.17	0.50
30:0:1522:A:H2'	30:0:1523:G:H5'	1.92	0.50
30:0:1811:A:C2	30:0:2752:C:H1'	2.46	0.50
30:0:2564:G:OP2	30:0:2565:C:H5"	2.11	0.50
30:0:2635:A:HO2'	30:0:2636:C:H5'	1.76	0.50
2:B:235:ARG:HH11	30:0:2092:G:P	2.33	0.50
7:G:16:LYS:O	7:G:20:VAL:HG23	2.11	0.50
13:M:71:SER:HB2	13:M:92:THR:CG2	2.35	0.50
17:Q:95:GLU:HA	30:0:949:U:H4'	1.94	0.50
30:0:73:U:H2'	30:0:74:G:C8	2.46	0.50
30:0:105:G:O2'	30:0:106:A:H5'	2.11	0.50
30:0:1015:C:O5'	30:0:1015:C:H6	1.94	0.50
30:0:1149:U:C5	30:0:1215:A:C5	3.00	0.50
30:0:1187:U:O2'	30:0:1189:A:H2	1.94	0.50
38:B:8995:HOH:O	30:0:2093:G:H5"	2.11	0.50
8:H:59:GLN:NE2	8:H:129:ARG:HE	2.10	0.50
14:N:37:ARG:NH1	31:9:6:C:OP1	2.44	0.50
16:P:114:LEU:HD22	16:P:118:GLN:HB3	1.93	0.50
16:P:135:ALA:O	16:P:139:ARG:HG3	2.11	0.50
30:0:119:A:H2'	30:0:120:A:C5'	2.42	0.50
30:0:372:A:C2	30:0:373:G:C4	2.99	0.50
30:0:451:C:O2'	30:0:452:G:H5'	2.12	0.50
30:0:556:C:O2'	30:0:557:C:H5'	2.11	0.50
30:0:738:G:O5'	30:0:738:G:H8	1.95	0.50
30:0:819:A:C4	30:0:821:U:C5	3.00	0.50
30:0:929:A:H5"	38:0:7060:HOH:O	2.11	0.50
30:0:2295:G:N3	30:0:2361:A:C2	2.80	0.50
30:0:2344:G:H2'	30:0:2344:G:N3	2.26	0.50
30:0:2506:A:C1'	38:0:6031:HOH:O	2.58	0.50
1:A:132:ASP:CG	1:A:133:ARG:H	2.15	0.50
1:A:178:LYS:HA	30:0:1653:A:H5'	1.94	0.50
26:Z:42:TYR:N	30:0:1829:A:H61	2.10	0.50
29:3:3:MET:O	29:3:90:PHE:HA	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:10:U:O4	30:0:532:A:H8	1.95	0.50
30:0:69:A:H8	30:0:69:A:C5'	2.24	0.50
30:0:79:G:N2	30:0:97:G:H1'	2.26	0.50
30:0:716:G:C6	30:0:717:C:N4	2.80	0.50
30:0:1666:C:H42	30:0:1667:A:N6	2.10	0.50
30:0:1705:C:O2	30:0:2735:U:H5"	2.11	0.50
30:0:2415:A:C2'	30:0:2416:G:H5'	2.40	0.50
30:0:2803:C:H2'	30:0:2804:C:H6	1.77	0.50
30:0:2823:G:O2'	30:0:2824:C:H5'	2.12	0.50
31:9:75:G:N2	31:9:106:U:O2	2.36	0.50
31:9:92:G:H2'	31:9:93:A:H8	1.73	0.50
1:A:100:PRO:HG2	1:A:103:VAL:HG21	1.94	0.50
3:C:22:PHE:HA	3:C:116:ALA:HA	1.94	0.50
13:M:77:HIS:CE1	13:M:86:GLN:HG2	2.47	0.50
13:M:82:ARG:HH22	13:M:85:ARG:NH2	2.08	0.50
14:N:38:LYS:HE2	14:N:107:ASN:HD21	1.75	0.50
22:V:56:ILE:O	22:V:60:GLN:HG3	2.12	0.50
29:3:10:TYR:HB2	29:3:17:HIS:CE1	2.47	0.50
30:0:59:A:C5'	38:0:4313:HOH:O	2.60	0.50
30:0:74:G:H1	30:0:103:C:N4	2.10	0.50
30:0:282:C:O2'	30:0:283:U:C4'	2.60	0.50
30:0:764:C:H2'	30:0:765:G:O4'	2.12	0.50
30:0:1878:G:C4'	38:0:6097:HOH:O	2.60	0.50
31:9:23:U:H2'	31:9:23:U:O2	2.12	0.50
1:A:141:PRO:HG2	30:0:1855:G:O6	2.12	0.50
2:B:18:ARG:HG3	2:B:256:GLN:HG3	1.93	0.50
3:C:101:ASP:HB2	30:0:750:A:O3'	2.12	0.50
12:L:24:ALA:HB2	12:L:30:ARG:HE	1.76	0.50
13:M:145:ASP:HB2	38:M:8865:HOH:O	2.11	0.50
20:T:71:VAL:HG11	20:T:90:PRO:CB	2.38	0.50
23:W:6:GLN:CB	23:W:26:ILE:HD11	2.40	0.50
23:W:130:HIS:O	23:W:136:GLY:HA3	2.12	0.50
24:X:26:ALA:HB2	24:X:63:ARG:HA	1.93	0.50
29:3:3:MET:SD	29:3:88:LEU:HD23	2.52	0.50
30:0:561:G:C2	30:0:562:A:C8	3.00	0.50
30:0:814:G:H2'	30:0:815:U:H6	1.77	0.50
30:0:2253:G:O2'	30:0:2254:G:H5'	2.11	0.50
30:0:2465:A:H3'	38:0:3637:HOH:O	2.12	0.50
31:9:42:C:H5'	31:9:43:G:OP2	2.12	0.50
2:B:66:GLU:OE1	2:B:328:ARG:HD2	2.12	0.49
4:D:58:VAL:CG1	4:D:60:GLU:HG2	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:159:VAL:CG1	33:M:8818:CL:CL	2.95	0.49
16:P:87:ARG:HG2	38:0:5919:HOH:O	2.10	0.49
30:0:47:G:N3	30:0:114:A:C2	2.80	0.49
30:0:952:G:N3	30:0:2302:A:H2'	2.26	0.49
30:0:1165:G:H21	30:0:1173:A:H5'	1.74	0.49
30:0:1268:C:H2'	30:0:1269:G:C8	2.46	0.49
30:0:1393:A:H2'	30:0:1394:C:C6	2.47	0.49
30:0:1601:G:H1'	38:0:9891:HOH:O	2.11	0.49
30:0:1933:G:O2'	30:0:1934:A:H5'	2.12	0.49
30:0:2854:A:C6	30:0:2905:A:C6	3.00	0.49
31:9:28:U:O2	31:9:57:A:N6	2.44	0.49
31:9:39:U:H1'	31:9:44:A:H61	1.77	0.49
4:D:35:ALA:HB2	38:D:5576:HOH:O	2.11	0.49
8:H:32:ALA:HB3	8:H:69:ARG:HH12	1.77	0.49
16:P:98:ILE:HD12	16:P:102:ARG:NE	2.27	0.49
18:R:18:LEU:O	18:R:142:ASP:HA	2.12	0.49
29:3:60:LYS:C	29:3:62:THR:H	2.15	0.49
30:0:134:U:C2	30:0:145:A:C2	2.99	0.49
30:0:589:U:H2'	30:0:590:A:H8	1.76	0.49
30:0:873:G:N2	38:0:9173:HOH:O	2.43	0.49
30:0:1226:G:H2'	30:0:1227:C:C6	2.44	0.49
30:0:1662:C:O5'	30:0:1662:C:H6	1.94	0.49
30:0:1902:G:N2	30:0:1936:C:C2	2.80	0.49
31:9:55:U:H4'	31:9:56:A:H8	1.71	0.49
10:J:131:THR:HG22	10:J:134:GLU:H	1.77	0.49
11:K:34:VAL:HB	38:K:7169:HOH:O	2.12	0.49
25:Y:212:ARG:HB2	30:0:1315:G:C4	2.47	0.49
30:0:316:A:N3	30:0:336:G:O2'	2.41	0.49
30:0:400:C:H2'	30:0:401:C:C6	2.47	0.49
30:0:1194:A:C2	30:0:1206:U:H1'	2.47	0.49
30:0:1787:C:C4'	30:0:2883:A:O4'	2.59	0.49
30:0:1800:G:H2'	30:0:1801:A:H8	1.77	0.49
30:0:2291:A:H2'	30:0:2291:A:N3	2.28	0.49
30:0:2617:G:C2	30:0:2618:G:C8	3.00	0.49
30:0:2846:C:H2'	30:0:2847:G:H8	1.77	0.49
1:A:47:HIS:CD2	30:0:1654:U:C2'	2.92	0.49
2:B:44:TYR:OH	2:B:148:PRO:HG3	2.11	0.49
2:B:215:VAL:O	2:B:219:GLY:HA2	2.13	0.49
6:F:110:ASP:O	6:F:114:LYS:HG3	2.12	0.49
9:I:93:ALA:HB3	9:I:132:VAL:HG22	1.95	0.49
17:Q:66:LYS:HB2	17:Q:70:ALA:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:115:ARG:NH2	30:0:1266:U:H4'	2.27	0.49
26:Z:60:ASP:HB3	26:Z:69:ASP:HB3	1.92	0.49
29:3:79:LEU:CD1	30:0:2456:A:H2	2.25	0.49
29:3:79:LEU:HD22	38:0:7515:HOH:O	2.13	0.49
30:0:36:C:C2	30:0:447:A:C2	3.00	0.49
30:0:814:G:H2'	30:0:815:U:C6	2.47	0.49
30:0:816:G:H5'	30:0:1598:A:H4'	1.94	0.49
30:0:1206:U:C5'	30:0:1206:U:H6	2.21	0.49
30:0:1255:A:H1'	38:0:7741:HOH:O	2.11	0.49
30:0:1339:G:C6	30:0:1340:G:N1	2.81	0.49
30:0:1381:A:N3	30:0:1382:G:H1'	2.28	0.49
30:0:1947:G:N2	30:0:1966:U:N3	2.60	0.49
30:0:2133:U:H4'	30:0:2134:G:H5'	1.93	0.49
30:0:2632:G:C6	30:0:2633:A:N6	2.81	0.49
30:0:2632:G:H2'	30:0:2633:A:C8	2.46	0.49
2:B:304:PRO:HD2	2:B:307:ARG:HE	1.78	0.49
14:N:58:LEU:N	14:N:58:LEU:HD12	2.27	0.49
30:0:494:C:H1'	30:0:498:A:N6	2.27	0.49
30:0:1370:G:H5"	38:0:5497:HOH:O	2.12	0.49
30:0:1555:G:H4'	30:0:1630:A:C2	2.47	0.49
30:0:1559:A:HO2'	30:0:1561:U:H5	1.60	0.49
30:0:1733:A:C5	30:0:1734:C:C2	3.00	0.49
30:0:1787:C:O4'	30:0:2883:A:H1'	2.11	0.49
30:0:1878:G:O2'	30:0:1879:U:H6	1.90	0.49
30:0:2118:A:H5'	38:0:3996:HOH:O	2.13	0.49
30:0:2366:C:O5'	30:0:2366:C:H6	1.95	0.49
8:H:27:PRO:HD3	8:H:123:ILE:CG2	2.43	0.49
10:J:130:VAL:HG12	10:J:131:THR:H	1.78	0.49
14:N:37:ARG:HG3	14:N:37:ARG:HH11	1.77	0.49
20:T:107:LYS:HD2	30:0:97:G:C2	2.47	0.49
30:0:29:C:O2'	30:0:30:U:H5'	2.12	0.49
30:0:1174:A:C5	30:0:1201:C:H4'	2.47	0.49
30:0:1189:A:O2'	30:0:1208:C:H2'	2.12	0.49
30:0:1517:C:O2	30:0:1670:A:C2	2.66	0.49
30:0:1626:A:O2'	30:0:1627:G:H5'	2.13	0.49
30:0:1682:A:O2'	30:0:1683:G:H5"	2.12	0.49
30:0:1871:U:O4'	30:0:1873:G:C8	2.66	0.49
30:0:2335:C:C2	30:0:2350:G:C2	3.01	0.49
2:B:307:ARG:HD2	38:B:9123:HOH:O	2.12	0.49
6:F:110:ASP:O	6:F:114:LYS:N	2.44	0.49
18:R:71:LYS:HE2	30:0:2831:C:O3'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:9:CYS:HB2	38:U:6796:HOH:O	2.11	0.49
29:3:12:PRO:HB3	30:0:2382:A:O2'	2.12	0.49
29:3:33:MET:HG2	30:0:1922:A:C2'	2.42	0.49
30:0:285:A:H2'	30:0:286:U:O4'	2.13	0.49
30:0:316:A:H1'	30:0:336:G:N3	2.27	0.49
30:0:549:A:C6	30:0:550:C:C4	3.00	0.49
30:0:862:U:H2'	30:0:863:G:H8	1.77	0.49
30:0:889:C:H4'	38:0:6368:HOH:O	2.13	0.49
30:0:1226:G:N3	30:0:1227:C:C6	2.81	0.49
30:0:2478:U:H2'	30:0:2479:A:C8	2.48	0.49
1:A:109:GLU:HG2	1:A:116:GLY:N	2.25	0.49
2:B:98:THR:HG22	2:B:99:GLU:N	2.28	0.49
2:B:162:MET:CE	2:B:308:LEU:HD21	2.42	0.49
3:C:233:THR:HG22	3:C:234:VAL:N	2.26	0.49
8:H:29:SER:HA	8:H:62:HIS:HD2	1.77	0.49
26:Z:47:ARG:HH22	30:0:1771:U:H1'	1.77	0.49
30:0:447:A:O2'	30:0:448:G:H5'	2.13	0.49
30:0:1183:C:N4	30:0:1184:C:N4	2.60	0.49
30:0:1583:U:O2'	30:0:1584:C:H5'	2.13	0.49
30:0:1706:G:C5	30:0:1707:G:C6	3.00	0.49
30:0:1760:G:H5'	30:0:1818:C:O2'	2.12	0.49
30:0:1921:A:C6	30:0:1922:A:C2	3.00	0.49
30:0:2326:C:H4'	30:0:2412:G:H4'	1.94	0.49
30:0:2826:G:H1'	30:0:2914:A:N6	2.28	0.49
31:9:110:G:N2	31:9:111:U:H1'	2.28	0.49
1:A:36:ASP:HB2	1:A:85:SER:H	1.77	0.49
14:N:25:ARG:HB3	30:0:2415:A:C2	2.47	0.49
25:Y:235:GLU:H	25:Y:235:GLU:CD	2.16	0.49
29:3:1:MET:HG2	29:3:87:ARG:O	2.11	0.49
30:0:717:C:H2'	30:0:718:C:H6	1.78	0.49
30:0:731:U:O2'	30:0:732:C:H5'	2.13	0.49
30:0:1116:U:C2	30:0:1246:A:N6	2.81	0.49
30:0:1343:C:H2'	30:0:1344:G:O5'	2.12	0.49
30:0:1453:G:C2	30:0:1675:C:C2	3.00	0.49
30:0:2103:A:N3	30:0:2103:A:H2'	2.28	0.49
30:0:2269:C:H2'	30:0:2270:G:O4'	2.12	0.49
31:9:105:A:H2'	31:9:106:U:O4'	2.12	0.49
14:N:178:THR:O	14:N:181:ASP:HB3	2.13	0.49
20:T:69:LYS:O	20:T:71:VAL:HG23	2.13	0.49
27:1:21:ARG:HD2	27:1:39:PHE:HB2	1.95	0.49
30:0:271:C:N4	30:0:378:A:H2	2.01	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1119:G:H22	30:0:1246:A:H2	1.46	0.49
30:0:1351:G:H1'	38:0:4648:HOH:O	2.13	0.49
30:0:1607:A:C4	30:0:1608:G:C8	3.01	0.49
30:0:1615:A:H5'	38:0:4169:HOH:O	2.12	0.49
30:0:2497:A:C2	30:0:2524:G:C2	3.01	0.49
30:0:2536:C:H6	38:0:4998:HOH:O	1.95	0.49
31:9:8:G:C6	31:9:9:C:C4	3.00	0.49
31:9:60:C:O2'	31:9:61:C:H5'	2.13	0.49
3:C:173:LYS:HE3	30:0:1311:G:O6	2.12	0.48
4:D:92:GLU:HB2	38:D:3862:HOH:O	2.13	0.48
6:F:63:ILE:HB	6:F:64:PRO:CD	2.37	0.48
13:M:52:GLN:OE1	13:M:116:ASN:HB3	2.13	0.48
25:Y:137:LYS:HD2	38:0:7590:HOH:O	2.11	0.48
29:3:88:LEU:HB3	29:3:90:PHE:CE1	2.48	0.48
30:0:191:A:H2'	30:0:237:G:O6	2.12	0.48
30:0:419:A:H1'	30:0:1921:A:C2	2.48	0.48
30:0:788:A:H4'	38:0:7005:HOH:O	2.12	0.48
30:0:1063:G:H4'	30:0:2307:A:H1'	1.95	0.48
30:0:1240:G:H1'	38:0:9360:HOH:O	2.12	0.48
30:0:1586:G:C2'	30:0:1587:U:H5'	2.43	0.48
30:0:1644:C:C2	30:0:1645:U:C5	3.01	0.48
30:0:2297:U:H2'	30:0:2298:C:H6	1.78	0.48
30:0:2639:G:C5	30:0:2640:U:C5	3.01	0.48
4:D:22:VAL:HG22	4:D:74:THR:HG22	1.95	0.48
5:E:11:VAL:HG12	5:E:12:ASP:N	2.28	0.48
11:K:98:VAL:HG11	11:K:102:GLU:HA	1.94	0.48
13:M:134:ILE:CG2	13:M:141:ILE:HD13	2.36	0.48
20:T:28:SER:O	20:T:32:ARG:HG3	2.14	0.48
21:U:19:THR:HG22	21:U:20:MET:N	2.28	0.48
30:0:106:A:C6	30:0:107:U:C4	3.00	0.48
30:0:1066:U:H2'	30:0:1067:A:C8	2.48	0.48
30:0:1765:G:O2'	30:0:1766:U:H5'	2.12	0.48
30:0:1916:C:O2'	30:0:1917:G:H5'	2.14	0.48
30:0:2646:G:C4	30:0:2647:C:C5	3.02	0.48
30:0:2713:G:O2'	30:0:2714:U:H5'	2.12	0.48
30:0:2864:U:O2'	30:0:2865:G:H5'	2.14	0.48
31:9:2:U:H4'	38:9:9107:HOH:O	2.13	0.48
31:9:19:G:C2	31:9:20:G:C8	3.00	0.48
8:H:52:LEU:HD13	8:H:153:PHE:HB3	1.95	0.48
16:P:124:ASP:O	30:0:801:U:H4'	2.13	0.48
30:0:334:G:C5	30:0:335:U:C5	3.00	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:595:U:O4'	33:0:8817:CL:CL	2.69	0.48
30:0:681:G:N3	30:0:681:G:H5'	2.28	0.48
30:0:1832:G:C2	30:0:1833:U:C6	3.00	0.48
30:0:1883:U:H2'	30:0:1884:G:H5'	1.94	0.48
30:0:2480:G:O2'	30:0:2481:G:H5'	2.13	0.48
30:0:2526:C:H3'	30:0:2526:C:C6	2.47	0.48
30:0:2827:A:C2	30:0:2914:A:C2	3.01	0.48
30:0:2898:G:H1'	38:0:7555:HOH:O	2.13	0.48
31:9:3:A:H2	31:9:21:G:N3	2.12	0.48
2:B:152:PRO:HD2	38:B:9102:HOH:O	2.12	0.48
8:H:35:LYS:HE3	30:0:968:G:H1'	1.95	0.48
13:M:84:LYS:HA	29:3:46:ILE:O	2.12	0.48
16:P:31:ILE:HG12	16:P:43:LEU:HD13	1.96	0.48
26:Z:42:TYR:H	30:0:1829:A:H61	1.61	0.48
30:0:120:A:H2'	30:0:120:A:N3	2.29	0.48
30:0:1015:C:H2'	30:0:1016:U:C6	2.48	0.48
30:0:1557:G:H2'	30:0:1558:C:H6	1.78	0.48
30:0:1632:A:C3'	30:0:1633:C:H5'	2.43	0.48
30:0:2700:G:H2'	30:0:2701:G:C5'	2.43	0.48
4:D:37:ALA:O	4:D:40:ILE:HG12	2.13	0.48
11:K:43:ARG:NH1	30:0:2712:G:OP1	2.46	0.48
12:L:117:GLU:HG3	12:L:117:GLU:O	2.13	0.48
14:N:78:MET:HB2	14:N:79:PRO:HD3	1.95	0.48
18:R:132:ARG:HG2	18:R:133:ALA:N	2.27	0.48
19:S:6:LYS:HB2	19:S:27:ALA:O	2.13	0.48
20:T:27:LEU:HB2	20:T:32:ARG:HG2	1.95	0.48
29:3:64:LYS:HE2	38:0:7638:HOH:O	2.12	0.48
30:0:100:C:C4	30:0:101:C:C5	3.01	0.48
30:0:222:A:H2'	30:0:223:G:O4'	2.13	0.48
30:0:677:C:H2'	30:0:678:G:H8	1.77	0.48
30:0:707:C:C2	30:0:708:A:C8	3.02	0.48
30:0:1434:A:O2'	30:0:1435:U:H6	1.92	0.48
30:0:1496:A:H5'	30:0:1572:A:H1'	1.94	0.48
30:0:1634:G:H2'	30:0:1635:U:H6	1.76	0.48
30:0:2255:A:C2	30:0:2256:G:C4	3.02	0.48
30:0:2505:G:C2'	30:0:2506:A:C5'	2.91	0.48
30:0:2672:C:H2'	30:0:2673:U:O4'	2.14	0.48
30:0:2755:G:H1'	38:0:4651:HOH:O	2.13	0.48
30:0:2772:G:O2'	30:0:2773:G:H5'	2.13	0.48
30:0:2854:A:H2'	30:0:2855:G:H8	1.78	0.48
30:0:2860:G:H2'	30:0:2861:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:36:PRO:HG3	2:B:169:GLY:H	1.77	0.48
4:D:51:ARG:HH11	4:D:68:PRO:HB3	1.78	0.48
5:E:139:GLU:OE2	30:0:2781:U:H1'	2.13	0.48
10:J:60:ARG:HD3	10:J:71:TYR:CE1	2.47	0.48
15:O:88:LYS:HB3	38:O:7061:HOH:O	2.13	0.48
29:3:43:ASN:HB2	29:3:52:PHE:CD1	2.48	0.48
30:0:200:C:H6	38:0:3433:HOH:O	1.96	0.48
30:0:611:U:H2'	30:0:612:U:C6	2.48	0.48
30:0:1182:C:C1'	30:0:1192:A:H8	2.26	0.48
30:0:1207:A:OP2	30:0:1208:C:H5	1.96	0.48
30:0:1970:G:H1'	38:0:3662:HOH:O	2.13	0.48
30:0:1970:G:H4'	30:0:1971:G:C5'	2.43	0.48
30:0:2133:U:H4'	30:0:2134:G:C5'	2.44	0.48
30:0:2598:U:O2	30:0:2600:A:C8	2.66	0.48
30:0:2617:G:H4'	38:0:4487:HOH:O	2.13	0.48
5:E:80:TRP:O	5:E:134:SER:HA	2.12	0.48
6:F:107:ASP:O	6:F:111:ILE:HG13	2.13	0.48
13:M:139:PRO:HA	13:M:142:GLN:HB2	1.95	0.48
16:P:94:TRP:CZ2	16:P:98:ILE:HG13	2.49	0.48
17:Q:28:ARG:HG2	38:9:9083:HOH:O	2.12	0.48
18:R:138:SER:HB2	38:0:5570:HOH:O	2.14	0.48
23:W:26:ILE:HB	38:W:5420:HOH:O	2.14	0.48
27:1:25:LYS:CD	28:2:49:GLU:H	2.25	0.48
30:0:31:C:H2'	38:0:7668:HOH:O	2.13	0.48
30:0:627:G:H2'	30:0:2071:C:C4	2.49	0.48
30:0:705:C:O2	30:0:705:C:C2'	2.62	0.48
30:0:1224:G:H2'	30:0:1225:C:C6	2.48	0.48
30:0:1520:G:H2'	30:0:1521:C:C6	2.49	0.48
30:0:1878:G:C2	30:0:1879:U:C2	3.02	0.48
30:0:1908:G:N1	30:0:1930:A:OP2	2.46	0.48
30:0:2569:A:H8	30:0:2569:A:O5'	1.96	0.48
30:0:2707:C:O2	30:0:2707:C:C2'	2.59	0.48
1:A:162:GLY:N	26:Z:91:GLY:HA2	2.29	0.48
9:I:133:THR:HG22	9:I:134:ILE:N	2.28	0.48
16:P:11:ALA:HB1	16:P:16:VAL:O	2.14	0.48
23:W:117:ARG:HH22	30:0:1264:U:P	2.36	0.48
27:1:1:THR:HB	38:1:2852:HOH:O	2.12	0.48
28:2:10:ARG:NH2	30:0:121:U:OP2	2.44	0.48
29:3:25:VAL:HA	38:3:9036:HOH:O	2.12	0.48
29:3:40:ARG:C	29:3:42:ARG:H	2.16	0.48
30:0:99:A:C8	30:0:100:C:C6	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:808:A:C5	30:0:809:G:H1'	2.48	0.48
30:0:858:U:H2'	30:0:859:C:C6	2.47	0.48
30:0:1023:C:O2'	30:0:1024:G:H5'	2.14	0.48
30:0:1029:U:O2'	30:0:1273:C:OP1	2.27	0.48
30:0:1063:G:H8	38:0:9856:HOH:O	1.96	0.48
30:0:2354:A:C2	30:0:2367:A:C8	3.02	0.48
30:0:2717:C:H2'	30:0:2718:C:H5'	1.93	0.48
1:A:71:PRO:HG2	1:A:91:GLY:HA2	1.95	0.48
4:D:51:ARG:NH1	4:D:68:PRO:HB3	2.28	0.48
8:H:157:TYR:HD1	8:H:157:TYR:C	2.18	0.48
30:0:69:A:C2'	30:0:70:A:OP2	2.62	0.48
30:0:432:G:H5"	38:0:6860:HOH:O	2.12	0.48
30:0:763:C:O2'	30:0:764:C:H5'	2.14	0.48
30:0:842:C:H4'	38:0:3427:HOH:O	2.13	0.48
30:0:920:C:C4'	30:0:921:G:C2	2.95	0.48
30:0:1177:A:H2'	30:0:1177:A:N3	2.28	0.48
30:0:1204:C:H2'	30:0:1205:U:O4'	2.14	0.48
30:0:2254:G:C2	30:0:2255:A:C8	3.01	0.48
30:0:2281:C:H5	38:0:3756:HOH:O	1.97	0.48
30:0:2505:G:H2'	30:0:2506:A:C5'	2.43	0.48
30:0:2587:OMU:H5	38:0:7464:HOH:O	2.13	0.48
30:0:2777:G:O2'	30:0:2778:A:H5'	2.13	0.48
31:9:39:U:C2'	31:9:40:C:OP1	2.62	0.48
1:A:161:GLY:HA3	38:Z:8705:HOH:O	2.13	0.48
1:A:217:ARG:HG2	1:A:229:ALA:HB2	1.95	0.48
2:B:226:LYS:HG2	2:B:230:GLN:HE21	1.78	0.48
6:F:58:GLU:HA	6:F:61:MET:SD	2.54	0.48
11:K:1:MET:N	30:0:2686:C:O2'	2.38	0.48
13:M:9:ARG:HD2	30:0:380:A:OP2	2.14	0.48
14:N:4:PRO:HG3	31:9:69:U:OP1	2.13	0.48
29:3:51:LYS:HG3	29:3:52:PHE:HD2	1.76	0.48
29:3:83:TRP:HB2	38:0:5759:HOH:O	2.14	0.48
30:0:202:U:C4	30:0:203:G:C6	3.01	0.48
30:0:1186:C:C4	30:0:1187:U:C4	3.02	0.48
30:0:1626:A:H2'	30:0:1627:G:O4'	2.14	0.48
3:C:162:VAL:O	3:C:162:VAL:HG13	2.13	0.47
9:I:69:PRO:HA	30:0:1164:U:OP1	2.14	0.47
18:R:15:LYS:HE3	38:R:8976:HOH:O	2.14	0.47
29:3:50:GLY:CA	30:0:170:U:H1'	2.43	0.47
30:0:151:A:H2'	30:0:152:A:O4'	2.14	0.47
30:0:625:U:H5"	30:0:1044:C:H42	1.71	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:870:G:H2'	30:0:871:G:C5'	2.34	0.47
30:0:1188:A:C5	30:0:1189:A:C2	3.02	0.47
30:0:1337:G:C6	30:0:1338:U:C4	3.01	0.47
30:0:1337:G:C5	30:0:1338:U:C5	3.02	0.47
30:0:1471:A:H2'	30:0:1472:C:C6	2.48	0.47
30:0:1745:G:H5'	38:0:4312:HOH:O	2.14	0.47
30:0:2458:U:H3'	38:0:3241:HOH:O	2.13	0.47
30:0:2474:A:H5'	30:0:2476:C:O5'	2.14	0.47
30:0:2474:A:N7	30:0:2621:PSU:H4'	2.29	0.47
30:0:2598:U:O2	30:0:2600:A:H8	1.96	0.47
30:0:2830:U:H2'	30:0:2831:C:H6	1.79	0.47
30:0:2848:G:O4'	30:0:2906:A:C2	2.66	0.47
1:A:27:LEU:HD21	1:A:55:VAL:CG2	2.44	0.47
2:B:84:LEU:O	2:B:99:GLU:HA	2.14	0.47
21:U:50:GLU:OE1	30:0:2866:U:H2'	2.13	0.47
30:0:373:G:O2'	30:0:374:U:H5'	2.14	0.47
30:0:968:G:O2'	30:0:969:G:H5'	2.14	0.47
30:0:2385:G:H2'	30:0:2386:U:C6	2.49	0.47
30:0:2855:G:C2	30:0:2904:U:N3	2.82	0.47
11:K:132:VAL:HG11	21:U:22:VAL:HG22	1.96	0.47
25:Y:234:VAL:HG12	25:Y:235:GLU:N	2.28	0.47
26:Z:40:ALA:HA	30:0:1773:G:H8	1.79	0.47
30:0:361:C:H2'	30:0:362:G:O4'	2.13	0.47
30:0:834:G:H3'	30:0:835:U:H4'	1.97	0.47
30:0:1947:G:OP1	30:0:1971:G:N7	2.47	0.47
30:0:2087:C:H2'	30:0:2088:C:H6	1.80	0.47
1:A:70:ALA:HB1	26:Z:89:THR:HG21	1.97	0.47
2:B:74:ILE:HD13	2:B:309:VAL:HG21	1.95	0.47
2:B:162:MET:HE1	2:B:308:LEU:HD21	1.96	0.47
2:B:201:ASP:CB	2:B:312:ARG:HD2	2.42	0.47
8:H:88:MET:HA	8:H:139:ALA:HA	1.96	0.47
21:U:56:ARG:HB2	30:0:2890:A:N7	2.29	0.47
22:V:12:THR:CG2	22:V:15:GLU:HG3	2.40	0.47
24:X:85:VAL:HG12	24:X:86:GLU:N	2.29	0.47
30:0:407:A:H5'	38:0:6000:HOH:O	2.14	0.47
30:0:681:G:N3	30:0:681:G:H2'	2.30	0.47
30:0:699:C:C2	30:0:744:G:C2	3.03	0.47
30:0:965:A:H5'	30:0:966:U:OP2	2.14	0.47
30:0:1275:C:H2'	30:0:1276:U:H5'	1.96	0.47
30:0:1389:G:N2	30:0:1391:G:H3'	2.29	0.47
30:0:1619:G:H2'	30:0:1620:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2379:G:H4'	30:0:2380:A:O5'	2.13	0.47
30:0:2719:A:H2'	30:0:2720:C:C5'	2.44	0.47
30:0:2724:U:O5'	30:0:2724:U:H6	1.96	0.47
30:0:2857:C:H1'	38:0:5328:HOH:O	2.15	0.47
8:H:59:GLN:HE22	8:H:96:GLN:HG2	1.79	0.47
11:K:118:ALA:HA	11:K:125:ALA:HB2	1.96	0.47
17:Q:11:ARG:HD3	38:0:6238:HOH:O	2.13	0.47
28:2:15:ASP:O	28:2:18:ASN:HB2	2.15	0.47
29:3:68:LYS:HG2	29:3:77:ALA:CB	2.44	0.47
29:3:88:LEU:CD2	33:3:8804:CL:CL	2.86	0.47
30:0:287:C:H6	30:0:287:C:O5'	1.97	0.47
30:0:371:U:C4	30:0:372:A:N7	2.83	0.47
30:0:558:C:HO2'	30:0:559:U:H5"	1.78	0.47
30:0:699:C:C6	30:0:744:G:N3	2.82	0.47
30:0:820:G:O2'	30:0:856:G:H4'	2.14	0.47
30:0:1210:G:N2	30:0:1211:G:H1'	2.29	0.47
30:0:1226:G:C4	30:0:1227:C:C6	3.02	0.47
30:0:1477:C:H4'	30:0:1868:G:OP1	2.15	0.47
30:0:1503:U:H2'	30:0:1504:A:C5'	2.45	0.47
30:0:1733:A:N7	30:0:1734:C:C4	2.82	0.47
30:0:2265:U:H2'	30:0:2266:A:H8	1.80	0.47
30:0:2781:U:C2'	30:0:2782:G:H5'	2.45	0.47
31:9:39:U:H3	31:9:42:C:H5"	1.79	0.47
31:9:73:A:H61	31:9:108:C:N4	2.13	0.47
1:A:135:VAL:HA	1:A:150:PRO:HD3	1.96	0.47
2:B:234:ARG:NH2	30:0:2039:A:OP2	2.47	0.47
7:G:64:ASN:N	7:G:64:ASN:ND2	2.62	0.47
11:K:97:ILE:HG22	11:K:98:VAL:H	1.79	0.47
13:M:68:ARG:HD2	30:0:1469:C:OP2	2.15	0.47
20:T:71:VAL:CG1	20:T:90:PRO:HB3	2.40	0.47
26:Z:34:SER:CA	30:0:797:A:H4'	2.44	0.47
29:3:9:THR:HG23	29:3:20:HIS:CE1	2.49	0.47
30:0:625:U:C5'	30:0:1044:C:N4	2.71	0.47
30:0:724:G:O2'	30:0:725:C:H5'	2.15	0.47
30:0:731:U:H2'	30:0:732:C:C6	2.50	0.47
30:0:1667:A:H5'	30:0:1667:A:C8	2.50	0.47
30:0:1760:G:C5	30:0:1761:U:C4	3.03	0.47
30:0:2375:A:H2'	30:0:2376:C:C6	2.50	0.47
30:0:2597:U:C2'	30:0:2598:U:H5'	2.45	0.47
31:9:5:G:C2'	31:9:6:C:H5'	2.45	0.47
1:A:94:LEU:HG	1:A:99:ILE:CD1	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:171:VAL:O	2:B:175:LEU:HB2	2.15	0.47
3:C:180:SER:HB2	38:C:8643:HOH:O	2.14	0.47
4:D:59:GLY:HA3	38:D:4886:HOH:O	2.14	0.47
8:H:6:ALA:HB3	30:0:2521:A:OP2	2.14	0.47
8:H:123:ILE:HD12	8:H:123:ILE:N	2.30	0.47
10:J:39:VAL:CG2	10:J:107:ASN:HA	2.44	0.47
13:M:15:PRO:HA	13:M:20:LEU:HD23	1.95	0.47
14:N:71:TRP:HZ2	38:N:8833:HOH:O	1.97	0.47
15:O:42:GLU:HB2	38:0:3736:HOH:O	2.15	0.47
16:P:13:VAL:HG13	16:P:14:LEU:N	2.29	0.47
20:T:41:ARG:NH1	20:T:42:VAL:O	2.47	0.47
20:T:51:LEU:HD11	20:T:97:ARG:HB2	1.97	0.47
23:W:21:LEU:HD21	23:W:48:VAL:HG11	1.96	0.47
23:W:77:ALA:HB3	38:W:5763:HOH:O	2.14	0.47
23:W:129:LYS:HE3	31:9:87:U:H2'	1.97	0.47
25:Y:151:SER:HB3	25:Y:154:ARG:HB3	1.97	0.47
30:0:432:G:H2'	30:0:433:C:H6	1.80	0.47
30:0:711:G:O2'	30:0:712:C:H5'	2.15	0.47
30:0:790:A:H1'	30:0:1710:A:H2'	1.97	0.47
30:0:1181:A:N1	30:0:1192:A:O2'	2.45	0.47
30:0:1210:G:O2'	30:0:1211:G:H5'	2.14	0.47
30:0:1333:U:H2'	30:0:1334:C:H6	1.80	0.47
30:0:1858:A:H2'	30:0:1859:A:C8	2.50	0.47
30:0:1988:C:H2'	30:0:1989:G:O4'	2.15	0.47
30:0:2509:A:H2'	30:0:2510:C:O4'	2.14	0.47
30:0:2727:A:C2'	30:0:2728:C:H5'	2.45	0.47
30:0:2781:U:H2'	30:0:2782:G:H5'	1.95	0.47
30:0:2837:U:H2'	38:0:6824:HOH:O	2.15	0.47
30:0:2858:U:H2'	30:0:2859:C:C6	2.49	0.47
30:0:2860:G:H2'	30:0:2861:G:H8	1.80	0.47
1:A:105:VAL:CG1	1:A:154:ALA:HB1	2.44	0.47
3:C:28:SER:HB2	38:C:8659:HOH:O	2.14	0.47
14:N:27:LEU:HD22	14:N:50:LEU:HD13	1.97	0.47
16:P:3:LEU:HA	16:P:6:GLN:OE1	2.14	0.47
22:V:64:GLY:O	22:V:65:ASP:HB2	2.15	0.47
23:W:128:VAL:HG22	30:0:1098:A:OP1	2.15	0.47
30:0:800:G:H8	30:0:800:G:O5'	1.98	0.47
30:0:835:U:H5"	38:0:9381:HOH:O	2.14	0.47
30:0:1168:C:H2'	30:0:1169:U:H5'	1.96	0.47
30:0:1446:U:H4'	30:0:1447:U:OP2	2.14	0.47
30:0:1857:A:N6	30:0:2247:C:H1'	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2059:U:H1'	38:0:4439:HOH:O	2.14	0.47
30:0:2460:A:C2	30:0:2461:U:C2	3.02	0.47
31:9:22:G:N7	31:9:55:U:C6	2.82	0.47
1:A:171:LYS:HB2	30:0:820:G:C5	2.50	0.47
2:B:212:GLN:HB2	2:B:257:THR:OG1	2.15	0.47
6:F:21:GLU:O	6:F:24:ARG:HG2	2.15	0.47
16:P:1:THR:O	30:0:1396:C:H1'	2.15	0.47
18:R:69:LYS:HB2	18:R:72:VAL:HG23	1.97	0.47
22:V:1:THR:HG23	22:V:2:VAL:N	2.29	0.47
23:W:72:PRO:HG2	38:W:5763:HOH:O	2.15	0.47
30:0:292:G:H2'	30:0:358:G:N2	2.30	0.47
30:0:561:G:H2'	30:0:562:A:H8	1.79	0.47
30:0:1889:C:O2'	30:0:1890:U:H5'	2.15	0.47
30:0:2490:A:H5"	38:0:7023:HOH:O	2.15	0.47
30:0:2858:U:H2'	30:0:2859:C:H6	1.80	0.47
30:0:2878:U:H2'	30:0:2879:A:O4'	2.14	0.47
13:M:193:LYS:HB3	30:0:392:U:C5'	2.45	0.47
14:N:170:GLU:O	14:N:174:GLU:HG3	2.14	0.47
16:P:41:ARG:NH2	30:0:1500:U:OP2	2.47	0.47
17:Q:34:ASP:O	17:Q:37:GLU:HB2	2.15	0.47
23:W:125:HIS:CE1	30:0:1097:A:C5'	2.95	0.47
30:0:249:G:O2'	30:0:250:C:H5'	2.15	0.47
30:0:1056:U:H2'	30:0:1057:A:O4'	2.14	0.47
30:0:1806:G:C4	30:0:1807:U:C6	3.03	0.47
30:0:1928:C:O2'	30:0:1929:G:H5'	2.15	0.47
30:0:2301:A:H5"	30:0:2302:A:H5'	1.96	0.47
4:D:22:VAL:HG21	30:0:2348:C:C5'	2.45	0.46
13:M:184:ARG:HG3	13:M:185:PRO:HA	1.97	0.46
16:P:13:VAL:HG13	16:P:14:LEU:H	1.80	0.46
19:S:6:LYS:HE3	19:S:29:ASP:HA	1.97	0.46
24:X:30:MET:HG2	30:0:1384:C:H5'	1.96	0.46
30:0:40:C:H5'	38:0:3836:HOH:O	2.14	0.46
30:0:137:U:OP1	30:0:259:G:O2'	2.33	0.46
30:0:589:U:H2'	30:0:590:A:C8	2.50	0.46
30:0:737:A:H2'	30:0:738:G:C8	2.49	0.46
30:0:806:A:H2'	30:0:807:A:O4'	2.15	0.46
30:0:1159:G:H1	30:0:1208:C:H42	1.63	0.46
30:0:1177:A:N1	30:0:1178:G:C4	2.82	0.46
30:0:1760:G:C6	30:0:1761:U:C4	3.03	0.46
30:0:1854:C:H2'	30:0:1875:A:H61	1.80	0.46
30:0:1942:A:O2'	30:0:1943:C:H5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2019:A:H2'	30:0:2020:C:C6	2.49	0.46
30:0:2379:G:H4'	30:0:2380:A:C5'	2.45	0.46
30:0:2388:C:O2'	30:0:2389:U:H5'	2.14	0.46
31:9:54:A:C2'	31:9:55:U:C5'	2.85	0.46
2:B:162:MET:CE	2:B:310:ARG:HD3	2.45	0.46
10:J:42:GLU:HG2	10:J:43:ARG:N	2.30	0.46
21:U:47:ARG:HG3	38:U:4381:HOH:O	2.15	0.46
26:Z:70:ARG:NH1	26:Z:83:TYR:HD1	2.11	0.46
27:1:10:LYS:HG3	38:1:2979:HOH:O	2.14	0.46
29:3:79:LEU:HD12	30:0:2456:A:C2	2.50	0.46
30:0:11:A:H2'	30:0:11:A:N3	2.30	0.46
30:0:61:G:C6	30:0:86:A:N6	2.83	0.46
30:0:154:C:O2'	30:0:155:C:H5'	2.14	0.46
30:0:703:G:C6	30:0:704:C:N4	2.83	0.46
30:0:1409:G:C2	30:0:1410:G:C8	3.03	0.46
30:0:1925:G:O2'	30:0:1926:G:H5'	2.15	0.46
30:0:2461:U:O2	30:0:2466:G:H1'	2.14	0.46
1:A:88:ILE:HD13	1:A:100:PRO:HD3	1.97	0.46
2:B:5:ARG:HD2	2:B:8:LYS:NZ	2.31	0.46
12:L:38:HIS:O	30:0:926:A:H1'	2.15	0.46
13:M:92:THR:HB	30:0:401:C:O2'	2.15	0.46
38:W:7804:HOH:O	30:0:1286:A:H5"	2.15	0.46
29:3:67:LEU:HD13	29:3:69:TYR:HE1	1.81	0.46
30:0:168:C:O5'	30:0:168:C:H6	1.98	0.46
30:0:214:U:H5'	38:0:6117:HOH:O	2.15	0.46
30:0:400:C:H2'	30:0:401:C:H6	1.80	0.46
30:0:432:G:C2	30:0:433:C:C5	3.02	0.46
30:0:604:G:H4'	30:0:605:C:O5'	2.15	0.46
30:0:1016:U:H1'	38:0:3652:HOH:O	2.15	0.46
30:0:1398:G:H4'	38:0:6650:HOH:O	2.15	0.46
30:0:1415:G:O2'	30:0:1416:G:H5'	2.15	0.46
30:0:1790:C:H2'	30:0:1791:U:H6	1.80	0.46
30:0:1825:U:O2'	30:0:1826:C:H5'	2.15	0.46
30:0:2259:C:C2	30:0:2260:A:C8	3.04	0.46
30:0:2658:G:C2	30:0:2659:U:C6	3.03	0.46
30:0:2871:G:C6	30:0:2887:G:N1	2.83	0.46
1:A:36:ASP:CB	1:A:85:SER:HB2	2.45	0.46
3:C:72:LYS:HG2	3:C:77:ALA:HA	1.96	0.46
4:D:138:GLY:HA2	31:9:29:C:O3'	2.15	0.46
10:J:90:LYS:HB2	33:J:8802:CL:CL	2.53	0.46
23:W:81:ASP:OD1	23:W:92:ASP:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1:42:SER:HB3	30:0:1473:U:C1'	2.45	0.46
29:3:64:LYS:HD3	29:3:82:GLY:O	2.14	0.46
30:0:10:U:C4	30:0:532:A:N7	2.84	0.46
30:0:100:C:H2'	30:0:101:C:H6	1.81	0.46
30:0:128:A:O2'	30:0:129:A:C5'	2.64	0.46
30:0:247:A:C2	30:0:265:U:C2	3.03	0.46
30:0:440:C:C4	30:0:441:A:C6	3.04	0.46
30:0:732:C:O2'	30:0:733:U:H5'	2.14	0.46
30:0:959:C:H1'	30:0:961:A:C6	2.50	0.46
30:0:1484:G:H2'	38:0:9110:HOH:O	2.16	0.46
30:0:1603:A:C5'	30:0:1605:G:C5'	2.91	0.46
30:0:1806:G:H2'	30:0:1807:U:H6	1.78	0.46
30:0:2520:G:O2'	30:0:2521:A:H5'	2.16	0.46
31:9:3:A:H2'	38:9:9044:HOH:O	2.14	0.46
1:A:212:PRO:HB2	38:0:4344:HOH:O	2.16	0.46
2:B:199:TYR:CE2	2:B:268:ARG:HB2	2.49	0.46
30:0:364:U:H2'	30:0:365:G:O4'	2.15	0.46
30:0:780:A:H2'	30:0:781:C:C6	2.50	0.46
30:0:815:U:H5	38:0:7423:HOH:O	1.98	0.46
30:0:1477:C:C5'	30:0:1868:G:C5'	2.94	0.46
30:0:1590:A:C2	30:0:1606:A:C1'	2.99	0.46
30:0:1626:A:H2'	30:0:1627:G:C5'	2.45	0.46
30:0:2004:U:H4'	38:0:5274:HOH:O	2.14	0.46
30:0:2355:G:H2'	30:0:2355:G:N3	2.31	0.46
30:0:2356:A:H2'	30:0:2357:G:O4'	2.16	0.46
30:0:2911:C:O2'	30:0:2912:C:H5'	2.15	0.46
1:A:94:LEU:HD12	1:A:98:GLU:HB2	1.96	0.46
2:B:304:PRO:HD2	2:B:307:ARG:NE	2.31	0.46
4:D:64:ARG:HB3	4:D:67:ASP:OD2	2.15	0.46
8:H:6:ALA:HA	8:H:61:ARG:NH1	2.30	0.46
9:I:87:PRO:HD3	38:0:7103:HOH:O	2.14	0.46
10:J:130:VAL:HG12	10:J:131:THR:N	2.31	0.46
14:N:147:ILE:HD12	38:9:9091:HOH:O	2.15	0.46
18:R:48:GLU:HA	18:R:51:ILE:HD12	1.98	0.46
23:W:68:THR:HG23	23:W:69:ARG:H	1.81	0.46
30:0:39:G:O6	30:0:441:A:C2	2.68	0.46
30:0:307:G:N2	30:0:309:C:C2	2.84	0.46
30:0:396:U:O2'	30:0:397:A:P	2.73	0.46
30:0:1215:A:O3'	30:0:1216:G:H4'	2.16	0.46
30:0:1524:U:H6	30:0:1524:U:H5"	1.81	0.46
30:0:2626:C:H2'	30:0:2627:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:89:LEU:HD21	30:0:262:A:C6	2.51	0.46
9:I:112:LEU:CD1	30:0:1162:G:H1'	2.45	0.46
14:N:42:HIS:HB3	14:N:62:HIS:HE1	1.80	0.46
15:O:51:TYR:CD2	30:0:721:A:H5"	2.51	0.46
24:X:43:VAL:HG12	24:X:47:ALA:HB3	1.98	0.46
30:0:421:C:H2'	30:0:422:G:C8	2.50	0.46
30:0:497:A:H5"	38:0:3588:HOH:O	2.16	0.46
30:0:662:U:H1'	30:0:748:C:H1'	1.98	0.46
30:0:1187:U:C2	30:0:1189:A:OP2	2.68	0.46
30:0:1200:A:H3'	38:0:5722:HOH:O	2.15	0.46
30:0:1427:A:O2'	30:0:1428:C:H5'	2.16	0.46
30:0:1773:G:H2'	30:0:1774:G:H5'	1.98	0.46
30:0:1829:A:H2'	30:0:1830:C:C5'	2.41	0.46
30:0:2017:U:O2'	30:0:2018:A:C8	2.53	0.46
30:0:2100:A:C5'	38:0:7373:HOH:O	2.57	0.46
30:0:2314:G:O2'	30:0:2315:C:H5'	2.15	0.46
30:0:2397:G:N2	38:0:6910:HOH:O	2.49	0.46
30:0:2471:G:C5	30:0:2472:C:C5	3.03	0.46
30:0:2828:G:O5'	30:0:2828:G:C8	2.68	0.46
9:I:124:VAL:C	9:I:126:THR:H	2.18	0.46
18:R:135:ALA:HB1	18:R:137:ASN:ND2	2.29	0.46
30:0:277:U:O2'	30:0:278:A:H5'	2.16	0.46
30:0:282:C:HO2'	30:0:368:C:N4	2.13	0.46
30:0:334:G:H2'	30:0:335:U:H6	1.81	0.46
30:0:567:U:C5'	38:0:5254:HOH:O	2.62	0.46
30:0:920:C:H5"	30:0:921:G:O5'	2.16	0.46
30:0:969:G:N1	30:0:999:C:N4	2.53	0.46
30:0:1187:U:O2'	30:0:1188:A:C8	2.69	0.46
30:0:1209:C:C2	30:0:1210:G:C8	3.03	0.46
30:0:1497:G:H4'	30:0:1627:G:O2'	2.16	0.46
30:0:2326:C:H4'	30:0:2412:G:C4'	2.46	0.46
30:0:2401:A:H2'	30:0:2402:A:C8	2.51	0.46
30:0:2612:A:H4'	38:0:3676:HOH:O	2.15	0.46
30:0:2912:C:O5'	30:0:2912:C:C6	2.66	0.46
10:J:131:THR:HG22	10:J:134:GLU:HG3	1.97	0.46
14:N:34:LEU:HD22	14:N:129:ILE:HD13	1.98	0.46
15:O:38:ARG:HD3	30:0:654:A:OP2	2.16	0.46
19:S:12:GLU:OE1	30:0:1444:G:H4'	2.15	0.46
20:T:48:VAL:HG23	20:T:98:VAL:HA	1.97	0.46
23:W:29:VAL:O	23:W:30:ASN:HB2	2.16	0.46
26:Z:34:SER:CB	30:0:797:A:H4'	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:488:U:C2'	38:0:3993:HOH:O	2.64	0.46
30:0:562:A:H2'	30:0:563:C:O4'	2.15	0.46
30:0:735:C:C5	30:0:736:A:C4	3.03	0.46
30:0:897:A:H2'	30:0:899:C:C5	2.50	0.46
30:0:1058:A:H2'	30:0:1060:C:H5"	1.97	0.46
30:0:1157:C:H2'	30:0:1158:G:H8	1.80	0.46
30:0:1790:C:H2'	30:0:1791:U:C6	2.51	0.46
30:0:1812:G:H4'	30:0:1814:G:O4'	2.15	0.46
30:0:2038:A:C2	30:0:2039:A:C5	3.04	0.46
30:0:2241:C:H2'	30:0:2242:U:C6	2.50	0.46
30:0:2456:A:H1'	38:0:6579:HOH:O	2.16	0.46
31:9:15:C:N4	31:9:16:G:C6	2.84	0.46
31:9:47:A:C2	31:9:48:C:C2	3.03	0.46
13:M:94:ARG:NH2	30:0:175:G:O6	2.49	0.46
13:M:164:THR:HG22	13:M:165:GLY:N	2.30	0.46
20:T:79:LEU:HG	20:T:89:ARG:HB2	1.98	0.46
24:X:21:PRO:HD3	38:X:6179:HOH:O	2.16	0.46
25:Y:214:ARG:HH12	25:Y:230:ASN:ND2	2.13	0.46
29:3:20:HIS:CE1	29:3:71:CYS:SG	3.09	0.46
30:0:212:A:H5'	30:0:214:U:H1'	1.98	0.46
30:0:938:G:C4	30:0:1031:G:N2	2.84	0.46
30:0:1119:G:N2	30:0:1246:A:H2	2.04	0.46
30:0:1236:A:C2'	30:0:1237:U:H5'	2.46	0.46
30:0:1504:A:C5'	38:0:4396:HOH:O	2.63	0.46
30:0:1512:G:H4'	38:0:4618:HOH:O	2.15	0.46
30:0:1707:G:H1'	30:0:1711:A:N6	2.31	0.46
30:0:1809:G:H2'	30:0:1811:A:OP2	2.16	0.46
30:0:1902:G:H2'	30:0:1903:U:O4'	2.16	0.46
30:0:2011:A:H5'	30:0:2013:G:C1'	2.46	0.46
30:0:2694:A:H3'	30:0:2695:C:H6	1.81	0.46
30:0:2831:C:C2	30:0:2910:A:N1	2.84	0.46
30:0:2860:G:H1'	38:0:6785:HOH:O	2.15	0.46
3:C:35:VAL:HG21	3:C:227:GLY:HA2	1.98	0.45
4:D:63:ILE:HG13	4:D:64:ARG:N	2.32	0.45
5:E:103:VAL:HG22	5:E:115:ARG:HB3	1.96	0.45
13:M:133:LEU:O	13:M:134:ILE:HD13	2.16	0.45
17:Q:64:GLU:HG3	17:Q:74:ASP:CG	2.36	0.45
30:0:56:G:H1'	38:0:5300:HOH:O	2.16	0.45
30:0:1217:G:C2	30:0:1218:U:C2	3.04	0.45
30:0:1490:G:H4'	30:0:1533:A:OP1	2.16	0.45
30:0:1516:U:H2'	30:0:1517:C:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1864:C:H2'	30:0:1865:A:O4'	2.16	0.45
1:A:35:GLY:O	1:A:37:VAL:HG22	2.17	0.45
1:A:94:LEU:HD23	1:A:94:LEU:N	2.31	0.45
1:A:186:TRP:CG	1:A:187:PRO:HA	2.50	0.45
2:B:320:GLN:HA	2:B:321:PRO:HD3	1.83	0.45
4:D:76:ARG:HD2	31:9:42:C:O2	2.16	0.45
8:H:157:TYR:C	8:H:157:TYR:CD1	2.89	0.45
9:I:83:GLY:H	30:0:1168:C:C5'	2.28	0.45
11:K:132:VAL:HG21	21:U:22:VAL:HG13	1.97	0.45
15:O:32:ARG:HH21	15:O:35:LYS:NZ	2.14	0.45
30:0:369:G:O2'	30:0:370:G:H5'	2.16	0.45
30:0:743:G:O2'	30:0:744:G:H5'	2.16	0.45
30:0:940:G:C5	30:0:1027:G:C2	3.04	0.45
30:0:1018:A:O5'	30:0:1018:A:H8	1.99	0.45
30:0:1074:G:H4'	30:0:1260:G:C6	2.52	0.45
30:0:1362:U:O2'	30:0:1363:G:H5'	2.17	0.45
30:0:1400:C:C2'	30:0:1401:G:H5'	2.46	0.45
30:0:1444:G:C6	30:0:1445:G:C5	3.05	0.45
30:0:1503:U:H2'	30:0:1504:A:H5'	1.98	0.45
30:0:1831:U:H2'	30:0:1832:G:H5'	1.98	0.45
30:0:1908:G:H1'	30:0:1931:A:N6	2.31	0.45
30:0:1987:C:O2'	30:0:1988:C:H5'	2.16	0.45
30:0:2134:G:N2	30:0:2242:U:C2	2.85	0.45
30:0:2577:A:H8	38:0:9606:HOH:O	1.99	0.45
30:0:2812:A:C2	30:0:2814:A:N7	2.85	0.45
31:9:39:U:N3	31:9:42:C:H5"	2.31	0.45
1:A:51:ARG:O	1:A:52:SER:HB2	2.16	0.45
8:H:46:TYR:HA	8:H:47:PRO:HD3	1.81	0.45
9:I:113:SER:HA	30:0:1186:C:H5'	1.98	0.45
20:T:114:SER:OG	20:T:117:ASP:HB2	2.16	0.45
29:3:12:PRO:HG2	29:3:13:HIS:CD2	2.49	0.45
30:0:99:A:C8	30:0:100:C:C5	3.05	0.45
30:0:154:C:H2'	30:0:155:C:H6	1.82	0.45
30:0:191:A:N6	30:0:435:A:H62	2.14	0.45
30:0:360:A:H2'	30:0:361:C:O4'	2.16	0.45
30:0:400:C:O2'	30:0:401:C:H5'	2.17	0.45
30:0:595:U:H2'	30:0:596:C:C6	2.52	0.45
30:0:793:A:H2'	30:0:794:U:H6	1.81	0.45
30:0:1116:U:N3	30:0:1246:A:N6	2.60	0.45
30:0:1213:C:O2'	30:0:1214:G:H5'	2.17	0.45
30:0:1603:A:H5'	30:0:1605:G:C5'	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1670:A:H2'	30:0:1671:U:O4'	2.16	0.45
30:0:1759:A:N3	30:0:1818:C:H2'	2.31	0.45
30:0:1948:G:H2'	30:0:1949:G:O4'	2.16	0.45
30:0:2293:G:C6	30:0:2294:C:C5	3.04	0.45
30:0:2757:A:H2'	30:0:2758:G:O4'	2.16	0.45
31:9:59:C:O5'	31:9:59:C:C6	2.63	0.45
2:B:254:GLN:HG2	2:B:255:GLY:N	2.30	0.45
13:M:30:GLU:HG2	38:M:8864:HOH:O	2.17	0.45
13:M:122:GLN:HB2	13:M:127:LYS:HG2	1.98	0.45
14:N:144:GLY:O	14:N:147:ILE:HG23	2.15	0.45
17:Q:15:LYS:HG3	30:0:2364:A:O3'	2.16	0.45
18:R:96:VAL:HG13	18:R:106:GLY:HA3	1.98	0.45
25:Y:144:ARG:CZ	38:Y:8916:HOH:O	2.65	0.45
26:Z:70:ARG:O	26:Z:81:CYS:SG	2.74	0.45
30:0:304:G:H8	30:0:304:G:O5'	2.00	0.45
30:0:734:U:H2'	30:0:736:A:OP2	2.16	0.45
30:0:790:A:H1'	30:0:1710:A:C2'	2.46	0.45
30:0:876:A:N3	30:0:876:A:C2'	2.79	0.45
30:0:912:A:C4	30:0:1294:A:C2	3.04	0.45
30:0:1178:G:C6	30:0:1179:C:N4	2.84	0.45
30:0:1819:G:H2'	30:0:1820:G:C4'	2.46	0.45
30:0:1964:U:H2'	30:0:1964:U:O2	2.15	0.45
30:0:1970:G:H2'	30:0:1970:G:N3	2.31	0.45
30:0:2005:G:H3'	30:0:2005:G:P	2.55	0.45
30:0:2092:G:H2'	30:0:2613:G:OP1	2.17	0.45
30:0:2438:G:H2'	30:0:2439:C:C6	2.51	0.45
31:9:29:C:C5	31:9:30:C:C5	3.04	0.45
2:B:162:MET:HE2	2:B:310:ARG:HD3	1.97	0.45
38:C:8558:HOH:O	30:0:751:U:H5'	2.16	0.45
5:E:152:THR:HG21	5:E:165:GLY:HA2	1.99	0.45
12:L:72:ASN:O	12:L:76:LEU:HG	2.17	0.45
18:R:18:LEU:HB2	18:R:143:VAL:CG1	2.46	0.45
23:W:5:VAL:HG11	23:W:153:MET:HE1	1.99	0.45
28:2:40:ARG:HG3	28:2:45:ASN:CB	2.45	0.45
29:3:59:ASP:OD1	30:0:2460:A:H5"	2.16	0.45
30:0:420:U:O4'	30:0:1920:C:C4	2.70	0.45
30:0:659:A:H5"	38:0:7082:HOH:O	2.17	0.45
30:0:940:G:N3	30:0:1032:A:C2	2.84	0.45
30:0:1524:U:H5"	30:0:1524:U:C6	2.51	0.45
30:0:1547:A:H2'	30:0:1548:U:C6	2.52	0.45
30:0:1940:C:H1'	38:0:9382:HOH:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2697:A:N3	30:0:2697:A:H2'	2.32	0.45
30:0:2718:C:H5'	30:0:2718:C:C6	2.50	0.45
30:0:2728:C:O5'	30:0:2728:C:H6	1.99	0.45
1:A:11:ARG:HD3	38:0:9222:HOH:O	2.16	0.45
1:A:204:GLY:N	30:0:2634:G:OP2	2.49	0.45
6:F:34:ASN:HA	13:M:4:ALA:HB2	1.98	0.45
9:I:82:THR:HG22	30:0:1168:C:H5"	1.97	0.45
12:L:57:VAL:O	12:L:57:VAL:HG12	2.17	0.45
13:M:34:GLU:HB3	13:M:38:GLU:HG3	1.99	0.45
14:N:33:ARG:HG3	38:N:8841:HOH:O	2.17	0.45
15:O:27:GLY:O	15:O:31:GLU:HG3	2.17	0.45
30:0:418:C:H2'	30:0:419:A:C8	2.52	0.45
30:0:790:A:H8	38:0:6078:HOH:O	1.98	0.45
30:0:960:G:N3	30:0:960:G:C2'	2.79	0.45
30:0:1149:U:C5	30:0:1215:A:N7	2.84	0.45
30:0:1151:G:N2	30:0:1214:G:C4	2.85	0.45
30:0:1406:A:H4'	30:0:1407:A:H5"	1.98	0.45
30:0:1434:A:H4'	30:0:1435:U:H5	1.82	0.45
30:0:1523:G:C6	30:0:1524:U:C4	3.05	0.45
30:0:1883:U:H5"	30:0:2013:G:OP2	2.17	0.45
30:0:2475:C:H5'	38:0:3664:HOH:O	2.16	0.45
31:9:61:C:H2'	31:9:62:A:C8	2.46	0.45
1:A:189:VAL:HA	30:0:1845:A:OP1	2.16	0.45
2:B:119:HIS:O	2:B:121:PRO:HD3	2.16	0.45
27:1:16:HIS:HE1	30:0:775:G:OP1	1.99	0.45
29:3:35:TRP:HZ3	30:0:2432:C:OP1	2.00	0.45
30:0:92:G:H2'	30:0:93:C:H6	1.82	0.45
30:0:2385:G:H2'	30:0:2386:U:H6	1.81	0.45
30:0:2515:C:H2'	30:0:2516:G:O4'	2.16	0.45
2:B:43:GLY:O	2:B:308:LEU:HD12	2.16	0.45
4:D:50:VAL:O	4:D:71:ALA:HA	2.17	0.45
6:F:96:ALA:HA	38:F:3111:HOH:O	2.15	0.45
10:J:43:ARG:HD3	38:J:8858:HOH:O	2.17	0.45
30:0:342:C:N4	30:0:343:C:H41	2.15	0.45
30:0:343:C:O2'	30:0:344:C:H5'	2.17	0.45
30:0:387:G:C2'	30:0:388:G:H5'	2.46	0.45
30:0:916:A:C6	30:0:917:U:C4	3.05	0.45
30:0:1405:U:H4'	30:0:1406:A:H5"	1.98	0.45
30:0:1902:G:O2'	30:0:1903:U:H5'	2.16	0.45
30:0:2361:A:H2'	30:0:2362:A:C8	2.51	0.45
30:0:2887:G:H2'	30:0:2888:U:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:30:C:O2	31:9:30:C:C2'	2.65	0.45
31:9:72:C:O2'	31:9:73:A:H5'	2.15	0.45
2:B:86:ALA:HA	38:B:9051:HOH:O	2.16	0.45
2:B:307:ARG:HH11	2:B:307:ARG:HG3	1.82	0.45
3:C:95:GLU:HG3	38:C:8669:HOH:O	2.16	0.45
5:E:102:VAL:HG11	5:E:148:ILE:HG12	1.98	0.45
5:E:121:ASP:HB2	38:E:5899:HOH:O	2.16	0.45
21:U:6:CYS:SG	21:U:31:PHE:HA	2.56	0.45
26:Z:35:SER:HB3	26:Z:47:ARG:HB2	1.98	0.45
30:0:228:C:H2'	30:0:229:G:C5'	2.46	0.45
30:0:281:U:H5	38:0:7575:HOH:O	1.99	0.45
30:0:862:U:H2'	30:0:863:G:C8	2.52	0.45
30:0:957:A:H8	30:0:957:A:O5'	2.00	0.45
30:0:1576:G:C2	30:0:1577:U:C2	3.05	0.45
30:0:1626:A:C2'	30:0:1627:G:H5'	2.46	0.45
30:0:1850:U:H2'	30:0:1851:G:C8	2.52	0.45
30:0:2842:G:H2'	30:0:2843:A:H5'	1.98	0.45
3:C:88:SER:O	3:C:91:PRO:HD3	2.17	0.45
13:M:86:GLN:NE2	38:M:8882:HOH:O	2.50	0.45
30:0:958:G:H2'	30:0:959:C:H6	1.75	0.45
30:0:969:G:N2	30:0:1000:C:C2	2.85	0.45
30:0:1041:U:H2'	30:0:1042:U:C5'	2.46	0.45
30:0:1477:C:C5'	30:0:1868:G:H5"	2.47	0.45
30:0:1543:G:N1	30:0:1641:A:OP2	2.36	0.45
30:0:1801:A:C2	30:0:1802:G:C4	3.04	0.45
30:0:2311:A:O2'	30:0:2312:G:H5'	2.17	0.45
30:0:2511:A:H2'	30:0:2512:U:H6	1.82	0.45
31:9:33:U:C6	31:9:43:G:C8	3.05	0.45
1:A:164:ARG:NH1	1:A:164:ARG:HB3	2.31	0.44
4:D:128:LEU:HD23	4:D:129:ASP:N	2.32	0.44
5:E:153:ARG:NH1	30:0:2778:A:C1'	2.81	0.44
8:H:83:GLU:HA	38:H:243:HOH:O	2.18	0.44
10:J:107:ASN:HD21	10:J:109:TYR:HB2	1.82	0.44
16:P:81:LYS:HE3	30:0:1813:U:O2'	2.18	0.44
18:R:34:GLU:HG2	18:R:46:TYR:OH	2.17	0.44
23:W:48:VAL:HG12	23:W:52:VAL:HB	1.98	0.44
26:Z:47:ARG:O	26:Z:51:ALA:HB2	2.16	0.44
30:0:163:U:O3'	30:0:896:C:H4'	2.16	0.44
30:0:198:A:C2	30:0:2444:U:H1'	2.53	0.44
30:0:283:U:H5"	30:0:284:C:OP2	2.17	0.44
30:0:339:A:C6	30:0:342:C:N3	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:581:G:H5'	38:0:7663:HOH:O	2.17	0.44
30:0:1181:A:O2'	30:0:1182:C:H5'	2.17	0.44
30:0:1392:A:C6	30:0:1395:C:C2	3.05	0.44
30:0:1524:U:H6	30:0:1524:U:C5'	2.29	0.44
30:0:1584:C:O2'	30:0:1585:C:H5'	2.17	0.44
30:0:1748:U:C5	30:0:1749:U:C4	3.06	0.44
30:0:2293:G:C6	30:0:2294:C:C4	3.05	0.44
30:0:2826:G:O6	30:0:2913:A:N6	2.50	0.44
31:9:3:A:OP2	31:9:25:G:N2	2.50	0.44
31:9:107:C:O2'	31:9:108:C:H5'	2.17	0.44
2:B:51:VAL:HG13	2:B:53:LEU:HD13	1.98	0.44
3:C:60:SER:HA	38:C:8575:HOH:O	2.17	0.44
3:C:129:HIS:HD2	3:C:165:ASP:OD2	2.01	0.44
10:J:15:ARG:HG2	10:J:16:ASP:OD1	2.17	0.44
12:L:41:HIS:CD2	30:0:926:A:O2'	2.69	0.44
13:M:76:ARG:HG3	38:M:8827:HOH:O	2.17	0.44
14:N:1:ALA:HB2	31:9:14:G:O2'	2.18	0.44
18:R:98:ASN:ND2	30:0:500:G:H21	2.12	0.44
20:T:81:LYS:HD2	20:T:87:VAL:HG11	1.98	0.44
23:W:10:GLU:O	23:W:13:MET:HB3	2.18	0.44
30:0:440:C:O5'	30:0:440:C:H6	2.00	0.44
30:0:711:G:C2'	30:0:712:C:H5'	2.47	0.44
30:0:1246:A:O2'	30:0:1247:A:H3'	2.17	0.44
30:0:1362:U:H2'	30:0:1363:G:C8	2.52	0.44
30:0:1434:A:H2'	30:0:1436:C:C5	2.52	0.44
9:I:130:LEU:HD21	30:0:1167:G:C4'	2.46	0.44
11:K:86:THR:HG22	11:K:87:ARG:N	2.32	0.44
13:M:71:SER:OG	13:M:72:ALA:N	2.51	0.44
18:R:59:PHE:O	18:R:63:ASN:HB3	2.18	0.44
22:V:12:THR:CG2	22:V:15:GLU:H	2.30	0.44
29:3:10:TYR:CD1	30:0:2408:A:H1'	2.52	0.44
30:0:57:C:H42	30:0:89:G:H1	1.64	0.44
30:0:372:A:O2'	30:0:373:G:H5'	2.17	0.44
30:0:729:C:C2	30:0:743:G:C2	3.05	0.44
30:0:877:G:N7	30:0:885:G:C5	2.85	0.44
30:0:1069:C:H2'	30:0:1070:A:O4'	2.18	0.44
30:0:1132:A:H2'	30:0:1133:A:C8	2.52	0.44
30:0:1202:A:C2'	30:0:1203:G:H5'	2.48	0.44
30:0:1391:G:N2	30:0:1434:A:H5"	2.32	0.44
30:0:1649:G:H1'	38:0:5049:HOH:O	2.17	0.44
30:0:1680:C:H2'	30:0:1681:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1701:A:H5"	30:0:1702:U:H3'	1.99	0.44
30:0:2276:U:H2'	30:0:2277:U:C6	2.52	0.44
2:B:244:PRO:HB3	30:0:1234:U:N3	2.32	0.44
4:D:153:THR:O	4:D:156:ARG:HB2	2.16	0.44
5:E:20:ILE:O	5:E:30:THR:HA	2.17	0.44
8:H:14:LYS:HG3	38:H:183:HOH:O	2.17	0.44
12:L:22:ARG:HG2	38:0:3223:HOH:O	2.15	0.44
19:S:11:THR:H	19:S:14:ALA:HB3	1.81	0.44
25:Y:182:PHE:HD2	25:Y:200:THR:O	2.00	0.44
25:Y:189:ASN:C	25:Y:189:ASN:HD22	2.21	0.44
26:Z:69:ASP:O	26:Z:71:VAL:N	2.45	0.44
29:3:5:ARG:HD2	29:3:21:GLU:HG2	1.98	0.44
30:0:625:U:H5'	38:0:3177:HOH:O	2.16	0.44
30:0:1415:G:C2'	30:0:1416:G:H5'	2.47	0.44
30:0:1556:G:O2'	30:0:1557:G:H5'	2.17	0.44
30:0:2507:G:H2'	30:0:2510:C:H42	1.81	0.44
30:0:2509:A:OP2	30:0:2510:C:H5	2.00	0.44
30:0:2775:A:N6	30:0:2799:A:C8	2.86	0.44
30:0:2911:C:H2'	30:0:2912:C:H6	1.82	0.44
18:R:80:TYR:O	30:0:2050:G:H5"	2.16	0.44
23:W:5:VAL:HG11	23:W:153:MET:CE	2.48	0.44
30:0:1043:C:H2'	38:0:3185:HOH:O	2.18	0.44
30:0:2345:A:C3'	30:0:2346:C:H6	2.23	0.44
1:A:233:THR:HB	30:0:1942:A:H5"	1.99	0.44
3:C:6:TYR:N	3:C:6:TYR:CD1	2.86	0.44
5:E:69:ILE:HA	5:E:72:MET:CE	2.48	0.44
8:H:8:MET:CE	30:0:2494:G:H4'	2.48	0.44
9:I:87:PRO:HG2	30:0:1181:A:O4'	2.18	0.44
13:M:66:SER:HB3	13:M:128:TRP:NE1	2.32	0.44
17:Q:40:HIS:HE1	30:0:949:U:O2'	2.01	0.44
20:T:97:ARG:NH2	30:0:309:C:OP1	2.51	0.44
23:W:129:LYS:CD	31:9:87:U:H2'	2.47	0.44
25:Y:99:ALA:HB2	25:Y:233:TYR:CE2	2.52	0.44
27:1:20:ARG:HB2	38:1:513:HOH:O	2.18	0.44
30:0:569:A:H5"	30:0:587:A:N1	2.32	0.44
30:0:821:U:H2'	30:0:822:C:H6	1.81	0.44
30:0:1016:U:O2'	30:0:2303:A:N7	2.40	0.44
30:0:1112:G:H1	30:0:1251:C:H42	1.65	0.44
30:0:1330:A:H2	38:0:4652:HOH:O	2.00	0.44
30:0:1519:U:O2'	30:0:1520:G:H5'	2.16	0.44
30:0:1706:G:C6	30:0:1707:G:N1	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1711:A:H2'	30:0:1712:A:H5'	1.99	0.44
30:0:1762:C:H2'	30:0:1763:C:H6	1.82	0.44
30:0:2005:G:OP2	30:0:2006:C:C5'	2.66	0.44
30:0:2377:U:O2'	30:0:2378:U:H5'	2.17	0.44
30:0:2457:U:H1'	38:0:7515:HOH:O	2.17	0.44
30:0:2552:C:C6	30:0:2577:A:N7	2.85	0.44
30:0:2781:U:H2'	30:0:2782:G:C5'	2.48	0.44
30:0:2834:G:H2'	30:0:2835:C:O5'	2.17	0.44
30:0:2854:A:C6	30:0:2905:A:N1	2.86	0.44
30:0:2872:U:C2	30:0:2873:C:C6	3.05	0.44
1:A:192:VAL:HG23	30:0:1882:C:OP1	2.17	0.44
2:B:5:ARG:NH1	30:0:2547:C:OP2	2.51	0.44
2:B:241:PRO:HB3	30:0:2609:G:N3	2.33	0.44
4:D:62:ASP:HA	38:D:4233:HOH:O	2.18	0.44
4:D:86:THR:O	4:D:89:PRO:HD2	2.18	0.44
19:S:55:GLN:CD	30:0:1446:U:H2'	2.37	0.44
38:T:2151:HOH:O	30:0:317:A:H5'	2.17	0.44
21:U:45:GLU:HB2	21:U:48:ASN:ND2	2.32	0.44
25:Y:204:ARG:NH2	30:0:1324:G:N2	2.65	0.44
30:0:929:A:O5'	30:0:929:A:H8	2.01	0.44
30:0:1309:U:C2'	30:0:1310:U:H5'	2.48	0.44
30:0:1427:A:C2'	30:0:1428:C:H5'	2.47	0.44
30:0:2250:G:N1	30:0:2251:G:N3	2.66	0.44
30:0:2541:U:H5'	30:0:2611:G:O6	2.18	0.44
30:0:2566:A:C2	30:0:2696:G:O4'	2.71	0.44
1:A:103:VAL:HA	1:A:104:PRO:HD3	1.89	0.44
1:A:194:MET:SD	30:0:875:A:C2	3.11	0.44
2:B:195:ARG:HE	2:B:323:LEU:HD13	1.83	0.44
8:H:59:GLN:HE21	8:H:129:ARG:HE	1.65	0.44
8:H:66:GLU:HA	38:H:239:HOH:O	2.17	0.44
8:H:87:LYS:HG3	8:H:140:TYR:HD1	1.83	0.44
13:M:80:GLY:O	13:M:81:ARG:HB2	2.18	0.44
14:N:47:LEU:HD13	14:N:47:LEU:HA	1.86	0.44
16:P:13:VAL:HG11	16:P:40:VAL:CG1	2.48	0.44
20:T:19:ARG:HD3	20:T:67:LEU:O	2.18	0.44
30:0:157:G:H3'	38:0:3945:HOH:O	2.18	0.44
30:0:304:G:H1'	30:0:347:A:N6	2.32	0.44
30:0:582:U:H2'	30:0:583:C:C6	2.53	0.44
30:0:703:G:C6	30:0:704:C:C4	3.06	0.44
30:0:821:U:O2'	30:0:822:C:H5'	2.18	0.44
30:0:868:G:C4	30:0:887:G:C8	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1202:A:H2'	30:0:1203:G:H5'	2.00	0.44
30:0:1789:G:H2'	30:0:1790:C:O5'	2.17	0.44
30:0:1950:G:H2'	30:0:1951:G:C8	2.53	0.44
30:0:1986:G:C6	30:0:1987:C:N4	2.86	0.44
30:0:2061:C:H2'	30:0:2062:A:H5'	1.99	0.44
30:0:2104:C:O2	30:0:2485:A:N1	2.50	0.44
31:9:26:C:H2'	31:9:27:C:H6	1.79	0.44
31:9:31:C:C2	31:9:50:G:C2	3.05	0.44
31:9:81:C:C2'	31:9:82:U:H5'	2.48	0.44
1:A:182:ARG:HB3	38:0:5133:HOH:O	2.18	0.44
2:B:54:VAL:HB	38:B:9083:HOH:O	2.17	0.44
2:B:279:THR:HG22	2:B:280:VAL:N	2.33	0.44
5:E:90:HIS:CE1	30:0:2694:A:H5"	2.53	0.44
8:H:39:LYS:O	30:0:969:G:H4'	2.18	0.44
10:J:75:PRO:HD3	10:J:136:SER:OG	2.18	0.44
16:P:54:LYS:HB2	30:0:1717:A:H5"	1.98	0.44
16:P:88:GLN:HB3	38:P:185:HOH:O	2.16	0.44
17:Q:25:PRO:HA	17:Q:26:PRO:HD3	1.78	0.44
29:3:10:TYR:CE2	30:0:2382:A:H1'	2.53	0.44
30:0:483:C:H2'	30:0:484:A:O4'	2.18	0.44
30:0:727:G:C2	30:0:728:C:C2	3.06	0.44
30:0:1522:A:H2'	30:0:1523:G:C5'	2.48	0.44
30:0:1937:U:O2'	30:0:1938:G:H5'	2.18	0.44
30:0:2250:G:C2	30:0:2251:G:C4	3.06	0.44
30:0:2431:C:H2'	30:0:2432:C:C6	2.53	0.44
30:0:2729:C:O2'	30:0:2730:G:H5'	2.18	0.44
3:C:174:ILE:CD1	30:0:338:C:H4'	2.48	0.43
4:D:103:ASN:ND2	4:D:133:ASN:HA	2.33	0.43
13:M:104:ARG:HG3	38:M:8866:HOH:O	2.18	0.43
14:N:12:ARG:HD3	14:N:18:THR:OG1	2.18	0.43
23:W:119:HIS:HE1	38:0:9568:HOH:O	2.00	0.43
25:Y:182:PHE:CG	25:Y:202:ALA:HB2	2.53	0.43
26:Z:45:VAL:O	26:Z:49:ARG:HG3	2.18	0.43
30:0:39:G:O2'	30:0:40:C:H5'	2.18	0.43
30:0:175:G:O2'	30:0:176:U:OP2	2.36	0.43
30:0:293:A:C5	30:0:360:A:C2	3.06	0.43
30:0:324:G:C6	30:0:325:U:C5	3.06	0.43
30:0:533:U:H3'	38:0:3742:HOH:O	2.18	0.43
30:0:634:G:O2'	30:0:1358:A:OP1	2.31	0.43
30:0:838:C:H4'	38:0:9187:HOH:O	2.18	0.43
30:0:1166:A:C6	30:0:1167:G:C5	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1167:G:O2'	30:0:1168:C:H5'	2.18	0.43
30:0:1185:U:C5'	38:0:7447:HOH:O	2.59	0.43
30:0:1421:C:O2'	30:0:1422:U:H5'	2.18	0.43
30:0:1544:U:H2'	30:0:1545:C:H6	1.82	0.43
30:0:1592:G:O2'	30:0:1593:C:O4'	2.36	0.43
30:0:1642:A:N7	30:0:1643:C:C4	2.86	0.43
30:0:2090:G:H2'	30:0:2091:G:C8	2.53	0.43
30:0:2435:U:H4'	38:0:9269:HOH:O	2.17	0.43
30:0:2851:G:O2'	30:0:2852:A:H5'	2.17	0.43
31:9:74:G:O2'	31:9:75:G:H5'	2.18	0.43
1:A:94:LEU:HD12	1:A:98:GLU:CB	2.48	0.43
1:A:215:ILE:HG22	1:A:227:ASP:O	2.18	0.43
2:B:84:LEU:HD23	2:B:142:LEU:HD23	2.00	0.43
2:B:202:VAL:HA	2:B:310:ARG:O	2.18	0.43
3:C:193:LEU:HD12	3:C:211:ASP:O	2.18	0.43
4:D:10:PHE:CG	4:D:11:HIS:N	2.86	0.43
13:M:65:VAL:HG21	13:M:105:ALA:HB2	2.00	0.43
23:W:13:MET:HE2	23:W:17:ILE:HG22	2.00	0.43
23:W:115:THR:HG23	38:W:5420:HOH:O	2.18	0.43
23:W:142:ASP:HB3	23:W:145:GLY:H	1.83	0.43
24:X:39:LYS:HE2	30:0:2834:G:OP1	2.17	0.43
26:Z:61:HIS:O	26:Z:69:ASP:HA	2.17	0.43
30:0:117:A:H2'	30:0:118:G:C8	2.53	0.43
30:0:692:A:N6	30:0:693:A:C2	2.86	0.43
30:0:827:A:H2'	30:0:828:G:O4'	2.18	0.43
30:0:1130:U:C2'	30:0:1131:G:H5'	2.48	0.43
30:0:1706:G:H1'	30:0:1712:A:N6	2.30	0.43
30:0:1916:C:C2	30:0:1924:A:C2	3.06	0.43
30:0:2135:A:O4'	30:0:2243:C:N4	2.51	0.43
30:0:2871:G:C4	30:0:2887:G:N2	2.86	0.43
31:9:2:U:OP2	31:9:3:A:H5'	2.18	0.43
1:A:38:ILE:HB	1:A:82:VAL:O	2.18	0.43
3:C:44:GLN:HA	38:C:8605:HOH:O	2.18	0.43
3:C:47:GLY:HA2	3:C:92:PRO:HB2	2.00	0.43
4:D:75:LEU:HD22	4:D:79:MET:HB3	2.00	0.43
20:T:14:ALA:HA	20:T:15:PRO:HD3	1.90	0.43
25:Y:154:ARG:HH21	30:0:1293:U:H5'	1.83	0.43
30:0:219:G:O5'	30:0:220:C:H5"	2.18	0.43
30:0:385:C:O5'	30:0:385:C:H6	2.02	0.43
30:0:665:A:C6	30:0:666:A:C6	3.06	0.43
30:0:820:G:H3'	30:0:820:G:N3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1210:G:C2	30:0:1211:G:C8	3.06	0.43
30:0:1298:U:H2'	30:0:1299:G:C8	2.53	0.43
30:0:1363:G:H2'	30:0:1364:G:C8	2.54	0.43
30:0:1815:A:H4'	30:0:2751:C:O4'	2.19	0.43
30:0:1816:C:H2'	30:0:1817:U:O4'	2.17	0.43
30:0:1949:G:N2	30:0:1964:U:C2	2.87	0.43
30:0:2112:A:H2'	30:0:2113:G:C8	2.53	0.43
30:0:2277:U:H1'	30:0:2469:A:N3	2.33	0.43
30:0:2429:A:C4'	38:0:7716:HOH:O	2.66	0.43
30:0:2594:C:O2'	30:0:2595:U:H5'	2.19	0.43
30:0:2793:A:N6	38:0:5853:HOH:O	2.50	0.43
30:0:2847:G:C2'	30:0:2848:G:H5'	2.48	0.43
3:C:6:TYR:N	3:C:6:TYR:HD1	2.17	0.43
5:E:84:MET:SD	38:E:3134:HOH:O	2.61	0.43
5:E:91:PHE:HA	5:E:92:PRO:HD3	1.89	0.43
5:E:126:ILE:HA	5:E:131:LEU:CD2	2.47	0.43
11:K:4:LEU:HD22	11:K:116:GLU:HB3	2.00	0.43
14:N:139:TRP:HA	14:N:139:TRP:CE3	2.53	0.43
30:0:36:C:H1'	38:0:3051:HOH:O	2.17	0.43
30:0:41:G:H8	30:0:41:G:O5'	2.00	0.43
30:0:152:A:O2'	30:0:153:C:H5'	2.18	0.43
30:0:234:A:H4'	30:0:437:A:O4'	2.18	0.43
30:0:1537:C:H2'	30:0:1538:C:H6	1.83	0.43
30:0:1878:G:O2'	30:0:1879:U:OP2	2.36	0.43
30:0:1980:U:O2	30:0:2008:U:H4'	2.18	0.43
31:9:115:C:C4	31:9:116:C:C5	3.06	0.43
2:B:154:VAL:HA	2:B:155:PRO:HD3	1.88	0.43
3:C:39:GLN:O	3:C:43:LYS:HD3	2.18	0.43
9:I:73:LEU:HD12	9:I:107:LYS:NZ	2.33	0.43
16:P:8:ARG:HG3	38:P:188:HOH:O	2.17	0.43
23:W:6:GLN:HB2	23:W:26:ILE:CD1	2.48	0.43
30:0:148:A:O2'	30:0:149:G:H5'	2.19	0.43
30:0:772:G:H2'	30:0:773:A:O4'	2.18	0.43
30:0:1024:G:C6	30:0:1025:C:C4	3.07	0.43
30:0:1503:U:H2'	30:0:1504:A:O4'	2.19	0.43
30:0:1520:G:C2	30:0:1521:C:C2	3.07	0.43
30:0:2070:G:H2'	30:0:2072:G:OP1	2.18	0.43
30:0:2354:A:H5'	30:0:2355:G:N7	2.33	0.43
30:0:2361:A:H5'	38:0:9191:HOH:O	2.19	0.43
30:0:2429:A:H4'	38:0:7716:HOH:O	2.16	0.43
30:0:2445:U:H2'	30:0:2446:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2451:G:H2'	30:0:2451:G:N3	2.32	0.43
30:0:2531:U:H2'	30:0:2532:A:O4'	2.19	0.43
30:0:2748:G:H1'	38:0:7881:HOH:O	2.18	0.43
30:0:2768:A:H3'	30:0:2768:A:N3	2.33	0.43
31:9:39:U:O2'	31:9:42:C:H5	2.01	0.43
1:A:71:PRO:O	1:A:160:ALA:HB2	2.18	0.43
4:D:104:PHE:CE2	4:D:132:VAL:HB	2.54	0.43
4:D:128:LEU:HB2	38:D:6007:HOH:O	2.18	0.43
5:E:107:PHE:CE2	5:E:108:LEU:HD13	2.54	0.43
6:F:60:VAL:O	6:F:62:HIS:N	2.52	0.43
10:J:70:PHE:HE1	30:0:2676:C:C4'	2.32	0.43
13:M:164:THR:HB	38:M:8820:HOH:O	2.17	0.43
14:N:32:PRO:HD2	14:N:99:GLU:O	2.18	0.43
14:N:77:ASN:OD1	14:N:79:PRO:HD2	2.18	0.43
17:Q:11:ARG:NH2	30:0:2363:G:C5'	2.81	0.43
26:Z:55:SER:HA	38:0:7562:HOH:O	2.19	0.43
29:3:59:ASP:HB3	29:3:63:LYS:HZ1	1.83	0.43
29:3:67:LEU:CD1	29:3:69:TYR:HE1	2.31	0.43
30:0:629:A:C2	30:0:2074:A:C2	3.07	0.43
30:0:1167:G:C2	30:0:1168:C:C2	3.06	0.43
30:0:1175:G:N3	30:0:1193:A:C6	2.86	0.43
30:0:1275:C:C2'	30:0:1276:U:H5'	2.49	0.43
30:0:1284:G:O2'	30:0:1285:U:H5'	2.18	0.43
30:0:1421:C:C2	30:0:1444:G:N2	2.87	0.43
30:0:1985:U:C2	30:0:1996:U:O4'	2.72	0.43
30:0:2429:A:N6	38:0:3326:HOH:O	2.51	0.43
30:0:2569:A:H2'	30:0:2570:G:O5'	2.19	0.43
30:0:2668:G:H2'	30:0:2669:U:H6	1.81	0.43
30:0:2692:G:N2	30:0:2701:G:C8	2.87	0.43
30:0:2886:C:O2'	30:0:2887:G:H5'	2.18	0.43
31:9:5:G:O2'	31:9:6:C:H5'	2.18	0.43
31:9:65:A:C4	31:9:113:C:C4	3.07	0.43
31:9:108:C:H2'	31:9:109:G:H8	1.82	0.43
2:B:27:ASN:HD21	30:0:2807:U:P	2.41	0.43
13:M:29:GLN:OE1	30:0:2244:A:H5"	2.18	0.43
13:M:70:GLY:HA3	13:M:73:ARG:HH21	1.77	0.43
14:N:91:ARG:O	14:N:94:GLU:HB2	2.19	0.43
26:Z:41:ARG:HD2	30:0:820:G:H22	1.83	0.43
30:0:85:C:H3'	30:0:86:A:H2'	2.01	0.43
30:0:102:A:C6	30:0:103:C:C4	3.06	0.43
30:0:273:G:H2'	30:0:274:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:284:C:OP2	30:0:284:C:H6	2.01	0.43
30:0:624:U:O4	30:0:628:1MA:H8	2.01	0.43
30:0:877:G:H3'	38:0:3106:HOH:O	2.19	0.43
30:0:1178:G:C5	30:0:1179:C:C4	3.07	0.43
30:0:1333:U:H2'	30:0:1334:C:C6	2.53	0.43
30:0:1519:U:H1'	38:0:3898:HOH:O	2.18	0.43
30:0:1552:G:C6	30:0:1634:G:C6	3.07	0.43
30:0:1602:C:H5'	38:0:6467:HOH:O	2.18	0.43
30:0:1665:G:C2	30:0:1666:C:C6	3.07	0.43
30:0:1705:C:O2	30:0:2735:U:C5'	2.65	0.43
30:0:2473:U:H2'	30:0:2476:C:H5	1.84	0.43
30:0:2507:G:H22	30:0:2512:U:H5"	1.84	0.43
30:0:2803:C:H2'	30:0:2804:C:C6	2.54	0.43
30:0:2855:G:C2	30:0:2904:U:C2	3.06	0.43
31:9:111:U:O2'	31:9:112:U:H5'	2.19	0.43
1:A:167:LYS:CE	26:Z:50:VAL:HG13	2.42	0.43
14:N:65:ASP:HB3	38:N:8820:HOH:O	2.19	0.43
16:P:58:SER:HB3	38:0:5593:HOH:O	2.18	0.43
21:U:6:CYS:HB2	21:U:13:ILE:CG1	2.49	0.43
25:Y:144:ARG:HB3	38:0:4369:HOH:O	2.18	0.43
29:3:22:VAL:HG12	29:3:90:PHE:HE2	1.83	0.43
30:0:79:G:H22	30:0:97:G:H1'	1.82	0.43
30:0:432:G:C2	30:0:433:C:C6	3.07	0.43
30:0:816:G:C6	30:0:817:G:N1	2.87	0.43
30:0:1159:G:C6	30:0:1160:G:C4	3.07	0.43
30:0:1202:A:H2'	30:0:1203:G:O4'	2.19	0.43
30:0:1255:A:H2'	30:0:1256:C:O5'	2.18	0.43
30:0:1703:G:C2	30:0:1716:A:C4	3.06	0.43
30:0:1788:U:C2	30:0:1805:G:C2	3.07	0.43
30:0:2094:G:C2	30:0:2652:U:O2	2.71	0.43
30:0:2510:C:H42	30:0:2564:G:H22	1.66	0.43
30:0:2727:A:C6	30:0:2756:U:N3	2.87	0.43
30:0:2780:C:C4	30:0:2781:U:C4	3.06	0.43
30:0:2812:A:H2	30:0:2814:A:H62	1.63	0.43
1:A:105:VAL:HG11	1:A:154:ALA:HB1	2.00	0.43
2:B:305:ASP:O	2:B:306:LYS:CB	2.66	0.43
5:E:7:ILE:HG23	5:E:45:ASP:O	2.19	0.43
5:E:95:VAL:O	5:E:126:ILE:HD12	2.18	0.43
10:J:99:GLU:HA	38:J:8871:HOH:O	2.19	0.43
16:P:134:VAL:O	16:P:137:LEU:HB3	2.19	0.43
18:R:18:LEU:HD12	18:R:143:VAL:CG1	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:39:THR:HB	18:R:42:GLU:CD	2.39	0.43
25:Y:235:GLU:CD	25:Y:235:GLU:N	2.72	0.43
29:3:17:HIS:ND1	30:0:2408:A:O2'	2.48	0.43
29:3:54:LYS:HE3	38:0:3005:HOH:O	2.18	0.43
30:0:191:A:H61	30:0:435:A:H62	1.67	0.43
30:0:1399:A:H2'	30:0:1400:C:C6	2.54	0.43
30:0:1667:A:H2'	30:0:1668:U:O4'	2.19	0.43
30:0:1697:G:H1'	38:0:7261:HOH:O	2.19	0.43
30:0:1712:A:H2'	30:0:1713:G:O4'	2.19	0.43
30:0:1882:C:H2'	30:0:1883:U:C6	2.53	0.43
30:0:2080:G:H2'	30:0:2081:A:C8	2.54	0.43
30:0:2328:U:C4	30:0:2329:C:C5	3.07	0.43
30:0:2332:A:H3'	30:0:2333:G:H8	1.84	0.43
31:9:11:A:H2	31:9:68:G:N3	2.17	0.43
31:9:39:U:H2'	31:9:40:C:OP1	2.18	0.43
1:A:72:GLU:HG2	26:Z:100:GLY:HA3	2.01	0.43
4:D:12:GLU:O	4:D:15:GLU:HG2	2.18	0.43
6:F:58:GLU:HB3	13:M:8:ILE:HG23	2.01	0.43
12:L:6:ARG:HD3	30:0:1299:G:O6	2.18	0.43
13:M:48:LYS:HE3	13:M:52:GLN:NE2	2.28	0.43
19:S:57:THR:C	19:S:59:ASP:H	2.21	0.43
20:T:28:SER:HA	20:T:97:ARG:HD3	1.99	0.43
30:0:67:A:H5"	30:0:69:A:C8	2.54	0.43
30:0:135:G:C2	30:0:144:A:N3	2.86	0.43
30:0:393:G:C2	30:0:394:G:C4	3.06	0.43
30:0:435:A:O2'	30:0:436:A:H5'	2.19	0.43
30:0:699:C:C2	30:0:744:G:N2	2.87	0.43
30:0:793:A:C2	30:0:822:C:C2	3.06	0.43
30:0:816:G:O5'	30:0:816:G:H8	2.02	0.43
30:0:1192:A:H4'	38:0:4383:HOH:O	2.18	0.43
30:0:1342:C:H2'	30:0:1343:C:H5'	1.99	0.43
30:0:1383:U:H2'	30:0:1384:C:C6	2.54	0.43
30:0:1504:A:H4'	30:0:1506:U:C5	2.53	0.43
30:0:1600:G:OP2	30:0:1600:G:H8	2.02	0.43
30:0:1933:G:C2'	30:0:1934:A:H5'	2.48	0.43
30:0:2095:A:OP1	30:0:2096:A:H4'	2.19	0.43
30:0:2293:G:C5	30:0:2294:C:C5	3.07	0.43
30:0:2476:C:H2'	30:0:2476:C:O2	2.19	0.43
30:0:2779:G:N7	30:0:2790:C:C2	2.86	0.43
30:0:2896:A:N3	30:0:2896:A:H2'	2.34	0.43
31:9:11:A:H4'	31:9:13:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:TYR:HB2	30:0:1872:C:C5	2.54	0.42
1:A:81:GLN:H	1:A:92:ASN:ND2	2.17	0.42
3:C:156:LEU:O	3:C:160:LEU:HG	2.19	0.42
4:D:67:ASP:HA	4:D:68:PRO:HD3	1.92	0.42
5:E:81:GLU:O	5:E:172:PRO:HD3	2.19	0.42
13:M:42:ARG:HA	13:M:43:PRO:HD3	1.86	0.42
15:O:57:THR:O	15:O:111:VAL:HG23	2.19	0.42
19:S:42:GLU:O	19:S:46:ASP:HA	2.19	0.42
21:U:34:SER:HB3	38:0:3126:HOH:O	2.17	0.42
30:0:248:A:H5'	30:0:249:G:OP2	2.19	0.42
30:0:349:U:O5'	30:0:349:U:H6	2.02	0.42
30:0:577:G:C2	30:0:581:G:C6	3.07	0.42
30:0:729:C:C2	30:0:743:G:N2	2.87	0.42
30:0:877:G:N7	30:0:885:G:C6	2.87	0.42
30:0:970:U:H2'	38:0:6308:HOH:O	2.18	0.42
30:0:1287:A:H8	38:0:7887:HOH:O	2.02	0.42
31:9:16:G:C2	31:9:66:G:O6	2.72	0.42
31:9:110:G:C6	31:9:111:U:C5	3.07	0.42
3:C:24:THR:HG23	3:C:25:PRO:HD2	2.02	0.42
4:D:137:PRO:O	31:9:30:C:OP1	2.37	0.42
13:M:112:LEU:HB3	13:M:133:LEU:HB3	2.02	0.42
23:W:11:VAL:O	23:W:12:ASN:HB2	2.19	0.42
24:X:43:VAL:HG12	24:X:44:ASP:N	2.34	0.42
24:X:49:ARG:NH1	30:0:1385:G:O3'	2.51	0.42
27:1:44:LYS:HG2	30:0:148:A:H5"	2.01	0.42
30:0:95:A:H5"	30:0:97:G:O4'	2.19	0.42
30:0:188:C:H6	30:0:188:C:O5'	2.02	0.42
30:0:726:C:C2	30:0:727:G:C8	3.07	0.42
30:0:1183:C:N3	30:0:1184:C:N4	2.67	0.42
30:0:1184:C:O2'	30:0:1185:U:OP2	2.32	0.42
30:0:1568:G:C2'	30:0:1569:U:H5'	2.49	0.42
30:0:1970:G:H4'	30:0:1971:G:O5'	2.19	0.42
30:0:1981:A:C6	30:0:2005:G:H4'	2.54	0.42
30:0:2005:G:OP2	30:0:2006:C:H5"	2.19	0.42
30:0:2512:U:H4'	30:0:2514:U:O4	2.19	0.42
30:0:2531:U:H4'	38:0:9596:HOH:O	2.17	0.42
30:0:2600:A:H2'	30:0:2601:A:O4'	2.19	0.42
30:0:2853:U:C4	30:0:2906:A:N6	2.87	0.42
3:C:46:TYR:CE1	30:0:450:C:H4'	2.54	0.42
3:C:151:GLN:HA	3:C:151:GLN:HE21	1.84	0.42
3:C:194:PHE:HB2	3:C:212:VAL:HG12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:76:ARG:NE	31:9:44:A:O4'	2.52	0.42
5:E:21:THR:HG23	5:E:30:THR:OG1	2.19	0.42
8:H:65:LEU:HA	8:H:65:LEU:HD12	1.80	0.42
26:Z:34:SER:HB3	30:0:797:A:H4'	2.00	0.42
30:0:107:U:H2'	30:0:108:U:H5'	2.01	0.42
30:0:111:C:H2'	30:0:112:G:O4'	2.19	0.42
30:0:314:G:N2	30:0:317:A:C8	2.87	0.42
30:0:354:A:H2'	30:0:355:C:C6	2.52	0.42
30:0:752:G:H2'	30:0:753:U:O4'	2.19	0.42
30:0:830:G:O2'	30:0:831:U:H5'	2.19	0.42
30:0:1115:U:H5"	30:0:1140:C:O2'	2.20	0.42
30:0:1474:C:O2'	30:0:1475:G:H5'	2.18	0.42
30:0:2248:C:O2'	30:0:2249:G:H5'	2.19	0.42
30:0:2374:G:H2'	30:0:2375:A:C8	2.53	0.42
2:B:57:GLU:HA	2:B:58:PRO:HD2	1.85	0.42
2:B:60:SER:HA	2:B:61:PRO:HD3	1.90	0.42
5:E:35:TYR:CD2	5:E:36:PRO:HD2	2.55	0.42
5:E:72:MET:O	5:E:76:VAL:HG22	2.19	0.42
5:E:106:ASN:ND2	5:E:109:GLY:HA2	2.34	0.42
12:L:38:HIS:CD2	12:L:39:GLU:HG3	2.54	0.42
19:S:57:THR:HG22	19:S:58:MET:N	2.34	0.42
20:T:24:ARG:HH21	20:T:39:ASN:ND2	2.17	0.42
26:Z:66:CYS:SG	26:Z:67:GLY:N	2.93	0.42
28:2:22:PRO:HG2	28:2:25:VAL:CG2	2.49	0.42
29:3:80:ARG:HH22	30:0:2381:C:H4'	1.84	0.42
30:0:282:C:O2'	30:0:368:C:N4	2.52	0.42
30:0:652:G:H2'	30:0:653:U:O4'	2.20	0.42
30:0:877:G:C6	30:0:885:G:C4	3.08	0.42
30:0:1195:G:N2	30:0:1205:U:C2	2.87	0.42
30:0:1350:U:H5"	38:0:5090:HOH:O	2.20	0.42
30:0:1789:G:C2'	30:0:1790:C:O5'	2.67	0.42
30:0:2362:A:H2'	30:0:2363:G:C8	2.54	0.42
30:0:2502:C:O2'	30:0:2503:A:H5'	2.19	0.42
30:0:2655:U:C4	30:0:2656:G:N7	2.87	0.42
30:0:2893:C:C2'	30:0:2894:C:H5'	2.49	0.42
31:9:36:C:C5	31:9:37:C:C4	3.08	0.42
31:9:57:A:N3	31:9:57:A:H5'	2.34	0.42
31:9:65:A:C2'	31:9:66:G:OP2	2.68	0.42
1:A:81:GLN:HB2	1:A:92:ASN:ND2	2.35	0.42
1:A:223:ARG:HH12	30:0:2270:G:C4'	2.27	0.42
2:B:162:MET:HG3	2:B:310:ARG:NH1	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:177:HIS:O	2:B:181:ILE:HG13	2.19	0.42
2:B:307:ARG:HG2	2:B:308:LEU:N	2.34	0.42
3:C:211:ASP:HB2	3:C:231:ARG:HH12	1.85	0.42
4:D:88:LEU:HB2	4:D:89:PRO:HD3	2.00	0.42
8:H:91:ARG:NH2	8:H:135:GLN:NE2	2.68	0.42
12:L:10:SER:O	12:L:11:ARG:HB3	2.19	0.42
15:O:105:ASN:HD21	15:O:109:SER:N	2.18	0.42
16:P:10:ALA:HA	16:P:13:VAL:HG12	2.02	0.42
24:X:12:ILE:HB	24:X:70:ILE:CG2	2.49	0.42
26:Z:38:PHE:HB3	26:Z:42:TYR:HD1	1.82	0.42
29:3:10:TYR:CD2	30:0:2382:A:H1'	2.55	0.42
30:0:138:U:P	30:0:139:C:H5	2.42	0.42
30:0:161:A:H2'	30:0:162:C:C6	2.53	0.42
30:0:165:A:H2'	30:0:166:A:OP1	2.19	0.42
30:0:265:U:C2	30:0:266:G:C8	3.07	0.42
30:0:690:G:H1'	30:0:731:U:O2'	2.20	0.42
30:0:776:A:C2	30:0:780:A:C6	3.08	0.42
30:0:1342:C:O2'	30:0:1343:C:H5'	2.18	0.42
30:0:1754:A:H8	30:0:1754:A:O5'	2.02	0.42
30:0:1757:U:H5	38:0:3214:HOH:O	2.02	0.42
30:0:1848:G:O2'	30:0:1849:G:H5'	2.19	0.42
30:0:1998:G:O2'	30:0:2026:C:H1'	2.20	0.42
30:0:2346:C:O2	30:0:2346:C:H2'	2.18	0.42
30:0:2470:A:H2'	30:0:2471:G:O5'	2.19	0.42
31:9:22:G:C6	31:9:55:U:C2	3.07	0.42
1:A:10:GLY:HA2	30:0:1861:C:O2	2.20	0.42
2:B:48:MET:O	30:0:2719:A:H5'	2.20	0.42
8:H:48:VAL:HG13	38:H:218:HOH:O	2.18	0.42
9:I:133:THR:HG22	9:I:134:ILE:H	1.83	0.42
13:M:185:PRO:HD3	38:0:9800:HOH:O	2.19	0.42
13:M:191:GLY:O	30:0:175:G:H3'	2.19	0.42
24:X:71:ARG:HD3	38:X:2171:HOH:O	2.20	0.42
27:1:37:CYS:SG	27:1:39:PHE:HB2	2.59	0.42
29:3:33:MET:CG	30:0:1922:A:H2'	2.50	0.42
30:0:221:G:H2'	30:0:222:A:C8	2.55	0.42
30:0:453:A:C4	30:0:479:G:N7	2.87	0.42
30:0:685:C:O2'	30:0:748:C:H5"	2.19	0.42
30:0:1047:U:O5'	30:0:1047:U:H6	2.03	0.42
30:0:1097:A:H2'	30:0:1098:A:C8	2.54	0.42
30:0:1367:A:H2'	30:0:1368:U:O4'	2.20	0.42
30:0:1391:G:H2'	30:0:1392:A:H5'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1573:A:C8	30:0:1574:C:C6	3.08	0.42
30:0:1603:A:H5'	30:0:1605:G:H5'	1.99	0.42
30:0:1643:C:O2'	30:0:1644:C:H5'	2.19	0.42
30:0:1680:C:H5'	30:0:1685:A:N6	2.34	0.42
30:0:1709:G:C6	30:0:1711:A:C5	3.07	0.42
30:0:2499:U:H2'	30:0:2500:C:O4'	2.20	0.42
30:0:2805:A:C8	30:0:2806:C:C5	3.07	0.42
30:0:2842:G:C2'	30:0:2843:A:H5'	2.50	0.42
31:9:108:C:H2'	31:9:109:G:C8	2.55	0.42
1:A:26:ASP:HB2	38:0:7291:HOH:O	2.18	0.42
2:B:223:ARG:HG3	2:B:232:TRP:C	2.40	0.42
8:H:59:GLN:HE21	8:H:129:ARG:HG2	1.85	0.42
10:J:116:LEU:HB2	10:J:119:THR:CG2	2.49	0.42
10:J:131:THR:O	10:J:134:GLU:HB2	2.19	0.42
13:M:70:GLY:HA3	13:M:73:ARG:CZ	2.50	0.42
13:M:159:VAL:HG13	13:M:160:PHE:N	2.35	0.42
14:N:169:PRO:O	14:N:172:PHE:HB3	2.20	0.42
20:T:75:GLU:O	20:T:76:ASP:HB2	2.19	0.42
30:0:462:A:N6	30:0:477:A:C2	2.88	0.42
30:0:583:C:H2'	30:0:584:U:H6	1.85	0.42
30:0:590:A:H2'	30:0:591:A:C5'	2.48	0.42
30:0:669:G:C4	30:0:670:G:C8	3.07	0.42
30:0:795:G:H2'	38:0:9823:HOH:O	2.20	0.42
30:0:1060:C:H6	30:0:1060:C:H5'	1.85	0.42
30:0:1255:A:C2'	30:0:1256:C:O5'	2.68	0.42
30:0:1523:G:C6	30:0:1524:U:O4	2.73	0.42
30:0:1965:C:O5'	30:0:1965:C:H6	2.02	0.42
30:0:2492:U:C4	30:0:2493:C:C4	3.07	0.42
30:0:2812:A:H2	30:0:2814:A:N7	2.17	0.42
30:0:2864:U:H2'	30:0:2865:G:H5'	2.02	0.42
1:A:160:ALA:CB	26:Z:89:THR:HB	2.49	0.42
38:C:8619:HOH:O	30:0:338:C:H5'	2.19	0.42
4:D:104:PHE:CD2	4:D:104:PHE:N	2.88	0.42
13:M:30:GLU:O	13:M:34:GLU:HG3	2.19	0.42
23:W:92:ASP:OD2	23:W:94:SER:HB2	2.20	0.42
24:X:25:ARG:HD2	38:X:5356:HOH:O	2.19	0.42
26:Z:37:ARG:HG3	26:Z:38:PHE:CD2	2.54	0.42
30:0:451:C:C2'	30:0:452:G:H5'	2.50	0.42
30:0:711:G:N2	30:0:718:C:N1	2.67	0.42
30:0:802:G:N2	30:0:812:A:C4	2.88	0.42
30:0:877:G:C2	30:0:885:G:O4'	2.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1241:G:H2'	30:0:1242:A:O4'	2.19	0.42
30:0:1537:C:O2'	30:0:1538:C:H5'	2.18	0.42
30:0:1541:G:O2'	30:0:1542:G:H5'	2.18	0.42
30:0:2256:G:H2'	30:0:2257:G:C5'	2.50	0.42
1:A:169:PHE:O	1:A:170:VAL:HB	2.20	0.42
2:B:8:LYS:HB3	2:B:218:TRP:O	2.19	0.42
2:B:316:ARG:HB2	30:0:2768:A:C8	2.55	0.42
3:C:87:ARG:NH2	30:0:894:A:C2	2.88	0.42
30:0:325:U:H3'	38:0:5512:HOH:O	2.19	0.42
30:0:387:G:O2'	30:0:388:G:H5'	2.20	0.42
30:0:473:A:C2'	30:0:474:C:H5'	2.49	0.42
30:0:485:A:N3	30:0:487:G:H5"	2.34	0.42
30:0:1183:C:H1'	30:0:1192:A:N6	2.35	0.42
30:0:1187:U:O2	30:0:1189:A:H5"	2.20	0.42
30:0:1413:A:H2'	30:0:1414:A:O4'	2.20	0.42
30:0:1819:G:H2'	30:0:1820:G:H5'	2.01	0.42
30:0:1840:A:H4'	30:0:1841:C:O5'	2.20	0.42
30:0:2355:G:N3	30:0:2355:G:C2'	2.83	0.42
30:0:2523:U:O2'	30:0:2524:G:H5'	2.19	0.42
31:9:74:G:C2	31:9:75:G:C8	3.08	0.42
31:9:92:G:C6	31:9:93:A:N6	2.88	0.42
5:E:77:THR:OG1	5:E:78:GLU:N	2.50	0.42
8:H:149:VAL:HG13	8:H:150:LYS:N	2.35	0.42
11:K:105:ARG:HD2	38:K:3385:HOH:O	2.19	0.42
16:P:40:VAL:O	16:P:44:VAL:HG23	2.20	0.42
17:Q:27:GLN:HB3	38:9:9083:HOH:O	2.20	0.42
23:W:10:GLU:HB3	38:W:1223:HOH:O	2.20	0.42
24:X:70:ILE:HG23	24:X:70:ILE:O	2.18	0.42
26:Z:61:HIS:CG	26:Z:95:PRO:HG3	2.55	0.42
28:2:41:HIS:CE1	30:0:1439:C:H5"	2.54	0.42
29:3:14:CYS:SG	38:3:9063:HOH:O	2.62	0.42
29:3:83:TRP:O	29:3:85:ALA:N	2.53	0.42
30:0:59:A:H5"	38:0:4313:HOH:O	2.18	0.42
30:0:67:A:H3'	30:0:67:A:OP2	2.20	0.42
30:0:293:A:C2	30:0:294:C:C6	3.08	0.42
30:0:868:G:H2'	38:0:3039:HOH:O	2.18	0.42
30:0:1015:C:H2'	30:0:1016:U:H6	1.82	0.42
30:0:2700:G:C2'	30:0:2701:G:H5'	2.49	0.42
30:0:2909:G:N2	30:0:2910:A:C5	2.88	0.42
31:9:114:G:C6	31:9:115:C:N4	2.88	0.42
2:B:203:ALA:HA	2:B:263:THR:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:224:LYS:HD3	2:B:224:LYS:HA	1.83	0.41
38:I:3512:HOH:O	30:0:1163:G:N2	2.53	0.41
12:L:35:ARG:HB2	12:L:43:HIS:CD2	2.55	0.41
12:L:53:ARG:N	33:L:8810:CL:CL	2.66	0.41
12:L:73:VAL:HG21	12:L:116:HIS:CE1	2.54	0.41
13:M:89:THR:HA	38:M:8950:HOH:O	2.19	0.41
15:O:39:THR:HB	38:0:4589:HOH:O	2.19	0.41
15:O:68:GLY:HA3	30:0:745:G:O6	2.20	0.41
21:U:56:ARG:NH1	30:0:2890:A:C2	2.88	0.41
22:V:39:ALA:C	22:V:41:GLU:H	2.23	0.41
28:2:48:ASP:O	28:2:49:GLU:HB2	2.20	0.41
29:3:62:THR:CG2	29:3:63:LYS:N	2.83	0.41
30:0:314:G:C2	30:0:317:A:C8	3.08	0.41
30:0:335:U:C2'	30:0:336:G:OP1	2.68	0.41
30:0:371:U:H2'	30:0:372:A:H8	1.85	0.41
30:0:628:1MA:H4'	38:0:3136:HOH:O	2.19	0.41
30:0:887:G:H2'	30:0:888:U:C6	2.54	0.41
30:0:1006:A:N3	30:0:2298:C:O2'	2.45	0.41
30:0:1182:C:H4'	30:0:1192:A:N7	2.35	0.41
30:0:1210:G:C2	30:0:1211:G:N9	2.88	0.41
30:0:1588:G:C6	30:0:1589:G:C6	3.08	0.41
30:0:1624:A:O4'	30:0:1626:A:C8	2.73	0.41
30:0:1789:G:N2	30:0:1790:C:H1'	2.35	0.41
30:0:1919:A:H4'	38:0:4820:HOH:O	2.19	0.41
30:0:2433:A:H2'	30:0:2434:A:C8	2.54	0.41
30:0:2478:U:H2'	30:0:2479:A:H8	1.85	0.41
30:0:2799:A:H5'	30:0:2800:A:P	2.59	0.41
1:A:51:ARG:NH2	1:A:53:ALA:HB3	2.35	0.41
1:A:199:HIS:CD2	1:A:200:PRO:HD2	2.55	0.41
4:D:76:ARG:CZ	31:9:44:A:C1'	2.98	0.41
9:I:96:SER:H	9:I:99:GLN:CD	2.22	0.41
10:J:19:MET:HE2	10:J:79:PHE:HA	2.02	0.41
11:K:4:LEU:HD23	11:K:4:LEU:HA	1.84	0.41
16:P:94:TRP:CH2	16:P:98:ILE:HG13	2.55	0.41
18:R:99:ALA:HB1	18:R:109:MET:HE2	2.01	0.41
22:V:23:LEU:HD22	22:V:49:LEU:HD23	2.01	0.41
23:W:13:MET:CE	23:W:17:ILE:HG22	2.50	0.41
26:Z:78:ILE:HB	38:Z:8715:HOH:O	2.19	0.41
27:1:31:LYS:O	27:1:33:VAL:HG23	2.20	0.41
29:3:5:ARG:HA	29:3:22:VAL:HG23	2.02	0.41
30:0:102:A:C6	30:0:103:C:N4	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:201:G:H1'	38:0:4539:HOH:O	2.19	0.41
30:0:272:A:N1	30:0:369:G:H5"	2.34	0.41
30:0:412:C:C2'	30:0:413:G:H5'	2.50	0.41
30:0:446:G:H3'	38:0:9539:HOH:O	2.20	0.41
30:0:495:A:O4'	30:0:1390:A:H1'	2.20	0.41
30:0:1163:G:C2	30:0:1184:C:N3	2.87	0.41
30:0:1178:G:H2'	30:0:1179:C:H6	1.79	0.41
30:0:1449:G:H4'	38:0:9213:HOH:O	2.20	0.41
30:0:1507:C:H4'	38:0:3595:HOH:O	2.20	0.41
30:0:1519:U:O5'	30:0:1519:U:H6	2.04	0.41
30:0:1915:U:O2	30:0:1925:G:C2	2.73	0.41
30:0:2004:U:O2	30:0:2004:U:H2'	2.20	0.41
30:0:2020:C:O2'	30:0:2021:C:H5'	2.20	0.41
30:0:2061:C:C2'	30:0:2062:A:H5'	2.51	0.41
30:0:2912:C:C2'	30:0:2913:A:H5'	2.50	0.41
31:9:50:G:C6	31:9:51:A:C6	3.08	0.41
31:9:56:A:C3'	31:9:57:A:C5'	2.93	0.41
2:B:75:GLU:C	2:B:77:PRO:HD3	2.40	0.41
2:B:211:THR:HG21	38:0:7438:HOH:O	2.20	0.41
4:D:84:LEU:HD23	4:D:84:LEU:HA	1.92	0.41
5:E:69:ILE:HA	5:E:72:MET:HE3	2.02	0.41
8:H:59:GLN:NE2	8:H:96:GLN:HG2	2.35	0.41
38:H:216:HOH:O	30:0:2517:A:H2	1.99	0.41
12:L:150:GLN:HB3	38:L:8869:HOH:O	2.19	0.41
21:U:31:PHE:CG	21:U:37:GLU:HG2	2.55	0.41
24:X:54:ILE:HD11	24:X:85:VAL:HG12	2.03	0.41
25:Y:157:ILE:HD13	38:0:4836:HOH:O	2.20	0.41
26:Z:34:SER:HA	30:0:797:A:C5'	2.50	0.41
30:0:38:G:C2'	30:0:39:G:H5'	2.50	0.41
30:0:236:A:H8	30:0:236:A:OP1	2.03	0.41
30:0:1079:A:N1	30:0:2068:G:O2'	2.43	0.41
30:0:1212:C:C5	30:0:1213:C:C5	3.09	0.41
30:0:1303:C:O2	30:0:1353:C:H1'	2.20	0.41
30:0:1419:U:H5'	30:0:1420:C:OP2	2.21	0.41
30:0:1554:C:O2'	30:0:1631:A:H1'	2.19	0.41
30:0:1804:A:H2'	30:0:1805:G:C8	2.55	0.41
30:0:1826:C:O2'	30:0:1827:G:H5'	2.21	0.41
30:0:1878:G:O2'	30:0:1879:U:P	2.78	0.41
30:0:2256:G:C2'	30:0:2257:G:H5'	2.51	0.41
30:0:2474:A:C8	30:0:2621:PSU:H4'	2.55	0.41
30:0:2782:G:O6	30:0:2790:C:H5"	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2795:C:O2'	30:0:2796:U:C5'	2.65	0.41
30:0:2799:A:N6	30:0:2801:A:C2	2.89	0.41
2:B:69:VAL:HA	2:B:70:PRO:HD3	1.77	0.41
5:E:107:PHE:O	5:E:110:GLU:HG3	2.20	0.41
15:O:26:TRP:HA	15:O:26:TRP:CE3	2.55	0.41
19:S:17:ASP:HB3	19:S:23:LYS:HB2	2.01	0.41
24:X:23:HIS:HE1	30:0:2044:G:OP1	2.03	0.41
26:Z:34:SER:HA	30:0:797:A:H5'	2.02	0.41
30:0:107:U:C2'	30:0:108:U:H5'	2.50	0.41
30:0:281:U:C2'	30:0:282:C:C5'	2.98	0.41
30:0:517:U:H2'	30:0:518:G:H5'	2.02	0.41
30:0:552:A:H5'	38:0:5878:HOH:O	2.19	0.41
30:0:1607:A:C5	30:0:1608:G:C8	3.09	0.41
30:0:1757:U:H6	30:0:1757:U:O5'	2.04	0.41
30:0:1769:C:C2'	30:0:1770:U:H5'	2.51	0.41
30:0:1819:G:C2'	30:0:1820:G:H5'	2.50	0.41
30:0:1894:C:N4	30:0:1939:U:H2'	2.34	0.41
30:0:1928:C:C2'	30:0:1929:G:H5'	2.50	0.41
30:0:1942:A:C1'	38:0:9045:HOH:O	2.69	0.41
30:0:1997:A:H2	30:0:2026:C:O2'	2.04	0.41
30:0:2710:U:H2'	30:0:2711:U:C6	2.55	0.41
30:0:2723:G:H1'	38:0:4812:HOH:O	2.19	0.41
30:0:2815:G:H4'	30:0:2816:A:OP2	2.20	0.41
31:9:58:G:C8	31:9:59:C:C4	3.08	0.41
31:9:110:G:C6	31:9:111:U:C4	3.08	0.41
1:A:212:PRO:HA	30:0:1943:C:O4'	2.20	0.41
2:B:222:LYS:HG3	30:0:2038:A:H5"	2.01	0.41
2:B:320:GLN:HE21	2:B:321:PRO:HD3	1.84	0.41
3:C:5:ILE:HG12	3:C:139:VAL:CG1	2.50	0.41
6:F:26:THR:HB	6:F:102:GLY:HA3	2.02	0.41
7:G:23:ILE:O	7:G:27:ILE:HG13	2.20	0.41
8:H:165:ARG:HD2	38:H:241:HOH:O	2.21	0.41
10:J:54:VAL:HG11	10:J:138:THR:HG21	2.02	0.41
10:J:76:ASP:HA	38:J:8863:HOH:O	2.20	0.41
11:K:66:ARG:NH1	30:0:1992:U:H3'	2.35	0.41
14:N:132:ASN:O	14:N:135:VAL:HG12	2.21	0.41
19:S:51:GLN:HE21	19:S:53:ASN:HD21	1.67	0.41
21:U:5:GLU:HG2	21:U:6:CYS:N	2.36	0.41
25:Y:130:ARG:HB2	25:Y:142:SER:O	2.20	0.41
25:Y:152:LYS:CB	25:Y:160:LYS:HG3	2.51	0.41
25:Y:189:ASN:HD22	25:Y:191:ASP:N	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:10:U:O4	30:0:532:A:OP2	2.38	0.41
30:0:343:C:H1'	38:0:5552:HOH:O	2.19	0.41
30:0:594:C:C4	30:0:595:U:C4	3.08	0.41
30:0:910:C:H2'	30:0:911:G:O4'	2.21	0.41
30:0:1063:G:O5'	30:0:2307:A:H1'	2.21	0.41
30:0:1271:A:H2'	30:0:1272:C:H6	1.84	0.41
30:0:1423:C:O2'	30:0:1424:A:H5'	2.20	0.41
30:0:1882:C:H2'	30:0:1883:U:H6	1.86	0.41
30:0:1898:G:H2'	30:0:1899:C:C6	2.55	0.41
30:0:2470:A:C2'	30:0:2471:G:O5'	2.68	0.41
30:0:2511:A:H2'	30:0:2512:U:C6	2.56	0.41
30:0:2854:A:N6	30:0:2905:A:N6	2.69	0.41
1:A:70:ALA:HA	1:A:71:PRO:HD3	1.82	0.41
2:B:241:PRO:HD2	38:B:9125:HOH:O	2.20	0.41
18:R:9:ASP:HA	18:R:10:PRO:HD2	1.90	0.41
19:S:52:VAL:HG22	19:S:66:VAL:HG13	2.03	0.41
23:W:122:ARG:NH2	38:0:5254:HOH:O	2.52	0.41
30:0:165:A:C2'	30:0:166:A:OP1	2.67	0.41
30:0:307:G:C2	30:0:309:C:C4	3.08	0.41
30:0:1278:A:O2'	30:0:1279:U:C2	2.65	0.41
30:0:1540:G:C4	30:0:1541:G:C8	3.09	0.41
30:0:1666:C:C2'	30:0:1667:A:H5'	2.32	0.41
30:0:1679:C:O2	30:0:1685:A:C2	2.73	0.41
30:0:2057:U:O5'	30:0:2057:U:H6	2.03	0.41
30:0:2255:A:H2'	30:0:2256:G:O4'	2.20	0.41
30:0:2692:G:N2	30:0:2701:G:C5	2.88	0.41
31:9:60:C:O2	31:9:60:C:H2'	2.19	0.41
8:H:89:THR:O	8:H:137:PHE:HD2	2.04	0.41
21:U:17:THR:HG21	38:U:2221:HOH:O	2.21	0.41
21:U:42:LEU:HB3	30:0:1810:C:O4'	2.21	0.41
26:Z:70:ARG:HB2	26:Z:81:CYS:HG	1.86	0.41
29:3:91:GLN:O	29:3:92:GLU:HB2	2.21	0.41
30:0:69:A:C8	30:0:69:A:C3'	3.04	0.41
30:0:213:G:O2'	30:0:214:U:OP2	2.39	0.41
30:0:268:U:O4	30:0:269:G:N1	2.54	0.41
30:0:393:G:C6	30:0:394:G:C6	3.09	0.41
30:0:631:A:C6	30:0:2074:A:H5'	2.56	0.41
30:0:677:C:O5'	30:0:677:C:H6	2.03	0.41
30:0:812:A:H1'	38:0:3946:HOH:O	2.20	0.41
30:0:862:U:O2'	30:0:863:G:H5'	2.20	0.41
30:0:870:G:C3'	30:0:871:G:H5"	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1012:A:H8	30:0:1012:A:O5'	2.04	0.41
30:0:1191:A:O5'	30:0:1191:A:C8	2.74	0.41
30:0:1196:C:H2'	30:0:1197:G:H5'	2.02	0.41
30:0:1438:G:N3	30:0:1438:G:H2'	2.35	0.41
30:0:1544:U:O2'	30:0:1545:C:H5'	2.20	0.41
30:0:1798:C:OP2	30:0:1799:G:H5"	2.20	0.41
30:0:2325:U:C2	30:0:2326:C:C6	3.09	0.41
30:0:2383:G:C6	30:0:2384:U:C4	3.08	0.41
30:0:2668:G:N2	30:0:2669:U:C2	2.88	0.41
30:0:2668:G:O4'	30:0:2827:A:C2	2.73	0.41
1:A:47:HIS:HD2	30:0:1654:U:O2'	2.03	0.41
1:A:199:HIS:HE1	30:0:1881:A:OP1	2.04	0.41
1:A:232:ARG:CZ	30:0:1939:U:H4'	2.50	0.41
2:B:195:ARG:HG2	2:B:323:LEU:HD22	2.03	0.41
4:D:20:LYS:HG2	4:D:133:ASN:HB3	2.02	0.41
8:H:91:ARG:NH1	8:H:138:THR:OG1	2.53	0.41
10:J:107:ASN:HA	10:J:108:PRO:HD2	1.98	0.41
14:N:83:LEU:HD13	14:N:175:LEU:HD23	2.03	0.41
16:P:89:ASN:HA	38:P:165:HOH:O	2.20	0.41
18:R:114:VAL:HG13	18:R:114:VAL:O	2.20	0.41
23:W:43:GLY:HA3	30:0:945:U:O2'	2.20	0.41
30:0:189:A:H2	30:0:205:U:O2	2.04	0.41
30:0:241:A:C2	30:0:378:A:H4'	2.55	0.41
30:0:383:A:H2'	30:0:384:G:O4'	2.21	0.41
30:0:1173:A:H2'	30:0:1177:A:H62	1.85	0.41
30:0:1209:C:O2'	30:0:1210:G:H5'	2.20	0.41
30:0:1621:G:H2'	30:0:1622:G:H8	1.86	0.41
30:0:1774:G:C2'	30:0:1775:A:H5'	2.51	0.41
30:0:1803:C:H2'	30:0:1804:A:C8	2.56	0.41
30:0:1913:C:H2'	30:0:1914:C:C6	2.54	0.41
30:0:1977:U:OP1	30:0:1977:U:H3'	2.20	0.41
30:0:2039:A:H2'	30:0:2040:C:C6	2.56	0.41
30:0:2324:G:H2'	30:0:2325:U:C6	2.56	0.41
30:0:2700:G:H2'	30:0:2701:G:O5'	2.21	0.41
31:9:82:U:H2'	31:9:83:G:C8	2.56	0.41
1:A:171:LYS:HB2	30:0:820:G:C6	2.55	0.41
2:B:74:ILE:HG13	38:B:9076:HOH:O	2.20	0.41
4:D:36:ASN:HA	38:D:7500:HOH:O	2.20	0.41
5:E:15:GLN:HG2	5:E:16:ASP:N	2.36	0.41
5:E:20:ILE:HD12	5:E:33:LEU:HD12	2.03	0.41
5:E:119:HIS:O	5:E:140:ALA:HB1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:145:ALA:HB1	5:E:168:ILE:CD1	2.49	0.41
6:F:61:MET:O	6:F:64:PRO:HD2	2.21	0.41
14:N:73:ALA:HB1	14:N:74:PRO:CD	2.51	0.41
16:P:61:ARG:NH2	30:0:2737:C:OP2	2.40	0.41
17:Q:41:LEU:HB3	17:Q:52:PHE:CZ	2.56	0.41
19:S:73:ASP:OD1	19:S:76:GLU:HG3	2.21	0.41
21:U:56:ARG:NH1	30:0:2890:A:C4	2.89	0.41
23:W:120:PRO:HG2	30:0:1095:U:O2	2.20	0.41
25:Y:152:LYS:HB3	25:Y:160:LYS:HG3	2.02	0.41
26:Z:47:ARG:HD2	38:Z:8718:HOH:O	2.20	0.41
30:0:20:G:H2'	30:0:21:G:O5'	2.21	0.41
30:0:51:G:C2	30:0:111:C:C2	3.08	0.41
30:0:61:G:C2	30:0:62:C:C2	3.09	0.41
30:0:265:U:C4	30:0:266:G:N7	2.89	0.41
30:0:279:C:H2'	30:0:280:C:H5'	2.01	0.41
30:0:844:A:C6	30:0:882:A:C6	3.09	0.41
30:0:1024:G:C5	30:0:1025:C:C4	3.09	0.41
30:0:1089:G:H1'	30:0:1290:G:N2	2.36	0.41
30:0:1168:C:C2'	30:0:1169:U:H5'	2.51	0.41
30:0:1193:A:C2	30:0:1194:A:N6	2.89	0.41
30:0:1207:A:H5'	30:0:1208:C:OP2	2.21	0.41
30:0:1226:G:C2	30:0:1227:C:C6	3.08	0.41
30:0:1339:G:C5	30:0:1340:G:C6	3.09	0.41
30:0:1362:U:H2'	30:0:1363:G:H8	1.86	0.41
30:0:1416:G:C2'	30:0:1417:G:H5'	2.51	0.41
30:0:1476:A:H1'	30:0:1867:G:O2'	2.21	0.41
30:0:1543:G:H2'	30:0:1544:U:C5	2.56	0.41
30:0:1553:C:O5'	30:0:1553:C:H6	2.04	0.41
30:0:1596:U:O2'	30:0:1598:A:N7	2.46	0.41
30:0:1619:G:H2'	30:0:1620:C:O4'	2.21	0.41
30:0:1748:U:C6	30:0:1749:U:C5	3.09	0.41
30:0:1973:A:H5'	30:0:1973:A:C8	2.53	0.41
30:0:2366:C:P	38:0:6939:HOH:O	2.79	0.41
30:0:2453:G:H2'	30:0:2454:C:C6	2.55	0.41
30:0:2599:A:C6	30:0:2600:A:N1	2.89	0.41
30:0:2695:C:N4	30:0:2701:G:N2	2.69	0.41
30:0:2801:A:C4	30:0:2802:C:C5	3.08	0.41
31:9:29:C:C6	31:9:30:C:C6	3.08	0.41
1:A:37:VAL:HG13	38:A:9088:HOH:O	2.21	0.41
2:B:288:GLY:HA2	30:0:2898:G:H4'	2.02	0.41
38:B:9106:HOH:O	30:0:2818:A:H2	2.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:23:GLU:HG2	5:E:28:SER:CB	2.51	0.41
5:E:81:GLU:HA	5:E:133:VAL:O	2.21	0.41
13:M:68:ARG:HB2	38:M:8932:HOH:O	2.19	0.41
18:R:130:MET:HG3	38:0:7551:HOH:O	2.21	0.41
23:W:132:VAL:HG21	23:W:140:LYS:O	2.21	0.41
30:0:23:G:H1'	30:0:520:A:N6	2.35	0.41
30:0:123:U:O2'	30:0:124:C:H5'	2.21	0.41
30:0:282:C:O2	30:0:282:C:C2'	2.62	0.41
30:0:714:U:O4'	30:0:716:G:C2	2.74	0.41
30:0:736:A:H5"	38:0:4253:HOH:O	2.21	0.41
30:0:965:A:N3	30:0:965:A:H2'	2.36	0.41
30:0:1103:C:C2	30:0:1241:G:N2	2.89	0.41
30:0:1195:G:N1	30:0:1205:U:N3	2.69	0.41
30:0:1208:C:H2'	30:0:1208:C:O2	2.19	0.41
30:0:1591:A:H5'	30:0:1603:A:H61	1.86	0.41
30:0:1634:G:C4	30:0:1635:U:C5	3.08	0.41
30:0:2016:U:H2'	30:0:2017:U:O4'	2.21	0.41
30:0:2098:C:O5'	30:0:2098:C:H6	2.04	0.41
30:0:2269:C:C4	30:0:2270:G:C5	3.08	0.41
30:0:2526:C:C6	30:0:2526:C:H5'	2.56	0.41
30:0:2617:G:H5"	38:0:3896:HOH:O	2.20	0.41
31:9:14:G:H8	31:9:14:G:C5'	2.13	0.41
31:9:110:G:N3	31:9:110:G:H2'	2.35	0.41
3:C:118:THR:HG21	3:C:233:THR:HB	2.03	0.40
4:D:28:GLY:CA	4:D:69:ILE:HG23	2.51	0.40
6:F:38:LYS:HE3	30:0:244:C:OP2	2.21	0.40
13:M:72:ALA:HB3	38:M:8950:HOH:O	2.21	0.40
13:M:75:ARG:HG3	38:M:8868:HOH:O	2.20	0.40
14:N:110:THR:HA	14:N:111:PRO:HD3	1.98	0.40
19:S:11:THR:CG2	30:0:1444:G:H5"	2.50	0.40
23:W:4:LEU:CD2	23:W:54:PHE:HB3	2.51	0.40
23:W:48:VAL:HG12	23:W:48:VAL:O	2.21	0.40
25:Y:125:LYS:HB2	25:Y:126:PRO:HD2	2.03	0.40
28:2:42:TRP:HZ2	30:0:1438:G:H1'	1.87	0.40
29:3:86:GLY:HA2	38:3:9032:HOH:O	2.21	0.40
30:0:257:G:N2	30:0:258:G:C4	2.89	0.40
30:0:797:A:H2'	30:0:798:G:O4'	2.21	0.40
30:0:1170:U:O2	30:0:1172:G:H8	2.04	0.40
30:0:1175:G:C5	30:0:1193:A:C2	3.10	0.40
30:0:1177:A:C6	30:0:1178:G:C5	3.09	0.40
30:0:1832:G:N3	30:0:1833:U:C6	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2330:U:H4'	30:0:2331:C:OP1	2.20	0.40
30:0:2414:A:N1	30:0:2415:A:C6	2.90	0.40
30:0:2635:A:H2'	30:0:2636:C:H5'	1.98	0.40
30:0:2692:G:N2	30:0:2701:G:C4	2.88	0.40
3:C:206:ASN:HB2	30:0:329:A:OP2	2.20	0.40
6:F:48:VAL:CG2	6:F:74:PHE:HB3	2.51	0.40
13:M:113:ARG:NH1	13:M:155:GLN:HB2	2.36	0.40
15:O:32:ARG:HD3	15:O:32:ARG:O	2.22	0.40
24:X:26:ALA:HB3	24:X:63:ARG:HG3	2.03	0.40
30:0:69:A:C8	30:0:69:A:C5'	2.98	0.40
30:0:312:U:O2	30:0:320:G:C2	2.75	0.40
30:0:366:U:H2'	30:0:367:G:O4'	2.20	0.40
30:0:534:C:H2'	30:0:2083:A:C2	2.57	0.40
30:0:594:C:H2'	30:0:595:U:C6	2.56	0.40
30:0:596:C:H6	30:0:596:C:O5'	2.03	0.40
30:0:962:C:H2'	30:0:963:C:H5'	2.03	0.40
30:0:1634:G:C6	30:0:1635:U:C4	3.10	0.40
30:0:1681:G:H5"	30:0:1682:A:H5'	2.03	0.40
30:0:1774:G:H2'	30:0:1775:A:C5'	2.51	0.40
30:0:2121:G:C2'	30:0:2122:C:H5'	2.51	0.40
30:0:2245:C:H6	30:0:2245:C:O5'	2.04	0.40
30:0:2300:A:H4'	30:0:2301:A:N3	2.37	0.40
30:0:2335:C:N3	30:0:2350:G:C2	2.89	0.40
30:0:2501:G:H1	30:0:2519:C:N4	2.18	0.40
30:0:2831:C:C2'	30:0:2832:C:C5'	2.93	0.40
30:0:2834:G:C2'	30:0:2835:C:O5'	2.69	0.40
2:B:5:ARG:NH2	30:0:2548:C:OP2	2.55	0.40
2:B:188:HIS:ND1	2:B:188:HIS:N	2.69	0.40
2:B:277:GLU:N	2:B:278:PRO:CD	2.84	0.40
6:F:50:VAL:HG11	6:F:60:VAL:HG11	2.03	0.40
13:M:46:LEU:O	13:M:50:ARG:HG3	2.21	0.40
22:V:12:THR:HG23	22:V:15:GLU:H	1.86	0.40
24:X:43:VAL:HG11	24:X:82:GLU:HA	2.04	0.40
29:3:39:GLN:O	29:3:52:PHE:HE1	2.04	0.40
30:0:238:C:H4'	30:0:287:C:OP1	2.22	0.40
30:0:249:G:O2'	30:0:266:G:H5'	2.21	0.40
30:0:462:A:H2'	38:0:4853:HOH:O	2.21	0.40
30:0:568:G:H21	30:0:590:A:H62	1.69	0.40
30:0:603:A:H4'	30:0:604:G:O5'	2.22	0.40
30:0:822:C:H2'	30:0:823:U:H6	1.86	0.40
30:0:1133:A:H2'	30:0:1134:G:H5'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1325:G:O2'	30:0:1326:C:H5'	2.21	0.40
30:0:1474:C:C6	30:0:1474:C:C5'	2.94	0.40
30:0:1521:C:O2'	30:0:1522:A:H5'	2.22	0.40
30:0:1613:C:C6	30:0:1613:C:H3'	2.57	0.40
30:0:2311:A:H3'	38:0:7660:HOH:O	2.20	0.40
30:0:2325:U:H5"	30:0:2417:C:O2'	2.22	0.40
30:0:2493:C:O2	30:0:2493:C:C2'	2.67	0.40
30:0:2510:C:H42	30:0:2564:G:N2	2.19	0.40
1:A:33:GLU:CD	1:A:33:GLU:N	2.75	0.40
2:B:73:VAL:HG21	2:B:284:PHE:HZ	1.86	0.40
3:C:100:LEU:HD22	30:0:751:U:H5"	2.03	0.40
4:D:14:ARG:HD3	31:9:56:A:O2'	2.22	0.40
5:E:23:GLU:HG2	5:E:28:SER:HB3	2.03	0.40
7:G:19:GLU:HG2	7:G:66:LEU:HD13	2.03	0.40
8:H:91:ARG:H	8:H:91:ARG:HG2	1.43	0.40
15:O:47:ARG:HG3	15:O:47:ARG:NH1	2.36	0.40
15:O:49:GLU:OE1	15:O:72:LYS:HG3	2.22	0.40
15:O:96:VAL:HG13	15:O:100:GLN:OE1	2.21	0.40
25:Y:132:ASP:OD1	25:Y:135:LYS:HD2	2.20	0.40
30:0:192:A:N6	30:0:194:A:C2	2.89	0.40
30:0:1102:C:H5	38:0:3479:HOH:O	2.04	0.40
30:0:1159:G:C2	30:0:1209:C:N3	2.89	0.40
30:0:1520:G:C6	30:0:1521:C:N4	2.89	0.40
30:0:1979:G:H1'	38:0:3061:HOH:O	2.21	0.40
30:0:2102:G:N2	30:0:2103:A:N1	2.69	0.40
30:0:2532:A:H8	30:0:2532:A:OP2	2.05	0.40
30:0:2672:C:H2'	30:0:2673:U:C6	2.53	0.40
31:9:81:C:O2'	31:9:82:U:H5'	2.21	0.40
31:9:89:C:O2'	31:9:90:G:H5'	2.22	0.40
1:A:20:SER:C	1:A:22:ARG:H	2.25	0.40
2:B:201:ASP:N	2:B:312:ARG:O	2.53	0.40
3:C:1:MET:HG2	3:C:2:GLN:N	2.34	0.40
3:C:104:ASP:O	3:C:108:GLN:HG3	2.22	0.40
4:D:135:VAL:HG22	4:D:136:ARG:N	2.36	0.40
5:E:84:MET:HA	5:E:167:TYR:O	2.22	0.40
6:F:59:ILE:CD1	30:0:263:U:C2	3.04	0.40
14:N:127:LEU:HD12	14:N:127:LEU:HA	1.93	0.40
15:O:32:ARG:HA	15:O:32:ARG:NE	2.35	0.40
16:P:13:VAL:HG21	16:P:41:ARG:HG2	2.03	0.40
16:P:78:GLY:O	30:0:1813:U:H4'	2.22	0.40
20:T:26:THR:HA	20:T:39:ASN:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:229:LEU:O	30:0:552:A:H5"	2.22	0.40
28:2:41:HIS:HE1	30:0:1439:C:OP1	2.05	0.40
29:3:17:HIS:CG	30:0:2409:C:H4'	2.57	0.40
30:0:37:A:H2'	30:0:38:G:H8	1.84	0.40
30:0:146:U:C4	30:0:147:G:C6	3.09	0.40
30:0:295:C:H2'	30:0:296:G:O4'	2.22	0.40
30:0:766:A:HO2'	30:0:767:A:H8	1.68	0.40
30:0:920:C:H5'	30:0:921:G:N3	2.37	0.40
30:0:1016:U:H2'	30:0:1017:U:O4'	2.21	0.40
30:0:1525:G:H4'	30:0:1525:G:OP1	2.21	0.40
30:0:1557:G:H2'	30:0:1558:C:C6	2.57	0.40
30:0:2004:U:H5"	30:0:2005:G:C8	2.57	0.40
30:0:2273:C:O2'	30:0:2274:A:H5'	2.22	0.40
31:9:2:U:H4'	31:9:2:U:OP2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	235/240 (98%)	200 (85%)	30 (13%)	5 (2%)	7 33
2	B	335/338 (99%)	305 (91%)	23 (7%)	7 (2%)	7 33
3	C	244/246 (99%)	216 (88%)	26 (11%)	2 (1%)	19 57
4	D	134/177 (76%)	105 (78%)	23 (17%)	6 (4%)	2 14
5	E	170/178 (96%)	158 (93%)	11 (6%)	1 (1%)	25 64
6	F	117/120 (98%)	97 (83%)	16 (14%)	4 (3%)	3 20
7	G	25/348 (7%)	22 (88%)	3 (12%)	0	100 100
8	H	156/177 (88%)	139 (89%)	16 (10%)	1 (1%)	25 64
9	I	68/162 (42%)	49 (72%)	16 (24%)	3 (4%)	2 15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
10	J	140/145 (97%)	128 (91%)	10 (7%)	2 (1%)	11 43
11	K	130/132 (98%)	120 (92%)	9 (7%)	1 (1%)	19 57
12	L	141/165 (86%)	116 (82%)	22 (16%)	3 (2%)	7 33
13	M	192/196 (98%)	171 (89%)	17 (9%)	4 (2%)	7 33
14	N	184/187 (98%)	163 (89%)	17 (9%)	4 (2%)	6 31
15	O	113/116 (97%)	106 (94%)	7 (6%)	0	100 100
16	P	141/149 (95%)	133 (94%)	8 (6%)	0	100 100
17	Q	93/96 (97%)	86 (92%)	5 (5%)	2 (2%)	6 31
18	R	148/155 (96%)	138 (93%)	9 (6%)	1 (1%)	22 60
19	S	79/85 (93%)	75 (95%)	4 (5%)	0	100 100
20	T	117/120 (98%)	108 (92%)	9 (8%)	0	100 100
21	U	51/67 (76%)	44 (86%)	6 (12%)	1 (2%)	7 34
22	V	63/71 (89%)	58 (92%)	4 (6%)	1 (2%)	9 40
23	W	152/154 (99%)	142 (93%)	9 (6%)	1 (1%)	22 60
24	X	80/92 (87%)	72 (90%)	6 (8%)	2 (2%)	5 28
25	Y	140/241 (58%)	132 (94%)	7 (5%)	1 (1%)	22 60
26	Z	71/116 (61%)	55 (78%)	12 (17%)	4 (6%)	2 10
27	1	54/57 (95%)	49 (91%)	5 (9%)	0	100 100
28	2	42/50 (84%)	41 (98%)	1 (2%)	0	100 100
29	3	90/92 (98%)	64 (71%)	17 (19%)	9 (10%)	0 2
All	All	3705/4472 (83%)	3292 (89%)	348 (9%)	65 (2%)	8 37

All (65) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	206	THR
2	B	306	LYS
4	D	137	PRO
6	F	61	MET
6	F	101	ALA
10	J	5	GLU
12	L	80	ASP
13	M	75	ARG
14	N	154	LEU
14	N	183	ASP

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Mol	Chain	Res	Type
14	N	184	ILE
21	U	44	ARG
26	Z	70	ARG
29	3	56	PRO
29	3	64	LYS
29	3	84	ARG
1	A	34	ASP
3	C	8	LEU
3	C	201	SER
5	E	128	GLY
12	L	21	ARG
12	L	82	ALA
13	M	81	ARG
17	Q	21	ARG
23	W	139	GLY
24	X	70	ILE
26	Z	39	GLY
29	3	4	PRO
29	3	68	LYS
29	3	72	GLY
29	3	73	GLU
2	B	169	GLY
4	D	56	ARG
9	I	83	GLY
9	I	107	LYS
11	K	10	GLN
14	N	165	ALA
26	Z	83	TYR
29	3	90	PHE
1	A	119	ALA
2	B	107	SER
2	B	184	ASP
4	D	65	GLU
10	J	7	ASP
13	M	86	GLN
17	Q	18	PRO
18	R	20	GLU
1	A	24	LYS
1	A	122	SER
1	A	132	ASP
2	B	2	GLN
2	B	185	GLY

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Mol	Chain	Res	Type
4	D	172	VAL
6	F	100	ASP
9	I	76	ASP
13	M	80	GLY
24	X	52	PRO
26	Z	105	ARG
29	3	62	THR
4	D	16	PRO
4	D	53	LYS
6	F	64	PRO
8	H	19	ARG
22	V	39	ALA
25	Y	111	ASP

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	179/182 (98%)	170 (95%)	9 (5%)	24	60
2	B	282/283 (100%)	263 (93%)	19 (7%)	16	49
3	C	193/193 (100%)	180 (93%)	13 (7%)	16	49
4	D	117/148 (79%)	110 (94%)	7 (6%)	19	53
5	E	152/156 (97%)	146 (96%)	6 (4%)	32	69
6	F	93/94 (99%)	92 (99%)	1 (1%)	73	90
7	G	27/282 (10%)	25 (93%)	2 (7%)	13	44
8	H	134/145 (92%)	124 (92%)	10 (8%)	13	43
9	I	58/130 (45%)	57 (98%)	1 (2%)	60	85
10	J	118/121 (98%)	109 (92%)	9 (8%)	13	43
11	K	106/106 (100%)	103 (97%)	3 (3%)	43	77
12	L	113/127 (89%)	106 (94%)	7 (6%)	18	52
13	M	158/160 (99%)	147 (93%)	11 (7%)	15	47
14	N	149/150 (99%)	146 (98%)	3 (2%)	55	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
15	O	93/94 (99%)	93 (100%)	0	100 100
16	P	113/117 (97%)	111 (98%)	2 (2%)	59 85
17	Q	79/80 (99%)	74 (94%)	5 (6%)	18 51
18	R	117/122 (96%)	113 (97%)	4 (3%)	37 72
19	S	71/74 (96%)	70 (99%)	1 (1%)	67 88
20	T	105/106 (99%)	98 (93%)	7 (7%)	16 49
21	U	44/53 (83%)	43 (98%)	1 (2%)	50 80
22	V	51/57 (90%)	51 (100%)	0	100 100
23	W	130/130 (100%)	126 (97%)	4 (3%)	40 75
24	X	66/74 (89%)	61 (92%)	5 (8%)	13 43
25	Y	120/196 (61%)	117 (98%)	3 (2%)	47 79
26	Z	60/94 (64%)	60 (100%)	0	100 100
27	1	46/47 (98%)	46 (100%)	0	100 100
28	2	42/46 (91%)	41 (98%)	1 (2%)	49 79
29	3	79/79 (100%)	73 (92%)	6 (8%)	13 43
All	All	3095/3646 (85%)	2955 (96%)	140 (4%)	27 64

All (140) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ARG
1	A	37	VAL
1	A	66	ARG
1	A	94	LEU
1	A	131	HIS
1	A	153	ARG
1	A	179	MET
1	A	190	ARG
1	A	217	ARG
2	B	7	ARG
2	B	11	LEU
2	B	27	ASN
2	B	49	THR
2	B	56	ASP
2	B	71	VAL
2	B	132	HIS
2	B	144	THR

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Mol	Chain	Res	Type
2	B	162	MET
2	B	171	VAL
2	B	180	ASP
2	B	188	HIS
2	B	190	MET
2	B	195	ARG
2	B	254	GLN
2	B	264	GLU
2	B	277	GLU
2	B	312	ARG
2	B	322	ARG
3	C	2	GLN
3	C	16	VAL
3	C	76	ARG
3	C	78	ARG
3	C	87	ARG
3	C	101	ASP
3	C	104	ASP
3	C	162	VAL
3	C	180	SER
3	C	187	ARG
3	C	236	THR
3	C	240	LEU
3	C	243	VAL
4	D	19	GLU
4	D	24	HIS
4	D	29	HIS
4	D	50	VAL
4	D	104	PHE
4	D	137	PRO
4	D	149	ARG
5	E	7	ILE
5	E	100	ASP
5	E	116	THR
5	E	126	ILE
5	E	155	ASN
5	E	156	ASP
6	F	12	LEU
7	G	64	ASN
7	G	72	ASP
8	H	33	GLN
8	H	62	HIS

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Mol	Chain	Res	Type
8	H	65	LEU
8	H	87	LYS
8	H	89	THR
8	H	91	ARG
8	H	99	ARG
8	H	122	LYS
8	H	157	TYR
8	H	172	GLU
9	I	110	ASP
10	J	39	VAL
10	J	45	VAL
10	J	46	ILE
10	J	52	GLN
10	J	74	ARG
10	J	79	PHE
10	J	107	ASN
10	J	120	SER
10	J	131	THR
11	K	10	GLN
11	K	24	THR
11	K	55	VAL
12	L	18	HIS
12	L	35	ARG
12	L	73	VAL
12	L	83	GLU
12	L	102	ASP
12	L	104	ASP
12	L	114	VAL
13	M	10	ASP
13	M	46	LEU
13	M	68	ARG
13	M	73	ARG
13	M	81	ARG
13	M	83	SER
13	M	84	LYS
13	M	89	THR
13	M	91	ILE
13	M	99	ARG
13	M	116	ASN
14	N	21	HIS
14	N	134	ASP
14	N	138	ASP

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Mol	Chain	Res	Type
16	P	91	LYS
16	P	98	ILE
17	Q	16	ASN
17	Q	18	PRO
17	Q	54	PRO
17	Q	75	ILE
17	Q	95	GLU
18	R	13	THR
18	R	39	THR
18	R	82	GLU
18	R	143	VAL
19	S	30	ASP
20	T	5	ASP
20	T	39	ASN
20	T	48	VAL
20	T	73	HIS
20	T	96	VAL
20	T	115	GLU
20	T	117	ASP
21	U	25	ASP
23	W	4	LEU
23	W	35	VAL
23	W	38	THR
23	W	146	ILE
24	X	27	ASP
24	X	52	PRO
24	X	72	VAL
24	X	79	GLU
24	X	82	GLU
25	Y	118	THR
25	Y	189	ASN
25	Y	203	VAL
28	2	18	ASN
29	3	7	PHE
29	3	15	ASN
29	3	17	HIS
29	3	56	PRO
29	3	71	CYS
29	3	90	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (88) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	HIS
1	A	92	ASN
1	A	176	HIS
1	A	177	HIS
1	A	199	HIS
2	B	27	ASN
2	B	106	HIS
2	B	145	HIS
2	B	238	ASN
2	B	256	GLN
2	B	260	HIS
2	B	320	GLN
2	B	332	ASN
3	C	73	GLN
3	C	129	HIS
4	D	103	ASN
4	D	133	ASN
5	E	55	ASN
5	E	68	HIS
5	E	74	HIS
5	E	90	HIS
5	E	106	ASN
5	E	143	GLN
7	G	64	ASN
8	H	59	GLN
8	H	135	GLN
9	I	106	GLN
10	J	25	GLN
10	J	52	GLN
10	J	107	ASN
10	J	126	ASN
11	K	10	GLN
11	K	42	ASN
11	K	44	HIS
11	K	119	GLN
12	L	18	HIS
12	L	38	HIS
12	L	41	HIS
12	L	43	HIS
12	L	116	HIS
13	M	24	GLN
13	M	58	GLN
13	M	77	HIS

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Mol	Chain	Res	Type
13	M	86	GLN
13	M	137	ASN
13	M	142	GLN
13	M	170	ASN
14	N	107	ASN
14	N	132	ASN
16	P	50	GLN
16	P	66	GLN
16	P	88	GLN
16	P	118	GLN
17	Q	27	GLN
17	Q	40	HIS
18	R	61	GLN
18	R	94	ASN
18	R	98	ASN
18	R	117	HIS
19	S	9	HIS
19	S	44	GLN
19	S	53	ASN
20	T	39	ASN
20	T	43	ASN
21	U	39	ASN
22	V	34	GLN
22	V	60	GLN
23	W	12	ASN
23	W	110	GLN
23	W	119	HIS
23	W	141	HIS
24	X	23	HIS
25	Y	129	ASN
25	Y	134	HIS
25	Y	149	GLN
25	Y	189	ASN
27	1	16	HIS
27	1	28	HIS
28	2	16	ASN
28	2	18	ASN
28	2	41	HIS
28	2	45	ASN
29	3	2	GLN
29	3	13	HIS
29	3	18	GLN

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Mol	Chain	Res	Type
29	3	20	HIS
29	3	30	GLN
29	3	78	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	0	2745/2923 (93%)	243 (8%)	22 (0%)
31	9	121/122 (99%)	19 (15%)	2 (1%)
All	All	2866/3045 (94%)	262 (9%)	24 (0%)

All (262) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	0	31	C
30	0	67	A
30	0	69	A
30	0	70	A
30	0	71	G
30	0	86	A
30	0	87	C
30	0	88	G
30	0	114	A
30	0	115	U
30	0	120	A
30	0	130	C
30	0	138	U
30	0	141	C
30	0	151	A
30	0	166	A
30	0	185	G
30	0	186	A
30	0	191	A
30	0	192	A
30	0	198	A
30	0	200	C
30	0	219	G
30	0	237	G
30	0	271	C
30	0	272	A
30	0	273	G

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Mol	Chain	Res	Type
30	0	283	U
30	0	284	C
30	0	285	A
30	0	308	U
30	0	309	C
30	0	318	U
30	0	336	G
30	0	337	A
30	0	342	C
30	0	358	G
30	0	368	C
30	0	381	G
30	0	397	A
30	0	417	G
30	0	457	U
30	0	461	C
30	0	487	G
30	0	498	A
30	0	510	U
30	0	511	A
30	0	514	G
30	0	537	G
30	0	538	C
30	0	539	G
30	0	542	A
30	0	545	G
30	0	553	G
30	0	559	U
30	0	588	G
30	0	604	G
30	0	605	C
30	0	620	A
30	0	632	A
30	0	644	G
30	0	660	A
30	0	688	A
30	0	698	A
30	0	701	U
30	0	702	G
30	0	746	A
30	0	759	C
30	0	777	U

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Mol	Chain	Res	Type
30	0	809	G
30	0	821	U
30	0	835	U
30	0	840	U
30	0	857	A
30	0	858	U
30	0	868	G
30	0	869	G
30	0	871	G
30	0	872	U
30	0	875	A
30	0	877	G
30	0	878	G
30	0	884	C
30	0	885	G
30	0	898	G
30	0	905	C
30	0	920	C
30	0	921	G
30	0	923	A
30	0	953	G
30	0	960	G
30	0	961	A
30	0	1006	A
30	0	1008	C
30	0	1011	C
30	0	1029	U
30	0	1045	G
30	0	1059	G
30	0	1060	C
30	0	1072	G
30	0	1080	C
30	0	1081	A
30	0	1088	A
30	0	1109	U
30	0	1110	G
30	0	1119	G
30	0	1130	U
30	0	1137	G
30	0	1151	G
30	0	1161	A
30	0	1166	A

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Mol	Chain	Res	Type
30	0	1174	A
30	0	1175	G
30	0	1185	U
30	0	1192	A
30	0	1193	A
30	0	1205	U
30	0	1206	U
30	0	1208	C
30	0	1216	G
30	0	1238	C
30	0	1239	G
30	0	1279	U
30	0	1289	C
30	0	1342	C
30	0	1353	C
30	0	1354	G
30	0	1360	C
30	0	1377	C
30	0	1378	G
30	0	1407	A
30	0	1460	G
30	0	1474	C
30	0	1485	A
30	0	1505	U
30	0	1506	U
30	0	1524	U
30	0	1525	G
30	0	1526	A
30	0	1528	A
30	0	1562	C
30	0	1592	G
30	0	1605	G
30	0	1617	C
30	0	1625	U
30	0	1626	A
30	0	1634	G
30	0	1656	A
30	0	1667	A
30	0	1682	A
30	0	1684	A
30	0	1685	A
30	0	1692	C

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Mol	Chain	Res	Type
30	0	1701	A
30	0	1710	A
30	0	1722	U
30	0	1723	G
30	0	1725	C
30	0	1730	G
30	0	1731	C
30	0	1752	G
30	0	1778	A
30	0	1798	C
30	0	1820	G
30	0	1829	A
30	0	1856	C
30	0	1879	U
30	0	1919	A
30	0	1942	A
30	0	1967	U
30	0	1968	A
30	0	1971	G
30	0	1973	A
30	0	1978	A
30	0	1979	G
30	0	1996	U
30	0	2006	C
30	0	2008	U
30	0	2011	A
30	0	2012	U
30	0	2013	G
30	0	2033	G
30	0	2034	U
30	0	2064	U
30	0	2072	G
30	0	2073	G
30	0	2074	A
30	0	2096	A
30	0	2101	A
30	0	2102	G
30	0	2110	G
30	0	2238	A
30	0	2243	C
30	0	2258	A
30	0	2271	G

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Mol	Chain	Res	Type
30	0	2272	G
30	0	2317	C
30	0	2321	A
30	0	2354	A
30	0	2361	A
30	0	2369	A
30	0	2422	U
30	0	2462	G
30	0	2465	A
30	0	2469	A
30	0	2476	C
30	0	2480	G
30	0	2483	A
30	0	2507	G
30	0	2509	A
30	0	2511	A
30	0	2533	C
30	0	2537	G
30	0	2541	U
30	0	2553	A
30	0	2564	G
30	0	2589	U
30	0	2601	A
30	0	2602	G
30	0	2608	C
30	0	2613	G
30	0	2638	G
30	0	2664	A
30	0	2681	A
30	0	2682	C
30	0	2718	C
30	0	2726	U
30	0	2747	C
30	0	2748	G
30	0	2749	U
30	0	2750	G
30	0	2762	C
30	0	2768	A
30	0	2792	A
30	0	2800	A
30	0	2811	A
30	0	2812	A

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Mol	Chain	Res	Type
30	0	2825	C
30	0	2876	G
30	0	2890	A
30	0	2896	A
30	0	2903	C
30	0	2914	A
31	9	2	U
31	9	7	G
31	9	14	G
31	9	22	G
31	9	23	U
31	9	24	U
31	9	25	G
31	9	39	U
31	9	40	C
31	9	41	C
31	9	43	G
31	9	44	A
31	9	52	A
31	9	57	A
31	9	65	A
31	9	66	G
31	9	77	A
31	9	114	G
31	9	122	C

All (24) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
30	0	129	A
30	0	341	C
30	0	396	U
30	0	545	G
30	0	603	A
30	0	604	G
30	0	644	G
30	0	699	C
30	0	834	G
30	0	857	A
30	0	871	G
30	0	877	G
30	0	1080	C

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Mol	Chain	Res	Type
30	0	1237	U
30	0	1352	A
30	0	1685	A
30	0	1970	G
30	0	2011	A
30	0	2536	C
30	0	2718	C
30	0	2761	A
30	0	2791	U
31	9	43	G
31	9	65	A

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

5 non-standard protein/DNA/RNA residues are 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	$\#\|Z\| > 2$
30	1MA	0	628	35,30	16,25,26	1.41	3 (18%)	18,37,40	1.06	2 (11%)
30	PSU	0	2621	30	18,21,22	1.49	2 (11%)	22,30,33	1.27	3 (13%)
30	OMU	0	2587	35,30	19,22,23	0.32	0	26,31,34	0.40	0
30	OMG	0	2588	30	18,26,27	1.11	2 (11%)	19,38,41	0.69	1 (5%)
30	UR3	0	2619	30	19,22,23	0.42	0	26,32,35	0.59	1 (3%)

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
30	1MA	0	628	35,30	-	0/3/25/26	0/3/3/3
30	PSU	0	2621	30	-	0/7/25/26	0/2/2/2
30	OMU	0	2587	35,30	-	0/9/27/28	0/2/2/2
30	OMG	0	2588	30	-	0/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	UR3	0	2619	30	-	0/7/25/26	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	0	2621	PSU	C2-N1	4.86	1.43	1.36
30	0	628	1MA	C2-N3	3.92	1.33	1.29
30	0	2588	OMG	C5-C6	-3.07	1.41	1.47
30	0	2621	PSU	C6-C5	2.81	1.38	1.35
30	0	628	1MA	C6-N6	2.58	1.34	1.27
30	0	2588	OMG	C8-N7	-2.46	1.30	1.35
30	0	628	1MA	C8-N7	-2.02	1.31	1.35

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
30	0	2621	PSU	C6-C5-C4	3.37	120.55	118.20
30	0	628	1MA	N1-C2-N3	2.87	129.36	126.02
30	0	2621	PSU	C6-N1-C2	-2.82	119.80	122.68
30	0	2621	PSU	O2-C2-N1	2.81	125.89	122.79
30	0	628	1MA	C5-C6-N1	2.49	117.61	113.90
30	0	2619	UR3	C4-N3-C2	2.35	126.78	124.56
30	0	2588	OMG	O6-C6-C5	2.05	128.37	124.37

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	0	628	1MA	2	0
30	0	2621	PSU	2	0
30	0	2587	OMU	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 305 ligands modelled in this entry, 305 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	237/240 (98%)	-0.60	1 (0%) 92 79	29, 65, 98, 115	0
2	B	337/338 (99%)	-0.73	0 100 100	31, 59, 87, 97	0
3	C	246/246 (100%)	-0.82	0 100 100	23, 47, 69, 80	0
4	D	140/177 (79%)	0.45	15 (10%) 6 2	74, 109, 132, 140	0
5	E	172/178 (96%)	-0.64	0 100 100	50, 74, 97, 103	0
6	F	119/120 (99%)	-0.30	1 (0%) 86 65	50, 73, 106, 113	0
7	G	29/348 (8%)	0.08	0 100 100	75, 96, 105, 109	0
8	H	160/177 (90%)	-0.49	0 100 100	48, 67, 99, 109	0
9	I	70/162 (43%)	1.80	29 (41%) 0 0	134, 152, 167, 169	0
10	J	142/145 (97%)	-0.79	1 (0%) 87 69	40, 58, 75, 97	0
11	K	132/132 (100%)	-0.87	0 100 100	39, 55, 81, 86	0
12	L	145/165 (87%)	-0.24	1 (0%) 87 69	35, 72, 113, 129	0
13	M	194/196 (98%)	-0.51	8 (4%) 37 14	31, 46, 99, 106	0
14	N	186/187 (99%)	-0.33	0 100 100	60, 80, 126, 132	0
15	O	115/116 (99%)	-0.86	0 100 100	43, 56, 74, 80	0
16	P	143/149 (95%)	-0.75	0 100 100	40, 59, 79, 85	0
17	Q	95/96 (98%)	-0.71	0 100 100	44, 56, 72, 88	0
18	R	150/155 (96%)	-0.83	0 100 100	33, 49, 70, 83	0
19	S	81/85 (95%)	-0.67	1 (1%) 79 54	40, 62, 82, 92	0
20	T	119/120 (99%)	-0.55	0 100 100	40, 59, 87, 116	0
21	U	53/67 (79%)	2.66	32 (60%) 0 0	107, 117, 125, 126	0
22	V	65/71 (91%)	-0.02	4 (6%) 20 7	46, 74, 118, 123	0
23	W	154/154 (100%)	-0.69	0 100 100	39, 54, 73, 87	0
24	X	82/92 (89%)	-0.45	1 (1%) 79 54	46, 65, 94, 108	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
25	Y	142/241 (58%)	-0.88	0 100 100	30, 49, 71, 92	0
26	Z	73/116 (62%)	3.62	45 (61%) 0 0	98, 116, 126, 130	0
27	1	56/57 (98%)	-0.78	0 100 100	28, 36, 43, 48	0
28	2	46/50 (92%)	-0.57	1 (2%) 62 33	31, 66, 97, 104	0
29	3	92/92 (100%)	4.21	71 (77%) 0 0	104, 119, 130, 134	0
30	0	2749/2923 (94%)	-0.83	2 (0%) 95 89	23, 51, 96, 175	0
31	9	122/122 (100%)	-0.97	1 (0%) 86 65	45, 75, 103, 154	0
All	All	6646/7517 (88%)	-0.53	214 (3%) 47 20	23, 57, 116, 175	0

All (214) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
26	Z	46	SER	17.2
26	Z	58	ASN	13.1
29	3	39	GLN	12.1
26	Z	36	GLY	11.6
29	3	34	LYS	11.4
26	Z	55	SER	11.0
29	3	38	ARG	10.8
29	3	35	TRP	10.6
29	3	41	GLU	10.3
26	Z	35	SER	10.1
26	Z	50	VAL	9.9
29	3	37	ASP	9.8
29	3	20	HIS	9.0
29	3	33	MET	9.0
29	3	42	ARG	8.9
26	Z	43	GLY	8.8
29	3	36	ILE	8.3
26	Z	59	GLU	8.3
29	3	82	GLY	8.2
26	Z	69	ASP	7.8
29	3	19	GLU	7.5
29	3	31	THR	7.5
13	M	71	SER	7.5
21	U	54	THR	7.4
26	Z	49	ARG	7.3
13	M	70	GLY	7.2
29	3	14	CYS	7.2
29	3	15	ASN	7.1

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Mol	Chain	Res	Type	RSRZ
29	3	11	CYS	7.0
29	3	40	ARG	6.7
29	3	32	GLY	6.7
26	Z	53	ILE	6.4
26	Z	54	GLU	6.4
26	Z	44	ARG	6.3
26	Z	34	SER	6.2
21	U	46	ALA	6.1
29	3	62	THR	6.0
29	3	43	ASN	6.0
29	3	71	CYS	5.8
26	Z	42	TYR	5.7
26	Z	48	ARG	5.6
26	Z	57	MET	5.5
29	3	56	PRO	5.5
21	U	9	CYS	5.4
13	M	80	GLY	5.4
21	U	11	THR	5.4
29	3	16	GLU	5.4
29	3	78	HIS	5.4
26	Z	47	ARG	5.3
29	3	48	ASN	5.3
21	U	39	ASN	5.2
26	Z	60	ASP	5.1
29	3	51	LYS	5.1
29	3	47	GLY	5.1
26	Z	82	SER	5.1
9	I	74	ILE	5.0
29	3	44	SER	5.0
26	Z	45	VAL	4.9
26	Z	81	CYS	4.9
29	3	81	GLU	4.9
26	Z	77	GLY	4.8
26	Z	51	ALA	4.7
29	3	12	PRO	4.7
29	3	18	GLN	4.7
26	Z	67	GLY	4.7
26	Z	56	GLU	4.6
21	U	55	ALA	4.5
9	I	93	ALA	4.5
29	3	85	ALA	4.5
29	3	21	GLU	4.4

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Mol	Chain	Res	Type	RSRZ
21	U	40	ALA	4.4
29	3	28	GLY	4.3
29	3	53	SER	4.3
9	I	71	ALA	4.3
21	U	32	CYS	4.3
9	I	92	VAL	4.2
29	3	30	GLN	4.2
1	A	237	GLY	4.1
29	3	59	ASP	4.1
9	I	106	GLN	4.1
29	3	27	SER	4.1
21	U	53	ASP	4.1
29	3	13	HIS	4.1
4	D	57	THR	4.1
9	I	66	GLY	4.0
21	U	6	CYS	4.0
9	I	100	VAL	4.0
21	U	5	GLU	4.0
21	U	12	ASP	4.0
29	3	23	GLU	4.0
29	3	74	CYS	4.0
21	U	48	ASN	3.9
29	3	10	TYR	3.8
22	V	1	THR	3.8
9	I	102	GLN	3.8
29	3	29	ARG	3.7
29	3	84	ARG	3.7
26	Z	63	CYS	3.7
9	I	70	THR	3.7
29	3	76	LYS	3.7
29	3	45	GLY	3.7
31	9	1	U	3.6
26	Z	71	VAL	3.6
29	3	75	GLY	3.5
21	U	52	THR	3.5
29	3	60	LYS	3.5
21	U	10	GLY	3.5
9	I	67	VAL	3.5
9	I	112	LEU	3.4
4	D	18	ILE	3.4
21	U	36	CYS	3.3
29	3	77	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
29	3	91	GLN	3.3
29	3	83	TRP	3.3
26	Z	61	HIS	3.3
29	3	9	THR	3.3
29	3	61	PRO	3.3
9	I	78	ALA	3.2
26	Z	52	GLU	3.2
9	I	99	GLN	3.2
21	U	29	THR	3.2
9	I	104	ALA	3.2
21	U	31	PHE	3.2
4	D	69	ILE	3.2
22	V	38	GLY	3.2
29	3	17	HIS	3.2
9	I	132	VAL	3.1
29	3	63	LYS	3.1
4	D	88	LEU	3.1
29	3	58	GLY	3.1
21	U	56	ARG	3.1
9	I	72	GLU	3.1
29	3	25	VAL	3.1
26	Z	80	GLN	3.0
26	Z	65	ASN	3.0
29	3	69	TYR	3.0
29	3	64	LYS	3.0
26	Z	68	GLU	2.9
29	3	72	GLY	2.9
9	I	76	ASP	2.9
24	X	88	GLU	2.9
21	U	28	THR	2.9
9	I	73	LEU	2.9
26	Z	70	ARG	2.9
9	I	128	THR	2.9
22	V	39	ALA	2.9
9	I	110	ASP	2.9
4	D	92	GLU	2.8
13	M	82	ARG	2.8
22	V	40	PRO	2.8
26	Z	104	ARG	2.8
26	Z	40	ALA	2.8
4	D	63	ILE	2.8
26	Z	39	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
21	U	30	HIS	2.7
29	3	49	ASP	2.7
13	M	79	ALA	2.7
21	U	8	TYR	2.7
21	U	24	LYS	2.7
29	3	73	GLU	2.7
29	3	8	ASN	2.7
29	3	1	MET	2.7
21	U	43	GLY	2.6
29	3	6	ARG	2.6
21	U	51	TRP	2.6
26	Z	37	ARG	2.6
29	3	65	THR	2.6
10	J	4	ALA	2.6
4	D	26	GLY	2.6
29	3	70	ARG	2.5
30	0	1198	U	2.5
21	U	4	ARG	2.5
26	Z	83	TYR	2.5
29	3	3	MET	2.5
9	I	105	GLU	2.5
4	D	93	LEU	2.4
4	D	44	ILE	2.4
13	M	72	ALA	2.4
26	Z	62	ALA	2.4
9	I	68	PRO	2.4
12	L	60	GLU	2.4
21	U	23	HIS	2.4
9	I	108	HIS	2.4
21	U	7	ASP	2.4
29	3	46	ILE	2.4
26	Z	92	SER	2.3
29	3	68	LYS	2.3
21	U	41	ASP	2.3
30	0	1172	G	2.3
21	U	49	LEU	2.3
4	D	135	VAL	2.3
29	3	88	LEU	2.3
9	I	79	GLY	2.3
4	D	87	ALA	2.3
9	I	94	ASP	2.2
9	I	75	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
9	I	113	SER	2.2
4	D	80	ALA	2.2
26	Z	85	ASP	2.2
26	Z	78	ILE	2.1
13	M	83	SER	2.1
19	S	81	ILE	2.1
9	I	80	PHE	2.1
9	I	81	GLU	2.1
28	2	39	ARG	2.1
6	F	106	ALA	2.1
4	D	27	ILE	2.1
26	Z	103	VAL	2.0
13	M	77	HIS	2.0
4	D	134	LEU	2.0
21	U	44	ARG	2.0
4	D	75	LEU	2.0
21	U	38	ASN	2.0
26	Z	66	CYS	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
30	1MA	0	628	23/24	0.98	0.14	31,36,38,38	0
30	OMU	0	2587	21/22	0.98	0.12	41,44,50,50	0
30	OMG	0	2588	24/25	0.98	0.13	39,41,42,45	0
30	UR3	0	2619	21/22	0.98	0.14	39,43,45,48	0
30	PSU	0	2621	20/21	0.98	0.18	40,43,44,44	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
34	SR	0	9006	1/1	0.31	0.83	180,180,180,180	0
35	NA	0	8557	1/1	0.41	0.08	59,59,59,59	0
34	SR	0	9004	1/1	0.44	1.01	200,200,200,200	0
34	SR	0	8985	1/1	0.45	0.12	182,182,182,182	0
35	NA	0	8567	1/1	0.50	0.30	68,68,68,68	0
35	NA	0	8563	1/1	0.53	0.68	65,65,65,65	0
34	SR	0	8997	1/1	0.54	0.83	194,194,194,194	0
34	SR	0	8971	1/1	0.54	0.11	170,170,170,170	0
33	CL	J	8802	1/1	0.54	0.08	76,76,76,76	0
34	SR	0	9001	1/1	0.55	0.08	166,166,166,166	0
34	SR	0	8959	1/1	0.56	0.28	200,200,200,200	0
34	SR	0	8957	1/1	0.57	0.73	200,200,200,200	0
34	SR	0	8974	1/1	0.57	0.14	164,164,164,164	0
34	SR	0	8979	1/1	0.61	0.18	198,198,198,198	0
35	NA	0	8553	1/1	0.62	0.33	70,70,70,70	0
34	SR	0	8986	1/1	0.63	0.45	200,200,200,200	0
35	NA	0	8528	1/1	0.63	0.91	83,83,83,83	0
34	SR	0	8975	1/1	0.64	0.11	171,171,171,171	0
34	SR	0	8962	1/1	0.67	0.08	179,179,179,179	0
34	SR	0	8977	1/1	0.72	0.11	181,181,181,181	0
32	MG	0	8091	1/1	0.73	0.07	58,58,58,58	0
37	CD	U	8701	1/1	0.74	0.35	200,200,200,200	0
34	SR	0	8998	1/1	0.75	0.30	184,184,184,184	0
34	SR	0	8922	1/1	0.75	0.29	169,169,169,169	0
36	K	0	8401	1/1	0.75	0.15	156,156,156,156	0
34	SR	9	8980	1/1	0.75	0.14	182,182,182,182	0
34	SR	0	8960	1/1	0.76	0.05	152,152,152,152	0
34	SR	0	8919	1/1	0.76	0.32	200,200,200,200	0
34	SR	0	8982	1/1	0.78	1.88	200,200,200,200	0
34	SR	0	8969	1/1	0.78	0.31	192,192,192,192	0
32	MG	0	8063	1/1	0.78	0.22	86,86,86,86	0
33	CL	0	8814	1/1	0.78	0.18	72,72,72,72	0
35	NA	0	8518	1/1	0.79	0.26	75,75,75,75	0
35	NA	0	8559	1/1	0.79	0.46	122,122,122,122	0
34	SR	0	8944	1/1	0.80	0.08	165,165,165,165	0
34	SR	0	8973	1/1	0.80	0.14	112,112,112,112	0
34	SR	0	8967	1/1	0.81	0.05	133,133,133,133	0
34	SR	0	8988	1/1	0.81	0.13	170,170,170,170	0
35	NA	0	8566	1/1	0.81	0.32	62,62,62,62	0
35	NA	0	8556	1/1	0.82	0.44	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
34	SR	0	8968	1/1	0.82	0.15	177,177,177,177	0
35	NA	0	8571	1/1	0.82	0.17	46,46,46,46	0
35	NA	0	8573	1/1	0.82	0.28	55,55,55,55	0
35	NA	9	8572	1/1	0.82	0.17	71,71,71,71	0
34	SR	0	9007	1/1	0.82	0.24	179,179,179,179	0
34	SR	3	8932	1/1	0.82	0.09	158,158,158,158	0
35	NA	0	8535	1/1	0.83	0.20	64,64,64,64	0
35	NA	0	8541	1/1	0.83	0.24	54,54,54,54	0
34	SR	0	8931	1/1	0.83	0.07	110,110,110,110	0
33	CL	0	8815	1/1	0.83	0.09	87,87,87,87	0
34	SR	0	8947	1/1	0.83	0.30	194,194,194,194	0
34	SR	0	9002	1/1	0.83	0.06	157,157,157,157	0
32	MG	A	8051	1/1	0.83	0.22	101,101,101,101	0
34	SR	0	8955	1/1	0.85	0.17	200,200,200,200	0
34	SR	0	8946	1/1	0.85	0.12	123,123,123,123	0
35	NA	0	8548	1/1	0.85	0.12	68,68,68,68	0
35	NA	0	8564	1/1	0.86	0.34	57,57,57,57	0
35	NA	0	8546	1/1	0.86	0.47	80,80,80,80	0
35	NA	0	8507	1/1	0.86	0.16	32,32,32,32	0
35	NA	0	8515	1/1	0.86	0.15	44,44,44,44	0
32	MG	0	8081	1/1	0.86	0.32	80,80,80,80	0
34	SR	A	8993	1/1	0.86	0.08	159,159,159,159	0
32	MG	2	8060	1/1	0.86	0.10	35,35,35,35	0
34	SR	0	8989	1/1	0.86	0.18	200,200,200,200	0
37	CD	Z	8703	1/1	0.86	0.28	200,200,200,200	0
32	MG	0	8093	1/1	0.87	0.05	28,28,28,28	0
35	NA	0	8525	1/1	0.87	0.25	85,85,85,85	0
34	SR	B	8987	1/1	0.87	0.39	200,200,200,200	0
35	NA	0	8545	1/1	0.88	0.24	33,33,33,33	0
34	SR	0	8953	1/1	0.88	0.07	200,200,200,200	0
34	SR	0	8915	1/1	0.88	0.07	118,118,118,118	0
34	SR	0	8991	1/1	0.88	0.35	193,193,193,193	0
34	SR	0	8964	1/1	0.88	0.08	129,129,129,129	0
35	NA	0	8530	1/1	0.88	0.37	49,49,49,49	0
34	SR	0	8939	1/1	0.88	0.08	152,152,152,152	0
35	NA	0	8562	1/1	0.88	0.53	89,89,89,89	0
34	SR	0	8942	1/1	0.88	0.07	130,130,130,130	0
33	CL	3	8804	1/1	0.89	0.19	120,120,120,120	0
35	NA	0	8570	1/1	0.89	0.07	25,25,25,25	0
34	SR	0	8928	1/1	0.89	0.09	146,146,146,146	0
32	MG	0	8071	1/1	0.89	0.13	31,31,31,31	0
37	CD	3	8704	1/1	0.89	0.71	200,200,200,200	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
32	MG	0	8047	1/1	0.90	0.15	67,67,67,67	0
32	MG	B	8042	1/1	0.90	0.08	56,56,56,56	0
35	NA	0	8522	1/1	0.90	0.21	45,45,45,45	0
34	SR	0	8976	1/1	0.90	0.23	197,197,197,197	0
32	MG	0	8069	1/1	0.90	0.19	55,55,55,55	0
35	NA	0	8549	1/1	0.90	0.17	77,77,77,77	0
35	NA	0	8552	1/1	0.90	0.26	58,58,58,58	0
32	MG	0	8036	1/1	0.90	0.05	37,37,37,37	0
32	MG	0	8032	1/1	0.91	0.05	27,27,27,27	0
34	SR	3	8999	1/1	0.91	0.28	172,172,172,172	0
34	SR	0	8981	1/1	0.91	0.13	157,157,157,157	0
34	SR	9	9003	1/1	0.91	0.09	177,177,177,177	0
35	NA	0	8505	1/1	0.91	1.13	53,53,53,53	0
34	SR	0	8956	1/1	0.91	0.05	151,151,151,151	0
34	SR	0	8965	1/1	0.91	0.07	127,127,127,127	0
32	MG	0	8050	1/1	0.91	0.08	52,52,52,52	0
32	MG	0	8052	1/1	0.91	0.04	51,51,51,51	0
35	NA	0	8565	1/1	0.92	0.94	70,70,70,70	0
34	SR	F	9005	1/1	0.92	0.09	131,131,131,131	0
35	NA	0	8519	1/1	0.92	0.27	51,51,51,51	0
32	MG	0	8075	1/1	0.92	0.09	83,83,83,83	0
32	MG	0	8049	1/1	0.92	0.38	74,74,74,74	0
32	MG	0	8068	1/1	0.92	0.11	49,49,49,49	0
34	SR	0	8984	1/1	0.92	0.07	105,105,105,105	0
34	SR	0	9000	1/1	0.92	0.31	200,200,200,200	0
32	MG	0	8046	1/1	0.92	0.13	26,26,26,26	0
35	NA	0	8509	1/1	0.92	0.14	54,54,54,54	0
32	MG	K	8054	1/1	0.92	0.15	40,40,40,40	0
32	MG	0	8010	1/1	0.93	0.17	24,24,24,24	0
35	NA	0	8511	1/1	0.93	0.09	48,48,48,48	0
34	SR	0	8937	1/1	0.93	0.17	100,100,100,100	0
34	SR	0	8994	1/1	0.93	0.24	200,200,200,200	0
32	MG	0	8016	1/1	0.93	0.22	48,48,48,48	0
35	NA	0	8521	1/1	0.93	0.20	53,53,53,53	0
33	CL	L	8810	1/1	0.93	0.10	64,64,64,64	0
33	CL	Y	8820	1/1	0.94	0.11	47,47,47,47	0
35	NA	0	8560	1/1	0.94	0.76	74,74,74,74	0
32	MG	0	8039	1/1	0.94	0.18	71,71,71,71	0
35	NA	J	8538	1/1	0.94	0.08	49,49,49,49	0
35	NA	R	8532	1/1	0.94	0.14	37,37,37,37	0
34	SR	0	8910	1/1	0.94	0.08	99,99,99,99	0
35	NA	0	8544	1/1	0.94	0.11	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
32	MG	0	8033	1/1	0.94	0.13	40,40,40,40	0
34	SR	0	8916	1/1	0.94	0.10	114,114,114,114	0
35	NA	0	8547	1/1	0.94	0.67	47,47,47,47	0
32	MG	0	8037	1/1	0.94	0.17	76,76,76,76	0
33	CL	J	8821	1/1	0.94	0.11	66,66,66,66	0
34	SR	0	8927	1/1	0.94	0.20	196,196,196,196	0
34	SR	0	8970	1/1	0.94	0.04	131,131,131,131	0
32	MG	0	8088	1/1	0.94	0.16	35,35,35,35	0
33	CL	N	8807	1/1	0.94	0.35	99,99,99,99	0
33	CL	R	8806	1/1	0.95	0.11	47,47,47,47	0
35	NA	0	8504	1/1	0.95	0.09	27,27,27,27	0
32	MG	0	8082	1/1	0.95	0.12	66,66,66,66	0
35	NA	0	8506	1/1	0.95	0.51	58,58,58,58	0
32	MG	0	8065	1/1	0.95	0.12	50,50,50,50	0
35	NA	0	8508	1/1	0.95	0.56	61,61,61,61	0
34	SR	0	8983	1/1	0.95	0.27	191,191,191,191	0
33	CL	0	8803	1/1	0.95	0.14	69,69,69,69	0
33	CL	K	8812	1/1	0.95	0.07	48,48,48,48	0
34	SR	0	8914	1/1	0.95	0.20	105,105,105,105	0
32	MG	0	8080	1/1	0.95	0.28	68,68,68,68	0
33	CL	0	8822	1/1	0.95	0.60	97,97,97,97	0
34	SR	0	8945	1/1	0.95	0.06	107,107,107,107	0
32	MG	0	8062	1/1	0.95	0.20	57,57,57,57	0
35	NA	0	8526	1/1	0.95	0.13	33,33,33,33	0
34	SR	0	8996	1/1	0.96	0.22	199,199,199,199	0
32	MG	B	8043	1/1	0.96	0.11	53,53,53,53	0
33	CL	0	8816	1/1	0.96	0.39	94,94,94,94	0
34	SR	0	8943	1/1	0.96	0.09	72,72,72,72	0
33	CL	0	8817	1/1	0.96	0.20	69,69,69,69	0
35	NA	0	8554	1/1	0.96	0.55	65,65,65,65	0
35	NA	0	8513	1/1	0.96	0.34	66,66,66,66	0
32	MG	0	8040	1/1	0.96	0.21	54,54,54,54	0
35	NA	0	8516	1/1	0.96	0.08	20,20,20,20	0
34	SR	0	8917	1/1	0.96	0.10	109,109,109,109	0
35	NA	0	8561	1/1	0.96	0.36	57,57,57,57	0
34	SR	A	8929	1/1	0.96	0.04	117,117,117,117	0
32	MG	0	8041	1/1	0.96	0.31	36,36,36,36	0
33	CL	J	8801	1/1	0.96	0.13	71,71,71,71	0
34	SR	0	8972	1/1	0.96	0.10	150,150,150,150	0
32	MG	0	8035	1/1	0.96	0.10	61,61,61,61	0
35	NA	0	8527	1/1	0.96	0.15	54,54,54,54	0
35	NA	M	8539	1/1	0.96	0.09	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
35	NA	Q	8540	1/1	0.96	0.11	67,67,67,67	0
35	NA	0	8533	1/1	0.96	0.08	53,53,53,53	0
35	NA	0	8574	1/1	0.96	0.35	54,54,54,54	0
34	SR	0	8990	1/1	0.96	0.15	125,125,125,125	0
35	NA	S	8510	1/1	0.96	0.04	26,26,26,26	0
35	NA	0	8501	1/1	0.96	0.14	43,43,43,43	0
32	MG	3	8090	1/1	0.96	0.12	80,80,80,80	0
32	MG	0	8004	1/1	0.96	0.18	21,21,21,21	0
32	MG	0	8055	1/1	0.97	0.10	45,45,45,45	0
35	NA	0	8529	1/1	0.97	0.18	41,41,41,41	0
32	MG	T	8057	1/1	0.97	0.04	63,63,63,63	0
32	MG	0	8020	1/1	0.97	0.14	29,29,29,29	0
35	NA	0	8534	1/1	0.97	0.18	37,37,37,37	0
32	MG	0	8064	1/1	0.97	0.06	33,33,33,33	0
35	NA	0	8536	1/1	0.97	0.06	40,40,40,40	0
34	SR	0	8920	1/1	0.97	0.05	106,106,106,106	0
34	SR	0	8948	1/1	0.97	0.08	103,103,103,103	0
32	MG	0	8083	1/1	0.97	0.12	71,71,71,71	0
34	SR	0	8924	1/1	0.97	0.17	133,133,133,133	0
32	MG	0	8025	1/1	0.97	0.10	30,30,30,30	0
32	MG	0	8089	1/1	0.97	0.17	59,59,59,59	0
34	SR	0	8995	1/1	0.97	0.14	140,140,140,140	0
35	NA	0	8550	1/1	0.97	0.27	47,47,47,47	0
32	MG	0	8027	1/1	0.97	0.12	26,26,26,26	0
32	MG	0	8029	1/1	0.97	0.07	68,68,68,68	0
33	CL	A	8809	1/1	0.97	0.35	100,100,100,100	0
32	MG	Y	8086	1/1	0.97	0.06	37,37,37,37	0
34	SR	0	8901	1/1	0.98	0.14	63,63,63,63	0
34	SR	0	8951	1/1	0.98	0.09	139,139,139,139	0
34	SR	0	8908	1/1	0.98	0.13	77,77,77,77	0
34	SR	0	8909	1/1	0.98	0.13	89,89,89,89	0
32	MG	0	8014	1/1	0.98	0.19	21,21,21,21	0
34	SR	0	8911	1/1	0.98	0.06	79,79,79,79	0
34	SR	0	8958	1/1	0.98	0.07	114,114,114,114	0
32	MG	0	8073	1/1	0.98	0.06	51,51,51,51	0
35	NA	0	8542	1/1	0.98	0.16	51,51,51,51	0
32	MG	0	8005	1/1	0.98	0.22	34,34,34,34	0
32	MG	0	8078	1/1	0.98	0.23	51,51,51,51	0
34	SR	0	8963	1/1	0.98	0.05	123,123,123,123	0
32	MG	0	8017	1/1	0.98	0.10	20,20,20,20	0
32	MG	0	8034	1/1	0.98	0.13	53,53,53,53	0
32	MG	0	8053	1/1	0.98	0.05	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
34	SR	0	8921	1/1	0.98	0.09	75,75,75,75	0
35	NA	0	8551	1/1	0.98	0.15	55,55,55,55	0
32	MG	0	8018	1/1	0.98	0.14	34,34,34,34	0
34	SR	0	8923	1/1	0.98	0.12	85,85,85,85	0
35	NA	R	8575	1/1	0.98	0.34	89,89,89,89	0
35	NA	0	8555	1/1	0.98	0.34	50,50,50,50	0
32	MG	0	8087	1/1	0.98	0.09	26,26,26,26	0
34	SR	0	8926	1/1	0.98	0.09	109,109,109,109	0
35	NA	0	8558	1/1	0.98	0.22	44,44,44,44	0
32	MG	0	8006	1/1	0.98	0.13	20,20,20,20	0
32	MG	0	8021	1/1	0.98	0.11	25,25,25,25	0
32	MG	0	8023	1/1	0.98	0.18	24,24,24,24	0
34	SR	0	8935	1/1	0.98	0.09	87,87,87,87	0
34	SR	0	8936	1/1	0.98	0.08	87,87,87,87	0
32	MG	0	8092	1/1	0.98	0.02	44,44,44,44	0
34	SR	0	8938	1/1	0.98	0.07	164,164,164,164	0
32	MG	0	8024	1/1	0.98	0.12	96,96,96,96	0
34	SR	0	8940	1/1	0.98	0.11	77,77,77,77	0
35	NA	0	8568	1/1	0.98	0.10	38,38,38,38	0
34	SR	0	8941	1/1	0.98	0.18	122,122,122,122	0
34	SR	B	8950	1/1	0.98	0.16	113,113,113,113	0
32	MG	0	8066	1/1	0.98	0.31	75,75,75,75	0
35	NA	0	8520	1/1	0.98	0.10	39,39,39,39	0
32	MG	0	8067	1/1	0.98	0.13	32,32,32,32	0
36	K	M	8402	1/1	0.98	0.11	60,60,60,60	0
34	SR	S	8961	1/1	0.98	0.05	126,126,126,126	0
37	CD	O	8705	1/1	0.98	0.08	93,93,93,93	0
32	MG	0	8009	1/1	0.98	0.21	24,24,24,24	0
32	MG	0	8002	1/1	0.98	0.08	29,29,29,29	0
34	SR	0	8992	1/1	0.98	0.08	130,130,130,130	0
35	NA	0	8523	1/1	0.99	0.11	51,51,51,51	0
35	NA	0	8524	1/1	0.99	0.40	54,54,54,54	0
32	MG	0	8003	1/1	0.99	0.17	22,22,22,22	0
32	MG	0	8001	1/1	0.99	0.12	26,26,26,26	0
32	MG	0	8056	1/1	0.99	0.08	75,75,75,75	0
32	MG	0	8058	1/1	0.99	0.06	22,22,22,22	0
34	SR	A	8930	1/1	0.99	0.07	125,125,125,125	0
32	MG	0	8084	1/1	0.99	0.14	24,24,24,24	0
35	NA	0	8531	1/1	0.99	0.10	15,15,15,15	0
32	MG	0	8085	1/1	0.99	0.12	67,67,67,67	0
32	MG	0	8059	1/1	0.99	0.12	53,53,53,53	0
32	MG	0	8061	1/1	0.99	0.18	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
32	MG	0	8038	1/1	0.99	0.05	61,61,61,61	0
34	SR	1	8913	1/1	0.99	0.11	100,100,100,100	0
32	MG	0	8012	1/1	0.99	0.14	15,15,15,15	0
34	SR	0	8949	1/1	0.99	0.05	102,102,102,102	0
32	MG	0	8019	1/1	0.99	0.15	23,23,23,23	0
32	MG	0	8030	1/1	0.99	0.34	86,86,86,86	0
34	SR	0	8902	1/1	0.99	0.16	67,67,67,67	0
34	SR	0	8905	1/1	0.99	0.23	62,62,62,62	0
32	MG	9	8074	1/1	0.99	0.05	63,63,63,63	0
34	SR	0	9008	1/1	0.99	0.17	97,97,97,97	0
32	MG	0	8044	1/1	0.99	0.14	52,52,52,52	0
33	CL	B	8819	1/1	0.99	0.15	59,59,59,59	0
35	NA	C	8503	1/1	0.99	0.17	45,45,45,45	0
32	MG	0	8045	1/1	0.99	0.10	24,24,24,24	0
32	MG	0	8031	1/1	0.99	0.23	52,52,52,52	0
32	MG	0	8013	1/1	0.99	0.04	24,24,24,24	0
32	MG	0	8070	1/1	0.99	0.10	40,40,40,40	0
32	MG	0	8048	1/1	0.99	0.21	20,20,20,20	0
34	SR	0	8966	1/1	0.99	0.07	97,97,97,97	0
34	SR	0	8918	1/1	0.99	0.09	71,71,71,71	0
35	NA	0	8502	1/1	0.99	0.05	56,56,56,56	0
33	CL	M	8818	1/1	0.99	0.05	39,39,39,39	0
32	MG	0	8072	1/1	0.99	0.08	47,47,47,47	0
33	CL	O	8808	1/1	0.99	0.11	87,87,87,87	0
32	MG	0	8008	1/1	0.99	0.14	26,26,26,26	0
32	MG	0	8022	1/1	0.99	0.12	17,17,17,17	0
32	MG	0	8076	1/1	0.99	0.11	27,27,27,27	0
34	SR	0	8925	1/1	0.99	0.15	94,94,94,94	0
35	NA	0	8569	1/1	0.99	0.20	67,67,67,67	0
35	NA	0	8512	1/1	0.99	0.08	36,36,36,36	0
32	MG	0	8077	1/1	0.99	0.10	43,43,43,43	0
35	NA	0	8514	1/1	0.99	0.19	17,17,17,17	0
33	CL	0	8805	1/1	0.99	0.14	70,70,70,70	0
35	NA	9	8543	1/1	0.99	0.11	38,38,38,38	0
33	CL	0	8811	1/1	0.99	0.38	79,79,79,79	0
35	NA	0	8517	1/1	0.99	0.15	21,21,21,21	0
33	CL	0	8813	1/1	0.99	0.03	46,46,46,46	0
34	SR	0	8933	1/1	0.99	0.07	126,126,126,126	0
34	SR	0	8934	1/1	0.99	0.09	99,99,99,99	0
32	MG	0	8015	1/1	0.99	0.13	25,25,25,25	0
32	MG	0	8079	1/1	0.99	0.11	36,36,36,36	0
34	SR	0	8906	1/1	1.00	0.20	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
34	SR	0	8954	1/1	1.00	0.12	103,103,103,103	0
34	SR	0	8907	1/1	1.00	0.12	40,40,40,40	0
34	SR	1	8952	1/1	1.00	0.11	72,72,72,72	0
34	SR	9	8978	1/1	1.00	0.07	125,125,125,125	0
32	MG	0	8028	1/1	1.00	0.13	19,19,19,19	0
32	MG	0	8011	1/1	1.00	0.21	24,24,24,24	0
34	SR	R	8912	1/1	1.00	0.12	86,86,86,86	0
32	MG	0	8026	1/1	1.00	0.04	27,27,27,27	0
34	SR	0	8903	1/1	1.00	0.13	46,46,46,46	0
34	SR	0	8904	1/1	1.00	0.17	58,58,58,58	0
35	NA	0	8537	1/1	1.00	0.17	29,29,29,29	0
37	CD	1	8702	1/1	1.00	0.13	61,61,61,61	0
32	MG	0	8007	1/1	1.00	0.19	18,18,18,18	0

6.5 Other polymers (i)

There are no such residues in this entry.