



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:04 AM UTC

PDB ID : 1YJ9 / pdb_00001yj9
Title : Crystal Structure Of The Mutant 50S Ribosomal Subunit Of Haloarcula Marismortui Containing a three residue deletion in L22
Authors : Tu, D.; Blaha, G.; Moore, P.B.; Steitz, T.A.
Deposited on : 2005-01-13
Resolution : 2.80 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:

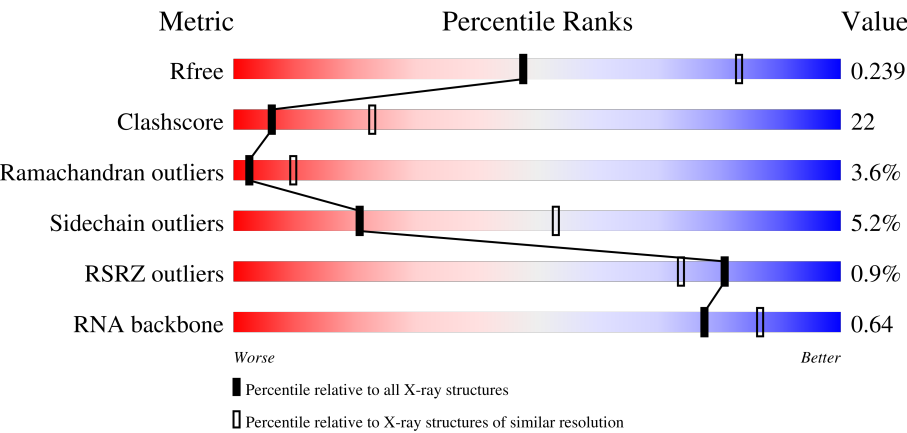
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.80 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.



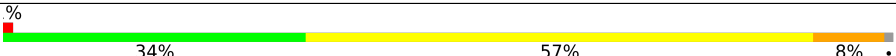
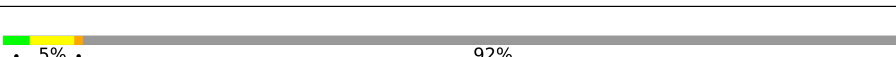
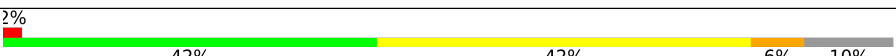
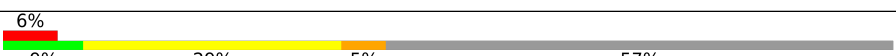
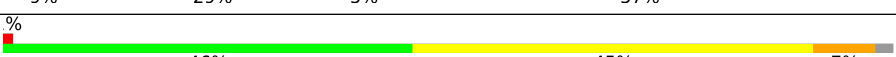
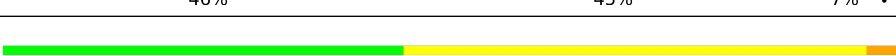
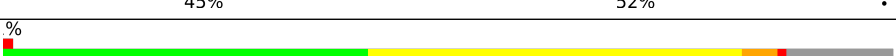
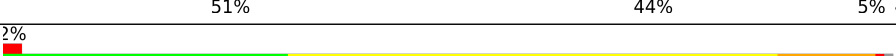
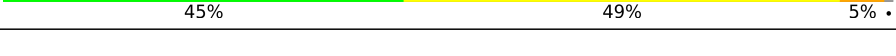
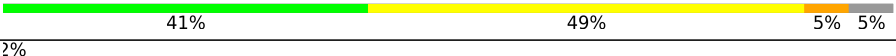
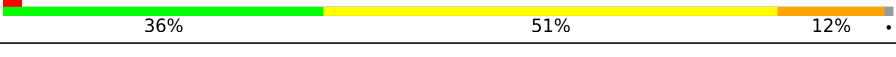
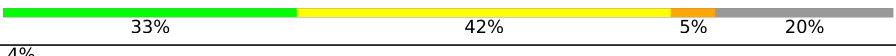
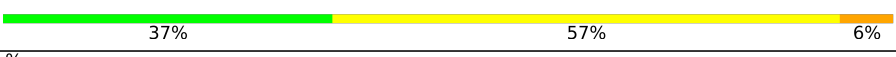
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)
RNA backbone	3983	1114 (3.00-2.60)

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 $\leq 5\%$. 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	0	2922	50%38%6%6%
2	9	122	2% 39%52%9%
3	A	240	% 47%42%10%
4	B	338	41%49%8%

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Mol	Chain	Length	Quality of chain
5	C	246	
6	D	177	
7	E	178	
8	F	120	
9	G	348	
10	H	177	
11	I	162	
12	J	145	
13	K	132	
14	L	165	
15	M	195	
16	N	187	
17	O	116	
18	P	149	
19	Q	96	
20	R	152	
21	S	85	
22	T	120	
23	U	66	
24	V	71	
25	W	154	
26	X	92	
27	Y	241	
28	Z	83	
29	1	57	

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Mol	Chain	Length	Quality of chain
30	2	50	
31	3	92	

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
34	NA	R	8586	-	-	-	X
35	CL	J	8801	-	-	X	-
35	CL	J	8802	-	-	X	-

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 99031 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 RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	2754	Total	C	N	O	P	0	1	0
			59041	26358	10875	19062	2746			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	628	1MA	A	modified residue	GB 55229667
0	2587	OMU	U	modified residue	GB 55229667
0	2588	OMG	G	modified residue	GB 55229667
0	2619	UR3	U	modified residue	GB 55229667
0	2621	PSU	U	modified residue	GB 55229667

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	9	122	Total	C	N	O	P	0	0	0
			2599	1160	471	847	121			

- Molecule 3 is a protein called 50S ribosomal protein L2P.

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

- Molecule 4 is a protein called 50S ribosomal protein L3P.

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

- Molecule 5 is a protein called 50S ribosomal protein L4E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	246	Total	C	N	O	S	0	0	0
			1859	1131	344	383	1			

- Molecule 6 is a protein called 50S ribosomal protein L5P.

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

- Molecule 7 is a protein called 50S ribosomal protein L6P.

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

- Molecule 8 is a protein called 50S ribosomal protein L7AE.

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

- Molecule 9 is a protein called ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG.

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

- Molecule 10 is a protein called 50S RIBOSOMAL PROTEIN L10E.

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

- Molecule 11 is a protein called 50S RIBOSOMAL PROTEIN L11P.

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

- Molecule 12 is a protein called 50S ribosomal protein L13P.

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

- Molecule 13 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	K	132	Total	C	N	O	S	0	0	0
			992	609	187	192	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	44	LEU	HIS	conflict	UNP P22450

- Molecule 14 is a protein called 50S ribosomal protein L15P.

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

- Molecule 15 is a protein called 50S Ribosomal Protein L15E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	M	194	Total	C	N	O	S	0	0	0
			1558	942	332	283	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	13	GLU	LYS	conflict	GB 55231501

- Molecule 16 is a protein called 50S ribosomal protein L18P.

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

- Molecule 17 is a protein called 50S ribosomal protein L18e.

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

- Molecule 18 is a protein called 50S ribosomal protein L19E.

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

- Molecule 19 is a protein called 50S ribosomal protein L21e.

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

- Molecule 20 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	R	147	Total	C	N	O	S	0	0	0
			1123	699	204	216	4			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	?	-	GLN	deletion	UNP P10970
R	?	-	GLN	deletion	UNP P10970
R	?	-	GLY	deletion	UNP P10970

- Molecule 21 is a protein called 50S ribosomal protein L23P.

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

- Molecule 22 is a protein called 50S ribosomal protein L24P.

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

- Molecule 23 is a protein called 50S ribosomal protein L24E.

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

- Molecule 24 is a protein called 50S ribosomal protein L29P.

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

- Molecule 25 is a protein called 50S ribosomal protein L30P.

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

- Molecule 26 is a protein called 50S ribosomal protein L31e.

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

- Molecule 27 is a protein called 50S ribosomal protein L32E.

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

- Molecule 28 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	Z	73	Total	C	N	O	S	0	0	0
			578	346	116	111	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	10	ARG	SER	conflict	GB 55231162

- Molecule 29 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 30 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	2	49	Total	C	N	O	S	0	0	0
			421	254	93	73	1			

- Molecule 31 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 32 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	0	107	Total	Mg	0	0
			107	107		
32	9	1	Total	Mg	0	0
			1	1		
32	A	2	Total	Mg	0	0
			2	2		
32	B	1	Total	Mg	0	0
			1	1		
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		

- Molecule 33 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	0	2	Total	K	0	0
			2	2		

- Molecule 34 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	74	Total	Na	0	0
			74	74		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	9	2	Total 2	Na 2	0	0
34	A	1	Total 1	Na 1	0	0
34	C	1	Total 1	Na 1	0	0
34	J	1	Total 1	Na 1	0	0
34	L	1	Total 1	Na 1	0	0
34	M	1	Total 1	Na 1	0	0
34	Q	1	Total 1	Na 1	0	0
34	R	2	Total 2	Na 2	0	0
34	S	1	Total 1	Na 1	0	0
34	T	1	Total 1	Na 1	0	0

- Molecule 35 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	0	9	Total 9	Cl 9	0	0
35	A	1	Total 1	Cl 1	0	0
35	B	1	Total 1	Cl 1	0	0
35	J	3	Total 3	Cl 3	0	0
35	L	1	Total 1	Cl 1	0	0
35	M	1	Total 1	Cl 1	0	0
35	N	1	Total 1	Cl 1	0	0
35	O	1	Total 1	Cl 1	0	0
35	Q	1	Total 1	Cl 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	R	1	Total 1	Cl 1	0	0
35	Y	1	Total 1	Cl 1	0	0
35	3	1	Total 1	Cl 1	0	0

- Molecule 36 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	O	1	Total 1	Cd 1	0	0
36	U	1	Total 1	Cd 1	0	0
36	Z	1	Total 1	Cd 1	0	0
36	1	1	Total 1	Cd 1	0	0
36	3	1	Total 1	Cd 1	0	0

- Molecule 37 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	0	5866	Total 5866	O 5866	0	0
37	9	143	Total 143	O 143	0	0
37	A	119	Total 119	O 119	0	0
37	B	148	Total 148	O 148	0	0
37	C	180	Total 180	O 180	0	0
37	D	46	Total 46	O 46	0	0
37	E	45	Total 45	O 45	0	0
37	F	27	Total 27	O 27	0	0
37	G	19	Total 19	O 19	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	H	69	Total 69	O 69	0	0
37	I	9	Total 9	O 9	0	0
37	J	57	Total 57	O 57	0	0
37	K	54	Total 54	O 54	0	0
37	L	84	Total 84	O 84	0	0
37	M	130	Total 130	O 130	0	0
37	N	64	Total 64	O 64	0	0
37	O	45	Total 45	O 45	0	0
37	P	64	Total 64	O 64	0	0
37	Q	53	Total 53	O 53	0	0
37	R	58	Total 58	O 58	0	0
37	S	34	Total 34	O 34	0	0
37	T	32	Total 32	O 32	0	0
37	U	26	Total 26	O 26	0	0
37	V	14	Total 14	O 14	0	0
37	W	72	Total 72	O 72	0	0
37	X	24	Total 24	O 24	0	0
37	Y	104	Total 104	O 104	0	0
37	Z	34	Total 34	O 34	0	0
37	1	63	Total 63	O 63	0	0
37	2	32	Total 32	O 32	0	0

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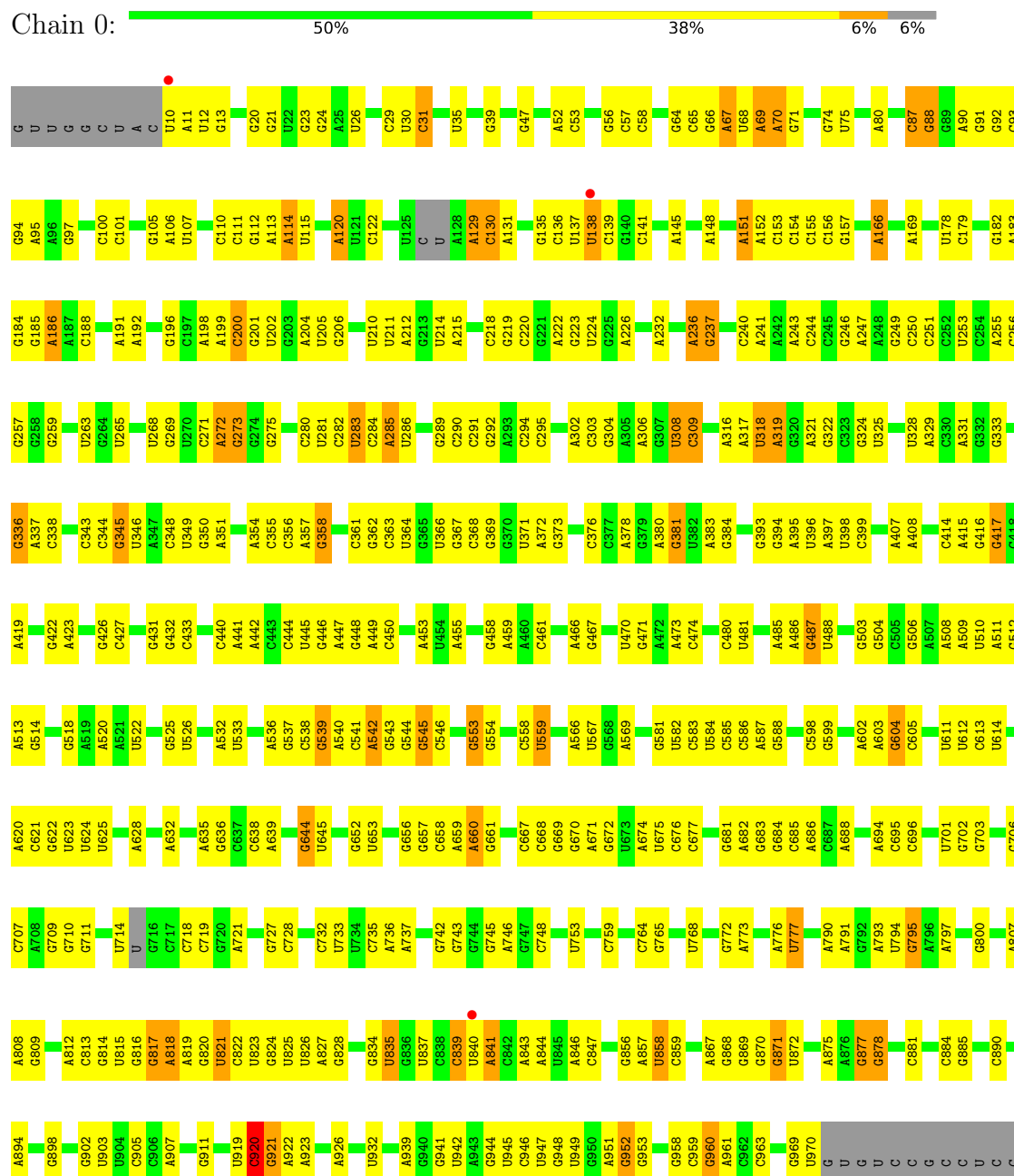
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	3	69	Total	O	0	0
			69	69		

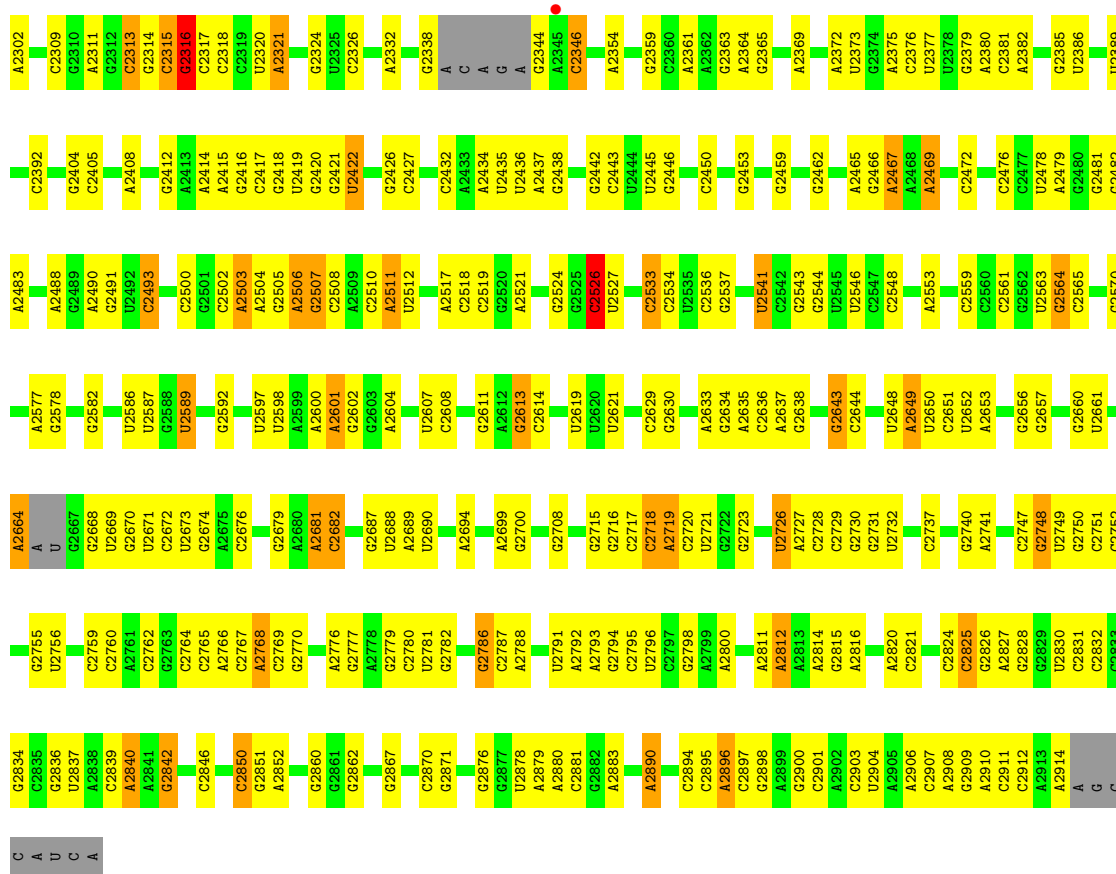
3 Residue-property plots

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.

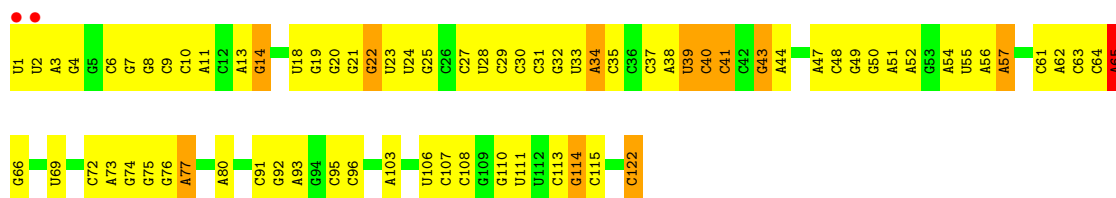
• Molecule 1: 23S Ribosomal RNA



U	G2080	G1974	C1894	A1815	C1735	G1634	U1544	U1457	G1351	C1243	A1166	A1067	G
A	A2081	A1978	A1904	C1816	U1741	U1635	C1545	U1461	A1352	U1244	G1167	A1070	A
C	C2084	G1979	U1905	U1817	A1742	G1636	G1546	C1462	C1353	C1245	C1168	G1071	A
C	A2085	U1980	U1905	G1819	G1743	A1637	A1547	U1463	C1360	A1246	A1171	G1072	A
G	G	G	G	G1820	G1743	A1641	C1549	G1468	C1361	C1250	G1172		G
G	A2089	U1996	A1909	A1821	A1746	A1642	G1552	G1468	U1362	C1251	A1173	A1078	G
C	G2090	A1997	A1910	A1822	A1747	C1643	C1553	C1469	C1366	C1254	A1174	A1079	A
G	G2091	G	G	G1823	G1751	U1645	C1554	A1470	C1366	C1254	G1175	C1080	U
U	G2094	G2000	C1916	U1825	G1752	G1649	G1555	A1471	C1370	A1261	C1176	A1081	C
U	A2095	C2002	U1918	G1826	A1755	U1653	G1556	U1472	G1370	A1261	A1177		G
G	A2096	U2003	C1920	G1827	G1756	A1654	C1557	C1474	U1371	U1266	A1086		G
A	C	U2004	G1828	A1829	U1757	U1655	G1558	C1477	C1377	C1267	G1087		G
C	A2101	G2005	A1921	C1830	U1758	A1656	U	U1488	G1378	C1268	A1088		A
U	G2102	C2006	A1922	U1834	A1759	A1657	A1559	C1477	A1379	G1269	U1091		C
U	A2007	A2007	G1923	A1839	U1759	A1657	A1561	C1483	G1378	G1273	A1092		C
C	G2105	U2008	A1924	C1834	G1760	A1657	C1562	G1484	A1379	C1273	U1185		C999
G	C2106	A	G1925	U1835	U1761	A1658	C1562	A1485	U1388	C1273	U1185		G1000
A	C2107	A	G1926	U1835	U1761	A1658	C1562	A1485	U1388	C1273	U1185		U1001
G	U2107	A	G1926	U1835	U1761	A1658	C1562	A1485	U1388	C1273	U1185		A1006
G	A2108	U2012	A1927	U1838	C1763	A1659	G1568	A1486	G1389	U1276	C1187		A1007
U	G2109	G2013	A1930	U1839	C1763	A1660	U1569	A1487	A1390	C1277	A1188		G1008
U	G2110	G2014	A1931	A1840	U1766	A1661	A1572	U1488	G1391	A1278	A1189		
A	G2111	A2015	A1931	C1841	U1767	C1662	A1573	A1493	A1392	U1279	G1190		
C	C	U2016	G1932	C1841	C1767	C1662	A1573	A1493	A1393	U1285	A1191		
C	U2115	U2028	G1933	A1845	C1768	C1666	A1573	A1494	C1394	U1285	A1192		A1012
G	U2116	C2029	A1934	U1846	U1770	A1667	G1576	A1495	C1395	U1285	A1193		A1013
C	G2121	G	U1937	G1848	C1772	C1679	A1580	G1497	C1396	C1289	A1194		A1014
C	U2032	U2032	U1938	G1849	C1773	C1679	A1580	U1500	C1397	G1290	G1195		U1015
U	G2128	G2033	U1939	U1850	G1774	A1682	U1587	U1500	A1399	U1297	G1197		U1016
A	A2251	U2034	C1940	G1851	U1778	G1683	U1587	U1503	C1400	U1298	C1127		
G	C2132	C2035	A1941	A1852	A1779	A1685	G1589	A1504	A1407	G1299	U1128		C1023
G	U2133	C2036	C1943	C1853	A1779	A1685	G1592	U1505	U1304	U1201	C1129		G1024
G	G2134	G2039	C1943	C1854	G1782	C1686	G1593	U1506	A1414	C1305	G1131		C1025
G	A2135	A	C1943	C1855	C1783	C1687	C1593	C1507	G1415	C1305	A1132		U1026
C	G2136	U2044	G1947	C1856	A1783	G1688	C1594	C1508	U1419	G1311	U1206		U1027
A	A	G2044	G1947	A1857	U1784	G1688	C1594	C1508	U1419	G1311	U1206		U1028
C	C	U2047	G1951	A1858	C1787	A1691	U1596	C1513	U1422	G1312	A1207		U1029
A	G	C2047	U	A1859	U1788	C1692	A1597	C1514	U1422	G1312	C1208		U1029
C	U	A	A	U1860	U1788	C1692	A1597	C1514	U1422	G1312	C1208		G1039
C	G	G2050	A	C1861	G1789	A1701	U1599	A1515	C1423	G1315	C1209		
C	U	G2053	C	C1862	C1790	U1702	U1599	U1516	C1426	G1316	G1214		C1043
U	G	G2053	U	G1863	U1791	G1703	G1600	C1517	A1427	G1319	A1215		C1044
G	C	U2057	A	C1864	U1791	G1703	C1602	A1518	C1428	G1319	G1216		G1045
A	C	U2057	U	C1864	G1794	A1711	A1603	G1523	U1429	A1328	G1217		C1051
C	C	U2063	G	G1868	C1798	A1712	G1604	U1524	G1430	G1329	U1218		G1052
A	G	U2064	A	C1872	C1798	A1717	G1605	G1525	A1330	G1329	G1151		G1053
C	A	U2064	C	C1872	C1798	A1717	G1605	G1525	A1330	G1329	G1151		G1054
C	U	A2067	C	G1873	C1803	A1717	C1613	A1526	C1439	A1154	A1154		G1055
A	A	G2068	C	U1874	A1804	U1722	G1613	A1527	U1440	G1155	C1156		U1056
G	G	C2068	U1964	A1875	G1805	U1722	G1614	A1528	G1441	C1229	C1157		G1057
U	U	G	C1965	C1876	G1806	U1724	A1442	G1529	A1442	C1334	C1158		A1057
U	U	C	U1966	G1877	U1807	C1725	C1617	G1535	U1446	C1335	C1159		A1058
G	C	C2071	U1967	G1878	G1808	C1725	A1624	C1536	U1446	G1340	G1236		A1059
A	A	G2072	U1967	U1878	G1808	C1725	A1624	C1536	U1446	G1340	A1236		G1060
A	C	G2073	U1968	U1879	G1809	C1731	U1625	C1537	G1449	A1161	G1160		
A	G	A2074	A1968	U1879	C1810	A1732	A1626	C1538	C1450	G1162	G1059		
U	C	U2074	G1971	C1882	A1811	A1732	U1539	C1538	C1451	G1239	G1163		U1064
U	U	U2078	U1972	U1883	G1812	A1733	A1632	G1540	C1451	G1239	G1163		U1065
C	C	C2079	A1972	G1884		C1734	C1632	U1260	C1456	U1164	G1065		U1066



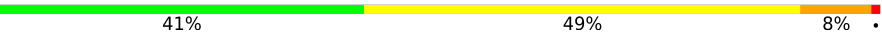
• Molecule 2: 5S Ribosomal RNA

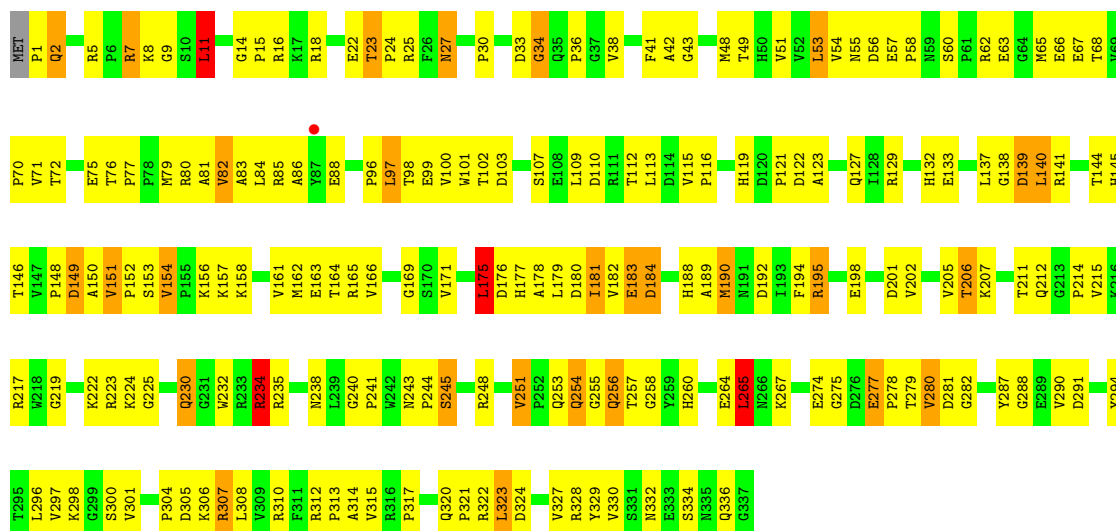


• Molecule 3: 50S ribosomal protein L2P



• Molecule 4: 50S ribosomal protein L3P

Chain B:  41% 49% 8% .



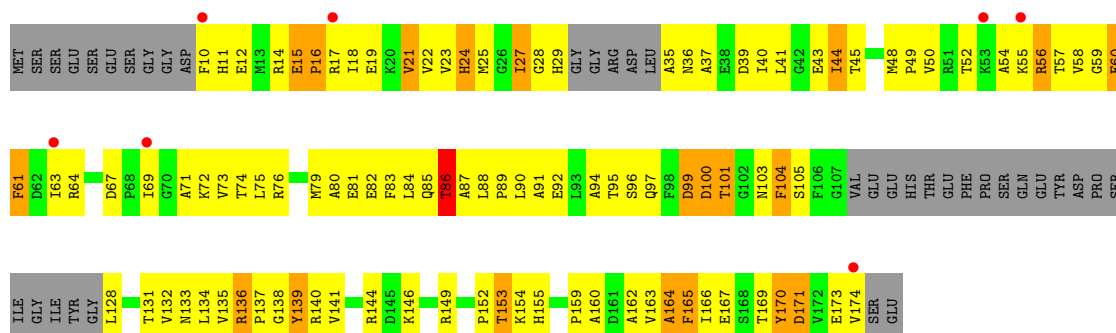
• Molecule 5: 50S ribosomal protein L4E

Chain C:  41% 51% 7% .

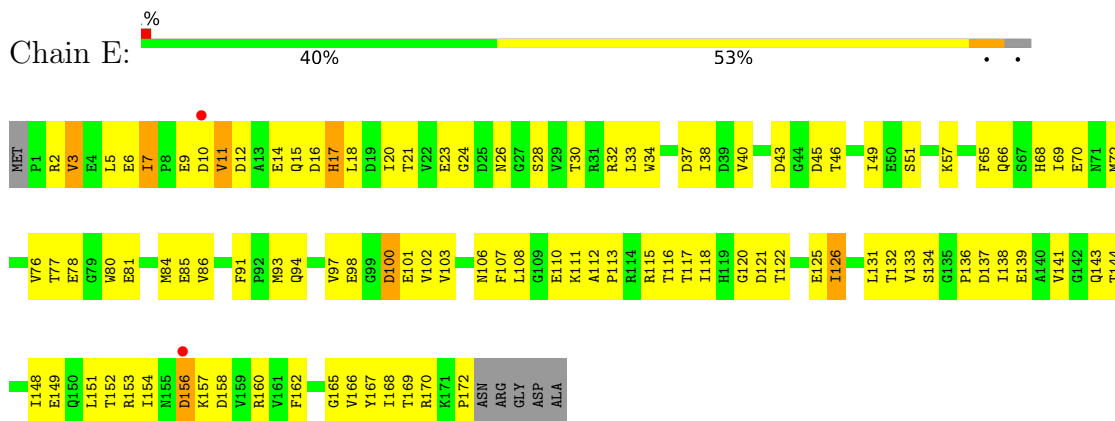


• Molecule 6: 50S ribosomal protein L5P

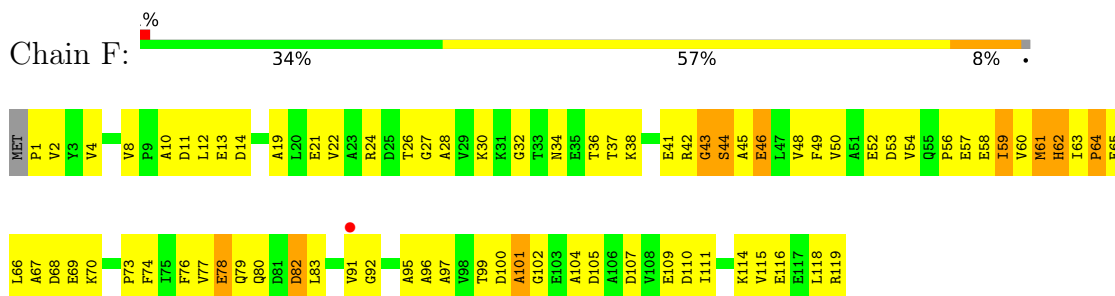
Chain D:  4% 20% 47% 11% 21% .



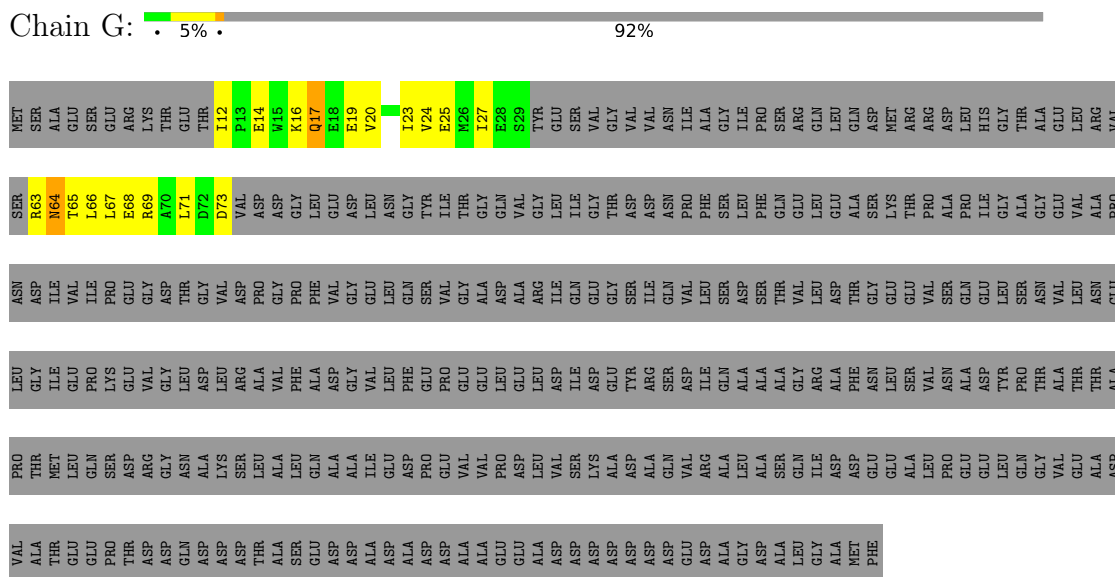
- Molecule 7: 50S ribosomal protein L6P



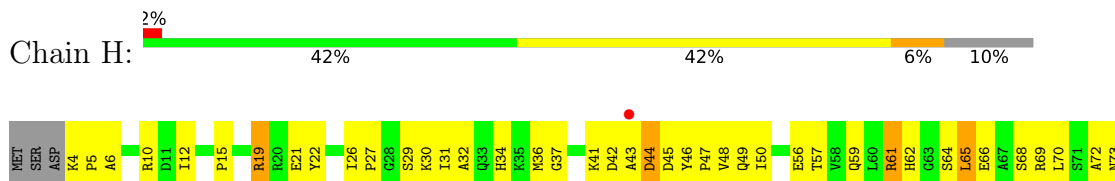
- Molecule 8: 50S ribosomal protein L7AE

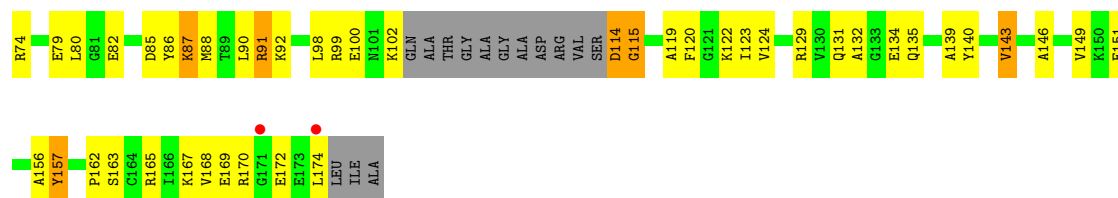


- Molecule 9: ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG

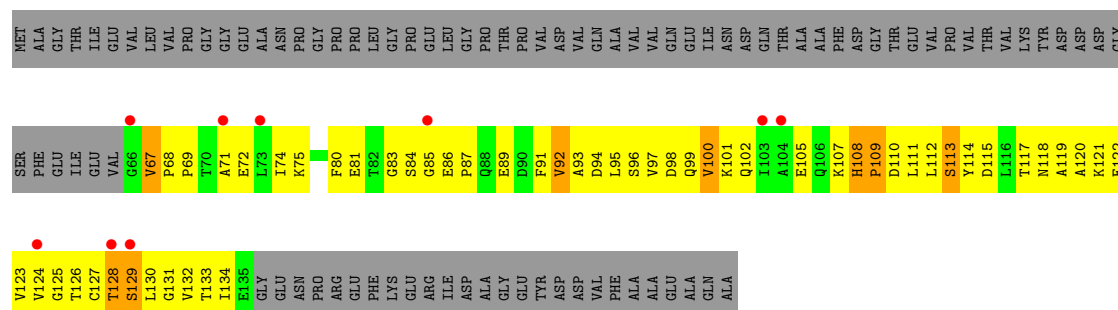
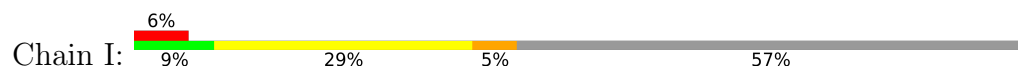


- Molecule 10: 50S RIBOSOMAL PROTEIN L10E

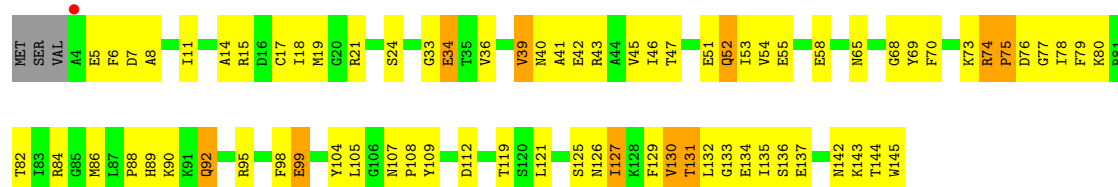




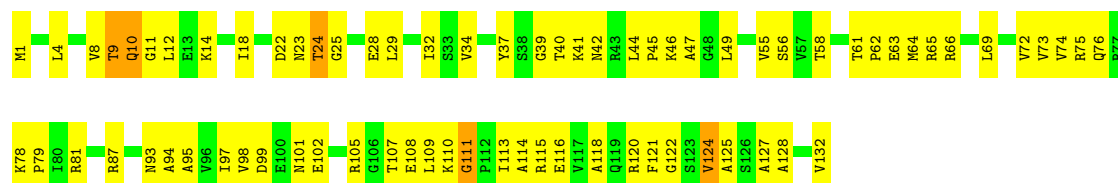
• Molecule 11: 50S RIBOSOMAL PROTEIN L11P



• Molecule 12: 50S ribosomal protein L13P

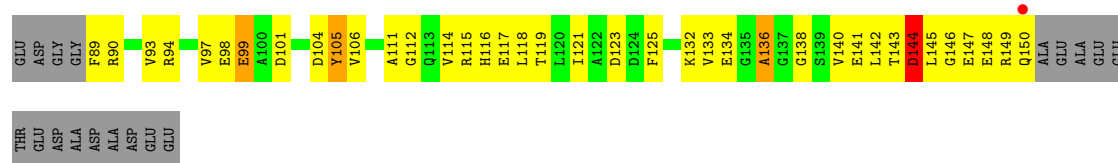


• Molecule 13: 50S ribosomal protein L14P

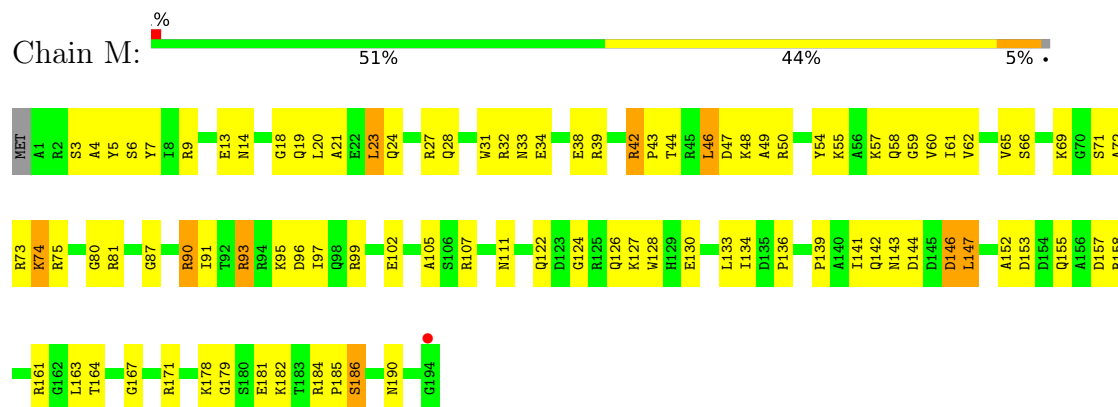


• Molecule 14: 50S ribosomal protein L15P

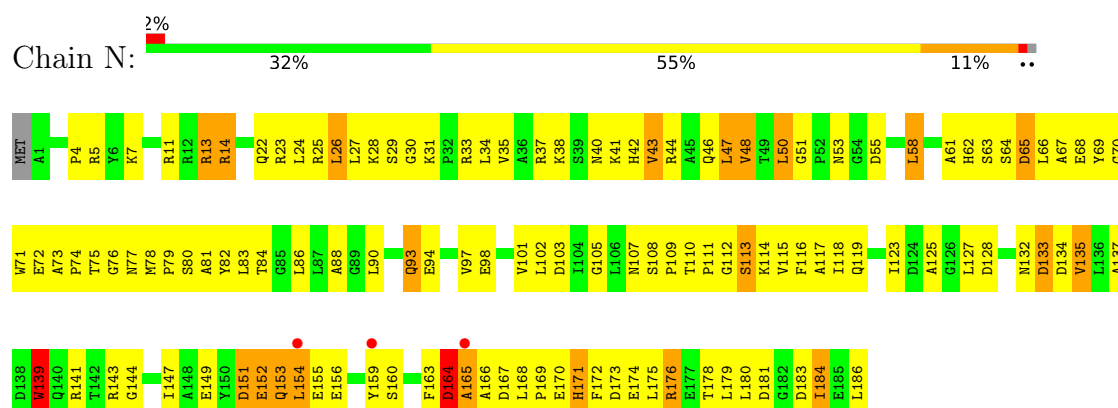




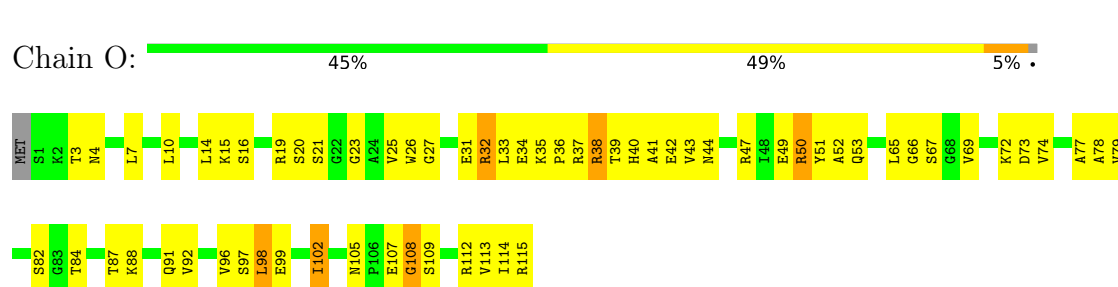
• Molecule 15: 50S Ribosomal Protein L15E



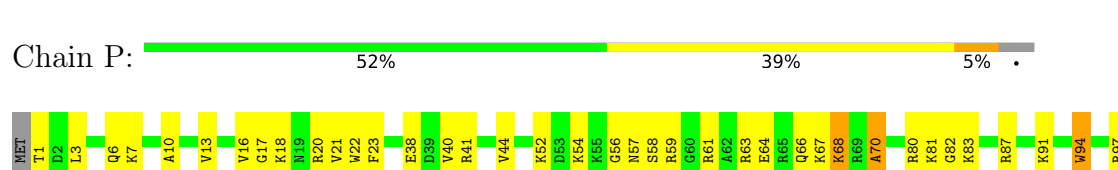
• Molecule 16: 50S ribosomal protein L18P



• Molecule 17: 50S ribosomal protein L18e



• Molecule 18: 50S ribosomal protein L19E





- Molecule 19: 50S ribosomal protein L21e



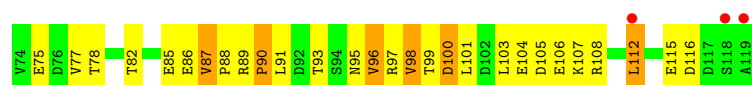
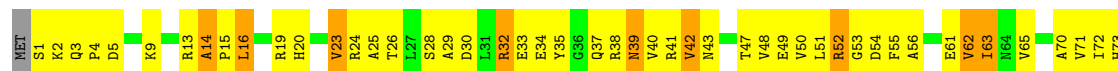
- Molecule 20: 50S ribosomal protein L22P



- Molecule 21: 50S ribosomal protein L23P

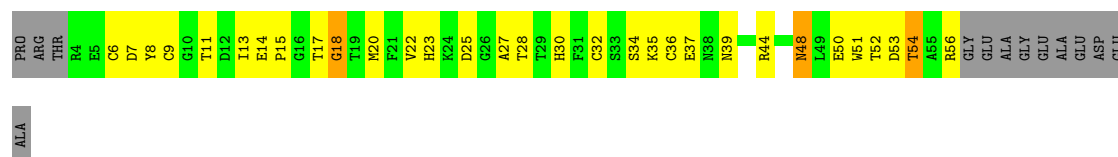


- Molecule 22: 50S ribosomal protein L24P

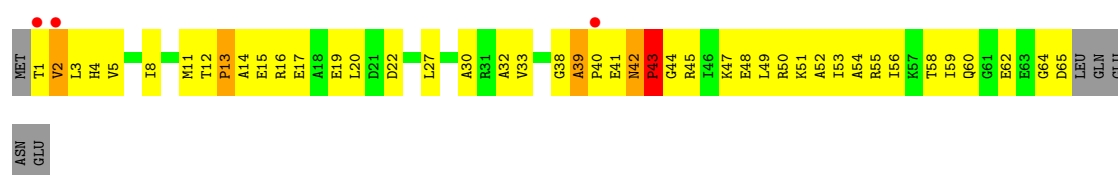


- Molecule 23: 50S ribosomal protein L24E

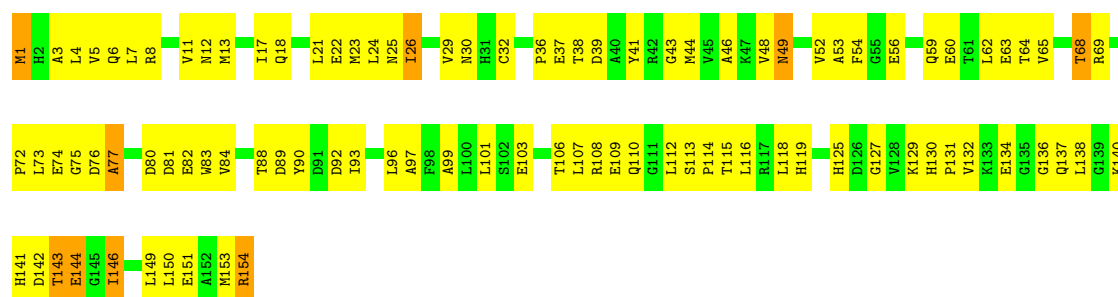
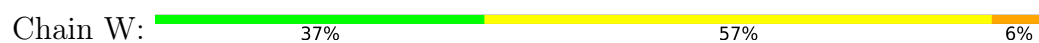




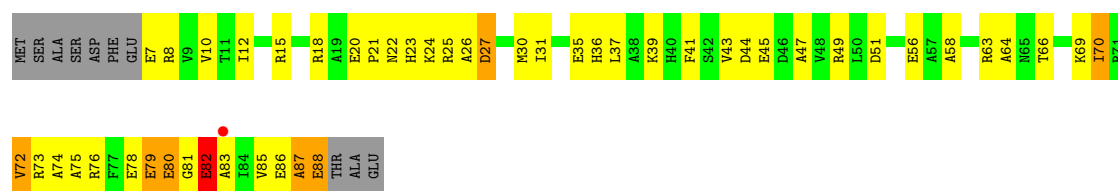
• Molecule 24: 50S ribosomal protein L29P



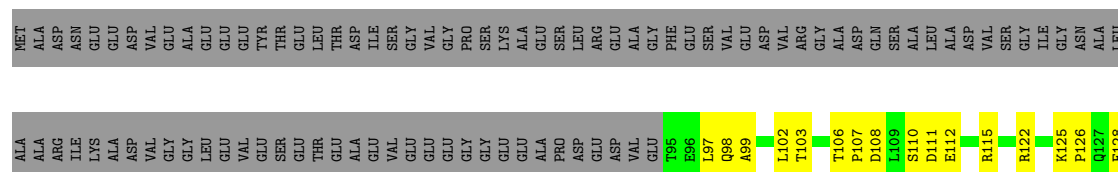
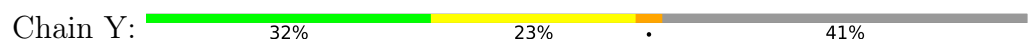
• Molecule 25: 50S ribosomal protein L30P

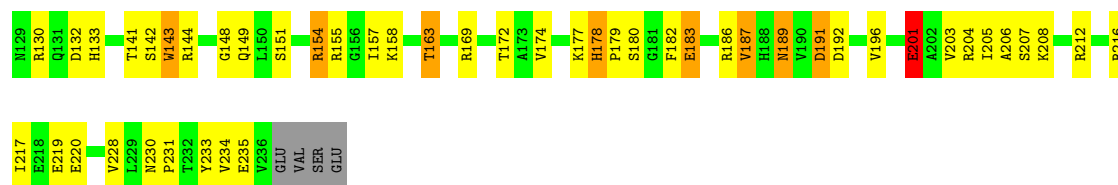


• Molecule 26: 50S ribosomal protein L31e

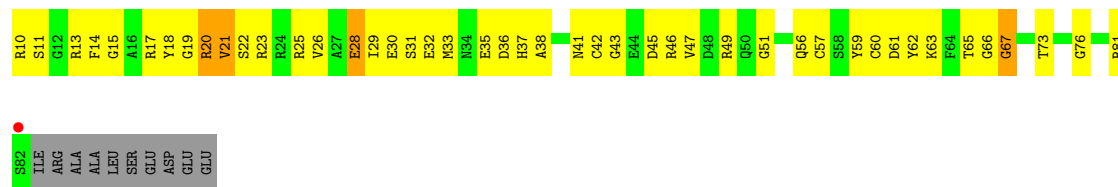


• Molecule 27: 50S ribosomal protein L32E

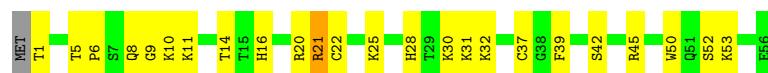




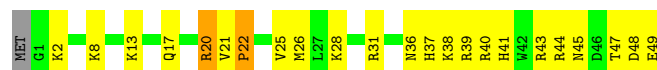
- Molecule 28: 50S ribosomal protein L37Ae



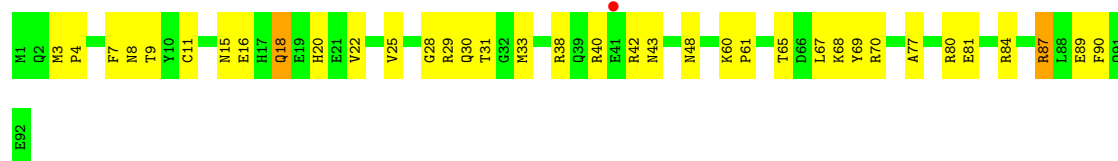
- Molecule 29: 50S ribosomal protein L37e



- Molecule 30: 50S ribosomal protein L39e



- Molecule 31: 50S ribosomal protein L44E



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	213.08Å 300.75Å 575.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.94 – 2.80 29.94 – 2.80	Depositor EDS
% Data completeness (in resolution range)	89.3 (29.94-2.80) 89.3 (29.94-2.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.81Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.184 , 0.242 0.183 , 0.239	Depositor DCC
R_{free} test set	3987 reflections (0.99%)	wwPDB-VP
Wilson B-factor (Å ²)	55.8	Xtriage
Anisotropy	0.325	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 62.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	99031	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: CL, PSU, NA, UR3, OMG, OMU, MG, 1MA, CD, 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	0	0.40	0/65980	0.62	18/102903 (0.0%)
2	9	0.39	0/2904	0.62	3/4526 (0.1%)
3	A	0.45	0/1786	1.03	12/2408 (0.5%)
4	B	0.46	0/2690	1.07	19/3652 (0.5%)
5	C	0.49	0/1884	1.04	10/2551 (0.4%)
6	D	0.39	0/1111	0.92	7/1498 (0.5%)
7	E	0.42	0/1382	0.90	1/1880 (0.1%)
8	F	0.39	0/901	0.96	3/1224 (0.2%)
9	G	0.36	0/241	0.90	1/324 (0.3%)
10	H	0.47	0/1302	1.04	8/1743 (0.5%)
11	I	0.40	0/526	0.95	3/716 (0.4%)
12	J	0.49	0/1136	0.95	4/1530 (0.3%)
13	K	0.46	0/1001	1.05	6/1347 (0.4%)
14	L	0.41	0/1130	1.00	5/1509 (0.3%)
15	M	0.45	0/1582	0.96	5/2117 (0.2%)
16	N	0.40	0/1474	1.10	12/1999 (0.6%)
17	O	0.46	0/874	0.97	3/1181 (0.3%)
18	P	0.43	0/1147	0.88	4/1528 (0.3%)
19	Q	0.51	0/749	1.15	6/1005 (0.6%)
20	R	0.52	0/1146	0.97	2/1544 (0.1%)
21	S	0.40	0/648	0.90	4/875 (0.5%)
22	T	0.43	0/958	1.02	11/1289 (0.9%)
23	U	0.41	0/417	0.95	2/562 (0.4%)
24	V	0.38	0/502	1.02	2/675 (0.3%)
25	W	0.51	0/1219	1.02	5/1655 (0.3%)
26	X	0.48	0/664	1.05	3/895 (0.3%)
27	Y	0.47	0/1146	0.99	6/1536 (0.4%)
28	Z	0.42	0/589	0.92	0/787
29	1	0.47	0/438	0.95	1/578 (0.2%)
30	2	0.50	0/427	0.89	0/566
31	3	0.45	0/771	0.86	1/1024 (0.1%)
All	All	0.42	0/98725	0.74	167/147627 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	46
2	9	0	1
All	All	0	47

There are no bond length outliers.

All (167) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	N	153	GLN	N-CA-C	-10.07	101.63	113.21
18	P	118	GLN	N-CA-C	-9.66	100.71	111.14
19	Q	17	LYS	N-CA-C	-8.91	98.89	109.93
4	B	323	LEU	N-CA-C	8.68	122.16	110.35
16	N	135	VAL	N-CA-C	-8.41	104.97	113.47
4	B	175	LEU	N-CA-C	-8.33	102.16	111.07
14	L	47	GLY	N-CA-C	8.23	120.58	111.85
10	H	163	SER	N-CA-C	-8.05	97.94	110.42
16	N	151	ASP	N-CA-C	-7.98	103.26	113.16
3	A	103	VAL	N-CA-C	7.86	116.57	107.77
25	W	143	THR	N-CA-C	-7.71	103.33	112.89
1	0	1942	A	C5'-C4'-C3'	7.65	127.47	116.00
19	Q	68	GLY	N-CA-C	-7.62	98.36	111.47
24	V	42	ASN	CA-C-N	7.49	129.21	119.84
24	V	42	ASN	C-N-CA	7.49	129.21	119.84
5	C	175	LYS	N-CA-C	7.42	119.89	110.24
7	E	11	VAL	N-CA-C	7.41	120.59	109.17
1	0	920	C	C2'-C3'-O3'	-7.35	102.68	113.70
4	B	157	LYS	N-CA-C	-7.24	104.31	113.43
15	M	13	GLU	N-CA-C	-7.19	103.44	111.28
16	N	102	LEU	N-CA-C	7.14	119.73	108.67
16	N	13	ARG	N-CA-C	-7.05	104.31	113.12
13	K	124	VAL	N-CA-C	-7.00	105.79	111.81
1	0	839	C	C2'-C3'-O3'	-7.00	103.20	113.70
22	T	63	ILE	N-CA-C	6.90	117.02	110.53
27	Y	143	TRP	N-CA-C	6.88	120.88	109.46
22	T	116	ASP	N-CA-C	6.85	118.54	111.14
3	A	222	GLY	N-CA-C	-6.84	105.75	114.37
3	A	235	ARG	N-CA-C	-6.80	105.11	113.41
4	B	151	VAL	CA-C-N	6.76	126.55	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	151	VAL	C-N-CA	6.76	126.55	119.05
1	0	2291	A	N9-C1'-C2'	6.70	122.05	112.00
4	B	154	VAL	CA-C-N	6.66	125.89	118.97
4	B	154	VAL	C-N-CA	6.66	125.89	118.97
3	A	148	LEU	N-CA-C	6.58	120.25	109.72
22	T	34	GLU	N-CA-C	6.53	118.40	111.28
5	C	219	ASN	N-CA-C	6.47	118.37	109.18
3	A	133	ARG	N-CA-C	-6.46	104.88	112.89
16	N	51	GLY	CA-C-N	6.41	127.86	119.84
16	N	51	GLY	C-N-CA	6.41	127.86	119.84
14	L	136	ALA	N-CA-C	-6.38	104.81	112.59
4	B	81	ALA	N-CA-C	-6.37	102.12	110.53
17	O	82	SER	N-CA-C	-6.35	102.60	110.41
15	M	42	ARG	CA-C-N	6.32	126.66	119.83
15	M	42	ARG	C-N-CA	6.32	126.66	119.83
1	0	1504	A	N9-C1'-C2'	6.32	121.48	112.00
10	H	10	ARG	N-CA-C	6.26	120.18	112.54
2	9	65	A	N9-C1'-C2'	6.23	121.35	112.00
6	D	170	TYR	N-CA-C	6.17	118.13	110.91
14	L	80	ASP	N-CA-C	6.16	119.13	109.96
3	A	213	LYS	N-CA-C	6.14	118.78	111.71
26	X	51	ASP	CA-C-N	6.14	127.52	119.84
26	X	51	ASP	C-N-CA	6.14	127.52	119.84
4	B	222	LYS	N-CA-C	-6.12	100.94	110.42
19	Q	47	VAL	CA-C-N	6.10	125.65	119.19
19	Q	47	VAL	C-N-CA	6.10	125.65	119.19
11	I	67	VAL	CA-C-N	6.08	126.64	120.38
11	I	67	VAL	C-N-CA	6.08	126.64	120.38
14	L	144	ASP	N-CA-C	-6.07	104.66	111.28
20	R	34	GLU	N-CA-C	6.07	117.97	111.36
14	L	20	ASN	N-CA-C	6.05	120.82	111.56
21	S	30	ASP	N-CA-C	6.04	120.12	112.87
26	X	79	GLU	N-CA-C	6.04	120.12	112.87
3	A	228	ILE	N-CA-C	6.02	117.06	108.93
22	T	87	VAL	N-CA-C	5.99	114.49	107.84
4	B	265	LEU	N-CA-C	5.95	119.79	110.32
12	J	68	GLY	N-CA-C	5.94	119.50	111.72
20	R	141	VAL	N-CA-C	5.93	117.91	108.89
3	A	198	ASP	N-CA-C	5.90	120.55	113.23
5	C	192	ILE	N-CA-C	5.90	116.68	109.30
23	U	50	GLU	N-CA-C	5.90	118.47	111.33
3	A	110	SER	N-CA-C	-5.88	104.85	112.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	100	ASP	N-CA-C	-5.88	107.09	114.56
27	Y	183	GLU	N-CA-C	-5.85	100.13	109.96
27	Y	178	HIS	N-CA-C	-5.84	101.79	110.20
16	N	14	ARG	N-CA-C	-5.83	104.84	111.07
4	B	282	GLY	N-CA-C	-5.82	107.35	114.92
6	D	136	ARG	CA-C-N	5.81	127.10	119.84
6	D	136	ARG	C-N-CA	5.81	127.10	119.84
31	3	81	GLU	N-CA-C	-5.81	102.45	110.35
16	N	171	HIS	N-CA-C	-5.79	105.05	111.71
25	W	115	THR	N-CA-C	5.79	118.33	108.90
16	N	48	VAL	N-CA-C	5.76	117.73	108.85
3	A	70	ALA	N-CA-C	5.75	117.23	109.24
19	Q	13	LYS	N-CA-C	5.75	118.32	111.71
4	B	234	ARG	N-CA-C	5.75	117.41	109.54
6	D	101	THR	N-CA-C	-5.69	106.23	112.72
21	S	10	VAL	N-CA-C	5.68	115.78	107.37
1	0	1261	A	N9-C1'-C2'	5.67	120.51	112.00
4	B	230	GLN	N-CA-C	5.67	119.92	112.89
16	N	176	ARG	N-CA-C	-5.67	105.00	111.07
12	J	112	ASP	N-CA-C	-5.66	103.05	110.53
1	0	834	G	C2'-C3'-O3'	-5.66	105.21	113.70
8	F	62	HIS	N-CA-C	5.65	118.38	111.82
4	B	161	VAL	N-CA-C	5.63	116.51	107.73
17	O	50	ARG	N-CA-C	5.63	117.42	111.28
25	W	68	THR	N-CA-C	5.62	117.49	111.36
5	C	78	ARG	N-CA-C	5.59	116.46	108.74
22	T	16	LEU	N-CA-C	5.57	120.55	111.37
10	H	115	GLY	N-CA-C	-5.55	100.01	113.18
25	W	75	GLY	N-CA-C	5.54	117.69	112.04
2	9	39	U	N1-C1'-C2'	5.52	120.29	112.00
5	C	91	PRO	CA-C-N	5.50	125.44	119.78
5	C	91	PRO	C-N-CA	5.50	125.44	119.78
18	P	44	VAL	N-CA-C	-5.49	105.37	110.53
10	H	172	GLU	N-CA-C	-5.48	104.85	112.30
21	S	57	THR	N-CA-C	5.45	118.18	110.50
4	B	324	ASP	CA-C-N	5.44	125.37	119.76
4	B	324	ASP	C-N-CA	5.44	125.37	119.76
22	T	52	ARG	N-CA-C	5.44	122.40	110.80
16	N	152	GLU	N-CA-C	-5.38	105.07	111.69
12	J	75	PRO	N-CA-C	-5.38	107.14	113.86
11	I	129	SER	N-CA-C	-5.35	105.46	112.41
1	0	2726	U	N1-C1'-C2'	5.35	120.02	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	W	25	ASN	N-CA-C	5.33	119.08	112.47
5	C	228	ALA	CA-C-N	5.32	125.32	120.21
5	C	228	ALA	C-N-CA	5.32	125.32	120.21
1	0	1450	C	C4'-C3'-O3'	5.31	120.97	113.00
6	D	15	GLU	CA-C-N	5.27	126.43	119.84
6	D	15	GLU	C-N-CA	5.27	126.43	119.84
27	Y	230	ASN	CA-C-N	5.27	126.40	120.66
27	Y	230	ASN	C-N-CA	5.27	126.40	120.66
22	T	14	ALA	CA-C-N	5.26	125.26	119.89
22	T	14	ALA	C-N-CA	5.26	125.26	119.89
13	K	108	GLU	N-CA-C	5.26	117.38	109.23
1	0	2664	A	N9-C1'-C2'	5.25	119.87	112.00
4	B	23	THR	CA-C-N	5.24	125.16	119.76
4	B	23	THR	C-N-CA	5.24	125.16	119.76
1	0	1419	U	N1-C1'-C2'	5.24	119.86	112.00
22	T	54	ASP	N-CA-C	-5.23	106.16	112.54
22	T	32	ARG	N-CA-C	-5.23	105.58	111.28
1	0	129	A	C2'-C3'-O3'	5.22	121.54	113.70
18	P	56	GLY	N-CA-C	-5.22	103.18	110.96
8	F	8	VAL	N-CA-C	5.21	112.30	107.56
2	9	65	A	C4'-C3'-O3'	-5.21	105.19	113.00
22	T	78	THR	N-CA-C	5.19	116.56	109.18
27	Y	201	GLU	N-CA-C	5.19	117.70	109.50
19	Q	11	ARG	N-CA-C	-5.17	105.54	111.07
1	0	206	G	C5'-C4'-C3'	-5.16	108.25	116.00
3	A	166	ASP	N-CA-C	5.16	116.98	111.36
3	A	135	VAL	N-CA-C	5.16	116.40	108.71
15	M	74	LYS	N-CA-C	5.15	117.89	109.59
4	B	11	LEU	N-CA-C	-5.15	107.51	112.97
13	K	8	VAL	N-CA-C	5.15	115.38	108.17
1	0	2526	C	N1-C1'-C2'	5.14	119.72	112.00
13	K	9	THR	N-CA-C	-5.14	100.14	108.41
10	H	65	LEU	N-CA-C	-5.13	104.95	111.11
12	J	39	VAL	N-CA-C	5.13	116.69	108.89
21	S	27	ALA	N-CA-C	-5.12	99.44	108.20
1	0	2316	G	C5'-C4'-C3'	-5.12	107.52	115.20
9	G	17	GLN	N-CA-C	-5.12	105.78	112.23
8	F	82	ASP	N-CA-C	-5.11	105.34	112.45
23	U	18	GLY	N-CA-C	5.11	120.79	112.61
13	K	25	GLY	N-CA-C	-5.11	107.75	114.95
1	0	1504	A	C1'-O4'-C4'	-5.11	104.80	109.90
1	0	2466	G	C4'-C3'-O3'	-5.10	105.34	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	H	91	ARG	N-CA-C	5.09	119.49	113.28
10	H	119	ALA	N-CA-C	5.08	119.34	113.20
15	M	90	ARG	N-CA-C	5.08	119.11	113.02
17	O	69	VAL	N-CA-C	5.07	115.42	108.12
10	H	162	PRO	N-CA-C	5.05	118.28	111.22
29	1	21	ARG	N-CA-C	5.03	119.28	112.04
5	C	80	VAL	CA-C-N	5.01	125.03	119.32
5	C	80	VAL	C-N-CA	5.01	125.03	119.32
13	K	46	LYS	N-CA-C	5.01	118.23	110.17
1	0	1006	A	N9-C1'-C2'	5.01	119.51	112.00
18	P	70	ALA	N-CA-C	-5.00	106.44	112.54

There are no chirality outliers.

All (47) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	1039	G	Sidechain
1	0	1078	A	Sidechain
1	0	1131	G	Sidechain
1	0	1340	G	Sidechain
1	0	1351	G	Sidechain
1	0	1430	G	Sidechain
1	0	148	A	Sidechain
1	0	1599	U	Sidechain
1	0	1635	U	Sidechain
1	0	1653	A	Sidechain
1	0	1684	A	Sidechain
1	0	1809	G	Sidechain
1	0	1829	A	Sidechain
1	0	1863	G	Sidechain
1	0	1877	G	Sidechain
1	0	1878	G	Sidechain
1	0	1972	U	Sidechain
1	0	2034	U	Sidechain
1	0	2101	A	Sidechain
1	0	2313	C	Sidechain
1	0	2315	C	Sidechain
1	0	2316	G	Sidechain
1	0	2493	C	Sidechain
1	0	2503	A	Sidechain
1	0	2506	A	Sidechain
1	0	2526	C	Sidechain

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Mol	Chain	Res	Type	Group
1	0	2564	G	Sidechain
1	0	26	U	Sidechain
1	0	2630	G	Sidechain
1	0	2643	G	Sidechain
1	0	2842	G	Sidechain
1	0	333	G	Sidechain
1	0	398	U	Sidechain
1	0	458	G	Sidechain
1	0	471	G	Sidechain
1	0	481	U	Sidechain
1	0	518	G	Sidechain
1	0	768	U	Sidechain
1	0	795	G	Sidechain
1	0	815	U	Sidechain
1	0	817	G	Sidechain
1	0	818	A	Sidechain
1	0	867	A	Sidechain
1	0	881	C	Sidechain
1	0	919	U	Sidechain
1	0	952	G	Sidechain
2	9	65	A	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	59041	0	29817	1167	0
2	9	2599	0	1325	86	0
3	A	1753	0	1766	152	0
4	B	2625	0	2533	211	0
5	C	1859	0	1816	164	0
6	D	1094	0	1085	144	0
7	E	1357	0	1266	91	0
8	F	890	0	843	83	0
9	G	240	0	231	24	0
10	H	1282	0	1292	97	0
11	I	519	0	500	63	0
12	J	1120	0	1098	86	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	K	992	0	1031	83	0
14	L	1118	0	1076	87	0
15	M	1558	0	1566	100	0
16	N	1445	0	1401	156	0
17	O	865	0	873	65	0
18	P	1136	0	1123	72	0
19	Q	735	0	729	38	0
20	R	1123	0	1099	77	0
21	S	641	0	605	40	0
22	T	950	0	923	101	0
23	U	410	0	364	34	0
24	V	499	0	511	48	0
25	W	1196	0	1137	134	0
26	X	654	0	653	57	0
27	Y	1130	0	1133	67	0
28	Z	578	0	539	43	0
29	1	431	0	426	35	0
30	2	421	0	437	36	0
31	3	755	0	728	32	0
32	0	107	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	2	0	0	0	0
32	B	1	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	2	0	0	0	0
34	0	74	0	0	0	0
34	9	2	0	0	0	0
34	A	1	0	0	0	0
34	C	1	0	0	0	0
34	J	1	0	0	0	0
34	L	1	0	0	0	0
34	M	1	0	0	0	0
34	Q	1	0	0	0	0
34	R	2	0	0	0	0
34	S	1	0	0	0	0
34	T	1	0	0	0	0
35	0	9	0	0	1	0
35	3	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	A	1	0	0	0	0
35	B	1	0	0	0	0
35	J	3	0	0	4	0
35	L	1	0	0	0	0
35	M	1	0	0	0	0
35	N	1	0	0	1	0
35	O	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	1	0	0	0	0
35	Y	1	0	0	0	0
36	1	1	0	0	0	0
36	3	1	0	0	0	0
36	O	1	0	0	0	0
36	U	1	0	0	0	0
36	Z	1	0	0	0	0
37	0	5866	0	0	247	0
37	1	63	0	0	8	0
37	2	32	0	0	3	0
37	3	69	0	0	8	0
37	9	143	0	0	12	0
37	A	119	0	0	23	0
37	B	148	0	0	31	0
37	C	180	0	0	34	0
37	D	46	0	0	18	0
37	E	45	0	0	11	0
37	F	27	0	0	8	0
37	G	19	0	0	2	0
37	H	69	0	0	12	0
37	I	9	0	0	5	0
37	J	57	0	0	8	0
37	K	54	0	0	10	0
37	L	84	0	0	17	0
37	M	130	0	0	11	0
37	N	64	0	0	22	0
37	O	45	0	0	12	0
37	P	64	0	0	10	0
37	Q	53	0	0	7	0
37	R	58	0	0	5	0
37	S	34	0	0	3	0
37	T	32	0	0	9	0
37	U	26	0	0	3	0
37	V	14	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	W	72	0	0	12	0
37	X	24	0	0	5	0
37	Y	104	0	0	15	0
37	Z	34	0	0	3	0
All	All	99031	0	59926	3351	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 22.

All (3351) 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)
5:C:127:ARG:NH2	5:C:225:PRO:HG2	1.66	1.09
6:D:25:MET:HE2	6:D:41:LEU:HG	1.35	1.09
5:C:236:THR:HG22	5:C:239:ALA:H	0.95	1.08
1:0:1160:G:H5'	1:0:1161:A:H5'	1.13	1.07
4:B:264:GLU:HG2	4:B:267:LYS:HE2	1.36	1.04
29:1:25:LYS:HD2	30:2:49:GLU:H	1.20	1.03
13:K:10:GLN:NE2	13:K:10:GLN:H	1.58	1.02
1:0:871:G:H5'	1:0:871:G:H8	1.21	1.01
24:V:12:THR:HG22	24:V:15:GLU:HG3	1.42	1.00
1:0:156:C:H5''	15:M:171:ARG:HD3	1.42	0.99
3:A:194:MET:HE3	3:A:199:HIS:HB2	1.44	0.98
1:0:1559:A:H1'	37:0:5655:HOH:O	1.61	0.98
1:0:1119:G:H2'	12:J:52:GLN:HE22	1.29	0.97
1:0:871:G:H5'	1:0:871:G:C8	1.98	0.96
1:0:381:G:H5''	37:0:4123:HOH:O	1.62	0.96
2:9:76:G:H3'	2:9:77:A:H5''	1.44	0.96
30:2:40:ARG:HD2	30:2:47:THR:HG22	1.46	0.96
5:C:236:THR:HG22	5:C:239:ALA:N	1.80	0.96
1:0:1242:A:H5'	12:J:82:THR:HG23	1.44	0.96
30:2:20:ARG:HG3	30:2:20:ARG:HH11	1.29	0.95
6:D:54:ALA:HB2	6:D:69:ILE:HD12	1.48	0.95
2:9:6:C:H5''	16:N:37:ARG:NH1	1.82	0.95
25:W:4:LEU:HD22	25:W:52:VAL:HG21	1.45	0.95
28:Z:10:ARG:HA	37:Z:8715:HOH:O	1.67	0.95
13:K:10:GLN:HE21	13:K:10:GLN:N	1.66	0.94
1:0:2270:G:H4'	3:A:223:ARG:HH12	1.33	0.94
1:0:2717:C:H2'	1:0:2718:C:H5''	1.46	0.94
5:C:233:THR:HG22	5:C:234:VAL:H	1.33	0.94
1:0:396:U:H1'	37:0:7397:HOH:O	1.66	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1474:C:H6	1:0:1474:C:H5'	1.34	0.93
5:C:76:ARG:HB3	5:C:76:ARG:HH11	1.30	0.93
4:B:202:VAL:HG11	4:B:301:VAL:HG13	1.51	0.92
1:0:541:C:H2'	1:0:542:A:H5''	1.51	0.92
1:0:1187:U:HO2'	1:0:1189:A:H2	1.03	0.92
25:W:5:VAL:HG11	25:W:153:MET:HE1	1.52	0.92
3:A:81:GLN:HB2	3:A:92:ASN:ND2	1.85	0.92
11:I:127:CYS:HB3	11:I:132:VAL:HB	1.51	0.92
18:P:115:SER:H	18:P:118:GLN:HE21	0.92	0.92
20:R:8:ALA:HB1	20:R:13:THR:HG21	1.51	0.92
1:0:1160:G:C5'	1:0:1161:A:H5'	1.99	0.92
3:A:211:LYS:HB3	3:A:212:PRO:HD2	1.52	0.92
12:J:74:ARG:HB3	12:J:74:ARG:HH11	1.35	0.91
16:N:97:VAL:HG12	16:N:127:LEU:HD11	1.53	0.91
6:D:94:ALA:HB3	6:D:97:GLN:HE21	1.34	0.91
28:Z:46:ARG:HD2	28:Z:59:TYR:HB2	1.53	0.91
1:0:1160:G:H5'	1:0:1161:A:C5'	2.01	0.90
18:P:115:SER:H	18:P:118:GLN:NE2	1.69	0.90
11:I:95:LEU:HD22	11:I:99:GLN:HB3	1.49	0.90
26:X:37:LEU:HD13	26:X:85:VAL:HG21	1.52	0.90
22:T:71:VAL:HG11	22:T:90:PRO:HB3	1.53	0.90
4:B:238:ASN:HD22	4:B:240:GLY:H	0.92	0.90
14:L:79:ASP:HB3	37:L:8862:HOH:O	1.70	0.90
11:I:107:LYS:HD2	11:I:110:ASP:HB2	1.51	0.90
10:H:59:GLN:HE21	10:H:129:ARG:HE	1.19	0.90
1:0:56:G:H5''	24:V:50:ARG:HH12	1.37	0.89
20:R:18:LEU:HB2	20:R:143:VAL:HG13	1.53	0.89
15:M:164:THR:HG23	15:M:167:GLY:H	1.35	0.89
25:W:88:THR:HG22	25:W:89:ASP:H	1.36	0.89
10:H:59:GLN:NE2	10:H:129:ARG:HE	1.72	0.88
3:A:35:GLY:O	3:A:36:ASP:HB3	1.72	0.88
25:W:6:GLN:HB2	25:W:26:ILE:HD12	1.55	0.88
1:0:2586:U:H3	1:0:2592:G:H22	1.20	0.87
1:0:1118:A:H8	1:0:1118:A:H3'	1.39	0.87
6:D:57:THR:HG23	6:D:63:ILE:HA	1.55	0.87
1:0:1835:U:H5	1:0:1840:A:N7	1.72	0.87
4:B:238:ASN:HD22	4:B:240:GLY:N	1.73	0.86
4:B:217:ARG:HG3	4:B:257:THR:HG22	1.57	0.86
1:0:2717:C:C2'	1:0:2718:C:H5''	2.06	0.86
6:D:146:LYS:NZ	16:N:107:ASN:HD21	1.73	0.85
18:P:115:SER:N	18:P:118:GLN:HE21	1.74	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:85:SER:HA	37:A:8909:HOH:O	1.74	0.85
14:L:77:ALA:HB3	37:L:8833:HOH:O	1.75	0.85
24:V:1:THR:HG23	24:V:2:VAL:H	1.40	0.85
4:B:238:ASN:ND2	4:B:240:GLY:H	1.74	0.85
12:J:105:LEU:HA	37:J:8866:HOH:O	1.77	0.85
25:W:21:LEU:HD21	25:W:48:VAL:HG11	1.56	0.85
13:K:29:LEU:HB3	13:K:55:VAL:HG11	1.57	0.85
1:O:182:G:H5'	37:O:4959:HOH:O	1.77	0.85
1:O:1162:G:H1'	11:I:112:LEU:HD11	1.59	0.85
4:B:55:ASN:HB3	4:B:63:GLU:HA	1.57	0.85
4:B:320:GLN:NE2	4:B:321:PRO:HD2	1.92	0.85
1:O:21:G:H5'	20:R:2:ILE:HA	1.58	0.84
1:O:870:G:H2'	1:O:871:G:H5''	1.57	0.84
10:H:41:LYS:HE2	10:H:45:ASP:HB3	1.59	0.84
10:H:168:VAL:HG13	37:H:213:HOH:O	1.76	0.84
4:B:201:ASP:HB2	4:B:312:ARG:HD2	1.58	0.84
8:F:96:ALA:HA	37:F:3111:HOH:O	1.78	0.84
16:N:23:ARG:HD3	37:N:8842:HOH:O	1.76	0.84
31:3:60:LYS:HG3	31:3:61:PRO:HD2	1.57	0.84
5:C:236:THR:HA	37:C:8660:HOH:O	1.77	0.83
10:H:49:GLN:HE21	10:H:140:TYR:HE2	1.25	0.83
5:C:236:THR:CG2	5:C:239:ALA:H	1.86	0.83
1:O:1118:A:H3'	1:O:1118:A:C8	2.13	0.83
10:H:102:LYS:HD3	10:H:122:LYS:HD3	1.58	0.83
12:J:107:ASN:ND2	12:J:109:TYR:H	1.76	0.83
8:F:61:MET:HB3	15:M:19:GLN:OE1	1.79	0.82
10:H:62:HIS:HA	10:H:65:LEU:HD23	1.59	0.82
18:P:59:ARG:NH2	18:P:66:GLN:HE22	1.77	0.82
7:E:20:ILE:HD11	7:E:40:VAL:HG11	1.62	0.82
1:O:1118:A:H62	1:O:1244:U:H3	1.27	0.82
30:2:41:HIS:HD2	30:2:44:ARG:H	1.27	0.82
1:O:1205:U:H2'	1:O:1206:U:H5'	1.62	0.82
14:L:149:ARG:O	14:L:150:GLN:HB2	1.79	0.82
1:O:1834:C:H2'	1:O:1840:A:N6	1.94	0.82
3:A:94:LEU:HG	3:A:99:ILE:HD11	1.59	0.82
3:A:191:GLY:HA2	3:A:194:MET:HE2	1.60	0.82
4:B:98:THR:HG22	4:B:99:GLU:H	1.45	0.82
1:O:541:C:C2'	1:O:542:A:H5''	2.10	0.81
4:B:7:ARG:NH1	4:B:11:LEU:HD21	1.94	0.81
1:O:1184:C:H1'	37:O:7238:HOH:O	1.79	0.81
1:O:2506:A:HO2'	1:O:2507:G:H8	1.28	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:99:ASP:CG	6:D:100:ASP:H	1.88	0.81
14:L:121:ILE:HG12	14:L:141:GLU:HB2	1.61	0.81
37:O:5022:HOH:O	13:K:39:GLY:HA2	1.80	0.81
24:V:39:ALA:H	24:V:40:PRO:HD2	1.46	0.81
13:K:74:VAL:HG11	13:K:113:ILE:HG12	1.61	0.81
3:A:192:VAL:HG12	3:A:207:GLN:HB3	1.60	0.81
1:O:1751:G:H2'	1:O:1752:G:H5''	1.60	0.81
13:K:98:VAL:HG11	13:K:102:GLU:HA	1.61	0.81
16:N:151:ASP:O	16:N:154:LEU:HB2	1.81	0.81
22:T:52:ARG:HB2	22:T:95:ASN:HB3	1.63	0.81
6:D:136:ARG:HD2	6:D:155:HIS:O	1.80	0.80
1:O:542:A:H5'	1:O:542:A:H8	1.46	0.80
25:W:13:MET:HE2	25:W:18:GLN:HA	1.62	0.80
8:F:58:GLU:HA	8:F:61:MET:HE2	1.62	0.80
29:1:21:ARG:HD2	29:1:39:PHE:HB2	1.62	0.80
1:O:2756:U:H3	1:O:2896:A:H2	1.30	0.80
1:O:2908:A:H2'	1:O:2909:G:O4'	1.81	0.80
2:9:14:G:H5'	2:9:14:G:H8	1.47	0.80
12:J:19:MET:HE3	12:J:132:LEU:HD11	1.62	0.80
2:9:56:A:H2'	2:9:57:A:H5''	1.64	0.80
25:W:21:LEU:HD21	25:W:48:VAL:CG1	2.11	0.80
5:C:27:ARG:HG2	5:C:30:LEU:HD12	1.63	0.79
14:L:55:GLN:HA	14:L:58:GLN:HE21	1.47	0.79
18:P:115:SER:OG	18:P:118:GLN:HG3	1.82	0.79
9:G:64:ASN:HD22	9:G:64:ASN:N	1.79	0.79
1:O:2364:A:H5''	19:Q:15:LYS:HD3	1.64	0.79
13:K:81:ARG:HB2	13:K:87:ARG:HH11	1.46	0.79
5:C:140:VAL:HB	37:C:8660:HOH:O	1.82	0.79
37:O:5326:HOH:O	15:M:58:GLN:HG3	1.82	0.79
21:S:22:ASN:ND2	21:S:68:LEU:HB2	1.98	0.79
1:O:1119:G:H2'	12:J:52:GLN:NE2	1.97	0.79
5:C:2:GLN:HB3	37:C:8588:HOH:O	1.83	0.79
1:O:1116:U:H3	1:O:1246:A:H62	1.27	0.79
37:O:5256:HOH:O	9:G:12:ILE:HA	1.82	0.79
4:B:177:HIS:O	4:B:181:ILE:HG13	1.82	0.79
9:G:27:ILE:HD13	9:G:71:LEU:HD23	1.63	0.79
13:K:10:GLN:H	13:K:10:GLN:HE21	0.84	0.79
21:S:57:THR:HG22	21:S:59:ASP:H	1.47	0.79
1:O:877:G:H5'	1:O:878:G:OP1	1.83	0.78
1:O:871:G:H8	1:O:871:G:C5'	1.97	0.78
1:O:1206:U:H5'	1:O:1206:U:H6	1.48	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:99:THR:HA	37:F:3461:HOH:O	1.82	0.78
13:K:118:ALA:HA	13:K:125:ALA:HB2	1.64	0.78
16:N:151:ASP:OD1	16:N:154:LEU:HD13	1.84	0.78
1:O:1684:A:H1'	30:2:43:ARG:HH22	1.49	0.78
37:C:8572:HOH:O	22:T:2:LYS:HE2	1.81	0.78
16:N:169:PRO:O	16:N:172:PHE:HB3	1.84	0.78
37:9:8671:HOH:O	16:N:147:ILE:HB	1.84	0.78
6:D:94:ALA:CB	6:D:97:GLN:HE21	1.96	0.78
6:D:104:PHE:HE2	6:D:132:VAL:HB	1.48	0.78
10:H:146:ALA:O	10:H:149:VAL:HG12	1.84	0.78
25:W:4:LEU:HD23	25:W:54:PHE:HB3	1.65	0.78
4:B:304:PRO:HD2	4:B:307:ARG:HD2	1.65	0.77
31:3:25:VAL:HG22	31:3:68:LYS:HG3	1.64	0.77
29:1:10:LYS:HG3	37:1:2979:HOH:O	1.84	0.77
1:O:272:A:H5'	1:O:273:G:OP2	1.83	0.77
3:A:121:ALA:O	3:A:124:VAL:HG22	1.84	0.77
10:H:165:ARG:HD3	37:H:238:HOH:O	1.84	0.77
16:N:80:SER:HB2	37:N:8832:HOH:O	1.83	0.77
26:X:43:VAL:HG12	26:X:44:ASP:H	1.49	0.77
1:O:21:G:C5'	20:R:2:ILE:HA	2.14	0.77
4:B:162:MET:HG3	4:B:310:ARG:HD3	1.67	0.77
6:D:28:GLY:HA2	6:D:69:ILE:HG23	1.65	0.77
1:O:272:A:H3'	37:0:7298:HOH:O	1.85	0.77
8:F:91:VAL:HG12	8:F:92:GLY:H	1.50	0.77
3:A:37:VAL:HG23	3:A:38:ILE:H	1.49	0.77
8:F:63:ILE:HB	8:F:64:PRO:HD3	1.65	0.77
1:O:1474:C:H5'	1:O:1474:C:C6	2.20	0.76
37:0:7226:HOH:O	4:B:211:THR:HG21	1.85	0.76
2:9:92:G:H2'	2:9:93:A:C8	2.20	0.76
24:V:12:THR:HG22	24:V:15:GLU:CG	2.15	0.76
3:A:223:ARG:HG3	37:A:8892:HOH:O	1.85	0.76
5:C:78:ARG:HH11	5:C:78:ARG:HG3	1.50	0.76
27:Y:219:GLU:HG3	27:Y:220:GLU:N	1.99	0.76
4:B:190:MET:HE2	4:B:194:PHE:CD1	2.20	0.76
29:1:8:GLN:HE22	29:1:11:LYS:NZ	1.84	0.76
27:Y:216:ARG:HD3	37:Y:8874:HOH:O	1.86	0.76
21:S:22:ASN:HD21	21:S:68:LEU:HB2	1.51	0.76
1:O:559:U:H6	1:O:559:U:H5'	1.50	0.76
37:0:4030:HOH:O	30:2:38:LYS:HE3	1.84	0.76
8:F:110:ASP:O	8:F:114:LYS:HG3	1.86	0.76
16:N:7:LYS:HE3	19:Q:21:ARG:O	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:545:G:H5'	1:0:545:G:H8	1.50	0.75
1:0:1979:G:H2'	37:0:9091:HOH:O	1.85	0.75
1:0:2426:G:H1'	37:0:5876:HOH:O	1.87	0.75
1:0:944:G:H21	25:W:44:MET:HE2	1.50	0.75
4:B:312:ARG:HD3	4:B:315:VAL:HG13	1.68	0.75
5:C:16:VAL:HG12	5:C:17:ASP:H	1.52	0.75
5:C:25:PRO:HD2	37:C:8638:HOH:O	1.84	0.75
26:X:43:VAL:HG11	26:X:82:GLU:HA	1.66	0.75
1:0:1450:C:H4'	1:0:1451:C:OP2	1.85	0.75
1:0:1634:G:H3'	37:0:3693:HOH:O	1.85	0.75
1:0:2243:C:H5''	37:0:3549:HOH:O	1.86	0.75
1:0:282:C:H1'	1:0:368:C:N4	2.01	0.75
6:D:104:PHE:CE2	6:D:132:VAL:HB	2.22	0.75
14:L:61:ALA:HA	37:L:8868:HOH:O	1.85	0.75
23:U:20:MET:HE2	23:U:30:HIS:NE2	2.01	0.75
1:0:506:G:H22	1:0:509:A:H5'	1.51	0.75
1:0:1446:U:H2'	21:S:55:GLN:NE2	2.02	0.75
1:0:1593:C:H5'	18:P:116:SER:O	1.86	0.75
1:0:1919:A:H4'	37:0:4649:HOH:O	1.86	0.75
14:L:138:GLY:HA3	37:L:8857:HOH:O	1.86	0.75
1:0:130:C:H2'	37:0:9961:HOH:O	1.86	0.74
1:0:154:C:H2'	1:0:155:C:H6	1.52	0.74
6:D:174:VAL:HG12	37:D:6555:HOH:O	1.87	0.74
14:L:80:ASP:HB2	14:L:90:ARG:O	1.87	0.74
2:9:75:G:H1	2:9:106:U:H3	1.34	0.74
21:S:37:VAL:O	21:S:41:VAL:HG23	1.87	0.74
29:1:25:LYS:HD2	30:2:49:GLU:N	2.00	0.74
1:0:2578:G:H5'	1:0:2578:G:H8	1.52	0.74
1:0:2769:C:H2'	1:0:2770:G:O4'	1.87	0.74
6:D:99:ASP:HA	37:D:5675:HOH:O	1.88	0.74
24:V:56:ILE:O	24:V:60:GLN:HG3	1.88	0.74
1:0:821:U:H2'	1:0:822:C:H6	1.51	0.74
1:0:2748:G:H5'	37:0:7309:HOH:O	1.87	0.74
8:F:46:GLU:O	8:F:73:PRO:HD2	1.87	0.74
18:P:59:ARG:HH22	18:P:66:GLN:HE22	1.33	0.74
23:U:9:CYS:HA	23:U:52:THR:HG23	1.69	0.74
25:W:72:PRO:HG2	25:W:77:ALA:HB3	1.68	0.74
30:2:41:HIS:H	30:2:45:ASN:HD22	1.31	0.74
7:E:43:ASP:HA	37:E:5864:HOH:O	1.87	0.74
1:0:200:C:H2'	37:0:3243:HOH:O	1.87	0.74
1:0:100:C:H4'	22:T:16:LEU:HB2	1.67	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:129:ALA:O	20:R:130:MET:HB2	1.87	0.74
1:O:2004:U:H4'	37:O:5105:HOH:O	1.86	0.74
5:C:184:ARG:HG2	37:C:8673:HOH:O	1.88	0.74
6:D:99:ASP:HB3	6:D:103:ASN:H	1.53	0.74
16:N:48:VAL:CG1	16:N:55:ASP:HB3	2.17	0.74
1:O:541:C:H2'	1:O:542:A:C5'	2.18	0.74
18:P:13:VAL:HG21	18:P:41:ARG:HG2	1.69	0.74
21:S:43:GLU:HB3	37:S:8543:HOH:O	1.88	0.73
22:T:32:ARG:NH1	22:T:38:ARG:HH12	1.85	0.73
1:O:236:A:H4'	1:O:237:G:OP1	1.87	0.73
37:B:8852:HOH:O	12:J:104:TYR:HA	1.87	0.73
21:S:57:THR:HG22	21:S:59:ASP:N	2.03	0.73
25:W:149:LEU:HG	25:W:153:MET:HE2	1.69	0.73
1:O:794:U:H3	1:O:819:A:H61	1.35	0.73
16:N:152:GLU:C	16:N:154:LEU:H	1.92	0.73
16:N:119:GLN:O	16:N:123:ILE:HG13	1.89	0.73
1:O:544:G:H2'	1:O:545:G:H5''	1.70	0.73
1:O:1835:U:C5	1:O:1840:A:N7	2.55	0.73
4:B:179:LEU:O	4:B:183:GLU:HG2	1.87	0.73
9:G:23:ILE:O	9:G:27:ILE:HG13	1.88	0.73
13:K:14:LYS:HB2	13:K:45:PRO:HG2	1.71	0.73
25:W:88:THR:HB	37:W:6679:HOH:O	1.89	0.73
1:O:2332:A:H5'	6:D:56:ARG:HH22	1.53	0.72
4:B:132:HIS:HB2	4:B:137:LEU:HD22	1.71	0.72
12:J:45:VAL:HG23	12:J:130:VAL:O	1.89	0.72
1:O:2840:A:OP1	4:B:211:THR:HG23	1.88	0.72
1:O:2851:G:O2'	1:O:2852:A:H5'	1.88	0.72
1:O:2862:G:H4'	4:B:336:GLN:O	1.89	0.72
4:B:235:ARG:HA	37:B:8895:HOH:O	1.89	0.72
13:K:32:ILE:HD11	13:K:56:SER:HB2	1.72	0.72
13:K:74:VAL:CG1	13:K:113:ILE:HG12	2.20	0.72
20:R:125:ARG:O	20:R:126:LYS:HB2	1.89	0.72
1:O:1328:A:OP1	27:Y:169:ARG:HD2	1.89	0.72
4:B:18:ARG:HG3	4:B:256:GLN:HG3	1.70	0.72
10:H:61:ARG:HH11	10:H:61:ARG:HG3	1.54	0.72
29:I:45:ARG:HB3	37:I:988:HOH:O	1.89	0.72
1:O:2524:G:H21	1:O:2526:C:N4	1.86	0.72
1:O:2812:A:H2	1:O:2814:A:H62	1.35	0.72
5:C:145:GLU:HG3	37:C:8578:HOH:O	1.88	0.72
16:N:132:ASN:O	16:N:135:VAL:HG12	1.88	0.72
25:W:130:HIS:O	25:W:136:GLY:HA3	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:944:G:H21	25:W:44:MET:CE	2.03	0.72
1:0:1234:U:N3	4:B:244:PRO:HB3	2.04	0.72
37:0:3789:HOH:O	5:C:188:ARG:HD3	1.89	0.72
3:A:153:ARG:HB2	3:A:153:ARG:HH11	1.54	0.72
1:0:558:C:H2'	1:0:559:U:H5'	1.71	0.72
5:C:127:ARG:HH21	5:C:225:PRO:HG2	1.55	0.72
25:W:82:GLU:HB2	37:W:2749:HOH:O	1.89	0.72
37:0:7197:HOH:O	22:T:9:LYS:HB2	1.89	0.71
5:C:242:GLU:HG3	37:C:8585:HOH:O	1.90	0.71
5:C:246:ARG:HB3	5:C:246:ARG:NH1	2.04	0.71
23:U:14:GLU:OE1	23:U:15:PRO:HD2	1.90	0.71
27:Y:141:THR:HG23	37:Y:8896:HOH:O	1.89	0.71
1:0:1080:C:H4'	1:0:1081:A:OP1	1.89	0.71
5:C:111:VAL:HB	37:C:8522:HOH:O	1.90	0.71
6:D:54:ALA:HB1	37:D:4069:HOH:O	1.89	0.71
8:F:91:VAL:HG12	8:F:92:GLY:N	2.04	0.71
1:0:1278:A:H4'	1:0:1279:U:C4	2.25	0.71
5:C:132:ASP:HB2	5:C:161:ASP:HB3	1.73	0.71
25:W:64:THR:O	25:W:68:THR:HG22	1.90	0.71
1:0:553:G:P	27:Y:204:ARG:HH22	2.13	0.71
17:O:42:GLU:HB2	37:O:2176:HOH:O	1.89	0.71
17:O:105:ASN:HD21	17:O:109:SER:H	1.39	0.71
3:A:192:VAL:CG1	3:A:207:GLN:HB3	2.20	0.71
4:B:264:GLU:HG2	4:B:267:LYS:CE	2.16	0.71
1:0:506:G:H22	1:0:509:A:C5'	2.04	0.71
18:P:64:GLU:HG2	37:P:169:HOH:O	1.91	0.71
1:0:1594:C:OP2	18:P:120:ARG:HD2	1.91	0.71
1:0:1733:A:H4'	4:B:212:GLN:HA	1.73	0.71
1:0:2890:A:H1'	23:U:56:ARG:NH2	2.06	0.71
9:G:64:ASN:HD22	9:G:64:ASN:H	1.38	0.71
22:T:106:GLU:HG3	37:T:4913:HOH:O	1.88	0.71
4:B:1:PRO:O	4:B:2:GLN:HB2	1.90	0.71
27:Y:186:ARG:HG2	27:Y:186:ARG:HH11	1.55	0.71
30:2:20:ARG:HH11	30:2:20:ARG:CG	2.04	0.71
1:0:459:A:H4'	37:0:9260:HOH:O	1.90	0.70
1:0:2548:C:OP2	4:B:5:ARG:NH2	2.24	0.70
3:A:217:ARG:HH11	3:A:217:ARG:HG3	1.55	0.70
5:C:236:THR:HG21	37:C:8578:HOH:O	1.90	0.70
24:V:44:GLY:O	24:V:48:GLU:HG2	1.91	0.70
4:B:305:ASP:O	4:B:306:LYS:HB2	1.89	0.70
26:X:76:ARG:HH11	26:X:76:ARG:HG3	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:285:A:H2'	1:0:286:U:O4'	1.90	0.70
1:0:902:G:N7	14:L:18:HIS:HD2	1.90	0.70
1:0:1120:U:H6	1:0:1120:U:H5'	1.55	0.70
1:0:2850:C:H6	1:0:2850:C:H5'	1.56	0.70
26:X:78:GLU:HG2	26:X:79:GLU:H	1.55	0.70
4:B:332:ASN:HB3	37:B:8861:HOH:O	1.91	0.70
1:0:447:A:P	22:T:1:SER:HB2	2.32	0.70
1:0:2506:A:O2'	1:0:2507:G:H8	1.73	0.70
3:A:217:ARG:HG2	3:A:229:ALA:HB2	1.74	0.70
12:J:107:ASN:HD21	12:J:109:TYR:HB2	1.57	0.70
18:P:115:SER:O	18:P:117:SER:N	2.23	0.70
1:0:1205:U:H2'	1:0:1206:U:C5'	2.21	0.70
1:0:1679:C:H5'	37:0:9135:HOH:O	1.90	0.70
4:B:195:ARG:HG2	4:B:323:LEU:HD22	1.74	0.70
22:T:48:VAL:HG13	22:T:97:ARG:O	1.92	0.70
2:9:73:A:H61	2:9:108:C:H42	1.39	0.70
1:0:1596:U:H2'	1:0:1598:A:OP2	1.92	0.70
10:H:49:GLN:HG3	10:H:140:TYR:CD2	2.27	0.70
1:0:88:G:H8	1:0:88:G:H5'	1.55	0.69
1:0:1118:A:H2'	1:0:1120:U:H5''	1.75	0.69
1:0:2291:A:C8	1:0:2309:C:H5'	2.26	0.69
4:B:36:PRO:HG3	4:B:169:GLY:H	1.56	0.69
12:J:19:MET:CE	12:J:132:LEU:HD11	2.22	0.69
1:0:1926:G:H2'	1:0:1927:A:C8	2.26	0.69
37:0:6135:HOH:O	4:B:298:LYS:HD3	1.91	0.69
2:9:56:A:C2'	2:9:57:A:H5''	2.21	0.69
20:R:72:VAL:CG1	20:R:75:TRP:HB3	2.22	0.69
4:B:162:MET:HE2	4:B:310:ARG:HD3	1.73	0.69
6:D:22:VAL:HG22	6:D:74:THR:HG22	1.74	0.69
7:E:6:GLU:HA	7:E:46:THR:HG22	1.72	0.69
13:K:98:VAL:CG1	13:K:102:GLU:HA	2.21	0.69
25:W:13:MET:HE2	25:W:18:GLN:CA	2.22	0.69
1:0:2491:G:H1'	37:0:6645:HOH:O	1.92	0.69
9:G:64:ASN:H	9:G:64:ASN:ND2	1.91	0.69
17:O:32:ARG:HH21	17:O:35:LYS:CD	2.05	0.69
21:S:81:ILE:HG12	37:S:8536:HOH:O	1.91	0.69
22:T:35:TYR:CD2	22:T:112:LEU:HD22	2.28	0.69
27:Y:99:ALA:HB2	27:Y:233:TYR:CZ	2.28	0.69
1:0:2363:G:O2'	19:Q:11:ARG:HG3	1.93	0.69
1:0:2559:C:H4'	37:0:7025:HOH:O	1.92	0.69
16:N:11:ARG:HG3	16:N:14:ARG:NH1	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:46:LEU:HG	37:M:8919:HOH:O	1.92	0.69
22:T:28:SER:O	22:T:32:ARG:HG3	1.91	0.69
24:V:5:VAL:HG23	37:V:2271:HOH:O	1.93	0.69
26:X:72:VAL:HG22	26:X:85:VAL:HG12	1.75	0.69
1:O:839:C:H4'	1:O:840[A]:U:H5'	1.73	0.69
1:O:1119:G:N2	1:O:1246:A:C2	2.60	0.69
14:L:73:VAL:HG21	14:L:116:HIS:CD2	2.27	0.69
21:S:33:SER:OG	21:S:36:GLU:HG3	1.92	0.69
29:1:42:SER:HB2	37:1:354:HOH:O	1.92	0.69
1:O:839:C:H5''	1:O:840[B]:U:OP1	1.93	0.69
1:O:1130:U:H5'	37:O:7441:HOH:O	1.91	0.69
1:O:1589:G:N2	1:O:1605:G:H1'	2.07	0.69
2:9:35:C:H5''	37:9:8659:HOH:O	1.91	0.69
1:O:1180:U:H4'	11:I:86:GLU:HG2	1.74	0.69
24:V:12:THR:HG23	24:V:14:ALA:H	1.57	0.69
2:9:56:A:C3'	2:9:57:A:H5''	2.23	0.68
3:A:36:ASP:HB2	3:A:84:VAL:N	2.09	0.68
4:B:119:HIS:O	4:B:121:PRO:HD3	1.93	0.68
37:O:4504:HOH:O	28:Z:51:GLY:HA3	1.93	0.68
15:M:80:GLY:O	15:M:81:ARG:HD2	1.94	0.68
27:Y:133:HIS:HD2	37:Y:8886:HOH:O	1.76	0.68
29:1:8:GLN:HE22	29:1:11:LYS:HZ2	1.41	0.68
1:O:1666:C:H2'	1:O:1667:A:H8	1.59	0.68
3:A:36:ASP:HA	3:A:83:GLY:HA3	1.75	0.68
4:B:5:ARG:HD2	4:B:8:LYS:NZ	2.09	0.68
9:G:71:LEU:C	9:G:73:ASP:H	2.00	0.68
24:V:11:MET:HE1	24:V:19:GLU:HB2	1.75	0.68
9:G:63:ARG:N	37:G:2569:HOH:O	2.26	0.68
17:O:32:ARG:HH21	17:O:35:LYS:HD2	1.57	0.68
25:W:39:ASP:HB2	37:W:3580:HOH:O	1.93	0.68
1:O:2392:C:H4'	37:Q:2875:HOH:O	1.91	0.68
13:K:74:VAL:HG13	13:K:113:ILE:HG23	1.75	0.68
1:O:1429:U:H1'	20:R:132:ARG:NH1	2.09	0.68
21:S:33:SER:O	21:S:37:VAL:HG23	1.94	0.68
22:T:101:LEU:HD13	22:T:112:LEU:HD11	1.76	0.68
26:X:30:MET:HE1	26:X:58:ALA:HB3	1.75	0.68
28:Z:37:HIS:HB2	28:Z:47:VAL:HB	1.75	0.68
1:O:1187:U:O2'	1:O:1189:A:H2	1.75	0.68
1:O:2502:C:C2'	1:O:2503:A:H5'	2.22	0.68
4:B:152:PRO:HD2	37:B:8931:HOH:O	1.92	0.68
10:H:12:ILE:HD12	10:H:57:THR:HG22	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:62:HIS:NE2	37:R:8831:HOH:O	2.26	0.68
1:O:2570:G:H5''	37:O:4714:HOH:O	1.93	0.67
2:9:6:C:H5''	16:N:37:ARG:HH12	1.57	0.67
27:Y:212:ARG:HD2	37:Y:8909:HOH:O	1.94	0.67
1:O:1741:U:H5'	1:O:1742:A:OP1	1.94	0.67
16:N:86:LEU:HD12	16:N:125:ALA:HB2	1.75	0.67
6:D:63:ILE:HG13	6:D:64:ARG:N	2.08	0.67
11:I:68:PRO:HB2	11:I:69:PRO:HD2	1.76	0.67
16:N:83:LEU:HD13	16:N:175:LEU:HD23	1.75	0.67
17:O:44:ASN:OD1	17:O:65:LEU:HB2	1.93	0.67
22:T:43:ASN:HD22	22:T:108:ARG:CZ	2.07	0.67
31:3:65:THR:HG22	31:3:67:LEU:HG	1.76	0.67
4:B:198:GLU:HA	37:B:8958:HOH:O	1.93	0.67
4:B:297:VAL:HB	37:B:8905:HOH:O	1.94	0.67
5:C:154:VAL:O	5:C:158:GLU:HG3	1.95	0.67
16:N:71:TRP:HE3	16:N:175:LEU:HD22	1.60	0.67
1:O:583:C:H2'	1:O:584:U:H6	1.60	0.67
1:O:870:G:C2'	1:O:871:G:H5''	2.23	0.67
17:O:49:GLU:OE1	17:O:72:LYS:HG3	1.94	0.67
26:X:43:VAL:HG12	26:X:44:ASP:N	2.08	0.67
4:B:84:LEU:HD23	4:B:178:ALA:HB1	1.77	0.67
12:J:74:ARG:O	12:J:78:ILE:HG12	1.95	0.67
15:M:28:GLN:O	15:M:32:ARG:HG3	1.94	0.67
1:O:1636:G:O2'	1:O:1637:A:H5'	1.94	0.67
22:T:48:VAL:HG11	22:T:96:VAL:HG13	1.76	0.67
24:V:64:GLY:O	24:V:65:ASP:HB2	1.94	0.67
3:A:5:GLN:HB3	37:A:8894:HOH:O	1.94	0.67
8:F:27:GLY:HA3	8:F:101:ALA:O	1.95	0.67
14:L:104:ASP:O	14:L:105:TYR:HB3	1.93	0.67
1:O:814:G:H4'	37:O:9934:HOH:O	1.95	0.67
1:O:2346:C:O2'	6:D:52:THR:HG21	1.95	0.67
1:O:2526:C:O2'	1:O:2527:U:H5'	1.94	0.67
5:C:16:VAL:HG12	5:C:17:ASP:N	2.10	0.67
14:L:148:GLU:HA	37:L:8876:HOH:O	1.95	0.67
1:O:840[B]:U:H5'	37:O:4709:HOH:O	1.95	0.67
1:O:1419:U:H2'	1:O:1685:A:C2	2.30	0.67
2:9:14:G:H5'	2:9:14:G:C8	2.28	0.67
12:J:52:GLN:HG3	12:J:53:ILE:N	2.09	0.67
17:O:87:THR:O	17:O:91:GLN:HG3	1.95	0.67
1:O:136:C:H2'	1:O:137:U:O4'	1.94	0.66
1:O:308:U:H5'	1:O:309:C:OP1	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:2637:A:H5'	37:O:9086:HOH:O	1.94	0.66
4:B:86:ALA:HA	37:B:8880:HOH:O	1.94	0.66
8:F:79:GLN:HB2	8:F:82:ASP:OD2	1.96	0.66
20:R:39:THR:HB	20:R:42:GLU:HG3	1.76	0.66
1:O:1043:C:H2'	37:O:7091:HOH:O	1.94	0.66
1:O:1244:U:OP1	12:J:18:ILE:HD13	1.95	0.66
25:W:4:LEU:HD22	25:W:52:VAL:CG2	2.24	0.66
1:O:1964:U:H2'	1:O:1964:U:O2	1.94	0.66
11:I:111:LEU:HD22	11:I:122:GLU:OE1	1.95	0.66
2:9:64:C:H2'	2:9:65:A:H5'	1.78	0.66
10:H:59:GLN:HE21	10:H:129:ARG:NE	1.91	0.66
1:O:21:G:H4'	20:R:2:ILE:HG22	1.78	0.66
1:O:1181:A:H2'	1:O:1182:C:H5'	1.76	0.66
7:E:11:VAL:HG12	7:E:12:ASP:N	2.10	0.66
10:H:26:ILE:HA	10:H:123:ILE:HG21	1.77	0.66
11:I:94:ASP:OD1	11:I:133:THR:HB	1.96	0.66
1:O:1717:A:H5''	18:P:54:LYS:HB2	1.78	0.66
16:N:154:LEU:O	16:N:155:GLU:HB3	1.95	0.66
25:W:38:THR:HG22	25:W:39:ASP:N	2.09	0.66
1:O:1926:G:H2'	1:O:1927:A:H8	1.60	0.66
6:D:135:VAL:HG21	6:D:139:TYR:CD1	2.31	0.66
10:H:43:ALA:O	10:H:170:ARG:NH1	2.28	0.66
13:K:22:ASP:HB2	37:K:5264:HOH:O	1.96	0.66
15:M:134:ILE:HG23	15:M:141:ILE:HD13	1.77	0.66
1:O:1589:G:H22	1:O:1605:G:H1'	1.60	0.66
4:B:98:THR:HG22	4:B:99:GLU:N	2.10	0.66
15:M:164:THR:HG23	15:M:167:GLY:N	2.10	0.66
19:Q:26:PRO:O	19:Q:30:VAL:HG23	1.95	0.66
25:W:21:LEU:HD22	25:W:26:ILE:CD1	2.26	0.66
30:2:40:ARG:CD	30:2:47:THR:HG22	2.24	0.66
3:A:88:ILE:O	3:A:88:ILE:HG22	1.94	0.66
5:C:76:ARG:HH11	5:C:76:ARG:CB	2.08	0.66
6:D:134:LEU:HD11	6:D:166:ILE:HD11	1.76	0.66
18:P:143:ALA:HA	37:P:193:HOH:O	1.95	0.66
1:O:1362:U:H5'	37:O:3068:HOH:O	1.96	0.66
13:K:62:PRO:HG3	13:K:65:ARG:HH21	1.59	0.66
23:U:52:THR:HG22	23:U:54:THR:H	1.60	0.66
25:W:88:THR:HG23	25:W:110:GLN:HB3	1.78	0.66
1:O:338:C:H4'	5:C:174:ILE:CD1	2.26	0.65
1:O:657:G:H2'	1:O:658:C:H6	1.61	0.65
21:S:17:ASP:HB3	21:S:23:LYS:HB2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:111:C:O2'	29:1:20:ARG:HG2	1.96	0.65
1:0:681:G:N3	1:0:681:G:H5'	2.11	0.65
1:0:1116:U:O2'	1:0:1118:A:H2	1.80	0.65
1:0:1319:G:H1'	37:0:4492:HOH:O	1.95	0.65
10:H:12:ILE:O	10:H:12:ILE:HG22	1.96	0.65
25:W:21:LEU:HD13	25:W:26:ILE:HD11	1.79	0.65
1:0:2053:G:H4'	20:R:136:TRP:CE3	2.31	0.65
1:0:2301:A:H5''	1:0:2302:A:H5'	1.78	0.65
11:I:127:CYS:C	11:I:129:SER:H	2.03	0.65
15:M:65:VAL:HG21	15:M:105:ALA:HB2	1.78	0.65
1:0:1790:C:H2'	1:0:1791:U:H6	1.60	0.65
1:0:1909:A:H2'	1:0:1910:A:C8	2.31	0.65
3:A:81:GLN:HB2	3:A:92:ASN:HD21	1.62	0.65
5:C:236:THR:H	5:C:239:ALA:HB3	1.61	0.65
16:N:4:PRO:HD2	37:N:8854:HOH:O	1.94	0.65
6:D:21:VAL:HG13	6:D:132:VAL:HG22	1.76	0.65
6:D:166:ILE:HB	37:D:6326:HOH:O	1.96	0.65
7:E:7:ILE:HD11	7:E:11:VAL:C	2.22	0.65
24:V:27:LEU:HA	24:V:49:LEU:HD13	1.79	0.65
1:0:2504:A:H4'	10:H:74:ARG:HH11	1.61	0.65
5:C:246:ARG:HB3	5:C:246:ARG:HH11	1.59	0.65
12:J:74:ARG:HH11	12:J:74:ARG:CB	2.06	0.65
16:N:166:ALA:HA	37:N:8824:HOH:O	1.95	0.65
1:0:450:C:OP1	5:C:184:ARG:NH2	2.30	0.65
16:N:37:ARG:HD3	35:N:8807:CL:CL	2.33	0.65
17:O:14:LEU:HD23	17:O:102:ILE:HD11	1.77	0.65
20:R:72:VAL:HG11	20:R:75:TRP:HB3	1.78	0.65
1:0:1525:G:H2'	1:0:1526:A:C8	2.32	0.65
1:0:1657:A:H2'	1:0:1658:A:C8	2.32	0.65
8:F:36:THR:HG23	8:F:97:ALA:HB2	1.78	0.65
17:O:73:ASP:HA	17:O:92:VAL:O	1.97	0.65
23:U:17:THR:HG22	23:U:18:GLY:N	2.10	0.65
1:0:657:G:H2'	1:0:658:C:C6	2.32	0.65
6:D:17:ARG:HG2	6:D:135:VAL:O	1.97	0.65
1:0:285:A:C2	1:0:368:C:H4'	2.31	0.65
1:0:1701:A:H4'	1:0:1702:U:H5''	1.79	0.65
3:A:200:PRO:HD3	37:A:8818:HOH:O	1.95	0.65
1:0:157:G:H4'	15:M:95:LYS:HE3	1.77	0.64
1:0:199:A:H5''	37:0:3331:HOH:O	1.97	0.64
1:0:246:G:H5'	37:0:5368:HOH:O	1.97	0.64
2:9:54:A:O2'	2:9:55:U:H5'	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:138:ILE:HG22	37:E:6457:HOH:O	1.96	0.64
13:K:24:THR:HB	13:K:64:MET:HE2	1.79	0.64
13:K:81:ARG:HD3	13:K:87:ARG:NH1	2.12	0.64
14:L:114:VAL:HG11	37:L:8877:HOH:O	1.96	0.64
15:M:102:GLU:OE1	15:M:164:THR:HG21	1.97	0.64
1:O:20:G:H21	20:R:117:HIS:HD2	1.44	0.64
1:O:1428:C:O2'	20:R:132:ARG:HB2	1.96	0.64
1:O:2272:G:H5'	3:A:223:ARG:HB2	1.77	0.64
1:O:2679:G:H2'	1:O:2681:A:OP2	1.97	0.64
4:B:51:VAL:CG1	4:B:53:LEU:HD13	2.26	0.64
9:G:16:LYS:O	9:G:20:VAL:HG23	1.98	0.64
25:W:52:VAL:HG22	25:W:53:ALA:H	1.61	0.64
27:Y:187:VAL:HG12	27:Y:205:ILE:HA	1.79	0.64
8:F:38:LYS:HZ1	15:M:3:SER:HA	1.63	0.64
10:H:174:LEU:HA	37:H:225:HOH:O	1.97	0.64
13:K:109:LEU:HD13	13:K:113:ILE:HD11	1.79	0.64
1:O:544:G:C2'	1:O:545:G:H5''	2.28	0.64
1:O:1377:C:H5'	1:O:1377:C:H6	1.63	0.64
3:A:94:LEU:HD23	3:A:94:LEU:N	2.12	0.64
12:J:126:ASN:HA	35:J:8801:CL:CL	2.35	0.64
14:L:143:THR:HG22	14:L:145:LEU:H	1.61	0.64
15:M:60:VAL:C	15:M:61:ILE:HD12	2.23	0.64
5:C:107:ARG:NE	37:C:8666:HOH:O	2.29	0.64
1:O:447:A:OP1	22:T:2:LYS:HG2	1.98	0.64
1:O:1687:C:O2	29:1:9:GLY:HA2	1.97	0.64
1:O:2904:U:H4'	26:X:8:ARG:NH1	2.13	0.64
25:W:6:GLN:HB2	25:W:26:ILE:CD1	2.28	0.64
4:B:62:ARG:HA	4:B:65:MET:HE3	1.80	0.64
4:B:83:ALA:HA	4:B:100:VAL:O	1.96	0.64
11:I:118:ASN:HA	11:I:121:LYS:CD	2.27	0.64
15:M:134:ILE:O	15:M:136:PRO:HD3	1.98	0.64
24:V:33:VAL:HG12	24:V:38:GLY:HA3	1.78	0.64
25:W:110:GLN:HA	25:W:110:GLN:HE21	1.62	0.64
26:X:20:GLU:OE1	26:X:21:PRO:HD2	1.97	0.64
1:O:1181:A:H5'	11:I:89:GLU:OE2	1.97	0.64
11:I:80:PHE:CD2	11:I:92:VAL:HG12	2.33	0.64
16:N:78:MET:HB2	16:N:79:PRO:HD3	1.79	0.64
3:A:33:GLU:O	3:A:34:ASP:HB2	1.95	0.64
4:B:162:MET:CE	4:B:308:LEU:HD21	2.27	0.64
5:C:14:GLY:O	5:C:15:GLU:HB3	1.97	0.64
12:J:39:VAL:HG12	12:J:40:ASN:CG	2.23	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:48:VAL:HG11	16:N:55:ASP:HB3	1.80	0.64
20:R:40:ALA:O	20:R:44:VAL:HG23	1.98	0.64
25:W:59:GLN:HE22	25:W:97:ALA:HB3	1.63	0.64
25:W:110:GLN:HA	25:W:110:GLN:NE2	2.13	0.64
1:0:621:C:H5'	27:Y:132:ASP:OD2	1.98	0.63
1:0:1804:A:H2'	1:0:1805:G:C8	2.33	0.63
2:9:1:U:H4'	2:9:3:A:OP1	1.99	0.63
19:Q:66:LYS:HB2	19:Q:70:ALA:O	1.98	0.63
37:0:6147:HOH:O	20:R:33:ARG:HG3	1.97	0.63
3:A:36:ASP:HB2	3:A:85:SER:H	1.63	0.63
6:D:86:THR:C	6:D:89:PRO:HD2	2.22	0.63
20:R:53:GLY:HA2	20:R:80:TYR:CD2	2.33	0.63
29:1:25:LYS:O	29:1:25:LYS:HG2	1.97	0.63
1:0:1804:A:H2'	1:0:1805:G:H8	1.63	0.63
6:D:63:ILE:HG13	6:D:64:ARG:H	1.60	0.63
16:N:165:ALA:HA	37:N:8821:HOH:O	1.96	0.63
25:W:60:GLU:HG2	37:W:705:HOH:O	1.98	0.63
28:Z:56:GLN:HG3	28:Z:62:TYR:O	1.98	0.63
1:0:56:G:H5''	24:V:50:ARG:NH1	2.11	0.63
1:0:1116:U:HO2'	1:0:1118:A:H2	1.44	0.63
25:W:52:VAL:HG22	25:W:53:ALA:N	2.13	0.63
1:0:653:U:H5''	37:O:7674:HOH:O	1.96	0.63
1:0:2073:G:OP2	1:0:2490:A:H5'	1.99	0.63
1:0:2681:A:H4'	1:0:2682:C:H5'	1.80	0.63
10:H:49:GLN:HB3	10:H:170:ARG:CG	2.29	0.63
12:J:75:PRO:HG2	12:J:105:LEU:HD21	1.80	0.63
1:0:1506:U:H6	1:0:1506:U:H5'	1.64	0.63
1:0:2827:A:H2'	1:0:2828:G:O4'	1.99	0.63
16:N:71:TRP:CE3	16:N:175:LEU:HD22	2.33	0.63
25:W:81:ASP:OD1	25:W:92:ASP:HB2	1.99	0.63
1:0:1603:A:H5'	1:0:1605:G:O4'	1.99	0.63
4:B:24:PRO:O	4:B:25:ARG:HD3	1.98	0.63
4:B:66:GLU:OE1	4:B:328:ARG:HD2	1.98	0.63
29:1:1:THR:HB	37:1:6858:HOH:O	1.99	0.63
1:0:584:U:H3'	37:0:5879:HOH:O	1.98	0.63
1:0:753:U:H3'	37:0:5320:HOH:O	1.99	0.63
1:0:1168:C:H5'	11:I:83:GLY:HA3	1.80	0.63
5:C:115:LEU:HD21	5:C:243:VAL:HG13	1.81	0.63
5:C:237:GLU:HB2	37:C:8640:HOH:O	1.97	0.63
14:L:140:VAL:HG23	37:L:8860:HOH:O	1.97	0.63
22:T:48:VAL:HG13	22:T:97:ARG:C	2.23	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:99:THR:O	22:T:100:ASP:HB2	1.98	0.63
1:0:69:A:H5'	1:0:69:A:H8	1.64	0.62
1:0:1197:G:H21	1:0:1202:A:H62	1.44	0.62
1:0:69:A:H5'	1:0:69:A:C8	2.34	0.62
1:0:800:G:H4'	37:0:6831:HOH:O	1.98	0.62
3:A:94:LEU:HG	3:A:99:ILE:CD1	2.26	0.62
16:N:78:MET:HE1	16:N:112:GLY:O	1.99	0.62
26:X:37:LEU:CD1	26:X:85:VAL:HG21	2.27	0.62
1:0:1118:A:C8	1:0:1118:A:C3'	2.78	0.62
1:0:2459:G:H3'	37:0:6782:HOH:O	1.97	0.62
2:9:48:C:H4'	16:N:141:ARG:HH21	1.64	0.62
7:E:166:VAL:HG12	37:E:3134:HOH:O	1.98	0.62
14:L:90:ARG:HA	14:L:119:THR:HB	1.81	0.62
1:0:1221:G:H8	37:0:5773:HOH:O	1.82	0.62
1:0:1632:A:H2'	1:0:1633:C:H5'	1.82	0.62
5:C:3:ALA:HA	37:C:8581:HOH:O	1.98	0.62
7:E:37:ASP:OD1	12:J:125:SER:HB3	1.99	0.62
1:0:694:A:H2'	1:0:695:C:H5'	1.81	0.62
14:L:133:VAL:HB	37:L:8860:HOH:O	1.98	0.62
25:W:13:MET:HE3	25:W:17:ILE:HG22	1.80	0.62
1:0:1441:G:H4'	20:R:130:MET:HE3	1.80	0.62
1:0:2256:G:O2'	1:0:2257:G:H5'	2.00	0.62
1:0:2332:A:H5'	6:D:56:ARG:NH2	2.15	0.62
3:A:43:VAL:O	3:A:76:VAL:HG13	2.00	0.62
8:F:21:GLU:HA	8:F:24:ARG:HD3	1.81	0.62
30:2:49:GLU:HB2	37:2:719:HOH:O	1.98	0.62
1:0:969:G:H1	1:0:999:C:N4	1.97	0.62
10:H:32:ALA:HB3	10:H:69:ARG:HH12	1.63	0.62
12:J:6:PHE:HB3	12:J:109:TYR:OH	1.99	0.62
13:K:55:VAL:HG12	13:K:56:SER:N	2.15	0.62
21:S:45:TYR:HE2	21:S:81:ILE:HD13	1.65	0.62
22:T:71:VAL:HG13	22:T:91:LEU:O	2.00	0.62
1:0:1285:U:H4'	25:W:74:GLU:OE1	2.00	0.62
29:1:25:LYS:CD	30:2:49:GLU:H	2.03	0.62
1:0:684:G:H5''	37:0:3862:HOH:O	1.99	0.62
1:0:1279:U:O2	1:0:1279:U:H2'	2.00	0.62
6:D:159:PRO:O	6:D:163:VAL:HG23	1.99	0.62
1:0:1528:A:H2'	1:0:1529:G:O4'	1.99	0.62
1:0:2346:C:H6	1:0:2346:C:O5'	1.83	0.62
3:A:194:MET:HE3	3:A:199:HIS:CB	2.25	0.62
8:F:28:ALA:HB3	8:F:99:THR:HG23	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:107:ASP:O	8:F:111:ILE:HG13	2.00	0.62
16:N:128:ASP:HA	37:N:8858:HOH:O	2.00	0.62
23:U:9:CYS:HA	23:U:52:THR:CG2	2.30	0.62
1:O:2251:G:H2'	1:O:2252:A:C8	2.35	0.61
1:O:2897:C:H2'	1:O:2898:G:H8	1.65	0.61
4:B:225:GLY:HA3	37:B:8866:HOH:O	1.99	0.61
7:E:93:MET:O	7:E:94:GLN:HG3	1.99	0.61
17:O:32:ARG:HB2	37:O:4656:HOH:O	1.98	0.61
4:B:149:ASP:HB2	37:B:8881:HOH:O	2.00	0.61
14:L:93:VAL:HG12	14:L:97:VAL:HG23	1.82	0.61
8:F:38:LYS:NZ	15:M:3:SER:HA	2.14	0.61
13:K:101:ASN:HA	37:K:6456:HOH:O	2.00	0.61
22:T:26:THR:HA	22:T:39:ASN:HB3	1.81	0.61
1:O:154:C:H2'	1:O:155:C:C6	2.33	0.61
37:O:6651:HOH:O	15:M:178:LYS:HB2	2.01	0.61
8:F:48:VAL:HG23	8:F:74:PHE:CB	2.29	0.61
25:W:73:LEU:O	25:W:74:GLU:HG3	2.01	0.61
26:X:43:VAL:HG22	26:X:76:ARG:NH1	2.15	0.61
1:O:1159:G:H21	1:O:1189:A:H8	1.48	0.61
1:O:1164:U:H3	1:O:1192:A:H2	1.48	0.61
1:O:1688:G:H4'	29:1:8:GLN:HG3	1.83	0.61
3:A:220:PRO:HD2	3:A:223:ARG:HD3	1.82	0.61
4:B:51:VAL:HG22	4:B:330:VAL:HG22	1.81	0.61
4:B:54:VAL:HB	37:B:8913:HOH:O	2.00	0.61
14:L:136:ALA:HB3	37:L:8877:HOH:O	1.99	0.61
15:M:31:TRP:HA	15:M:34:GLU:HG3	1.81	0.61
26:X:72:VAL:HG22	26:X:85:VAL:CG1	2.30	0.61
1:O:1008:C:H5''	10:H:19:ARG:HH12	1.65	0.61
1:O:2488:A:H61	1:O:2534:C:H42	1.48	0.61
3:A:211:LYS:HB2	37:A:8914:HOH:O	2.00	0.61
14:L:133:VAL:HA	37:L:8877:HOH:O	2.00	0.61
4:B:313:PRO:HA	37:B:8896:HOH:O	2.01	0.61
7:E:132:THR:HB	37:E:2227:HOH:O	2.00	0.61
10:H:30:LYS:H	10:H:62:HIS:CD2	2.18	0.61
10:H:88:MET:HA	10:H:139:ALA:HA	1.83	0.61
25:W:125:HIS:HD2	25:W:127:GLY:H	1.47	0.61
1:O:290:C:H2'	1:O:291:C:H6	1.64	0.61
1:O:2414:A:H2'	1:O:2415:A:C8	2.35	0.61
1:O:2895:C:H2'	37:O:9379:HOH:O	2.00	0.61
37:O:3868:HOH:O	15:M:97:ILE:HB	2.00	0.61
4:B:217:ARG:HG3	4:B:257:THR:CG2	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:118:ILE:HG23	7:E:144:THR:HG21	1.82	0.61
2:9:34:A:H2'	2:9:35:C:O4'	2.00	0.61
5:C:136:VAL:HA	5:C:137:PRO:C	2.25	0.61
6:D:146:LYS:HE2	16:N:107:ASN:ND2	2.16	0.61
1:0:447:A:OP2	22:T:1:SER:HB2	2.00	0.61
1:0:856:G:H2'	37:0:5225:HOH:O	2.00	0.61
4:B:129:ARG:O	4:B:133:GLU:HG3	2.00	0.61
6:D:99:ASP:CG	6:D:100:ASP:N	2.59	0.61
23:U:9:CYS:CA	23:U:52:THR:HG23	2.29	0.61
26:X:31:ILE:O	26:X:35:GLU:HG3	1.99	0.61
6:D:55:LYS:O	6:D:56:ARG:HB2	2.01	0.60
13:K:49:LEU:HD21	13:K:74:VAL:O	2.00	0.60
16:N:110:THR:HG22	37:N:8848:HOH:O	2.01	0.60
16:N:43:VAL:O	16:N:84:THR:HG21	2.01	0.60
18:P:135:ALA:HB1	18:P:139:ARG:HH12	1.66	0.60
27:Y:234:VAL:HG12	27:Y:235:GLU:N	2.16	0.60
1:0:1422:U:H2'	1:0:1423:C:C6	2.37	0.60
1:0:1691:A:H5''	37:0:9946:HOH:O	2.01	0.60
1:0:2421:G:H3'	1:0:2422:U:H5''	1.83	0.60
1:0:2502:C:H2'	1:0:2503:A:H5'	1.83	0.60
16:N:149:GLU:HA	16:N:152:GLU:HB2	1.83	0.60
21:S:73:ASP:O	21:S:77:VAL:HG23	2.01	0.60
1:0:1845:A:OP2	3:A:190:ARG:NH1	2.35	0.60
1:0:2094:G:H4'	4:B:245:SER:HB3	1.82	0.60
3:A:105:VAL:HG13	3:A:155:THR:O	2.02	0.60
4:B:162:MET:HG3	4:B:310:ARG:CD	2.29	0.60
5:C:127:ARG:HG2	5:C:127:ARG:HH11	1.65	0.60
19:Q:28:ARG:HG2	37:Q:4350:HOH:O	2.00	0.60
1:0:506:G:H5'	37:0:5722:HOH:O	2.00	0.60
1:0:714:U:H3'	37:0:6721:HOH:O	2.00	0.60
1:0:2690:U:O2'	7:E:111:LYS:HE3	2.01	0.60
4:B:154:VAL:HG12	4:B:156:LYS:HG2	1.84	0.60
7:E:172:PRO:HB3	37:E:6931:HOH:O	2.02	0.60
12:J:107:ASN:C	12:J:107:ASN:HD22	2.08	0.60
12:J:133:GLY:O	12:J:137:GLU:HG3	2.01	0.60
14:L:134:GLU:HG3	37:L:8860:HOH:O	2.01	0.60
20:R:4:TYR:CE1	20:R:17:MET:HE2	2.35	0.60
15:M:122:GLN:OE1	15:M:127:LYS:HE2	2.01	0.60
22:T:38:ARG:HG3	22:T:38:ARG:HH11	1.67	0.60
1:0:545:G:H5'	1:0:545:G:C8	2.34	0.60
1:0:1311:G:O6	5:C:173:LYS:HE3	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:140:LEU:HA	37:B:8880:HOH:O	2.01	0.60
4:B:279:THR:OG1	4:B:290:VAL:HB	2.01	0.60
7:E:20:ILE:HD11	7:E:40:VAL:CG1	2.31	0.60
10:H:66:GLU:HA	37:H:235:HOH:O	2.01	0.60
2:9:114:G:O6	16:N:11:ARG:HD3	2.01	0.60
5:C:20:ASP:HB2	37:C:8601:HOH:O	2.00	0.60
6:D:40:ILE:O	6:D:44:ILE:HG22	2.02	0.60
7:E:125:GLU:HB2	7:E:132:THR:CG2	2.30	0.60
1:0:709:G:O2'	17:O:25:VAL:HG12	2.02	0.60
5:C:78:ARG:HG3	5:C:78:ARG:NH1	2.16	0.60
7:E:84:MET:HE2	7:E:133:VAL:HG23	1.84	0.60
7:E:126:ILE:HB	7:E:131:LEU:HD23	1.83	0.60
8:F:56:PRO:CG	15:M:44:THR:HA	2.31	0.60
8:F:58:GLU:CD	15:M:27:ARG:HH22	2.09	0.60
11:I:113:SER:HB2	11:I:118:ASN:HB2	1.83	0.60
12:J:19:MET:HE1	12:J:132:LEU:HD21	1.82	0.60
27:Y:106:THR:HG23	27:Y:107:PRO:HD2	1.82	0.60
29:1:28:HIS:HD2	29:1:30:LYS:H	1.49	0.60
1:0:1803:C:H2'	1:0:1804:A:C8	2.36	0.60
1:0:2676:C:H4'	12:J:70:PHE:CE1	2.37	0.60
4:B:132:HIS:HB2	4:B:137:LEU:CD2	2.32	0.60
4:B:162:MET:HE1	4:B:308:LEU:HD21	1.84	0.60
16:N:154:LEU:HD12	16:N:156:GLU:O	2.01	0.60
1:0:354:A:H2'	1:0:355:C:C6	2.36	0.59
1:0:1523:G:H2'	1:0:1524:U:O4'	2.02	0.59
1:0:1878:G:H1'	37:0:5905:HOH:O	2.02	0.59
16:N:67:ALA:HA	16:N:71:TRP:HB3	1.84	0.59
20:R:25:PHE:CE2	20:R:29:LYS:HE2	2.37	0.59
28:Z:60:CYS:O	28:Z:61:ASP:HB2	2.02	0.59
29:1:28:HIS:O	29:1:32:LYS:N	2.35	0.59
1:0:1213:C:O2'	1:0:1214:G:H5'	2.01	0.59
1:0:1535:G:H2'	1:0:1536:C:C6	2.37	0.59
4:B:55:ASN:ND2	4:B:67:GLU:OE2	2.35	0.59
8:F:100:ASP:HB3	37:F:5691:HOH:O	2.01	0.59
12:J:52:GLN:HG3	12:J:53:ILE:H	1.65	0.59
27:Y:187:VAL:HG22	27:Y:192:ASP:HB2	1.83	0.59
1:0:558:C:H2'	1:0:559:U:C5'	2.32	0.59
1:0:1189:A:H1'	1:0:1209:C:O4'	2.02	0.59
11:I:120:ALA:O	11:I:124:VAL:HG23	2.02	0.59
12:J:74:ARG:NH1	12:J:76:ASP:HB2	2.17	0.59
14:L:94:ARG:HA	14:L:106:VAL:HG21	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:139:TRP:HA	16:N:139:TRP:HE3	1.67	0.59
21:S:57:THR:C	21:S:59:ASP:H	2.10	0.59
25:W:151:GLU:O	25:W:154:ARG:HB3	2.02	0.59
1:0:2719:A:C2	4:B:70:PRO:HG3	2.37	0.59
1:0:2769:C:O2'	1:0:2770:G:H5'	2.03	0.59
2:9:38:A:H2'	2:9:39:U:C6	2.37	0.59
4:B:141:ARG:HD2	4:B:163:GLU:OE2	2.03	0.59
13:K:81:ARG:HB2	13:K:87:ARG:NH1	2.17	0.59
1:0:1342:C:C2'	1:0:1343:C:H5'	2.32	0.59
4:B:307:ARG:HH11	4:B:307:ARG:HB2	1.66	0.59
13:K:37:TYR:HB3	37:K:7169:HOH:O	2.02	0.59
28:Z:46:ARG:CD	28:Z:59:TYR:HB2	2.29	0.59
1:0:671:A:O2'	1:0:672:G:H2'	2.01	0.59
4:B:102:THR:HG23	4:B:182:VAL:HG12	1.85	0.59
11:I:108:HIS:N	11:I:109:PRO:HD2	2.17	0.59
16:N:113:SER:HB2	37:N:8856:HOH:O	2.01	0.59
22:T:24:ARG:HG2	22:T:24:ARG:HH11	1.66	0.59
25:W:21:LEU:HD22	25:W:26:ILE:HD11	1.85	0.59
27:Y:130:ARG:HB2	27:Y:142:SER:O	2.01	0.59
1:0:87:C:H2'	30:2:28:LYS:O	2.02	0.59
1:0:2740:G:H2'	1:0:2741:A:O4'	2.03	0.59
3:A:179:MET:HA	3:A:179:MET:HE3	1.85	0.59
4:B:85:ARG:NH1	37:B:8935:HOH:O	2.36	0.59
17:O:88:LYS:HB3	37:O:7061:HOH:O	2.01	0.59
22:T:87:VAL:HB	37:T:5545:HOH:O	2.03	0.59
1:0:871:G:C8	1:0:871:G:C5'	2.76	0.59
1:0:1189:A:H3'	37:0:7449:HOH:O	2.03	0.59
1:0:2521:A:OP2	10:H:6:ALA:HB3	2.03	0.59
2:9:13:A:O2'	2:9:14:G:H5''	2.02	0.59
6:D:101:THR:O	6:D:101:THR:HG22	2.03	0.59
13:K:113:ILE:HD12	13:K:128:ALA:HB2	1.83	0.59
24:V:13:PRO:O	24:V:17:GLU:HG3	2.02	0.59
1:0:837:U:H4'	37:0:3192:HOH:O	2.02	0.59
5:C:170:ASP:O	5:C:171:GLU:HG3	2.03	0.59
6:D:50:VAL:O	6:D:71:ALA:HA	2.03	0.59
25:W:65:VAL:HA	25:W:68:THR:HG22	1.83	0.59
1:0:711:G:H1'	37:0:6868:HOH:O	2.03	0.59
10:H:49:GLN:HB3	10:H:170:ARG:HG3	1.84	0.59
12:J:90:LYS:HB2	35:J:8802:CL:CL	2.39	0.59
13:K:65:ARG:HD3	37:K:5358:HOH:O	2.02	0.59
31:3:3:MET:HG3	31:3:4:PRO:HD2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1819:G:H2'	1:0:1820:G:H4'	1.83	0.58
1:0:1874:U:OP1	3:A:51:ARG:HD2	2.03	0.58
1:0:2716:G:H5''	4:B:206:THR:HG21	1.85	0.58
3:A:134:ASN:O	3:A:150:PRO:HD3	2.02	0.58
14:L:143:THR:HG22	14:L:144:ASP:N	2.18	0.58
1:0:1537:C:H1'	37:0:6368:HOH:O	2.02	0.58
1:0:1666:C:H2'	1:0:1667:A:C8	2.37	0.58
1:0:2880:A:H2'	1:0:2881:C:H5'	1.85	0.58
4:B:267:LYS:HE3	4:B:300:SER:O	2.03	0.58
5:C:3:ALA:O	5:C:15:GLU:HB2	2.03	0.58
10:H:57:THR:HG23	10:H:131:GLN:HA	1.85	0.58
17:O:105:ASN:ND2	17:O:109:SER:H	2.00	0.58
20:R:39:THR:HG23	20:R:107:GLU:O	2.02	0.58
27:Y:186:ARG:HG2	27:Y:186:ARG:NH1	2.18	0.58
1:0:80:A:H3'	22:T:43:ASN:OD1	2.02	0.58
2:9:64:C:C2'	2:9:65:A:H5'	2.34	0.58
4:B:51:VAL:HG12	4:B:53:LEU:HD13	1.83	0.58
7:E:10:ASP:HA	37:E:6017:HOH:O	2.03	0.58
15:M:164:THR:CG2	15:M:167:GLY:H	2.10	0.58
16:N:163:PHE:O	16:N:164:ASP:O	2.20	0.58
25:W:7:LEU:HD12	25:W:53:ALA:HB2	1.85	0.58
28:Z:26:VAL:O	28:Z:30:GLU:HG3	2.02	0.58
30:2:48:ASP:O	30:2:49:GLU:HB2	2.02	0.58
1:0:1500:U:P	18:P:41:ARG:HH22	2.26	0.58
1:0:1735:C:OP2	4:B:234:ARG:HG3	2.03	0.58
1:0:1778:A:H2'	1:0:1779:A:H5'	1.84	0.58
1:0:1850:U:H2'	1:0:1851:G:H8	1.68	0.58
1:0:2635:A:O2'	1:0:2636:C:H5'	2.04	0.58
37:0:9986:HOH:O	15:M:9:ARG:HG3	2.04	0.58
3:A:199:HIS:CD2	3:A:201:PHE:H	2.21	0.58
5:C:133:ARG:HE	5:C:138:VAL:HG22	1.69	0.58
25:W:1:MET:H2	25:W:37:GLU:HG3	1.68	0.58
1:0:952:G:OP1	19:Q:42:LYS:HE2	2.02	0.58
37:0:3784:HOH:O	22:T:82:THR:HA	2.02	0.58
4:B:264:GLU:CG	4:B:267:LYS:HE2	2.24	0.58
7:E:5:LEU:HD21	7:E:66:GLN:HG3	1.86	0.58
8:F:28:ALA:CB	8:F:99:THR:HG23	2.34	0.58
8:F:56:PRO:HG2	15:M:44:THR:HA	1.85	0.58
10:H:42:ASP:HB2	10:H:45:ASP:OD1	2.04	0.58
16:N:64:SER:C	16:N:66:LEU:H	2.11	0.58
1:0:1441:G:C4'	20:R:130:MET:HE3	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1641:A:H2'	1:0:1642:A:H5'	1.84	0.58
1:0:2053:G:OP1	20:R:138:SER:HB3	2.04	0.58
4:B:275:GLY:O	4:B:291:ASP:HA	2.03	0.58
4:B:329:TYR:HE2	23:U:15:PRO:HG2	1.69	0.58
7:E:81:GLU:HG2	7:E:134:SER:HB3	1.86	0.58
7:E:125:GLU:HB2	7:E:132:THR:HG23	1.86	0.58
16:N:139:TRP:HA	16:N:139:TRP:CE3	2.36	0.58
17:O:78:ALA:O	17:O:98:LEU:HD13	2.04	0.58
3:A:8:ARG:HG2	37:A:8849:HOH:O	2.02	0.58
7:E:137:ASP:OD1	7:E:139:GLU:HB2	2.04	0.58
10:H:44:ASP:HA	10:H:170:ARG:HH12	1.68	0.58
12:J:19:MET:CE	12:J:132:LEU:HD21	2.34	0.58
1:0:419:A:H1'	1:0:1921:A:C2	2.38	0.58
1:0:1060:C:H6	1:0:1060:C:H5'	1.69	0.58
1:0:1183:C:N4	1:0:1184:C:H41	2.02	0.58
1:0:2524:G:H21	1:0:2526:C:H41	1.52	0.58
7:E:85:GLU:HG3	7:E:169:THR:OG1	2.04	0.58
10:H:79:GLU:C	10:H:80:LEU:HD23	2.29	0.58
11:I:118:ASN:HA	11:I:121:LYS:HD2	1.85	0.58
15:M:57:LYS:NZ	15:M:144:ASP:HB2	2.19	0.58
27:Y:112:GLU:HA	27:Y:112:GLU:OE1	2.04	0.58
1:0:841:A:P	37:0:6689:HOH:O	2.61	0.58
1:0:1766:U:O2	1:0:1778:A:H5'	2.04	0.58
5:C:2:GLN:HA	5:C:17:ASP:HA	1.86	0.58
1:0:214:U:H5'	37:0:5924:HOH:O	2.03	0.57
1:0:1624:A:H5'	1:0:1626:A:O4'	2.04	0.57
3:A:179:MET:HG2	3:A:186:TRP:CB	2.34	0.57
4:B:144:THR:HB	37:B:8925:HOH:O	2.04	0.57
6:D:88:LEU:HB2	6:D:89:PRO:HD3	1.87	0.57
7:E:126:ILE:HB	7:E:131:LEU:CD2	2.34	0.57
23:U:6:CYS:C	23:U:8:TYR:H	2.12	0.57
25:W:137:GLN:HE21	25:W:141:HIS:HE1	1.52	0.57
27:Y:126:PRO:HG2	27:Y:128:PHE:CE1	2.38	0.57
1:0:282:C:H2'	1:0:283:U:O4'	2.05	0.57
1:0:960:G:H3'	1:0:960:G:N3	2.19	0.57
1:0:1561:U:H5'	37:0:7201:HOH:O	2.04	0.57
4:B:22:GLU:HG2	37:B:8851:HOH:O	2.04	0.57
4:B:56:ASP:OD1	4:B:322:ARG:HB3	2.04	0.57
4:B:62:ARG:HG2	4:B:65:MET:HE3	1.86	0.57
14:L:17:SER:C	14:L:19:LYS:H	2.12	0.57
1:0:1015:C:H2'	1:0:1016:U:H6	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1400:C:H4'	26:X:56:GLU:HG2	1.86	0.57
1:0:2467:A:H2'	37:0:5254:HOH:O	2.03	0.57
3:A:88:ILE:HD13	3:A:100:PRO:HD3	1.87	0.57
8:F:19:ALA:O	8:F:22:VAL:HG22	2.04	0.57
16:N:27:LEU:HD22	16:N:50:LEU:HD22	1.86	0.57
25:W:1:MET:HE3	25:W:101:LEU:HD23	1.86	0.57
27:Y:115:ARG:NE	37:Y:8857:HOH:O	2.37	0.57
1:0:316:A:N3	1:0:336:G:O2'	2.36	0.57
1:0:1201:C:H2'	1:0:1202:A:H5'	1.87	0.57
8:F:50:VAL:HG21	8:F:63:ILE:HG21	1.85	0.57
23:U:14:GLU:O	23:U:17:THR:HB	2.05	0.57
25:W:13:MET:HE1	25:W:21:LEU:HD12	1.87	0.57
1:0:657:G:OP1	5:C:27:ARG:NH2	2.37	0.57
2:9:48:C:H4'	16:N:141:ARG:NH2	2.18	0.57
20:R:125:ARG:HH12	20:R:134:SER:HB2	1.70	0.57
24:V:64:GLY:O	24:V:65:ASP:CB	2.53	0.57
26:X:25:ARG:NH1	37:X:3861:HOH:O	2.38	0.57
28:Z:46:ARG:O	28:Z:57:CYS:HA	2.05	0.57
1:0:232:A:H4'	37:0:5867:HOH:O	2.05	0.57
1:0:583:C:H2'	1:0:584:U:C6	2.40	0.57
1:0:585:C:H6	37:0:5879:HOH:O	1.88	0.57
1:0:2338:G:OP1	6:D:97:GLN:HG2	2.05	0.57
11:I:108:HIS:N	11:I:109:PRO:CD	2.67	0.57
1:0:263:U:C4	8:F:54:VAL:HG13	2.38	0.57
1:0:2751:C:H3'	37:0:7037:HOH:O	2.03	0.57
3:A:153:ARG:HD3	37:A:8826:HOH:O	2.05	0.57
3:A:211:LYS:HB3	3:A:212:PRO:CD	2.30	0.57
4:B:27:ASN:HD22	4:B:27:ASN:H	1.51	0.57
10:H:29:SER:HA	10:H:62:HIS:HD2	1.70	0.57
30:2:39:ARG:HG2	37:2:3143:HOH:O	2.05	0.57
1:0:702:G:O2'	1:0:703:G:H5'	2.05	0.57
1:0:1164:U:C1'	1:0:1166:A:H5'	2.34	0.57
1:0:2344:G:H2'	1:0:2344:G:N3	2.19	0.57
1:0:2472:C:O2'	1:0:2634:G:H4'	2.04	0.57
1:0:2694:A:H4'	7:E:91:PHE:HE1	1.70	0.57
4:B:41:PHE:HB3	4:B:190:MET:HE1	1.86	0.57
5:C:7:ASP:OD2	5:C:9:ASP:HB2	2.05	0.57
5:C:236:THR:O	5:C:237:GLU:C	2.47	0.57
8:F:2:VAL:HG22	8:F:57:GLU:OE1	2.05	0.57
15:M:24:GLN:NE2	15:M:27:ARG:HH11	2.03	0.57
17:O:32:ARG:NH2	17:O:35:LYS:HD2	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:42:ASN:HB3	37:V:7247:HOH:O	2.03	0.57
26:X:18:ARG:NH1	37:X:4132:HOH:O	2.37	0.57
1:0:732:C:H2'	1:0:733:U:H6	1.70	0.57
1:0:1751:G:C2'	1:0:1752:G:H5''	2.34	0.57
1:0:2050:G:OP1	20:R:79:ARG:HB3	2.05	0.57
1:0:2563:U:H2'	1:0:2565:C:O5'	2.05	0.57
7:E:84:MET:HE1	7:E:148:ILE:CD1	2.35	0.57
12:J:105:LEU:HD23	37:J:8866:HOH:O	2.05	0.57
16:N:170:GLU:HA	16:N:173:ASP:OD2	2.04	0.57
31:3:38:ARG:HB3	31:3:42:ARG:HH12	1.70	0.57
1:0:1508:C:H5'	21:S:21:GLN:NE2	2.20	0.57
1:0:2670:G:O2'	1:0:2671:U:H5'	2.05	0.57
5:C:198:ASP:C	5:C:199:GLU:HG3	2.29	0.57
6:D:84:LEU:C	6:D:86:THR:H	2.13	0.57
7:E:84:MET:HE2	7:E:133:VAL:CG2	2.34	0.57
8:F:22:VAL:HG23	8:F:104:ALA:HB2	1.87	0.57
24:V:49:LEU:O	24:V:53:ILE:HG13	2.04	0.57
1:0:120:A:H2'	1:0:120:A:N3	2.20	0.56
1:0:558:C:O2'	1:0:559:U:H5''	2.05	0.56
1:0:2737:C:OP2	18:P:61:ARG:NH2	2.37	0.56
37:0:3401:HOH:O	3:A:236:GLY:HA3	2.03	0.56
2:9:11:A:P	19:Q:19:ARG:HH21	2.28	0.56
2:9:69:U:OP1	16:N:4:PRO:HG3	2.04	0.56
6:D:36:ASN:HA	37:D:7500:HOH:O	2.05	0.56
7:E:3:VAL:HG22	7:E:49:ILE:HB	1.87	0.56
7:E:84:MET:HG2	7:E:168:ILE:HD13	1.86	0.56
25:W:88:THR:HG23	25:W:110:GLN:NE2	2.20	0.56
1:0:1333:U:H2'	1:0:1334:C:C6	2.41	0.56
1:0:1711:A:O2'	1:0:1712:A:H5'	2.05	0.56
1:0:2359:G:H3'	37:0:5484:HOH:O	2.05	0.56
6:D:21:VAL:HA	6:D:131:THR:O	2.05	0.56
6:D:54:ALA:HB2	6:D:69:ILE:CD1	2.30	0.56
10:H:49:GLN:NE2	10:H:140:TYR:HE2	2.00	0.56
12:J:74:ARG:HH12	12:J:76:ASP:HB2	1.71	0.56
14:L:149:ARG:O	14:L:150:GLN:CB	2.52	0.56
18:P:134:VAL:O	18:P:137:LEU:HB3	2.04	0.56
21:S:19:ASP:O	21:S:20:PHE:HD2	1.88	0.56
22:T:23:VAL:C	22:T:93:THR:HG21	2.30	0.56
1:0:1007:A:H2'	10:H:22:TYR:CZ	2.40	0.56
1:0:1164:U:O4'	1:0:1166:A:H5'	2.05	0.56
1:0:1834:C:H2'	1:0:1840:A:H62	1.67	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1971:G:H2'	37:0:3091:HOH:O	2.04	0.56
3:A:101:GLU:O	3:A:103:VAL:HG23	2.06	0.56
4:B:329:TYR:CE2	23:U:15:PRO:HG2	2.39	0.56
6:D:64:ARG:HG2	6:D:67:ASP:HB3	1.87	0.56
8:F:48:VAL:HG23	8:F:74:PHE:HB3	1.86	0.56
12:J:74:ARG:HD3	37:J:8859:HOH:O	2.04	0.56
16:N:82:TYR:C	16:N:82:TYR:CD2	2.84	0.56
17:O:14:LEU:CD2	17:O:102:ILE:HD11	2.34	0.56
17:O:41:ALA:HA	37:O:5104:HOH:O	2.06	0.56
23:U:52:THR:HG22	23:U:54:THR:N	2.20	0.56
25:W:54:PHE:CZ	25:W:140:LYS:HB2	2.41	0.56
1:0:2715:G:N2	4:B:264:GLU:OE1	2.36	0.56
3:A:105:VAL:CG1	3:A:154:ALA:HB1	2.35	0.56
3:A:153:ARG:HB2	3:A:153:ARG:NH1	2.20	0.56
5:C:21:VAL:C	5:C:23:GLU:H	2.13	0.56
10:H:69:ARG:HB3	37:H:235:HOH:O	2.05	0.56
11:I:80:PHE:HB2	11:I:93:ALA:HB2	1.88	0.56
16:N:152:GLU:C	16:N:154:LEU:N	2.63	0.56
4:B:102:THR:CG2	4:B:182:VAL:HG12	2.36	0.56
16:N:24:LEU:HD13	19:Q:26:PRO:HB3	1.87	0.56
27:Y:205:ILE:O	27:Y:206:ALA:C	2.49	0.56
1:0:1180:U:H2'	1:0:1181:A:C8	2.39	0.56
1:0:1701:A:H4'	1:0:1702:U:C5'	2.36	0.56
1:0:2816:A:H4'	37:0:3702:HOH:O	2.05	0.56
2:9:49:G:H5''	37:9:8671:HOH:O	2.04	0.56
3:A:217:ARG:HH11	3:A:217:ARG:CG	2.18	0.56
4:B:294:TYR:HE2	37:B:8951:HOH:O	1.87	0.56
6:D:64:ARG:NE	6:D:67:ASP:HB3	2.20	0.56
8:F:57:GLU:HB2	15:M:23:LEU:HD11	1.88	0.56
13:K:62:PRO:HG3	13:K:65:ARG:NH2	2.19	0.56
15:M:99:ARG:HG2	37:M:8857:HOH:O	2.05	0.56
17:O:27:GLY:O	17:O:31:GLU:HG3	2.06	0.56
1:0:797:A:C4'	28:Z:10:ARG:N	2.68	0.56
1:0:922:A:N7	1:0:2281:C:H5'	2.21	0.56
2:9:44:A:O4'	6:D:76:ARG:NE	2.37	0.56
3:A:199:HIS:HD2	3:A:201:PHE:H	1.54	0.56
8:F:56:PRO:HG2	15:M:43:PRO:O	2.05	0.56
10:H:157:TYR:CD1	10:H:157:TYR:C	2.83	0.56
14:L:54:PRO:HG2	14:L:57:VAL:HG21	1.87	0.56
24:V:39:ALA:C	24:V:41:GLU:H	2.14	0.56
27:Y:189:ASN:HA	27:Y:217:ILE:HD11	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1477:C:H5'	1:0:1868:G:C5'	2.36	0.56
1:0:1504:A:H5''	37:0:5392:HOH:O	2.06	0.56
1:0:2661:U:H3	1:0:2812:A:H62	1.52	0.56
12:J:92:GLN:HB3	37:J:8829:HOH:O	2.06	0.56
20:R:125:ARG:HA	20:R:140:GLN:OE1	2.06	0.56
1:0:638:C:H2'	1:0:639:A:C8	2.41	0.56
1:0:820:G:C6	3:A:171:LYS:HB2	2.40	0.56
1:0:1299:G:O6	14:L:6:ARG:HD3	2.06	0.56
1:0:1702:U:H5'	37:0:3224:HOH:O	2.05	0.56
1:0:2256:G:C2'	1:0:2257:G:H5'	2.36	0.56
1:0:2270:G:H4'	3:A:223:ARG:NH1	2.13	0.56
12:J:41:ALA:HB3	37:J:8866:HOH:O	2.05	0.56
14:L:115:ARG:O	14:L:116:HIS:ND1	2.39	0.56
17:O:32:ARG:HD2	37:O:3240:HOH:O	2.05	0.56
25:W:13:MET:HE3	25:W:17:ILE:CG2	2.35	0.56
1:0:31:C:H4'	37:0:7197:HOH:O	2.06	0.56
1:0:1176:C:H1'	37:0:3728:HOH:O	2.06	0.56
1:0:2265:U:H2'	1:0:2266:A:C8	2.41	0.56
1:0:2694:A:H4'	7:E:91:PHE:CE1	2.40	0.56
1:0:2768:A:O2'	1:0:2769:C:H5'	2.05	0.56
6:D:23:VAL:HG23	6:D:23:VAL:O	2.06	0.56
14:L:73:VAL:HG21	14:L:116:HIS:HD2	1.67	0.56
1:0:282:C:O2'	1:0:283:U:H5'	2.06	0.55
1:0:793:A:H5''	18:P:83:LYS:HG2	1.87	0.55
4:B:202:VAL:HG11	4:B:301:VAL:CG1	2.32	0.55
5:C:139:VAL:HG13	37:C:8657:HOH:O	2.06	0.55
10:H:157:TYR:C	10:H:157:TYR:HD1	2.14	0.55
13:K:34:VAL:HB	37:K:7169:HOH:O	2.05	0.55
13:K:113:ILE:HG22	13:K:114:ALA:O	2.04	0.55
16:N:13:ARG:NH1	16:N:13:ARG:O	2.38	0.55
19:Q:64:GLU:OE1	19:Q:64:GLU:HA	2.06	0.55
20:R:91:LEU:HD22	20:R:143:VAL:HG22	1.88	0.55
28:Z:57:CYS:SG	28:Z:59:TYR:HB3	2.46	0.55
1:0:90:A:H2'	1:0:91:G:O4'	2.05	0.55
1:0:2831:C:H2'	1:0:2832:C:H5'	1.88	0.55
5:C:7:ASP:O	5:C:9:ASP:N	2.38	0.55
5:C:165:ASP:OD2	5:C:191:SER:HB2	2.06	0.55
6:D:170:TYR:O	6:D:171:ASP:HB3	2.05	0.55
9:G:71:LEU:C	9:G:73:ASP:N	2.65	0.55
10:H:72:ALA:HB2	10:H:156:ALA:HB2	1.88	0.55
18:P:59:ARG:HH22	18:P:66:GLN:NE2	2.01	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:3:16:GLU:HB2	37:3:8864:HOH:O	2.06	0.55
37:0:3554:HOH:O	22:T:9:LYS:HD3	2.06	0.55
4:B:109:LEU:HD11	4:B:113:LEU:HD12	1.87	0.55
4:B:320:GLN:HE21	4:B:321:PRO:HD2	1.71	0.55
6:D:89:PRO:C	6:D:91:ALA:H	2.14	0.55
10:H:61:ARG:HG3	10:H:61:ARG:NH1	2.20	0.55
26:X:78:GLU:HG2	26:X:79:GLU:N	2.22	0.55
1:0:263:U:O4	8:F:54:VAL:HG13	2.06	0.55
3:A:105:VAL:HG11	3:A:154:ALA:HB1	1.89	0.55
5:C:5:ILE:HG22	5:C:6:TYR:N	2.22	0.55
8:F:12:LEU:HD23	8:F:12:LEU:O	2.06	0.55
16:N:22:GLN:HG2	16:N:26:LEU:CD2	2.36	0.55
16:N:170:GLU:O	16:N:174:GLU:HG3	2.07	0.55
27:Y:235:GLU:N	27:Y:235:GLU:CD	2.64	0.55
1:0:280:C:H2'	1:0:281:U:O4'	2.07	0.55
1:0:558:C:H5'	37:0:5056:HOH:O	2.07	0.55
1:0:1702:U:H5''	37:0:6988:HOH:O	2.05	0.55
1:0:1826:C:H3'	37:0:7325:HOH:O	2.06	0.55
1:0:2427:C:OP2	31:3:84:ARG:HD2	2.05	0.55
2:9:6:C:OP1	16:N:37:ARG:NH1	2.37	0.55
4:B:132:HIS:CE1	4:B:171:VAL:HG23	2.41	0.55
8:F:48:VAL:HG12	8:F:97:ALA:CB	2.36	0.55
16:N:37:ARG:NH2	37:N:8830:HOH:O	2.39	0.55
19:Q:94:GLN:O	19:Q:95:GLU:HB2	2.06	0.55
22:T:99:THR:O	22:T:100:ASP:CB	2.54	0.55
5:C:37:ALA:O	5:C:41:ASN:ND2	2.39	0.55
5:C:240:LEU:HD23	5:C:240:LEU:O	2.06	0.55
11:I:67:VAL:CG1	11:I:68:PRO:HD2	2.37	0.55
11:I:96:SER:H	11:I:99:GLN:HB2	1.71	0.55
20:R:39:THR:HG22	20:R:42:GLU:H	1.72	0.55
22:T:49:GLU:OE2	22:T:97:ARG:HD2	2.06	0.55
22:T:55:PHE:O	22:T:56:ALA:C	2.48	0.55
25:W:65:VAL:HA	25:W:68:THR:CG2	2.36	0.55
1:0:1058:A:H2'	1:0:1060:C:H5''	1.87	0.55
3:A:200:PRO:HG2	3:A:225:VAL:HG21	1.87	0.55
5:C:7:ASP:C	5:C:9:ASP:H	2.15	0.55
8:F:69:GLU:O	8:F:70:LYS:HG2	2.07	0.55
13:K:66:ARG:HG2	13:K:66:ARG:HH11	1.71	0.55
15:M:72:ALA:HB2	15:M:93:ARG:HG2	1.89	0.55
22:T:101:LEU:HB2	22:T:103:LEU:HD21	1.87	0.55
25:W:77:ALA:HA	37:W:6694:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:797:A:H4'	28:Z:10:ARG:N	2.22	0.55
1:0:2780:C:H1'	7:E:143:GLN:HE21	1.71	0.55
4:B:145:HIS:HD2	4:B:146:THR:O	1.90	0.55
15:M:96:ASP:OD1	15:M:99:ARG:HD3	2.06	0.55
15:M:190:ASN:HB2	37:M:8820:HOH:O	2.07	0.55
16:N:67:ALA:C	16:N:69:TYR:H	2.14	0.55
28:Z:22:SER:O	28:Z:26:VAL:HG23	2.07	0.55
1:0:1044:C:H5	37:0:6383:HOH:O	1.89	0.55
1:0:1593:C:OP1	18:P:117:SER:HB3	2.06	0.55
1:0:1756:G:H1'	37:0:6047:HOH:O	2.07	0.55
1:0:2769:C:C2'	1:0:2770:G:H5'	2.37	0.55
7:E:18:LEU:HD13	7:E:34:TRP:CD1	2.42	0.55
8:F:111:ILE:O	8:F:115:VAL:HG23	2.06	0.55
12:J:95:ARG:O	12:J:99:GLU:HB2	2.07	0.55
13:K:14:LYS:CB	13:K:45:PRO:HG2	2.35	0.55
16:N:73:ALA:HB1	16:N:74:PRO:CD	2.37	0.55
20:R:12:THR:HG22	20:R:149:GLU:OE1	2.06	0.55
22:T:32:ARG:NH1	22:T:38:ARG:NH1	2.55	0.55
1:0:1116:U:H3	1:0:1246:A:N6	2.02	0.55
1:0:1189:A:H1'	1:0:1209:C:C1'	2.37	0.55
1:0:2111:G:H1'	37:0:8867:HOH:O	2.07	0.55
3:A:153:ARG:HH11	3:A:153:ARG:CB	2.19	0.55
4:B:171:VAL:O	4:B:175:LEU:HB2	2.07	0.55
27:Y:107:PRO:HB3	27:Y:182:PHE:CE2	2.42	0.55
1:0:945:U:H2'	1:0:946:C:C6	2.43	0.54
1:0:2361:A:H5'	37:0:4877:HOH:O	2.05	0.54
1:0:2415:A:O2'	16:N:29:SER:HB3	2.07	0.54
5:C:47:GLY:HA2	5:C:92:PRO:HB2	1.88	0.54
12:J:19:MET:HE2	12:J:79:PHE:HA	1.89	0.54
13:K:49:LEU:HD23	13:K:73:VAL:O	2.07	0.54
16:N:33:ARG:NH1	16:N:103:ASP:OD2	2.39	0.54
22:T:48:VAL:HG11	22:T:96:VAL:CG1	2.36	0.54
23:U:39:ASN:ND2	23:U:44:ARG:HH11	2.04	0.54
25:W:88:THR:HG22	25:W:89:ASP:N	2.15	0.54
1:0:65:C:O2'	1:0:66:G:H5'	2.07	0.54
1:0:449:A:N7	5:C:43:LYS:HG2	2.22	0.54
1:0:1701:A:H5'	37:0:6068:HOH:O	2.07	0.54
1:0:2546:U:H4'	37:B:8886:HOH:O	2.06	0.54
1:0:2755:G:H1'	37:0:4482:HOH:O	2.07	0.54
3:A:37:VAL:HG23	3:A:38:ILE:N	2.21	0.54
4:B:162:MET:HG3	4:B:310:ARG:CZ	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:81:GLU:C	6:D:83:PHE:H	2.15	0.54
15:M:66:SER:HB3	15:M:128:TRP:CD1	2.43	0.54
17:O:52:ALA:HB1	17:O:74:VAL:HG11	1.90	0.54
1:O:544:G:C3'	1:O:545:G:H5''	2.37	0.54
1:O:1168:C:H5''	11:I:83:GLY:H	1.72	0.54
1:O:1342:C:O2'	1:O:1343:C:H5'	2.07	0.54
1:O:2316:G:H4'	37:O:5876:HOH:O	2.08	0.54
1:O:2793:A:H5'	37:O:4360:HOH:O	2.08	0.54
10:H:49:GLN:HB2	10:H:170:ARG:HD2	1.89	0.54
12:J:107:ASN:HD22	12:J:108:PRO:N	2.05	0.54
20:R:9:ASP:O	20:R:13:THR:HG22	2.06	0.54
25:W:118:LEU:HD12	25:W:153:MET:HE3	1.88	0.54
1:O:732:C:H2'	1:O:733:U:C6	2.43	0.54
1:O:2469:A:H1'	37:O:3045:HOH:O	2.06	0.54
1:O:2604:A:H5'	37:O:5579:HOH:O	2.06	0.54
3:A:61:GLU:C	3:A:63:GLY:H	2.14	0.54
3:A:140:LEU:HB3	3:A:141:PRO:HD2	1.88	0.54
8:F:21:GLU:O	8:F:24:ARG:HG2	2.07	0.54
13:K:49:LEU:HD21	13:K:74:VAL:C	2.32	0.54
16:N:47:LEU:CD1	16:N:97:VAL:HG11	2.38	0.54
20:R:22:GLN:CG	20:R:140:GLN:HE21	2.21	0.54
22:T:25:ALA:O	22:T:39:ASN:HB2	2.08	0.54
22:T:55:PHE:CD2	22:T:77:VAL:HG13	2.42	0.54
1:O:111:C:H2'	1:O:112:G:O4'	2.08	0.54
4:B:140:LEU:HD23	37:B:8880:HOH:O	2.06	0.54
8:F:30:LYS:HA	37:F:5719:HOH:O	2.06	0.54
16:N:38:LYS:HD2	16:N:114:LYS:HE3	1.88	0.54
25:W:65:VAL:HG12	25:W:116:LEU:HD13	1.90	0.54
1:O:1882:C:H4'	37:O:4269:HOH:O	2.08	0.54
1:O:2044:G:OP1	26:X:23:HIS:HE1	1.91	0.54
1:O:2434:A:O3'	31:3:28:GLY:HA3	2.08	0.54
1:O:2504:A:H2'	1:O:2505:G:O4'	2.08	0.54
1:O:2837:U:H1'	4:B:307:ARG:HH12	1.73	0.54
1:O:399:C:H5'	15:M:179:GLY:O	2.08	0.54
3:A:96:LEU:HD22	3:A:128:LEU:HD13	1.89	0.54
5:C:21:VAL:HG23	5:C:22:PHE:CD1	2.42	0.54
8:F:53:ASP:OD1	8:F:80:GLN:HB2	2.08	0.54
10:H:135:GLN:HG3	37:H:236:HOH:O	2.07	0.54
16:N:72:GLU:HB3	16:N:171:HIS:HE1	1.73	0.54
18:P:80:ARG:HG2	18:P:87:ARG:CZ	2.38	0.54
20:R:14:ALA:HB3	20:R:147:LEU:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:52:VAL:HG22	21:S:66:VAL:HG22	1.89	0.54
25:W:65:VAL:CG1	25:W:116:LEU:HD13	2.38	0.54
26:X:70:ILE:HG23	26:X:70:ILE:O	2.08	0.54
29:1:28:HIS:ND1	29:1:31:LYS:HE2	2.22	0.54
30:2:36:ASN:C	30:2:38:LYS:H	2.15	0.54
1:0:947:U:O2'	1:0:948:G:H5'	2.07	0.54
1:0:1617:C:C4	1:0:1643:C:H4'	2.43	0.54
1:0:1787:C:H4'	1:0:2883:A:O4'	2.08	0.54
1:0:1972:U:H2'	1:0:1973:A:H5'	1.90	0.54
1:0:2718:C:H6	1:0:2718:C:H5'	1.73	0.54
2:9:122:C:H5'	37:9:8628:HOH:O	2.07	0.54
4:B:82:VAL:O	4:B:82:VAL:HG12	2.06	0.54
11:I:113:SER:CB	11:I:118:ASN:HB2	2.38	0.54
18:P:16:VAL:HG12	18:P:17:GLY:N	2.22	0.54
25:W:68:THR:HG23	25:W:69:ARG:HG2	1.90	0.54
1:0:542:A:H2'	1:0:543:G:O4'	2.08	0.54
1:0:1847:A:OP1	3:A:175:LYS:HG3	2.08	0.54
1:0:2824:C:H5''	1:0:2825:C:H5'	1.90	0.54
37:0:6155:HOH:O	29:1:30:LYS:HE2	2.08	0.54
6:D:154:LYS:H	6:D:154:LYS:HD2	1.71	0.54
10:H:100:GLU:HB3	10:H:124:VAL:HG11	1.88	0.54
15:M:107:ARG:HD2	37:M:8875:HOH:O	2.08	0.54
23:U:17:THR:CG2	23:U:18:GLY:N	2.71	0.54
24:V:4:HIS:O	24:V:8:ILE:HG13	2.07	0.54
24:V:11:MET:HB3	24:V:15:GLU:HB2	1.88	0.54
28:Z:11:SER:CB	28:Z:23:ARG:HB2	2.38	0.54
1:0:1701:A:H5''	1:0:1702:U:H3'	1.90	0.54
3:A:86:ALA:HB1	3:A:92:ASN:HD22	1.72	0.54
4:B:7:ARG:CZ	4:B:11:LEU:HD21	2.38	0.54
4:B:212:GLN:HB2	4:B:257:THR:HG21	1.88	0.54
5:C:26:VAL:N	37:C:8558:HOH:O	2.41	0.54
27:Y:234:VAL:HG12	27:Y:235:GLU:H	1.73	0.54
1:0:1614:G:H2'	37:0:4429:HOH:O	2.07	0.53
1:0:2795:C:O2'	1:0:2796:U:H5'	2.07	0.53
2:9:76:G:C3'	2:9:77:A:H5''	2.29	0.53
5:C:95:GLU:HG3	37:C:8684:HOH:O	2.06	0.53
6:D:95:THR:OG1	6:D:174:VAL:HG13	2.08	0.53
13:K:75:ARG:NH2	37:K:4172:HOH:O	2.41	0.53
16:N:176:ARG:HE	16:N:180:LEU:HD21	1.73	0.53
20:R:100:ASP:C	20:R:102:GLN:H	2.14	0.53
26:X:87:ALA:O	26:X:88:GLU:CB	2.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:49:GLN:HG3	10:H:140:TYR:CE2	2.43	0.53
12:J:130:VAL:HG11	12:J:135:ILE:HG13	1.90	0.53
15:M:59:GLY:C	15:M:141:ILE:HD11	2.34	0.53
25:W:1:MET:N	25:W:37:GLU:HG3	2.22	0.53
30:2:41:HIS:CD2	30:2:44:ARG:H	2.17	0.53
1:0:324:G:O2'	1:0:325:U:H5'	2.08	0.53
1:0:542:A:H5'	1:0:542:A:C8	2.35	0.53
1:0:719:C:O2'	17:O:112:ARG:NH2	2.41	0.53
1:0:2036:C:O4'	13:K:44:LEU:HG	2.08	0.53
1:0:2597:U:H2'	1:0:2598:U:H5'	1.89	0.53
3:A:107:ASN:N	3:A:119:ALA:O	2.38	0.53
5:C:1:MET:HG2	5:C:2:GLN:H	1.73	0.53
5:C:218:VAL:HG12	37:C:8633:HOH:O	2.07	0.53
11:I:119:ALA:O	11:I:123:VAL:HG23	2.07	0.53
13:K:64:MET:HE1	13:K:105:ARG:HE	1.72	0.53
20:R:47:LEU:O	20:R:51:ILE:HG13	2.09	0.53
22:T:48:VAL:HG12	22:T:49:GLU:N	2.23	0.53
22:T:51:LEU:HD11	22:T:97:ARG:HB2	1.91	0.53
1:0:88:G:H1'	37:0:6850:HOH:O	2.08	0.53
1:0:870:G:OP2	3:A:3:ARG:HD3	2.09	0.53
1:0:1505:U:H6	1:0:1505:U:H5'	1.71	0.53
1:0:2237:G:H1'	37:0:4653:HOH:O	2.08	0.53
1:0:2252:A:C5	1:0:2253:G:H1'	2.44	0.53
4:B:7:ARG:HD3	4:B:9:GLY:O	2.08	0.53
7:E:116:THR:HG22	7:E:151:LEU:HD22	1.91	0.53
9:G:12:ILE:HG22	9:G:17:GLN:NE2	2.23	0.53
17:O:44:ASN:HB3	17:O:67:SER:O	2.08	0.53
1:0:67:A:H5''	1:0:69:A:C8	2.43	0.53
1:0:677:C:H4'	5:C:246:ARG:NH2	2.23	0.53
1:0:1185:U:H5'	37:0:7238:HOH:O	2.08	0.53
1:0:1334:C:H2'	1:0:1335:C:H6	1.74	0.53
1:0:1632:A:C2'	1:0:1633:C:H5'	2.39	0.53
1:0:2314:G:C2'	1:0:2315:C:H5'	2.39	0.53
1:0:2578:G:H5'	1:0:2578:G:C8	2.40	0.53
8:F:48:VAL:HG12	8:F:97:ALA:HB2	1.89	0.53
22:T:55:PHE:HB2	37:T:6384:HOH:O	2.08	0.53
25:W:4:LEU:O	25:W:32:CYS:HA	2.09	0.53
26:X:85:VAL:HG12	26:X:86:GLU:N	2.23	0.53
31:3:30:GLN:HB3	37:3:8852:HOH:O	2.08	0.53
1:0:635:A:H2'	1:0:636:G:H5''	1.89	0.53
1:0:2276:U:H2'	1:0:2277:U:C6	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:36:ASP:CB	3:A:85:SER:H	2.22	0.53
3:A:121:ALA:H	3:A:124:VAL:CG2	2.20	0.53
6:D:44:ILE:O	6:D:44:ILE:HG12	2.08	0.53
6:D:55:LYS:O	6:D:56:ARG:CB	2.56	0.53
9:G:23:ILE:HG22	9:G:27:ILE:HD11	1.90	0.53
20:R:39:THR:HB	20:R:42:GLU:CG	2.38	0.53
1:0:290:C:H2'	1:0:291:C:C6	2.43	0.53
1:0:338:C:H5''	37:0:3599:HOH:O	2.08	0.53
1:0:2672:C:OP2	4:B:25:ARG:NH1	2.40	0.53
1:0:2748:G:H2'	37:0:7309:HOH:O	2.08	0.53
7:E:80:TRP:O	7:E:134:SER:HA	2.08	0.53
9:G:19:GLU:HG2	9:G:66:LEU:HD12	1.90	0.53
10:H:27:PRO:HD3	10:H:123:ILE:CG2	2.39	0.53
10:H:114:ASP:HB2	37:H:199:HOH:O	2.07	0.53
17:O:38:ARG:NH1	37:O:7674:HOH:O	2.42	0.53
21:S:7:HIS:CD2	21:S:27:ALA:HB3	2.44	0.53
25:W:76:ASP:O	25:W:77:ALA:C	2.52	0.53
1:0:656:G:H5'	17:O:3:THR:HB	1.91	0.53
1:0:2533:C:H5'	1:0:2533:C:H6	1.74	0.53
1:0:2896:A:H5''	37:0:5883:HOH:O	2.08	0.53
5:C:136:VAL:HG22	5:C:137:PRO:HA	1.90	0.53
6:D:18:ILE:HG12	6:D:134:LEU:CD2	2.39	0.53
7:E:93:MET:HE1	7:E:165:GLY:N	2.24	0.53
12:J:33:GLY:O	12:J:34:GLU:C	2.52	0.53
18:P:20:ARG:NH1	18:P:54:LYS:HD3	2.22	0.53
27:Y:107:PRO:HB3	27:Y:182:PHE:CD2	2.44	0.53
28:Z:73:THR:O	28:Z:76:GLY:N	2.42	0.53
1:0:122:C:H5''	37:0:3387:HOH:O	2.08	0.53
1:0:1120:U:H5'	1:0:1120:U:C6	2.40	0.53
1:0:1132:A:N6	1:0:1229:C:H2'	2.24	0.53
1:0:1527:A:H1'	1:0:1528:A:C8	2.43	0.53
1:0:1762:C:H4'	37:0:4456:HOH:O	2.08	0.53
1:0:1874:U:H2'	3:A:120:ARG:HG3	1.91	0.53
1:0:2028:U:H2'	1:0:2029:C:C6	2.43	0.53
4:B:150:ALA:O	4:B:152:PRO:HD3	2.09	0.53
10:H:30:LYS:H	10:H:62:HIS:HD2	1.55	0.53
18:P:135:ALA:HB1	18:P:139:ARG:NH1	2.24	0.53
20:R:61:GLN:CD	37:R:8831:HOH:O	2.51	0.53
29:1:10:LYS:N	37:1:2979:HOH:O	2.41	0.53
1:0:1790:C:H2'	1:0:1791:U:C6	2.43	0.53
1:0:2405:C:H5'	37:0:6375:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2445:U:H2'	1:0:2446:G:C8	2.44	0.53
1:0:2786:G:H2'	37:0:6957:HOH:O	2.08	0.53
1:0:2798:G:H3'	37:0:4196:HOH:O	2.08	0.53
4:B:51:VAL:HG13	4:B:327:VAL:HG13	1.92	0.53
11:I:95:LEU:HD23	11:I:99:GLN:OE1	2.08	0.53
21:S:42:GLU:HG2	21:S:49:VAL:HG23	1.91	0.53
24:V:16:ARG:HB2	37:V:874:HOH:O	2.09	0.53
26:X:87:ALA:O	26:X:88:GLU:HB3	2.09	0.53
27:Y:203:VAL:HG22	37:Y:8875:HOH:O	2.09	0.53
1:0:138:U:OP2	1:0:139:C:H5	1.92	0.52
1:0:1333:U:H2'	1:0:1334:C:H6	1.74	0.52
1:0:1391:G:H2'	1:0:1392:A:H5'	1.91	0.52
37:0:5256:HOH:O	9:G:12:ILE:HG23	2.10	0.52
37:0:6839:HOH:O	20:R:33:ARG:HD3	2.08	0.52
15:M:152:ALA:HB1	37:M:8941:HOH:O	2.07	0.52
27:Y:235:GLU:CD	27:Y:235:GLU:H	2.17	0.52
1:0:660:A:H4'	1:0:661:G:O5'	2.09	0.52
1:0:1268:C:H2'	1:0:1269:G:H8	1.74	0.52
1:0:1477:C:H5'	1:0:1868:G:H5''	1.92	0.52
3:A:65:ARG:C	3:A:66:ARG:HG3	2.33	0.52
3:A:69:LEU:HB3	37:A:8871:HOH:O	2.08	0.52
4:B:14:GLY:HA2	4:B:15:PRO:C	2.34	0.52
4:B:253:GLN:HA	37:B:8924:HOH:O	2.10	0.52
31:3:69:TYR:O	31:3:77:ALA:HA	2.09	0.52
1:0:1119:G:H5'	12:J:52:GLN:HE21	1.74	0.52
1:0:1815:A:H2'	1:0:1816:C:O4'	2.09	0.52
1:0:1882:C:O2'	1:0:2012:U:OP2	2.25	0.52
6:D:41:LEU:HA	6:D:44:ILE:HG22	1.91	0.52
11:I:133:THR:HG22	11:I:134:ILE:N	2.24	0.52
12:J:107:ASN:ND2	12:J:107:ASN:C	2.67	0.52
12:J:127:ILE:N	35:J:8801:CL:CL	2.75	0.52
16:N:86:LEU:O	16:N:90:LEU:HG	2.10	0.52
20:R:13:THR:HG23	37:R:8856:HOH:O	2.08	0.52
20:R:82:GLU:O	20:R:86:LYS:HG3	2.09	0.52
23:U:23:HIS:HB2	23:U:27:ALA:HB3	1.90	0.52
27:Y:178:HIS:CG	27:Y:179:PRO:HD2	2.45	0.52
1:0:513:A:N3	37:0:3459:HOH:O	2.33	0.52
1:0:2910:A:H5''	37:0:3932:HOH:O	2.09	0.52
37:0:7477:HOH:O	5:C:94:THR:HG21	2.09	0.52
4:B:254:GLN:HG2	4:B:255:GLY:N	2.24	0.52
5:C:34:ALA:HA	5:C:102:LEU:CD2	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:146:LYS:CE	16:N:107:ASN:HD21	2.21	0.52
8:F:50:VAL:CG2	8:F:63:ILE:HG21	2.39	0.52
11:I:117:THR:O	11:I:121:LYS:HG3	2.09	0.52
18:P:126:ALA:C	18:P:128:GLY:H	2.17	0.52
1:O:256:C:H2'	1:O:257:G:O4'	2.09	0.52
1:O:440:C:O2'	1:O:441:A:H5'	2.09	0.52
1:O:536:A:H3'	37:O:4850:HOH:O	2.10	0.52
1:O:2015:A:H2'	1:O:2016:U:O4'	2.08	0.52
1:O:2776:A:H2'	1:O:2777:G:O4'	2.09	0.52
2:9:29:C:H2'	2:9:30:C:H5'	1.91	0.52
8:F:26:THR:HG21	8:F:102:GLY:C	2.34	0.52
8:F:34:ASN:HA	15:M:4:ALA:HB2	1.92	0.52
16:N:58:LEU:N	16:N:58:LEU:HD12	2.24	0.52
18:P:38:GLU:HA	18:P:41:ARG:NH1	2.24	0.52
18:P:138:GLU:C	18:P:140:TYR:H	2.17	0.52
26:X:69:LYS:O	26:X:70:ILE:HB	2.10	0.52
27:Y:180:SER:HA	37:Y:8844:HOH:O	2.08	0.52
31:3:42:ARG:HB2	31:3:42:ARG:HH11	1.75	0.52
1:O:1741:U:O2'	1:O:2723:G:H4'	2.10	0.52
1:O:1762:C:H2'	1:O:1763:C:H6	1.75	0.52
3:A:52:SER:HB2	3:A:164:ARG:HH11	1.74	0.52
4:B:53:LEU:HD12	4:B:327:VAL:HA	1.91	0.52
5:C:26:VAL:HG21	5:C:123:LEU:HD11	1.91	0.52
5:C:84:VAL:O	5:C:85:LYS:HB2	2.09	0.52
5:C:127:ARG:HG2	5:C:127:ARG:NH1	2.25	0.52
5:C:219:ASN:O	5:C:222:ASP:OD1	2.28	0.52
11:I:98:ASP:C	11:I:100:VAL:H	2.17	0.52
14:L:68:GLU:O	14:L:69:ILE:C	2.53	0.52
19:Q:28:ARG:HD3	19:Q:92:ARG:HH12	1.73	0.52
27:Y:189:ASN:C	27:Y:189:ASN:HD22	2.17	0.52
1:O:2768:A:H2'	1:O:2769:C:O4'	2.09	0.52
4:B:223:ARG:HG3	4:B:232:TRP:O	2.10	0.52
5:C:131:PHE:CD2	5:C:232:LEU:HD22	2.45	0.52
6:D:25:MET:CE	6:D:37:ALA:HB1	2.40	0.52
16:N:143:ARG:HA	16:N:172:PHE:CD2	2.44	0.52
17:O:49:GLU:HG2	37:O:5191:HOH:O	2.09	0.52
25:W:48:VAL:O	25:W:48:VAL:HG12	2.10	0.52
26:X:80:GLU:O	26:X:80:GLU:HG2	2.08	0.52
1:O:625:U:H5'	37:O:9987:HOH:O	2.10	0.52
1:O:820:G:C5	3:A:171:LYS:HB2	2.44	0.52
1:O:821:U:H2'	1:O:822:C:C6	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1187:U:H2'	37:0:6675:HOH:O	2.09	0.52
1:0:2478:U:O2'	1:0:2479:A:H5'	2.09	0.52
1:0:2721:U:H4'	13:K:87:ARG:HG3	1.92	0.52
1:0:2837:U:H2'	37:0:6615:HOH:O	2.10	0.52
4:B:82:VAL:HG12	4:B:101:TRP:CE3	2.45	0.52
5:C:235:PHE:CE2	5:C:243:VAL:HG21	2.44	0.52
16:N:159:TYR:HB2	37:N:8828:HOH:O	2.09	0.52
21:S:50:GLU:CG	21:S:69:SER:HA	2.40	0.52
22:T:41:ARG:NH1	22:T:42:VAL:O	2.43	0.52
1:0:289:G:O2'	1:0:290:C:H5'	2.09	0.52
1:0:1495:C:H1'	1:0:1573:A:H1'	1.91	0.52
1:0:1771:U:O2'	1:0:1773:G:N7	2.38	0.52
6:D:146:LYS:HZ1	16:N:107:ASN:HD21	1.54	0.52
7:E:24:GLY:HA3	7:E:76:VAL:HB	1.90	0.52
7:E:77:THR:OG1	7:E:78:GLU:N	2.42	0.52
16:N:22:GLN:HG2	16:N:26:LEU:HD22	1.90	0.52
16:N:43:VAL:HG13	16:N:118:ILE:HD11	1.91	0.52
20:R:39:THR:O	20:R:40:ALA:C	2.51	0.52
28:Z:46:ARG:HA	37:Z:8730:HOH:O	2.10	0.52
1:0:2064:U:H4'	1:0:2653:A:OP1	2.09	0.52
1:0:2256:G:H2'	1:0:2257:G:C5'	2.40	0.52
1:0:2443:C:H3'	37:0:3275:HOH:O	2.09	0.52
1:0:2481:G:C3'	1:0:2482:G:H5''	2.40	0.52
3:A:103:VAL:O	3:A:105:VAL:HG23	2.10	0.52
4:B:75:GLU:C	4:B:77:PRO:HD3	2.35	0.52
14:L:142:LEU:HG	14:L:146:GLY:HA3	1.92	0.52
18:P:127:GLY:HA3	37:P:152:HOH:O	2.08	0.52
1:0:685:C:O2	1:0:748:C:H4'	2.09	0.51
1:0:1398:G:H2'	1:0:1399:A:C8	2.46	0.51
1:0:1428:C:O2	20:R:132:ARG:HD3	2.10	0.51
4:B:72:THR:HB	37:B:8905:HOH:O	2.09	0.51
5:C:114:ALA:HB1	5:C:223:LEU:HB3	1.91	0.51
22:T:38:ARG:HG3	22:T:38:ARG:NH1	2.25	0.51
27:Y:196:VAL:HG13	27:Y:201:GLU:HG3	1.91	0.51
1:0:2629:C:H41	3:A:206:ARG:HH21	1.56	0.51
2:9:57:A:O2'	6:D:152:PRO:HD2	2.10	0.51
3:A:39:ALA:HB3	3:A:61:GLU:OE2	2.10	0.51
3:A:84:VAL:O	3:A:98:GLU:HG3	2.10	0.51
4:B:43:GLY:HA3	4:B:76:THR:HG22	1.92	0.51
4:B:154:VAL:CG1	4:B:156:LYS:HG2	2.40	0.51
7:E:103:VAL:HG22	7:E:115:ARG:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:48:VAL:CG1	22:T:96:VAL:HG22	2.39	0.51
1:0:74:G:H1'	37:0:9872:HOH:O	2.09	0.51
1:0:100:C:C4'	22:T:16:LEU:HB2	2.39	0.51
1:0:188:C:H5''	15:M:163:LEU:HD21	1.91	0.51
1:0:396:U:OP2	31:3:38:ARG:HD2	2.10	0.51
1:0:1120:U:H6	1:0:1120:U:C5'	2.22	0.51
6:D:138:GLY:N	37:D:7597:HOH:O	2.42	0.51
6:D:140:ARG:O	6:D:144:ARG:HG2	2.11	0.51
16:N:152:GLU:OE1	16:N:152:GLU:HA	2.10	0.51
16:N:179:LEU:C	16:N:181:ASP:H	2.18	0.51
18:P:67:LYS:O	18:P:68:LYS:C	2.53	0.51
31:3:70:ARG:HD3	37:3:8868:HOH:O	2.09	0.51
1:0:138:U:H5''	1:0:139:C:OP2	2.10	0.51
1:0:2420:G:O2'	1:0:2421:G:H5'	2.10	0.51
1:0:2815:G:N7	12:J:80:LYS:NZ	2.59	0.51
3:A:53:ALA:HB3	37:A:8898:HOH:O	2.10	0.51
4:B:48:MET:N	37:B:8858:HOH:O	2.44	0.51
25:W:21:LEU:HB3	25:W:26:ILE:HG12	1.93	0.51
1:0:318:U:O2'	1:0:338:C:H2'	2.11	0.51
1:0:736:A:H2'	1:0:737:A:O4'	2.10	0.51
1:0:1703:G:H21	18:P:57:ASN:HD21	1.57	0.51
1:0:1734:C:OP1	4:B:234:ARG:HD3	2.11	0.51
1:0:2768:A:H5''	37:0:4229:HOH:O	2.11	0.51
6:D:167:GLU:C	6:D:169:THR:H	2.19	0.51
12:J:108:PRO:HG2	12:J:109:TYR:HD1	1.75	0.51
16:N:47:LEU:HD11	16:N:97:VAL:HG11	1.93	0.51
1:0:105:G:O2'	1:0:106:A:H5'	2.10	0.51
1:0:581:G:O2'	1:0:582:U:H5'	2.11	0.51
1:0:746:A:C6	17:O:65:LEU:HD13	2.46	0.51
1:0:1029:U:O2'	1:0:1273:C:OP1	2.26	0.51
1:0:1215:A:O3'	1:0:1216:G:H4'	2.11	0.51
1:0:1562:C:N4	37:0:5655:HOH:O	2.44	0.51
1:0:1973:A:H2'	1:0:1974:G:O4'	2.10	0.51
1:0:2597:U:H5''	37:0:3625:HOH:O	2.11	0.51
14:L:17:SER:C	14:L:19:LYS:N	2.68	0.51
14:L:104:ASP:O	14:L:105:TYR:CB	2.58	0.51
21:S:32:ALA:HA	21:S:36:GLU:OE1	2.10	0.51
25:W:11:VAL:O	25:W:12:ASN:HB2	2.11	0.51
31:3:65:THR:CG2	31:3:67:LEU:HG	2.39	0.51
1:0:453:A:H4'	1:0:455:A:N7	2.26	0.51
1:0:1072:G:OP2	27:Y:154:ARG:NH2	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:1313:A:H5'	27:Y:208:LYS:O	2.11	0.51
3:A:9:ARG:HG2	3:A:16:PHE:CD2	2.45	0.51
3:A:194:MET:CE	3:A:199:HIS:HB2	2.29	0.51
4:B:66:GLU:O	4:B:67:GLU:HG3	2.11	0.51
5:C:127:ARG:HD2	5:C:229:PRO:O	2.11	0.51
7:E:149:GLU:OE1	7:E:167:TYR:HA	2.11	0.51
19:Q:26:PRO:HG3	37:Q:2847:HOH:O	2.11	0.51
28:Z:11:SER:HB3	28:Z:23:ARG:HB2	1.92	0.51
37:O:3089:HOH:O	13:K:9:THR:HA	2.10	0.51
5:C:107:ARG:CZ	37:C:8666:HOH:O	2.59	0.51
7:E:20:ILE:O	7:E:30:THR:HA	2.10	0.51
11:I:127:CYS:C	11:I:129:SER:N	2.67	0.51
12:J:39:VAL:HG12	12:J:40:ASN:ND2	2.26	0.51
22:T:50:VAL:HG12	22:T:56:ALA:HA	1.93	0.51
22:T:73:HIS:HD2	22:T:88:PRO:CG	2.24	0.51
23:U:30:HIS:HD2	37:U:6215:HOH:O	1.93	0.51
1:O:243:A:H61	1:O:269:G:H1'	1.76	0.51
1:O:1439:C:OP1	30:2:41:HIS:HE1	1.93	0.51
4:B:243:ASN:HA	4:B:244:PRO:C	2.35	0.51
12:J:75:PRO:HG2	12:J:105:LEU:CD2	2.40	0.51
13:K:29:LEU:HB3	13:K:55:VAL:CG1	2.34	0.51
15:M:122:GLN:HG3	15:M:122:GLN:O	2.11	0.51
20:R:99:ALA:HB1	20:R:109:MET:HE2	1.93	0.51
24:V:12:THR:CG2	24:V:15:GLU:HG3	2.29	0.51
25:W:7:LEU:CD1	25:W:53:ALA:HB2	2.41	0.51
28:Z:20:ARG:O	28:Z:21:VAL:C	2.54	0.51
28:Z:36:ASP:HB3	28:Z:45:ASP:HB3	1.93	0.51
1:O:226:A:H1'	1:O:393:G:C5	2.46	0.51
1:O:1761:U:H5'	18:P:81:LYS:O	2.11	0.51
1:O:1882:C:H2'	1:O:1883:U:H6	1.76	0.51
4:B:310:ARG:HB3	37:B:8949:HOH:O	2.09	0.51
7:E:84:MET:HE1	7:E:148:ILE:HD12	1.93	0.51
11:I:101:LYS:O	11:I:105:GLU:HG3	2.11	0.51
13:K:65:ARG:O	13:K:66:ARG:HB2	2.11	0.51
16:N:143:ARG:HG2	16:N:172:PHE:CE2	2.45	0.51
20:R:111:ILE:HG23	20:R:145:LEU:CD1	2.40	0.51
22:T:23:VAL:O	22:T:93:THR:HG21	2.10	0.51
23:U:14:GLU:OE1	23:U:15:PRO:CD	2.59	0.51
25:W:18:GLN:O	25:W:22:GLU:HG3	2.11	0.51
25:W:107:LEU:O	25:W:112:LEU:HB2	2.11	0.51
1:O:110:C:H3'	37:O:5423:HOH:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:152:A:O2'	1:0:153:C:H5'	2.11	0.50
1:0:1266:U:H4'	27:Y:115:ARG:HH21	1.76	0.50
1:0:1439:C:O5'	1:0:1439:C:H6	1.94	0.50
1:0:2338:G:H4'	6:D:105:SER:O	2.11	0.50
3:A:100:PRO:HG2	3:A:103:VAL:HG21	1.92	0.50
6:D:146:LYS:CE	16:N:107:ASN:ND2	2.74	0.50
8:F:58:GLU:HG3	8:F:61:MET:HE2	1.93	0.50
10:H:169:GLU:OE1	10:H:169:GLU:HA	2.11	0.50
14:L:149:ARG:NH2	37:L:8890:HOH:O	2.44	0.50
15:M:61:ILE:CG2	15:M:62:VAL:N	2.73	0.50
1:0:558:C:C2'	1:0:559:U:C5'	2.89	0.50
1:0:1504:A:H5'	37:0:4218:HOH:O	2.11	0.50
1:0:2727:A:H2'	1:0:2728:C:H5'	1.93	0.50
2:9:1:U:O3'	2:9:3:A:H5'	2.11	0.50
3:A:58:VAL:O	3:A:65:ARG:HD2	2.12	0.50
4:B:88:GLU:O	4:B:88:GLU:HG3	2.11	0.50
5:C:132:ASP:O	5:C:161:ASP:HB2	2.11	0.50
5:C:159:ALA:O	5:C:160:LEU:HG	2.11	0.50
16:N:5:ARG:HG2	19:Q:18:PRO:HB3	1.92	0.50
27:Y:106:THR:HG22	27:Y:107:PRO:O	2.11	0.50
1:0:2089:A:O2'	1:0:2090:G:H5'	2.11	0.50
1:0:2248:C:H3'	37:0:5240:HOH:O	2.10	0.50
11:I:72:GLU:C	11:I:74:ILE:N	2.69	0.50
12:J:130:VAL:CG1	12:J:135:ILE:HG13	2.41	0.50
13:K:18:ILE:HG22	13:K:93:ASN:HB2	1.93	0.50
13:K:109:LEU:CD1	13:K:113:ILE:HD11	2.41	0.50
14:L:36:ASP:HB2	37:L:8839:HOH:O	2.09	0.50
14:L:57:VAL:O	14:L:57:VAL:HG12	2.11	0.50
25:W:108:ARG:HE	25:W:114:PRO:CG	2.24	0.50
26:X:73:ARG:O	26:X:85:VAL:HG13	2.11	0.50
27:Y:174:VAL:O	27:Y:177:LYS:HB2	2.12	0.50
27:Y:219:GLU:HG3	27:Y:220:GLU:H	1.76	0.50
1:0:1441:G:O2'	1:0:1442:A:H5'	2.11	0.50
1:0:1450:C:O2'	1:0:1494:A:H5'	2.11	0.50
1:0:1595:G:O2'	1:0:1596:U:H5'	2.11	0.50
1:0:1655:G:H3'	37:0:6195:HOH:O	2.11	0.50
2:9:55:U:H4'	2:9:56:A:C8	2.46	0.50
4:B:195:ARG:N	4:B:198:GLU:OE1	2.43	0.50
7:E:11:VAL:HG12	7:E:12:ASP:H	1.76	0.50
1:0:1053:G:OP1	10:H:15:PRO:HG3	2.11	0.50
1:0:1328:A:N7	1:0:1329:G:C5	2.80	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1937:U:O2'	1:0:1938:G:H5'	2.12	0.50
13:K:23:ASN:HD21	13:K:107:THR:H	1.59	0.50
24:V:3:LEU:HD23	24:V:52:ALA:HB1	1.94	0.50
27:Y:219:GLU:CG	27:Y:220:GLU:N	2.74	0.50
1:0:1025:C:H5'	25:W:23:MET:O	2.12	0.50
1:0:1166:A:OP2	1:0:1174:A:H4'	2.12	0.50
1:0:1649:G:H1'	37:0:4882:HOH:O	2.11	0.50
1:0:1783:A:O2'	1:0:1784:U:H5'	2.11	0.50
1:0:2132:C:H1'	15:M:124:GLY:HA3	1.94	0.50
2:9:28:U:H5''	16:N:40:ASN:HD21	1.77	0.50
2:9:57:A:H5'	37:9:8717:HOH:O	2.11	0.50
2:9:61:C:H2'	2:9:62:A:H8	1.77	0.50
4:B:312:ARG:HG2	4:B:313:PRO:N	2.26	0.50
4:B:313:PRO:O	4:B:314:ALA:C	2.54	0.50
6:D:21:VAL:HG23	6:D:80:ALA:HB1	1.94	0.50
6:D:144:ARG:CZ	37:D:3839:HOH:O	2.59	0.50
13:K:55:VAL:HG12	13:K:56:SER:H	1.75	0.50
14:L:68:GLU:HB2	37:L:8873:HOH:O	2.10	0.50
15:M:71:SER:O	15:M:73:ARG:NH1	2.44	0.50
24:V:19:GLU:O	24:V:22:ASP:HB2	2.12	0.50
1:0:1811:A:H2'	1:0:1812:G:H5'	1.94	0.50
37:0:9348:HOH:O	18:P:81:LYS:HG2	2.11	0.50
4:B:217:ARG:CG	4:B:257:THR:HG22	2.36	0.50
5:C:1:MET:HG2	5:C:2:GLN:NE2	2.26	0.50
26:X:75:ALA:O	26:X:83:ALA:HA	2.11	0.50
1:0:827:A:H2'	1:0:828:G:O4'	2.12	0.50
1:0:2377:U:H6	1:0:2377:U:O5'	1.94	0.50
1:0:2404:G:O5'	19:Q:68:GLY:HA3	2.12	0.50
5:C:165:ASP:O	5:C:168:ARG:HB3	2.10	0.50
6:D:94:ALA:HB3	6:D:97:GLN:NE2	2.15	0.50
7:E:16:ASP:O	7:E:17:HIS:HB2	2.11	0.50
8:F:91:VAL:CG1	8:F:92:GLY:H	2.23	0.50
14:L:145:LEU:HD23	14:L:145:LEU:O	2.11	0.50
19:Q:46:SER:O	19:Q:48:PRO:HD3	2.11	0.50
25:W:8:ARG:HB3	37:W:1427:HOH:O	2.12	0.50
25:W:125:HIS:CD2	25:W:127:GLY:H	2.29	0.50
1:0:354:A:H2'	1:0:355:C:H6	1.76	0.50
1:0:1015:C:H2'	1:0:1016:U:C6	2.47	0.50
1:0:1276:U:H3'	17:O:19:ARG:NH1	2.26	0.50
1:0:1805:G:O2'	1:0:1806:G:H5'	2.12	0.50
1:0:2320:U:H4'	1:0:2321:A:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:32:VAL:O	3:A:33:GLU:C	2.54	0.50
6:D:39:ASP:HB2	37:D:5583:HOH:O	2.12	0.50
6:D:138:GLY:O	6:D:140:ARG:N	2.45	0.50
7:E:45:ASP:OD2	7:E:46:THR:HG23	2.12	0.50
15:M:47:ASP:CG	15:M:48:LYS:N	2.69	0.50
22:T:16:LEU:O	22:T:19:ARG:HB2	2.12	0.50
22:T:41:ARG:O	22:T:42:VAL:C	2.55	0.50
23:U:13:ILE:HG12	23:U:32:CYS:HB3	1.92	0.50
1:O:383:A:H2'	1:O:384:G:O4'	2.12	0.49
1:O:969:G:H1	1:O:999:C:H42	1.60	0.49
1:O:1299:G:N7	14:L:6:ARG:NH1	2.60	0.49
1:O:1393:A:H2'	1:O:1394:C:C6	2.47	0.49
1:O:2115:U:H2'	1:O:2116:U:C6	2.47	0.49
1:O:2764:C:H2'	1:O:2765:C:H6	1.76	0.49
37:O:4720:HOH:O	15:M:14:ASN:HB3	2.12	0.49
5:C:20:ASP:O	5:C:23:GLU:HB2	2.12	0.49
10:H:73:ASN:HB2	10:H:88:MET:CE	2.42	0.49
12:J:34:GLU:HA	12:J:34:GLU:OE1	2.11	0.49
20:R:44:VAL:O	20:R:48:GLU:HG3	2.11	0.49
1:O:130:C:O2'	1:O:131:A:N7	2.45	0.49
1:O:1139:U:H2'	1:O:1140:C:C6	2.47	0.49
1:O:1470:A:OP1	15:M:93:ARG:HD2	2.12	0.49
1:O:1568:G:O2'	1:O:1569:U:H5'	2.12	0.49
1:O:2300:A:H4'	1:O:2301:A:O5'	2.12	0.49
1:O:2587:OMU:O5'	1:O:2587:OMU:H6	2.12	0.49
2:9:43:G:H5'	37:9:8611:HOH:O	2.11	0.49
3:A:120:ARG:HA	3:A:159:VAL:HG21	1.93	0.49
4:B:248:ARG:O	4:B:251:VAL:HG13	2.11	0.49
6:D:58:VAL:CG1	6:D:60:GLU:HG2	2.42	0.49
7:E:12:ASP:HA	37:E:1750:HOH:O	2.11	0.49
8:F:50:VAL:HG13	8:F:60:VAL:HG11	1.94	0.49
15:M:134:ILE:CG2	15:M:141:ILE:HD13	2.41	0.49
16:N:73:ALA:HB1	16:N:74:PRO:HD2	1.94	0.49
18:P:105:LEU:CD2	18:P:137:LEU:HD21	2.43	0.49
25:W:21:LEU:HD22	25:W:26:ILE:HD13	1.94	0.49
27:Y:172:THR:N	37:Y:8848:HOH:O	2.45	0.49
31:3:40:ARG:HD3	37:3:8856:HOH:O	2.12	0.49
1:O:470:U:O2'	29:1:16:HIS:HD2	1.94	0.49
5:C:235:PHE:HE2	5:C:243:VAL:HG21	1.76	0.49
13:K:64:MET:HE1	13:K:105:ARG:NE	2.27	0.49
14:L:144:ASP:O	14:L:147:GLU:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:28:GLN:HA	15:M:31:TRP:HB2	1.94	0.49
16:N:29:SER:OG	16:N:101:VAL:HG21	2.12	0.49
17:O:107:GLU:O	17:O:108:GLY:C	2.55	0.49
19:Q:64:GLU:HG3	19:Q:74:ASP:OD2	2.12	0.49
24:V:1:THR:HG23	24:V:2:VAL:N	2.18	0.49
28:Z:67:GLY:HA3	28:Z:73:THR:CG2	2.42	0.49
1:0:361:C:H2'	1:0:362:G:O4'	2.13	0.49
1:0:522:U:O2'	1:0:1366:C:H5'	2.12	0.49
1:0:669:G:O2'	1:0:670:G:H5'	2.12	0.49
1:0:1525:G:N2	1:0:1526:A:H2'	2.27	0.49
1:0:1768:C:H2'	1:0:1769:C:O4'	2.12	0.49
1:0:2780:C:H2'	1:0:2781:U:C6	2.48	0.49
1:0:2840:A:H3'	37:0:7417:HOH:O	2.11	0.49
6:D:164:ALA:O	6:D:165:PHE:C	2.56	0.49
16:N:112:GLY:HA2	16:N:137:ALA:HB2	1.93	0.49
24:V:55:ARG:O	24:V:59:ILE:HG12	2.12	0.49
25:W:38:THR:CG2	25:W:39:ASP:N	2.75	0.49
25:W:65:VAL:CA	25:W:68:THR:HG22	2.42	0.49
1:0:506:G:H3'	37:0:3569:HOH:O	2.11	0.49
1:0:602:A:O2'	1:0:605:C:H4'	2.11	0.49
1:0:1167:G:H4'	11:I:130:LEU:HD22	1.95	0.49
1:0:2036:C:C1'	13:K:44:LEU:HG	2.42	0.49
6:D:81:GLU:C	6:D:83:PHE:N	2.70	0.49
7:E:81:GLU:HB3	37:E:4761:HOH:O	2.12	0.49
14:L:81:VAL:O	14:L:81:VAL:HG12	2.13	0.49
16:N:127:LEU:HB2	37:N:8853:HOH:O	2.12	0.49
25:W:108:ARG:HE	25:W:114:PRO:HG3	1.76	0.49
25:W:129:LYS:HG2	37:W:1990:HOH:O	2.12	0.49
26:X:7:GLU:HG2	26:X:8:ARG:N	2.26	0.49
29:1:52:SER:HA	37:1:4248:HOH:O	2.12	0.49
1:0:545:G:H2'	1:0:546:C:O4'	2.12	0.49
1:0:1205:U:C2'	1:0:1206:U:H5'	2.40	0.49
1:0:1925:G:H5''	31:3:29:ARG:HH22	1.76	0.49
1:0:2676:C:H4'	12:J:70:PHE:HE1	1.76	0.49
1:0:2851:G:C2'	1:0:2852:A:H5'	2.42	0.49
37:0:6801:HOH:O	3:A:211:LYS:HG2	2.10	0.49
2:9:28:U:H5''	16:N:40:ASN:ND2	2.28	0.49
3:A:171:LYS:HB3	28:Z:18:TYR:HE2	1.78	0.49
4:B:138:GLY:O	4:B:139:ASP:O	2.29	0.49
6:D:39:ASP:O	6:D:43:GLU:HG3	2.13	0.49
7:E:154:ILE:HD11	7:E:157:LYS:HE2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:52:GLU:HG3	8:F:77:VAL:O	2.11	0.49
11:I:128:THR:HG22	11:I:128:THR:O	2.12	0.49
15:M:164:THR:CG2	15:M:167:GLY:N	2.73	0.49
16:N:11:ARG:NH2	37:N:8817:HOH:O	2.45	0.49
20:R:117:HIS:HA	37:R:8826:HOH:O	2.11	0.49
24:V:39:ALA:N	24:V:40:PRO:HD2	2.22	0.49
27:Y:151:SER:HB3	27:Y:154:ARG:HB3	1.94	0.49
1:0:363:C:H2'	1:0:364:U:C6	2.47	0.49
1:0:1066:U:H2'	1:0:1067:A:C8	2.47	0.49
1:0:1289:C:O2'	1:0:1290:G:H5'	2.13	0.49
1:0:1468:G:H5''	37:0:7227:HOH:O	2.11	0.49
1:0:1486:A:C4	30:2:2:LYS:HG3	2.47	0.49
1:0:1561:U:H2'	37:0:3944:HOH:O	2.11	0.49
1:0:1600:G:H4'	37:0:5444:HOH:O	2.11	0.49
1:0:1603:A:H5''	1:0:1605:G:H5'	1.93	0.49
1:0:1850:U:H2'	1:0:1851:G:C8	2.47	0.49
1:0:1972:U:H2'	1:0:1973:A:C5'	2.43	0.49
1:0:2072:G:H4'	37:0:6811:HOH:O	2.12	0.49
1:0:2507:G:H2'	1:0:2510:C:H42	1.78	0.49
3:A:192:VAL:HB	37:A:8884:HOH:O	2.11	0.49
5:C:72:LYS:HG2	5:C:77:ALA:HA	1.95	0.49
5:C:195:VAL:HA	5:C:213:ALA:O	2.13	0.49
26:X:81:GLY:O	26:X:82:GLU:HB3	2.12	0.49
1:0:303:C:H2'	1:0:304:G:O4'	2.13	0.49
1:0:525:G:H2'	1:0:526:U:O4'	2.12	0.49
1:0:894:A:C2	5:C:87:ARG:NH2	2.81	0.49
1:0:1661:A:H2'	1:0:1662:C:O4'	2.12	0.49
1:0:1825:U:O2'	1:0:1826:C:H5'	2.12	0.49
1:0:2577:A:H5'	37:0:7522:HOH:O	2.12	0.49
2:9:18:U:OP2	6:D:154:LYS:HE2	2.12	0.49
4:B:62:ARG:HA	4:B:65:MET:CE	2.43	0.49
5:C:230:GLY:N	37:C:8547:HOH:O	2.42	0.49
13:K:49:LEU:HA	13:K:73:VAL:HG12	1.93	0.49
15:M:178:LYS:NZ	37:M:8918:HOH:O	2.45	0.49
18:P:121:ASP:O	18:P:125:LYS:HG3	2.13	0.49
24:V:4:HIS:HB3	37:V:6622:HOH:O	2.13	0.49
25:W:36:PRO:HD2	25:W:41:TYR:CE1	2.48	0.49
30:2:41:HIS:CD2	30:2:43:ARG:H	2.31	0.49
1:0:343:C:O2'	1:0:344:C:H5'	2.12	0.49
1:0:445:U:H2'	1:0:446:G:H8	1.78	0.49
1:0:1496:A:H5'	1:0:1572:A:H1'	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2582:G:O3'	13:K:41:LYS:HA	2.13	0.49
37:0:4773:HOH:O	10:H:61:ARG:HG3	2.12	0.49
3:A:43:VAL:O	3:A:76:VAL:HG22	2.12	0.49
6:D:60:GLU:O	6:D:61:PHE:C	2.55	0.49
8:F:48:VAL:CG2	8:F:74:PHE:HB3	2.42	0.49
17:O:44:ASN:HA	17:O:65:LEU:O	2.13	0.49
24:V:27:LEU:CA	24:V:49:LEU:HD13	2.43	0.49
26:X:43:VAL:HG12	26:X:47:ALA:HB3	1.93	0.49
1:0:816:G:H5'	1:0:1598:A:H4'	1.94	0.49
1:0:1250:C:O2'	1:0:1251:C:H5'	2.12	0.49
1:0:1513:C:O2'	1:0:1514:C:H5'	2.12	0.49
1:0:2002:C:H2'	1:0:2003:U:H5'	1.95	0.49
3:A:199:HIS:HD2	3:A:201:PHE:HB2	1.77	0.49
5:C:27:ARG:NH2	17:O:4:ASN:ND2	2.61	0.49
13:K:132:VAL:HG11	23:U:22:VAL:HG22	1.95	0.49
14:L:65:ASP:CG	14:L:111:ALA:HB3	2.37	0.49
15:M:61:ILE:HD12	15:M:61:ILE:N	2.28	0.49
15:M:153:ASP:HB2	37:M:8910:HOH:O	2.13	0.49
17:O:50:ARG:HD2	17:O:51:TYR:CE1	2.48	0.49
18:P:109:ARG:C	18:P:111:GLU:H	2.20	0.49
20:R:129:ALA:O	20:R:130:MET:CB	2.61	0.49
24:V:39:ALA:O	24:V:41:GLU:N	2.42	0.49
25:W:46:ALA:O	25:W:49:ASN:HB2	2.13	0.49
31:3:11:CYS:HB2	31:3:20:HIS:CE1	2.48	0.49
1:0:321:A:O2'	1:0:322:G:H5'	2.12	0.48
1:0:415:A:O2'	1:0:416:G:H5'	2.13	0.48
1:0:661:G:C5	1:0:686:A:C2	3.01	0.48
1:0:1119:G:N2	1:0:1246:A:H2	2.08	0.48
2:9:73:A:H61	2:9:108:C:N4	2.08	0.48
3:A:57:ALA:HA	3:A:67:LEU:HD23	1.95	0.48
4:B:162:MET:HG3	4:B:310:ARG:NH1	2.28	0.48
5:C:132:ASP:O	5:C:133:ARG:HB2	2.12	0.48
7:E:20:ILE:CD1	7:E:40:VAL:HG11	2.37	0.48
11:I:129:SER:O	11:I:130:LEU:HD23	2.13	0.48
12:J:54:VAL:HG12	12:J:58:GLU:HG3	1.95	0.48
15:M:99:ARG:HD2	15:M:167:GLY:HA2	1.95	0.48
16:N:115:VAL:HG23	16:N:116:PHE:H	1.77	0.48
1:0:23:G:C6	1:0:24:G:N1	2.81	0.48
1:0:94:G:N2	37:0:4913:HOH:O	2.38	0.48
1:0:380:A:H2'	37:0:6998:HOH:O	2.13	0.48
1:0:485:A:N3	1:0:487:G:H5''	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:797:A:H5'	28:Z:10:ARG:N	2.27	0.48
3:A:86:ALA:HB1	3:A:92:ASN:ND2	2.29	0.48
4:B:23:THR:HG22	4:B:25:ARG:HE	1.78	0.48
5:C:5:ILE:HG23	37:C:8640:HOH:O	2.13	0.48
10:H:167:LYS:HE2	10:H:169:GLU:OE1	2.13	0.48
12:J:80:LYS:HE2	12:J:98:PHE:CZ	2.48	0.48
15:M:57:LYS:HG2	15:M:58:GLN:H	1.77	0.48
16:N:67:ALA:C	16:N:69:TYR:N	2.69	0.48
18:P:103:THR:HA	18:P:106:ARG:NH1	2.27	0.48
22:T:40:VAL:HG22	22:T:41:ARG:N	2.28	0.48
28:Z:33:MET:SD	28:Z:49:ARG:HD2	2.53	0.48
1:0:503:G:H2'	1:0:504:G:H8	1.78	0.48
1:0:539:G:H2'	1:0:540:A:C8	2.48	0.48
1:0:1377:C:H5'	1:0:1377:C:C6	2.45	0.48
1:0:2372:A:H2'	1:0:2373:U:C6	2.48	0.48
1:0:2443:C:O3'	14:L:56:LYS:HE3	2.13	0.48
1:0:2505:G:O2'	1:0:2506:A:H5'	2.14	0.48
2:9:39:U:H3'	2:9:40:C:H5''	1.94	0.48
12:J:34:GLU:O	12:J:36:VAL:HG23	2.13	0.48
18:P:3:LEU:HA	18:P:6:GLN:OE1	2.13	0.48
21:S:57:THR:CG2	21:S:58:MET:N	2.77	0.48
25:W:29:VAL:O	25:W:30:ASN:HB2	2.12	0.48
26:X:76:ARG:HG3	26:X:76:ARG:NH1	2.26	0.48
1:0:1342:C:H2'	1:0:1343:C:H5'	1.96	0.48
1:0:1762:C:H2'	1:0:1763:C:C6	2.48	0.48
1:0:2561:C:OP1	7:E:153:ARG:NH2	2.47	0.48
2:9:73:A:N6	2:9:108:C:H42	2.09	0.48
4:B:314:ALA:HB3	4:B:317:PRO:HG3	1.95	0.48
6:D:146:LYS:HZ3	16:N:107:ASN:HD21	1.56	0.48
16:N:37:ARG:NE	37:N:8830:HOH:O	2.46	0.48
26:X:10:VAL:HG11	26:X:36:HIS:HE1	1.78	0.48
26:X:86:GLU:O	26:X:87:ALA:O	2.32	0.48
1:0:371:U:H2'	1:0:372:A:H8	1.79	0.48
1:0:807:A:H2'	1:0:808:A:C8	2.49	0.48
1:0:1155:G:H2'	1:0:1156:C:C6	2.48	0.48
1:0:1297:U:H1'	37:0:3185:HOH:O	2.13	0.48
1:0:1545:C:H2'	1:0:1546:G:O4'	2.14	0.48
4:B:23:THR:HB	4:B:25:ARG:HH21	1.79	0.48
7:E:21:THR:HG23	7:E:30:THR:OG1	2.13	0.48
11:I:68:PRO:CB	11:I:69:PRO:HD2	2.42	0.48
12:J:42:GLU:O	12:J:131:THR:HG23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:76:LEU:HB3	14:L:79:ASP:OD2	2.14	0.48
16:N:93:GLN:HG2	37:N:8853:HOH:O	2.14	0.48
17:O:79:VAL:HA	37:O:6810:HOH:O	2.13	0.48
18:P:98:ILE:HD12	18:P:102:ARG:NE	2.28	0.48
29:1:5:THR:HB	29:1:6:PRO:CD	2.43	0.48
1:0:667:C:H2'	1:0:668:C:H6	1.77	0.48
1:0:1398:G:O2'	1:0:1399:A:H5'	2.13	0.48
2:9:91:C:H2'	2:9:92:G:O4'	2.14	0.48
4:B:139:ASP:CB	4:B:165:ARG:HE	2.26	0.48
5:C:109:LEU:HD12	5:C:109:LEU:O	2.13	0.48
8:F:115:VAL:O	8:F:118:LEU:N	2.47	0.48
11:I:67:VAL:HG13	11:I:68:PRO:HD2	1.94	0.48
14:L:98:GLU:C	14:L:99:GLU:HG3	2.39	0.48
1:0:682:A:H2'	1:0:683:G:O4'	2.13	0.48
1:0:1884:G:O6	3:A:190:ARG:HD2	2.13	0.48
1:0:1923:G:H4'	31:3:31:THR:O	2.13	0.48
1:0:2047:C:H5'	37:0:9623:HOH:O	2.12	0.48
1:0:2081:A:H4'	12:J:69:TYR:CE1	2.49	0.48
4:B:24:PRO:C	4:B:25:ARG:HD3	2.39	0.48
5:C:140:VAL:HG12	5:C:141:SER:N	2.27	0.48
5:C:233:THR:HG22	5:C:234:VAL:N	2.14	0.48
6:D:27:ILE:HG22	6:D:28:GLY:N	2.28	0.48
8:F:119:ARG:HD3	8:F:119:ARG:C	2.37	0.48
11:I:115:ASP:C	11:I:117:THR:N	2.69	0.48
12:J:17:CYS:HA	12:J:119:THR:O	2.14	0.48
14:L:125:PHE:CZ	14:L:140:VAL:HG13	2.49	0.48
19:Q:30:VAL:HG12	19:Q:30:VAL:O	2.14	0.48
24:V:50:ARG:HD3	37:V:2826:HOH:O	2.12	0.48
1:0:224:U:H1'	37:0:9698:HOH:O	2.14	0.48
1:0:581:G:H4'	1:0:1254:C:O2'	2.13	0.48
1:0:624:U:H5''	37:0:9327:HOH:O	2.14	0.48
1:0:1189:A:O2'	1:0:1208:C:H2'	2.14	0.48
1:0:2389:U:H4'	19:Q:53:HIS:CD2	2.49	0.48
2:9:6:C:C5'	16:N:37:ARG:NH1	2.67	0.48
4:B:41:PHE:HB3	4:B:190:MET:CE	2.43	0.48
4:B:201:ASP:CB	4:B:312:ARG:HD2	2.38	0.48
16:N:34:LEU:HD13	16:N:47:LEU:CD2	2.44	0.48
22:T:103:LEU:C	22:T:105:ASP:H	2.21	0.48
1:0:656:G:OP2	17:O:37:ARG:HD2	2.14	0.48
1:0:1165:G:H4'	1:0:1166:A:OP2	2.14	0.48
1:0:1234:U:C4	4:B:244:PRO:HB3	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:2500:C:H1'	37:O:4465:HOH:O	2.14	0.48
5:C:26:VAL:HG21	5:C:123:LEU:CD1	2.44	0.48
5:C:129:HIS:CE1	5:C:231:ARG:HA	2.49	0.48
6:D:146:LYS:NZ	16:N:107:ASN:ND2	2.53	0.48
9:G:23:ILE:HD13	9:G:67:LEU:HD23	1.96	0.48
17:O:15:LYS:O	17:O:16:SER:C	2.56	0.48
1:O:210:U:O2'	1:O:211:U:H5'	2.14	0.48
1:O:422:G:H2'	1:O:423:A:H8	1.79	0.48
1:O:835:U:H3'	37:O:9181:HOH:O	2.13	0.48
1:O:1184:C:O2'	1:O:1185:U:OP2	2.23	0.48
1:O:1205:U:C2'	1:O:1206:U:C5'	2.90	0.48
1:O:1656:A:H5'	37:O:4205:HOH:O	2.13	0.48
1:O:2266:A:OP2	15:M:90:ARG:NH2	2.47	0.48
1:O:2629:C:N4	3:A:206:ARG:HH21	2.12	0.48
1:O:2672:C:O2'	1:O:2673:U:H5'	2.14	0.48
1:O:2906:A:H5'	1:O:2907:C:O4'	2.14	0.48
37:O:4785:HOH:O	5:C:219:ASN:HB2	2.14	0.48
2:9:57:A:C8	6:D:141:VAL:HG21	2.49	0.48
3:A:35:GLY:HA3	37:A:8887:HOH:O	2.13	0.48
4:B:63:GLU:HG3	4:B:63:GLU:O	2.14	0.48
4:B:211:THR:HA	4:B:255:GLY:O	2.14	0.48
5:C:142:ASP:OD1	5:C:236:THR:HG23	2.13	0.48
8:F:105:ASP:O	8:F:109:GLU:HB2	2.13	0.48
12:J:41:ALA:N	37:J:8866:HOH:O	2.46	0.48
12:J:45:VAL:HG21	12:J:129:PHE:CD1	2.49	0.48
14:L:147:GLU:C	37:L:8856:HOH:O	2.57	0.48
15:M:54:TYR:CG	15:M:55:LYS:N	2.82	0.48
20:R:39:THR:HB	20:R:42:GLU:CD	2.39	0.48
25:W:4:LEU:CD2	25:W:54:PHE:HB3	2.41	0.48
1:O:317:A:H4'	37:O:3570:HOH:O	2.13	0.47
1:O:553:G:H2'	1:O:554:G:H5'	1.96	0.47
1:O:710:G:H5'	17:O:25:VAL:CG1	2.43	0.47
1:O:1572:A:H2'	1:O:1573:A:C8	2.49	0.47
1:O:2256:G:H2'	1:O:2257:G:H5'	1.96	0.47
2:9:114:G:H2'	2:9:115:C:C6	2.49	0.47
4:B:96:PRO:HG3	37:B:8935:HOH:O	2.14	0.47
7:E:101:GLU:HB3	7:E:117:THR:HA	1.96	0.47
8:F:91:VAL:CG1	8:F:92:GLY:N	2.75	0.47
10:H:87:LYS:HB2	10:H:87:LYS:NZ	2.29	0.47
12:J:19:MET:HE1	12:J:78:ILE:HG22	1.96	0.47
13:K:4:LEU:HD21	13:K:120:ARG:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:72:ASN:O	14:L:76:LEU:HG	2.13	0.47
18:P:7:LYS:HD3	18:P:21:VAL:CG2	2.45	0.47
18:P:83:LYS:NZ	37:P:201:HOH:O	2.47	0.47
19:Q:3:SER:HB3	37:Q:5998:HOH:O	2.13	0.47
20:R:113:HIS:HE1	20:R:144:GLU:CD	2.21	0.47
23:U:36:CYS:O	23:U:37:GLU:C	2.56	0.47
25:W:6:GLN:CB	25:W:26:ILE:HD12	2.36	0.47
1:O:1200:A:H3'	37:O:5546:HOH:O	2.14	0.47
1:O:1372:A:H3'	37:O:6959:HOH:O	2.13	0.47
1:O:2105:C:H2'	1:O:2106:C:C6	2.49	0.47
37:O:5264:HOH:O	9:G:65:THR:HG23	2.12	0.47
2:9:3:A:H2	2:9:21:G:N3	2.12	0.47
2:9:33:U:H2'	37:9:8651:HOH:O	2.12	0.47
4:B:238:ASN:ND2	4:B:240:GLY:N	2.47	0.47
5:C:150:THR:O	5:C:152:GLU:N	2.47	0.47
5:C:232:LEU:HA	37:C:8505:HOH:O	2.14	0.47
6:D:135:VAL:HG22	6:D:136:ARG:N	2.29	0.47
8:F:10:ALA:O	8:F:13:GLU:HB3	2.13	0.47
11:I:95:LEU:CD2	11:I:99:GLN:HB3	2.34	0.47
18:P:94:TRP:CZ2	18:P:98:ILE:HG13	2.49	0.47
25:W:38:THR:HG22	25:W:39:ASP:H	1.77	0.47
27:Y:110:SER:O	27:Y:111:ASP:C	2.56	0.47
1:O:1086:A:C6	25:W:11:VAL:HG11	2.48	0.47
1:O:2050:G:H5''	20:R:80:TYR:O	2.14	0.47
1:O:2072:G:C6	1:O:2533:C:H1'	2.49	0.47
1:O:2421:G:H3'	1:O:2422:U:C5'	2.39	0.47
5:C:246:ARG:NE	37:C:8633:HOH:O	2.46	0.47
6:D:153:THR:C	6:D:155:HIS:H	2.22	0.47
7:E:120:GLY:C	7:E:122:THR:H	2.21	0.47
8:F:67:ALA:C	8:F:69:GLU:H	2.22	0.47
13:K:62:PRO:CG	13:K:65:ARG:HH21	2.27	0.47
19:Q:32:GLU:HA	19:Q:71:TYR:OH	2.15	0.47
22:T:47:THR:HB	22:T:100:ASP:HB3	1.95	0.47
25:W:38:THR:HG21	37:W:5390:HOH:O	2.15	0.47
25:W:108:ARG:C	25:W:110:GLN:N	2.72	0.47
27:Y:102:LEU:HG	37:Y:8888:HOH:O	2.14	0.47
27:Y:189:ASN:ND2	27:Y:192:ASP:H	2.12	0.47
1:O:255:A:H2'	1:O:256:C:O4'	2.14	0.47
1:O:306:A:P	22:T:38:ARG:HH21	2.37	0.47
1:O:466:A:H2'	1:O:467:G:O4'	2.14	0.47
1:O:512:G:O3'	1:O:513:A:H8	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:711:G:C2	1:0:718:C:C2	3.02	0.47
1:0:1441:G:C5'	20:R:130:MET:HE3	2.44	0.47
1:0:1909:A:N1	1:0:2128:G:H1'	2.30	0.47
2:9:55:U:H4'	2:9:56:A:H8	1.80	0.47
3:A:217:ARG:CG	3:A:217:ARG:NH1	2.76	0.47
4:B:57:GLU:O	4:B:63:GLU:HB3	2.14	0.47
4:B:277:GLU:N	4:B:278:PRO:HD2	2.29	0.47
4:B:279:THR:HG22	4:B:280:VAL:N	2.29	0.47
7:E:137:ASP:O	7:E:141:VAL:HG23	2.15	0.47
10:H:139:ALA:HB3	37:H:232:HOH:O	2.15	0.47
12:J:108:PRO:HG2	12:J:109:TYR:CD1	2.49	0.47
17:O:47:ARG:HA	17:O:50:ARG:NH1	2.29	0.47
18:P:87:ARG:HA	37:P:188:HOH:O	2.13	0.47
21:S:39:ASP:O	21:S:40:ALA:C	2.57	0.47
25:W:69:ARG:NH2	25:W:119:HIS:HB2	2.28	0.47
26:X:88:GLU:OE1	26:X:88:GLU:O	2.32	0.47
1:0:656:G:H4'	37:C:8561:HOH:O	2.14	0.47
1:0:1167:G:H2'	1:0:1168:C:C6	2.49	0.47
1:0:1185:U:O2'	1:0:1186:C:H5'	2.15	0.47
1:0:1878:G:O2'	1:0:1879:U:C6	2.64	0.47
1:0:2598:U:O2	1:0:2600:A:H8	1.97	0.47
1:0:2717:C:O2'	1:0:2718:C:H5''	2.15	0.47
3:A:206:ARG:HH12	3:A:208:HIS:CE1	2.33	0.47
6:D:12:GLU:HB3	37:D:3359:HOH:O	2.14	0.47
10:H:68:SER:O	10:H:69:ARG:C	2.57	0.47
11:I:102:GLN:HA	11:I:105:GLU:OE2	2.15	0.47
16:N:110:THR:HB	16:N:113:SER:OG	2.15	0.47
25:W:73:LEU:HD12	25:W:73:LEU:HA	1.70	0.47
31:3:69:TYR:CZ	31:3:80:ARG:HD2	2.50	0.47
1:0:506:G:N2	1:0:509:A:H5'	2.26	0.47
1:0:675:U:H2'	1:0:676:C:H5'	1.96	0.47
1:0:1388:U:H2'	1:0:1389:G:O4'	2.14	0.47
1:0:2381:C:H2'	1:0:2382:A:H8	1.78	0.47
2:9:41:C:H5''	6:D:48:MET:HE2	1.97	0.47
4:B:122:ASP:O	4:B:123:ALA:C	2.57	0.47
6:D:58:VAL:HG12	6:D:60:GLU:HG2	1.97	0.47
6:D:163:VAL:O	6:D:167:GLU:HB2	2.15	0.47
8:F:100:ASP:O	8:F:101:ALA:O	2.32	0.47
10:H:43:ALA:HB1	10:H:140:TYR:CE2	2.49	0.47
11:I:94:ASP:O	11:I:95:LEU:HG	2.14	0.47
13:K:87:ARG:NE	37:K:4854:HOH:O	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:59:GLY:HA3	15:M:141:ILE:CD1	2.45	0.47
16:N:61:ALA:HB3	16:N:88:ALA:HB2	1.96	0.47
16:N:179:LEU:HD23	16:N:184:ILE:CD1	2.45	0.47
27:Y:108:ASP:OD1	27:Y:108:ASP:N	2.48	0.47
27:Y:154:ARG:NH1	27:Y:155:ARG:HG3	2.30	0.47
1:0:113:A:OP2	1:0:114:A:H2'	2.15	0.47
1:0:212:A:O4'	1:0:214:U:C6	2.68	0.47
1:0:682:A:H5''	37:0:3492:HOH:O	2.15	0.47
1:0:695:C:O2'	1:0:696:C:H5'	2.14	0.47
1:0:1189:A:H1'	1:0:1209:C:H1'	1.97	0.47
1:0:1485:A:H4'	37:0:3088:HOH:O	2.14	0.47
1:0:1486:A:C5	30:2:2:LYS:HG3	2.49	0.47
1:0:1798:C:C4'	18:P:66:GLN:HG2	2.45	0.47
1:0:2453:G:H4'	14:L:50:GLY:C	2.39	0.47
1:0:2656:G:C2'	1:0:2657:G:H5'	2.45	0.47
1:0:2699:A:H2'	1:0:2700:G:O4'	2.15	0.47
5:C:55:ARG:HB2	37:C:8510:HOH:O	2.14	0.47
5:C:104:ASP:O	5:C:108:GLN:HG3	2.14	0.47
10:H:41:LYS:HD3	10:H:46:TYR:CZ	2.50	0.47
11:I:69:PRO:HG2	11:I:72:GLU:HB2	1.97	0.47
16:N:115:VAL:HG23	16:N:116:PHE:N	2.30	0.47
22:T:24:ARG:HG2	22:T:24:ARG:NH1	2.30	0.47
25:W:140:LYS:C	25:W:141:HIS:HD2	2.23	0.47
31:3:3:MET:O	31:3:90:PHE:HA	2.14	0.47
1:0:11:A:H5'	1:0:12:U:OP2	2.15	0.47
1:0:292:G:H2'	1:0:358:G:N2	2.29	0.47
1:0:2781:U:C2'	1:0:2782:G:H5'	2.44	0.47
37:0:3634:HOH:O	15:M:48:LYS:NZ	2.44	0.47
37:0:9363:HOH:O	25:W:119:HIS:HE1	1.96	0.47
4:B:41:PHE:HA	4:B:79:MET:CE	2.45	0.47
4:B:62:ARG:NH2	4:B:66:GLU:O	2.47	0.47
4:B:79:MET:C	4:B:80:ARG:HG3	2.40	0.47
6:D:23:VAL:CG2	6:D:73:VAL:HB	2.44	0.47
6:D:44:ILE:O	6:D:44:ILE:HG23	2.15	0.47
10:H:48:VAL:HA	10:H:170:ARG:O	2.15	0.47
12:J:39:VAL:HG11	12:J:107:ASN:HB2	1.97	0.47
14:L:89:PHE:CD1	14:L:89:PHE:N	2.82	0.47
15:M:69:LYS:HG3	15:M:126:GLN:CA	2.45	0.47
15:M:99:ARG:HG2	15:M:99:ARG:HH11	1.80	0.47
17:O:14:LEU:HA	17:O:102:ILE:HD11	1.96	0.47
18:P:18:LYS:O	18:P:21:VAL:HG22	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:111:ILE:HG23	20:R:145:LEU:HD11	1.95	0.47
21:S:52:VAL:CG2	21:S:66:VAL:HG13	2.44	0.47
1:0:183:A:O2'	1:0:184:G:H5'	2.15	0.47
1:0:1685:A:H4'	1:0:1686:C:OP2	2.15	0.47
1:0:1882:C:H2'	1:0:1883:U:C6	2.49	0.47
1:0:2003:U:H4'	1:0:2004:U:H5	1.79	0.47
1:0:2681:A:H4'	1:0:2682:C:C5'	2.45	0.47
1:0:2842:G:H5'	20:R:68:HIS:O	2.15	0.47
37:0:3490:HOH:O	7:E:143:GLN:HG2	2.15	0.47
4:B:27:ASN:HD22	4:B:27:ASN:N	2.11	0.47
4:B:178:ALA:O	4:B:179:LEU:C	2.57	0.47
4:B:258:GLY:H	4:B:260:HIS:CE1	2.33	0.47
7:E:107:PHE:CE1	7:E:152:THR:HB	2.50	0.47
14:L:143:THR:CG2	14:L:144:ASP:N	2.78	0.47
15:M:57:LYS:HZ3	15:M:144:ASP:HB2	1.79	0.47
18:P:38:GLU:HA	18:P:41:ARG:HH11	1.80	0.47
22:T:70:ALA:O	22:T:71:VAL:HG23	2.14	0.47
25:W:108:ARG:C	25:W:110:GLN:H	2.23	0.47
25:W:131:PRO:HG2	25:W:134:GLU:HB2	1.96	0.47
28:Z:28:GLU:O	28:Z:29:ILE:C	2.58	0.47
1:0:157:G:H3'	37:0:3755:HOH:O	2.15	0.47
1:0:710:G:O2'	1:0:711:G:H5'	2.14	0.47
1:0:1930:A:H2'	1:0:1931:A:C8	2.50	0.47
1:0:2503:A:H2	1:0:2517:A:N7	2.13	0.47
2:9:51:A:H5'	16:N:160:SER:HB3	1.96	0.47
3:A:36:ASP:O	3:A:37:VAL:C	2.58	0.47
4:B:53:LEU:HD11	4:B:327:VAL:HG22	1.97	0.47
5:C:21:VAL:C	5:C:23:GLU:N	2.73	0.47
6:D:64:ARG:CD	6:D:67:ASP:HB3	2.45	0.47
6:D:84:LEU:HA	6:D:87:ALA:HB3	1.97	0.47
10:H:86:TYR:C	10:H:86:TYR:CD1	2.93	0.47
14:L:54:PRO:HG2	14:L:57:VAL:CG2	2.44	0.47
14:L:82:ALA:O	14:L:83:GLU:C	2.58	0.47
15:M:47:ASP:CG	15:M:48:LYS:H	2.22	0.47
23:U:13:ILE:HG12	23:U:32:CYS:CB	2.45	0.47
24:V:1:THR:C	24:V:3:LEU:H	2.23	0.47
1:0:694:A:C2'	1:0:695:C:H5'	2.45	0.46
1:0:1186:C:H2'	1:0:1187:U:O4'	2.15	0.46
1:0:1477:C:C5'	1:0:1868:G:H5''	2.45	0.46
1:0:1735:C:H5'	4:B:235:ARG:HH21	1.79	0.46
1:0:1883:U:O2'	1:0:1884:G:H5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2436:U:H5'	31:3:68:LYS:HE2	1.96	0.46
1:0:2570:G:H8	37:0:4714:HOH:O	1.98	0.46
4:B:56:ASP:HB3	4:B:322:ARG:HE	1.80	0.46
6:D:59:GLY:O	6:D:61:PHE:N	2.49	0.46
7:E:158:ASP:OD1	7:E:160:ARG:N	2.49	0.46
11:I:98:ASP:HA	11:I:101:LYS:HG3	1.97	0.46
17:O:26:TRP:N	37:O:3062:HOH:O	2.48	0.46
20:R:33:ARG:HH11	20:R:60:LYS:HG3	1.79	0.46
23:U:6:CYS:SG	23:U:8:TYR:HB3	2.55	0.46
26:X:43:VAL:CG1	26:X:44:ASP:H	2.25	0.46
30:2:41:HIS:HB3	30:2:44:ARG:HB2	1.97	0.46
1:0:742:G:O2'	1:0:743:G:H5'	2.15	0.46
1:0:1587:U:H2'	1:0:1588:G:O4'	2.14	0.46
1:0:2067:A:H2'	1:0:2068:G:O4'	2.15	0.46
1:0:2730:G:O2'	1:0:2731:G:H5'	2.16	0.46
1:0:2781:U:O2'	1:0:2782:G:H5'	2.15	0.46
4:B:214:PRO:HD2	37:B:8820:HOH:O	2.15	0.46
10:H:31:ILE:HA	10:H:66:GLU:OE1	2.15	0.46
10:H:49:GLN:O	10:H:169:GLU:HB2	2.15	0.46
10:H:98:LEU:O	10:H:124:VAL:HG22	2.15	0.46
18:P:138:GLU:C	18:P:140:TYR:N	2.73	0.46
21:S:45:TYR:CE2	21:S:81:ILE:HD13	2.47	0.46
25:W:26:ILE:O	25:W:26:ILE:CG1	2.63	0.46
28:Z:30:GLU:HA	28:Z:33:MET:HE2	1.98	0.46
28:Z:60:CYS:SG	28:Z:62:TYR:HB2	2.55	0.46
30:2:36:ASN:HB3	30:2:39:ARG:HE	1.80	0.46
1:0:444:C:H1'	37:0:7106:HOH:O	2.14	0.46
1:0:776:A:OP1	29:1:28:HIS:HE1	1.98	0.46
1:0:825:U:H5'	1:0:826:U:OP1	2.16	0.46
1:0:843:A:C2	1:0:846:A:C8	3.03	0.46
1:0:1070:A:O5'	1:0:1070:A:H8	1.99	0.46
1:0:1603:A:C5'	1:0:1605:G:H5'	2.45	0.46
8:F:22:VAL:CG2	8:F:104:ALA:HB2	2.45	0.46
10:H:50:ILE:HB	37:H:232:HOH:O	2.14	0.46
13:K:115:ARG:HG3	13:K:116:GLU:N	2.30	0.46
14:L:55:GLN:HA	14:L:58:GLN:NE2	2.25	0.46
14:L:73:VAL:HG11	14:L:118:LEU:HD21	1.97	0.46
21:S:8:PRO:HD2	24:V:32:ALA:HA	1.96	0.46
21:S:56:ASN:O	30:2:8:LYS:NZ	2.47	0.46
22:T:49:GLU:HG3	22:T:97:ARG:HB3	1.98	0.46
23:U:6:CYS:C	23:U:8:TYR:N	2.74	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Z:13:ARG:NH1	28:Z:14:PHE:CZ	2.83	0.46
29:1:21:ARG:HD2	29:1:37:CYS:SG	2.54	0.46
1:0:952:G:H4'	37:0:6512:HOH:O	2.16	0.46
37:0:3833:HOH:O	5:C:149:LYS:HE3	2.14	0.46
4:B:30:PRO:HG2	4:B:313:PRO:HD2	1.96	0.46
7:E:11:VAL:CG1	7:E:12:ASP:N	2.77	0.46
7:E:93:MET:HE1	7:E:165:GLY:H	1.80	0.46
7:E:156:ASP:OD1	7:E:156:ASP:N	2.47	0.46
8:F:13:GLU:OE2	8:F:78:GLU:HG2	2.15	0.46
13:K:41:LYS:O	13:K:42:ASN:HB2	2.15	0.46
13:K:113:ILE:HD12	13:K:128:ALA:CB	2.45	0.46
16:N:58:LEU:HD12	16:N:58:LEU:H	1.80	0.46
19:Q:11:ARG:HD2	37:Q:5620:HOH:O	2.15	0.46
22:T:50:VAL:HG11	22:T:55:PHE:HB2	1.96	0.46
1:0:338:C:H4'	5:C:174:ILE:HD11	1.96	0.46
1:0:348:C:H2'	1:0:349:U:H6	1.80	0.46
1:0:407:A:H2'	1:0:408:A:C8	2.51	0.46
1:0:816:G:C6	1:0:817:G:N1	2.83	0.46
1:0:1613:C:H2'	1:0:1614:G:O4'	2.15	0.46
1:0:2324:G:H4'	1:0:2418:G:O2'	2.15	0.46
3:A:9:ARG:O	3:A:11:ARG:N	2.49	0.46
3:A:171:LYS:HB3	28:Z:18:TYR:CE2	2.50	0.46
4:B:248:ARG:O	4:B:251:VAL:CG1	2.64	0.46
5:C:129:HIS:HD2	5:C:165:ASP:OD2	1.98	0.46
6:D:35:ALA:C	6:D:37:ALA:H	2.22	0.46
6:D:92:GLU:HB2	37:D:3862:HOH:O	2.16	0.46
7:E:9:GLU:HG3	7:E:10:ASP:N	2.29	0.46
14:L:35:ARG:HB2	14:L:43:HIS:CD2	2.51	0.46
20:R:100:ASP:C	20:R:102:GLN:N	2.74	0.46
24:V:12:THR:H	24:V:15:GLU:HB2	1.81	0.46
1:0:130:C:H5'	37:0:5015:HOH:O	2.15	0.46
1:0:1561:U:C5'	37:0:7201:HOH:O	2.61	0.46
1:0:2668:G:H2'	1:0:2669:U:C6	2.51	0.46
1:0:2911:C:H2'	1:0:2912:C:H6	1.81	0.46
2:9:8:G:O6	16:N:11:ARG:NH1	2.47	0.46
3:A:1:GLY:N	37:A:8900:HOH:O	2.48	0.46
4:B:205:VAL:N	37:B:8954:HOH:O	2.49	0.46
8:F:66:LEU:O	8:F:69:GLU:HG2	2.15	0.46
15:M:31:TRP:C	15:M:33:ASN:H	2.24	0.46
16:N:42:HIS:HA	16:N:75:THR:O	2.16	0.46
16:N:98:GLU:O	16:N:127:LEU:HD12	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:4:LEU:HD23	25:W:54:PHE:CB	2.41	0.46
26:X:30:MET:CE	26:X:58:ALA:HB3	2.44	0.46
1:O:35:U:H5'	5:C:47:GLY:O	2.16	0.46
1:O:612:U:H2'	1:O:613:C:C6	2.51	0.46
1:O:727:G:H3'	1:O:728:C:H6	1.81	0.46
1:O:1197:G:N2	1:O:1202:A:H62	2.12	0.46
1:O:1268:C:H2'	1:O:1269:G:C8	2.50	0.46
1:O:1353:C:P	37:O:4479:HOH:O	2.74	0.46
1:O:2787:C:H2'	1:O:2788:A:O4'	2.14	0.46
1:O:2894:C:O2'	1:O:2895:C:H5'	2.15	0.46
3:A:223:ARG:O	3:A:223:ARG:HG2	2.14	0.46
5:C:141:SER:C	5:C:143:ASP:H	2.23	0.46
12:J:131:THR:HB	12:J:134:GLU:OE1	2.15	0.46
17:O:78:ALA:C	17:O:98:LEU:HD13	2.41	0.46
19:Q:28:ARG:HD3	19:Q:92:ARG:NH1	2.30	0.46
25:W:6:GLN:HG2	25:W:29:VAL:HA	1.97	0.46
25:W:26:ILE:O	25:W:26:ILE:HG13	2.16	0.46
1:O:625:U:H5''	1:O:1044:C:N4	2.31	0.46
1:O:812:A:H1'	37:O:3756:HOH:O	2.16	0.46
1:O:858:U:H2'	1:O:859:C:C6	2.50	0.46
1:O:1072:G:P	27:Y:154:ARG:NH2	2.88	0.46
1:O:1175:G:H4'	37:O:6633:HOH:O	2.16	0.46
1:O:1829:A:H2'	1:O:1830:C:H5'	1.98	0.46
1:O:1878:G:O2'	1:O:1879:U:P	2.74	0.46
1:O:2878:U:H2'	1:O:2879:A:O4'	2.15	0.46
4:B:79:MET:O	4:B:80:ARG:HG3	2.15	0.46
6:D:10:PHE:CG	6:D:11:HIS:N	2.83	0.46
6:D:103:ASN:ND2	6:D:134:LEU:H	2.13	0.46
10:H:80:LEU:HD12	10:H:86:TYR:CD2	2.51	0.46
14:L:123:ASP:OD1	14:L:145:LEU:HB3	2.16	0.46
19:Q:25:PRO:HA	19:Q:26:PRO:HD3	1.84	0.46
22:T:101:LEU:CD1	22:T:112:LEU:HD11	2.45	0.46
25:W:13:MET:HE1	25:W:21:LEU:CD1	2.44	0.46
1:O:1245:C:O5'	1:O:1245:C:H6	1.98	0.46
1:O:1334:C:H2'	1:O:1335:C:C6	2.51	0.46
3:A:9:ARG:O	3:A:10:GLY:C	2.59	0.46
3:A:173:GLY:O	3:A:176:HIS:HB3	2.16	0.46
9:G:20:VAL:O	9:G:24:VAL:HG23	2.16	0.46
11:I:72:GLU:C	11:I:74:ILE:H	2.24	0.46
12:J:84:ARG:HB2	12:J:98:PHE:CE1	2.51	0.46
18:P:105:LEU:HD21	18:P:137:LEU:HD21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:41:ARG:HG2	22:T:41:ARG:HH11	1.80	0.46
25:W:80:ASP:HB2	37:W:3312:HOH:O	2.16	0.46
31:3:7:PHE:CD1	31:3:7:PHE:C	2.93	0.46
1:0:29:C:O2'	1:0:30:U:H5'	2.16	0.46
1:0:247:A:H2'	37:0:3722:HOH:O	2.16	0.46
1:0:926:A:O2'	14:L:41:HIS:CD2	2.68	0.46
1:0:945:U:O2'	25:W:43:GLY:HA3	2.16	0.46
1:0:1855:G:O6	3:A:142:SER:HB3	2.16	0.46
1:0:2442:G:H2'	37:0:9007:HOH:O	2.15	0.46
37:0:3554:HOH:O	22:T:9:LYS:CD	2.63	0.46
2:9:1:U:C4'	2:9:3:A:OP1	2.64	0.46
2:9:44:A:H1'	6:D:76:ARG:NH2	2.31	0.46
4:B:16:ARG:NH2	37:B:8854:HOH:O	2.32	0.46
4:B:115:VAL:HA	4:B:116:PRO:HD3	1.87	0.46
5:C:135:GLU:O	5:C:136:VAL:HB	2.15	0.46
6:D:24:HIS:HB2	6:D:72:LYS:HB3	1.98	0.46
10:H:73:ASN:HB2	10:H:88:MET:HE2	1.97	0.46
12:J:126:ASN:O	12:J:129:PHE:HE2	1.99	0.46
14:L:26:HIS:HB2	37:L:8812:HOH:O	2.16	0.46
18:P:59:ARG:NH2	18:P:66:GLN:NE2	2.57	0.46
21:S:50:GLU:HG2	21:S:69:SER:HA	1.99	0.46
22:T:29:ALA:N	37:T:5241:HOH:O	2.48	0.46
25:W:13:MET:CE	25:W:17:ILE:HG22	2.44	0.46
1:0:97:G:N1	22:T:107:LYS:HG3	2.31	0.45
1:0:558:C:C2'	1:0:559:U:H5''	2.45	0.45
1:0:611:U:H2'	1:0:612:U:C6	2.51	0.45
1:0:652:G:H5''	37:0:9812:HOH:O	2.16	0.45
1:0:1461:U:H2'	1:0:1462:C:C6	2.51	0.45
1:0:1553:C:H2'	1:0:1554:C:H6	1.81	0.45
1:0:2032:U:H2'	1:0:2033:G:C5'	2.46	0.45
1:0:2241:C:H2'	1:0:2242:U:C6	2.51	0.45
1:0:2314:G:H2'	1:0:2315:C:H5'	1.97	0.45
1:0:2526:C:C2'	1:0:2527:U:H5'	2.46	0.45
5:C:21:VAL:HG23	5:C:22:PHE:HD1	1.79	0.45
5:C:149:LYS:HB2	5:C:152:GLU:HG3	1.98	0.45
6:D:95:THR:OG1	6:D:174:VAL:HA	2.16	0.45
7:E:84:MET:HB2	7:E:131:LEU:HB2	1.98	0.45
16:N:70:GLY:O	16:N:71:TRP:C	2.57	0.45
16:N:73:ALA:N	37:N:8863:HOH:O	2.46	0.45
16:N:77:ASN:OD1	16:N:79:PRO:HD2	2.16	0.45
24:V:58:THR:O	24:V:62:GLU:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:13:MET:HE2	25:W:18:GLN:N	2.30	0.45
29:1:37:CYS:SG	29:1:39:PHE:HB2	2.56	0.45
1:0:317:A:OP1	22:T:52:ARG:O	2.34	0.45
1:0:470:U:O2'	29:1:16:HIS:CD2	2.69	0.45
1:0:1159:G:P	37:0:4097:HOH:O	2.74	0.45
37:0:9753:HOH:O	26:X:23:HIS:HD2	1.98	0.45
3:A:36:ASP:CG	3:A:85:SER:H	2.25	0.45
3:A:77:GLY:O	3:A:78:ASP:C	2.60	0.45
4:B:148:PRO:HD2	37:B:8881:HOH:O	2.16	0.45
5:C:16:VAL:CG1	5:C:17:ASP:H	2.27	0.45
10:H:91:ARG:H	10:H:91:ARG:HG2	1.64	0.45
11:I:108:HIS:H	11:I:109:PRO:HD2	1.81	0.45
11:I:125:GLY:HA3	37:I:3512:HOH:O	2.15	0.45
16:N:5:ARG:HB2	37:N:8854:HOH:O	2.15	0.45
19:Q:72:LYS:HG2	19:Q:85:ILE:HD13	1.98	0.45
22:T:9:LYS:CE	22:T:13:ARG:NH1	2.79	0.45
31:3:18:GLN:HG3	37:3:8861:HOH:O	2.16	0.45
1:0:290:C:H2'	1:0:291:C:O4'	2.15	0.45
1:0:920:C:H5'	1:0:921:G:C4	2.51	0.45
1:0:958:G:H2'	1:0:959:C:C6	2.51	0.45
1:0:2053:G:H4'	20:R:136:TRP:CD2	2.51	0.45
1:0:2326:C:H4'	1:0:2412:G:H4'	1.98	0.45
3:A:235:ARG:HD3	37:A:8833:HOH:O	2.15	0.45
4:B:5:ARG:HD2	4:B:8:LYS:HZ1	1.80	0.45
6:D:40:ILE:HG23	37:D:5583:HOH:O	2.15	0.45
6:D:64:ARG:O	6:D:67:ASP:OD1	2.34	0.45
11:I:95:LEU:HD22	11:I:99:GLN:CB	2.35	0.45
11:I:126:THR:C	37:I:7439:HOH:O	2.59	0.45
15:M:42:ARG:HA	15:M:43:PRO:HD3	1.81	0.45
18:P:109:ARG:NH1	18:P:119:TYR:CE2	2.84	0.45
22:T:50:VAL:HG11	37:T:6384:HOH:O	2.16	0.45
25:W:76:ASP:O	25:W:77:ALA:O	2.35	0.45
30:2:20:ARG:CG	30:2:20:ARG:NH1	2.72	0.45
1:0:1515:A:H2'	1:0:1516:U:C6	2.51	0.45
1:0:1940:C:H4'	37:0:7117:HOH:O	2.14	0.45
1:0:2246:U:N3	1:0:2256:G:C2	2.85	0.45
4:B:280:VAL:CG1	4:B:281:ASP:N	2.78	0.45
5:C:16:VAL:CG1	5:C:17:ASP:N	2.80	0.45
7:E:14:GLU:HG2	7:E:15:GLN:N	2.31	0.45
7:E:84:MET:HE1	7:E:148:ILE:HD13	1.98	0.45
8:F:58:GLU:OE2	15:M:20:LEU:HD13	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:63:ILE:HB	8:F:64:PRO:CD	2.42	0.45
19:Q:25:PRO:HB2	37:Q:4350:HOH:O	2.17	0.45
21:S:6:LYS:HB2	21:S:27:ALA:O	2.14	0.45
22:T:9:LYS:NZ	22:T:13:ARG:NH1	2.64	0.45
27:Y:97:LEU:CD2	27:Y:235:GLU:HG3	2.46	0.45
28:Z:25:ARG:O	28:Z:29:ILE:HG13	2.17	0.45
1:O:23:G:H1'	1:O:520:A:N6	2.32	0.45
1:O:80:A:H5''	22:T:41:ARG:CZ	2.47	0.45
1:O:903:U:O4	14:L:18:HIS:HB2	2.17	0.45
1:O:1163:G:H5'	11:I:110:ASP:O	2.17	0.45
1:O:1855:G:H4'	1:O:1856:C:O5'	2.16	0.45
1:O:2437:A:H2'	1:O:2438:G:C8	2.51	0.45
1:O:2541:U:H5'	1:O:2611:G:O6	2.16	0.45
1:O:2543:G:H2'	1:O:2544:G:O4'	2.16	0.45
7:E:23:GLU:HG2	7:E:28:SER:HB3	1.99	0.45
10:H:149:VAL:HG21	37:H:232:HOH:O	2.16	0.45
13:K:110:LYS:O	13:K:111:GLY:O	2.34	0.45
16:N:175:LEU:HD12	16:N:175:LEU:HA	1.81	0.45
21:S:25:GLN:HG2	21:S:65:VAL:HG22	1.98	0.45
22:T:52:ARG:C	22:T:56:ALA:HB2	2.42	0.45
27:Y:99:ALA:HB2	27:Y:233:TYR:CE2	2.51	0.45
30:2:21:VAL:O	30:2:22:PRO:C	2.58	0.45
1:O:394:G:H1	15:M:181:GLU:CD	2.24	0.45
1:O:395:A:H5''	37:O:3721:HOH:O	2.17	0.45
1:O:1067:A:H5'	37:O:4151:HOH:O	2.15	0.45
1:O:1127:C:C5	1:O:1128:U:C4	3.05	0.45
1:O:1894:C:C2	1:O:1939:U:C4	3.04	0.45
1:O:2084:C:H2'	1:O:2085:A:H8	1.82	0.45
1:O:2506:A:O2'	1:O:2507:G:C8	2.56	0.45
1:O:2904:U:H4'	26:X:8:ARG:HH12	1.80	0.45
3:A:30:ARG:HE	3:A:30:ARG:HB3	1.55	0.45
4:B:148:PRO:HB2	4:B:156:LYS:O	2.16	0.45
6:D:10:PHE:HA	37:D:7345:HOH:O	2.17	0.45
8:F:4:VAL:HA	8:F:76:PHE:CE1	2.51	0.45
10:H:65:LEU:H	10:H:65:LEU:HD22	1.82	0.45
11:I:85:GLY:C	11:I:86:GLU:HG3	2.41	0.45
11:I:86:GLU:O	11:I:89:GLU:HB2	2.16	0.45
11:I:87:PRO:HD3	37:I:6825:HOH:O	2.16	0.45
15:M:74:LYS:HE2	37:M:8928:HOH:O	2.16	0.45
25:W:21:LEU:HD21	25:W:48:VAL:HG13	1.96	0.45
27:Y:143:TRP:C	37:Y:8921:HOH:O	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1173:A:H2	37:0:6065:HOH:O	2.00	0.45
1:0:2897:C:O2'	1:0:2898:G:H5'	2.17	0.45
5:C:88:SER:O	5:C:91:PRO:HD3	2.17	0.45
6:D:49:PRO:HA	6:D:73:VAL:HG22	1.99	0.45
6:D:162:ALA:C	6:D:164:ALA:N	2.73	0.45
10:H:48:VAL:HG21	10:H:143:VAL:HA	1.99	0.45
10:H:122:LYS:HB2	10:H:122:LYS:HE3	1.81	0.45
13:K:23:ASN:HD21	13:K:107:THR:HB	1.81	0.45
17:O:66:GLY:HA3	17:O:84:THR:HG22	1.97	0.45
18:P:67:LYS:O	18:P:70:ALA:N	2.50	0.45
25:W:132:VAL:HG23	25:W:138:LEU:O	2.17	0.45
27:Y:163:THR:HB	37:Y:8908:HOH:O	2.16	0.45
1:0:338:C:H4'	5:C:174:ILE:HD12	1.99	0.45
1:0:344:C:H2'	1:0:345:G:O4'	2.17	0.45
1:0:1181:A:H2'	1:0:1182:C:C5'	2.43	0.45
1:0:1500:U:OP2	18:P:41:ARG:NH2	2.49	0.45
1:0:1517:C:H2'	1:0:1518:A:C8	2.51	0.45
1:0:1539:U:O2'	1:0:1540:G:H5'	2.17	0.45
1:0:1735:C:H5'	4:B:235:ARG:NH2	2.32	0.45
1:0:2239:C:H6	37:0:6451:HOH:O	1.99	0.45
37:0:3035:HOH:O	14:L:22:ARG:HG2	2.16	0.45
37:0:3324:HOH:O	21:S:13:LYS:HE2	2.16	0.45
12:J:99:GLU:HA	37:J:8876:HOH:O	2.15	0.45
1:0:10:U:O4	1:0:532:A:OP2	2.33	0.45
1:0:603:A:H4'	1:0:604:G:O5'	2.16	0.45
1:0:745:G:H5''	1:0:746:A:OP1	2.16	0.45
1:0:1942:A:O3'	3:A:213:LYS:HE2	2.16	0.45
1:0:2488:A:H2	37:0:7044:HOH:O	2.00	0.45
1:0:2587:OMU:H2'	1:0:2589:U:H5''	1.98	0.45
1:0:2787:C:H5	37:0:4434:HOH:O	1.99	0.45
37:0:4033:HOH:O	20:R:17:MET:HE3	2.16	0.45
37:0:9331:HOH:O	20:R:139:PRO:HD3	2.15	0.45
2:9:95:C:O2'	2:9:96:C:H5'	2.17	0.45
3:A:145:MET:HG2	37:A:8828:HOH:O	2.15	0.45
4:B:141:ARG:HB3	4:B:164:THR:O	2.16	0.45
5:C:139:VAL:CG1	37:C:8657:HOH:O	2.63	0.45
5:C:180:SER:N	37:C:8579:HOH:O	2.47	0.45
6:D:128:LEU:O	6:D:128:LEU:HD23	2.17	0.45
11:I:124:VAL:O	11:I:124:VAL:HG12	2.17	0.45
13:K:75:ARG:HH21	13:K:94:ALA:HB2	1.82	0.45
13:K:132:VAL:HG21	23:U:22:VAL:HG11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:115:VAL:O	16:N:118:ILE:HB	2.16	0.45
16:N:139:TRP:CZ2	16:N:176:ARG:NH1	2.85	0.45
17:O:32:ARG:HG2	17:O:32:ARG:NH1	2.32	0.45
19:Q:75:ILE:CD1	19:Q:84:ILE:HD11	2.47	0.45
21:S:16:ASN:O	21:S:20:PHE:N	2.50	0.45
25:W:106:THR:OG1	25:W:109:GLU:HG3	2.17	0.45
1:0:586:C:H5''	37:0:7055:HOH:O	2.17	0.45
1:0:612:U:H2'	1:0:613:C:H6	1.81	0.45
1:0:645:U:OP2	14:L:4:LYS:HE2	2.17	0.45
1:0:746:A:H5'	37:0:5310:HOH:O	2.17	0.45
1:0:941:G:C5	1:0:942:U:C4	3.05	0.45
1:0:1071:G:H4'	27:Y:154:ARG:NH2	2.32	0.45
1:0:1072:G:P	27:Y:154:ARG:HH22	2.39	0.45
1:0:1643:C:O2'	1:0:1644:C:H5'	2.16	0.45
1:0:1682:A:H5''	37:0:9263:HOH:O	2.17	0.45
1:0:1942:A:H3'	37:0:7117:HOH:O	2.17	0.45
1:0:2057:U:O5'	1:0:2057:U:H6	1.99	0.45
1:0:2318:C:H1'	37:0:3939:HOH:O	2.17	0.45
1:0:2651:C:H2'	1:0:2652:U:O4'	2.17	0.45
3:A:32:VAL:O	3:A:34:ASP:N	2.49	0.45
3:A:36:ASP:HB2	3:A:84:VAL:H	1.81	0.45
3:A:37:VAL:O	3:A:38:ILE:C	2.60	0.45
16:N:67:ALA:O	16:N:69:TYR:N	2.50	0.45
19:Q:93:ARG:HG3	19:Q:93:ARG:HH11	1.81	0.45
20:R:125:ARG:NH1	20:R:125:ARG:HB3	2.32	0.45
22:T:9:LYS:HE3	22:T:13:ARG:NH1	2.31	0.45
23:U:52:THR:CG2	23:U:54:THR:HB	2.47	0.45
28:Z:38:ALA:N	37:Z:8725:HOH:O	2.50	0.45
1:0:241:A:C2	1:0:378:A:H4'	2.51	0.44
1:0:1755:A:H2'	1:0:1756:G:O4'	2.17	0.44
37:0:7197:HOH:O	22:T:9:LYS:HD2	2.16	0.44
2:9:110:G:C2'	2:9:111:U:H5'	2.47	0.44
5:C:20:ASP:O	5:C:23:GLU:N	2.47	0.44
5:C:194:PHE:HA	5:C:234:VAL:HG13	1.98	0.44
5:C:200:PRO:HB3	5:C:212:VAL:HG23	1.99	0.44
7:E:143:GLN:O	7:E:144:THR:C	2.60	0.44
16:N:184:ILE:HG23	16:N:184:ILE:O	2.18	0.44
21:S:57:THR:C	21:S:59:ASP:N	2.75	0.44
22:T:89:ARG:HD2	22:T:89:ARG:C	2.41	0.44
25:W:80:ASP:O	25:W:81:ASP:C	2.60	0.44
29:1:8:GLN:NE2	29:1:11:LYS:NZ	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:2:41:HIS:H	30:2:45:ASN:ND2	2.09	0.44
1:0:106:A:H2'	1:0:107:U:O4'	2.18	0.44
1:0:506:G:N2	1:0:508:A:H3'	2.32	0.44
1:0:1020:A:H1'	37:Q:6976:HOH:O	2.16	0.44
1:0:1151:G:OP1	9:G:63:ARG:NH1	2.50	0.44
1:0:1154:A:H2'	1:0:1155:G:C8	2.52	0.44
1:0:1496:A:N6	37:0:6898:HOH:O	2.49	0.44
1:0:2453:G:H3'	37:0:5707:HOH:O	2.16	0.44
1:0:2633:A:H2'	1:0:2634:G:H5'	1.99	0.44
1:0:2720:C:O2	13:K:87:ARG:NH2	2.49	0.44
1:0:2831:C:C2'	1:0:2832:C:H5'	2.48	0.44
4:B:139:ASP:HB2	4:B:165:ARG:HE	1.81	0.44
4:B:304:PRO:CG	4:B:307:ARG:NH1	2.80	0.44
5:C:126:ASP:C	5:C:128:GLY:N	2.69	0.44
6:D:28:GLY:O	6:D:29:HIS:HB3	2.17	0.44
7:E:101:GLU:HG3	7:E:101:GLU:O	2.16	0.44
10:H:41:LYS:HD3	10:H:46:TYR:CE1	2.52	0.44
10:H:50:ILE:HD12	10:H:149:VAL:CG1	2.48	0.44
16:N:114:LYS:O	16:N:117:ALA:HB3	2.17	0.44
19:Q:31:GLU:CD	19:Q:93:ARG:HH12	2.25	0.44
23:U:17:THR:HG22	23:U:18:GLY:H	1.81	0.44
26:X:74:ALA:CB	26:X:85:VAL:HG22	2.48	0.44
31:3:15:ASN:HB2	37:3:8846:HOH:O	2.17	0.44
1:0:222:A:H2'	1:0:223:G:O4'	2.17	0.44
1:0:1044:C:H5''	37:0:8844:HOH:O	2.17	0.44
1:0:1822:A:O2'	1:0:1823:G:H5'	2.17	0.44
1:0:2831:C:H2'	1:0:2832:C:C5'	2.46	0.44
1:0:2850:C:H5'	1:0:2850:C:C6	2.44	0.44
2:9:3:A:N6	2:9:22:G:H1'	2.33	0.44
3:A:94:LEU:CG	3:A:99:ILE:HD11	2.40	0.44
4:B:38:VAL:HA	4:B:166:VAL:HG22	2.00	0.44
4:B:240:GLY:HA3	37:B:8829:HOH:O	2.17	0.44
7:E:32:ARG:O	7:E:33:LEU:HD23	2.17	0.44
10:H:6:ALA:HA	10:H:61:ARG:NH1	2.32	0.44
10:H:87:LYS:HB2	10:H:87:LYS:HZ2	1.82	0.44
17:O:7:LEU:HD22	37:O:5650:HOH:O	2.16	0.44
18:P:13:VAL:HG11	18:P:40:VAL:CG1	2.47	0.44
20:R:9:ASP:C	20:R:13:THR:HG22	2.42	0.44
22:T:48:VAL:HG12	22:T:96:VAL:HG22	2.00	0.44
30:2:22:PRO:HG2	30:2:25:VAL:CG2	2.47	0.44
1:0:1872:C:H5	3:A:20:SER:HB3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1947:G:N2	1:0:1966:U:C2	2.85	0.44
1:0:2265:U:H2'	1:0:2266:A:H8	1.81	0.44
1:0:2508:C:H2'	37:0:6533:HOH:O	2.17	0.44
5:C:214:THR:HG23	5:C:216:SER:H	1.82	0.44
6:D:164:ALA:O	6:D:167:GLU:N	2.50	0.44
7:E:170:ARG:NH2	37:E:4761:HOH:O	2.49	0.44
8:F:60:VAL:O	8:F:61:MET:C	2.61	0.44
10:H:151:GLU:OE1	10:H:151:GLU:HA	2.17	0.44
11:I:84:SER:N	37:I:7210:HOH:O	2.50	0.44
11:I:127:CYS:N	37:I:5371:HOH:O	2.45	0.44
17:O:10:LEU:HD13	17:O:99:GLU:HG3	1.98	0.44
23:U:25:ASP:OD2	23:U:27:ALA:HB2	2.17	0.44
24:V:12:THR:O	24:V:15:GLU:N	2.48	0.44
25:W:96:LEU:O	25:W:99:ALA:N	2.51	0.44
25:W:132:VAL:HG21	25:W:141:HIS:CD2	2.52	0.44
27:Y:122:ARG:NH2	37:Y:8835:HOH:O	2.50	0.44
28:Z:14:PHE:O	28:Z:15:GLY:C	2.61	0.44
1:0:820:G:O2'	1:0:856:G:H4'	2.17	0.44
1:0:1174:A:H5'	37:0:4217:HOH:O	2.17	0.44
1:0:1314:U:H5''	1:0:1316:G:O4'	2.17	0.44
1:0:1845:A:O3'	3:A:187:PRO:HB2	2.16	0.44
2:9:13:A:OP1	2:9:113:C:H5'	2.16	0.44
3:A:51:ARG:NH2	37:A:8843:HOH:O	2.49	0.44
5:C:27:ARG:HH11	5:C:27:ARG:HG3	1.82	0.44
5:C:133:ARG:HD2	37:C:8615:HOH:O	2.17	0.44
6:D:36:ASN:C	37:D:7500:HOH:O	2.61	0.44
10:H:4:LYS:HB3	10:H:5:PRO:CD	2.48	0.44
10:H:79:GLU:O	10:H:80:LEU:HD23	2.17	0.44
10:H:131:GLN:O	10:H:134:GLU:HG3	2.18	0.44
12:J:47:THR:O	12:J:53:ILE:HD11	2.18	0.44
12:J:131:THR:HG22	12:J:133:GLY:N	2.33	0.44
14:L:101:ASP:OD1	14:L:101:ASP:N	2.51	0.44
14:L:145:LEU:O	14:L:148:GLU:HG3	2.18	0.44
15:M:49:ALA:HB1	15:M:54:TYR:HB2	1.99	0.44
16:N:108:SER:HA	16:N:109:PRO:HD3	1.83	0.44
22:T:48:VAL:HG22	22:T:98:VAL:HA	1.99	0.44
22:T:73:HIS:HD2	22:T:88:PRO:HG3	1.82	0.44
26:X:26:ALA:HB2	26:X:63:ARG:HA	1.99	0.44
30:2:26:MET:O	30:2:31:ARG:N	2.43	0.44
1:0:820:G:H5'	1:0:821:U:H5'	1.98	0.44
1:0:1149:U:C5	1:0:1215:A:C5	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1450:C:C4'	1:0:1451:C:OP2	2.61	0.44
1:0:1471:A:H2'	1:0:1472:C:C6	2.53	0.44
1:0:1484:G:H2'	37:0:8922:HOH:O	2.17	0.44
1:0:1506:U:H5'	1:0:1506:U:C6	2.50	0.44
1:0:1864:C:C5	15:M:75:ARG:HD2	2.53	0.44
1:0:2379:G:H4'	1:0:2380:A:H5''	1.98	0.44
1:0:2860:G:H1'	37:0:6361:HOH:O	2.18	0.44
2:9:80:A:C2	2:9:103:A:C4	3.06	0.44
10:H:36:MET:HB3	10:H:73:ASN:ND2	2.32	0.44
10:H:91:ARG:HD3	10:H:135:GLN:HB2	1.99	0.44
11:I:71:ALA:O	11:I:75:LYS:HG3	2.16	0.44
16:N:144:GLY:O	16:N:147:ILE:CG2	2.65	0.44
22:T:71:VAL:HG11	22:T:90:PRO:CB	2.37	0.44
24:V:33:VAL:CG1	24:V:38:GLY:HA3	2.44	0.44
25:W:48:VAL:CG1	25:W:48:VAL:O	2.66	0.44
26:X:43:VAL:CG1	26:X:44:ASP:N	2.79	0.44
1:0:777:U:O2'	29:1:11:LYS:HG2	2.17	0.44
1:0:793:A:C5'	18:P:83:LYS:HG2	2.48	0.44
1:0:1001:U:H1'	37:H:219:HOH:O	2.17	0.44
1:0:2281:C:H2'	1:0:2282:U:H5'	2.00	0.44
1:0:2764:C:H2'	1:0:2765:C:C6	2.53	0.44
2:9:31:C:H2'	2:9:32:G:O4'	2.18	0.44
3:A:35:GLY:O	3:A:36:ASP:CB	2.53	0.44
4:B:189:ALA:O	4:B:192:ASP:HB2	2.18	0.44
6:D:10:PHE:CD2	6:D:11:HIS:N	2.85	0.44
6:D:94:ALA:HA	6:D:174:VAL:O	2.17	0.44
6:D:104:PHE:N	6:D:104:PHE:CD2	2.86	0.44
8:F:1:PRO:HB2	37:F:5897:HOH:O	2.18	0.44
11:I:127:CYS:O	11:I:130:LEU:N	2.50	0.44
22:T:14:ALA:HA	22:T:15:PRO:HD3	1.88	0.44
25:W:142:ASP:HB2	37:W:2729:HOH:O	2.18	0.44
28:Z:28:GLU:O	28:Z:31:SER:N	2.51	0.44
1:0:249:G:H2'	1:0:250:C:C6	2.53	0.44
1:0:533:U:H3'	37:0:3547:HOH:O	2.16	0.44
1:0:945:U:H2'	1:0:946:C:H6	1.81	0.44
1:0:1056:U:H2'	1:0:1057:A:O4'	2.18	0.44
1:0:1086:A:N6	25:W:11:VAL:HG11	2.33	0.44
1:0:1743:G:O4'	13:K:78:LYS:HD3	2.17	0.44
1:0:2107:U:O2'	1:0:2108:A:H5'	2.18	0.44
1:0:2438:G:H5'	37:0:5953:HOH:O	2.18	0.44
3:A:206:ARG:NH1	3:A:208:HIS:NE2	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:115:LEU:HD13	5:C:115:LEU:HA	1.85	0.44
7:E:23:GLU:HG2	7:E:28:SER:CB	2.47	0.44
15:M:153:ASP:C	15:M:155:GLN:H	2.26	0.44
16:N:144:GLY:O	16:N:147:ILE:HG22	2.18	0.44
18:P:82:GLY:HA2	37:P:174:HOH:O	2.17	0.44
22:T:16:LEU:HA	22:T:19:ARG:HG3	2.00	0.44
22:T:20:HIS:O	22:T:23:VAL:HG23	2.18	0.44
22:T:37:GLN:HB3	37:T:6711:HOH:O	2.16	0.44
23:U:35:LYS:HB2	37:U:774:HOH:O	2.17	0.44
30:2:49:GLU:CD	37:2:719:HOH:O	2.60	0.44
1:0:363:C:H2'	1:0:364:U:H6	1.82	0.44
1:0:812:A:H2'	1:0:813:C:O4'	2.18	0.44
1:0:1160:G:O2'	1:0:1190:G:H1'	2.17	0.44
1:0:1462:C:O2'	1:0:1463:U:H5'	2.18	0.44
1:0:1782:G:O2'	1:0:1783:A:H5'	2.18	0.44
1:0:1943:C:O4'	3:A:212:PRO:HA	2.18	0.44
1:0:2064:U:H5'	1:0:2652:U:H4'	2.00	0.44
1:0:2846:C:H4'	4:B:156:LYS:HB3	2.00	0.44
4:B:215:VAL:O	4:B:219:GLY:HA2	2.18	0.44
4:B:224:LYS:HD3	4:B:224:LYS:HA	1.79	0.44
11:I:97:VAL:HG12	11:I:101:LYS:HE3	1.99	0.44
25:W:96:LEU:O	25:W:97:ALA:C	2.59	0.44
26:X:22:ASN:C	26:X:24:LYS:H	2.26	0.44
1:0:74:G:H2'	1:0:75:U:C6	2.52	0.43
1:0:321:A:C2'	1:0:322:G:H5'	2.48	0.43
1:0:969:G:H2'	1:0:970:U:C6	2.52	0.43
1:0:1555:G:O2'	1:0:1556:G:H5'	2.18	0.43
1:0:1723:G:H2'	37:0:9433:HOH:O	2.18	0.43
1:0:2281:C:C2'	1:0:2282:U:H5'	2.48	0.43
37:0:9600:HOH:O	13:K:39:GLY:HA3	2.18	0.43
2:9:49:G:O2'	2:9:50:G:H5'	2.17	0.43
5:C:57:PRO:O	5:C:58:ALA:C	2.61	0.43
14:L:35:ARG:O	14:L:40:PHE:HA	2.18	0.43
15:M:158:ARG:HB2	15:M:163:LEU:HB2	1.99	0.43
16:N:37:ARG:NH2	16:N:105:GLY:CA	2.81	0.43
16:N:93:GLN:HG3	16:N:125:ALA:O	2.18	0.43
1:0:169:A:H1'	31:3:48:ASN:ND2	2.33	0.43
1:0:371:U:H2'	1:0:372:A:C8	2.52	0.43
1:0:920:C:H4'	1:0:921:G:C2	2.52	0.43
1:0:958:G:O2'	1:0:959:C:H5'	2.18	0.43
1:0:1023:C:H2'	1:0:1024:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1414:A:H2'	1:0:1415:G:O4'	2.19	0.43
1:0:1504:A:O2'	1:0:1506:U:OP2	2.31	0.43
1:0:1556:G:O2'	1:0:1557:G:H5'	2.17	0.43
1:0:1644:C:H2'	1:0:1645:U:H6	1.84	0.43
1:0:1659:A:H2'	1:0:1660:G:O4'	2.17	0.43
3:A:93:THR:HG23	3:A:154:ALA:O	2.18	0.43
4:B:180:ASP:O	4:B:181:ILE:C	2.60	0.43
5:C:13:ASP:OD1	5:C:13:ASP:O	2.36	0.43
5:C:21:VAL:HG23	5:C:22:PHE:N	2.34	0.43
5:C:84:VAL:O	5:C:85:LYS:CB	2.66	0.43
8:F:32:GLY:N	37:F:3111:HOH:O	2.51	0.43
13:K:11:GLY:O	13:K:12:LEU:HD23	2.18	0.43
13:K:115:ARG:CG	13:K:116:GLU:N	2.81	0.43
16:N:115:VAL:HG23	37:N:8856:HOH:O	2.18	0.43
16:N:179:LEU:HA	16:N:184:ILE:CD1	2.48	0.43
17:O:35:LYS:HB3	17:O:36:PRO:HD2	1.99	0.43
17:O:39:THR:O	17:O:115:ARG:NH2	2.51	0.43
20:R:22:GLN:HG2	20:R:140:GLN:HE21	1.83	0.43
21:S:52:VAL:HG22	21:S:66:VAL:HG13	2.00	0.43
22:T:55:PHE:CD1	22:T:55:PHE:N	2.86	0.43
23:U:17:THR:CG2	23:U:18:GLY:H	2.30	0.43
23:U:34:SER:HA	23:U:37:GLU:OE1	2.17	0.43
24:V:42:ASN:O	24:V:44:GLY:N	2.52	0.43
25:W:144:GLU:O	25:W:144:GLU:HG3	2.14	0.43
27:Y:126:PRO:HG2	27:Y:128:PHE:CZ	2.53	0.43
1:0:92:G:O2'	1:0:93:C:H5'	2.18	0.43
1:0:1181:A:C2	1:0:1192:A:C8	3.06	0.43
1:0:1426:C:H4'	1:0:1427:A:C8	2.52	0.43
1:0:2820:A:H2'	1:0:2821:C:O4'	2.18	0.43
3:A:82:VAL:HG13	3:A:93:THR:HB	2.00	0.43
3:A:132:ASP:OD1	3:A:133:ARG:N	2.48	0.43
10:H:4:LYS:N	37:H:221:HOH:O	2.52	0.43
11:I:127:CYS:O	11:I:129:SER:N	2.51	0.43
12:J:70:PHE:N	37:J:8869:HOH:O	2.51	0.43
14:L:17:SER:O	14:L:19:LYS:N	2.51	0.43
14:L:105:TYR:CD1	14:L:105:TYR:C	2.96	0.43
14:L:112:GLY:O	14:L:132:LYS:NZ	2.36	0.43
15:M:31:TRP:C	15:M:33:ASN:N	2.76	0.43
16:N:179:LEU:C	16:N:181:ASP:N	2.75	0.43
18:P:138:GLU:O	18:P:140:TYR:N	2.51	0.43
20:R:19:ARG:HA	20:R:142:ASP:OD1	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:91:LEU:CD2	20:R:143:VAL:HG22	2.49	0.43
22:T:35:TYR:CG	22:T:112:LEU:HD22	2.53	0.43
31:3:22:VAL:HG11	31:3:67:LEU:HD13	1.99	0.43
1:0:31:C:H2'	37:0:7457:HOH:O	2.17	0.43
1:0:259:G:H21	15:M:58:GLN:NE2	2.15	0.43
1:0:541:C:O2'	1:0:542:A:H5''	2.17	0.43
1:0:2121:G:H3'	37:0:6357:HOH:O	2.19	0.43
1:0:2432:C:H1'	37:0:6075:HOH:O	2.17	0.43
1:0:2793:A:H2'	1:0:2794:G:H5'	1.99	0.43
37:0:9572:HOH:O	14:L:41:HIS:HE1	2.01	0.43
2:9:73:A:H2'	2:9:74:G:C8	2.54	0.43
3:A:48:ASP:HB3	37:A:8898:HOH:O	2.16	0.43
7:E:16:ASP:O	7:E:16:ASP:CG	2.61	0.43
12:J:77:GLY:O	12:J:78:ILE:C	2.59	0.43
15:M:87:GLY:O	15:M:91:ILE:HD11	2.19	0.43
22:T:48:VAL:CG1	22:T:96:VAL:HG13	2.45	0.43
25:W:60:GLU:O	25:W:63:GLU:HB2	2.18	0.43
25:W:140:LYS:C	25:W:141:HIS:CD2	2.97	0.43
30:2:41:HIS:N	30:2:45:ASN:HD22	2.09	0.43
31:3:31:THR:HB	31:3:33:MET:HE3	2.00	0.43
1:0:215:A:OP1	14:L:52:LYS:NZ	2.47	0.43
1:0:368:C:H2'	1:0:369:G:H5'	2.00	0.43
1:0:818:A:O2'	28:Z:13:ARG:HD3	2.19	0.43
1:0:1181:A:C2'	1:0:1182:C:H5'	2.47	0.43
1:0:1182:C:O5'	1:0:1182:C:H6	2.01	0.43
1:0:1557:G:O2'	1:0:1558:C:H5'	2.18	0.43
1:0:1688:G:H2'	1:0:1692:C:H42	1.83	0.43
1:0:1798:C:H4'	18:P:66:GLN:HG2	1.99	0.43
1:0:2266:A:H2'	1:0:2267:G:C8	2.53	0.43
1:0:2434:A:H2'	1:0:2435:U:O4'	2.18	0.43
4:B:77:PRO:HG2	4:B:151:VAL:HG22	2.00	0.43
4:B:79:MET:HG2	4:B:146:THR:HG22	2.01	0.43
4:B:280:VAL:HG13	4:B:334:SER:HA	2.00	0.43
5:C:98:ARG:NH1	37:C:8559:HOH:O	2.51	0.43
6:D:104:PHE:N	6:D:104:PHE:HD2	2.17	0.43
6:D:136:ARG:O	6:D:138:GLY:N	2.50	0.43
7:E:103:VAL:HG21	7:E:115:ARG:NH2	2.33	0.43
10:H:27:PRO:HD3	10:H:123:ILE:HG22	1.98	0.43
12:J:11:ILE:HD11	12:J:109:TYR:CD2	2.54	0.43
15:M:133:LEU:O	15:M:134:ILE:HD13	2.18	0.43
22:T:49:GLU:CD	22:T:97:ARG:HD2	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:62:VAL:N	37:T:3851:HOH:O	2.51	0.43
22:T:85:GLU:HG2	22:T:86:GLU:H	1.83	0.43
25:W:21:LEU:HB3	25:W:26:ILE:CG1	2.49	0.43
27:Y:125:LYS:HB2	27:Y:126:PRO:HD2	2.00	0.43
1:0:88:G:H5'	1:0:88:G:C8	2.43	0.43
1:0:185:G:H4'	1:0:186:A:H4'	2.01	0.43
1:0:263:U:O4'	8:F:59:ILE:HD13	2.17	0.43
1:0:275:G:C2	1:0:376:C:N3	2.87	0.43
1:0:638:C:H2'	1:0:639:A:H8	1.83	0.43
1:0:1091:U:O2'	1:0:1092:A:H5'	2.19	0.43
1:0:1145:G:H1	1:0:1218:U:H3	1.66	0.43
1:0:1157:C:H2'	1:0:1158:G:H8	1.82	0.43
1:0:2311:A:H5'	10:H:120:PHE:CD1	2.53	0.43
1:0:2834:G:OP1	26:X:39:LYS:HE2	2.18	0.43
2:9:63:C:O2'	2:9:64:C:H5'	2.19	0.43
3:A:61:GLU:C	3:A:63:GLY:N	2.77	0.43
3:A:164:ARG:HE	3:A:164:ARG:HB3	1.60	0.43
10:H:56:GLU:C	10:H:132:ALA:HB2	2.43	0.43
11:I:107:LYS:CD	11:I:110:ASP:HB2	2.36	0.43
12:J:127:ILE:O	12:J:127:ILE:HG12	2.19	0.43
15:M:184:ARG:HG3	15:M:185:PRO:HA	2.00	0.43
19:Q:93:ARG:HG3	19:Q:93:ARG:NH1	2.34	0.43
22:T:48:VAL:HG11	22:T:96:VAL:HG22	2.01	0.43
22:T:65:VAL:HG22	22:T:72:ILE:HG22	2.01	0.43
23:U:48:ASN:ND2	37:U:3104:HOH:O	2.50	0.43
25:W:90:TYR:CD1	25:W:90:TYR:N	2.86	0.43
25:W:125:HIS:HE1	37:W:3071:HOH:O	2.01	0.43
26:X:12:ILE:O	26:X:69:LYS:HA	2.17	0.43
30:2:41:HIS:O	30:2:45:ASN:HB2	2.18	0.43
1:0:100:C:H2'	1:0:101:C:H6	1.84	0.43
1:0:153:C:P	37:0:6629:HOH:O	2.76	0.43
1:0:250:C:O5'	1:0:250:C:H6	2.01	0.43
1:0:350:G:O2'	1:0:351:A:H5'	2.18	0.43
1:0:1544:U:H2'	1:0:1545:C:H6	1.84	0.43
1:0:1588:G:C6	1:0:1589:G:N1	2.86	0.43
1:0:1840:A:H4'	1:0:1841:C:O5'	2.18	0.43
1:0:1942:A:O2'	1:0:1943:C:H5'	2.19	0.43
1:0:2381:C:H2'	1:0:2382:A:C8	2.53	0.43
37:0:6069:HOH:O	27:Y:158:LYS:HD3	2.17	0.43
3:A:60:PHE:HD1	3:A:64:ASP:O	2.02	0.43
3:A:165:THR:O	3:A:165:THR:HG22	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:215:ILE:HG13	3:A:216:SER:N	2.32	0.43
4:B:62:ARG:CA	4:B:65:MET:HE3	2.47	0.43
5:C:168:ARG:NH2	5:C:190:ALA:O	2.51	0.43
7:E:112:ALA:HA	7:E:113:PRO:HD3	1.83	0.43
13:K:55:VAL:CG1	13:K:56:SER:N	2.81	0.43
15:M:55:LYS:O	15:M:57:LYS:N	2.52	0.43
15:M:61:ILE:HG22	15:M:62:VAL:N	2.33	0.43
16:N:34:LEU:HD13	16:N:47:LEU:HD23	1.99	0.43
16:N:171:HIS:CE1	37:N:8863:HOH:O	2.71	0.43
18:P:10:ALA:HA	18:P:13:VAL:HG12	2.01	0.43
18:P:94:TRP:CH2	18:P:98:ILE:HG13	2.54	0.43
19:Q:28:ARG:CD	19:Q:92:ARG:NH1	2.81	0.43
1:0:795:G:H1'	1:0:817:G:N2	2.33	0.43
1:0:835:U:OP1	4:B:230:GLN:NE2	2.48	0.43
1:0:911:G:H5'	1:0:932:U:OP1	2.19	0.43
1:0:1014:A:H2'	1:0:1015:C:H5'	1.99	0.43
1:0:1079:A:N1	1:0:2068:G:O2'	2.51	0.43
1:0:1808:C:O2'	1:0:1809:G:H5'	2.19	0.43
1:0:1811:A:C2	1:0:2752:C:H1'	2.54	0.43
1:0:2830:U:H4'	37:0:9892:HOH:O	2.19	0.43
37:0:3038:HOH:O	11:I:87:PRO:HG2	2.19	0.43
3:A:232:ARG:NH2	3:A:236:GLY:O	2.51	0.43
4:B:76:THR:N	4:B:77:PRO:HD3	2.34	0.43
5:C:188:ARG:HD2	37:C:8677:HOH:O	2.19	0.43
6:D:94:ALA:HB3	6:D:97:GLN:HG3	1.99	0.43
8:F:45:ALA:HA	37:F:3461:HOH:O	2.18	0.43
18:P:16:VAL:HG13	18:P:20:ARG:CZ	2.49	0.43
24:V:11:MET:HE2	24:V:15:GLU:HB3	2.00	0.43
27:Y:149:GLN:NE2	37:Y:8910:HOH:O	2.50	0.43
1:0:622:G:P	27:Y:148:GLY:HA3	2.58	0.43
1:0:644:G:H5'	1:0:644:G:N3	2.34	0.43
1:0:902:G:N7	14:L:18:HIS:CD2	2.79	0.43
1:0:951:A:C2'	1:0:952:G:H5'	2.49	0.43
1:0:1163:G:N2	37:0:5830:HOH:O	2.51	0.43
1:0:1350:U:H1'	37:0:9473:HOH:O	2.19	0.43
1:0:1379:A:H1'	37:0:9503:HOH:O	2.19	0.43
2:9:51:A:C5	16:N:41:LYS:HE2	2.54	0.43
2:9:61:C:H2'	2:9:62:A:C8	2.53	0.43
3:A:55:VAL:CG1	3:A:67:LEU:HB3	2.48	0.43
5:C:5:ILE:CG2	5:C:6:TYR:N	2.82	0.43
5:C:35:VAL:HG21	5:C:227:GLY:HA2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:107:PHE:O	7:E:108:LEU:C	2.60	0.43
13:K:10:GLN:NE2	13:K:10:GLN:N	2.42	0.43
15:M:33:ASN:HB2	37:M:8866:HOH:O	2.19	0.43
1:O:166:A:N7	14:L:25:GLY:HA2	2.34	0.43
1:O:204:A:H2'	1:O:205:U:H5'	2.00	0.43
1:O:1827:G:H2'	1:O:1828:G:C8	2.54	0.43
1:O:1828:G:H5'	37:O:3780:HOH:O	2.18	0.43
1:O:2870:C:O2'	1:O:2871:G:H5'	2.18	0.43
37:O:4471:HOH:O	15:M:4:ALA:HB3	2.19	0.43
2:9:22:G:H5'	37:9:8723:HOH:O	2.19	0.43
2:9:56:A:O2'	6:D:14:ARG:HD3	2.19	0.43
4:B:182:VAL:O	4:B:184:ASP:N	2.52	0.43
5:C:150:THR:C	5:C:152:GLU:N	2.74	0.43
6:D:35:ALA:C	6:D:37:ALA:N	2.77	0.43
7:E:106:ASN:O	7:E:107:PHE:C	2.59	0.43
8:F:37:THR:O	8:F:41:GLU:HG3	2.18	0.43
17:O:14:LEU:CG	17:O:102:ILE:HD11	2.49	0.43
17:O:26:TRP:HA	17:O:26:TRP:CE3	2.53	0.43
20:R:75:TRP:CG	20:R:76:ASP:H	2.37	0.43
22:T:63:ILE:HD11	22:T:75:GLU:OE1	2.19	0.43
25:W:1:MET:N	25:W:103:GLU:OE2	2.52	0.43
26:X:8:ARG:NH1	37:X:2479:HOH:O	2.52	0.43
27:Y:189:ASN:HD22	27:Y:191:ASP:N	2.17	0.43
1:O:240:C:O2	1:O:240:C:H2'	2.19	0.42
1:O:275:G:N2	1:O:376:C:C2	2.87	0.42
1:O:319:A:H4'	1:O:338:C:C4	2.53	0.42
1:O:764:C:H2'	1:O:765:G:O4'	2.19	0.42
1:O:795:G:N3	1:O:817:G:C2	2.87	0.42
1:O:1759:A:N3	1:O:1818:C:H2'	2.34	0.42
1:O:1876:C:C4	3:A:123:GLY:HA3	2.54	0.42
1:O:2385:G:H2'	1:O:2386:U:C6	2.54	0.42
1:O:2518:C:H2'	1:O:2519:C:O4'	2.19	0.42
1:O:2669:U:H2'	1:O:2670:G:C8	2.53	0.42
1:O:2673:U:C2'	1:O:2674:G:H5'	2.48	0.42
1:O:2781:U:H2'	1:O:2782:G:H5'	2.01	0.42
3:A:74:VAL:O	28:Z:65:THR:HG23	2.19	0.42
3:A:191:GLY:O	3:A:194:MET:HG3	2.19	0.42
4:B:55:ASN:CB	4:B:63:GLU:HA	2.40	0.42
4:B:175:LEU:C	4:B:175:LEU:CD2	2.91	0.42
4:B:176:ASP:O	4:B:177:HIS:C	2.60	0.42
4:B:277:GLU:N	4:B:278:PRO:CD	2.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:51:TYR:CE2	29:1:53:LYS:HB3	2.54	0.42
6:D:89:PRO:O	6:D:91:ALA:N	2.52	0.42
6:D:91:ALA:HB1	37:D:5198:HOH:O	2.18	0.42
6:D:95:THR:C	6:D:97:GLN:N	2.76	0.42
6:D:138:GLY:O	6:D:141:VAL:HG23	2.19	0.42
20:R:125:ARG:O	20:R:126:LYS:CB	2.62	0.42
22:T:48:VAL:CG1	22:T:49:GLU:N	2.81	0.42
26:X:27:ASP:OD2	26:X:27:ASP:N	2.48	0.42
1:O:64:G:H2'	1:O:65:C:O4'	2.19	0.42
1:O:488:U:H2'	37:O:3801:HOH:O	2.19	0.42
1:O:695:C:H2'	1:O:696:C:H6	1.84	0.42
1:O:1353:C:H6	37:O:4479:HOH:O	2.01	0.42
1:O:2001:G:O2'	1:O:2002:C:H5'	2.19	0.42
1:O:2064:U:H5'	1:O:2652:U:O3'	2.19	0.42
1:O:2506:A:O2'	1:O:2507:G:O5'	2.38	0.42
1:O:2607:U:H4'	37:O:9249:HOH:O	2.18	0.42
1:O:2687:G:O2'	1:O:2688:U:H5'	2.18	0.42
37:O:4423:HOH:O	3:A:6:GLY:HA3	2.19	0.42
2:9:28:U:H2'	2:9:29:C:C6	2.54	0.42
4:B:57:GLU:OE1	4:B:60:SER:HB2	2.19	0.42
5:C:15:GLU:O	5:C:15:GLU:HG3	2.19	0.42
5:C:201:SER:O	5:C:202:THR:C	2.60	0.42
6:D:35:ALA:N	37:D:5576:HOH:O	2.52	0.42
6:D:169:THR:O	6:D:169:THR:HG22	2.19	0.42
7:E:84:MET:HE3	7:E:131:LEU:CB	2.49	0.42
8:F:48:VAL:HG23	8:F:74:PHE:HB2	2.00	0.42
13:K:98:VAL:HG12	13:K:99:ASP:N	2.34	0.42
15:M:43:PRO:HD2	37:M:8919:HOH:O	2.19	0.42
16:N:119:GLN:HG2	16:N:123:ILE:HD11	2.01	0.42
17:O:32:ARG:C	17:O:32:ARG:HD3	2.44	0.42
18:P:16:VAL:HG12	18:P:17:GLY:H	1.83	0.42
19:Q:40:HIS:CE1	19:Q:94:GLN:HA	2.54	0.42
21:S:29:ASP:OD1	21:S:31:ARG:NH1	2.53	0.42
21:S:77:VAL:O	21:S:80:ARG:HG2	2.20	0.42
22:T:28:SER:HB2	37:T:4606:HOH:O	2.19	0.42
26:X:25:ARG:HD3	26:X:64:ALA:O	2.19	0.42
1:O:39:G:N2	1:O:444:C:C2	2.87	0.42
1:O:480:C:H4'	37:O:7494:HOH:O	2.18	0.42
1:O:823:U:H2'	1:O:824:G:O4'	2.19	0.42
1:O:1055:G:OP2	10:H:99:ARG:NH1	2.52	0.42
1:O:1215:A:O3'	1:O:1216:G:C4'	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1496:A:H2'	1:0:1497:G:C8	2.54	0.42
1:0:1933:G:O2'	1:0:1934:A:H5'	2.18	0.42
4:B:162:MET:HE2	4:B:310:ARG:CD	2.46	0.42
4:B:241:PRO:HD2	37:B:8956:HOH:O	2.19	0.42
5:C:19:PRO:HD2	5:C:240:LEU:HD21	2.02	0.42
5:C:27:ARG:NH1	5:C:29:ASP:OD2	2.52	0.42
7:E:93:MET:HG2	7:E:94:GLN:H	1.84	0.42
9:G:14:GLU:C	9:G:16:LYS:N	2.76	0.42
10:H:12:ILE:HD12	10:H:57:THR:CG2	2.46	0.42
12:J:39:VAL:CG1	12:J:107:ASN:HB2	2.49	0.42
12:J:88:PRO:HA	35:J:8802:CL:CL	2.57	0.42
13:K:34:VAL:HG22	13:K:47:ALA:HB2	2.01	0.42
15:M:69:LYS:HG3	15:M:126:GLN:HA	2.00	0.42
15:M:139:PRO:HA	15:M:142:GLN:HB2	2.01	0.42
16:N:28:LYS:C	16:N:30:GLY:N	2.76	0.42
16:N:81:ALA:O	16:N:82:TYR:C	2.63	0.42
16:N:132:ASN:O	16:N:133:ASP:C	2.62	0.42
22:T:71:VAL:CG1	22:T:72:ILE:N	2.81	0.42
25:W:110:GLN:HE21	25:W:110:GLN:CA	2.27	0.42
26:X:12:ILE:HB	26:X:70:ILE:CG2	2.49	0.42
1:0:345:G:N2	1:0:346:U:H1'	2.34	0.42
1:0:445:U:H2'	1:0:446:G:C8	2.53	0.42
1:0:659:A:N1	17:O:42:GLU:OE2	2.52	0.42
1:0:2011:A:H5'	1:0:2013:G:H1'	2.01	0.42
1:0:2248:C:C2	1:0:2254:G:C2	3.07	0.42
3:A:134:ASN:C	37:A:8886:HOH:O	2.61	0.42
5:C:19:PRO:HD2	5:C:240:LEU:CD2	2.49	0.42
7:E:65:PHE:O	7:E:66:GLN:C	2.62	0.42
7:E:81:GLU:HA	7:E:133:VAL:O	2.20	0.42
7:E:101:GLU:CB	7:E:117:THR:HA	2.50	0.42
24:V:12:THR:C	24:V:14:ALA:N	2.77	0.42
25:W:83:TRP:O	25:W:84:VAL:C	2.61	0.42
27:Y:144:ARG:CZ	37:Y:8921:HOH:O	2.66	0.42
28:Z:42:CYS:SG	28:Z:43:GLY:N	2.92	0.42
1:0:733:U:H5''	37:0:9658:HOH:O	2.18	0.42
1:0:1221:G:C8	37:0:5773:HOH:O	2.57	0.42
1:0:1853:C:O2'	3:A:217:ARG:NH2	2.53	0.42
1:0:1878:G:C1'	37:0:5905:HOH:O	2.65	0.42
1:0:1916:C:H2'	1:0:1917:G:O4'	2.20	0.42
1:0:2408:A:H4'	31:3:15:ASN:O	2.20	0.42
1:0:2673:U:H2'	1:0:2674:G:H5'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:110:G:H2'	2:9:111:U:H5'	2.01	0.42
5:C:144:PHE:HE1	5:C:153:VAL:HG13	1.84	0.42
5:C:246:ARG:CZ	37:C:8633:HOH:O	2.67	0.42
6:D:170:TYR:CD1	6:D:170:TYR:N	2.87	0.42
8:F:43:GLY:C	8:F:45:ALA:H	2.27	0.42
8:F:77:VAL:HG21	8:F:83:LEU:HD13	2.01	0.42
9:G:12:ILE:HG22	9:G:12:ILE:O	2.19	0.42
10:H:34:HIS:HD2	10:H:90:LEU:O	2.03	0.42
13:K:63:GLU:HG2	37:K:6344:HOH:O	2.19	0.42
13:K:122:GLY:C	13:K:124:VAL:N	2.76	0.42
14:L:73:VAL:HG23	14:L:74:THR:N	2.35	0.42
16:N:23:ARG:NH1	37:N:8842:HOH:O	2.52	0.42
16:N:116:PHE:O	16:N:119:GLN:HB3	2.19	0.42
16:N:132:ASN:N	37:N:8851:HOH:O	2.52	0.42
17:O:14:LEU:HA	17:O:102:ILE:CD1	2.49	0.42
22:T:30:ASP:O	22:T:33:GLU:HB3	2.20	0.42
22:T:103:LEU:O	22:T:105:ASP:N	2.53	0.42
24:V:42:ASN:N	24:V:43:PRO:HD3	2.34	0.42
27:Y:98:GLN:HA	37:Y:8839:HOH:O	2.19	0.42
1:0:282:C:H1'	1:0:368:C:H41	1.79	0.42
1:0:567:U:H5''	37:0:6184:HOH:O	2.20	0.42
1:0:949:U:O2'	19:Q:40:HIS:HE1	2.03	0.42
1:0:1166:A:H1'	1:0:1192:A:C2	2.55	0.42
1:0:1213:C:C2'	1:0:1214:G:H5'	2.50	0.42
1:0:1396:C:H1'	18:P:1:THR:O	2.20	0.42
1:0:1473:U:C1'	29:1:42:SER:HB3	2.50	0.42
1:0:2291:A:N9	1:0:2309:C:H5'	2.35	0.42
1:0:2759:C:OP1	4:B:207:LYS:NZ	2.51	0.42
1:0:2909:G:H2'	1:0:2910:A:H8	1.84	0.42
37:0:5502:HOH:O	7:E:57:LYS:HE2	2.19	0.42
37:0:9010:HOH:O	5:C:107:ARG:NH1	2.53	0.42
2:9:4:G:H1'	37:9:8716:HOH:O	2.20	0.42
2:9:47:A:C2	2:9:48:C:C2	3.08	0.42
2:9:56:A:H1'	6:D:14:ARG:HG2	2.02	0.42
2:9:72:C:O2'	2:9:73:A:H5'	2.20	0.42
3:A:180:LYS:HB2	37:A:8916:HOH:O	2.20	0.42
5:C:40:ALA:O	5:C:43:LYS:HB2	2.20	0.42
5:C:214:THR:CG2	5:C:216:SER:H	2.32	0.42
7:E:26:ASN:HB3	7:E:76:VAL:C	2.45	0.42
8:F:42:ARG:C	8:F:44:SER:H	2.28	0.42
10:H:92:LYS:HA	10:H:92:LYS:HD3	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:66:SER:HB3	15:M:128:TRP:NE1	2.34	0.42
15:M:146:ASP:O	15:M:147:LEU:HG	2.18	0.42
22:T:103:LEU:HD22	22:T:112:LEU:CD1	2.49	0.42
23:U:53:ASP:O	23:U:54:THR:C	2.61	0.42
25:W:1:MET:SD	25:W:1:MET:C	3.03	0.42
30:2:48:ASP:O	30:2:49:GLU:CB	2.66	0.42
1:0:328:U:O4'	5:C:202:THR:HG22	2.20	0.42
1:0:417:G:P	37:0:7190:HOH:O	2.77	0.42
1:0:1235:G:N2	37:0:4680:HOH:O	2.51	0.42
1:0:1441:G:H5'	20:R:130:MET:HE3	2.02	0.42
1:0:2132:C:H2'	37:0:7327:HOH:O	2.20	0.42
1:0:2689:A:H2'	1:0:2690:U:H5'	2.02	0.42
1:0:2694:A:C4'	7:E:91:PHE:HE1	2.31	0.42
1:0:2717:C:OP1	4:B:207:LYS:HG3	2.19	0.42
3:A:70:ALA:HA	3:A:71:PRO:HD3	1.84	0.42
3:A:129:LEU:CD1	3:A:145:MET:HE1	2.50	0.42
4:B:71:VAL:HG11	4:B:296:LEU:HB3	2.02	0.42
5:C:170:ASP:C	5:C:171:GLU:HG3	2.43	0.42
6:D:23:VAL:HG22	6:D:73:VAL:HB	2.02	0.42
6:D:166:ILE:H	6:D:166:ILE:HG13	1.68	0.42
7:E:100:ASP:HB2	37:E:2789:HOH:O	2.18	0.42
13:K:23:ASN:HA	37:K:7075:HOH:O	2.19	0.42
15:M:18:GLY:O	15:M:21:ALA:HB3	2.19	0.42
15:M:24:GLN:O	15:M:28:GLN:HG3	2.19	0.42
16:N:176:ARG:O	16:N:180:LEU:HD13	2.19	0.42
18:P:58:SER:HB3	37:P:184:HOH:O	2.20	0.42
20:R:66:VAL:HG13	20:R:79:ARG:HE	1.85	0.42
20:R:141:VAL:HG12	20:R:142:ASP:N	2.34	0.42
1:0:414:C:H5'	37:0:5897:HOH:O	2.20	0.42
1:0:1335:C:OP2	27:Y:207:SER:CB	2.67	0.42
1:0:1684:A:H1'	30:2:43:ARG:NH2	2.28	0.42
1:0:2000:G:O2'	1:0:2001:G:H5'	2.20	0.42
1:0:2002:C:C2'	1:0:2003:U:H5'	2.49	0.42
1:0:2766:A:O2'	4:B:265:LEU:O	2.33	0.42
37:0:5206:HOH:O	3:A:164:ARG:CZ	2.67	0.42
37:0:6661:HOH:O	3:A:165:THR:HG23	2.18	0.42
6:D:11:HIS:CG	6:D:12:GLU:N	2.88	0.42
14:L:105:TYR:N	37:L:8868:HOH:O	2.53	0.42
16:N:165:ALA:C	16:N:167:ASP:H	2.28	0.42
22:T:71:VAL:HG13	22:T:91:LEU:H	1.85	0.42
26:X:45:GLU:HG3	37:X:6178:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:3:87:ARG:HG2	37:3:8869:HOH:O	2.19	0.42
1:0:52:A:H2'	1:0:53:C:O4'	2.20	0.42
1:0:57:C:H2'	1:0:58:C:O4'	2.20	0.42
1:0:281:U:H2'	1:0:282:C:O4'	2.19	0.42
1:0:319:A:H4'	1:0:338:C:C5	2.54	0.42
1:0:366:U:H2'	1:0:367:G:O4'	2.20	0.42
1:0:426:G:H2'	1:0:427:C:O4'	2.20	0.42
1:0:432:G:N2	1:0:433:C:C2	2.87	0.42
1:0:598:C:H2'	1:0:599:G:H8	1.82	0.42
1:0:1008:C:OP1	10:H:19:ARG:NH2	2.51	0.42
1:0:1276:U:H3'	17:O:19:ARG:HH11	1.85	0.42
1:0:1311:G:C2	1:0:1312:G:C8	3.08	0.42
1:0:1449:G:H2'	1:0:1493:A:C2	2.55	0.42
1:0:2134:G:N2	1:0:2242:U:C2	2.88	0.42
4:B:88:GLU:HB3	4:B:97:LEU:HG	2.01	0.42
4:B:279:THR:CG2	4:B:280:VAL:N	2.83	0.42
6:D:87:ALA:O	6:D:88:LEU:C	2.63	0.42
8:F:11:ASP:HA	8:F:14:ASP:OD2	2.19	0.42
8:F:60:VAL:O	8:F:62:HIS:N	2.53	0.42
10:H:57:THR:N	10:H:132:ALA:HB2	2.34	0.42
11:I:91:PHE:CD2	11:I:131:GLY:HA2	2.55	0.42
12:J:42:GLU:HG2	12:J:43:ARG:HG3	2.01	0.42
12:J:121:LEU:HD21	12:J:129:PHE:CD2	2.55	0.42
13:K:41:LYS:HE3	37:K:7871:HOH:O	2.18	0.42
13:K:72:VAL:O	13:K:95:ALA:HA	2.19	0.42
13:K:78:LYS:HA	13:K:79:PRO:HD3	1.86	0.42
14:L:67:ARG:O	14:L:71:GLU:HG3	2.20	0.42
14:L:74:THR:C	14:L:76:LEU:N	2.77	0.42
15:M:139:PRO:O	15:M:143:ASN:ND2	2.53	0.42
16:N:168:LEU:C	16:N:170:GLU:N	2.77	0.42
27:Y:103:THR:O	27:Y:103:THR:HG22	2.20	0.42
27:Y:234:VAL:CG1	27:Y:235:GLU:N	2.82	0.42
28:Z:66:GLY:O	28:Z:67:GLY:C	2.63	0.42
1:0:383:A:H4'	37:0:5126:HOH:O	2.19	0.42
1:0:613:C:H2'	1:0:614:U:H6	1.85	0.42
1:0:907:A:H4'	1:0:1328:A:C2	2.55	0.42
1:0:1758:U:H2'	1:0:1759:A:O4'	2.20	0.42
1:0:1846:U:O2'	3:A:172:ALA:HB2	2.19	0.42
1:0:1860:U:H2'	1:0:1861:C:O4'	2.19	0.42
1:0:2764:C:O2'	1:0:2765:C:H5'	2.20	0.42
1:0:2825:C:H4'	1:0:2826:G:O5'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:206:ARG:HH11	3:A:208:HIS:CD2	2.38	0.42
4:B:7:ARG:CZ	4:B:7:ARG:HB2	2.50	0.42
5:C:93:LYS:HB3	5:C:95:GLU:OE1	2.20	0.42
12:J:51:GLU:O	12:J:55:GLU:HG3	2.19	0.42
16:N:43:VAL:O	16:N:43:VAL:HG12	2.20	0.42
16:N:62:HIS:O	16:N:65:ASP:OD1	2.38	0.42
21:S:7:HIS:HB2	21:S:8:PRO:CD	2.50	0.42
22:T:3:GLN:HA	22:T:4:PRO:HD3	1.97	0.42
26:X:22:ASN:O	26:X:25:ARG:HG3	2.20	0.42
1:O:790:A:H2'	1:O:791:A:O4'	2.20	0.41
1:O:858:U:H2'	1:O:859:C:H6	1.85	0.41
1:O:1044:C:C5'	37:O:8844:HOH:O	2.67	0.41
1:O:1601:G:H1'	37:O:9701:HOH:O	2.18	0.41
1:O:1703:G:N2	18:P:57:ASN:HD21	2.18	0.41
1:O:1996:U:O2'	1:O:1997:A:H5'	2.20	0.41
1:O:2248:C:H2'	1:O:2249:G:H8	1.85	0.41
1:O:2392:C:O5'	1:O:2392:C:H6	2.03	0.41
1:O:2511:A:H2'	1:O:2512:U:O4'	2.19	0.41
1:O:2896:A:P	26:X:15:ARG:NH1	2.93	0.41
2:9:3:A:C8	2:9:3:A:O5'	2.74	0.41
2:9:9:C:H2'	2:9:10:C:H5'	2.02	0.41
3:A:194:MET:HE1	37:A:8814:HOH:O	2.20	0.41
4:B:119:HIS:C	4:B:121:PRO:HD3	2.45	0.41
6:D:87:ALA:C	6:D:89:PRO:HD2	2.44	0.41
6:D:160:ALA:C	6:D:162:ALA:N	2.78	0.41
7:E:97:VAL:C	37:E:4191:HOH:O	2.63	0.41
8:F:49:PHE:N	8:F:49:PHE:CD1	2.87	0.41
8:F:99:THR:HG23	8:F:99:THR:O	2.20	0.41
9:G:24:VAL:HA	9:G:27:ILE:HD12	2.02	0.41
13:K:61:THR:C	13:K:63:GLU:N	2.77	0.41
17:O:32:ARG:HG2	17:O:32:ARG:HH11	1.85	0.41
17:O:77:ALA:HB1	17:O:98:LEU:HD12	2.02	0.41
17:O:96:VAL:HG12	17:O:97:SER:N	2.35	0.41
21:S:39:ASP:HB3	21:S:43:GLU:OE2	2.20	0.41
24:V:45:ARG:C	24:V:47:LYS:N	2.78	0.41
1:O:253:U:H1'	1:O:256:C:H41	1.86	0.41
1:O:372:A:H2'	1:O:373:G:H8	1.86	0.41
1:O:794:U:H3	1:O:819:A:N6	2.11	0.41
1:O:844:A:H2'	37:O:9368:HOH:O	2.19	0.41
1:O:847:C:H5	37:O:9056:HOH:O	2.02	0.41
1:O:1194:A:O5'	1:O:1194:A:H8	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1503:U:H2'	1:0:1504:A:O4'	2.20	0.41
1:0:1771:U:H4'	1:0:1772:C:OP2	2.19	0.41
1:0:2096:A:N3	1:0:2096:A:H3'	2.35	0.41
1:0:2135:A:O2'	1:0:2136:G:H5'	2.19	0.41
1:0:2365:G:H4'	19:Q:45:PRO:O	2.20	0.41
1:0:2420:G:H2'	1:0:2421:G:C8	2.55	0.41
1:0:2506:A:H1'	37:O:3545:HOH:O	2.20	0.41
1:0:2729:C:H2'	1:0:2730:G:H8	1.85	0.41
37:O:3151:HOH:O	19:Q:16:ASN:HB2	2.19	0.41
2:9:41:C:O4'	6:D:50:VAL:HG22	2.21	0.41
2:9:73:A:N1	2:9:108:C:N3	2.68	0.41
5:C:141:SER:C	5:C:143:ASP:N	2.78	0.41
6:D:140:ARG:HH11	6:D:140:ARG:HG3	1.84	0.41
7:E:2:ARG:HA	7:E:49:ILE:O	2.20	0.41
8:F:119:ARG:C	8:F:119:ARG:CD	2.93	0.41
10:H:46:TYR:HE2	10:H:85:ASP:O	2.03	0.41
12:J:21:ARG:HH11	12:J:21:ARG:HG2	1.85	0.41
14:L:117:GLU:HG3	14:L:117:GLU:O	2.21	0.41
16:N:64:SER:C	16:N:66:LEU:N	2.76	0.41
16:N:67:ALA:HA	16:N:71:TRP:CB	2.48	0.41
16:N:178:THR:O	16:N:181:ASP:HB3	2.20	0.41
20:R:6:VAL:HG21	20:R:113:HIS:CD2	2.54	0.41
20:R:125:ARG:NH1	20:R:134:SER:HB2	2.33	0.41
22:T:49:GLU:CG	22:T:97:ARG:HB3	2.50	0.41
25:W:36:PRO:HD2	25:W:41:TYR:CD1	2.55	0.41
25:W:89:ASP:C	25:W:90:TYR:CD1	2.98	0.41
28:Z:17:ARG:HB2	28:Z:18:TYR:CE1	2.54	0.41
1:0:329:A:OP2	5:C:206:ASN:HB2	2.19	0.41
1:0:447:A:O2'	1:0:448:G:H5'	2.20	0.41
1:0:474:C:O3'	5:C:73:LEU:CD2	2.68	0.41
1:0:566:A:H2'	1:0:567:U:O4'	2.20	0.41
1:0:890:C:O2'	29:1:50:TRP:O	2.35	0.41
1:0:1353:C:N3	14:L:5:LYS:NZ	2.68	0.41
1:0:1439:C:H4'	20:R:132:ARG:NH1	2.34	0.41
1:0:1548:U:O2'	1:0:1549:C:H5'	2.20	0.41
1:0:1576:G:H2'	1:0:1577:U:O4'	2.21	0.41
1:0:1773:G:H2'	1:0:1774:G:H5'	2.02	0.41
1:0:1773:G:C2'	1:0:1774:G:H5'	2.50	0.41
1:0:1856:C:H5'	1:0:1858:A:O4'	2.21	0.41
1:0:2039:A:H4'	1:0:2760:C:O2'	2.21	0.41
1:0:2079:G:H2'	1:0:2080:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2416:G:H2'	1:0:2417:C:C6	2.55	0.41
1:0:2766:A:O2'	1:0:2767:C:H5'	2.20	0.41
2:9:27:C:N3	37:9:8644:HOH:O	2.37	0.41
3:A:54:PRO:HG2	3:A:160:ALA:HB3	2.02	0.41
3:A:94:LEU:N	3:A:94:LEU:CD2	2.81	0.41
3:A:206:ARG:NH1	3:A:208:HIS:CD2	2.88	0.41
4:B:57:GLU:HA	4:B:58:PRO:HD2	1.90	0.41
4:B:112:THR:OG1	4:B:158:LYS:HG3	2.21	0.41
5:C:2:GLN:HB3	37:C:8537:HOH:O	2.20	0.41
6:D:128:LEU:N	37:D:6007:HOH:O	2.52	0.41
10:H:37:GLY:HA3	10:H:87:LYS:HA	2.01	0.41
12:J:14:ALA:O	12:J:15:ARG:C	2.62	0.41
12:J:125:SER:O	12:J:126:ASN:CG	2.63	0.41
14:L:40:PHE:CD1	14:L:40:PHE:C	2.99	0.41
16:N:170:GLU:H	16:N:170:GLU:CD	2.28	0.41
17:O:47:ARG:HA	17:O:50:ARG:HH12	1.85	0.41
22:T:9:LYS:HE3	22:T:13:ARG:HD2	2.01	0.41
25:W:68:THR:HG23	25:W:69:ARG:N	2.36	0.41
25:W:93:ILE:HB	37:W:4301:HOH:O	2.19	0.41
26:X:21:PRO:HG2	26:X:24:LYS:HD3	2.01	0.41
1:0:178:U:H2'	1:0:179:C:H6	1.84	0.41
1:0:182:G:O3'	15:M:157:ASP:OD2	2.38	0.41
1:0:201:G:N2	35:0:8805:CL:CL	2.91	0.41
1:0:1194:A:O2'	1:0:1195:G:H5'	2.21	0.41
1:0:1246:A:H5'	1:0:1246:A:H8	1.85	0.41
1:0:1266:U:O2'	1:0:1267:C:H5'	2.20	0.41
1:0:1711:A:C2'	1:0:1712:A:H5'	2.50	0.41
1:0:2090:G:H2'	1:0:2091:G:C8	2.55	0.41
1:0:2613:G:O2'	1:0:2614:C:H5'	2.20	0.41
37:0:5207:HOH:O	14:L:34:GLY:HA2	2.19	0.41
2:9:19:G:O2'	2:9:20:G:H5'	2.21	0.41
4:B:138:GLY:O	4:B:139:ASP:C	2.63	0.41
6:D:19:GLU:HG3	37:D:6165:HOH:O	2.20	0.41
6:D:81:GLU:O	6:D:83:PHE:N	2.53	0.41
10:H:50:ILE:HD12	10:H:149:VAL:HG11	2.03	0.41
12:J:24:SER:HA	12:J:86:MET:SD	2.61	0.41
12:J:73:LYS:O	12:J:136:SER:OG	2.32	0.41
13:K:76:GLN:HA	13:K:93:ASN:HA	2.01	0.41
14:L:34:GLY:C	14:L:36:ASP:H	2.29	0.41
15:M:134:ILE:O	15:M:136:PRO:CD	2.67	0.41
17:O:26:TRP:HA	17:O:26:TRP:HE3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:135:ALA:O	18:P:139:ARG:HG3	2.20	0.41
21:S:7:HIS:HD2	21:S:27:ALA:HB3	1.83	0.41
31:3:43:ASN:ND2	37:3:8806:HOH:O	2.54	0.41
1:0:569:A:H5''	1:0:587:A:N1	2.35	0.41
1:0:622:G:O2'	1:0:623:U:H5'	2.19	0.41
1:0:721:A:H5''	17:O:51:TYR:CE2	2.55	0.41
1:0:963:C:O5'	1:0:963:C:H6	2.03	0.41
1:0:1051:C:H2'	1:0:1052:G:O4'	2.21	0.41
1:0:1746:A:O4'	1:0:1747:A:C2	2.73	0.41
37:0:6465:HOH:O	22:T:38:ARG:NH1	2.54	0.41
3:A:48:ASP:HA	3:A:49:PRO:HD3	1.93	0.41
4:B:36:PRO:CG	4:B:169:GLY:H	2.27	0.41
4:B:84:LEU:HD13	4:B:84:LEU:C	2.46	0.41
5:C:94:THR:HG22	37:C:8684:HOH:O	2.21	0.41
7:E:84:MET:HA	7:E:167:TYR:O	2.20	0.41
14:L:90:ARG:NH2	14:L:121:ILE:HD11	2.36	0.41
20:R:32:ALA:O	20:R:33:ARG:C	2.63	0.41
20:R:59:PHE:HZ	20:R:81:PRO:HG3	1.85	0.41
20:R:89:LEU:HD23	20:R:89:LEU:HA	1.85	0.41
25:W:52:VAL:CG2	25:W:53:ALA:N	2.82	0.41
25:W:90:TYR:CE2	25:W:99:ALA:HB2	2.56	0.41
26:X:25:ARG:HB3	26:X:66:THR:HG22	2.03	0.41
26:X:43:VAL:HG22	26:X:76:ARG:HH12	1.84	0.41
26:X:43:VAL:CG1	26:X:47:ALA:HB3	2.50	0.41
1:0:243:A:H61	1:0:269:G:C1'	2.33	0.41
1:0:251:C:C2	1:0:259:G:C2	3.09	0.41
1:0:1634:G:H2'	1:0:1635:U:C6	2.54	0.41
1:0:1667:A:H2'	1:0:1668:U:C6	2.55	0.41
1:0:2839:C:H2'	1:0:2840:A:H5''	2.02	0.41
1:0:2911:C:H2'	1:0:2912:C:C6	2.56	0.41
37:9:8645:HOH:O	16:N:41:LYS:HD2	2.20	0.41
5:C:5:ILE:HD11	5:C:16:VAL:HG23	2.03	0.41
10:H:64:SER:O	10:H:65:LEU:C	2.62	0.41
16:N:74:PRO:HG2	16:N:159:TYR:CZ	2.56	0.41
16:N:113:SER:N	37:N:8848:HOH:O	2.53	0.41
16:N:155:GLU:HG2	16:N:156:GLU:HG3	2.03	0.41
18:P:22:TRP:C	18:P:23:PHE:HD1	2.28	0.41
24:V:51:LYS:O	24:V:54:ALA:HB3	2.21	0.41
25:W:73:LEU:HD12	25:W:113:SER:HA	2.03	0.41
31:3:8:ASN:O	31:3:9:THR:HB	2.20	0.41
1:0:151:A:C2	1:0:442:A:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:183:A:H1'	15:M:161:ARG:NH1	2.36	0.41
1:0:302:A:H5''	37:0:7219:HOH:O	2.21	0.41
1:0:338:C:H5''	37:0:5626:HOH:O	2.20	0.41
1:0:431:G:O2'	1:0:432:G:H5'	2.21	0.41
1:0:440:C:H2'	1:0:441:A:C8	2.56	0.41
1:0:1552:G:C6	1:0:1553:C:C4	3.08	0.41
1:0:1761:U:H4'	18:P:82:GLY:O	2.20	0.41
1:0:1789:G:H2'	1:0:1790:C:O5'	2.21	0.41
1:0:1849:G:H1'	1:0:2011:A:N1	2.35	0.41
1:0:2898:G:H4'	4:B:288:GLY:HA2	2.02	0.41
37:0:9502:HOH:O	15:M:182:LYS:HE3	2.20	0.41
2:9:4:G:O2'	16:N:44:ARG:NH2	2.54	0.41
2:9:106:U:O2'	2:9:107:C:H5'	2.21	0.41
4:B:314:ALA:CB	4:B:317:PRO:HG3	2.50	0.41
7:E:68:HIS:O	7:E:72:MET:HG3	2.21	0.41
8:F:46:GLU:N	37:F:3461:HOH:O	2.53	0.41
8:F:115:VAL:O	8:F:116:GLU:C	2.63	0.41
10:H:123:ILE:N	10:H:123:ILE:CD1	2.84	0.41
12:J:142:ASN:O	12:J:144:THR:HG23	2.21	0.41
13:K:125:ALA:C	13:K:127:ALA:H	2.29	0.41
16:N:37:ARG:HD3	16:N:37:ARG:HA	1.94	0.41
16:N:90:LEU:HD23	16:N:125:ALA:HB1	2.03	0.41
17:O:33:LEU:HA	17:O:40:HIS:NE2	2.36	0.41
17:O:77:ALA:HA	17:O:96:VAL:O	2.21	0.41
25:W:24:LEU:O	25:W:26:ILE:HG23	2.21	0.41
1:0:12:U:H2'	1:0:13:G:H5'	2.01	0.41
1:0:68:U:O2'	1:0:69:A:H5''	2.21	0.41
1:0:218:C:C5	1:0:220:C:C4	3.08	0.41
1:0:244:C:OP1	8:F:42:ARG:NH2	2.51	0.41
1:0:290:C:O2'	1:0:291:C:H5'	2.19	0.41
1:0:318:U:O2'	1:0:319:A:OP1	2.35	0.41
1:0:356:C:H3'	1:0:357:A:H2'	2.02	0.41
1:0:485:A:O2'	1:0:487:G:H5'	2.21	0.41
1:0:1079:A:H4'	1:0:2078:U:H5'	2.03	0.41
1:0:1838:U:O2'	1:0:2644:C:H5'	2.21	0.41
1:0:1904:A:H2'	1:0:1905:U:O4'	2.21	0.41
1:0:2296:C:H2'	1:0:2297:U:H6	1.86	0.41
1:0:2506:A:N6	1:0:2511:A:O2'	2.52	0.41
1:0:2598:U:O2	1:0:2600:A:C8	2.73	0.41
1:0:2900:G:H2'	1:0:2901:C:O4'	2.20	0.41
3:A:87:GLU:HB2	37:A:8918:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:211:LYS:CB	37:A:8914:HOH:O	2.64	0.41
6:D:15:GLU:O	6:D:16:PRO:O	2.39	0.41
6:D:35:ALA:HB3	37:D:6716:HOH:O	2.20	0.41
6:D:128:LEU:HD23	6:D:128:LEU:C	2.45	0.41
7:E:38:ILE:HA	7:E:51:SER:HB2	2.02	0.41
10:H:32:ALA:N	10:H:66:GLU:OE1	2.44	0.41
13:K:28:GLU:HG2	13:K:58:THR:HB	2.03	0.41
16:N:35:VAL:HB	16:N:46:GLN:HB2	2.03	0.41
17:O:14:LEU:HG	17:O:102:ILE:HD11	2.03	0.41
18:P:97:ARG:HD2	37:P:162:HOH:O	2.21	0.41
24:V:39:ALA:H	24:V:40:PRO:CD	2.25	0.41
25:W:62:LEU:HD23	25:W:97:ALA:HB1	2.02	0.41
25:W:131:PRO:O	25:W:136:GLY:N	2.48	0.41
26:X:18:ARG:NH1	37:X:2351:HOH:O	2.53	0.41
1:O:154:C:C2	1:O:155:C:C5	3.09	0.41
1:O:196:G:H1'	1:O:198:A:N7	2.35	0.41
1:O:249:G:H1'	1:O:265:U:O2	2.21	0.41
1:O:764:C:OP1	5:C:87:ARG:NH1	2.54	0.41
1:O:772:G:H2'	1:O:773:A:O4'	2.20	0.41
1:O:944:G:N2	25:W:44:MET:HE2	2.27	0.41
1:O:1064:U:H2'	1:O:1065:G:C8	2.56	0.41
1:O:1120:U:H2'	1:O:1121:G:H5'	2.02	0.41
1:O:1191:A:H3'	1:O:1192:A:H5''	2.02	0.41
1:O:1473:U:O4'	29:1:42:SER:HB3	2.20	0.41
1:O:1553:C:H2'	1:O:1554:C:C6	2.56	0.41
1:O:1767:A:O2'	1:O:1768:C:H5'	2.21	0.41
1:O:1794:G:P	18:P:133:SER:HB2	2.60	0.41
1:O:2028:U:H2'	1:O:2029:C:H6	1.86	0.41
1:O:2032:U:H1'	37:O:6047:HOH:O	2.21	0.41
1:O:2445:U:H2'	1:O:2446:G:H8	1.86	0.41
1:O:2676:C:H4'	12:J:70:PHE:CD1	2.56	0.41
1:O:2731:G:H2'	1:O:2732:U:O4'	2.20	0.41
1:O:2765:C:H2'	1:O:2766:A:C8	2.56	0.41
37:O:9389:HOH:O	15:M:186:SER:HB3	2.21	0.41
2:9:38:A:H2	2:9:43:G:H5''	1.85	0.41
2:9:39:U:H3'	37:9:8707:HOH:O	2.20	0.41
4:B:33:ASP:O	4:B:34:GLY:O	2.38	0.41
4:B:56:ASP:CG	4:B:322:ARG:HB3	2.46	0.41
4:B:162:MET:HG3	4:B:310:ARG:NE	2.35	0.41
4:B:182:VAL:O	4:B:183:GLU:C	2.63	0.41
5:C:57:PRO:HD2	5:C:73:LEU:HD22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:120:ASP:CG	5:C:123:LEU:HG	2.46	0.41
6:D:89:PRO:C	6:D:91:ALA:N	2.79	0.41
6:D:95:THR:O	6:D:97:GLN:N	2.54	0.41
10:H:140:TYR:CD1	10:H:140:TYR:N	2.89	0.41
11:I:114:TYR:CD1	11:I:114:TYR:N	2.88	0.41
12:J:52:GLN:O	12:J:53:ILE:C	2.63	0.41
12:J:129:PHE:CD1	12:J:129:PHE:C	2.98	0.41
12:J:130:VAL:HG11	12:J:135:ILE:CG1	2.51	0.41
13:K:40:THR:O	13:K:41:LYS:C	2.64	0.41
13:K:99:ASP:OD1	13:K:99:ASP:C	2.64	0.41
14:L:89:PHE:O	14:L:119:THR:N	2.50	0.41
15:M:34:GLU:HB3	15:M:38:GLU:HG3	2.02	0.41
15:M:46:LEU:HD22	15:M:50:ARG:CD	2.51	0.41
16:N:76:GLY:N	37:N:8840:HOH:O	2.50	0.41
17:O:25:VAL:HG23	17:O:26:TRP:N	2.36	0.41
18:P:13:VAL:HG11	18:P:40:VAL:HG12	2.02	0.41
18:P:63:ARG:HA	18:P:66:GLN:HB2	2.02	0.41
19:Q:77:ASP:N	19:Q:80:LYS:O	2.53	0.41
20:R:104:PHE:HE2	20:R:149:GLU:CD	2.29	0.41
22:T:61:GLU:N	37:T:4772:HOH:O	2.53	0.41
22:T:103:LEU:N	22:T:103:LEU:HD23	2.35	0.41
25:W:3:ALA:O	25:W:54:PHE:HA	2.21	0.41
29:1:25:LYS:NZ	37:1:3076:HOH:O	2.52	0.41
30:2:13:LYS:O	30:2:17:GLN:HG3	2.20	0.41
1:0:135:G:OP1	15:M:39:ARG:NH1	2.53	0.41
1:0:215:A:P	14:L:52:LYS:HZ1	2.44	0.41
1:0:696:C:H4'	37:0:7047:HOH:O	2.21	0.41
1:0:735:C:N4	31:3:15:ASN:HD21	2.19	0.41
1:0:1304:U:H2'	1:0:1305:C:C6	2.56	0.41
1:0:1821:A:O2'	1:0:1822:A:H5'	2.20	0.41
1:0:2134:G:C6	1:0:2258:A:C8	3.09	0.41
1:0:2909:G:H2'	1:0:2910:A:C8	2.56	0.41
37:0:9900:HOH:O	27:Y:212:ARG:HB3	2.20	0.41
3:A:66:ARG:HG2	37:A:8907:HOH:O	2.21	0.41
3:A:199:HIS:CD2	3:A:201:PHE:HB2	2.56	0.41
5:C:57:PRO:HG2	5:C:73:LEU:HD13	2.03	0.41
5:C:157:LEU:HD22	5:C:162:VAL:CG1	2.51	0.41
5:C:169:ALA:HB3	5:C:208:ALA:O	2.21	0.41
5:C:236:THR:HG23	5:C:238:SER:H	1.86	0.41
6:D:17:ARG:HG3	6:D:18:ILE:N	2.35	0.41
6:D:67:ASP:O	6:D:69:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:75:LEU:HD22	6:D:79:MET:HB3	2.02	0.41
8:F:19:ALA:C	8:F:22:VAL:HG22	2.46	0.41
14:L:89:PHE:N	14:L:117:GLU:O	2.54	0.41
16:N:47:LEU:HD22	16:N:47:LEU:HA	1.79	0.41
19:Q:86:VAL:HG22	19:Q:87:THR:N	2.35	0.41
21:S:23:LYS:HE2	37:S:8522:HOH:O	2.21	0.41
23:U:51:TRP:CD1	23:U:51:TRP:H	2.38	0.41
24:V:12:THR:HG23	24:V:14:ALA:N	2.31	0.41
24:V:39:ALA:C	24:V:41:GLU:N	2.79	0.41
25:W:56:GLU:O	25:W:143:THR:HG23	2.20	0.41
25:W:108:ARG:O	25:W:110:GLN:N	2.54	0.41
28:Z:47:VAL:HA	28:Z:56:GLN:O	2.20	0.41
1:0:204:A:C2'	1:0:205:U:H5'	2.51	0.40
1:0:268:U:H1'	37:0:3602:HOH:O	2.20	0.40
1:0:532:A:N1	1:0:2660:G:O2'	2.46	0.40
1:0:706:G:N2	1:0:707:C:H41	2.18	0.40
1:0:727:G:H3'	1:0:728:C:C6	2.56	0.40
1:0:1097:A:H5''	25:W:125:HIS:CE1	2.56	0.40
1:0:2071:C:H5'	37:0:9338:HOH:O	2.21	0.40
1:0:2296:C:H2'	1:0:2297:U:C6	2.57	0.40
1:0:2600:A:H2'	1:0:2601:A:O4'	2.21	0.40
1:0:2649:A:H5'	1:0:2649:A:H8	1.86	0.40
1:0:2708:G:N2	13:K:1:MET:O	2.54	0.40
2:9:34:A:H1'	16:N:153:GLN:HE22	1.85	0.40
2:9:49:G:OP1	16:N:78:MET:HG2	2.21	0.40
4:B:109:LEU:CD1	4:B:113:LEU:HD12	2.50	0.40
4:B:321:PRO:HA	37:B:8958:HOH:O	2.19	0.40
5:C:93:LYS:HA	37:C:8555:HOH:O	2.21	0.40
6:D:85:GLN:O	6:D:86:THR:HG23	2.21	0.40
8:F:4:VAL:HA	8:F:76:PHE:CZ	2.56	0.40
10:H:49:GLN:NE2	10:H:140:TYR:CE2	2.83	0.40
12:J:6:PHE:O	12:J:8:ALA:N	2.45	0.40
13:K:69:LEU:HD12	13:K:97:ILE:HD13	2.03	0.40
14:L:34:GLY:C	14:L:36:ASP:N	2.79	0.40
16:N:94:GLU:HG3	16:N:186:LEU:HD12	2.03	0.40
17:O:113:VAL:O	17:O:114:ILE:HD13	2.21	0.40
25:W:118:LEU:HD23	25:W:118:LEU:N	2.36	0.40
25:W:146:ILE:O	25:W:150:LEU:HG	2.21	0.40
1:0:939:A:C2	1:0:1027:G:N3	2.90	0.40
1:0:1494:A:C4	1:0:1495:C:C5	3.09	0.40
1:0:2779:G:H21	7:E:143:GLN:NE2	2.18	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:37:C:H4'	16:N:111:PRO:HD2	2.02	0.40
5:C:124:VAL:HA	5:C:230:GLY:O	2.20	0.40
6:D:28:GLY:CA	6:D:69:ILE:HG23	2.43	0.40
6:D:105:SER:HB2	6:D:131:THR:HG23	2.03	0.40
8:F:46:GLU:OE1	8:F:100:ASP:HA	2.20	0.40
9:G:14:GLU:C	9:G:16:LYS:H	2.29	0.40
16:N:31:LYS:HB2	16:N:101:VAL:HG23	2.04	0.40
17:O:77:ALA:C	17:O:98:LEU:HD11	2.46	0.40
19:Q:86:VAL:CG2	19:Q:87:THR:N	2.84	0.40
22:T:71:VAL:CG1	22:T:90:PRO:HB3	2.37	0.40
26:X:41:PHE:CZ	26:X:74:ALA:HB3	2.56	0.40
27:Y:189:ASN:C	27:Y:189:ASN:ND2	2.80	0.40
29:1:53:LYS:HA	29:1:53:LYS:HD3	1.93	0.40
1:0:66:G:H2'	37:0:9911:HOH:O	2.20	0.40
1:0:69:A:C2'	1:0:70:A:OP2	2.70	0.40
1:0:201:G:N2	1:0:202:U:C2	2.90	0.40
1:0:294:C:H2'	1:0:295:C:O4'	2.22	0.40
1:0:695:C:H2'	1:0:696:C:C6	2.57	0.40
1:0:1370:G:H5''	37:R:8838:HOH:O	2.21	0.40
1:0:1456:C:H2'	1:0:1457:U:C6	2.56	0.40
1:0:1771:U:O2	28:Z:19:GLY:HA2	2.21	0.40
1:0:1845:A:P	3:A:190:ARG:HH11	2.45	0.40
1:0:2493:C:H2'	1:0:2493:C:O2	2.22	0.40
3:A:76:VAL:HG23	28:Z:63:LYS:HB3	2.02	0.40
5:C:1:MET:HG2	5:C:2:GLN:HE21	1.86	0.40
5:C:175:LYS:HD3	5:C:184:ARG:O	2.21	0.40
6:D:64:ARG:CG	6:D:67:ASP:HB3	2.49	0.40
7:E:162:PHE:CD1	7:E:162:PHE:N	2.89	0.40
9:G:64:ASN:O	9:G:68:GLU:HG3	2.20	0.40
9:G:69:ARG:NH1	37:G:3513:HOH:O	2.54	0.40
10:H:46:TYR:HA	10:H:47:PRO:HD3	1.77	0.40
15:M:19:GLN:N	37:M:8864:HOH:O	2.54	0.40
16:N:62:HIS:O	16:N:64:SER:N	2.55	0.40
17:O:53:GLN:NE2	17:O:112:ARG:HH21	2.19	0.40
18:P:103:THR:HB	37:P:180:HOH:O	2.21	0.40
20:R:119:VAL:O	20:R:119:VAL:HG12	2.21	0.40
22:T:103:LEU:C	22:T:105:ASP:N	2.78	0.40
1:0:145:A:N3	15:M:111:ASN:HB3	2.37	0.40
1:0:1127:C:H2'	1:0:1128:U:H5'	2.03	0.40
1:0:1839:A:H5'	1:0:2643:G:H4'	2.02	0.40
1:0:1851:G:O2'	1:0:1852:A:H5'	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2419:U:H5''	1:0:2420:G:H5'	2.03	0.40
1:0:2479:A:H5''	37:0:4453:HOH:O	2.21	0.40
1:0:2768:A:H3'	37:0:4229:HOH:O	2.21	0.40
3:A:150:PRO:HD3	37:A:8886:HOH:O	2.21	0.40
4:B:42:ALA:HB1	4:B:308:LEU:HD11	2.04	0.40
4:B:79:MET:HB2	4:B:188:HIS:CE1	2.57	0.40
4:B:127:GLN:HG3	37:B:8943:HOH:O	2.21	0.40
4:B:153:SER:HB2	4:B:287:TYR:CZ	2.57	0.40
6:D:80:ALA:O	6:D:84:LEU:HG	2.20	0.40
7:E:69:ILE:O	7:E:70:GLU:C	2.65	0.40
12:J:143:LYS:HA	12:J:145:TRP:CZ3	2.56	0.40
13:K:120:ARG:HB3	13:K:121:PHE:CE1	2.55	0.40
15:M:5:TYR:O	15:M:7:TYR:N	2.55	0.40
17:O:23:GLY:C	37:O:3062:HOH:O	2.64	0.40
18:P:124:ASP:HA	37:P:167:HOH:O	2.20	0.40
20:R:63:ASN:OD1	20:R:63:ASN:N	2.54	0.40
25:W:137:GLN:HE21	25:W:141:HIS:CE1	2.35	0.40
27:Y:177:LYS:HG3	27:Y:183:GLU:OE2	2.21	0.40
28:Z:57:CYS:C	28:Z:59:TYR:H	2.29	0.40
29:1:22:CYS:HA	37:1:2086:HOH:O	2.20	0.40
1:0:47:G:N3	1:0:114:A:C2	2.90	0.40
1:0:95:A:H5''	1:0:97:G:O4'	2.21	0.40
1:0:645:U:OP2	14:L:4:LYS:CE	2.69	0.40
1:0:694:A:H2'	1:0:695:C:C5'	2.51	0.40
1:0:1012:A:O5'	1:0:1012:A:H8	2.05	0.40
1:0:1483:C:O2'	1:0:1484:G:H5'	2.21	0.40
1:0:1641:A:C2'	1:0:1642:A:H5'	2.51	0.40
1:0:2375:A:H2'	1:0:2376:C:C6	2.57	0.40
1:0:2419:U:H5''	1:0:2420:G:C5'	2.51	0.40
1:0:2450:C:H6	1:0:2450:C:O5'	2.04	0.40
1:0:2769:C:H2'	1:0:2770:G:C5'	2.51	0.40
1:0:2880:A:C2'	1:0:2881:C:H5'	2.48	0.40
3:A:186:TRP:CG	3:A:187:PRO:HA	2.57	0.40
8:F:49:PHE:O	8:F:95:ALA:HB1	2.21	0.40
11:I:72:GLU:O	11:I:74:ILE:N	2.54	0.40
16:N:22:GLN:HA	16:N:25:ARG:CZ	2.52	0.40
16:N:42:HIS:CG	16:N:62:HIS:HE1	2.40	0.40
16:N:108:SER:C	16:N:110:THR:H	2.30	0.40
24:V:27:LEU:O	24:V:30:ALA:HB3	2.21	0.40
28:Z:17:ARG:C	28:Z:18:TYR:CD1	2.99	0.40
28:Z:32:GLU:HA	28:Z:35:GLU:HG3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:2:20:ARG:HG3	30:2:20:ARG:NH1	2.11	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	
3	A	235/240 (98%)	191 (81%)	31 (13%)	13 (6%)	1	4
4	B	335/338 (99%)	291 (87%)	35 (10%)	9 (3%)	4	15
5	C	244/246 (99%)	201 (82%)	32 (13%)	11 (4%)	2	7
6	D	134/177 (76%)	85 (63%)	31 (23%)	18 (13%)	0	0
7	E	170/178 (96%)	150 (88%)	15 (9%)	5 (3%)	3	13
8	F	117/120 (98%)	93 (80%)	17 (14%)	7 (6%)	1	3
9	G	25/348 (7%)	23 (92%)	2 (8%)	0	100	100
10	H	156/177 (88%)	134 (86%)	17 (11%)	5 (3%)	3	11
11	I	68/162 (42%)	49 (72%)	14 (21%)	5 (7%)	1	2
12	J	140/145 (97%)	121 (86%)	14 (10%)	5 (4%)	2	10
13	K	130/132 (98%)	111 (85%)	17 (13%)	2 (2%)	8	28
14	L	141/165 (86%)	114 (81%)	25 (18%)	2 (1%)	9	30
15	M	192/195 (98%)	169 (88%)	20 (10%)	3 (2%)	7	27
16	N	184/187 (98%)	149 (81%)	23 (12%)	12 (6%)	1	3
17	O	113/116 (97%)	102 (90%)	8 (7%)	3 (3%)	4	15
18	P	141/149 (95%)	125 (89%)	12 (8%)	4 (3%)	4	14
19	Q	93/96 (97%)	86 (92%)	5 (5%)	2 (2%)	5	19
20	R	145/152 (95%)	122 (84%)	18 (12%)	5 (3%)	3	11
21	S	79/85 (93%)	69 (87%)	9 (11%)	1 (1%)	9	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	T	117/120 (98%)	92 (79%)	19 (16%)	6 (5%)	1	5
23	U	51/66 (77%)	43 (84%)	7 (14%)	1 (2%)	6	21
24	V	63/71 (89%)	50 (79%)	9 (14%)	4 (6%)	1	3
25	W	152/154 (99%)	136 (90%)	14 (9%)	2 (1%)	9	31
26	X	80/92 (87%)	69 (86%)	8 (10%)	3 (4%)	2	9
27	Y	140/241 (58%)	138 (99%)	2 (1%)	0	100	100
28	Z	71/83 (86%)	56 (79%)	10 (14%)	5 (7%)	1	2
29	1	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
30	2	47/50 (94%)	44 (94%)	1 (2%)	2 (4%)	2	7
31	3	90/92 (98%)	84 (93%)	6 (7%)	0	100	100
All	All	3707/4434 (84%)	3148 (85%)	424 (11%)	135 (4%)	2	10

All (135) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	34	ASP
4	B	34	GLY
4	B	139	ASP
4	B	206	THR
5	C	8	LEU
6	D	16	PRO
6	D	56	ARG
6	D	139	TYR
6	D	165	PHE
6	D	173	GLU
8	F	101	ALA
14	L	105	TYR
16	N	154	LEU
16	N	164	ASP
16	N	184	ILE
18	P	116	SER
20	R	121	GLU
20	R	135	ALA
22	T	100	ASP
24	V	43	PRO
25	W	77	ALA
26	X	70	ILE
26	X	87	ALA

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Mol	Chain	Res	Type
28	Z	20	ARG
28	Z	81	ARG
3	A	10	GLY
3	A	33	GLU
3	A	37	VAL
3	A	38	ILE
3	A	87	GLU
3	A	119	ALA
4	B	184	ASP
5	C	13	ASP
5	C	15	GLU
5	C	58	ALA
5	C	151	GLN
5	C	234	VAL
6	D	60	GLU
6	D	61	PHE
6	D	90	LEU
6	D	99	ASP
6	D	137	PRO
6	D	171	ASP
7	E	110	GLU
8	F	44	SER
8	F	61	MET
8	F	68	ASP
10	H	143	VAL
12	J	34	GLU
12	J	89	HIS
13	K	111	GLY
15	M	6	SER
16	N	113	SER
16	N	134	ASP
16	N	183	ASP
17	O	20	SER
17	O	21	SER
20	R	20	GLU
22	T	104	GLU
28	Z	21	VAL
30	2	37	HIS
3	A	122	SER
4	B	183	GLU
5	C	178	GLN
5	C	244	ALA

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Mol	Chain	Res	Type
6	D	96	SER
8	F	64	PRO
11	I	113	SER
11	I	128	THR
12	J	5	GLU
12	J	65	ASN
16	N	63	SER
16	N	65	ASP
16	N	133	ASP
18	P	139	ARG
20	R	126	LYS
23	U	7	ASP
30	2	22	PRO
3	A	101	GLU
4	B	107	SER
5	C	85	LYS
5	C	232	LEU
6	D	82	GLU
6	D	86	THR
7	E	121	ASP
10	H	19	ARG
10	H	70	LEU
10	H	115	GLY
13	K	24	THR
16	N	68	GLU
17	O	108	GLY
18	P	68	LYS
20	R	130	MET
26	X	82	GLU
28	Z	28	GLU
3	A	35	GLY
3	A	236	GLY
4	B	2	GLN
6	D	44	ILE
7	E	17	HIS
7	E	98	GLU
10	H	82	GLU
12	J	7	ASP
16	N	165	ALA
19	Q	89	ALA
24	V	39	ALA
25	W	49	ASN

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Mol	Chain	Res	Type
28	Z	67	GLY
5	C	142	ASP
6	D	45	THR
6	D	164	ALA
11	I	100	VAL
15	M	146	ASP
15	M	147	LEU
16	N	139	TRP
18	P	117	SER
24	V	20	LEU
3	A	102	GLY
11	I	109	PRO
24	V	2	VAL
3	A	192	VAL
7	E	136	PRO
8	F	43	GLY
11	I	92	VAL
14	L	69	ILE
21	S	47	VAL
22	T	53	GLY
4	B	181	ILE
6	D	27	ILE
4	B	82	VAL
8	F	59	ILE
22	T	42	VAL
22	T	62	VAL
22	T	90	PRO
19	Q	18	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	179/182 (98%)	170 (95%)	9 (5%)	22	54
4	B	282/283 (100%)	258 (92%)	24 (8%)	10	31
5	C	193/193 (100%)	180 (93%)	13 (7%)	15	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	D	117/148 (79%)	110 (94%)	7 (6%)	17	47
7	E	152/156 (97%)	145 (95%)	7 (5%)	24	58
8	F	93/94 (99%)	90 (97%)	3 (3%)	34	70
9	G	27/283 (10%)	25 (93%)	2 (7%)	13	37
10	H	134/145 (92%)	128 (96%)	6 (4%)	24	58
11	I	58/130 (45%)	56 (97%)	2 (3%)	32	68
12	J	118/121 (98%)	110 (93%)	8 (7%)	14	42
13	K	106/106 (100%)	105 (99%)	1 (1%)	70	89
14	L	113/127 (89%)	109 (96%)	4 (4%)	32	67
15	M	158/159 (99%)	153 (97%)	5 (3%)	34	70
16	N	149/150 (99%)	140 (94%)	9 (6%)	17	47
17	O	93/94 (99%)	87 (94%)	6 (6%)	15	43
18	P	113/117 (97%)	108 (96%)	5 (4%)	25	59
19	Q	79/80 (99%)	77 (98%)	2 (2%)	42	76
20	R	114/120 (95%)	110 (96%)	4 (4%)	32	67
21	S	71/74 (96%)	67 (94%)	4 (6%)	19	50
22	T	105/106 (99%)	98 (93%)	7 (7%)	15	42
23	U	44/52 (85%)	40 (91%)	4 (9%)	9	28
24	V	51/57 (90%)	49 (96%)	2 (4%)	28	64
25	W	130/130 (100%)	125 (96%)	5 (4%)	29	64
26	X	66/74 (89%)	60 (91%)	6 (9%)	9	28
27	Y	120/196 (61%)	111 (92%)	9 (8%)	12	37
28	Z	60/68 (88%)	59 (98%)	1 (2%)	53	83
29	1	46/47 (98%)	45 (98%)	1 (2%)	45	78
30	2	45/46 (98%)	44 (98%)	1 (2%)	45	78
31	3	79/79 (100%)	76 (96%)	3 (4%)	29	64
All	All	3095/3617 (86%)	2935 (95%)	160 (5%)	21	53

All (160) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	3	ARG
3	A	33	GLU

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Mol	Chain	Res	Type
3	A	36	ASP
3	A	69	LEU
3	A	94	LEU
3	A	153	ARG
3	A	175	LYS
3	A	179	MET
3	A	217	ARG
4	B	7	ARG
4	B	11	LEU
4	B	27	ASN
4	B	49	THR
4	B	53	LEU
4	B	68	THR
4	B	97	LEU
4	B	103	ASP
4	B	110	ASP
4	B	140	LEU
4	B	149	ASP
4	B	175	LEU
4	B	190	MET
4	B	195	ARG
4	B	234	ARG
4	B	245	SER
4	B	251	VAL
4	B	254	GLN
4	B	256	GLN
4	B	265	LEU
4	B	274	GLU
4	B	277	GLU
4	B	280	VAL
4	B	307	ARG
5	C	2	GLN
5	C	42	ARG
5	C	76	ARG
5	C	78	ARG
5	C	91	PRO
5	C	115	LEU
5	C	187	ARG
5	C	214	THR
5	C	222	ASP
5	C	233	THR
5	C	234	VAL

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Mol	Chain	Res	Type
5	C	236	THR
5	C	237	GLU
6	D	21	VAL
6	D	24	HIS
6	D	86	THR
6	D	104	PHE
6	D	133	ASN
6	D	149	ARG
6	D	153	THR
7	E	3	VAL
7	E	7	ILE
7	E	86	VAL
7	E	100	ASP
7	E	102	VAL
7	E	126	ILE
7	E	156	ASP
8	F	46	GLU
8	F	65	GLU
8	F	78	GLU
9	G	25	GLU
9	G	64	ASN
10	H	21	GLU
10	H	44	ASP
10	H	61	ARG
10	H	87	LYS
10	H	114	ASP
10	H	157	TYR
11	I	81	GLU
11	I	108	HIS
12	J	46	ILE
12	J	52	GLN
12	J	74	ARG
12	J	92	GLN
12	J	99	GLU
12	J	127	ILE
12	J	130	VAL
12	J	131	THR
13	K	10	GLN
14	L	18	HIS
14	L	35	ARG
14	L	99	GLU
14	L	144	ASP

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Mol	Chain	Res	Type
15	M	23	LEU
15	M	46	LEU
15	M	93	ARG
15	M	130	GLU
15	M	186	SER
16	N	26	LEU
16	N	43	VAL
16	N	47	LEU
16	N	50	LEU
16	N	53	ASN
16	N	58	LEU
16	N	93	GLN
16	N	139	TRP
16	N	164	ASP
17	O	32	ARG
17	O	34	GLU
17	O	38	ARG
17	O	43	VAL
17	O	98	LEU
17	O	102	ILE
18	P	52	LYS
18	P	91	LYS
18	P	94	TRP
18	P	98	ILE
18	P	110	ASP
19	Q	57	ASP
19	Q	95	GLU
20	R	39	THR
20	R	82	GLU
20	R	109	MET
20	R	143	VAL
21	S	10	VAL
21	S	30	ASP
21	S	71	ASP
21	S	72	ASP
22	T	5	ASP
22	T	23	VAL
22	T	39	ASN
22	T	96	VAL
22	T	98	VAL
22	T	112	LEU
22	T	115	GLU

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Mol	Chain	Res	Type
23	U	11	THR
23	U	28	THR
23	U	48	ASN
23	U	54	THR
24	V	13	PRO
24	V	43	PRO
25	W	1	MET
25	W	26	ILE
25	W	144	GLU
25	W	146	ILE
25	W	154	ARG
26	X	27	ASP
26	X	49	ARG
26	X	72	VAL
26	X	80	GLU
26	X	82	GLU
26	X	88	GLU
27	Y	154	ARG
27	Y	157	ILE
27	Y	163	THR
27	Y	187	VAL
27	Y	189	ASN
27	Y	191	ASP
27	Y	201	GLU
27	Y	228	VAL
27	Y	231	PRO
28	Z	41	ASN
29	1	14	THR
30	2	20	ARG
31	3	18	GLN
31	3	87	ARG
31	3	89	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (111) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	29	HIS
3	A	47	HIS
3	A	125	ASN
3	A	199	HIS
3	A	218	ASN
4	B	2	GLN

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Mol	Chain	Res	Type
4	B	27	ASN
4	B	145	HIS
4	B	188	HIS
4	B	191	ASN
4	B	221	GLN
4	B	238	ASN
4	B	243	ASN
4	B	256	GLN
4	B	260	HIS
4	B	320	GLN
4	B	332	ASN
5	C	2	GLN
5	C	39	GLN
5	C	108	GLN
5	C	129	HIS
5	C	163	HIS
6	D	47	GLN
6	D	97	GLN
6	D	103	ASN
6	D	133	ASN
7	E	66	GLN
7	E	143	GLN
8	F	80	GLN
9	G	17	GLN
9	G	64	ASN
10	H	34	HIS
10	H	59	GLN
10	H	62	HIS
10	H	73	ASN
10	H	131	GLN
10	H	135	GLN
10	H	148	HIS
11	I	88	GLN
11	I	106	GLN
12	J	25	GLN
12	J	29	GLN
12	J	52	GLN
12	J	92	GLN
12	J	107	ASN
12	J	142	ASN
13	K	10	GLN
13	K	67	GLN

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Mol	Chain	Res	Type
14	L	7	GLN
14	L	18	HIS
14	L	41	HIS
14	L	42	ASN
14	L	43	HIS
14	L	58	GLN
15	M	24	GLN
15	M	52	GLN
15	M	58	GLN
15	M	170	ASN
16	N	22	GLN
16	N	40	ASN
16	N	107	ASN
16	N	132	ASN
16	N	140	GLN
16	N	153	GLN
17	O	53	GLN
17	O	105	ASN
18	P	50	GLN
18	P	57	ASN
18	P	66	GLN
18	P	118	GLN
19	Q	16	ASN
19	Q	40	HIS
19	Q	59	GLN
19	Q	94	GLN
20	R	61	GLN
20	R	98	ASN
20	R	113	HIS
20	R	117	HIS
20	R	140	GLN
21	S	53	ASN
22	T	11	GLN
22	T	39	ASN
22	T	43	ASN
22	T	64	ASN
22	T	73	HIS
23	U	39	ASN
24	V	60	GLN
25	W	14	HIS
25	W	28	HIS
25	W	59	GLN

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Mol	Chain	Res	Type
25	W	110	GLN
25	W	119	HIS
25	W	125	HIS
25	W	141	HIS
26	X	22	ASN
26	X	23	HIS
26	X	36	HIS
27	Y	119	GLN
27	Y	133	HIS
27	Y	149	GLN
27	Y	189	ASN
29	1	8	GLN
29	1	16	HIS
29	1	28	HIS
30	2	16	ASN
30	2	41	HIS
30	2	45	ASN
31	3	15	ASN
31	3	30	GLN
31	3	43	ASN
31	3	48	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2744/2922 (93%)	250 (9%)	26 (0%)
2	9	121/122 (99%)	17 (14%)	1 (0%)
All	All	2865/3044 (94%)	267 (9%)	27 (0%)

All (267) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	31	C
1	0	67	A
1	0	69	A
1	0	70	A
1	0	71	G
1	0	87	C
1	0	88	G
1	0	114	A
1	0	115	U

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Mol	Chain	Res	Type
1	0	120	A
1	0	130	C
1	0	138	U
1	0	141	C
1	0	151	A
1	0	166	A
1	0	186	A
1	0	191	A
1	0	192	A
1	0	200	C
1	0	219	G
1	0	236	A
1	0	237	G
1	0	271	C
1	0	272	A
1	0	273	G
1	0	283	U
1	0	284	C
1	0	285	A
1	0	308	U
1	0	309	C
1	0	319	A
1	0	331	A
1	0	336	G
1	0	337	A
1	0	345	G
1	0	358	G
1	0	381	G
1	0	397	A
1	0	417	G
1	0	461	C
1	0	473	A
1	0	486	A
1	0	487	G
1	0	510	U
1	0	511	A
1	0	514	G
1	0	537	G
1	0	538	C
1	0	539	G
1	0	542	A
1	0	545	G

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Mol	Chain	Res	Type
1	0	553	G
1	0	559	U
1	0	588	G
1	0	604	G
1	0	620	A
1	0	632	A
1	0	644	G
1	0	660	A
1	0	674	A
1	0	688	A
1	0	701	U
1	0	759	C
1	0	777	U
1	0	809	G
1	0	821	U
1	0	835	U
1	0	841	A
1	0	857	A
1	0	858	U
1	0	868	G
1	0	869	G
1	0	871	G
1	0	872	U
1	0	875	A
1	0	877	G
1	0	878	G
1	0	884	C
1	0	885	G
1	0	898	G
1	0	905	C
1	0	920	C
1	0	921	G
1	0	923	A
1	0	953	G
1	0	960	G
1	0	961	A
1	0	1006	A
1	0	1008	C
1	0	1029	U
1	0	1045	G
1	0	1059	G
1	0	1060	C

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Mol	Chain	Res	Type
1	0	1072	G
1	0	1081	A
1	0	1088	A
1	0	1109	U
1	0	1110	G
1	0	1119	G
1	0	1120	U
1	0	1127	C
1	0	1130	U
1	0	1137	G
1	0	1151	G
1	0	1164	U
1	0	1166	A
1	0	1174	A
1	0	1175	G
1	0	1185	U
1	0	1193	A
1	0	1206	U
1	0	1208	C
1	0	1216	G
1	0	1237	U
1	0	1238	C
1	0	1239	G
1	0	1279	U
1	0	1289	C
1	0	1331	G
1	0	1342	C
1	0	1353	C
1	0	1360	C
1	0	1377	C
1	0	1407	A
1	0	1451	C
1	0	1457	U
1	0	1474	C
1	0	1485	A
1	0	1488	U
1	0	1505	U
1	0	1506	U
1	0	1524	U
1	0	1528	A
1	0	1562	C
1	0	1580	A

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Mol	Chain	Res	Type
1	0	1592	G
1	0	1617	C
1	0	1625	U
1	0	1626	A
1	0	1634	G
1	0	1656	A
1	0	1682	A
1	0	1684	A
1	0	1685	A
1	0	1692	C
1	0	1701	A
1	0	1722	U
1	0	1723	G
1	0	1725	C
1	0	1730	G
1	0	1731	C
1	0	1752	G
1	0	1778	A
1	0	1779	A
1	0	1798	C
1	0	1819	G
1	0	1820	G
1	0	1829	A
1	0	1856	C
1	0	1873	G
1	0	1879	U
1	0	1919	A
1	0	1942	A
1	0	1968	A
1	0	1971	G
1	0	1973	A
1	0	1974	G
1	0	1978	A
1	0	1979	G
1	0	1980	U
1	0	1996	U
1	0	2004	U
1	0	2006	C
1	0	2008	U
1	0	2011	A
1	0	2012	U
1	0	2013	G

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Mol	Chain	Res	Type
1	0	2033	G
1	0	2034	U
1	0	2063	U
1	0	2064	U
1	0	2072	G
1	0	2073	G
1	0	2074	A
1	0	2096	A
1	0	2101	A
1	0	2102	G
1	0	2110	G
1	0	2133	U
1	0	2238	A
1	0	2243	C
1	0	2258	A
1	0	2271	G
1	0	2272	G
1	0	2291	A
1	0	2317	C
1	0	2321	A
1	0	2346	C
1	0	2354	A
1	0	2369	A
1	0	2422	U
1	0	2462	G
1	0	2465	A
1	0	2467	A
1	0	2469	A
1	0	2476	C
1	0	2483	A
1	0	2507	G
1	0	2511	A
1	0	2533	C
1	0	2537	G
1	0	2541	U
1	0	2553	A
1	0	2564	G
1	0	2589	U
1	0	2601	A
1	0	2602	G
1	0	2608	C
1	0	2613	G

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Mol	Chain	Res	Type
1	0	2638	G
1	0	2648	U
1	0	2649	A
1	0	2650	U
1	0	2664	A
1	0	2681	A
1	0	2682	C
1	0	2718	C
1	0	2719	A
1	0	2726	U
1	0	2747	C
1	0	2748	G
1	0	2749	U
1	0	2750	G
1	0	2762	C
1	0	2768	A
1	0	2786	G
1	0	2792	A
1	0	2800	A
1	0	2811	A
1	0	2812	A
1	0	2825	C
1	0	2836	G
1	0	2840	A
1	0	2850	C
1	0	2867	G
1	0	2876	G
1	0	2890	A
1	0	2896	A
1	0	2903	C
1	0	2914	A
2	9	2	U
2	9	7	G
2	9	14	G
2	9	22	G
2	9	23	U
2	9	24	U
2	9	25	G
2	9	34	A
2	9	40	C
2	9	41	C
2	9	43	G

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Mol	Chain	Res	Type
2	9	52	A
2	9	57	A
2	9	66	G
2	9	77	A
2	9	114	G
2	9	122	C

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	69	A
1	0	129	A
1	0	318	U
1	0	644	G
1	0	857	A
1	0	871	G
1	0	877	G
1	0	898	G
1	0	1080	C
1	0	1120	U
1	0	1237	U
1	0	1246	A
1	0	1352	A
1	0	1377	C
1	0	1450	C
1	0	1506	U
1	0	1942	A
1	0	1979	G
1	0	2011	A
1	0	2313	C
1	0	2467	A
1	0	2526	C
1	0	2536	C
1	0	2649	A
1	0	2718	C
1	0	2791	U
2	9	65	A

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

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	$\# Z > 2$
1	PSU	0	2621	1	18,21,22	1.60	2 (11%)	21,30,33	1.26	3 (14%)
1	UR3	0	2619	1	19,22,23	0.36	0	26,32,35	0.70	1 (3%)
1	OMG	0	2588	1	23,26,27	0.30	0	32,38,41	0.44	0
1	1MA	0	628	1	21,25,26	0.73	1 (4%)	30,37,40	0.77	1 (3%)
1	OMU	0	2587	1	19,22,23	0.36	0	25,31,34	0.42	0

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
1	PSU	0	2621	1	-	0/7/25/26	0/2/2/2
1	UR3	0	2619	1	-	0/7/25/26	0/2/2/2
1	OMG	0	2588	1	-	1/9/27/28	0/3/3/3
1	1MA	0	628	1	-	2/7/25/26	0/3/3/3
1	OMU	0	2587	1	-	0/9/27/28	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	2621	PSU	C2-N1	5.37	1.43	1.36
1	0	2621	PSU	C6-C5	3.25	1.38	1.35
1	0	628	1MA	C6-N6	2.55	1.34	1.28

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2621	PSU	C6-C5-C4	2.93	120.15	118.17
1	0	2621	PSU	O2-C2-N1	2.90	125.78	122.79
1	0	2621	PSU	C6-N1-C2	-2.86	120.04	122.69
1	0	628	1MA	N1-C2-N3	2.83	129.36	126.00
1	0	2619	UR3	C4-N3-C2	2.76	126.80	124.58

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	0	2588	OMG	C3'-C2'-O2'-CM2
1	0	628	1MA	C2'-C1'-N9-C4
1	0	628	1MA	C2'-C1'-N9-C8

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	0	2587	OMU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 231 ligands modelled in this entry, 231 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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, 95th 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	0	2749/2922 (94%)	-0.60	11 (0%) 88 84	29, 55, 100, 157	1 (0%)
2	9	122/122 (100%)	-0.35	2 (1%) 70 61	44, 68, 95, 159	0
3	A	237/240 (98%)	-0.14	3 (1%) 75 66	34, 62, 95, 116	0
4	B	337/338 (99%)	-0.17	1 (0%) 90 86	32, 64, 90, 97	0
5	C	246/246 (100%)	-0.22	0 100 100	29, 58, 81, 90	0
6	D	140/177 (79%)	0.68	7 (5%) 34 26	62, 107, 129, 138	0
7	E	172/178 (96%)	0.04	2 (1%) 76 68	52, 75, 97, 101	0
8	F	119/120 (99%)	0.16	1 (0%) 82 75	65, 84, 105, 117	0
9	G	29/348 (8%)	0.51	0 100 100	76, 98, 106, 107	0
10	H	160/177 (90%)	-0.12	3 (1%) 66 57	40, 61, 96, 107	0
11	I	70/162 (43%)	1.12	9 (12%) 7 6	112, 126, 144, 147	0
12	J	142/145 (97%)	-0.16	1 (0%) 84 77	43, 58, 82, 95	0
13	K	132/132 (100%)	-0.07	0 100 100	40, 61, 84, 89	0
14	L	145/165 (87%)	0.09	2 (1%) 73 64	29, 75, 115, 126	0
15	M	194/195 (99%)	-0.33	1 (0%) 87 82	40, 55, 69, 79	0
16	N	186/187 (99%)	0.14	3 (1%) 70 61	46, 71, 115, 125	0
17	O	115/116 (99%)	-0.13	0 100 100	47, 65, 81, 83	0
18	P	143/149 (95%)	-0.09	0 100 100	44, 66, 80, 86	0
19	Q	95/96 (98%)	-0.37	0 100 100	39, 51, 64, 79	0
20	R	147/152 (96%)	-0.13	5 (3%) 48 39	41, 56, 114, 128	0
21	S	81/85 (95%)	-0.15	0 100 100	52, 72, 88, 95	0
22	T	119/120 (99%)	-0.04	3 (2%) 58 48	51, 69, 94, 111	0
23	U	53/66 (80%)	-0.12	0 100 100	51, 64, 79, 85	0
24	V	65/71 (91%)	0.34	3 (4%) 37 29	63, 85, 118, 122	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	W	154/154 (100%)	-0.41	0 100 100	41, 56, 76, 85	0
26	X	82/92 (89%)	-0.06	1 (1%) 76 68	49, 66, 87, 101	0
27	Y	142/241 (58%)	-0.39	0 100 100	31, 53, 79, 95	0
28	Z	73/83 (87%)	0.23	1 (1%) 73 64	53, 69, 86, 102	0
29	1	56/57 (98%)	-0.72	0 100 100	35, 43, 49, 58	0
30	2	49/50 (98%)	0.09	0 100 100	40, 66, 94, 104	0
31	3	92/92 (100%)	-0.16	1 (1%) 78 70	42, 63, 76, 91	0
All	All	6646/7478 (88%)	-0.29	60 (0%) 81 74	29, 61, 106, 159	1 (0%)

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	9	1	U	5.1
1	0	840[A]	U	4.8
10	H	174	LEU	4.7
10	H	171	GLY	4.0
1	0	1175	G	3.7
24	V	1	THR	3.6
11	I	71	ALA	3.5
6	D	63	ILE	3.5
14	L	82	ALA	3.3
16	N	154	LEU	3.2
20	R	121	GLU	3.1
28	Z	82	SER	3.1
7	E	10	ASP	3.0
1	0	10	U	3.0
6	D	10	PHE	2.9
11	I	73	LEU	2.9
1	0	1171	A	2.8
1	0	1176	C	2.8
20	R	134	SER	2.8
24	V	2	VAL	2.7
11	I	128	THR	2.7
4	B	87	TYR	2.6
2	9	2	U	2.6
1	0	138	U	2.5
1	0	2345	A	2.5
6	D	53	LYS	2.5
22	T	119	ALA	2.5
24	V	40	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
6	D	69	ILE	2.5
20	R	135	ALA	2.5
6	D	55	LYS	2.4
1	0	1161	A	2.3
6	D	17	ARG	2.3
11	I	104	ALA	2.3
3	A	37	VAL	2.3
11	I	85	GLY	2.3
1	0	1130	U	2.2
1	0	1177	A	2.2
11	I	103	ILE	2.2
16	N	165	ALA	2.2
3	A	36	ASP	2.2
16	N	159	TYR	2.2
22	T	118	SER	2.2
11	I	66	GLY	2.2
8	F	91	VAL	2.1
15	M	194	GLY	2.1
31	3	41	GLU	2.1
3	A	237	GLY	2.1
22	T	112	LEU	2.1
10	H	43	ALA	2.1
11	I	129	SER	2.1
14	L	150	GLN	2.1
6	D	174	VAL	2.1
11	I	124	VAL	2.1
20	R	120	GLY	2.1
1	0	1279	U	2.0
20	R	129	ALA	2.0
12	J	4	ALA	2.0
26	X	83	ALA	2.0
7	E	156	ASP	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, 95th 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
1	OMU	0	2587	21/22	0.97	0.07	39,42,43,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	OMG	0	2588	24/25	0.98	0.06	40,42,44,44	0
1	UR3	0	2619	21/22	0.98	0.04	40,42,43,46	0
1	PSU	0	2621	20/21	0.98	0.05	40,41,43,44	0
1	1MA	0	628	23/24	0.99	0.05	32,37,39,39	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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, 95th 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($\text{\AA}^2$)	Q<0.9
34	NA	R	8586	1/1	0.70	0.41	81,81,81,81	0
32	MG	0	8038	1/1	0.74	0.15	38,38,38,38	0
34	NA	0	8568	1/1	0.75	0.33	84,84,84,84	0
34	NA	0	8569	1/1	0.81	0.18	66,66,66,66	0
32	MG	0	8050	1/1	0.85	0.08	97,97,97,97	0
32	MG	0	8104	1/1	0.86	0.13	61,61,61,61	0
34	NA	0	8513	1/1	0.86	0.07	72,72,72,72	0
34	NA	0	8567	1/1	0.86	0.24	70,70,70,70	0
32	MG	0	8049	1/1	0.86	0.12	70,70,70,70	0
32	MG	0	8014	1/1	0.86	0.07	20,20,20,20	0
34	NA	0	8582	1/1	0.86	0.19	78,78,78,78	0
32	MG	0	8087	1/1	0.86	0.10	81,81,81,81	0
35	CL	0	8815	1/1	0.86	0.28	112,112,112,112	0
34	NA	0	8507	1/1	0.87	0.10	61,61,61,61	0
32	MG	0	8043	1/1	0.87	0.09	62,62,62,62	0
34	NA	0	8571	1/1	0.87	0.25	61,61,61,61	0
34	NA	0	8526	1/1	0.87	0.31	78,78,78,78	0
34	NA	9	8551	1/1	0.87	0.24	46,46,46,46	0
34	NA	9	8583	1/1	0.87	0.11	71,71,71,71	0
34	NA	0	8566	1/1	0.87	0.08	68,68,68,68	0
32	MG	2	8076	1/1	0.87	0.10	69,69,69,69	0
34	NA	0	8527	1/1	0.88	0.22	69,69,69,69	0
34	NA	0	8557	1/1	0.88	0.10	65,65,65,65	0
34	NA	0	8584	1/1	0.89	0.12	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
34	NA	0	8585	1/1	0.89	0.27	60,60,60,60	0
34	NA	0	8528	1/1	0.89	0.17	61,61,61,61	0
32	MG	0	8041	1/1	0.89	0.15	59,59,59,59	0
34	NA	0	8572	1/1	0.89	0.19	69,69,69,69	0
34	NA	0	8563	1/1	0.89	0.15	51,51,51,51	0
34	NA	0	8524	1/1	0.90	0.14	68,68,68,68	0
32	MG	0	8031	1/1	0.90	0.09	34,34,34,34	0
34	NA	0	8533	1/1	0.90	0.17	49,49,49,49	0
34	NA	R	8537	1/1	0.90	0.08	51,51,51,51	0
34	NA	0	8541	1/1	0.90	0.08	53,53,53,53	0
34	NA	0	8556	1/1	0.90	0.15	58,58,58,58	0
35	CL	A	8809	1/1	0.90	0.14	82,82,82,82	0
34	NA	0	8529	1/1	0.91	0.14	79,79,79,79	0
34	NA	0	8564	1/1	0.91	0.10	40,40,40,40	0
32	MG	0	8092	1/1	0.91	0.13	80,80,80,80	0
34	NA	0	8540	1/1	0.91	0.08	40,40,40,40	0
32	MG	0	8114	1/1	0.91	0.09	47,47,47,47	0
34	NA	0	8552	1/1	0.91	0.22	62,62,62,62	0
32	MG	0	8115	1/1	0.91	0.05	70,70,70,70	0
34	NA	S	8512	1/1	0.91	0.05	48,48,48,48	0
34	NA	0	8516	1/1	0.91	0.07	61,61,61,61	0
34	NA	0	8573	1/1	0.91	0.09	73,73,73,73	0
32	MG	T	8073	1/1	0.92	0.05	68,68,68,68	0
34	NA	0	8532	1/1	0.92	0.21	47,47,47,47	0
34	NA	0	8560	1/1	0.92	0.24	61,61,61,61	0
34	NA	0	8508	1/1	0.92	0.14	73,73,73,73	0
34	NA	0	8574	1/1	0.92	0.19	63,63,63,63	0
35	CL	B	8819	1/1	0.92	0.18	74,74,74,74	0
35	CL	J	8802	1/1	0.92	0.07	75,75,75,75	0
35	CL	N	8807	1/1	0.92	0.09	74,74,74,74	0
35	CL	O	8808	1/1	0.92	0.16	99,99,99,99	0
35	CL	Y	8820	1/1	0.92	0.12	55,55,55,55	0
34	NA	0	8530	1/1	0.93	0.07	72,72,72,72	0
35	CL	0	8805	1/1	0.93	0.08	77,77,77,77	0
32	MG	0	8089	1/1	0.93	0.07	69,69,69,69	0
32	MG	0	8099	1/1	0.93	0.06	62,62,62,62	0
34	NA	0	8505	1/1	0.93	0.07	49,49,49,49	0
34	NA	A	8545	1/1	0.93	0.07	46,46,46,46	0
34	NA	C	8504	1/1	0.93	0.04	48,48,48,48	0
34	NA	0	8579	1/1	0.93	0.15	62,62,62,62	0
32	MG	0	8100	1/1	0.93	0.12	66,66,66,66	0
35	CL	3	8804	1/1	0.93	0.09	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	MG	0	8103	1/1	0.94	0.12	67,67,67,67	0
32	MG	0	8093	1/1	0.94	0.14	50,50,50,50	0
32	MG	0	8105	1/1	0.94	0.16	63,63,63,63	0
34	NA	0	8577	1/1	0.94	0.16	72,72,72,72	0
32	MG	0	8094	1/1	0.94	0.10	67,67,67,67	0
32	MG	0	8097	1/1	0.94	0.08	51,51,51,51	0
34	NA	0	8534	1/1	0.94	0.10	55,55,55,55	0
35	CL	J	8801	1/1	0.94	0.06	67,67,67,67	0
32	MG	9	8095	1/1	0.94	0.06	54,54,54,54	0
32	MG	0	8046	1/1	0.94	0.08	55,55,55,55	0
34	NA	0	8550	1/1	0.94	0.14	56,56,56,56	0
35	CL	R	8806	1/1	0.94	0.10	63,63,63,63	0
34	NA	0	8570	1/1	0.94	0.21	66,66,66,66	0
32	MG	0	8042	1/1	0.94	0.06	55,55,55,55	0
36	CD	3	8704	1/1	0.94	0.06	72,72,72,72	0
35	CL	0	8817	1/1	0.95	0.08	74,74,74,74	0
35	CL	0	8822	1/1	0.95	0.11	79,79,79,79	0
34	NA	0	8520	1/1	0.95	0.06	33,33,33,33	0
32	MG	0	8051	1/1	0.95	0.09	67,67,67,67	0
32	MG	0	8107	1/1	0.95	0.10	65,65,65,65	0
32	MG	0	8082	1/1	0.95	0.13	76,76,76,76	0
34	NA	0	8559	1/1	0.95	0.13	66,66,66,66	0
34	NA	0	8514	1/1	0.95	0.14	39,39,39,39	0
34	NA	T	8543	1/1	0.95	0.10	43,43,43,43	0
34	NA	0	8562	1/1	0.95	0.17	81,81,81,81	0
32	MG	0	8045	1/1	0.95	0.07	59,59,59,59	0
35	CL	0	8816	1/1	0.95	0.16	79,79,79,79	0
32	MG	0	8057	1/1	0.96	0.13	67,67,67,67	0
34	NA	0	8517	1/1	0.96	0.06	52,52,52,52	0
32	MG	0	8088	1/1	0.96	0.07	34,34,34,34	0
34	NA	0	8561	1/1	0.96	0.11	50,50,50,50	0
34	NA	L	8580	1/1	0.96	0.15	72,72,72,72	0
34	NA	M	8547	1/1	0.96	0.09	45,45,45,45	0
34	NA	0	8523	1/1	0.96	0.12	37,37,37,37	0
32	MG	0	8062	1/1	0.96	0.06	65,65,65,65	0
32	MG	K	8069	1/1	0.96	0.04	62,62,62,62	0
34	NA	0	8565	1/1	0.96	0.10	49,49,49,49	0
32	MG	0	8101	1/1	0.96	0.06	70,70,70,70	0
35	CL	0	8814	1/1	0.96	0.10	71,71,71,71	0
32	MG	Y	8108	1/1	0.96	0.06	48,48,48,48	0
32	MG	0	8102	1/1	0.96	0.06	71,71,71,71	0
33	K	0	8401	1/1	0.96	0.28	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
33	K	0	8402	1/1	0.96	0.10	69,69,69,69	0
32	MG	0	8063	1/1	0.96	0.12	73,73,73,73	0
34	NA	0	8506	1/1	0.96	0.19	51,51,51,51	0
32	MG	0	8075	1/1	0.96	0.07	54,54,54,54	0
32	MG	0	8040	1/1	0.96	0.05	57,57,57,57	0
35	CL	L	8810	1/1	0.96	0.08	73,73,73,73	0
34	NA	0	8575	1/1	0.96	0.10	58,58,58,58	0
34	NA	0	8544	1/1	0.96	0.04	33,33,33,33	0
32	MG	0	8096	1/1	0.96	0.03	53,53,53,53	0
32	MG	0	8112	1/1	0.96	0.06	64,64,64,64	0
34	NA	0	8555	1/1	0.96	0.12	67,67,67,67	0
34	NA	0	8515	1/1	0.96	0.12	65,65,65,65	0
32	MG	0	8044	1/1	0.97	0.11	51,51,51,51	0
34	NA	0	8509	1/1	0.97	0.10	37,37,37,37	0
34	NA	Q	8548	1/1	0.97	0.07	49,49,49,49	0
34	NA	0	8510	1/1	0.97	0.12	40,40,40,40	0
34	NA	0	8511	1/1	0.97	0.04	43,43,43,43	0
32	MG	0	8047	1/1	0.97	0.05	59,59,59,59	0
32	MG	0	8048	1/1	0.97	0.05	62,62,62,62	0
35	CL	0	8803	1/1	0.97	0.08	80,80,80,80	0
34	NA	0	8536	1/1	0.97	0.05	52,52,52,52	0
35	CL	0	8812	1/1	0.97	0.10	65,65,65,65	0
35	CL	0	8813	1/1	0.97	0.08	67,67,67,67	0
34	NA	0	8538	1/1	0.97	0.06	61,61,61,61	0
32	MG	0	8098	1/1	0.97	0.06	30,30,30,30	0
32	MG	0	8064	1/1	0.97	0.08	43,43,43,43	0
32	MG	0	8091	1/1	0.97	0.06	53,53,53,53	0
34	NA	0	8518	1/1	0.97	0.04	32,32,32,32	0
34	NA	0	8519	1/1	0.97	0.04	34,34,34,34	0
34	NA	0	8554	1/1	0.97	0.08	38,38,38,38	0
34	NA	0	8578	1/1	0.97	0.14	77,77,77,77	0
34	NA	0	8502	1/1	0.97	0.06	49,49,49,49	0
34	NA	0	8522	1/1	0.97	0.22	68,68,68,68	0
34	NA	0	8503	1/1	0.97	0.25	70,70,70,70	0
34	NA	0	8558	1/1	0.97	0.21	107,107,107,107	0
35	CL	Q	8811	1/1	0.97	0.09	72,72,72,72	0
32	MG	0	8071	1/1	0.97	0.06	80,80,80,80	0
34	NA	0	8525	1/1	0.97	0.06	50,50,50,50	0
32	MG	0	8052	1/1	0.97	0.05	44,44,44,44	0
32	MG	A	8066	1/1	0.97	0.05	88,88,88,88	0
32	MG	0	8109	1/1	0.98	0.08	33,33,33,33	0
32	MG	0	8111	1/1	0.98	0.04	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	MG	0	8070	1/1	0.98	0.06	54,54,54,54	0
34	NA	0	8576	1/1	0.98	0.06	51,51,51,51	0
34	NA	0	8501	1/1	0.98	0.03	29,29,29,29	0
34	NA	0	8531	1/1	0.98	0.07	55,55,55,55	0
32	MG	0	8113	1/1	0.98	0.07	49,49,49,49	0
34	NA	0	8581	1/1	0.98	0.06	52,52,52,52	0
32	MG	0	8024	1/1	0.98	0.05	45,45,45,45	0
32	MG	0	8061	1/1	0.98	0.04	36,36,36,36	0
34	NA	0	8535	1/1	0.98	0.21	73,73,73,73	0
32	MG	0	8081	1/1	0.98	0.07	74,74,74,74	0
34	NA	0	8521	1/1	0.98	0.10	73,73,73,73	0
34	NA	0	8539	1/1	0.98	0.03	26,26,26,26	0
35	CL	J	8821	1/1	0.98	0.07	54,54,54,54	0
32	MG	A	8065	1/1	0.98	0.05	43,43,43,43	0
35	CL	M	8818	1/1	0.98	0.05	60,60,60,60	0
34	NA	J	8546	1/1	0.98	0.04	48,48,48,48	0
32	MG	0	8025	1/1	0.98	0.03	58,58,58,58	0
34	NA	0	8542	1/1	0.98	0.12	51,51,51,51	0
32	MG	0	8084	1/1	0.98	0.06	54,54,54,54	0
32	MG	0	8027	1/1	0.98	0.04	63,63,63,63	0
32	MG	0	8053	1/1	0.98	0.10	47,47,47,47	0
36	CD	O	8705	1/1	0.98	0.04	98,98,98,98	0
34	NA	0	8553	1/1	0.98	0.04	36,36,36,36	0
32	MG	0	8003	1/1	0.99	0.04	47,47,47,47	0
32	MG	0	8034	1/1	0.99	0.03	36,36,36,36	0
32	MG	3	8078	1/1	0.99	0.04	43,43,43,43	0
32	MG	0	8036	1/1	0.99	0.03	44,44,44,44	0
32	MG	0	8067	1/1	0.99	0.04	54,54,54,54	0
32	MG	0	8068	1/1	0.99	0.03	70,70,70,70	0
32	MG	0	8037	1/1	0.99	0.04	51,51,51,51	0
32	MG	0	8015	1/1	0.99	0.02	41,41,41,41	0
32	MG	0	8072	1/1	0.99	0.03	61,61,61,61	0
32	MG	0	8074	1/1	0.99	0.02	40,40,40,40	0
32	MG	0	8039	1/1	0.99	0.10	44,44,44,44	0
32	MG	0	8080	1/1	0.99	0.04	47,47,47,47	0
32	MG	0	8106	1/1	0.99	0.03	38,38,38,38	0
32	MG	0	8016	1/1	0.99	0.02	48,48,48,48	0
32	MG	0	8018	1/1	0.99	0.04	50,50,50,50	0
32	MG	0	8110	1/1	0.99	0.03	59,59,59,59	0
32	MG	0	8005	1/1	0.99	0.03	45,45,45,45	0
34	NA	0	8549	1/1	0.99	0.06	54,54,54,54	0
32	MG	0	8085	1/1	0.99	0.04	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	MG	0	8086	1/1	0.99	0.04	46,46,46,46	0
32	MG	0	8056	1/1	0.99	0.04	49,49,49,49	0
32	MG	0	8012	1/1	0.99	0.02	33,33,33,33	0
32	MG	0	8116	1/1	0.99	0.06	39,39,39,39	0
32	MG	0	8058	1/1	0.99	0.05	46,46,46,46	0
32	MG	0	8090	1/1	0.99	0.03	59,59,59,59	0
32	MG	0	8059	1/1	0.99	0.03	44,44,44,44	0
32	MG	B	8055	1/1	0.99	0.06	46,46,46,46	0
32	MG	0	8060	1/1	0.99	0.03	50,50,50,50	0
36	CD	Z	8703	1/1	0.99	0.02	71,71,71,71	0
32	MG	0	8013	1/1	0.99	0.03	54,54,54,54	0
32	MG	0	8011	1/1	1.00	0.04	32,32,32,32	0
32	MG	0	8028	1/1	1.00	0.03	48,48,48,48	0
32	MG	0	8083	1/1	1.00	0.06	52,52,52,52	0
32	MG	0	8029	1/1	1.00	0.02	55,55,55,55	0
32	MG	0	8030	1/1	1.00	0.02	34,34,34,34	0
32	MG	0	8001	1/1	1.00	0.02	33,33,33,33	0
32	MG	0	8054	1/1	1.00	0.02	43,43,43,43	0
32	MG	0	8032	1/1	1.00	0.03	32,32,32,32	0
32	MG	0	8033	1/1	1.00	0.02	37,37,37,37	0
32	MG	0	8004	1/1	1.00	0.02	43,43,43,43	0
32	MG	0	8035	1/1	1.00	0.02	58,58,58,58	0
32	MG	0	8002	1/1	1.00	0.04	35,35,35,35	0
32	MG	0	8006	1/1	1.00	0.01	37,37,37,37	0
32	MG	0	8007	1/1	1.00	0.03	29,29,29,29	0
32	MG	0	8017	1/1	1.00	0.04	33,33,33,33	0
32	MG	0	8008	1/1	1.00	0.02	35,35,35,35	0
32	MG	0	8019	1/1	1.00	0.02	39,39,39,39	0
32	MG	0	8020	1/1	1.00	0.03	31,31,31,31	0
32	MG	0	8021	1/1	1.00	0.01	31,31,31,31	0
32	MG	0	8022	1/1	1.00	0.02	42,42,42,42	0
32	MG	0	8023	1/1	1.00	0.02	42,42,42,42	0
32	MG	0	8009	1/1	1.00	0.04	36,36,36,36	0
32	MG	0	8010	1/1	1.00	0.02	45,45,45,45	0
32	MG	0	8077	1/1	1.00	0.03	32,32,32,32	0
36	CD	U	8701	1/1	1.00	0.01	76,76,76,76	0
32	MG	0	8079	1/1	1.00	0.02	43,43,43,43	0
36	CD	1	8702	1/1	1.00	0.04	68,68,68,68	0
32	MG	0	8026	1/1	1.00	0.01	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.