



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 04:10 am GMT

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

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

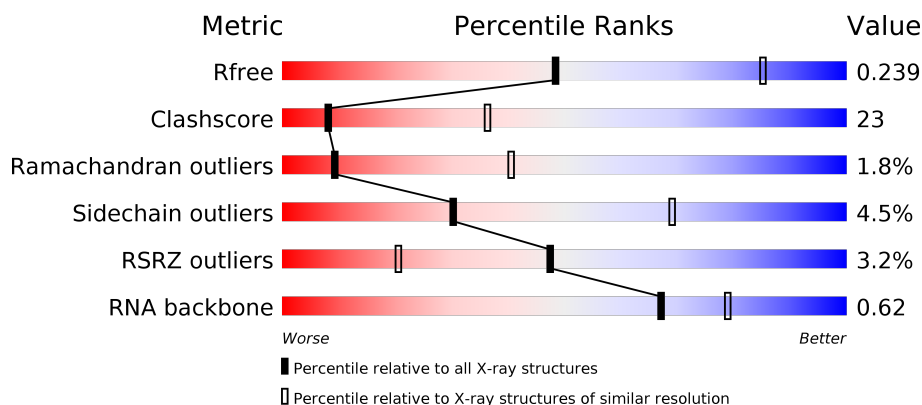
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*





The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	111664	1851 (3.00-3.00)
Clashscore	122126	2167 (3.00-3.00)
Ramachandran outliers	120053	2101 (3.00-3.00)
Sidechain outliers	120020	2104 (3.00-3.00)
RSRZ outliers	108989	1751 (3.00-3.00)
RNA backbone	2636	1017 (3.30-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	A	240	 62% 33% 5% 2%
2	B	338	 58% 37% 5%
3	C	246	 68% 27% 5%
4	D	177	 8% 42% 35% 15%

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

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

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

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

## 2 Entry composition

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	93	Total 93	Sr 93	0	0
34	1	2	Total 2	Sr 2	0	0
34	B	2	Total 2	Sr 2	0	0
34	3	2	Total 2	Sr 2	0	0
34	A	3	Total 3	Sr 3	0	0
34	R	1	Total 1	Sr 1	0	0
34	9	3	Total 3	Sr 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	S	1	Total 1	Sr 1	0	0
34	F	1	Total 1	Sr 1	0	0

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

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

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

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

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

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

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

- Molecule 38 is water.

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

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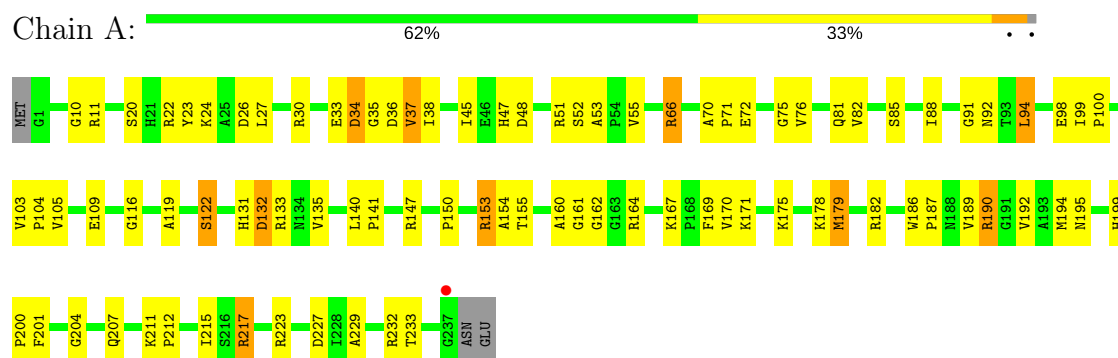
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	R	75	Total 75	O 75	0	0
38	S	37	Total 37	O 37	0	0
38	T	40	Total 40	O 40	0	0
38	U	28	Total 28	O 28	0	0
38	V	15	Total 15	O 15	0	0
38	W	69	Total 69	O 69	0	0
38	X	22	Total 22	O 22	0	0
38	Y	100	Total 100	O 100	0	0
38	Z	28	Total 28	O 28	0	0
38	1	61	Total 61	O 61	0	0
38	2	45	Total 45	O 45	0	0
38	3	76	Total 76	O 76	0	0
38	0	5897	Total 5897	O 5897	0	0
38	9	154	Total 154	O 154	0	0

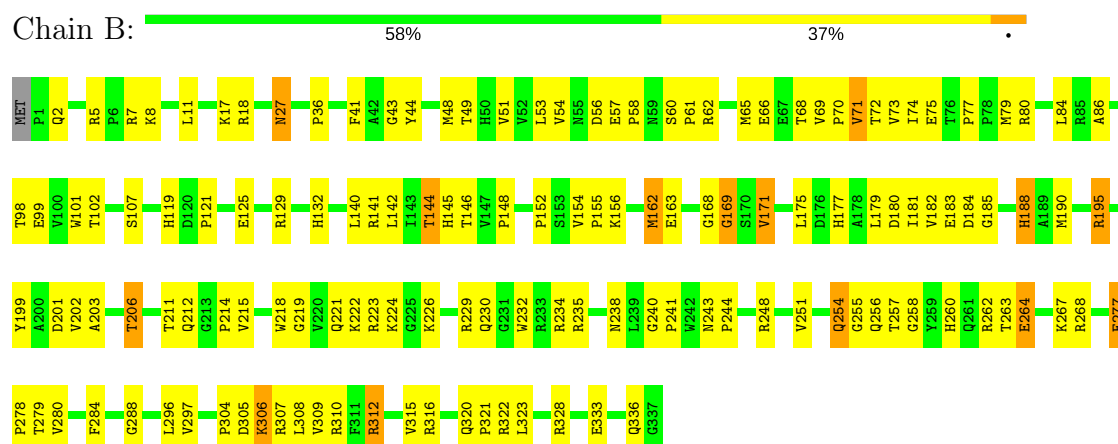
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

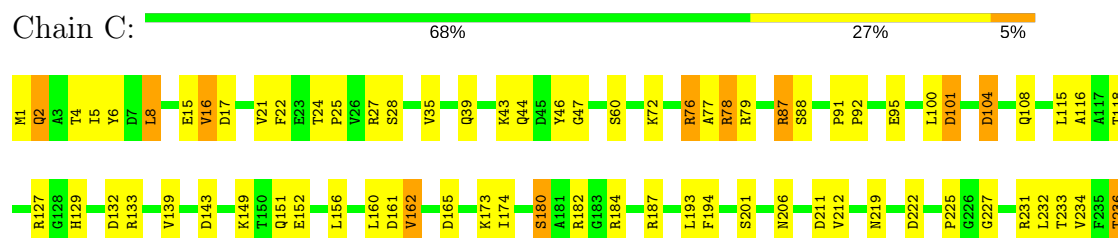
#### • Molecule 1: 50S ribosomal protein L2P



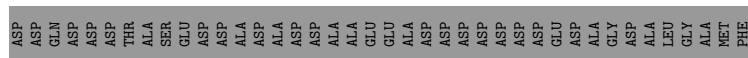
#### • Molecule 2: 50S ribosomal protein L3P



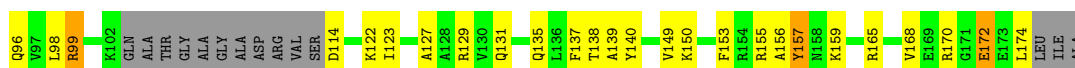
#### • Molecule 3: 50S ribosomal protein L4P



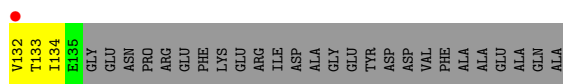




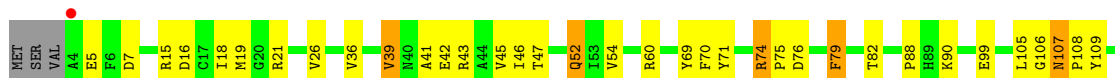
- Chain H:  57% 28% 5% 10%



- Chain I: 



- Chain J:  %

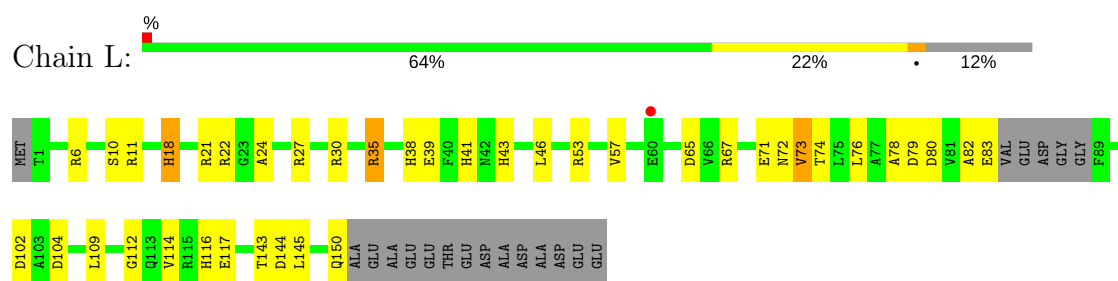


- Chain K:  72% 27%

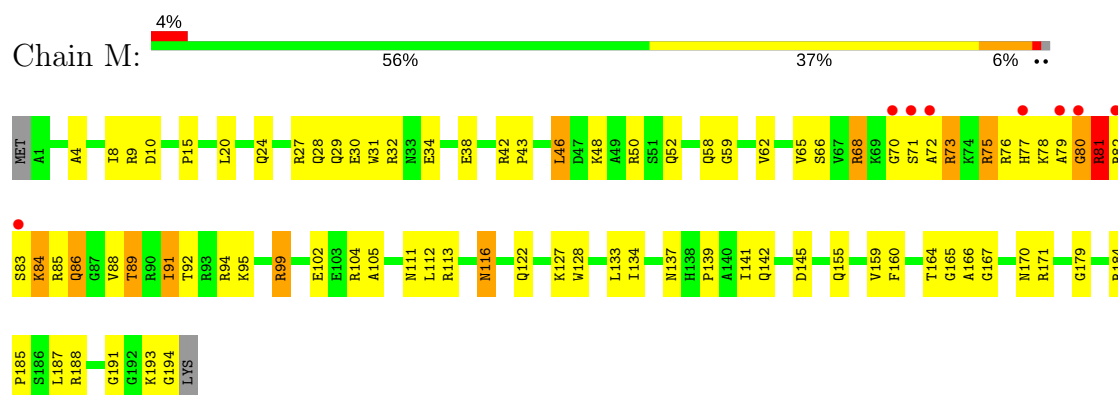


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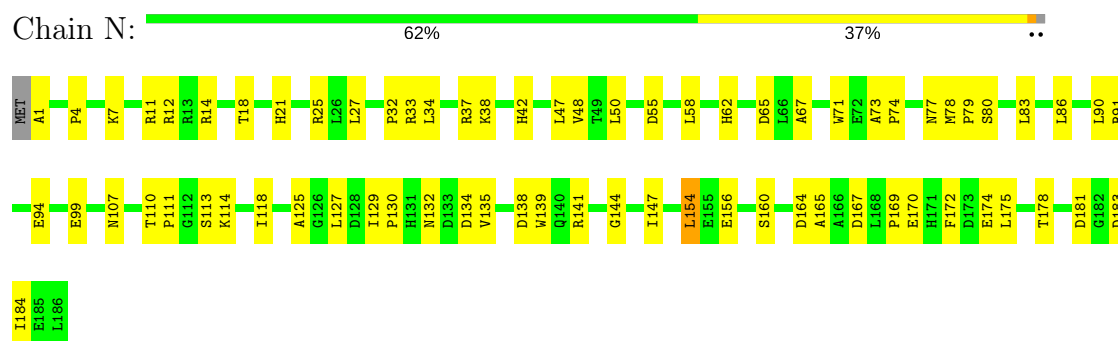




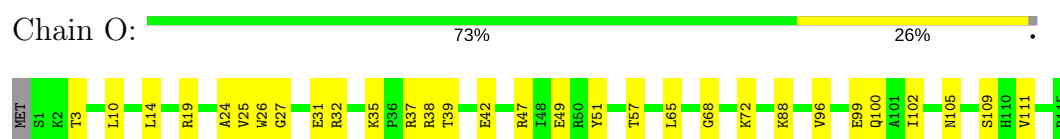
- Molecule 13: 50S ribosomal protein L15e



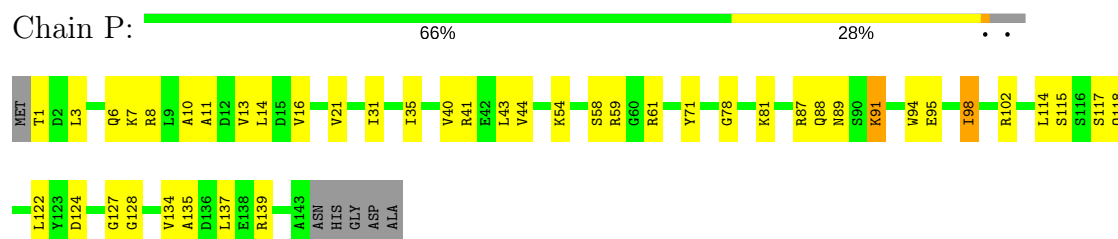
- Molecule 14: 50S ribosomal protein L18P



- Molecule 15: 50S ribosomal protein L18e



- Molecule 16: 50S ribosomal protein L19e



- Molecule 17: 50S ribosomal protein L21e

Chain Q:  69% 27% ..



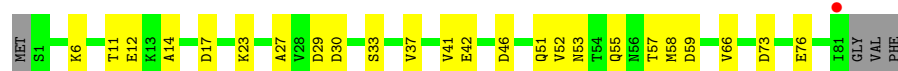
- Molecule 18: 50S ribosomal protein L22P

Chain R:  68% 26% . .



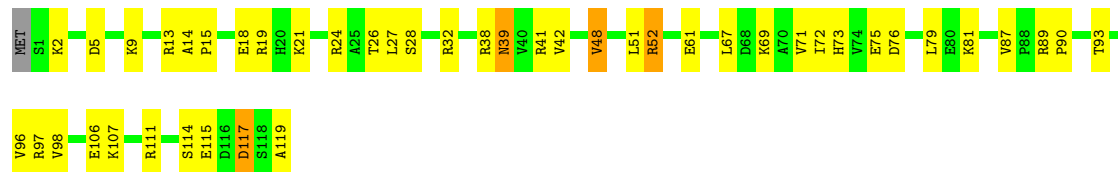
- Molecule 19: 50S ribosomal protein L23P

Chain S:  % 67% 28% 5%



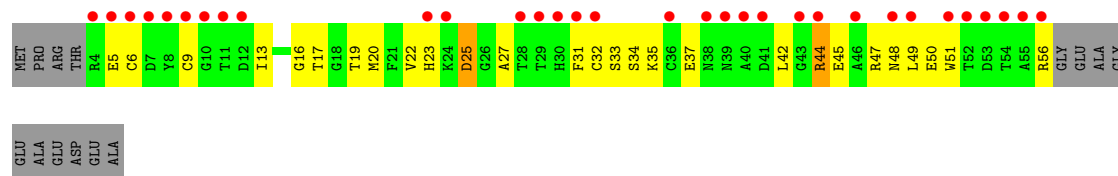
- Molecule 20: 50S ribosomal protein L24P

Chain T:  62% 34% ..



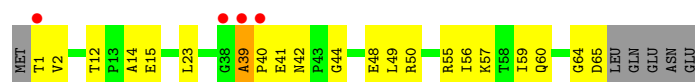
- Molecule 21: 50S ribosomal protein L24e

Chain U:  48% 39% 37% 21%

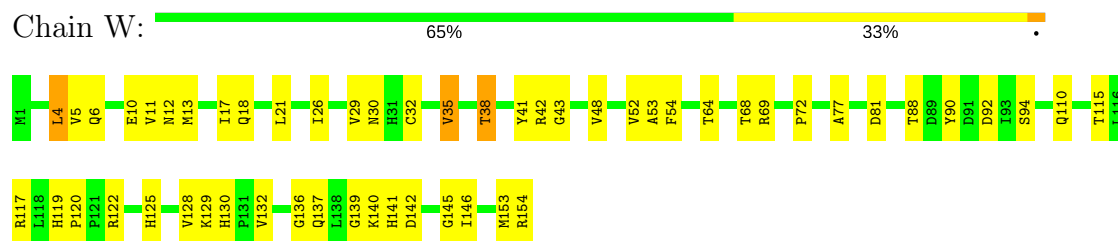


- Molecule 22: 50S ribosomal protein L29P

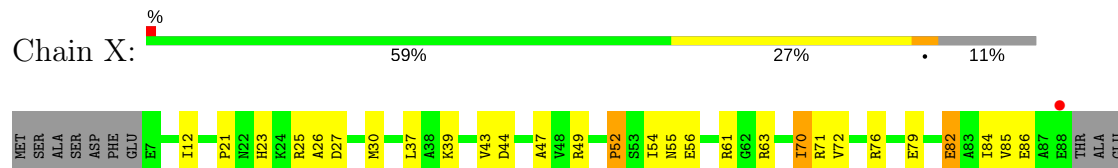
Chain V:  6% 62% 28% 8%



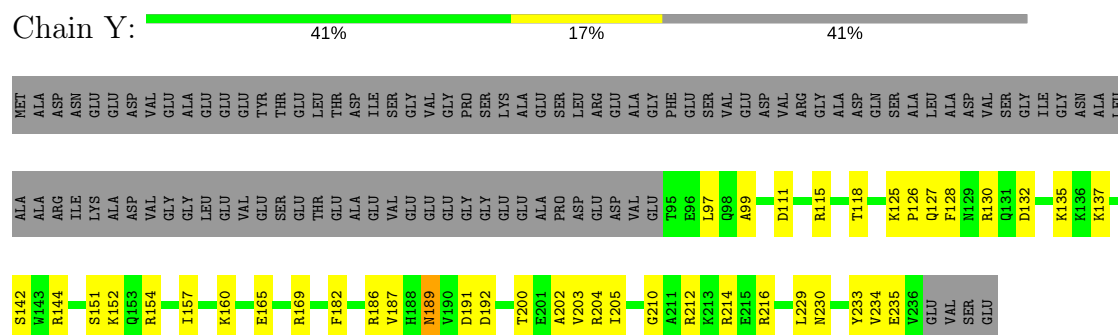
- Molecule 23: 50S ribosomal protein L30P



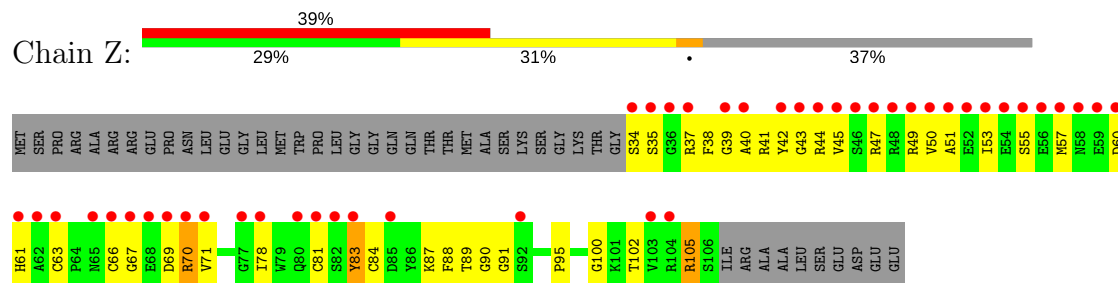
- Molecule 24: 50S ribosomal protein L31e



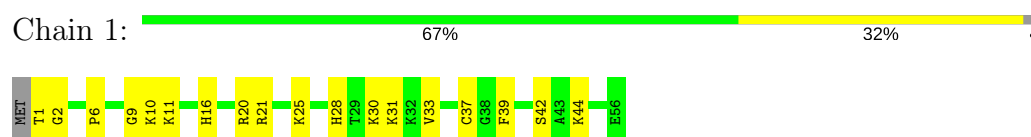
- Molecule 25: 50S ribosomal protein L32e



- Molecule 26: 50S ribosomal protein L37Ae

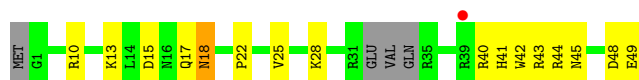


- Molecule 27: 50S ribosomal protein L37e

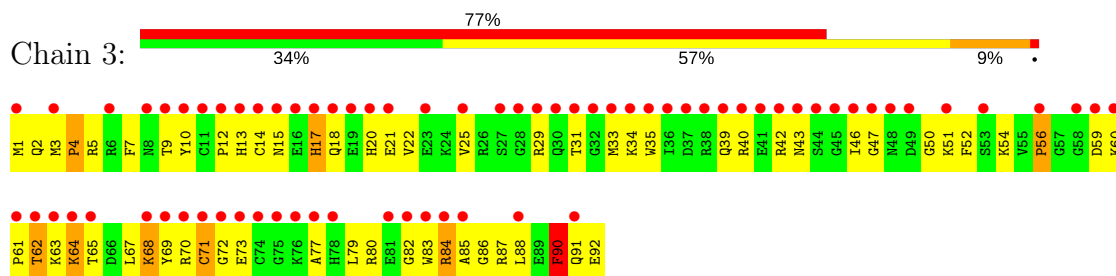


- Molecule 28: 50S ribosomal protein L39e

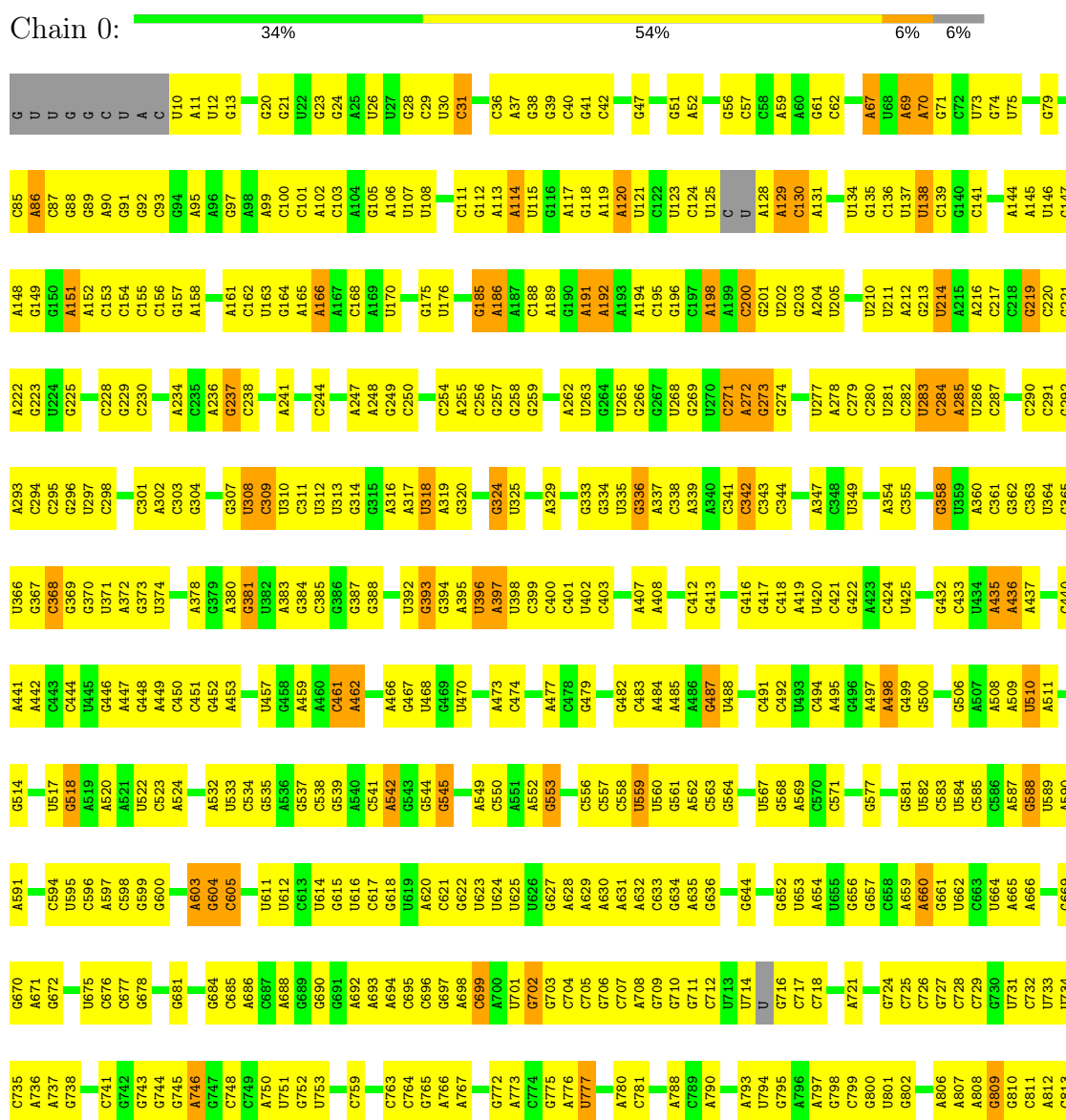




• Molecule 29: 50S ribosomal protein L44E



• Molecule 30: 23S RIBOSOMAL RNA



A1924	C1856	A1778	C1705	G1523	G1555	G1475	U1405	C1251	C1186	G1112	C1025	G964	G887	G814
G1925	A1857	A1778	G1706	A1624	G1556	A1476	A1406	C1255	U1187	U1115	U1026	A965	U888	U815
G1926	A1858	C1787	G1707	U1625	C1557	C1477	A1407	C1256	A1188	U1116	U1028	U967	C899	G816
A1927	A1859	C1787	G1708	A1626	C1558	U1478	A1408	C1256	A1189	U1116	U1028	U967	C899	G817
G1928	U1860	G1788	G1709	G1627	U1559	U1478	G1409	C1260	G1190	A1117	U1029	G968	A894	A818
G1929	C1861	G1789	A1710	U1630	U1561	A1485	G1410	C1260	A1191	A1118	U1030	G969	A895	A819
A1930	C1862	C1790	A1711	A1630	C1562	A1485	U1411	U1264	A1192	G1119	U1031	U970	A896	G820
A1931	C1863	U1791	G1712	A1631	C1563	G1490	A1413	U1264	A1193	U1120	A1032	U	C896	G821
G1932	C1864	A1796	G1713	A1632	C1563	U1490	A1414	U1265	A1194	G1121	U1041	U	C897	G822
G1933	A1865	A1797	A1716	A1633	C1566	C1495	G1415	U1266	A1195	C1127	U1042	G	C898	U823
A1934	A1866	C1798	A1717	C1634	G1567	A1496	G1416	C1267	C1196	C1127	U1043	U	C899	G824
G1935	G1867	G1799	G1718	U1635	G1568	G1497	G1417	C1268	G1197	U1128	C1043	C	G902	U825
C1936	G1868	G1800	G1719	U1635	G1568	G1497	G1417	C1269	U1198	G1129	C1044	C	U903	U826
U1937	A1841	U1800	G1719	A1641	U1569	U1500	U1419	U1270	A1199	U1130	G1045	G	U904	U827
G1938	U1871	A1801	U1722	A1642	U1570	U1500	C1420	U1271	A1200	U1131	U1046	C	U904	G828
U1939	C1872	G1802	U1722	A1643	A1572	U1503	C1421	C1271	G1131	A1132	U1047	C	C905	G829
G1940	G1873	C1803	G1723	U1644	A1573	A1504	U1422	C1272	A1201	A1133	U1047	U	G	G830
A1941	U1874	A1804	U1724	C1645	C1574	A1504	C1423	C1273	A1202	G1134	G1052	C	C910	G911
A1942	A1875	G1805	C1725	U1645	C1575	U1505	C1424	C1275	G1203	G1134	G1053	C	G911	G912
C1943	C1876	G1806	C1725	G1649	G1576	C1507	G1425	U1276	U1205	G1137	G1054	G	A912	G834
G1947	G1877	U1807	G1730	A1653	U1577	C1507	C1426	U1277	U1206	G1137	G1055	A	A913	G835
G1948	C1878	C1808	C1731	U1654	C1578	U1511	C1427	U1278	U1139	U1139	U1056	G	A916	C838
G1949	U1879	G1809	A1732	U1654	C1578	G1512	C1428	U1279	C1208	C1140	A1057	A	U917	C839
G1950	A1880	C1810	A1733	G1655	U1583	G1513	U1429	U1284	C1209	U1149	A1058	G	U917	U840
G1951	C1882	G1812	C1735	U1656	C1585	G1514	G1430	U1285	G1211	A1150	C1060	A	C920	A841
U	U1883	U1813	A1736	C1662	C1586	A1515	A1434	U1285	G1211	A1150	C1061	G	G921	C842
A	C1884	G1814	A1736	G1663	U1587	U1516	U1435	A1286	C1212	G1151	U1062	U	A922	A843
C	A1885	A1815	A1742	A1664	U1588	A1517	U1436	A1287	C1213	A1154	G1063	G	A923	A844
A	C1886	C1816	A1742	G1665	G1589	A1518	C1437	U1288	G1214	G1155	U1066	C	G924	C848
U	A1887	U1817	G1743	C1666	U1590	U1519	U1438	C1289	A1215	C1156	U1067	C	C925	C848
A	C1889	G1818	G1744	A1667	A1591	G1520	C1439	G1290	G1217	C1157	A1067	C	A926	C848
U	U1890	G1819	G1745	U1668	G1592	C1521	U1440	A1291	G1217	G1158	C1068	A	U927	C853
G	C1891	G1820	G1745	U1669	C1593	A1522	G1441	U1293	U1218	G1159	C1069	C	G928	G854
A	C1892	U1820	U1748	A1670	C1594	G1523	A1442	A1294	U1219	G1160	A1070	A	A929	U855
C	U1825	U1825	U1749	U1671	U1595	U1524	G1443	U1294	U1220	A1161	G1071	C999	G938	C856
C	G1898	C1826	G1752	C1675	U1596	G1525	G1444	U1298	G1224	G1162	A1073	C1000	A939	A857
C	C1899	G1827	C1753	G1676	A1597	A1526	G1445	U1299	C1225	G1163	A1073	U1003	G940	U858
U1964	G1902	G1828	C1754	U1677	U1598	A1527	G1446	G1300	G1226	U1164	G1074	U1003	G941	C859
C1965	U1903	A1829	A1755	A1678	U1599	A1528	U1447	C1303	C1227	G1165	G1074	C1004	U942	C859
U1966	A1904	C1830	G1755	A1679	G1600	G1529	A1448	C1303	C1228	A1166	A1079	C1005	U942	U862
U1967	U1905	U1831	G1756	C1679	G1601	G1530	G1449	U1304	C1229	G1167	C1080	A1006	U942	C863
A1968	U1906	G1832	U1757	C1680	G1602	G1531	G1450	C1305	C1229	G1168	A1081	C1008	U945	C863
C	C1907	U1833	U1758	G1681	A1603	A1533	C1451	C1305	C1229	U1169	A1081	C1008	C946	C863
G1970	U1907	C1834	A1759	A1682	G1604	C1537	G1452	U1309	U1234	U1170	G1087	U1009	U947	G868
G1971	G1908	U1835	G1760	G1683	G1605	C1538	G1453	U1310	G1235	A1171	A1088	U1009	U947	G869
U1972	A1909	A1884	U1761	A1684	A1606	U1539	U1454	G1311	A1236	G1172	G1089	C1010	G948	G870
A1973	A1910	C1840	C1763	A1685	A1607	G1540	G1461	G1312	U1237	G1173	G1089	C1011	U949	G871
G1974	C1913	C1841	C1764	C1686	G1608	G1541	G1462	G1313	C1238	A1174	U1095	A1012	G950	U872
U1977	C1914	C1844	G1765	C1687	C1613	G1542	U1461	U1314	G1240	A1174	U1096	A1013	A951	C873
G1978	U1915	A1845	U1766	A1691	G1614	G1543	U1462	U1315	G1241	G1175	A1097	A1014	G952	A874
G1979	C1916	C1692	U1766	C1692	A1615	U1544	U1463	G1316	G1242	C1176	A1097	C1015	G953	A875
U1980	G1917	G1848	C1769	G1697	A1616	G1545	C1464	G1324	G1243	U1177	A1098	U1016	G956	A876
A1981	U1918	G1849	U1770	G1697	C1617	G1546	U1470	G1325	C1243	G1178	A1098	U1017	U957	G877
U1985	C1920	U1851	G1772	A1701	G1618	U1547	A1471	C1326	U1244	G1179	C1102	U1018	G958	G878
G1986	A1921	U1702	G1773	G1619	G1619	U1548	U1472	G1327	C1245	U1180	C1103	C1019	G959	C878
C1987	A1922	U1703	G1774	C1620	G1620	U1549	C1472	C1328	C1246	A1181	C1104	A1020	C960	A882
C1988	G1923	G1622	A1775	C1554	C1554	G1552	C1473	G1329	A1247	C1182	U1109	G1021	G960	A883
										C1183	G1110	A1022	A961	C884
										U1111	C1184	C1023	C962	A885
												G1024	C963	A886

U1989	A2062	U2133	G2253	A2397	G2397	A2465	C2526	A2604	G2674	G2750	G2815	U2878
U2063	U2063	G2134	G2254	U2328	A2401	G2466	U2527	U2607	A2675	C2751	A2816	A2879
U1992	U2064	G2135	G2255	U2329	A2402	G2467	U2531	C2608	C2676	C2752	A2817	A2883
C1993	G2065	G2136	G2256	U2330	A2403	A2468	A2532	C2609	A2681	G2755	A2819	C2886
A1994	C2066	A	G2257	U2331	G2403	A2469	C2533	U2610	C2682	U2756	A2820	C2887
G1995	A2067	C	G2258	A2332	G2404	A2470	C2536	G2611	G2686	A2757	C2821	U2888
U1996	G2068	G	C2259	G2333	G2407	A2471	C2537	A2612	C2687	C2758	C2822	U2889
A1997	U2069	U	A2260	C2334	A2408	C2472	C2538	G2613	A2689	C2759	G2823	U2890
G1998	G2070	G	G2263	G2335	A2409	C2473	U2539	C2614	U2690	C2760	A2824	A2891
G2001	C2071	U	A2264	G2336	G2410	A2474	U2540	G2615	A2691	A2761	C2825	A2892
C2002	G2072	C	G2265	G2337	G2411	C2475	G2541	G2616	A2692	C2762	A2826	G2893
U2003	A2073	G	U2266	A	G2412	C2476	U2541	G2617	C2692	A2763	A2827	C2894
U2004	G2074	C	A2267	C	A2413	C2477	G2544	G2618	U2693	A2766	G2828	C2895
G2005	U2076	A	C2269	A	A2414	U2478	G2544	U2621	A2694	C2767	U2830	A2896
C2006	G2077	C	G2270	G	A2415	A2479	C2547	U2622	C2695	A2768	U2831	C2897
U2007	U2078	C	G2271	A	G2416	G2480	C2548	A2624	G2696	C2769	C2832	G2898
G2008	G2079	U	G2272	G2344	C2417	G2481	C2549	G2625	A2697	G2770	C2833	A2899
G2009	G2080	G	G2273	A2345	G2418	G2482	C2549	G2626	G2698	G2771	G2834	C2900
A2010	G2081	U	A2274	C2346	U2419	A2483	C2552	G2627	A2699	G2772	G2835	C2901
A2011	G2082	G	U2275	C2347	G2420	A2484	A2553	G2632	G2700	G2773	U2836	A2902
U2012	A2083	C	U2276	C2348	G2421	A2485	U2553	G2633	G2701	U2774	U2837	C2903
C2013	G2087	A	U2277	G2350	U2422	A2486	C2487	G2634	A2702	A2775	A2840	U2904
U2016	C2088	G	C2281	A2353	U2424	C2487	U2563	G2635	A2703	A2776	A2841	A2905
U2017	A2089	A	U2282	A2354	A2425	A2490	C2565	G2636	C2704	G2777	G2842	A2906
A2018	G2090	U	C2289	G2355	G2426	G2491	A2566	A2637	U2705	A2778	A2843	C2907
A2019	G2091	C	U2290	U2356	A2429	U2492	C2569	G2638	A2706	C2779	U2844	U2908
C2020	G2092	A	A2291	C2357	A2430	C2493	C2570	G2639	G2707	C2780	C2845	C2909
G2021	G2093	C	G2292	C2357	A2431	G2494	C2571	U2640	G2708	U2781	C2846	A2910
C2026	G2094	C	C2293	A2361	C2432	A2497	G2572	C2641	G2709	U2782	G2847	C2911
U2032	A2095	C	G2294	A2362	C2433	C2498	U2572	G2642	G2712	A2784	G2848	C2912
G2033	C2097	G	C2295	G2363	A2434	U2499	A2576	G2643	G2713	C2785	U2851	A2914
U2034	A2098	C	C2296	A2364	U2435	U2500	A2577	G2644	U2714	C2787	A2852	A
G2037	A2100	G	U2297	G2365	U2436	G2501	G2578	U2645	G2715	C2790	A2853	G
A2038	A2101	U	G2298	C2366	A2437	C2502	U2581	G2646	G2716	U2791	A2854	C
A2039	G2102	C	G2299	A2367	G2438	A2503	G2582	U2647	C2717	A2792	G2855	A
C2040	A2103	A	A2300	A2368	C2439	A2504	G2583	A2649	C2718	A2793	A2856	U
G2041	C2104	U	A2301	A2369	C2440	G2505	G2584	U2650	A2719	G2794	U2857	U
U2042	C2105	C	A2302	A2370	G2443	G2506	G2585	U2651	C2720	C2795	U2858	C
U2043	U2107	A	A2303	A2371	U2444	C2507	U2586	U2652	G2723	U2724	G2859	A
G2044	A2108	G	A2307	G2374	U2445	A2508	U2587	C2654	U2724	U2725	G2860	U
G2045	U2109	A	A2311	A2375	G2446	C2509	G2588	U2655	G2725	A2799	G2861	
C2047	G2110	G	G2312	U2376	G2449	A2511	U2589	U2656	U2726	A2800	G2862	
G2050	G2111	G	G2313	U2377	C2450	U2512	U2590	G2657	A2727	A2801	G2863	
G2053	A2112	U	G2314	G2378	G2451	A2513	C2591	U2658	C2728	C2802	U2864	
A2054	G2113	C	C2315	A2380	U2452	U2514	G2592	U2659	C2729	C2803	G2865	
A2055	C2114	A	G2316	C2381	G2453	C2515	C2593		G2730	C2804	G2866	
C2056	G2118	C	C2317	A2382	G2454	U2516	C2594	A2664	U2735	A2805	C2867	
C2056	C2119	C	U2320	G2383	A2455	C2517	U2595	A	U2736	C2806	G2868	
U2057	G2120	G	A2321	U2384	U2456	G2518	A2596	U	U2737	G2807	C2869	
G2058	G2121	C	C2322	G2385	U2457	C2519	U2597	G2667	C2737	U2808	C2870	
U2059	G2122	C	G2323	U2386	U2458	A2521	U2598	U2668	C2738	C2809	U2872	
A2060	G2128	U	G2324	U2387	G2459	G2522	A2600	G2670	G2744	A2811	G2874	
C2061		G	U2325	U2388	A2460	U2523	A2601	U2671	C2747	A2812	A2875	
			A2252	U2389	U2461	G2524	G2602	U2672	C2748	C2813	G2876	
						G2525	G2603	U2673	U2749	A2814	G2877	

• Molecule 31: 5S RIBOSOMAL RNA



U1	U2	U3	A3	G4	G5	G6	G7	G8	C9	C10	A11	C12	A13	G14	C15	G16	C17	U18	C19	C20	G21	G22	U23	U24	A25	C26	C27	U28	C29	C30	C31	G32	U33	A34	C35	C36	C37	A38	U39	C40	C41	C42	G43	A44	A47	C48	C49	G50	A51	A52	G53	A54	U55	A56	A57	G58	C59	C60	C61
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A62	C63	C64	A65	G66	C67	G68	U69	C72	A73	G74	G75	G76	A77	C81	U82	G83	U87	G88	C89	G90	C91	G92	A93	A105	U106	C107	C108	G109	G110	U111	U112	C113	G114	C115	C116	C122
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------

## 4 Data and refinement statistics

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

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

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: MG, OMG, CL, SR, NA, K, CD, OMU, UR3, 1MA, PSU

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

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

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

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

There are no bond length outliers.

All (5) bond angle outliers are listed below:

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

There are no chirality outliers.

All (20) planarity outliers are listed below:

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

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

## 5.2 Too-close contacts

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

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

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

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

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 23.

All (3377) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:871:G:C8	30:0:871:G:H5'	1.74	1.22
30:0:1160:G:H5'	30:0:1161:A:C5'	1.70	1.20
30:0:1160:G:C5'	30:0:1161:A:H5'	1.73	1.18
30:0:1278:A:H4'	30:0:1279:U:C4	1.81	1.16
13:M:171:ARG:HD3	30:0:156:C:H5''	1.15	1.13
14:N:37:ARG:NH1	31:9:6:C:H5''	1.65	1.12
30:0:1559:A:H1'	38:0:5836:HOH:O	1.48	1.11
10:J:82:THR:HG23	30:0:1242:A:H5'	1.30	1.10
30:0:236:A:H4'	30:0:237:G:H5'	1.26	1.09
14:N:37:ARG:HH12	31:9:6:C:H5''	1.04	1.08
30:0:1205:U:H2'	30:0:1206:U:C5'	1.83	1.07
30:0:1205:U:H2'	30:0:1206:U:H5'	1.32	1.06
2:B:264:GLU:HG2	2:B:267:LYS:HE2	1.35	1.06
30:0:545:G:H8	30:0:545:G:H5'	1.18	1.05
29:3:88:LEU:HD22	33:3:8804:CL:CL	1.95	1.03
30:0:871:G:H5'	30:0:871:G:H8	0.89	1.02
31:9:54:A:O2'	31:9:55:U:H5'	1.58	1.02
30:0:2506:A:HO2'	30:0:2507:G:H8	1.04	1.01
30:0:1118:A:H3'	30:0:1118:A:H8	1.24	1.01
31:9:14:G:H5'	31:9:14:G:H8	1.25	1.01
22:V:50:ARG:HH12	30:0:56:G:H5''	1.25	1.01
30:0:960:G:H4'	38:0:7414:HOH:O	1.61	0.99
30:0:558:C:C2'	30:0:559:U:H5''	1.92	0.99
30:0:2372:A:H2'	30:0:2373:U:H6	1.28	0.99
29:3:68:LYS:HD3	29:3:70:ARG:HH21	1.28	0.99
30:0:1603:A:H5'	30:0:1605:G:O4'	1.61	0.98
30:0:1834:C:H2'	30:0:1840:A:N6	1.78	0.98
31:9:76:G:H3'	31:9:77:A:H5''	1.44	0.98
29:3:47:GLY:HA2	30:0:2121:G:H4'	1.43	0.98
30:0:1666:C:O2'	30:0:1667:A:H5''	1.62	0.98
18:R:8:ALA:HB1	18:R:13:THR:HG21	1.46	0.97
30:0:694:A:H2'	30:0:695:C:H5'	1.44	0.97
30:0:877:G:H5'	30:0:878:G:OP1	1.65	0.97
2:B:238:ASN:HD22	2:B:240:GLY:H	1.09	0.97
30:0:2717:C:C2'	30:0:2718:C:H5''	1.95	0.96
21:U:51:TRP:HD1	30:0:2865:G:HO2'	1.07	0.96
30:0:1118:A:H3'	30:0:1118:A:C8	1.99	0.96
30:0:1305:C:H5'	38:0:9833:HOH:O	1.66	0.96
30:0:1209:C:H2'	30:0:1210:G:H8	1.31	0.95
31:9:29:C:H2'	31:9:30:C:H5'	1.49	0.95
30:0:2717:C:O2'	30:0:2718:C:H5''	1.65	0.95
30:0:363:C:H1'	38:0:5247:HOH:O	1.67	0.95

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

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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2896:A:H5''	38:0:6075:HOH:O	1.77	0.83
31:9:14:G:C8	31:9:14:G:H5'	2.14	0.83
30:0:271:C:H41	30:0:378:A:H2	1.22	0.82
30:0:1644:C:H2'	30:0:1645:U:H6	1.44	0.82
30:0:810:G:H2'	30:0:811:C:C6	2.13	0.82
30:0:2437:A:H2'	30:0:2438:G:C8	2.14	0.82
22:V:12:THR:HG22	22:V:15:GLU:HG3	1.60	0.82
30:0:1205:U:C2'	30:0:1206:U:C5'	2.57	0.82
30:0:1206:U:H5'	30:0:1206:U:H6	1.43	0.82
30:0:236:A:C4'	30:0:237:G:H5'	2.09	0.82
4:D:25:MET:SD	4:D:40:ILE:HD11	2.19	0.82
15:O:3:THR:CG2	30:0:656:G:H5'	2.09	0.82
3:C:236:THR:HG22	3:C:239:ALA:H	1.44	0.82
30:0:2345:A:H3'	30:0:2346:C:C6	2.15	0.82
30:0:2426:G:H1'	38:0:6068:HOH:O	1.79	0.82
30:0:2502:C:C2'	30:0:2503:A:H5'	2.10	0.82
13:M:134:ILE:HG23	13:M:141:ILE:HD13	1.62	0.81
30:0:1116:U:O2'	30:0:1118:A:H2	1.62	0.81
30:0:1191:A:H2'	30:0:1193:A:H5'	1.62	0.81
30:0:1278:A:H4'	30:0:1279:U:C5	2.15	0.81
30:0:614:U:O2'	30:0:615:G:H5'	1.80	0.81
30:0:2604:A:H5'	38:0:5760:HOH:O	1.79	0.81
30:0:185:G:H4'	30:0:186:A:OP1	1.78	0.81
26:Z:42:TYR:HA	30:0:1829:A:H61	1.45	0.81
30:0:282:C:O2'	30:0:283:U:H5'	1.79	0.81
14:N:67:ALA:HA	14:N:71:TRP:HB3	1.62	0.81
18:R:39:THR:HG22	18:R:42:GLU:H	1.44	0.80
13:M:171:ARG:CD	30:0:156:C:H5''	2.06	0.80
31:9:56:A:C2'	31:9:57:A:H5''	2.11	0.80
30:0:1632:A:H2'	30:0:1633:C:H5'	1.61	0.80
29:3:2:GLN:O	30:0:2320:U:H2'	1.80	0.80
6:F:91:VAL:HG12	6:F:92:GLY:H	1.47	0.80
30:0:1119:G:N2	30:0:1246:A:C2	2.48	0.80
30:0:2467:A:H3'	38:0:5416:HOH:O	1.82	0.80
31:9:59:C:H2'	31:9:60:C:C6	2.16	0.80
30:0:558:C:O2'	30:0:559:U:H5''	1.81	0.80
30:0:1185:U:H2'	30:0:1186:C:H6	1.46	0.80
22:V:50:ARG:NH1	30:0:56:G:H5''	1.95	0.80
11:K:14:LYS:HB2	11:K:45:PRO:HG2	1.63	0.80
31:9:29:C:C2'	31:9:30:C:H5'	2.12	0.79
19:S:55:GLN:NE2	30:0:1446:U:H2'	1.97	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:LYS:HE2	26:Z:50:VAL:HG13	1.63	0.79
30:0:1116:U:HO2'	30:0:1118:A:H2	0.80	0.79
30:0:1603:A:H5''	30:0:1605:G:H5'	1.65	0.79
28:2:41:HIS:H	28:2:45:ASN:HD22	1.31	0.79
21:U:56:ARG:HD2	30:0:2890:A:N9	1.97	0.79
13:M:58:GLN:NE2	30:0:259:G:H21	1.81	0.79
30:0:2506:A:O2'	30:0:2507:G:H8	1.66	0.79
1:A:199:HIS:CD2	1:A:201:PHE:H	2.00	0.79
13:M:159:VAL:HG12	33:M:8818:CL:CL	2.20	0.79
30:0:2717:C:H2'	30:0:2718:C:C5'	2.13	0.79
31:9:73:A:H2'	31:9:74:G:C8	2.17	0.79
30:0:2604:A:H4'	38:0:7586:HOH:O	1.83	0.79
30:0:282:C:H1'	30:0:368:C:H41	1.46	0.79
30:0:282:C:H1'	30:0:368:C:N4	1.98	0.79
30:0:2783:A:H3'	38:0:5197:HOH:O	1.82	0.78
30:0:2769:C:O2'	30:0:2770:G:H5'	1.84	0.78
30:0:1829:A:H2'	30:0:1830:C:H5'	1.65	0.78
30:0:2533:C:H5'	30:0:2533:C:H6	1.47	0.78
30:0:2906:A:H5'	30:0:2907:C:O4'	1.83	0.78
31:9:55:U:H5''	38:9:9146:HOH:O	1.82	0.78
30:0:541:C:C2'	30:0:542:A:H5''	2.13	0.78
30:0:853:C:H3'	38:0:4528:HOH:O	1.83	0.78
30:0:2416:G:H2'	30:0:2417:C:H6	1.49	0.78
2:B:221:GLN:HE22	11:K:42:ASN:HD22	1.32	0.78
10:J:74:ARG:HB3	10:J:74:ARG:HH11	1.48	0.78
13:M:70:GLY:HA3	13:M:73:ARG:NH2	1.99	0.78
30:0:2237:G:H1'	38:0:4824:HOH:O	1.83	0.78
30:0:297:U:H2'	30:0:298:C:H6	1.49	0.78
31:9:56:A:C3'	31:9:57:A:H5''	2.12	0.78
30:0:1189:A:H1'	30:0:1209:C:O4'	1.84	0.77
30:0:1426:C:H2'	38:0:9600:HOH:O	1.83	0.77
30:0:1617:C:C4	30:0:1643:C:H4'	2.19	0.77
30:0:1741:U:H5'	30:0:1742:A:OP1	1.83	0.77
13:M:171:ARG:HD3	30:0:156:C:C5'	2.07	0.77
30:0:1942:A:H5'	38:0:7329:HOH:O	1.84	0.77
30:0:2440:C:H5''	38:0:3808:HOH:O	1.83	0.77
30:0:603:A:H1'	30:0:605:C:C2	2.19	0.77
30:0:1118:A:C3'	30:0:1118:A:C8	2.66	0.77
4:D:105:SER:OG	30:0:2338:G:H1'	1.83	0.77
30:0:2769:C:H2'	30:0:2770:G:O4'	1.82	0.77
10:J:70:PHE:CE1	30:0:2676:C:H4'	2.19	0.77

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

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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:58:VAL:HB	4:D:62:ASP:HB3	1.72	0.72
13:M:76:ARG:HB2	13:M:88:VAL:HG13	1.72	0.72
30:0:1372:A:H3'	38:0:7172:HOH:O	1.88	0.72
18:R:132:ARG:NH2	30:0:2055:A:H4'	2.05	0.72
30:0:2467:A:H1'	38:0:9049:HOH:O	1.89	0.72
30:0:2898:G:O2'	30:0:2899:A:H5'	1.89	0.72
30:0:1316:G:H5''	38:0:5285:HOH:O	1.88	0.72
30:0:2831:C:O2'	30:0:2832:C:H5'	1.88	0.72
30:0:1178:G:H2'	30:0:1179:C:C6	2.25	0.72
30:0:1713:G:H1'	38:0:5039:HOH:O	1.89	0.72
30:0:2297:U:H1'	38:0:5144:HOH:O	1.88	0.72
30:0:272:A:H5'	30:0:273:G:OP2	1.90	0.72
30:0:2253:G:H2'	30:0:2254:G:H8	1.55	0.72
30:0:595:U:O2'	30:0:596:C:H5'	1.90	0.71
30:0:603:A:H5''	30:0:604:G:OP1	1.89	0.71
31:9:26:C:O2'	31:9:27:C:H5'	1.91	0.71
30:0:1979:G:H3'	38:0:3283:HOH:O	1.88	0.71
30:0:958:G:H2'	30:0:959:C:C6	2.24	0.71
30:0:1477:C:H5'	30:0:1868:G:H5'	1.72	0.71
18:R:2:ILE:HG22	30:0:21:G:H4'	1.71	0.71
30:0:1801:A:H3'	38:0:7596:HOH:O	1.90	0.71
30:0:2321:A:H2	30:0:2378:U:N3	1.88	0.71
27:1:25:LYS:HD2	28:2:49:GLU:H	1.55	0.71
23:W:125:HIS:CE1	30:0:1097:A:H5''	2.25	0.71
25:Y:187:VAL:HG23	25:Y:192:ASP:CB	2.21	0.71
30:0:1197:G:H1'	30:0:1203:G:N2	2.06	0.71
30:0:1398:G:H2'	30:0:1399:A:C8	2.25	0.71
30:0:2769:C:H2'	30:0:2770:G:C5'	2.20	0.71
5:E:143:GLN:NE2	30:0:2779:G:H21	1.89	0.71
30:0:2780:C:H2'	30:0:2781:U:C6	2.26	0.71
30:0:920:C:H4'	30:0:921:G:C2	2.26	0.71
14:N:33:ARG:HH21	14:N:48:VAL:HG11	1.55	0.71
26:Z:84:CYS:HB3	30:0:1604:G:H22	1.56	0.71
31:9:55:U:H4'	31:9:56:A:C8	2.25	0.71
21:U:56:ARG:HG3	21:U:56:ARG:HH11	1.56	0.71
30:0:1666:C:C2'	30:0:1667:A:C5'	2.69	0.71
3:C:139:VAL:HG13	38:C:8645:HOH:O	1.91	0.70
30:0:1185:U:H2'	30:0:1186:C:C6	2.25	0.70
30:0:2321:A:C2	30:0:2378:U:N3	2.55	0.70
30:0:2524:G:H21	30:0:2526:C:N4	1.88	0.70
30:0:1118:A:N6	30:0:1244:U:H3	1.89	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2416:G:H2'	30:0:2417:C:C6	2.26	0.70
3:C:78:ARG:HH11	3:C:78:ARG:HG3	1.56	0.70
30:0:1972:U:H2'	30:0:1973:A:H5'	1.73	0.70
30:0:2312:G:H2'	30:0:2313:C:H5'	1.72	0.70
30:0:2717:C:C2'	30:0:2718:C:C5'	2.68	0.70
22:V:57:LYS:HA	22:V:60:GLN:HE21	1.57	0.70
14:N:4:PRO:HB2	30:0:1010:C:H4'	1.73	0.70
30:0:1596:U:H2'	30:0:1598:A:OP2	1.90	0.70
30:0:2565:C:H4'	38:0:4806:HOH:O	1.91	0.70
26:Z:43:GLY:O	26:Z:47:ARG:HG2	1.91	0.70
30:0:1829:A:C2'	30:0:1830:C:H5'	2.21	0.70
30:0:2539:U:H1'	38:0:7770:HOH:O	1.90	0.70
13:M:164:THR:HG22	13:M:166:ALA:H	1.57	0.70
1:A:223:ARG:HH12	30:0:2270:G:H4'	1.55	0.70
14:N:11:ARG:HD3	31:9:114:G:O6	1.90	0.70
38:C:8565:HOH:O	20:T:2:LYS:HE3	1.92	0.70
29:3:40:ARG:HA	29:3:52:PHE:CE1	2.26	0.70
30:0:1226:G:H2'	30:0:1227:C:H6	1.57	0.70
31:9:59:C:O5'	31:9:59:C:H6	1.74	0.69
30:0:1589:G:H5'	38:0:6843:HOH:O	1.91	0.69
30:0:2415:A:H2'	30:0:2416:G:H5'	1.74	0.69
30:0:522:U:O2'	30:0:1366:C:H5'	1.92	0.69
30:0:1181:A:C2'	30:0:1182:C:H5'	2.22	0.69
30:0:2404:G:H5''	38:0:5177:HOH:O	1.91	0.69
30:0:714:U:H4'	38:0:5705:HOH:O	1.93	0.69
1:A:135:VAL:HG11	1:A:147:ARG:NH2	2.07	0.69
7:G:64:ASN:N	7:G:64:ASN:HD22	1.90	0.69
10:J:70:PHE:CD1	30:0:2676:C:H4'	2.27	0.69
30:0:2667:G:H1'	30:0:2914:A:N3	2.08	0.69
8:H:168:VAL:HG13	38:H:218:HOH:O	1.91	0.69
29:3:20:HIS:HD2	29:3:69:TYR:HB3	1.56	0.69
26:Z:37:ARG:HB3	38:0:4665:HOH:O	1.91	0.69
30:0:1205:U:C2'	30:0:1206:U:H5''	2.23	0.69
30:0:545:G:C5'	30:0:545:G:H8	1.99	0.69
14:N:37:ARG:NH1	31:9:6:C:C5'	2.50	0.69
30:0:735:C:H2'	30:0:736:A:O4'	1.93	0.69
2:B:258:GLY:H	2:B:260:HIS:CE1	2.10	0.69
3:C:76:ARG:HH11	3:C:76:ARG:HB3	1.57	0.69
30:0:1741:U:O2'	30:0:2723:G:H4'	1.91	0.69
15:O:32:ARG:HE	15:O:35:LYS:HD2	1.58	0.69
30:0:2705:U:H2'	30:0:2706:A:C8	2.28	0.69

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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1528:A:H2'	30:0:1529:G:O4'	1.95	0.67
30:0:541:C:H2'	30:0:542:A:H5''	1.74	0.67
8:H:57:THR:HG23	8:H:131:GLN:HA	1.76	0.67
30:0:2524:G:H5''	38:0:4698:HOH:O	1.94	0.67
30:0:1787:C:H4'	30:0:2883:A:O4'	1.94	0.67
13:M:91:ILE:HG23	38:0:7530:HOH:O	1.94	0.67
30:0:2894:C:O2'	30:0:2895:C:H5'	1.95	0.67
28:2:28:LYS:HE2	30:0:86:A:H1'	1.77	0.67
13:M:73:ARG:HH22	30:0:2263:G:H5''	1.58	0.67
21:U:19:THR:HG22	21:U:20:MET:H	1.59	0.67
30:0:119:A:H2'	30:0:120:A:H5''	1.77	0.67
30:0:370:G:O2'	30:0:371:U:H5'	1.93	0.67
31:9:76:G:C3'	31:9:77:A:H5''	2.23	0.67
30:0:2780:C:H2'	30:0:2781:U:H6	1.59	0.67
30:0:2829:G:N2	30:0:2912:C:C2	2.63	0.67
12:L:46:LEU:O	30:0:2430:A:H4'	1.95	0.67
30:0:1641:A:H2'	30:0:1642:A:H5'	1.77	0.67
30:0:256:C:H2'	30:0:257:G:O4'	1.95	0.67
30:0:810:G:H2'	30:0:811:C:H6	1.56	0.67
29:3:60:LYS:HG3	29:3:61:PRO:HD2	1.77	0.67
4:D:154:LYS:HD2	4:D:154:LYS:H	1.60	0.67
5:E:91:PHE:HE1	30:0:2694:A:H4'	1.58	0.67
10:J:75:PRO:HG2	10:J:105:LEU:HD21	1.77	0.67
11:K:20:CYS:HB2	11:K:29:LEU:HG	1.77	0.67
16:P:59:ARG:HD3	38:0:6249:HOH:O	1.95	0.66
1:A:135:VAL:HG21	1:A:147:ARG:HB3	1.77	0.66
30:0:2785:C:H5'	38:0:7694:HOH:O	1.95	0.66
30:0:596:C:H2'	30:0:597:A:C8	2.29	0.66
14:N:33:ARG:NH2	14:N:48:VAL:HG11	2.10	0.66
30:0:468:U:H3'	38:0:7549:HOH:O	1.93	0.66
29:3:68:LYS:HD3	29:3:70:ARG:NH2	2.07	0.66
15:O:14:LEU:HD23	15:O:102:ILE:HD11	1.77	0.66
30:0:1041:U:H2'	30:0:1042:U:H5'	1.78	0.66
30:0:869:G:H1'	38:0:3302:HOH:O	1.95	0.66
13:M:48:LYS:HE3	13:M:52:GLN:HE21	1.60	0.66
30:0:1120:U:H5'	30:0:1121:G:OP2	1.95	0.66
11:K:12:LEU:HB2	11:K:47:ALA:HB3	1.77	0.66
30:0:1205:U:C2'	30:0:1206:U:H5'	2.18	0.66
30:0:123:U:H5'	38:0:6635:HOH:O	1.96	0.66
30:0:1942:A:H3'	38:0:7329:HOH:O	1.95	0.66
30:0:2329:C:O2'	30:0:2330:U:H5'	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:113:SER:HB2	38:N:8852:HOH:O	1.94	0.66
30:0:1063:G:H5''	38:0:9856:HOH:O	1.94	0.66
30:0:1167:G:H2'	30:0:1168:C:C6	2.31	0.66
28:2:43:ARG:NH2	30:0:1684:A:H1'	2.10	0.66
30:0:2032:U:H2'	30:0:2033:G:C5'	2.26	0.66
30:0:2760:C:H5''	38:0:5294:HOH:O	1.95	0.66
30:0:318:U:H5'	30:0:339:A:C2	2.31	0.66
30:0:704:C:H2'	30:0:705:C:H6	1.60	0.66
31:9:7:G:H5'	38:9:9102:HOH:O	1.95	0.66
2:B:27:ASN:H	2:B:27:ASN:HD22	1.44	0.66
30:0:2533:C:C6	30:0:2533:C:H5'	2.31	0.66
3:C:184:ARG:NH2	30:0:450:C:OP1	2.29	0.66
30:0:559:U:C6	30:0:559:U:H5'	2.23	0.66
30:0:921:G:H4'	30:0:924:G:N1	2.11	0.66
30:0:1249:U:H2'	30:0:1250:C:C6	2.30	0.65
30:0:1603:A:H5'	30:0:1605:G:C4'	2.26	0.65
30:0:449:A:H3'	38:0:6214:HOH:O	1.95	0.65
26:Z:44:ARG:NH2	30:0:1771:U:H5'	2.09	0.65
30:0:2851:G:H2'	30:0:2902:A:H61	1.60	0.65
30:0:559:U:H6	30:0:559:U:C5'	2.09	0.65
2:B:179:LEU:O	2:B:183:GLU:HG2	1.96	0.65
12:L:143:THR:HG22	12:L:144:ASP:H	1.61	0.65
14:N:80:SER:HB2	38:N:8833:HOH:O	1.95	0.65
20:T:9:LYS:HE3	20:T:13:ARG:NH1	2.12	0.65
30:0:368:C:H2'	30:0:369:G:H5'	1.77	0.65
31:9:29:C:C5	31:9:30:C:C6	2.84	0.65
26:Z:78:ILE:HG21	26:Z:87:LYS:HE2	1.78	0.65
30:0:2707:C:H2'	30:0:2707:C:O2	1.96	0.65
38:D:7597:HOH:O	31:9:56:A:H2	1.79	0.65
16:P:88:GLN:NE2	30:0:1800:G:H1'	2.10	0.65
1:A:122:SER:HB2	1:A:164:ARG:NH1	2.11	0.65
21:U:56:ARG:HD2	30:0:2890:A:C1'	2.25	0.65
30:0:1061:C:H3'	38:0:5051:HOH:O	1.97	0.65
30:0:1132:A:N6	30:0:1229:C:H2'	2.12	0.65
30:0:1666:C:C2'	30:0:1667:A:H5''	2.27	0.65
30:0:213:G:N2	30:0:225:G:H2'	2.11	0.65
30:0:2597:U:H2'	30:0:2598:U:H5'	1.77	0.65
30:0:416:G:H5''	38:0:7402:HOH:O	1.96	0.65
30:0:696:C:H4'	38:0:7263:HOH:O	1.96	0.65
5:E:91:PHE:CE1	30:0:2694:A:H4'	2.32	0.65
9:I:110:ASP:O	30:0:1163:G:H5'	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:115:ARG:HH21	30:0:1266:U:H4'	1.60	0.65
30:0:1385:G:H1'	38:0:4024:HOH:O	1.97	0.65
30:0:290:C:O2'	30:0:291:C:H5'	1.96	0.65
30:0:42:C:H1'	38:0:4645:HOH:O	1.97	0.65
38:O:1484:HOH:O	30:0:710:G:H1'	1.97	0.65
30:0:812:A:H2'	30:0:813:C:C6	2.31	0.65
2:B:238:ASN:HD22	2:B:240:GLY:N	1.90	0.65
30:0:2119:C:O2'	30:0:2120:U:H5'	1.97	0.65
16:P:81:LYS:O	30:0:1761:U:H5'	1.97	0.65
30:0:1586:G:O2'	30:0:1587:U:H5'	1.97	0.64
30:0:2892:G:C6	30:0:2893:C:C4	2.85	0.64
30:0:696:C:O2'	30:0:697:G:H5'	1.97	0.64
31:9:61:C:H2'	31:9:62:A:H8	1.62	0.64
30:0:1377:C:H5'	30:0:1377:C:C6	2.33	0.64
30:0:1422:U:H2'	30:0:1423:C:C6	2.32	0.64
30:0:1735:C:O2'	30:0:1736:A:H5'	1.97	0.64
30:0:1862:C:H1'	38:0:7203:HOH:O	1.96	0.64
38:B:8996:HOH:O	30:0:2766:A:H5'	1.97	0.64
30:0:441:A:H1'	30:0:442:A:N7	2.13	0.64
1:A:47:HIS:HD2	30:0:1654:U:H2'	1.61	0.64
30:0:1819:G:H5'	38:0:4680:HOH:O	1.96	0.64
30:0:1972:U:C2'	30:0:1973:A:H5''	2.27	0.64
30:0:671:A:O2'	30:0:672:G:H2'	1.97	0.64
2:B:36:PRO:HA	2:B:168:GLY:HA3	1.78	0.64
21:U:56:ARG:HD2	30:0:2890:A:C8	2.33	0.64
27:1:9:GLY:HA2	30:0:1687:C:O2	1.98	0.64
30:0:281:U:H2'	30:0:282:C:O4'	1.98	0.64
30:0:693:A:H2'	30:0:694:A:C8	2.33	0.64
2:B:312:ARG:HD3	2:B:315:VAL:HG13	1.80	0.64
30:0:1706:G:H1'	30:0:1712:A:H61	1.61	0.64
30:0:2768:A:O2'	30:0:2769:C:H5'	1.97	0.64
27:1:21:ARG:HD2	27:1:37:CYS:SG	2.38	0.64
5:E:143:GLN:HE22	30:0:2779:G:H21	1.44	0.64
5:E:20:ILE:HD11	5:E:40:VAL:HG11	1.79	0.64
23:W:6:GLN:HB2	23:W:26:ILE:HD11	1.79	0.64
26:Z:70:ARG:HH11	26:Z:83:TYR:HD1	1.46	0.64
3:C:78:ARG:HG3	3:C:78:ARG:NH1	2.13	0.64
30:0:1181:A:H2'	30:0:1182:C:H5'	1.80	0.64
30:0:1973:A:H2'	30:0:1974:G:O4'	1.96	0.64
30:0:2088:C:H2'	30:0:2089:A:H8	1.62	0.64
25:Y:154:ARG:HH22	30:0:1071:G:H4'	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:169:ARG:HD2	30:0:1328:A:OP1	1.98	0.64
30:0:459:A:H5''	38:0:9055:HOH:O	1.96	0.64
3:C:16:VAL:HG12	3:C:17:ASP:H	1.62	0.64
14:N:86:LEU:HD12	14:N:125:ALA:HB2	1.78	0.64
30:0:1748:U:C5	30:0:1749:U:C5	2.85	0.63
11:K:66:ARG:HH22	30:0:1994:A:P	2.21	0.63
8:H:27:PRO:HD3	8:H:123:ILE:HG22	1.79	0.63
21:U:23:HIS:HD2	21:U:27:ALA:HB3	1.63	0.63
30:0:2867:G:H2'	30:0:2868:C:C6	2.33	0.63
30:0:541:C:H2'	30:0:542:A:H5'	1.77	0.63
3:C:132:ASP:O	3:C:133:ARG:HG3	1.98	0.63
3:C:236:THR:HG21	38:C:8571:HOH:O	1.97	0.63
11:K:98:VAL:CG1	11:K:102:GLU:HA	2.28	0.63
18:R:40:ALA:O	18:R:44:VAL:HG23	1.99	0.63
8:H:19:ARG:HH12	30:0:1008:C:H5''	1.63	0.63
30:0:1116:U:O2'	30:0:1118:A:C2	2.40	0.63
30:0:2727:A:H2'	30:0:2728:C:H5'	1.80	0.63
30:0:541:C:O2'	30:0:542:A:H5''	1.97	0.63
31:9:17:G:O2'	31:9:18:U:H5'	1.97	0.63
17:Q:26:PRO:O	17:Q:30:VAL:HG23	1.97	0.63
30:0:1835:U:H3'	38:0:5539:HOH:O	1.97	0.63
30:0:2032:U:O2'	30:0:2033:G:H5''	1.98	0.63
13:M:66:SER:HB3	13:M:128:TRP:CD1	2.33	0.63
13:M:164:THR:HG22	13:M:166:ALA:N	2.13	0.63
30:0:2659:U:H5''	38:0:4112:HOH:O	1.98	0.63
30:0:506:G:H22	30:0:509:A:H5'	1.63	0.63
23:W:88:THR:HG22	23:W:110:GLN:HB3	1.81	0.63
30:0:1985:U:H1'	38:0:4497:HOH:O	1.98	0.63
30:0:90:A:H2'	30:0:91:G:O4'	1.98	0.63
29:3:65:THR:O	29:3:82:GLY:HA3	1.99	0.63
31:9:91:C:H2'	31:9:92:G:O4'	1.99	0.63
1:A:211:LYS:HB3	1:A:212:PRO:HD2	1.79	0.63
26:Z:38:PHE:HB3	26:Z:42:TYR:CD1	2.33	0.63
30:0:1149:U:H5''	30:0:1151:G:O4'	1.98	0.63
30:0:1644:C:H2'	30:0:1645:U:C6	2.31	0.63
30:0:2291:A:H8	38:0:6453:HOH:O	1.81	0.63
30:0:2675:A:H1'	30:0:2813:A:C2	2.34	0.63
30:0:2824:C:H5''	30:0:2825:C:H5'	1.80	0.63
14:N:164:ASP:OD1	14:N:167:ASP:HA	1.98	0.63
14:N:37:ARG:HH12	31:9:6:C:C5'	1.95	0.63
30:0:2250:G:H2'	30:0:2251:G:O4'	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2766:A:O2'	30:0:2767:C:H5'	1.99	0.63
29:3:59:ASP:HB3	29:3:63:LYS:NZ	2.13	0.63
29:3:2:GLN:HB3	29:3:91:GLN:CD	2.19	0.63
2:B:280:VAL:HG13	2:B:333:GLU:O	1.99	0.63
4:D:131:THR:HG21	30:0:2348:C:H1'	1.79	0.63
22:V:42:ASN:HB3	38:V:7247:HOH:O	1.98	0.63
30:0:2782:G:H3'	38:0:5004:HOH:O	1.98	0.63
5:E:60:SER:OG	30:0:2784:A:H1'	1.98	0.63
30:0:279:C:C2'	30:0:280:C:H5'	2.29	0.63
30:0:630:A:H5''	38:0:4722:HOH:O	1.99	0.63
30:0:956:G:C8	38:0:9387:HOH:O	2.50	0.63
28:2:41:HIS:HB3	28:2:44:ARG:HB2	1.80	0.63
11:K:74:VAL:CG1	11:K:113:ILE:HG12	2.29	0.63
30:0:1165:G:H21	30:0:1173:A:C5'	2.12	0.62
30:0:2349:G:H2'	30:0:2350:G:H8	1.62	0.62
12:L:57:VAL:HG21	30:0:2443:C:H5'	1.80	0.62
27:1:2:GLY:O	27:1:6:PRO:HG2	1.99	0.62
20:T:72:ILE:HD13	20:T:93:THR:HG22	1.81	0.62
26:Z:34:SER:HB2	38:0:7481:HOH:O	1.99	0.62
26:Z:41:ARG:HD2	30:0:1830:C:O2	1.98	0.62
30:0:1921:A:O2'	30:0:1922:A:H5'	1.98	0.62
29:3:54:LYS:HE2	30:0:2468:A:N7	2.14	0.62
30:0:1527:A:H1'	30:0:1528:A:C8	2.34	0.62
30:0:1351:G:H5'	38:0:3619:HOH:O	1.99	0.62
30:0:1878:G:H1'	38:0:6097:HOH:O	2.00	0.62
30:0:1889:C:H2'	30:0:1890:U:O4'	2.00	0.62
4:D:54:ALA:HB2	4:D:69:ILE:HD12	1.80	0.62
14:N:160:SER:HB3	31:9:51:A:H5'	1.82	0.62
21:U:49:LEU:HD12	38:U:3805:HOH:O	1.99	0.62
30:0:1477:C:H5'	30:0:1868:G:C5'	2.29	0.62
8:H:15:PRO:HG3	30:0:1053:G:OP1	2.00	0.62
30:0:790:A:H1'	30:0:1710:A:O2'	1.99	0.62
30:0:229:G:O2'	30:0:230:C:H5'	2.00	0.62
5:E:153:ARG:HH12	30:0:2778:A:H1'	1.65	0.62
20:T:61:GLU:HG2	38:T:3851:HOH:O	1.99	0.62
30:0:1226:G:H5'	38:0:4509:HOH:O	1.98	0.62
29:3:68:LYS:NZ	30:0:2436:U:H5'	2.14	0.62
3:C:246:ARG:NH2	30:0:677:C:H4'	2.14	0.62
30:0:2510:C:H5'	30:0:2511:A:OP2	1.99	0.62
15:O:51:TYR:CE2	30:0:721:A:H5''	2.35	0.62
30:0:920:C:H4'	30:0:921:G:N2	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:2:22:PRO:HG2	28:2:25:VAL:HG23	1.82	0.62
22:V:39:ALA:H	22:V:40:PRO:HD2	1.65	0.62
26:Z:53:ILE:O	26:Z:57:MET:HB2	2.00	0.62
30:0:1752:G:H2'	38:0:7531:HOH:O	2.00	0.62
30:0:303:C:O2'	30:0:304:G:H5'	2.00	0.62
30:0:630:A:H5'	38:0:9372:HOH:O	1.98	0.62
17:Q:14:LEU:HD21	17:Q:43:ILE:HD12	1.82	0.62
30:0:1131:G:H1'	38:0:3907:HOH:O	1.99	0.61
30:0:1279:U:C2'	30:0:1279:U:O2	2.48	0.61
30:0:2251:G:H2'	30:0:2252:A:C8	2.35	0.61
30:0:2300:A:H4'	30:0:2301:A:O5'	2.00	0.61
30:0:236:A:H4'	30:0:237:G:C5'	2.17	0.61
30:0:2439:C:H5'	38:0:5449:HOH:O	1.99	0.61
30:0:2775:A:C6	30:0:2799:A:C8	2.88	0.61
31:9:91:C:H1'	38:9:9149:HOH:O	1.98	0.61
3:C:129:HIS:CE1	3:C:231:ARG:HA	2.35	0.61
23:W:64:THR:O	23:W:68:THR:HG22	2.00	0.61
30:0:1477:C:O2'	30:0:1478:U:H5'	1.99	0.61
30:0:2576:A:H2'	38:0:7732:HOH:O	2.00	0.61
30:0:825:U:H5''	30:0:826:U:OP1	2.00	0.61
9:I:130:LEU:CD2	30:0:1167:G:H4'	2.29	0.61
22:V:55:ARG:O	22:V:59:ILE:HG12	2.01	0.61
30:0:2314:G:C2'	30:0:2315:C:H5'	2.30	0.61
25:Y:186:ARG:HG2	25:Y:186:ARG:HH11	1.65	0.61
30:0:1711:A:O2'	30:0:1712:A:H5'	2.00	0.61
30:0:2912:C:O5'	30:0:2912:C:H6	1.83	0.61
30:0:301:C:O2'	30:0:302:A:H5'	2.00	0.61
2:B:262:ARG:HG3	30:0:2716:G:H5'	1.83	0.61
7:G:12:ILE:HG23	38:0:5418:HOH:O	1.98	0.61
13:M:75:ARG:NH2	13:M:78:LYS:HE2	2.16	0.61
23:W:52:VAL:HG22	23:W:53:ALA:H	1.63	0.61
24:X:71:ARG:HD2	38:X:7542:HOH:O	1.99	0.61
30:0:1118:A:H8	30:0:1119:G:H5''	1.64	0.61
1:A:20:SER:HB3	30:0:1872:C:H5	1.65	0.61
2:B:336:GLN:O	30:0:2862:G:H4'	2.00	0.61
30:0:39:G:N2	30:0:444:C:C2	2.68	0.61
2:B:320:GLN:HE21	2:B:321:PRO:HD2	1.65	0.61
9:I:91:PHE:HD2	9:I:131:GLY:HA2	1.66	0.61
12:L:67:ARG:HB2	12:L:112:GLY:HA3	1.83	0.61
30:0:2526:C:H3'	30:0:2526:C:H6	1.65	0.61
30:0:705:C:H2'	30:0:705:C:O2	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:130:LEU:HD21	30:0:1167:G:H4'	1.81	0.61
23:W:13:MET:HE1	23:W:18:GLN:HA	1.81	0.61
30:0:1774:G:O2'	30:0:1775:A:H5'	2.01	0.61
30:0:228:C:H2'	30:0:229:G:H5'	1.80	0.61
30:0:877:G:C5'	30:0:878:G:OP1	2.46	0.61
31:9:20:G:H3'	38:9:9057:HOH:O	2.00	0.61
22:V:12:THR:HG22	22:V:15:GLU:CG	2.31	0.61
30:0:1676:G:O2'	30:0:1677:U:H5'	2.01	0.61
30:0:1856:C:H5'	30:0:1858:A:O4'	2.01	0.61
30:0:282:C:O2	30:0:282:C:H2'	2.00	0.61
30:0:2834:G:C2	30:0:2835:C:H1'	2.35	0.61
23:W:145:GLY:HA3	38:W:6373:HOH:O	2.00	0.61
30:0:1398:G:H2'	30:0:1399:A:H8	1.64	0.61
30:0:283:U:C5	30:0:284:C:C4	2.88	0.61
30:0:807:A:H2'	30:0:808:A:C8	2.36	0.61
31:9:39:U:HO2'	31:9:42:C:H5	1.48	0.61
30:0:1701:A:H4'	30:0:1702:U:C5'	2.30	0.61
30:0:558:C:H2'	30:0:559:U:H5'	1.81	0.61
8:H:174:LEU:HD21	30:0:1220:U:H4'	1.82	0.61
11:K:10:GLN:N	11:K:10:GLN:HE21	1.96	0.61
30:0:1878:G:HO2'	30:0:1879:U:H6	1.42	0.60
38:3:9025:HOH:O	30:0:2468:A:H5'	2.00	0.60
30:0:31:C:H4'	38:0:7408:HOH:O	2.00	0.60
1:A:140:LEU:HB3	1:A:141:PRO:HD2	1.83	0.60
10:J:47:THR:HB	38:0:4807:HOH:O	2.01	0.60
30:0:1175:G:H1'	30:0:1193:A:C2'	2.31	0.60
30:0:1697:G:H4'	38:0:9347:HOH:O	2.02	0.60
30:0:2281:C:H2'	30:0:2282:U:H5'	1.82	0.60
29:3:9:THR:HG23	29:3:20:HIS:ND1	2.15	0.60
2:B:102:THR:HG23	2:B:182:VAL:HG12	1.81	0.60
2:B:320:GLN:HE21	2:B:321:PRO:CD	2.14	0.60
3:C:27:ARG:NH2	30:0:657:G:OP1	2.34	0.60
30:0:2071:C:H5'	38:0:9540:HOH:O	2.00	0.60
30:0:2312:G:C2'	30:0:2313:C:H5'	2.30	0.60
30:0:282:C:O2'	30:0:283:U:C5'	2.49	0.60
30:0:2872:U:H2'	30:0:2873:C:O4'	2.02	0.60
11:K:74:VAL:HG12	11:K:75:ARG:HG3	1.83	0.60
30:0:1201:C:H5''	38:0:6211:HOH:O	2.00	0.60
30:0:1495:C:H1'	30:0:1573:A:H1'	1.83	0.60
26:Z:84:CYS:HB3	30:0:1604:G:N2	2.15	0.60
30:0:38:G:O2'	30:0:39:G:H5'	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:407:A:H3'	38:0:4438:HOH:O	2.01	0.60
25:Y:126:PRO:HG2	25:Y:128:PHE:CE1	2.36	0.60
30:0:1205:U:O2'	30:0:1206:U:H5''	2.01	0.60
30:0:1398:G:O2'	30:0:1399:A:H5'	2.02	0.60
30:0:1407:A:O2'	30:0:1408:U:H3'	2.01	0.60
30:0:1972:U:C2'	30:0:1973:A:C5'	2.80	0.60
30:0:2420:G:C2'	30:0:2421:G:H5'	2.30	0.60
30:0:51:G:H1'	38:0:9033:HOH:O	2.01	0.60
30:0:947:U:H2'	30:0:948:G:C8	2.36	0.60
2:B:72:THR:HB	38:B:9076:HOH:O	2.02	0.60
11:K:74:VAL:HG13	11:K:113:ILE:HG12	1.82	0.60
20:T:48:VAL:HG22	20:T:97:ARG:O	2.01	0.60
30:0:146:U:C2'	30:0:147:G:H5'	2.31	0.60
16:P:41:ARG:HH22	30:0:1500:U:P	2.24	0.60
30:0:2893:C:O2'	30:0:2894:C:H5'	2.01	0.60
31:9:18:U:H2'	31:9:19:G:C8	2.37	0.60
31:9:23:U:O2'	31:9:24:U:H4'	2.01	0.60
7:G:16:LYS:HE2	7:G:63:ARG:HH12	1.67	0.60
13:M:102:GLU:OE1	13:M:164:THR:HG21	2.01	0.60
30:0:2353:A:H4'	30:0:2354:A:O5'	2.01	0.60
29:3:31:THR:OG1	29:3:34:LYS:HD3	2.01	0.60
8:H:72:ALA:HB2	8:H:156:ALA:HB2	1.81	0.60
15:O:14:LEU:CD2	15:O:102:ILE:HD11	2.32	0.60
18:R:135:ALA:HB1	18:R:137:ASN:HD21	1.67	0.60
30:0:1844:C:H6	30:0:1844:C:O5'	1.84	0.60
30:0:2608:C:H3'	38:0:7790:HOH:O	2.02	0.60
31:9:26:C:H2'	31:9:27:C:C6	2.36	0.60
31:9:29:C:H2'	31:9:30:C:C5'	2.28	0.60
31:9:3:A:C6	31:9:22:G:H1'	2.36	0.60
33:B:8819:CL:CL	38:B:8997:HOH:O	2.54	0.60
13:M:188:ARG:HD3	30:0:155:C:OP2	2.02	0.60
10:J:82:THR:CG2	30:0:1242:A:H5'	2.20	0.60
30:0:307:G:H3'	38:0:6667:HOH:O	2.01	0.60
30:0:567:U:H5''	38:0:5254:HOH:O	2.02	0.60
2:B:79:MET:HB2	2:B:188:HIS:CE1	2.36	0.60
18:R:46:TYR:O	18:R:50:VAL:HG23	2.00	0.60
30:0:74:G:H2'	30:0:75:U:C6	2.37	0.60
30:0:947:U:H2'	30:0:948:G:H8	1.65	0.60
29:3:43:ASN:HB2	29:3:52:PHE:CE1	2.36	0.60
6:F:58:GLU:CD	13:M:27:ARG:HH22	2.05	0.60
30:0:1878:G:O2'	30:0:1879:U:C6	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:319:A:H4'	30:0:338:C:C4	2.37	0.59
30:0:324:G:O2'	30:0:325:U:H5'	2.02	0.59
31:9:63:C:O2'	31:9:64:C:H5'	2.01	0.59
2:B:235:ARG:HD3	30:0:2091:G:H5''	1.83	0.59
16:P:91:LYS:O	16:P:95:GLU:HG3	2.02	0.59
30:0:1590:A:H1'	30:0:1606:A:C2	2.36	0.59
30:0:2686:C:C2	30:0:2709:G:N2	2.70	0.59
27:1:20:ARG:HG2	30:0:111:C:O2'	2.01	0.59
31:9:65:A:N6	31:9:112:U:C6	2.71	0.59
11:K:130:MET:SD	21:U:25:ASP:O	2.60	0.59
13:M:82:ARG:HH22	13:M:85:ARG:HH21	1.49	0.59
30:0:2403:C:H5'	38:0:6001:HOH:O	2.01	0.59
30:0:2718:C:H6	30:0:2718:C:H5'	1.67	0.59
30:0:2820:A:H2'	30:0:2821:C:C6	2.36	0.59
1:A:94:LEU:HG	1:A:99:ILE:HD11	1.84	0.59
3:C:236:THR:HA	38:C:8648:HOH:O	2.01	0.59
5:E:145:ALA:HB1	5:E:168:ILE:HD11	1.85	0.59
30:0:2867:G:H2'	30:0:2868:C:H6	1.67	0.59
30:0:653:U:H2'	30:0:654:A:C8	2.37	0.59
30:0:834:G:H4'	30:0:835:U:OP2	2.02	0.59
2:B:101:TRP:HB2	2:B:119:HIS:CD2	2.38	0.59
2:B:156:LYS:HB3	30:0:2846:C:H4'	1.84	0.59
12:L:79:ASP:HB3	38:L:8859:HOH:O	2.03	0.59
14:N:86:LEU:O	14:N:90:LEU:HG	2.02	0.59
30:0:1585:C:H2'	30:0:1586:G:C8	2.37	0.59
30:0:2809:G:H2'	30:0:2810:G:C8	2.37	0.59
30:0:2831:C:H2'	30:0:2832:C:H5'	1.82	0.59
30:0:2874:G:H3'	38:0:9586:HOH:O	2.02	0.59
30:0:652:G:C2	30:0:653:U:H1'	2.37	0.59
1:A:179:MET:HG2	1:A:186:TRP:CB	2.32	0.59
1:A:33:GLU:H	1:A:33:GLU:CD	2.06	0.59
2:B:62:ARG:HG2	2:B:65:MET:HE3	1.85	0.59
6:F:13:GLU:OE2	6:F:78:GLU:HG2	2.01	0.59
38:B:8993:HOH:O	30:0:2549:C:H1'	2.03	0.59
4:D:58:VAL:HG12	4:D:60:GLU:HG2	1.83	0.59
30:0:1702:U:H5''	38:0:7201:HOH:O	2.01	0.59
30:0:2846:C:H4'	38:0:5047:HOH:O	2.03	0.59
30:0:812:A:H2'	30:0:813:C:H6	1.68	0.59
8:H:37:GLY:HA3	8:H:87:LYS:HA	1.85	0.59
30:0:1380:U:C4	30:0:2748:G:C4	2.91	0.59
30:0:2065:C:O2'	30:0:2066:C:H5'	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:542:A:H5'	30:0:542:A:C8	2.29	0.59
30:0:590:A:H2'	30:0:591:A:H5'	1.83	0.59
2:B:215:VAL:HB	38:B:9089:HOH:O	2.02	0.59
8:H:155:ARG:NH1	30:0:2503:A:H5''	2.18	0.59
30:0:1563:G:H4'	38:0:4215:HOH:O	2.01	0.59
30:0:1566:C:O2'	30:0:1567:G:H5'	2.03	0.59
30:0:1972:U:H2'	30:0:1973:A:H5''	1.83	0.59
30:0:499:G:O2'	30:0:500:G:H5'	2.02	0.59
30:0:702:G:O2'	30:0:703:G:H5'	2.02	0.59
30:0:921:G:H4'	30:0:924:G:C6	2.37	0.59
31:9:54:A:C2	31:9:55:U:C2	2.91	0.59
2:B:145:HIS:HD2	2:B:146:THR:O	1.85	0.59
4:D:159:PRO:O	4:D:163:VAL:HG23	2.02	0.59
11:K:41:LYS:HA	30:0:2582:G:O3'	2.03	0.59
16:P:7:LYS:HD3	16:P:21:VAL:HG22	1.85	0.59
18:R:39:THR:HG23	18:R:107:GLU:O	2.03	0.59
24:X:37:LEU:HD13	24:X:85:VAL:HG21	1.84	0.59
10:J:88:PRO:HD3	30:0:1104:C:H4'	1.85	0.59
13:M:137:ASN:ND2	30:0:145:A:H4'	2.18	0.59
30:0:255:A:H2'	30:0:256:C:H6	1.67	0.59
30:0:281:U:C2'	30:0:282:C:H5'	2.33	0.59
6:F:30:LYS:HB2	6:F:97:ALA:HB3	1.84	0.59
10:J:69:TYR:CE1	30:0:2081:A:H4'	2.38	0.59
30:0:1568:G:O2'	30:0:1569:U:H5'	2.03	0.58
30:0:2563:U:H2'	30:0:2565:C:O5'	2.02	0.58
30:0:2724:U:H2'	30:0:2725:G:O4'	2.03	0.58
30:0:2826:G:C6	30:0:2913:A:C6	2.90	0.58
30:0:925:C:H3'	38:0:3826:HOH:O	2.02	0.58
26:Z:40:ALA:HA	30:0:1773:G:C8	2.38	0.58
30:0:1245:C:O5'	30:0:1245:C:H6	1.85	0.58
25:Y:169:ARG:HD3	30:0:1328:A:C8	2.38	0.58
30:0:2825:C:H4'	30:0:2826:G:O5'	2.03	0.58
30:0:28:G:H1'	38:0:4650:HOH:O	2.03	0.58
29:3:47:GLY:HA2	30:0:2121:G:C4'	2.25	0.58
2:B:243:ASN:HB3	38:0:6624:HOH:O	2.02	0.58
2:B:297:VAL:HB	38:B:9076:HOH:O	2.03	0.58
8:H:98:LEU:HD11	8:H:127:ALA:HB2	1.85	0.58
30:0:1158:G:O2'	30:0:1159:G:H5'	2.03	0.58
9:I:83:GLY:H	30:0:1168:C:H5''	1.68	0.58
30:0:1187:U:H2'	38:0:6880:HOH:O	2.01	0.58
30:0:1290:G:H4'	38:0:7465:HOH:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2467:A:H5''	38:0:4285:HOH:O	2.03	0.58
30:0:951:A:C2'	30:0:952:G:H5'	2.33	0.58
3:C:79:ARG:O	3:C:87:ARG:HG2	2.04	0.58
4:D:28:GLY:HA2	4:D:69:ILE:HG23	1.85	0.58
12:L:145:LEU:HB2	38:L:8836:HOH:O	2.03	0.58
13:M:28:GLN:HA	13:M:31:TRP:HB2	1.85	0.58
26:Z:34:SER:HA	30:0:797:A:H4'	1.83	0.58
30:0:1186:C:H42	30:0:1190:G:H22	1.48	0.58
30:0:2590:U:H2'	30:0:2591:C:H5'	1.85	0.58
30:0:293:A:C4	30:0:360:A:C2	2.91	0.58
20:T:52:ARG:HD2	30:0:317:A:H5''	1.85	0.58
30:0:1711:A:C2'	30:0:1712:A:H5'	2.33	0.58
30:0:204:A:H2'	30:0:205:U:H5'	1.85	0.58
30:0:2784:A:H8	30:0:2784:A:O5'	1.87	0.58
3:C:182:ARG:HH12	30:0:450:C:H3'	1.67	0.58
12:L:18:HIS:HD2	30:0:902:G:N7	2.01	0.58
25:Y:234:VAL:HG12	25:Y:235:GLU:H	1.66	0.58
30:0:1520:G:C6	30:0:1521:C:C4	2.92	0.58
10:J:127:ILE:HG22	33:J:8801:CL:CL	2.40	0.58
26:Z:70:ARG:HB2	26:Z:81:CYS:SG	2.44	0.58
30:0:1503:U:C2'	30:0:1504:A:H5'	2.34	0.58
30:0:164:G:H3'	38:0:3636:HOH:O	2.03	0.58
30:0:368:C:C2'	30:0:369:G:H5'	2.34	0.58
30:0:271:C:N4	30:0:378:A:C2	2.66	0.58
31:9:39:U:H1'	31:9:44:A:N6	2.19	0.58
2:B:162:MET:HG3	2:B:310:ARG:HD3	1.84	0.58
5:E:100:ASP:HB3	38:E:2789:HOH:O	2.02	0.58
30:0:1662:C:H2'	30:0:1663:G:O4'	2.03	0.58
30:0:2073:G:OP2	30:0:2490:A:H5'	2.03	0.58
30:0:2493:C:O2	30:0:2493:C:H2'	2.02	0.58
30:0:2505:G:H2'	30:0:2506:A:H5'	1.86	0.58
30:0:2624:A:H1'	38:0:9769:HOH:O	2.04	0.58
30:0:482:G:H4'	30:0:508:A:N1	2.19	0.58
30:0:951:A:O2'	30:0:952:G:H5'	2.03	0.58
31:9:54:A:C2	31:9:55:U:N3	2.72	0.58
2:B:267:LYS:HA	38:B:8996:HOH:O	2.04	0.58
17:Q:11:ARG:NH2	30:0:2363:G:H5''	2.19	0.58
26:Z:42:TYR:HA	30:0:1829:A:N6	2.16	0.58
30:0:1585:C:H2'	30:0:1586:G:H8	1.68	0.58
30:0:1634:G:H2'	30:0:1635:U:C6	2.38	0.58
30:0:1973:A:H5'	30:0:1973:A:H8	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2511:A:H2'	30:0:2512:U:O4'	2.03	0.58
30:0:2581:U:H1'	38:0:4452:HOH:O	2.03	0.58
30:0:412:C:O2'	30:0:413:G:H5'	2.02	0.58
30:0:544:G:H2'	30:0:545:G:H5''	1.85	0.58
30:0:625:U:H3'	38:0:3244:HOH:O	2.03	0.58
8:H:172:GLU:HB2	38:H:248:HOH:O	2.04	0.58
22:V:1:THR:HG23	22:V:2:VAL:H	1.69	0.58
30:0:1041:U:C2'	30:0:1042:U:H5'	2.34	0.58
30:0:1160:G:H5'	30:0:1161:A:H5'	0.78	0.58
30:0:1300:G:H1'	38:0:4652:HOH:O	2.03	0.58
30:0:2812:A:N7	38:0:7497:HOH:O	2.32	0.58
30:0:51:G:O2'	30:0:52:A:H5'	2.03	0.58
30:0:1057:A:H1'	30:0:2492:U:O2'	2.03	0.57
30:0:12:U:C2'	30:0:13:G:H5'	2.32	0.57
4:D:76:ARG:CZ	31:9:44:A:H1'	2.34	0.57
1:A:75:GLY:HA2	26:Z:88:PHE:HA	1.86	0.57
2:B:125:GLU:O	2:B:129:ARG:HG3	2.03	0.57
3:C:236:THR:CG2	3:C:239:ALA:H	2.16	0.57
11:K:20:CYS:SG	11:K:22:ASP:OD1	2.62	0.57
15:O:10:LEU:HD13	15:O:99:GLU:HG3	1.84	0.57
30:0:2705:U:H2'	30:0:2706:A:H8	1.68	0.57
30:0:2748:G:H5'	38:0:7523:HOH:O	2.04	0.57
30:0:820:G:H5'	30:0:821:U:H5'	1.86	0.57
10:J:70:PHE:HE1	30:0:2676:C:H4'	1.68	0.57
20:T:111:ARG:HB3	20:T:119:ALA:HB2	1.85	0.57
30:0:1166:A:H61	30:0:1180:U:H3	1.51	0.57
30:0:1216:G:H2'	30:0:1217:G:O4'	2.03	0.57
30:0:1256:C:H6	38:0:7140:HOH:O	1.87	0.57
30:0:1342:C:C2'	30:0:1343:C:H5'	2.34	0.57
30:0:590:A:C2'	30:0:591:A:H5'	2.33	0.57
30:0:821:U:H3'	38:0:3764:HOH:O	2.03	0.57
1:A:53:ALA:HB2	1:A:122:SER:OG	2.05	0.57
14:N:48:VAL:HG13	14:N:55:ASP:HB3	1.86	0.57
26:Z:90:GLY:HA3	26:Z:95:PRO:O	2.04	0.57
30:0:1503:U:O2'	30:0:1504:A:H5'	2.04	0.57
30:0:2712:G:H5'	38:0:5187:HOH:O	2.02	0.57
30:0:283:U:H5	30:0:284:C:C4	2.22	0.57
30:0:916:A:C2	30:0:928:G:C4	2.93	0.57
3:C:236:THR:HG22	3:C:239:ALA:N	2.15	0.57
20:T:18:GLU:O	20:T:21:LYS:HG2	2.03	0.57
30:0:1552:G:H2'	30:0:1553:C:C6	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1555:G:H4'	30:0:1630:A:H2	1.69	0.57
30:0:1883:U:C2'	30:0:1884:G:H5'	2.34	0.57
30:0:694:A:H2'	30:0:695:C:C5'	2.27	0.57
30:0:727:G:H3'	30:0:728:C:H6	1.68	0.57
29:3:51:LYS:HG3	29:3:52:PHE:CD2	2.40	0.57
11:K:14:LYS:CB	11:K:45:PRO:HG2	2.35	0.57
30:0:1754:A:H5''	38:0:9757:HOH:O	2.04	0.57
30:0:1819:G:H2'	30:0:1820:G:H4'	1.85	0.57
30:0:2078:U:O2'	30:0:2079:G:H5'	2.05	0.57
30:0:2240:U:O2'	30:0:2241:C:H5'	2.04	0.57
30:0:2335:C:H2'	30:0:2336:G:H8	1.67	0.57
30:0:2828:G:H8	30:0:2828:G:O5'	1.87	0.57
30:0:544:G:C2'	30:0:545:G:H5''	2.35	0.57
3:C:8:LEU:HD11	3:C:143:ASP:O	2.04	0.57
5:E:125:GLU:HB2	5:E:132:THR:HG23	1.86	0.57
30:0:1189:A:H1'	30:0:1209:C:C1'	2.35	0.57
30:0:1577:U:O2'	30:0:1578:C:H5'	2.05	0.57
30:0:2001:G:O2'	30:0:2002:C:H5'	2.04	0.57
3:C:127:ARG:HD3	3:C:129:HIS:HE1	1.70	0.57
21:U:56:ARG:HG3	21:U:56:ARG:NH1	2.19	0.57
24:X:43:VAL:HG22	24:X:76:ARG:NH1	2.20	0.57
30:0:138:U:OP2	30:0:139:C:C5	2.58	0.57
30:0:1718:G:O2'	30:0:1719:G:H5'	2.04	0.57
30:0:2010:A:H2'	38:0:5933:HOH:O	2.03	0.57
18:R:68:HIS:O	30:0:2842:G:H5'	2.05	0.57
30:0:371:U:O2'	30:0:372:A:H5'	2.05	0.57
30:0:403:C:H3'	38:0:6286:HOH:O	2.05	0.57
1:A:153:ARG:HD3	38:A:9011:HOH:O	2.04	0.57
2:B:214:PRO:HD2	38:B:8989:HOH:O	2.05	0.57
5:E:153:ARG:NH1	30:0:2778:A:H1'	2.19	0.57
14:N:160:SER:CB	31:9:51:A:H5'	2.34	0.57
15:O:19:ARG:NH1	30:0:1276:U:H3'	2.19	0.57
21:U:13:ILE:HG12	21:U:32:CYS:HB3	1.86	0.57
21:U:33:SER:O	21:U:37:GLU:HG3	2.04	0.57
25:Y:216:ARG:HD2	38:Y:8871:HOH:O	2.03	0.57
26:Z:45:VAL:HG13	26:Z:49:ARG:HE	1.70	0.57
30:0:1182:C:H1'	30:0:1192:A:H8	1.69	0.57
30:0:1971:G:H5'	38:0:7053:HOH:O	2.05	0.57
30:0:2407:G:O2'	30:0:2408:A:H5'	2.05	0.57
31:9:23:U:H2'	31:9:24:U:H4'	1.87	0.57
31:9:64:C:C2'	31:9:65:A:H5'	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:ARG:HD2	30:0:1884:G:O6	2.03	0.57
2:B:41:PHE:CZ	2:B:79:MET:HG3	2.40	0.57
13:M:68:ARG:HD3	13:M:68:ARG:O	2.05	0.57
20:T:24:ARG:HH21	20:T:39:ASN:HD22	1.53	0.57
24:X:30:MET:HE1	24:X:55:ASN:HA	1.86	0.57
30:0:1079:A:OP2	30:0:1080:C:N4	2.36	0.56
30:0:10:U:C4	30:0:532:A:C8	2.94	0.56
30:0:2251:G:H2'	30:0:2252:A:H8	1.70	0.56
30:0:2769:C:C2'	30:0:2770:G:C5'	2.78	0.56
30:0:312:U:O2'	30:0:313:U:H5'	2.05	0.56
30:0:407:A:H2'	30:0:408:A:C8	2.40	0.56
10:J:116:LEU:HB2	10:J:119:THR:HG21	1.87	0.56
30:0:1020:A:H2'	30:0:1021:G:C8	2.40	0.56
30:0:1173:A:H4'	30:0:1174:A:C8	2.40	0.56
13:M:82:ARG:HD2	30:0:170:U:OP2	2.05	0.56
30:0:2110:G:O2'	30:0:2111:G:H5'	2.05	0.56
30:0:2265:U:H2'	30:0:2266:A:C8	2.40	0.56
30:0:2698:G:H2'	30:0:2699:A:O4'	2.05	0.56
30:0:2700:G:H3'	38:0:3575:HOH:O	2.05	0.56
31:9:54:A:HO2'	31:9:55:U:H5'	1.67	0.56
11:K:32:ILE:HD11	11:K:56:SER:HB2	1.86	0.56
30:0:1616:A:H5''	30:0:1617:C:OP1	2.05	0.56
30:0:1948:G:O2'	30:0:1949:G:H5'	2.05	0.56
30:0:2011:A:H5'	30:0:2013:G:H1'	1.87	0.56
30:0:695:C:O2'	30:0:696:C:H5'	2.04	0.56
30:0:947:U:O2'	30:0:948:G:H5'	2.05	0.56
14:N:48:VAL:CG1	14:N:55:ASP:HB3	2.35	0.56
23:W:38:THR:O	23:W:42:ARG:HB2	2.04	0.56
30:0:1183:C:N4	30:0:1184:C:H41	2.03	0.56
30:0:1928:C:H2'	30:0:1929:G:O4'	2.05	0.56
30:0:280:C:H2'	30:0:281:U:O4'	2.06	0.56
28:2:40:ARG:HG3	28:2:45:ASN:HB2	1.85	0.56
29:3:34:LYS:HB3	38:3:9001:HOH:O	2.05	0.56
11:K:98:VAL:HG13	11:K:102:GLU:HA	1.85	0.56
14:N:141:ARG:NH2	31:9:48:C:H4'	2.21	0.56
30:0:162:C:H2'	30:0:163:U:H5'	1.87	0.56
30:0:1735:C:H2'	30:0:1736:A:C8	2.40	0.56
13:M:171:ARG:NH2	30:0:189:A:OP1	2.38	0.56
30:0:2659:U:H3'	38:0:4379:HOH:O	2.05	0.56
31:9:33:U:H2'	38:9:9068:HOH:O	2.04	0.56
2:B:17:LYS:O	2:B:260:HIS:HD2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:49:GLN:NE2	8:H:140:TYR:HE2	1.95	0.56
15:O:24:ALA:HB3	30:0:710:G:OP1	2.05	0.56
17:Q:45:PRO:O	30:0:2365:G:H4'	2.06	0.56
13:M:68:ARG:HG3	30:0:1469:C:OP1	2.05	0.56
30:0:1904:A:H2'	30:0:1905:U:O4'	2.05	0.56
30:0:2289:G:O2'	30:0:2290:U:H5'	2.06	0.56
30:0:2349:G:H2'	30:0:2350:G:C8	2.38	0.56
30:0:2064:U:H4'	30:0:2653:A:OP1	2.05	0.56
30:0:26:U:H5	38:0:3099:HOH:O	1.89	0.56
30:0:1042:U:O2'	30:0:1043:C:H5'	2.05	0.56
30:0:113:A:OP2	30:0:114:A:H2'	2.06	0.56
30:0:1434:A:O2'	30:0:1435:U:H2'	2.05	0.56
30:0:2502:C:H2'	30:0:2503:A:C5'	2.34	0.56
30:0:473:A:O2'	30:0:474:C:H5'	2.06	0.56
30:0:799:C:O2'	30:0:800:G:H5'	2.05	0.56
29:3:65:THR:HG23	33:3:8804:CL:CL	2.43	0.56
2:B:223:ARG:HD3	33:B:8819:CL:CL	2.43	0.56
30:0:1127:C:C5	30:0:1128:U:C4	2.94	0.56
30:0:138:U:OP2	30:0:139:C:H5	1.88	0.56
30:0:2595:U:O2'	30:0:2596:A:H5'	2.05	0.56
26:Z:34:SER:HA	30:0:797:A:C4'	2.36	0.56
29:3:18:GLN:HB3	38:3:9013:HOH:O	2.06	0.56
31:9:54:A:H2'	31:9:55:U:H5'	1.82	0.56
2:B:199:TYR:HE2	2:B:268:ARG:HB2	1.71	0.56
12:L:27:ARG:NH2	12:L:30:ARG:HD3	2.21	0.56
16:P:127:GLY:HA3	38:P:152:HOH:O	2.05	0.56
25:Y:165:GLU:HB3	38:0:6689:HOH:O	2.05	0.56
30:0:1292:G:HO2'	30:0:1293:U:H6	1.52	0.56
13:M:94:ARG:HD2	30:0:158:A:OP2	2.06	0.56
30:0:2241:C:O2'	30:0:2242:U:H5'	2.05	0.56
30:0:2514:U:OP1	30:0:2572:G:H1'	2.04	0.56
21:U:56:ARG:HD2	30:0:2890:A:H1'	1.87	0.56
27:1:28:HIS:HE1	30:0:776:A:OP1	1.88	0.56
30:0:473:A:O2'	30:0:890:C:H5'	2.05	0.56
1:A:27:LEU:HD21	1:A:55:VAL:HG21	1.88	0.56
3:C:4:THR:HA	3:C:15:GLU:HB3	1.88	0.56
13:M:24:GLN:HE22	13:M:27:ARG:HH11	1.53	0.56
21:U:44:ARG:HD3	21:U:49:LEU:CD1	2.35	0.56
30:0:1679:C:H5'	38:0:9332:HOH:O	2.06	0.56
30:0:1788:U:C2	30:0:1805:G:N2	2.73	0.56
30:0:2673:U:C4	30:0:2674:G:C6	2.94	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:18:U:H2'	31:9:19:G:H8	1.71	0.56
15:O:47:ARG:HG3	15:O:47:ARG:HH11	1.71	0.56
30:0:1020:A:H2'	30:0:1021:G:H8	1.71	0.56
30:0:1181:A:H2'	30:0:1182:C:O4'	2.06	0.56
30:0:2314:G:H2'	30:0:2315:C:H5'	1.87	0.56
30:0:2578:G:C8	30:0:2578:G:H5'	2.36	0.56
30:0:2911:C:H2'	30:0:2912:C:C6	2.42	0.56
3:C:174:ILE:HD11	30:0:338:C:H4'	1.89	0.56
30:0:660:A:H4'	30:0:661:G:O5'	2.06	0.56
12:L:41:HIS:HD2	30:0:926:A:O2'	1.89	0.56
31:9:49:G:H2'	31:9:50:G:O4'	2.06	0.56
2:B:68:THR:HG21	21:U:16:GLY:HA3	1.87	0.56
21:U:23:HIS:CD2	21:U:27:ALA:HB3	2.40	0.56
25:Y:142:SER:HB2	38:Y:8902:HOH:O	2.05	0.56
30:0:1116:U:H3	30:0:1246:A:N6	1.96	0.55
1:A:47:HIS:HD2	30:0:1654:U:C2'	2.18	0.55
30:0:1878:G:C1'	38:0:6097:HOH:O	2.53	0.55
30:0:558:C:C2'	30:0:559:U:C5'	2.68	0.55
30:0:1613:C:H2'	30:0:1614:G:O4'	2.06	0.55
29:3:33:MET:HG2	30:0:1922:A:H2'	1.88	0.55
30:0:2271:G:N3	30:0:2271:G:H2'	2.20	0.55
30:0:2325:U:O2'	30:0:2411:C:H1'	2.06	0.55
30:0:2852:A:H5''	38:0:5199:HOH:O	2.05	0.55
30:0:339:A:H2'	38:0:4203:HOH:O	2.06	0.55
30:0:684:G:H5''	38:0:4053:HOH:O	2.06	0.55
30:0:858:U:H2'	30:0:859:C:H6	1.71	0.55
5:E:49:ILE:HD11	5:E:69:ILE:HD12	1.88	0.55
25:Y:99:ALA:HB2	25:Y:233:TYR:CZ	2.42	0.55
30:0:1165:G:H21	30:0:1173:A:H5''	1.72	0.55
30:0:1172:G:H1'	38:0:4940:HOH:O	2.05	0.55
30:0:1183:C:H41	30:0:1192:A:H5'	1.72	0.55
30:0:1512:G:O2'	30:0:1513:C:H5'	2.05	0.55
30:0:2113:G:C6	30:0:2114:C:C4	2.94	0.55
30:0:735:C:C6	30:0:736:A:C8	2.94	0.55
3:C:115:LEU:HD21	3:C:243:VAL:HG13	1.86	0.55
23:W:52:VAL:HG22	23:W:53:ALA:N	2.20	0.55
30:0:2668:G:H2'	30:0:2669:U:C6	2.42	0.55
30:0:913:A:O5'	30:0:913:A:H8	1.90	0.55
30:0:920:C:H5'	30:0:921:G:C4	2.41	0.55
3:C:1:MET:HG2	3:C:2:GLN:H	1.72	0.55
25:Y:210:GLY:HA2	38:0:5285:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:44:ARG:HB2	30:0:1886:A:O2'	2.05	0.55
30:0:1625:U:C6	30:0:1625:U:C3'	2.85	0.55
2:B:229:ARG:NH2	30:0:1753:C:O2	2.39	0.55
30:0:2250:G:N2	30:0:2251:G:H1'	2.21	0.55
30:0:310:U:H2'	30:0:311:C:C6	2.41	0.55
29:3:59:ASP:HB3	29:3:63:LYS:HZ3	1.72	0.55
3:C:21:VAL:HG13	38:C:8594:HOH:O	2.05	0.55
7:G:16:LYS:HE2	7:G:63:ARG:NH1	2.21	0.55
24:X:76:ARG:HH11	24:X:76:ARG:HG3	1.72	0.55
38:Y:8879:HOH:O	30:0:1355:A:H5''	2.06	0.55
30:0:1562:C:N4	38:0:5836:HOH:O	2.38	0.55
30:0:1909:A:H2'	30:0:1910:A:C8	2.42	0.55
29:3:47:GLY:CA	30:0:2121:G:H4'	2.29	0.55
30:0:956:G:H3'	38:0:9387:HOH:O	2.06	0.55
3:C:149:LYS:HB2	3:C:152:GLU:HG3	1.89	0.55
3:C:162:VAL:HG22	3:C:232:LEU:HD21	1.87	0.55
10:J:19:MET:HE1	10:J:132:LEU:HD21	1.87	0.55
26:Z:63:CYS:SG	26:Z:81:CYS:CB	2.94	0.55
30:0:1691:A:H5''	38:0:3140:HOH:O	2.06	0.55
30:0:1736:A:H1'	38:0:7566:HOH:O	2.07	0.55
30:0:212:A:O4'	30:0:214:U:C6	2.59	0.55
30:0:545:G:C5'	30:0:545:G:C8	2.81	0.55
30:0:571:C:O5'	30:0:571:C:H6	1.90	0.55
30:0:822:C:C2	30:0:823:U:C5	2.94	0.55
30:0:835:U:H3'	38:0:9381:HOH:O	2.06	0.55
2:B:36:PRO:HA	2:B:168:GLY:CA	2.36	0.55
23:W:119:HIS:HD2	23:W:120:PRO:O	1.89	0.55
30:0:2274:A:H2'	30:0:2275:G:C8	2.42	0.55
30:0:2868:C:H1'	38:0:7107:HOH:O	2.07	0.55
30:0:401:C:H2'	30:0:402:U:H6	1.72	0.55
30:0:696:C:HO2'	30:0:697:G:H5'	1.71	0.55
29:3:90:PHE:CD1	29:3:90:PHE:N	2.75	0.55
31:9:59:C:C2	31:9:60:C:C5	2.94	0.55
2:B:102:THR:HG21	2:B:182:VAL:O	2.07	0.55
4:D:140:ARG:HG3	4:D:140:ARG:HH11	1.72	0.55
13:M:111:ASN:HB2	38:M:8852:HOH:O	2.07	0.55
30:0:1156:C:O2'	30:0:1157:C:H5'	2.07	0.55
30:0:1175:G:H2'	30:0:1176:C:C6	2.42	0.55
30:0:1166:A:C6	30:0:1181:A:C2	2.95	0.55
30:0:1200:A:N1	30:0:1201:C:C2	2.75	0.55
30:0:130:C:O2'	30:0:131:A:N7	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:291:C:H2'	30:0:292:G:O4'	2.07	0.55
28:2:43:ARG:HH22	30:0:1684:A:C1'	2.16	0.55
5:E:132:THR:HB	38:E:2227:HOH:O	2.06	0.55
13:M:70:GLY:CA	30:0:2263:G:H4'	2.37	0.55
19:S:37:VAL:O	19:S:41:VAL:HG23	2.05	0.55
30:0:1905:U:H2'	30:0:1906:C:H6	1.72	0.55
30:0:1849:G:H1'	30:0:2011:A:N1	2.22	0.55
30:0:2584:G:H4'	38:0:7102:HOH:O	2.07	0.55
30:0:2689:A:C2'	30:0:2690:U:H5'	2.37	0.55
30:0:2790:C:HO2'	30:0:2791:U:H6	1.55	0.55
30:0:777:U:OP2	30:0:777:U:H4'	2.07	0.55
5:E:118:ILE:HG23	5:E:144:THR:HG21	1.89	0.55
5:E:53:GLU:HB3	5:E:55:ASN:ND2	2.21	0.55
30:0:1377:C:H6	30:0:1377:C:C5'	2.20	0.54
30:0:1903:U:O2'	30:0:1904:A:N7	2.40	0.54
30:0:1909:A:N1	30:0:2128:G:H1'	2.22	0.54
30:0:2782:G:N2	30:0:2783:A:N6	2.55	0.54
30:0:690:G:H4'	30:0:741:C:O2	2.06	0.54
30:0:820:G:H5'	30:0:821:U:C5'	2.37	0.54
30:0:941:G:C5	30:0:942:U:C4	2.95	0.54
3:C:132:ASP:HB2	3:C:161:ASP:HB3	1.89	0.54
3:C:2:GLN:HB3	38:C:8581:HOH:O	2.07	0.54
14:N:110:THR:HB	14:N:113:SER:OG	2.07	0.54
1:A:76:VAL:HG23	26:Z:87:LYS:HB3	1.88	0.54
30:0:1593:C:H1'	38:0:6083:HOH:O	2.06	0.54
30:0:363:C:O2'	30:0:364:U:H5'	2.07	0.54
30:0:814:G:H2'	30:0:815:U:O4'	2.07	0.54
30:0:960:G:H8	38:0:5945:HOH:O	1.89	0.54
29:3:12:PRO:HG2	29:3:13:HIS:HD2	1.71	0.54
31:9:58:G:N7	31:9:59:C:C4	2.75	0.54
2:B:232:TRP:CZ3	30:0:2614:C:H5''	2.41	0.54
5:E:108:LEU:HD11	5:E:164:ASP:HB2	1.88	0.54
4:D:146:LYS:NZ	14:N:107:ASN:HD21	2.05	0.54
30:0:1015:C:H4'	38:0:6566:HOH:O	2.06	0.54
30:0:1175:G:H4'	38:0:6842:HOH:O	2.07	0.54
30:0:2032:U:C2'	30:0:2033:G:C5'	2.86	0.54
30:0:2032:U:C2'	30:0:2033:G:H5''	2.38	0.54
30:0:2524:G:H21	30:0:2526:C:H41	1.55	0.54
30:0:2869:G:H5'	38:0:5457:HOH:O	2.07	0.54
27:1:28:HIS:HD2	27:1:30:LYS:H	1.53	0.54
2:B:140:LEU:HA	38:B:9051:HOH:O	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:41:PHE:CE1	2:B:79:MET:HG3	2.43	0.54
9:I:78:ALA:HB2	9:I:95:LEU:HD21	1.89	0.54
14:N:114:LYS:O	14:N:118:ILE:HG13	2.07	0.54
14:N:130:PRO:HA	38:N:8837:HOH:O	2.06	0.54
30:0:1447:U:OP1	30:0:1506:U:N3	2.39	0.54
30:0:1876:C:H4'	30:0:1877:G:OP2	2.08	0.54
30:0:2281:C:C2'	30:0:2282:U:H5'	2.38	0.54
31:9:27:C:H2'	31:9:28:U:O4'	2.08	0.54
5:E:85:GLU:HG2	5:E:130:GLU:HG2	1.89	0.54
6:F:2:VAL:HG22	6:F:57:GLU:OE1	2.08	0.54
13:M:59:GLY:HA3	13:M:141:ILE:HD12	1.90	0.54
30:0:1139:U:H2'	30:0:1140:C:H6	1.72	0.54
15:O:19:ARG:HH22	30:0:1278:A:P	2.31	0.54
1:A:223:ARG:NH1	30:0:2270:G:H4'	2.22	0.54
30:0:2477:C:O2'	30:0:2478:U:H5'	2.07	0.54
31:9:36:C:C5	31:9:37:C:C5	2.96	0.54
1:A:192:VAL:CG1	1:A:207:GLN:HB3	2.38	0.54
9:I:87:PRO:HD2	30:0:1180:U:H1'	1.89	0.54
9:I:91:PHE:CD2	9:I:131:GLY:HA2	2.42	0.54
12:L:143:THR:HG22	12:L:144:ASP:N	2.22	0.54
13:M:99:ARG:HE	13:M:170:ASN:ND2	1.96	0.54
30:0:1697:G:H5'	38:0:5475:HOH:O	2.08	0.54
30:0:2081:A:H2'	30:0:2082:G:O4'	2.08	0.54
30:0:2107:U:O2'	30:0:2108:A:H5'	2.07	0.54
30:0:2321:A:C4	30:0:2323:G:C8	2.95	0.54
30:0:236:A:H4'	30:0:237:G:OP1	2.08	0.54
30:0:2831:C:H3'	38:0:7197:HOH:O	2.07	0.54
30:0:312:U:C2	30:0:320:G:N2	2.76	0.54
30:0:710:G:O2'	30:0:711:G:H5'	2.08	0.54
1:A:195:ASN:ND2	30:0:877:G:C8	2.76	0.54
30:0:963:C:O2	30:0:1005:A:N1	2.40	0.54
29:3:60:LYS:HB3	29:3:62:THR:O	2.07	0.54
12:L:67:ARG:O	12:L:71:GLU:HG3	2.08	0.54
30:0:1617:C:C5	30:0:1643:C:H4'	2.42	0.54
30:0:2078:U:H2'	30:0:2079:G:C8	2.42	0.54
30:0:2892:G:C5	30:0:2893:C:C5	2.95	0.54
30:0:461:C:N3	30:0:479:G:H5'	2.22	0.54
30:0:623:U:O2'	30:0:624:U:H5'	2.08	0.54
30:0:661:G:C5	30:0:686:A:C2	2.96	0.54
30:0:706:G:HO2'	30:0:707:C:H6	1.53	0.54
30:0:960:G:N3	30:0:960:G:C3'	2.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:19:ARG:HH21	31:9:11:A:P	2.30	0.54
16:P:35:ILE:HD13	38:P:171:HOH:O	2.08	0.54
30:0:1175:G:H1'	30:0:1193:A:H2'	1.89	0.54
30:0:1676:G:H1'	38:0:9441:HOH:O	2.08	0.54
30:0:1850:U:H2'	30:0:1851:G:H8	1.73	0.54
30:0:2045:G:H5''	38:0:7204:HOH:O	2.06	0.54
30:0:2256:G:O2'	30:0:2257:G:H5'	2.08	0.54
30:0:2670:G:O2'	30:0:2671:U:H5'	2.08	0.54
27:1:16:HIS:HD2	30:0:470:U:O2'	1.91	0.54
31:9:30:C:O2	31:9:30:C:H2'	2.08	0.54
2:B:62:ARG:HA	2:B:65:MET:HE3	1.88	0.54
4:D:135:VAL:HG21	4:D:139:TYR:CD1	2.43	0.54
5:E:116:THR:HG22	5:E:151:LEU:HD22	1.90	0.54
18:R:99:ALA:HB1	18:R:109:MET:CE	2.37	0.54
15:O:19:ARG:HH11	30:0:1276:U:H3'	1.73	0.54
30:0:1625:U:H5''	38:0:5995:HOH:O	2.07	0.54
30:0:2487:C:H5	38:0:4858:HOH:O	1.91	0.54
30:0:2787:C:H5	38:0:4605:HOH:O	1.90	0.54
30:0:2908:A:H8	30:0:2908:A:O5'	1.91	0.54
30:0:334:G:C4	30:0:335:U:C6	2.96	0.54
13:M:164:THR:CG2	13:M:165:GLY:N	2.70	0.54
30:0:2831:C:H2'	30:0:2832:C:C5'	2.38	0.54
30:0:541:C:C2'	30:0:542:A:C5'	2.78	0.54
30:0:853:C:H2'	30:0:854:G:O4'	2.08	0.54
28:2:13:LYS:O	28:2:17:GLN:HG3	2.07	0.54
31:9:23:U:C2'	31:9:24:U:H4'	2.38	0.54
30:0:1453:G:H2'	30:0:1454:U:O4'	2.07	0.53
30:0:1525:G:H5'	30:0:1526:A:OP2	2.08	0.53
30:0:2106:C:H2'	30:0:2107:U:C6	2.43	0.53
30:0:2599:A:H5''	38:0:3367:HOH:O	2.08	0.53
30:0:30:U:H5''	38:0:5777:HOH:O	2.08	0.53
30:0:338:C:H5''	38:0:3793:HOH:O	2.07	0.53
30:0:354:A:H2'	30:0:355:C:H6	1.73	0.53
1:A:179:MET:HG2	1:A:186:TRP:HB2	1.91	0.53
2:B:238:ASN:ND2	2:B:240:GLY:H	1.92	0.53
8:H:99:ARG:NH1	30:0:1055:G:OP2	2.41	0.53
14:N:132:ASN:HD22	30:0:2413:A:H4'	1.72	0.53
25:Y:97:LEU:HA	25:Y:234:VAL:O	2.08	0.53
30:0:1268:C:H2'	30:0:1269:G:H8	1.73	0.53
30:0:2321:A:C5	30:0:2323:G:C8	2.96	0.53
30:0:2379:G:N3	30:0:2418:G:H2'	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2553:A:N3	30:0:2553:A:H2'	2.23	0.53
30:0:2563:U:O2'	30:0:2564:G:H3'	2.08	0.53
30:0:2769:C:H2'	30:0:2770:G:C4'	2.37	0.53
9:I:111:LEU:HD23	30:0:1163:G:H4'	1.90	0.53
15:O:105:ASN:HD21	15:O:109:SER:H	1.56	0.53
16:P:7:LYS:HD3	16:P:21:VAL:CG2	2.38	0.53
30:0:1226:G:C4	30:0:1227:C:C5	2.96	0.53
30:0:1311:G:C2	30:0:1312:G:C8	2.97	0.53
2:B:212:GLN:HA	30:0:1733:A:H4'	1.89	0.53
30:0:2465:A:H5'	38:0:6910:HOH:O	2.07	0.53
30:0:421:C:H2'	30:0:422:G:H8	1.74	0.53
31:9:73:A:H61	31:9:108:C:H42	1.57	0.53
1:A:33:GLU:O	1:A:34:ASP:HB2	2.08	0.53
18:R:25:PHE:HB3	38:R:8914:HOH:O	2.07	0.53
23:W:35:VAL:HG23	23:W:41:TYR:CD2	2.43	0.53
30:0:1754:A:H2'	30:0:1755:A:O4'	2.09	0.53
1:A:20:SER:HB3	30:0:1872:C:C5	2.44	0.53
30:0:2703:A:H2'	30:0:2704:C:C6	2.40	0.53
30:0:491:C:O2'	30:0:492:C:H5'	2.09	0.53
30:0:869:G:OP2	30:0:869:G:C8	2.62	0.53
31:9:114:G:H2'	31:9:115:C:C6	2.43	0.53
12:L:11:ARG:O	30:0:903:U:C2	2.61	0.53
23:W:5:VAL:HG22	23:W:32:CYS:HB2	1.91	0.53
30:0:1271:A:H2'	30:0:1272:C:C6	2.43	0.53
30:0:1741:U:C4	30:0:2033:G:C8	2.96	0.53
30:0:1762:C:O2'	30:0:1763:C:H5'	2.08	0.53
30:0:2119:C:C2'	30:0:2120:U:H5'	2.38	0.53
30:0:213:G:H22	30:0:225:G:H2'	1.72	0.53
30:0:2831:C:C2	30:0:2910:A:C2	2.96	0.53
30:0:2895:C:H2'	38:0:9579:HOH:O	2.08	0.53
30:0:549:A:C2	30:0:550:C:C2	2.97	0.53
30:0:597:A:O2'	30:0:598:C:H5'	2.08	0.53
30:0:718:C:C2'	30:0:718:C:O2	2.55	0.53
8:H:49:GLN:HG3	8:H:140:TYR:CE2	2.43	0.53
16:P:71:TYR:CE2	30:0:1790:C:H5	2.26	0.53
30:0:1278:A:C4'	30:0:1279:U:C4	2.74	0.53
30:0:2078:U:H2'	30:0:2079:G:H8	1.74	0.53
30:0:2321:A:H2'	30:0:2321:A:N3	2.24	0.53
30:0:2501:G:H1	30:0:2519:C:H42	1.56	0.53
21:U:56:ARG:CD	30:0:2890:A:H1'	2.38	0.53
30:0:466:A:H2'	30:0:467:G:O4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:535:G:C5	30:0:2063:U:C4	2.96	0.53
29:3:68:LYS:HZ1	30:0:2436:U:H5'	1.73	0.53
31:9:58:G:C8	31:9:59:C:C5	2.97	0.53
8:H:69:ARG:HD3	38:H:239:HOH:O	2.08	0.53
11:K:89:LYS:HA	38:K:7064:HOH:O	2.08	0.53
30:0:1706:G:C6	30:0:1707:G:C6	2.97	0.53
30:0:1806:G:C5	30:0:1807:U:C5	2.97	0.53
30:0:1819:G:H5'	38:0:5785:HOH:O	2.07	0.53
29:3:31:THR:O	30:0:1923:G:H4'	2.09	0.53
30:0:195:C:H2'	30:0:196:G:H5'	1.91	0.53
30:0:1972:U:O2'	30:0:1973:A:H5''	2.09	0.53
30:0:2321:A:H4'	30:0:2322:U:OP1	2.08	0.53
30:0:398:U:H2'	30:0:399:C:C6	2.44	0.53
30:0:561:G:N3	30:0:562:A:C8	2.77	0.53
2:B:305:ASP:O	2:B:306:LYS:HB2	2.09	0.53
14:N:11:ARG:HG3	14:N:14:ARG:NH1	2.23	0.53
25:Y:154:ARG:NH2	30:0:1071:G:H4'	2.23	0.53
30:0:1167:G:H2'	30:0:1168:C:H6	1.71	0.53
30:0:1769:C:O2'	30:0:1770:U:H5'	2.09	0.53
30:0:191:A:H61	30:0:435:A:N6	2.06	0.53
30:0:2250:G:C2	30:0:2251:G:H1'	2.44	0.53
30:0:2613:G:O2'	30:0:2614:C:H5'	2.09	0.53
30:0:2864:U:C2'	30:0:2865:G:H5'	2.38	0.53
13:M:179:GLY:O	30:0:399:C:H5'	2.08	0.53
30:0:424:C:H2'	30:0:425:U:C6	2.44	0.53
23:W:154:ARG:NH1	30:0:588:G:O6	2.40	0.53
30:0:69:A:H2'	30:0:70:A:OP2	2.09	0.53
30:0:735:C:C5	30:0:736:A:C5	2.97	0.53
1:A:164:ARG:HB3	1:A:164:ARG:HH11	1.73	0.53
1:A:199:HIS:HD2	1:A:201:PHE:N	2.00	0.53
2:B:141:ARG:HD2	2:B:163:GLU:OE2	2.08	0.53
10:J:39:VAL:HG22	10:J:107:ASN:HA	1.91	0.53
11:K:41:LYS:O	11:K:42:ASN:HB2	2.09	0.53
13:M:187:LEU:CD2	13:M:194:GLY:HA3	2.38	0.53
14:N:154:LEU:C	14:N:156:GLU:H	2.11	0.53
22:V:44:GLY:O	22:V:48:GLU:HG2	2.08	0.53
30:0:1158:G:C2'	30:0:1159:G:H5'	2.39	0.53
30:0:1913:C:H2'	30:0:1914:C:H6	1.73	0.53
30:0:1922:A:N1	30:0:2449:G:O2'	2.38	0.53
30:0:1968:A:H2'	30:0:1969:A:C8	2.44	0.53
30:0:2336:G:H2'	38:0:6275:HOH:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:334:G:H2'	30:0:335:U:O4'	2.08	0.53
2:B:62:ARG:HA	2:B:65:MET:CE	2.38	0.53
8:H:6:ALA:HA	8:H:61:ARG:HH12	1.74	0.53
10:J:41:ALA:HB3	38:J:8863:HOH:O	2.09	0.53
16:P:115:SER:OG	16:P:118:GLN:HG3	2.08	0.53
30:0:74:G:H1	30:0:103:C:H42	1.55	0.53
30:0:1844:C:O2'	30:0:1845:A:H5'	2.08	0.53
30:0:2642:G:H2'	30:0:2643:G:O4'	2.09	0.53
9:I:108:HIS:H	9:I:109:PRO:HD2	1.74	0.53
14:N:38:LYS:HE2	14:N:107:ASN:ND2	2.24	0.53
30:0:1014:A:H2'	30:0:1015:C:H5'	1.90	0.52
30:0:1188:A:C6	30:0:1189:A:C6	2.97	0.52
30:0:1244:U:H4'	30:0:1246:A:O4'	2.09	0.52
30:0:1451:C:H5'	30:0:1505:U:C5	2.44	0.52
30:0:2037:C:H3'	38:0:6684:HOH:O	2.09	0.52
30:0:216:A:O2'	30:0:217:C:H5'	2.09	0.52
30:0:2719:A:H2'	30:0:2720:C:H5'	1.90	0.52
30:0:488:U:H2'	38:0:3993:HOH:O	2.08	0.52
31:9:20:G:O2'	31:9:21:G:H5'	2.09	0.52
31:9:37:C:O2	31:9:47:A:H1'	2.09	0.52
31:9:58:G:C6	31:9:59:C:C2	2.97	0.52
1:A:105:VAL:HG13	1:A:155:THR:O	2.09	0.52
1:A:45:ILE:HG22	26:Z:78:ILE:HG12	1.89	0.52
8:H:26:ILE:HA	8:H:123:ILE:HG21	1.91	0.52
8:H:159:LYS:HG2	30:0:2519:C:O2	2.09	0.52
30:0:1164:U:H5	38:0:6024:HOH:O	1.91	0.52
30:0:675:U:H2'	30:0:676:C:H5'	1.90	0.52
15:O:25:VAL:HG13	30:0:709:G:O3'	2.10	0.52
23:W:4:LEU:HD22	23:W:54:PHE:HB3	1.90	0.52
30:0:125:U:H2'	38:0:3760:HOH:O	2.10	0.52
30:0:1515:A:H2'	30:0:1516:U:C6	2.44	0.52
30:0:1557:G:O2'	30:0:1558:C:H5'	2.09	0.52
30:0:1684:A:O2'	30:0:1685:A:H5''	2.10	0.52
13:M:73:ARG:HH21	30:0:2263:G:H5''	1.70	0.52
30:0:271:C:C2	30:0:273:G:O4'	2.61	0.52
30:0:2901:C:H6	30:0:2901:C:O5'	1.93	0.52
3:C:43:LYS:HG2	30:0:449:A:N7	2.24	0.52
30:0:622:G:O2'	30:0:623:U:H5'	2.10	0.52
31:9:1:U:C4'	31:9:3:A:OP1	2.58	0.52
5:E:126:ILE:HA	5:E:131:LEU:HD23	1.91	0.52
13:M:24:GLN:NE2	13:M:27:ARG:HH11	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:33:SER:O	19:S:37:VAL:HG23	2.10	0.52
30:0:1359:U:O5'	30:0:1360:C:H5''	2.10	0.52
30:0:1664:A:OP1	30:0:1664:A:H8	1.92	0.52
30:0:1865:A:H2'	30:0:1866:A:C8	2.44	0.52
30:0:2320:U:H4'	30:0:2321:A:O4'	2.09	0.52
30:0:2407:G:H2'	30:0:2408:A:O4'	2.09	0.52
30:0:249:G:N2	30:0:250:C:C2	2.77	0.52
30:0:2783:A:O2'	30:0:2784:A:H5'	2.09	0.52
30:0:40:C:H6	30:0:40:C:O5'	1.93	0.52
30:0:24:G:N2	30:0:518:G:H1'	2.24	0.52
28:2:49:GLU:HB2	38:2:131:HOH:O	2.08	0.52
31:9:38:A:C2	31:9:39:U:C4	2.97	0.52
11:K:66:ARG:HH12	30:0:1992:U:H3'	1.75	0.52
20:T:26:THR:HG23	20:T:97:ARG:HG3	1.90	0.52
23:W:130:HIS:NE2	31:9:88:G:OP1	2.42	0.52
30:0:1590:A:C2	30:0:1606:A:H1'	2.44	0.52
30:0:204:A:C2'	30:0:205:U:H5'	2.39	0.52
30:0:916:A:C2	30:0:928:G:N3	2.78	0.52
29:3:68:LYS:HG2	29:3:77:ALA:HB3	1.91	0.52
14:N:55:ASP:OD2	31:9:7:G:H4'	2.09	0.52
2:B:226:LYS:HG2	2:B:230:GLN:NE2	2.25	0.52
6:F:53:ASP:OD1	6:F:80:GLN:HB2	2.10	0.52
13:M:81:ARG:HB3	13:M:86:GLN:HG2	1.91	0.52
30:0:1139:U:H2'	30:0:1140:C:C6	2.45	0.52
30:0:1180:U:O2'	30:0:1181:A:H5'	2.10	0.52
30:0:1641:A:C2'	30:0:1642:A:H5'	2.40	0.52
30:0:1649:G:H1'	38:0:5498:HOH:O	2.09	0.52
30:0:1087:G:O2'	33:0:8822:CL:CL	2.55	0.52
31:9:49:G:O2'	31:9:50:G:H5'	2.08	0.52
1:A:66:ARG:HH11	1:A:66:ARG:HB2	1.74	0.52
4:D:18:ILE:HD13	4:D:84:LEU:HD12	1.91	0.52
5:E:153:ARG:HH12	30:0:2778:A:C1'	2.22	0.52
18:R:111:ILE:HG23	18:R:145:LEU:HD11	1.90	0.52
18:R:132:ARG:HH22	30:0:2055:A:H4'	1.74	0.52
20:T:106:GLU:HG3	38:T:4913:HOH:O	2.09	0.52
30:0:1052:G:H2'	30:0:1052:G:N3	2.24	0.52
30:0:1886:A:H4'	38:0:9333:HOH:O	2.09	0.52
30:0:1890:U:H4'	30:0:2010:A:C6	2.44	0.52
30:0:1930:A:H2'	30:0:1931:A:C8	2.44	0.52
30:0:2041:G:O2'	30:0:2042:U:H5'	2.10	0.52
30:0:228:C:C2'	30:0:229:G:H5'	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2526:C:C6	30:0:2526:C:C3'	2.93	0.52
25:Y:132:ASP:OD2	30:0:621:C:H5'	2.10	0.52
28:2:18:ASN:HD21	28:2:40:ARG:HB3	1.74	0.52
31:9:58:G:C5	31:9:59:C:C2	2.98	0.52
2:B:223:ARG:HG3	2:B:232:TRP:O	2.10	0.52
38:I:1549:HOH:O	30:0:1180:U:H1'	2.10	0.52
30:0:2637:A:C5'	38:0:4897:HOH:O	2.55	0.52
30:0:2651:C:H2'	30:0:2652:U:O4'	2.10	0.52
30:0:506:G:N2	30:0:509:A:H5''	2.18	0.52
30:0:595:U:H3'	38:0:6474:HOH:O	2.09	0.52
30:0:734:U:O2'	30:0:736:A:N7	2.33	0.52
30:0:800:G:H2'	30:0:801:U:C6	2.45	0.52
27:1:11:LYS:HG2	30:0:777:U:O2'	2.10	0.52
31:9:34:A:H2'	31:9:35:C:O4'	2.10	0.52
18:R:18:LEU:HB2	18:R:143:VAL:HG13	1.91	0.52
30:0:1183:C:C4	30:0:1184:C:N4	2.78	0.52
30:0:1522:A:C2'	30:0:1523:G:H5'	2.40	0.52
30:0:2672:C:H2'	30:0:2673:U:H6	1.74	0.52
30:0:599:G:H2'	30:0:600:G:H8	1.74	0.52
30:0:615:G:H2'	30:0:616:U:C6	2.44	0.52
30:0:793:A:C5	30:0:794:U:C5	2.98	0.52
2:B:243:ASN:HB2	30:0:2607:U:OP2	2.10	0.52
6:F:91:VAL:HG12	6:F:92:GLY:N	2.20	0.52
7:G:63:ARG:O	7:G:67:LEU:HG	2.10	0.52
12:L:73:VAL:HG23	12:L:74:THR:H	1.75	0.52
30:0:1154:A:H2'	30:0:1155:G:C8	2.44	0.52
30:0:1422:U:H2'	30:0:1423:C:H6	1.72	0.52
30:0:1504:A:H5'	38:0:4396:HOH:O	2.10	0.52
30:0:2088:C:H2'	30:0:2089:A:C8	2.44	0.52
30:0:308:U:C4	30:0:342:C:H1'	2.45	0.52
30:0:818:A:C6	30:0:819:A:N1	2.78	0.52
29:3:4:PRO:HA	29:3:91:GLN:O	2.09	0.52
13:M:73:ARG:HD2	13:M:73:ARG:N	2.25	0.52
30:0:1175:G:N7	30:0:1176:C:C4	2.78	0.51
30:0:1191:A:C2'	30:0:1193:A:H5'	2.38	0.51
30:0:1309:U:O2'	30:0:1310:U:H5'	2.10	0.51
30:0:1743:G:H2'	30:0:1744:G:O4'	2.10	0.51
30:0:2872:U:H2'	30:0:2873:C:H6	1.76	0.51
30:0:818:A:C6	30:0:819:A:C2	2.98	0.51
12:L:78:ALA:HB3	38:L:8860:HOH:O	2.11	0.51
13:M:43:PRO:HG3	13:M:62:VAL:HG21	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:49:ARG:HD3	24:X:84:ILE:HG12	1.92	0.51
30:0:1395:C:H2'	30:0:1396:C:C6	2.46	0.51
30:0:2498:C:O2'	30:0:2499:U:H5'	2.10	0.51
30:0:2900:G:H2'	30:0:2901:C:O4'	2.10	0.51
30:0:395:A:H2'	30:0:397:A:H62	1.74	0.51
2:B:144:THR:HB	38:B:9096:HOH:O	2.10	0.51
14:N:7:LYS:HE3	17:Q:21:ARG:O	2.09	0.51
17:Q:87:THR:HB	38:Q:1295:HOH:O	2.10	0.51
20:T:52:ARG:HH12	30:0:308:U:H2'	1.75	0.51
26:Z:38:PHE:HB3	26:Z:42:TYR:CE1	2.46	0.51
30:0:1667:A:H8	30:0:1667:A:H5'	1.75	0.51
30:0:1992:U:H2'	30:0:1994:A:OP2	2.10	0.51
30:0:2544:G:H5'	38:0:3418:HOH:O	2.10	0.51
30:0:20:G:H5''	30:0:510:U:O4	2.09	0.51
25:Y:205:ILE:HB	25:Y:230:ASN:HD21	1.75	0.51
30:0:1641:A:H2'	30:0:1642:A:C5'	2.40	0.51
30:0:2032:U:H2'	30:0:2033:G:H5''	1.92	0.51
29:3:54:LYS:HE2	30:0:2468:A:C8	2.45	0.51
30:0:2614:C:O2'	30:0:2615:U:H5'	2.10	0.51
9:I:120:ALA:O	9:I:124:VAL:HG23	2.09	0.51
30:0:1160:G:H2'	38:0:5597:HOH:O	2.11	0.51
30:0:1167:G:H2'	30:0:1168:C:O4'	2.11	0.51
30:0:1395:C:H2'	30:0:1396:C:H6	1.76	0.51
31:9:56:A:H3'	31:9:57:A:H5''	1.89	0.51
1:A:175:LYS:HE2	33:A:8809:CL:CL	2.48	0.51
15:O:65:LEU:HD13	30:0:746:A:C6	2.45	0.51
17:Q:7:LEU:HD12	30:0:2424:U:H1'	1.93	0.51
30:0:254:C:C2'	30:0:254:C:O2	2.57	0.51
30:0:2700:G:O2'	30:0:2701:G:H5'	2.09	0.51
30:0:2846:C:H3'	38:0:7070:HOH:O	2.11	0.51
30:0:2851:G:H2'	30:0:2902:A:N6	2.26	0.51
30:0:660:A:N6	30:0:746:A:O4'	2.43	0.51
30:0:702:G:C2	30:0:703:G:C8	2.98	0.51
31:9:58:G:H3'	31:9:59:C:C5	2.45	0.51
3:C:127:ARG:HD3	3:C:129:HIS:CE1	2.45	0.51
10:J:21:ARG:HH21	30:0:1244:U:H5''	1.76	0.51
11:K:91:GLU:HG3	38:U:151:HOH:O	2.11	0.51
30:0:1019:C:O2'	30:0:1020:A:H5'	2.11	0.51
30:0:128:A:O2'	30:0:129:A:H5'	2.10	0.51
2:B:234:ARG:HG3	30:0:1735:C:OP2	2.11	0.51
30:0:1947:G:N2	30:0:1966:U:C2	2.79	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2032:U:H2'	30:0:2033:G:H5'	1.93	0.51
30:0:2719:A:C2'	30:0:2720:C:H5'	2.41	0.51
30:0:37:A:H2'	30:0:38:G:C8	2.46	0.51
30:0:633:C:O2'	30:0:634:G:H5'	2.10	0.51
29:3:40:ARG:HA	29:3:52:PHE:HE1	1.73	0.51
29:3:83:TRP:NE1	30:0:2380:A:H2	2.09	0.51
5:E:137:ASP:OD1	5:E:139:GLU:HB2	2.11	0.51
8:H:114:ASP:HA	38:H:204:HOH:O	2.11	0.51
17:Q:94:GLN:O	17:Q:95:GLU:HB2	2.11	0.51
24:X:56:GLU:HG2	30:0:1400:C:H4'	1.92	0.51
30:0:1236:A:O2'	30:0:1237:U:H5'	2.11	0.51
30:0:2047:C:H5'	38:0:9814:HOH:O	2.10	0.51
30:0:210:U:O2'	30:0:211:U:H5'	2.11	0.51
30:0:2456:A:O2'	30:0:2457:U:H5'	2.10	0.51
30:0:2689:A:H2'	30:0:2690:U:H5'	1.92	0.51
15:O:37:ARG:HD2	30:0:656:G:OP2	2.11	0.51
30:0:727:G:H3'	30:0:728:C:C6	2.45	0.51
30:0:822:C:N3	30:0:823:U:C5	2.79	0.51
3:C:149:LYS:HE3	38:0:4023:HOH:O	2.10	0.51
3:C:219:ASN:O	3:C:222:ASP:HB2	2.11	0.51
6:F:91:VAL:HG11	30:0:262:A:OP2	2.10	0.51
6:F:36:THR:HG23	6:F:97:ALA:HB2	1.93	0.51
7:G:64:ASN:HD22	7:G:64:ASN:H	1.58	0.51
13:M:28:GLN:O	13:M:32:ARG:HG3	2.10	0.51
20:T:32:ARG:NH1	20:T:38:ARG:NH1	2.58	0.51
26:Z:53:ILE:HG23	38:Z:8719:HOH:O	2.10	0.51
26:Z:78:ILE:HD12	38:Z:8715:HOH:O	2.11	0.51
30:0:1890:U:H1'	30:0:2013:G:N2	2.26	0.51
11:K:66:ARG:NH2	30:0:1994:A:OP1	2.44	0.51
30:0:2589:U:H2'	30:0:2590:U:C6	2.46	0.51
30:0:2712:G:C5'	38:0:5187:HOH:O	2.58	0.51
30:0:523:C:H2'	30:0:524:A:C8	2.46	0.51
16:P:128:GLY:HA3	30:0:801:U:O4'	2.11	0.51
8:H:61:ARG:HH11	8:H:61:ARG:HG3	1.75	0.51
24:X:61:ARG:O	30:0:2744:G:H5''	2.11	0.51
25:Y:127:GLN:HA	38:Y:8909:HOH:O	2.11	0.51
30:0:1186:C:N4	30:0:1187:U:C4	2.79	0.51
30:0:1568:G:H2'	30:0:1569:U:O4'	2.10	0.51
30:0:1819:G:H2'	30:0:1820:G:C5'	2.41	0.51
30:0:2526:C:O2'	30:0:2527:U:H5'	2.10	0.51
30:0:255:A:H2'	30:0:256:C:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:39:G:C2	30:0:444:C:C2	2.99	0.51
30:0:617:C:H2'	30:0:618:G:O4'	2.11	0.51
29:3:22:VAL:HG12	29:3:90:PHE:CE2	2.46	0.51
2:B:80:ARG:HB2	2:B:145:HIS:CE1	2.45	0.51
8:H:31:ILE:HD11	8:H:65:LEU:HB3	1.93	0.51
16:P:118:GLN:O	16:P:122:LEU:HG	2.11	0.51
9:I:83:GLY:HA3	30:0:1168:C:H5'	1.93	0.50
30:0:1226:G:C5	30:0:1227:C:C5	2.99	0.50
30:0:553:G:O4'	30:0:1325:G:H5'	2.10	0.50
30:0:1441:G:O2'	30:0:1442:A:H5'	2.11	0.50
30:0:1511:U:O2'	30:0:1512:G:H5'	2.11	0.50
30:0:1642:A:C8	30:0:1643:C:C5	2.99	0.50
30:0:1796:A:H8	30:0:1796:A:O5'	1.94	0.50
30:0:1805:G:O2'	30:0:1806:G:H5'	2.11	0.50
30:0:2587:OMU:H2'	30:0:2589:U:H5''	1.93	0.50
30:0:560:U:H2'	30:0:561:G:H8	1.75	0.50
2:B:71:VAL:HG21	2:B:296:LEU:HB3	1.92	0.50
7:G:20:VAL:O	7:G:24:VAL:HG23	2.11	0.50
11:K:97:ILE:HG22	11:K:98:VAL:N	2.25	0.50
22:V:12:THR:HG23	22:V:14:ALA:H	1.76	0.50
26:Z:102:THR:HG23	26:Z:105:ARG:HD2	1.93	0.50
30:0:1167:G:N2	30:0:1180:U:C2	2.79	0.50
30:0:134:U:O2	30:0:145:A:C2	2.63	0.50
30:0:2087:C:O2'	30:0:2088:C:H5'	2.11	0.50
30:0:2672:C:C2	30:0:2673:U:C6	3.00	0.50
30:0:2847:G:O2'	30:0:2848:G:H5'	2.11	0.50
3:C:127:ARG:HH21	3:C:225:PRO:HG2	1.71	0.50
25:Y:210:GLY:N	30:0:1313:A:H5''	2.27	0.50
30:0:1087:G:H4'	30:0:1088:A:OP1	2.12	0.50
30:0:1216:G:N2	30:0:1217:G:H1'	2.26	0.50
30:0:1461:U:H2'	30:0:1462:C:C6	2.46	0.50
30:0:1735:C:H2'	30:0:1736:A:H8	1.75	0.50
30:0:2899:A:O2'	30:0:2900:G:H5'	2.12	0.50
30:0:523:C:H2'	30:0:524:A:H8	1.76	0.50
30:0:876:A:H2'	30:0:876:A:N3	2.26	0.50
27:1:16:HIS:CD2	30:0:470:U:O2'	2.64	0.50
29:3:29:ARG:HA	38:3:9012:HOH:O	2.11	0.50
2:B:248:ARG:O	2:B:251:VAL:HG22	2.11	0.50
3:C:193:LEU:HA	3:C:211:ASP:O	2.10	0.50
3:C:236:THR:HG22	3:C:239:ALA:CB	2.41	0.50
5:E:7:ILE:HG13	5:E:11:VAL:HB	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:35:LYS:HA	30:0:2755:G:OP1	2.11	0.50
30:0:1181:A:H2'	30:0:1182:C:C5'	2.41	0.50
30:0:1463:U:H2'	30:0:1464:C:C6	2.47	0.50
30:0:1474:C:H6	30:0:1474:C:C5'	2.17	0.50
30:0:1522:A:H2'	30:0:1523:G:H5'	1.92	0.50
30:0:2564:G:OP2	30:0:2565:C:H5''	2.11	0.50
30:0:2635:A:HO2'	30:0:2636:C:H5'	1.76	0.50
30:0:1811:A:C2	30:0:2752:C:H1'	2.46	0.50
30:0:40:C:H2'	30:0:41:G:C8	2.46	0.50
29:3:10:TYR:CE1	30:0:2408:A:H1'	2.46	0.50
29:3:10:TYR:HB2	29:3:17:HIS:HE1	1.76	0.50
10:J:107:ASN:HD22	10:J:107:ASN:C	2.15	0.50
12:L:65:ASP:HA	12:L:109:LEU:O	2.11	0.50
30:0:1015:C:O5'	30:0:1015:C:H6	1.94	0.50
30:0:105:G:O2'	30:0:106:A:H5'	2.11	0.50
30:0:1187:U:O2'	30:0:1189:A:H2	1.94	0.50
30:0:1149:U:C5	30:0:1215:A:C5	3.00	0.50
30:0:73:U:H2'	30:0:74:G:C8	2.46	0.50
17:Q:95:GLU:HA	30:0:949:U:H4'	1.94	0.50
2:B:235:ARG:HH11	30:0:2092:G:P	2.33	0.50
7:G:16:LYS:O	7:G:20:VAL:HG23	2.11	0.50
13:M:71:SER:HB2	13:M:92:THR:CG2	2.35	0.50
30:0:119:A:H2'	30:0:120:A:C5'	2.42	0.50
38:B:8995:HOH:O	30:0:2093:G:H5''	2.11	0.50
30:0:2344:G:N3	30:0:2344:G:H2'	2.26	0.50
30:0:2295:G:N3	30:0:2361:A:C2	2.80	0.50
30:0:2506:A:C1'	38:0:6031:HOH:O	2.58	0.50
30:0:372:A:C2	30:0:373:G:C4	2.99	0.50
30:0:451:C:O2'	30:0:452:G:H5'	2.12	0.50
30:0:556:C:O2'	30:0:557:C:H5'	2.11	0.50
30:0:738:G:O5'	30:0:738:G:H8	1.95	0.50
30:0:819:A:C4	30:0:821:U:C5	3.00	0.50
30:0:929:A:H5''	38:0:7060:HOH:O	2.11	0.50
8:H:59:GLN:NE2	8:H:129:ARG:HE	2.10	0.50
14:N:37:ARG:NH1	31:9:6:C:OP1	2.44	0.50
16:P:114:LEU:HD22	16:P:118:GLN:HB3	1.93	0.50
16:P:135:ALA:O	16:P:139:ARG:HG3	2.11	0.50
30:0:10:U:O4	30:0:532:A:H8	1.95	0.50
30:0:1666:C:H42	30:0:1667:A:N6	2.10	0.50
26:Z:42:TYR:N	30:0:1829:A:H61	2.10	0.50
30:0:2415:A:C2'	30:0:2416:G:H5'	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1705:C:O2	30:0:2735:U:H5''	2.11	0.50
30:0:2803:C:H2'	30:0:2804:C:H6	1.77	0.50
30:0:2823:G:O2'	30:0:2824:C:H5'	2.12	0.50
30:0:69:A:C5'	30:0:69:A:H8	2.24	0.50
30:0:716:G:C6	30:0:717:C:N4	2.80	0.50
30:0:79:G:N2	30:0:97:G:H1'	2.26	0.50
29:3:3:MET:O	29:3:90:PHE:HA	2.11	0.50
31:9:75:G:N2	31:9:106:U:O2	2.36	0.50
31:9:92:G:H2'	31:9:93:A:H8	1.73	0.50
1:A:132:ASP:CG	1:A:133:ARG:H	2.15	0.50
1:A:178:LYS:HA	30:0:1653:A:H5'	1.94	0.50
30:0:74:G:H1	30:0:103:C:N4	2.10	0.50
30:0:1878:G:C4'	38:0:6097:HOH:O	2.60	0.50
30:0:282:C:O2'	30:0:283:U:C4'	2.60	0.50
30:0:59:A:C5'	38:0:4313:HOH:O	2.60	0.50
30:0:764:C:H2'	30:0:765:G:O4'	2.12	0.50
29:3:10:TYR:HB2	29:3:17:HIS:CE1	2.47	0.50
31:9:23:U:H2'	31:9:23:U:O2	2.12	0.50
1:A:100:PRO:HG2	1:A:103:VAL:HG21	1.94	0.50
3:C:22:PHE:HA	3:C:116:ALA:HA	1.94	0.50
13:M:82:ARG:HH22	13:M:85:ARG:NH2	2.08	0.50
13:M:77:HIS:CE1	13:M:86:GLN:HG2	2.47	0.50
14:N:38:LYS:HE2	14:N:107:ASN:HD21	1.75	0.50
22:V:56:ILE:O	22:V:60:GLN:HG3	2.12	0.50
30:0:2253:G:O2'	30:0:2254:G:H5'	2.11	0.50
30:0:2465:A:H3'	38:0:3637:HOH:O	2.12	0.50
30:0:561:G:C2	30:0:562:A:C8	3.00	0.50
3:C:101:ASP:HB2	30:0:750:A:O3'	2.12	0.50
30:0:814:G:H2'	30:0:815:U:H6	1.77	0.50
29:3:3:MET:SD	29:3:88:LEU:HD23	2.52	0.50
31:9:42:C:H5'	31:9:43:G:OP2	2.12	0.50
1:A:141:PRO:HG2	30:0:1855:G:O6	2.12	0.50
2:B:18:ARG:HG3	2:B:256:GLN:HG3	1.93	0.50
12:L:24:ALA:HB2	12:L:30:ARG:HE	1.76	0.50
13:M:145:ASP:HB2	38:M:8865:HOH:O	2.11	0.50
20:T:71:VAL:HG11	20:T:90:PRO:CB	2.38	0.50
23:W:130:HIS:O	23:W:136:GLY:HA3	2.12	0.50
23:W:6:GLN:CB	23:W:26:ILE:HD11	2.40	0.50
24:X:26:ALA:HB2	24:X:63:ARG:HA	1.93	0.50
30:0:47:G:N3	30:0:114:A:C2	2.80	0.49
30:0:1165:G:H21	30:0:1173:A:H5'	1.74	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1268:C:H2'	30:0:1269:G:C8	2.46	0.49
30:0:1393:A:H2'	30:0:1394:C:C6	2.47	0.49
30:0:1601:G:H1'	38:0:9891:HOH:O	2.11	0.49
30:0:1933:G:O2'	30:0:1934:A:H5'	2.12	0.49
30:0:2854:A:C6	30:0:2905:A:C6	3.00	0.49
30:0:952:G:N3	30:0:2302:A:H2'	2.26	0.49
31:9:28:U:O2	31:9:57:A:N6	2.44	0.49
31:9:39:U:H1'	31:9:44:A:H61	1.77	0.49
2:B:66:GLU:OE1	2:B:328:ARG:HD2	2.12	0.49
4:D:58:VAL:CG1	4:D:60:GLU:HG2	2.41	0.49
13:M:159:VAL:CG1	33:M:8818:CL:CL	2.95	0.49
16:P:87:ARG:HG2	38:0:5919:HOH:O	2.10	0.49
30:0:1226:G:H2'	30:0:1227:C:C6	2.44	0.49
30:0:134:U:C2	30:0:145:A:C2	2.99	0.49
30:0:1662:C:H6	30:0:1662:C:O5'	1.94	0.49
30:0:1902:G:N2	30:0:1936:C:C2	2.80	0.49
30:0:589:U:H2'	30:0:590:A:H8	1.76	0.49
30:0:873:G:N2	38:0:9173:HOH:O	2.43	0.49
29:3:60:LYS:C	29:3:62:THR:H	2.15	0.49
31:9:55:U:H4'	31:9:56:A:H8	1.71	0.49
4:D:35:ALA:HB2	38:D:5576:HOH:O	2.11	0.49
8:H:32:ALA:HB3	8:H:69:ARG:HH12	1.77	0.49
16:P:98:ILE:HD12	16:P:102:ARG:NE	2.27	0.49
18:R:18:LEU:O	18:R:142:ASP:HA	2.12	0.49
30:0:1194:A:C2	30:0:1206:U:H1'	2.47	0.49
25:Y:212:ARG:HB2	30:0:1315:G:C4	2.47	0.49
30:0:1800:G:H2'	30:0:1801:A:H8	1.77	0.49
30:0:2291:A:N3	30:0:2291:A:H2'	2.28	0.49
30:0:2617:G:C2	30:0:2618:G:C8	3.00	0.49
30:0:2846:C:H2'	30:0:2847:G:H8	1.77	0.49
30:0:1787:C:C4'	30:0:2883:A:O4'	2.59	0.49
30:0:316:A:N3	30:0:336:G:O2'	2.41	0.49
30:0:400:C:H2'	30:0:401:C:C6	2.47	0.49
10:J:131:THR:HG22	10:J:134:GLU:H	1.77	0.49
11:K:34:VAL:HB	38:K:7169:HOH:O	2.12	0.49
30:0:1206:U:C5'	30:0:1206:U:H6	2.21	0.49
30:0:1255:A:H1'	38:0:7741:HOH:O	2.11	0.49
25:Y:115:ARG:NH2	30:0:1266:U:H4'	2.27	0.49
30:0:1339:G:C6	30:0:1340:G:N1	2.81	0.49
30:0:1381:A:N3	30:0:1382:G:H1'	2.28	0.49
1:A:47:HIS:CD2	30:0:1654:U:C2'	2.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1947:G:N2	30:0:1966:U:N3	2.60	0.49
30:0:2133:U:H4'	30:0:2134:G:H5'	1.93	0.49
30:0:2632:G:C6	30:0:2633:A:N6	2.81	0.49
30:0:2632:G:H2'	30:0:2633:A:C8	2.46	0.49
30:0:36:C:C2	30:0:447:A:C2	3.00	0.49
30:0:814:G:H2'	30:0:815:U:C6	2.47	0.49
30:0:816:G:H5'	30:0:1598:A:H4'	1.94	0.49
29:3:79:LEU:CD1	30:0:2456:A:H2	2.25	0.49
29:3:79:LEU:HD22	38:0:7515:HOH:O	2.13	0.49
2:B:44:TYR:OH	2:B:148:PRO:HG3	2.11	0.49
2:B:215:VAL:O	2:B:219:GLY:HA2	2.13	0.49
6:F:110:ASP:O	6:F:114:LYS:HG3	2.12	0.49
9:I:93:ALA:HB3	9:I:132:VAL:HG22	1.95	0.49
17:Q:66:LYS:HB2	17:Q:70:ALA:O	2.13	0.49
26:Z:60:ASP:HB3	26:Z:69:ASP:HB3	1.92	0.49
30:0:1370:G:H5''	38:0:5497:HOH:O	2.12	0.49
30:0:1559:A:HO2'	30:0:1561:U:H5	1.60	0.49
30:0:1555:G:H4'	30:0:1630:A:C2	2.47	0.49
30:0:1733:A:C5	30:0:1734:C:C2	3.00	0.49
30:0:1878:G:O2'	30:0:1879:U:H6	1.90	0.49
30:0:2118:A:H5'	38:0:3996:HOH:O	2.13	0.49
30:0:2366:C:O5'	30:0:2366:C:H6	1.95	0.49
30:0:1787:C:O4'	30:0:2883:A:H1'	2.11	0.49
30:0:494:C:H1'	30:0:498:A:N6	2.27	0.49
2:B:304:PRO:HD2	2:B:307:ARG:HE	1.78	0.49
14:N:58:LEU:HD12	14:N:58:LEU:N	2.27	0.49
30:0:1189:A:O2'	30:0:1208:C:H2'	2.12	0.49
30:0:1174:A:C5	30:0:1201:C:H4'	2.47	0.49
30:0:1626:A:O2'	30:0:1627:G:H5'	2.13	0.49
30:0:1517:C:O2	30:0:1670:A:C2	2.66	0.49
30:0:1682:A:O2'	30:0:1683:G:H5''	2.12	0.49
30:0:1871:U:O4'	30:0:1873:G:C8	2.66	0.49
30:0:2335:C:C2	30:0:2350:G:C2	3.01	0.49
30:0:29:C:O2'	30:0:30:U:H5'	2.12	0.49
20:T:107:LYS:HD2	30:0:97:G:C2	2.47	0.49
8:H:27:PRO:HD3	8:H:123:ILE:CG2	2.43	0.49
10:J:130:VAL:HG12	10:J:131:THR:H	1.78	0.49
14:N:37:ARG:HG3	14:N:37:ARG:HH11	1.77	0.49
30:0:1226:G:N3	30:0:1227:C:C6	2.81	0.49
29:3:33:MET:HG2	30:0:1922:A:C2'	2.42	0.49
30:0:2478:U:H2'	30:0:2479:A:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:71:LYS:HE2	30:0:2831:C:O3'	2.13	0.49
30:0:285:A:H2'	30:0:286:U:O4'	2.13	0.49
30:0:316:A:H1'	30:0:336:G:N3	2.27	0.49
30:0:549:A:C6	30:0:550:C:C4	3.00	0.49
30:0:862:U:H2'	30:0:863:G:H8	1.77	0.49
30:0:889:C:H4'	38:0:6368:HOH:O	2.13	0.49
29:3:12:PRO:HB3	30:0:2382:A:O2'	2.12	0.49
2:B:307:ARG:HD2	38:B:9123:HOH:O	2.12	0.49
6:F:110:ASP:O	6:F:114:LYS:N	2.44	0.49
21:U:9:CYS:HB2	38:U:6796:HOH:O	2.11	0.49
30:0:1183:C:N4	30:0:1184:C:N4	2.60	0.49
30:0:1583:U:O2'	30:0:1584:C:H5'	2.13	0.49
30:0:1706:G:C5	30:0:1707:G:C6	3.00	0.49
30:0:1760:G:H5'	30:0:1818:C:O2'	2.12	0.49
30:0:1921:A:C6	30:0:1922:A:C2	3.00	0.49
30:0:2326:C:H4'	30:0:2412:G:H4'	1.94	0.49
30:0:2826:G:H1'	30:0:2914:A:N6	2.28	0.49
30:0:447:A:O2'	30:0:448:G:H5'	2.13	0.49
31:9:110:G:N2	31:9:111:U:H1'	2.28	0.49
1:A:109:GLU:HG2	1:A:116:GLY:N	2.25	0.49
2:B:162:MET:CE	2:B:308:LEU:HD21	2.42	0.49
2:B:98:THR:HG22	2:B:99:GLU:N	2.28	0.49
3:C:233:THR:HG22	3:C:234:VAL:N	2.26	0.49
8:H:29:SER:HA	8:H:62:HIS:HD2	1.77	0.49
26:Z:47:ARG:HH22	30:0:1771:U:H1'	1.77	0.49
30:0:1116:U:C2	30:0:1246:A:N6	2.81	0.49
30:0:1343:C:H2'	30:0:1344:G:O5'	2.12	0.49
30:0:1453:G:C2	30:0:1675:C:C2	3.00	0.49
30:0:2103:A:N3	30:0:2103:A:H2'	2.28	0.49
30:0:2269:C:H2'	30:0:2270:G:O4'	2.12	0.49
30:0:717:C:H2'	30:0:718:C:H6	1.78	0.49
30:0:731:U:O2'	30:0:732:C:H5'	2.13	0.49
29:3:1:MET:HG2	29:3:87:ARG:O	2.11	0.49
31:9:105:A:H2'	31:9:106:U:O4'	2.12	0.49
1:A:36:ASP:HB2	1:A:85:SER:H	1.77	0.49
14:N:25:ARG:HB3	30:0:2415:A:C2	2.47	0.49
25:Y:235:GLU:CD	25:Y:235:GLU:H	2.16	0.49
30:0:1119:G:H22	30:0:1246:A:H2	1.46	0.49
30:0:1351:G:H1'	38:0:4648:HOH:O	2.13	0.49
30:0:1607:A:C4	30:0:1608:G:C8	3.01	0.49
30:0:1615:A:H5'	38:0:4169:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2497:A:C2	30:0:2524:G:C2	3.01	0.49
30:0:2536:C:H6	38:0:4998:HOH:O	1.95	0.49
30:0:271:C:N4	30:0:378:A:H2	2.01	0.49
27:1:21:ARG:HD2	27:1:39:PHE:HB2	1.95	0.49
31:9:60:C:O2'	31:9:61:C:H5'	2.13	0.49
31:9:8:G:C6	31:9:9:C:C4	3.00	0.49
14:N:178:THR:O	14:N:181:ASP:HB3	2.13	0.49
20:T:69:LYS:O	20:T:71:VAL:HG23	2.13	0.49
30:0:1063:G:H4'	30:0:2307:A:H1'	1.95	0.48
30:0:1240:G:H1'	38:0:9360:HOH:O	2.12	0.48
30:0:1586:G:C2'	30:0:1587:U:H5'	2.43	0.48
30:0:1644:C:C2	30:0:1645:U:C5	3.01	0.48
30:0:191:A:H2'	30:0:237:G:O6	2.12	0.48
30:0:419:A:H1'	30:0:1921:A:C2	2.48	0.48
30:0:2297:U:H2'	30:0:2298:C:H6	1.78	0.48
30:0:2639:G:C5	30:0:2640:U:C5	3.01	0.48
30:0:788:A:H4'	38:0:7005:HOH:O	2.12	0.48
29:3:88:LEU:HB3	29:3:90:PHE:CE1	2.48	0.48
3:C:173:LYS:HE3	30:0:1311:G:O6	2.12	0.48
4:D:92:GLU:HB2	38:D:3862:HOH:O	2.13	0.48
6:F:63:ILE:HB	6:F:64:PRO:CD	2.37	0.48
13:M:52:GLN:OE1	13:M:116:ASN:HB3	2.13	0.48
25:Y:137:LYS:HD2	38:0:7590:HOH:O	2.11	0.48
30:0:1066:U:H2'	30:0:1067:A:C8	2.48	0.48
30:0:106:A:C6	30:0:107:U:C4	3.00	0.48
30:0:1765:G:O2'	30:0:1766:U:H5'	2.12	0.48
30:0:1916:C:O2'	30:0:1917:G:H5'	2.14	0.48
30:0:2646:G:C4	30:0:2647:C:C5	3.02	0.48
30:0:2713:G:O2'	30:0:2714:U:H5'	2.12	0.48
30:0:2864:U:O2'	30:0:2865:G:H5'	2.14	0.48
31:9:19:G:C2	31:9:20:G:C8	3.00	0.48
31:9:2:U:H4'	38:9:9107:HOH:O	2.13	0.48
4:D:22:VAL:HG22	4:D:74:THR:HG22	1.95	0.48
5:E:11:VAL:HG12	5:E:12:ASP:N	2.28	0.48
11:K:98:VAL:HG11	11:K:102:GLU:HA	1.94	0.48
13:M:134:ILE:CG2	13:M:141:ILE:HD13	2.36	0.48
20:T:28:SER:O	20:T:32:ARG:HG3	2.14	0.48
21:U:19:THR:HG22	21:U:20:MET:N	2.28	0.48
30:0:1832:G:C2	30:0:1833:U:C6	3.00	0.48
30:0:1883:U:H2'	30:0:1884:G:H5'	1.94	0.48
30:0:2480:G:O2'	30:0:2481:G:H5'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2526:C:H3'	30:0:2526:C:C6	2.47	0.48
30:0:2827:A:C2	30:0:2914:A:C2	3.01	0.48
30:0:2898:G:H1'	38:0:7555:HOH:O	2.13	0.48
30:0:334:G:C5	30:0:335:U:C5	3.00	0.48
30:0:595:U:O4'	33:0:8817:CL:CL	2.69	0.48
30:0:681:G:N3	30:0:681:G:H5'	2.28	0.48
31:9:3:A:H2	31:9:21:G:N3	2.12	0.48
8:H:52:LEU:HD13	8:H:153:PHE:HB3	1.95	0.48
16:P:124:ASP:O	30:0:801:U:H4'	2.13	0.48
30:0:1015:C:H2'	30:0:1016:U:C6	2.48	0.48
30:0:120:A:H2'	30:0:120:A:N3	2.29	0.48
30:0:1557:G:H2'	30:0:1558:C:H6	1.78	0.48
30:0:1632:A:C3'	30:0:1633:C:H5'	2.43	0.48
26:Z:42:TYR:H	30:0:1829:A:H61	1.61	0.48
30:0:2700:G:H2'	30:0:2701:G:C5'	2.43	0.48
8:H:35:LYS:HE3	30:0:968:G:H1'	1.95	0.48
2:B:152:PRO:HD2	38:B:9102:HOH:O	2.12	0.48
13:M:84:LYS:HA	29:3:46:ILE:O	2.12	0.48
16:P:31:ILE:HG12	16:P:43:LEU:HD13	1.96	0.48
30:0:100:C:C4	30:0:101:C:C5	3.01	0.48
30:0:1434:A:O2'	30:0:1435:U:H6	1.92	0.48
30:0:1496:A:H5'	30:0:1572:A:H1'	1.94	0.48
30:0:1634:G:H2'	30:0:1635:U:H6	1.76	0.48
30:0:222:A:H2'	30:0:223:G:O4'	2.13	0.48
30:0:2255:A:C2	30:0:2256:G:C4	3.02	0.48
30:0:2505:G:C2'	30:0:2506:A:C5'	2.91	0.48
30:0:2672:C:H2'	30:0:2673:U:O4'	2.14	0.48
11:K:43:ARG:NH1	30:0:2712:G:OP1	2.46	0.48
30:0:2755:G:H1'	38:0:4651:HOH:O	2.13	0.48
30:0:2772:G:O2'	30:0:2773:G:H5'	2.13	0.48
30:0:2854:A:H2'	30:0:2855:G:H8	1.78	0.48
30:0:2860:G:H2'	30:0:2861:G:C8	2.48	0.48
30:0:677:C:H2'	30:0:678:G:H8	1.77	0.48
30:0:707:C:C2	30:0:708:A:C8	3.02	0.48
29:3:64:LYS:HE2	38:0:7638:HOH:O	2.12	0.48
4:D:37:ALA:O	4:D:40:ILE:HG12	2.13	0.48
12:L:117:GLU:HG3	12:L:117:GLU:O	2.13	0.48
14:N:78:MET:HB2	14:N:79:PRO:HD3	1.95	0.48
18:R:132:ARG:HG2	18:R:133:ALA:N	2.27	0.48
19:S:6:LYS:HB2	19:S:27:ALA:O	2.13	0.48
20:T:27:LEU:HB2	20:T:32:ARG:HG2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1182:C:C1'	30:0:1192:A:H8	2.26	0.48
30:0:1207:A:OP2	30:0:1208:C:H5	1.96	0.48
30:0:1970:G:H1'	38:0:3662:HOH:O	2.13	0.48
30:0:1970:G:H4'	30:0:1971:G:C5'	2.43	0.48
30:0:200:C:H6	38:0:3433:HOH:O	1.96	0.48
30:0:2133:U:H4'	30:0:2134:G:C5'	2.44	0.48
30:0:2598:U:O2	30:0:2600:A:C8	2.66	0.48
30:0:2617:G:H4'	38:0:4487:HOH:O	2.13	0.48
5:E:139:GLU:OE2	30:0:2781:U:H1'	2.13	0.48
30:0:611:U:H2'	30:0:612:U:C6	2.48	0.48
29:3:43:ASN:HB2	29:3:52:PHE:CD1	2.48	0.48
2:B:36:PRO:HG3	2:B:169:GLY:H	1.77	0.48
4:D:51:ARG:HH11	4:D:68:PRO:HB3	1.78	0.48
10:J:60:ARG:HD3	10:J:71:TYR:CE1	2.47	0.48
15:O:88:LYS:HB3	38:O:7061:HOH:O	2.13	0.48
30:0:1224:G:H2'	30:0:1225:C:C6	2.48	0.48
30:0:1520:G:H2'	30:0:1521:C:C6	2.49	0.48
30:0:1878:G:C2	30:0:1879:U:C2	3.02	0.48
30:0:1908:G:N1	30:0:1930:A:OP2	2.46	0.48
30:0:627:G:H2'	30:0:2071:C:C4	2.49	0.48
30:0:2569:A:O5'	30:0:2569:A:H8	1.96	0.48
30:0:2707:C:C2'	30:0:2707:C:O2	2.59	0.48
30:0:31:C:H2'	38:0:7668:HOH:O	2.13	0.48
30:0:705:C:C2'	30:0:705:C:O2	2.62	0.48
27:1:25:LYS:CD	28:2:49:GLU:H	2.25	0.48
5:E:80:TRP:O	5:E:134:SER:HA	2.12	0.48
6:F:107:ASP:O	6:F:111:ILE:HG13	2.13	0.48
13:M:139:PRO:HA	13:M:142:GLN:HB2	1.95	0.48
16:P:94:TRP:CZ2	16:P:98:ILE:HG13	2.49	0.48
17:Q:28:ARG:HG2	38:9:9083:HOH:O	2.12	0.48
18:R:138:SER:HB2	38:0:5570:HOH:O	2.14	0.48
23:W:26:ILE:HB	38:W:5420:HOH:O	2.14	0.48
30:0:1023:C:O2'	30:0:1024:G:H5'	2.14	0.48
30:0:1063:G:H8	38:0:9856:HOH:O	1.96	0.48
28:2:10:ARG:NH2	30:0:121:U:OP2	2.44	0.48
30:0:1029:U:O2'	30:0:1273:C:OP1	2.27	0.48
30:0:2354:A:C2	30:0:2367:A:C8	3.02	0.48
30:0:2717:C:H2'	30:0:2718:C:H5'	1.93	0.48
30:0:808:A:C5	30:0:809:G:H1'	2.48	0.48
30:0:858:U:H2'	30:0:859:C:C6	2.47	0.48
30:0:99:A:C8	30:0:100:C:C6	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1:1:THR:HB	38:1:2852:HOH:O	2.12	0.48
29:3:25:VAL:HA	38:3:9036:HOH:O	2.12	0.48
29:3:40:ARG:C	29:3:42:ARG:H	2.16	0.48
9:I:133:THR:HG22	9:I:134:ILE:N	2.28	0.48
16:P:11:ALA:HB1	16:P:16:VAL:O	2.14	0.48
23:W:117:ARG:HH22	30:0:1264:U:P	2.36	0.48
1:A:162:GLY:N	26:Z:91:GLY:HA2	2.29	0.48
30:0:1177:A:N3	30:0:1177:A:H2'	2.28	0.48
30:0:1204:C:H2'	30:0:1205:U:O4'	2.14	0.48
30:0:2254:G:C2	30:0:2255:A:C8	3.01	0.48
30:0:2281:C:H5	38:0:3756:HOH:O	1.97	0.48
30:0:2505:G:H2'	30:0:2506:A:C5'	2.43	0.48
30:0:2587:OMU:H5	38:0:7464:HOH:O	2.13	0.48
30:0:2777:G:O2'	30:0:2778:A:H5'	2.13	0.48
30:0:432:G:H5''	38:0:6860:HOH:O	2.12	0.48
30:0:69:A:C2'	30:0:70:A:OP2	2.62	0.48
30:0:763:C:O2'	30:0:764:C:H5'	2.14	0.48
30:0:842:C:H4'	38:0:3427:HOH:O	2.13	0.48
30:0:920:C:C4'	30:0:921:G:C2	2.95	0.48
31:9:39:U:C2'	31:9:40:C:OP1	2.62	0.48
1:A:71:PRO:HG2	1:A:91:GLY:HA2	1.95	0.48
4:D:51:ARG:NH1	4:D:68:PRO:HB3	2.28	0.48
8:H:157:TYR:C	8:H:157:TYR:HD1	2.18	0.48
30:0:1186:C:C4	30:0:1187:U:C4	3.02	0.48
30:0:1626:A:H2'	30:0:1627:G:O4'	2.14	0.48
30:0:202:U:C4	30:0:203:G:C6	3.01	0.48
11:K:1:MET:N	30:0:2686:C:O2'	2.38	0.48
13:M:9:ARG:HD2	30:0:380:A:OP2	2.14	0.48
29:3:51:LYS:HG3	29:3:52:PHE:HD2	1.76	0.48
29:3:83:TRP:HB2	38:0:5759:HOH:O	2.14	0.48
14:N:4:PRO:HG3	31:9:69:U:OP1	2.13	0.48
1:A:161:GLY:HA3	38:Z:8705:HOH:O	2.13	0.48
1:A:217:ARG:HG2	1:A:229:ALA:HB2	1.95	0.48
2:B:226:LYS:HG2	2:B:230:GLN:HE21	1.78	0.48
6:F:58:GLU:HA	6:F:61:MET:SD	2.54	0.48
9:I:69:PRO:HA	30:0:1164:U:OP1	2.14	0.47
30:0:1188:A:C5	30:0:1189:A:C2	3.02	0.47
30:0:1337:G:C6	30:0:1338:U:C4	3.01	0.47
30:0:1337:G:C5	30:0:1338:U:C5	3.02	0.47
30:0:1471:A:H2'	30:0:1472:C:C6	2.48	0.47
30:0:151:A:H2'	30:0:152:A:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:50:GLY:CA	30:0:170:U:H1'	2.43	0.47
30:0:1745:G:H5'	38:0:4312:HOH:O	2.14	0.47
30:0:2458:U:H3'	38:0:3241:HOH:O	2.13	0.47
30:0:2474:A:H5'	30:0:2476:C:O5'	2.14	0.47
30:0:2474:A:N7	30:0:2621:PSU:H4'	2.29	0.47
30:0:2598:U:O2	30:0:2600:A:H8	1.96	0.47
30:0:2830:U:H2'	30:0:2831:C:H6	1.79	0.47
30:0:2848:G:O4'	30:0:2906:A:C2	2.66	0.47
30:0:625:U:H5''	30:0:1044:C:H42	1.71	0.47
30:0:870:G:H2'	30:0:871:G:C5'	2.34	0.47
3:C:162:VAL:HG13	3:C:162:VAL:O	2.13	0.47
18:R:15:LYS:HE3	38:R:8976:HOH:O	2.14	0.47
30:0:2385:G:H2'	30:0:2386:U:C6	2.49	0.47
21:U:50:GLU:OE1	30:0:2866:U:H2'	2.13	0.47
30:0:2855:G:C2	30:0:2904:U:N3	2.82	0.47
30:0:373:G:O2'	30:0:374:U:H5'	2.14	0.47
30:0:968:G:O2'	30:0:969:G:H5'	2.14	0.47
1:A:27:LEU:HD21	1:A:55:VAL:CG2	2.44	0.47
2:B:84:LEU:O	2:B:99:GLU:HA	2.14	0.47
30:0:1947:G:OP1	30:0:1971:G:N7	2.47	0.47
30:0:2087:C:H2'	30:0:2088:C:H6	1.80	0.47
30:0:361:C:H2'	30:0:362:G:O4'	2.13	0.47
30:0:834:G:H3'	30:0:835:U:H4'	1.97	0.47
11:K:132:VAL:HG11	21:U:22:VAL:HG22	1.96	0.47
25:Y:234:VAL:HG12	25:Y:235:GLU:N	2.28	0.47
26:Z:40:ALA:HA	30:0:1773:G:H8	1.79	0.47
30:0:1275:C:H2'	30:0:1276:U:H5'	1.96	0.47
30:0:1389:G:N2	30:0:1391:G:H3'	2.29	0.47
30:0:1619:G:H2'	30:0:1620:C:C6	2.49	0.47
30:0:2379:G:H4'	30:0:2380:A:O5'	2.13	0.47
30:0:2719:A:H2'	30:0:2720:C:C5'	2.44	0.47
30:0:2724:U:H6	30:0:2724:U:O5'	1.96	0.47
30:0:2857:C:H1'	38:0:5328:HOH:O	2.15	0.47
30:0:407:A:H5'	38:0:6000:HOH:O	2.14	0.47
30:0:681:G:N3	30:0:681:G:H2'	2.30	0.47
30:0:699:C:C2	30:0:744:G:C2	3.03	0.47
30:0:965:A:H5'	30:0:966:U:OP2	2.14	0.47
1:A:70:ALA:HB1	26:Z:89:THR:HG21	1.97	0.47
2:B:162:MET:HE1	2:B:308:LEU:HD21	1.96	0.47
2:B:74:ILE:HD13	2:B:309:VAL:HG21	1.95	0.47
2:B:201:ASP:CB	2:B:312:ARG:HD2	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:88:MET:HA	8:H:139:ALA:HA	1.96	0.47
21:U:56:ARG:HB2	30:0:2890:A:N7	2.29	0.47
22:V:12:THR:CG2	22:V:15:GLU:HG3	2.40	0.47
24:X:85:VAL:HG12	24:X:86:GLU:N	2.29	0.47
30:0:1210:G:N2	30:0:1211:G:H1'	2.29	0.47
30:0:1226:G:C4	30:0:1227:C:C6	3.02	0.47
30:0:1503:U:H2'	30:0:1504:A:C5'	2.45	0.47
30:0:1733:A:N7	30:0:1734:C:C4	2.82	0.47
30:0:1477:C:H4'	30:0:1868:G:OP1	2.15	0.47
30:0:2265:U:H2'	30:0:2266:A:H8	1.80	0.47
30:0:2781:U:C2'	30:0:2782:G:H5'	2.45	0.47
30:0:287:C:H6	30:0:287:C:O5'	1.97	0.47
30:0:371:U:C4	30:0:372:A:N7	2.83	0.47
30:0:558:C:HO2'	30:0:559:U:H5''	1.78	0.47
30:0:699:C:C6	30:0:744:G:N3	2.82	0.47
30:0:820:G:O2'	30:0:856:G:H4'	2.14	0.47
28:2:15:ASP:O	28:2:18:ASN:HB2	2.15	0.47
29:3:68:LYS:HG2	29:3:77:ALA:CB	2.44	0.47
29:3:88:LEU:CD2	33:3:8804:CL:CL	2.86	0.47
31:9:73:A:H61	31:9:108:C:N4	2.13	0.47
31:9:39:U:H3	31:9:42:C:H5''	1.79	0.47
8:H:59:GLN:HE22	8:H:96:GLN:HG2	1.79	0.47
11:K:118:ALA:HA	11:K:125:ALA:HB2	1.96	0.47
17:Q:11:ARG:HD3	38:0:6238:HOH:O	2.13	0.47
30:0:625:U:C5'	30:0:1044:C:N4	2.71	0.47
13:M:68:ARG:HD2	30:0:1469:C:OP2	2.15	0.47
30:0:1667:A:H5'	30:0:1667:A:C8	2.50	0.47
30:0:1760:G:C5	30:0:1761:U:C4	3.03	0.47
2:B:234:ARG:NH2	30:0:2039:A:OP2	2.47	0.47
30:0:2375:A:H2'	30:0:2376:C:C6	2.50	0.47
30:0:2597:U:C2'	30:0:2598:U:H5'	2.45	0.47
30:0:724:G:O2'	30:0:725:C:H5'	2.15	0.47
30:0:731:U:H2'	30:0:732:C:C6	2.50	0.47
26:Z:34:SER:CA	30:0:797:A:H4'	2.44	0.47
29:3:9:THR:HG23	29:3:20:HIS:CE1	2.49	0.47
31:9:5:G:C2'	31:9:6:C:H5'	2.45	0.47
1:A:135:VAL:HA	1:A:150:PRO:HD3	1.96	0.47
7:G:64:ASN:ND2	7:G:64:ASN:N	2.62	0.47
11:K:97:ILE:HG22	11:K:98:VAL:H	1.79	0.47
20:T:71:VAL:CG1	20:T:90:PRO:HB3	2.40	0.47
30:0:1181:A:N1	30:0:1192:A:O2'	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1210:G:O2'	30:0:1211:G:H5'	2.14	0.47
30:0:2509:A:H2'	30:0:2510:C:O4'	2.14	0.47
8:H:6:ALA:HB3	30:0:2521:A:OP2	2.14	0.47
30:0:2781:U:H2'	30:0:2782:G:H5'	1.95	0.47
30:0:2860:G:H2'	30:0:2861:G:H8	1.80	0.47
30:0:432:G:H2'	30:0:433:C:H6	1.80	0.47
1:A:94:LEU:HG	1:A:99:ILE:CD1	2.44	0.47
8:H:123:ILE:HD12	8:H:123:ILE:N	2.30	0.47
10:J:39:VAL:CG2	10:J:107:ASN:HA	2.44	0.47
15:O:42:GLU:HB2	38:0:3736:HOH:O	2.15	0.47
20:T:41:ARG:NH1	20:T:42:VAL:O	2.47	0.47
20:T:51:LEU:HD11	20:T:97:ARG:HB2	1.97	0.47
23:W:21:LEU:HD21	23:W:48:VAL:HG11	1.96	0.47
25:Y:151:SER:HB3	25:Y:154:ARG:HB3	1.97	0.47
30:0:1333:U:H2'	30:0:1334:C:H6	1.80	0.47
30:0:790:A:H1'	30:0:1710:A:H2'	1.97	0.47
30:0:1858:A:H2'	30:0:1859:A:C8	2.50	0.47
30:0:1988:C:H2'	30:0:1989:G:O4'	2.15	0.47
30:0:2727:A:C2'	30:0:2728:C:H5'	2.45	0.47
30:0:2837:U:H2'	38:0:6824:HOH:O	2.15	0.47
30:0:2858:U:H2'	30:0:2859:C:C6	2.49	0.47
30:0:711:G:O2'	30:0:712:C:H5'	2.15	0.47
2:B:171:VAL:O	2:B:175:LEU:HB2	2.15	0.47
3:C:180:SER:HB2	38:C:8643:HOH:O	2.14	0.47
4:D:59:GLY:HA3	38:D:4886:HOH:O	2.14	0.47
13:M:15:PRO:HA	13:M:20:LEU:HD23	1.95	0.47
14:N:71:TRP:HZ2	38:N:8833:HOH:O	1.97	0.47
16:P:13:VAL:HG13	16:P:14:LEU:N	2.29	0.47
23:W:129:LYS:HE3	31:9:87:U:H2'	1.97	0.47
23:W:77:ALA:HB3	38:W:5763:HOH:O	2.14	0.47
30:0:1168:C:H2'	30:0:1169:U:H5'	1.96	0.47
30:0:1446:U:H4'	30:0:1447:U:OP2	2.14	0.47
30:0:1857:A:N6	30:0:2247:C:H1'	2.30	0.47
30:0:2059:U:H1'	38:0:4439:HOH:O	2.14	0.47
30:0:2460:A:C2	30:0:2461:U:C2	3.02	0.47
30:0:800:G:H8	30:0:800:G:O5'	1.98	0.47
30:0:835:U:H5''	38:0:9381:HOH:O	2.14	0.47
31:9:22:G:N7	31:9:55:U:C6	2.82	0.47
1:A:105:VAL:CG1	1:A:154:ALA:HB1	2.44	0.47
3:C:28:SER:HB2	38:C:8659:HOH:O	2.14	0.47
14:N:27:LEU:HD22	14:N:50:LEU:HD13	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:3:LEU:HA	16:P:6:GLN:OE1	2.14	0.47
22:V:64:GLY:O	22:V:65:ASP:HB2	2.15	0.47
23:W:128:VAL:HG22	30:0:1098:A:OP1	2.15	0.47
30:0:1889:C:O2'	30:0:1890:U:H5'	2.15	0.47
30:0:2490:A:H5''	38:0:7023:HOH:O	2.15	0.47
30:0:2858:U:H2'	30:0:2859:C:H6	1.80	0.47
30:0:2878:U:H2'	30:0:2879:A:O4'	2.14	0.47
30:0:292:G:H2'	30:0:358:G:N2	2.30	0.47
30:0:561:G:H2'	30:0:562:A:H8	1.79	0.47
1:A:171:LYS:HB2	30:0:820:G:C5	2.50	0.47
2:B:212:GLN:HB2	2:B:257:THR:OG1	2.15	0.47
6:F:21:GLU:O	6:F:24:ARG:HG2	2.15	0.47
16:P:1:THR:O	30:0:1396:C:H1'	2.15	0.47
18:R:69:LYS:HB2	18:R:72:VAL:HG23	1.97	0.47
22:V:1:THR:HG23	22:V:2:VAL:N	2.29	0.47
23:W:72:PRO:HG2	38:W:5763:HOH:O	2.15	0.47
30:0:1056:U:H2'	30:0:1057:A:O4'	2.14	0.47
23:W:125:HIS:CE1	30:0:1097:A:C5'	2.95	0.47
16:P:41:ARG:NH2	30:0:1500:U:OP2	2.47	0.47
30:0:1806:G:C4	30:0:1807:U:C6	3.03	0.47
30:0:1928:C:O2'	30:0:1929:G:H5'	2.15	0.47
30:0:2301:A:H5''	30:0:2302:A:H5'	1.96	0.47
30:0:249:G:O2'	30:0:250:C:H5'	2.15	0.47
13:M:193:LYS:HB3	30:0:392:U:C5'	2.45	0.47
14:N:170:GLU:O	14:N:174:GLU:HG3	2.14	0.47
17:Q:34:ASP:O	17:Q:37:GLU:HB2	2.15	0.47
30:0:1177:A:N1	30:0:1178:G:C4	2.82	0.46
30:0:1159:G:H1	30:0:1208:C:H42	1.63	0.46
30:0:137:U:OP1	30:0:259:G:O2'	2.33	0.46
24:X:30:MET:HG2	30:0:1384:C:H5'	1.96	0.46
30:0:1760:G:C6	30:0:1761:U:C4	3.03	0.46
30:0:1854:C:H2'	30:0:1875:A:H61	1.80	0.46
30:0:1942:A:O2'	30:0:1943:C:H5'	2.15	0.46
30:0:2019:A:H2'	30:0:2020:C:C6	2.49	0.46
4:D:22:VAL:HG21	30:0:2348:C:C5'	2.45	0.46
30:0:2379:G:H4'	30:0:2380:A:C5'	2.45	0.46
30:0:2388:C:O2'	30:0:2389:U:H5'	2.14	0.46
30:0:40:C:H5'	38:0:3836:HOH:O	2.14	0.46
30:0:589:U:H2'	30:0:590:A:C8	2.50	0.46
30:0:737:A:H2'	30:0:738:G:C8	2.49	0.46
30:0:806:A:H2'	30:0:807:A:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:54:A:C2'	31:9:55:U:C5'	2.85	0.46
13:M:184:ARG:HG3	13:M:185:PRO:HA	1.97	0.46
16:P:13:VAL:HG13	16:P:14:LEU:H	1.80	0.46
19:S:6:LYS:HE3	19:S:29:ASP:HA	1.97	0.46
30:0:11:A:N3	30:0:11:A:H2'	2.30	0.46
30:0:1409:G:C2	30:0:1410:G:C8	3.03	0.46
30:0:154:C:O2'	30:0:155:C:H5'	2.14	0.46
30:0:1925:G:O2'	30:0:1926:G:H5'	2.15	0.46
29:3:79:LEU:HD12	30:0:2456:A:C2	2.50	0.46
30:0:2461:U:O2	30:0:2466:G:H1'	2.14	0.46
30:0:703:G:C6	30:0:704:C:N4	2.83	0.46
30:0:61:G:C6	30:0:86:A:N6	2.83	0.46
27:1:10:LYS:HG3	38:1:2979:HOH:O	2.14	0.46
2:B:162:MET:CE	2:B:310:ARG:HD3	2.45	0.46
10:J:42:GLU:HG2	10:J:43:ARG:N	2.30	0.46
21:U:47:ARG:HG3	38:U:4381:HOH:O	2.15	0.46
26:Z:70:ARG:NH1	26:Z:83:TYR:HD1	2.11	0.46
30:0:1016:U:H1'	38:0:3652:HOH:O	2.15	0.46
38:W:7804:HOH:O	30:0:1286:A:H5''	2.15	0.46
30:0:1398:G:H4'	38:0:6650:HOH:O	2.15	0.46
30:0:1415:G:O2'	30:0:1416:G:H5'	2.15	0.46
30:0:168:C:H6	30:0:168:C:O5'	1.98	0.46
30:0:1790:C:H2'	30:0:1791:U:H6	1.80	0.46
30:0:1825:U:O2'	30:0:1826:C:H5'	2.15	0.46
30:0:214:U:H5'	38:0:6117:HOH:O	2.15	0.46
30:0:2259:C:C2	30:0:2260:A:C8	3.04	0.46
30:0:2658:G:C2	30:0:2659:U:C6	3.03	0.46
30:0:2871:G:C6	30:0:2887:G:N1	2.83	0.46
30:0:400:C:H2'	30:0:401:C:H6	1.80	0.46
30:0:432:G:C2	30:0:433:C:C5	3.02	0.46
30:0:604:G:H4'	30:0:605:C:O5'	2.15	0.46
12:L:38:HIS:O	30:0:926:A:H1'	2.15	0.46
29:3:67:LEU:HD13	29:3:69:TYR:HE1	1.81	0.46
1:A:88:ILE:HD13	1:A:100:PRO:HD3	1.97	0.46
2:B:5:ARG:HD2	2:B:8:LYS:NZ	2.31	0.46
13:M:92:THR:HB	30:0:401:C:O2'	2.15	0.46
30:0:100:C:H2'	30:0:101:C:H6	1.81	0.46
30:0:10:U:C4	30:0:532:A:N7	2.84	0.46
30:0:128:A:O2'	30:0:129:A:C5'	2.64	0.46
30:0:1484:G:H2'	38:0:9110:HOH:O	2.16	0.46
30:0:1603:A:C5'	30:0:1605:G:C5'	2.91	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1806:G:H2'	30:0:1807:U:H6	1.78	0.46
30:0:247:A:C2	30:0:265:U:C2	3.03	0.46
30:0:2520:G:O2'	30:0:2521:A:H5'	2.16	0.46
30:0:440:C:C4	30:0:441:A:C6	3.04	0.46
30:0:732:C:O2'	30:0:733:U:H5'	2.14	0.46
30:0:959:C:H1'	30:0:961:A:C6	2.50	0.46
27:1:42:SER:HB3	30:0:1473:U:C1'	2.45	0.46
29:3:64:LYS:HD3	29:3:82:GLY:O	2.14	0.46
4:D:138:GLY:HA2	31:9:29:C:O3'	2.15	0.46
31:9:3:A:H2'	38:9:9044:HOH:O	2.14	0.46
1:A:36:ASP:CB	1:A:85:SER:HB2	2.45	0.46
3:C:72:LYS:HG2	3:C:77:ALA:HA	1.96	0.46
10:J:90:LYS:HB2	33:J:8802:CL:CL	2.53	0.46
23:W:81:ASP:OD1	23:W:92:ASP:HB2	2.16	0.46
30:0:1477:C:C5'	30:0:1868:G:C5'	2.94	0.46
30:0:1590:A:C2	30:0:1606:A:C1'	2.99	0.46
30:0:1626:A:H2'	30:0:1627:G:C5'	2.45	0.46
30:0:2004:U:H4'	38:0:5274:HOH:O	2.14	0.46
30:0:2355:G:N3	30:0:2355:G:H2'	2.31	0.46
30:0:2356:A:H2'	30:0:2357:G:O4'	2.16	0.46
30:0:2911:C:O2'	30:0:2912:C:H5'	2.15	0.46
30:0:364:U:H2'	30:0:365:G:O4'	2.15	0.46
30:0:780:A:H2'	30:0:781:C:C6	2.50	0.46
30:0:815:U:H5	38:0:7423:HOH:O	1.98	0.46
1:A:212:PRO:HB2	38:0:4344:HOH:O	2.16	0.46
2:B:199:TYR:CE2	2:B:268:ARG:HB2	2.49	0.46
30:0:1215:A:O3'	30:0:1216:G:H4'	2.16	0.46
30:0:1524:U:H5''	30:0:1524:U:H6	1.81	0.46
30:0:2626:C:H2'	30:0:2627:G:C8	2.51	0.46
30:0:307:G:N2	30:0:309:C:C2	2.84	0.46
30:0:396:U:O2'	30:0:397:A:P	2.73	0.46
30:0:39:G:O6	30:0:441:A:C2	2.68	0.46
1:A:94:LEU:HD12	1:A:98:GLU:HB2	1.96	0.46
2:B:304:PRO:HD2	2:B:307:ARG:NE	2.31	0.46
4:D:64:ARG:HB3	4:D:67:ASP:OD2	2.15	0.46
8:H:6:ALA:HA	8:H:61:ARG:NH1	2.30	0.46
9:I:87:PRO:HD3	38:0:7103:HOH:O	2.14	0.46
10:J:130:VAL:HG12	10:J:131:THR:N	2.31	0.46
14:N:147:ILE:HD12	38:9:9091:HOH:O	2.15	0.46
18:R:48:GLU:HA	18:R:51:ILE:HD12	1.98	0.46
23:W:68:THR:HG23	23:W:69:ARG:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1187:U:C2	30:0:1189:A:OP2	2.68	0.46
30:0:1200:A:H3'	38:0:5722:HOH:O	2.15	0.46
30:0:1427:A:O2'	30:0:1428:C:H5'	2.16	0.46
30:0:1773:G:H2'	30:0:1774:G:H5'	1.98	0.46
30:0:1829:A:H2'	30:0:1830:C:C5'	2.41	0.46
30:0:2017:U:O2'	30:0:2018:A:C8	2.53	0.46
30:0:2100:A:C5'	38:0:7373:HOH:O	2.57	0.46
30:0:2314:G:O2'	30:0:2315:C:H5'	2.15	0.46
30:0:2397:G:N2	38:0:6910:HOH:O	2.49	0.46
30:0:2471:G:C5	30:0:2472:C:C5	3.03	0.46
30:0:2828:G:O5'	30:0:2828:G:C8	2.68	0.46
30:0:421:C:H2'	30:0:422:G:C8	2.50	0.46
30:0:497:A:H5''	38:0:3588:HOH:O	2.16	0.46
30:0:662:U:H1'	30:0:748:C:H1'	1.98	0.46
6:F:89:LEU:HD21	30:0:262:A:C6	2.51	0.46
9:I:112:LEU:CD1	30:0:1162:G:H1'	2.45	0.46
14:N:42:HIS:HB3	14:N:62:HIS:HE1	1.80	0.46
15:O:51:TYR:CD2	30:0:721:A:H5''	2.51	0.46
24:X:43:VAL:HG12	24:X:47:ALA:HB3	1.98	0.46
30:0:1187:U:O2'	30:0:1188:A:C8	2.69	0.46
30:0:1209:C:C2	30:0:1210:G:C8	3.03	0.46
30:0:1497:G:H4'	30:0:1627:G:O2'	2.16	0.46
30:0:2401:A:H2'	30:0:2402:A:C8	2.51	0.46
30:0:2326:C:H4'	30:0:2412:G:C4'	2.46	0.46
30:0:2612:A:H4'	38:0:3676:HOH:O	2.15	0.46
30:0:277:U:O2'	30:0:278:A:H5'	2.16	0.46
30:0:282:C:HO2'	30:0:368:C:N4	2.13	0.46
30:0:2912:C:C6	30:0:2912:C:O5'	2.66	0.46
30:0:334:G:H2'	30:0:335:U:H6	1.81	0.46
30:0:567:U:C5'	38:0:5254:HOH:O	2.62	0.46
30:0:920:C:H5''	30:0:921:G:O5'	2.16	0.46
30:0:969:G:N1	30:0:999:C:N4	2.53	0.46
9:I:124:VAL:C	9:I:126:THR:H	2.18	0.46
18:R:135:ALA:HB1	18:R:137:ASN:ND2	2.29	0.46
30:0:1058:A:H2'	30:0:1060:C:H5''	1.97	0.46
30:0:1157:C:H2'	30:0:1158:G:H8	1.80	0.46
19:S:12:GLU:OE1	30:0:1444:G:H4'	2.15	0.46
30:0:1790:C:H2'	30:0:1791:U:C6	2.51	0.46
30:0:1812:G:H4'	30:0:1814:G:O4'	2.15	0.46
30:0:2038:A:C2	30:0:2039:A:C5	3.04	0.46
30:0:2241:C:H2'	30:0:2242:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2456:A:H1'	38:0:6579:HOH:O	2.16	0.46
30:0:488:U:C2'	38:0:3993:HOH:O	2.64	0.46
30:0:562:A:H2'	30:0:563:C:O4'	2.15	0.46
30:0:735:C:C5	30:0:736:A:C4	3.03	0.46
26:Z:34:SER:CB	30:0:797:A:H4'	2.46	0.46
30:0:897:A:H2'	30:0:899:C:C5	2.50	0.46
31:9:15:C:N4	31:9:16:G:C6	2.84	0.46
31:9:47:A:C2	31:9:48:C:C2	3.03	0.46
10:J:131:THR:HG22	10:J:134:GLU:HG3	1.97	0.46
14:N:34:LEU:HD22	14:N:129:ILE:HD13	1.98	0.46
15:O:38:ARG:HD3	30:0:654:A:OP2	2.16	0.46
20:T:48:VAL:HG23	20:T:98:VAL:HA	1.97	0.46
23:W:29:VAL:O	23:W:30:ASN:HB2	2.16	0.46
30:0:1119:G:N2	30:0:1246:A:H2	2.04	0.46
30:0:1236:A:C2'	30:0:1237:U:H5'	2.46	0.46
30:0:1504:A:C5'	38:0:4396:HOH:O	2.63	0.46
30:0:1512:G:H4'	38:0:4618:HOH:O	2.15	0.46
30:0:1707:G:H1'	30:0:1711:A:N6	2.31	0.46
30:0:1809:G:H2'	30:0:1811:A:OP2	2.16	0.46
30:0:1902:G:H2'	30:0:1903:U:O4'	2.16	0.46
30:0:2011:A:H5'	30:0:2013:G:C1'	2.46	0.46
30:0:212:A:H5'	30:0:214:U:H1'	1.98	0.46
30:0:2694:A:H3'	30:0:2695:C:H6	1.81	0.46
30:0:2831:C:C2	30:0:2910:A:N1	2.84	0.46
30:0:2860:G:H1'	38:0:6785:HOH:O	2.15	0.46
30:0:938:G:C4	30:0:1031:G:N2	2.84	0.46
29:3:20:HIS:CE1	29:3:71:CYS:SG	3.09	0.46
13:M:164:THR:HG22	13:M:165:GLY:N	2.30	0.46
13:M:94:ARG:NH2	30:0:175:G:O6	2.49	0.46
20:T:79:LEU:HG	20:T:89:ARG:HB2	1.98	0.46
24:X:21:PRO:HD3	38:X:6179:HOH:O	2.16	0.46
25:Y:214:ARG:HH12	25:Y:230:ASN:ND2	2.13	0.46
30:0:1217:G:C2	30:0:1218:U:C2	3.04	0.45
30:0:1516:U:H2'	30:0:1517:C:O4'	2.17	0.45
30:0:1490:G:H4'	30:0:1533:A:OP1	2.16	0.45
30:0:1864:C:H2'	30:0:1865:A:O4'	2.16	0.45
30:0:56:G:H1'	38:0:5300:HOH:O	2.16	0.45
3:C:35:VAL:HG21	3:C:227:GLY:HA2	1.98	0.45
4:D:63:ILE:HG13	4:D:64:ARG:N	2.32	0.45
5:E:103:VAL:HG22	5:E:115:ARG:HB3	1.96	0.45
13:M:133:LEU:O	13:M:134:ILE:HD13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:64:GLU:HG3	17:Q:74:ASP:CG	2.36	0.45
30:0:1018:A:H8	30:0:1018:A:O5'	1.99	0.45
30:0:940:G:C5	30:0:1027:G:C2	3.04	0.45
30:0:1074:G:H4'	30:0:1260:G:C6	2.52	0.45
30:0:1362:U:O2'	30:0:1363:G:H5'	2.17	0.45
30:0:1400:C:C2'	30:0:1401:G:H5'	2.46	0.45
30:0:1444:G:C6	30:0:1445:G:C5	3.05	0.45
30:0:1503:U:H2'	30:0:1504:A:H5'	1.98	0.45
30:0:1831:U:H2'	30:0:1832:G:H5'	1.98	0.45
30:0:1908:G:H1'	30:0:1931:A:N6	2.31	0.45
30:0:1987:C:O2'	30:0:1988:C:H5'	2.16	0.45
30:0:2134:G:N2	30:0:2242:U:C2	2.85	0.45
30:0:2577:A:H8	38:0:9606:HOH:O	1.99	0.45
30:0:2812:A:C2	30:0:2814:A:N7	2.85	0.45
30:0:369:G:O2'	30:0:370:G:H5'	2.16	0.45
30:0:743:G:O2'	30:0:744:G:H5'	2.16	0.45
31:9:39:U:N3	31:9:42:C:H5''	2.31	0.45
4:D:76:ARG:HD2	31:9:42:C:O2	2.16	0.45
1:A:186:TRP:CG	1:A:187:PRO:HA	2.50	0.45
1:A:35:GLY:O	1:A:37:VAL:HG22	2.17	0.45
1:A:94:LEU:N	1:A:94:LEU:HD23	2.31	0.45
2:B:320:GLN:HA	2:B:321:PRO:HD3	1.83	0.45
8:H:157:TYR:CD1	8:H:157:TYR:C	2.89	0.45
9:I:83:GLY:H	30:0:1168:C:C5'	2.28	0.45
11:K:132:VAL:HG21	21:U:22:VAL:HG13	1.97	0.45
15:O:32:ARG:HH21	15:O:35:LYS:NZ	2.14	0.45
30:0:99:A:C8	30:0:100:C:C5	3.05	0.45
9:I:113:SER:HA	30:0:1186:C:H5'	1.98	0.45
30:0:1213:C:O2'	30:0:1214:G:H5'	2.17	0.45
30:0:1116:U:N3	30:0:1246:A:N6	2.60	0.45
30:0:154:C:H2'	30:0:155:C:H6	1.82	0.45
30:0:1603:A:H5'	30:0:1605:G:C5'	2.46	0.45
30:0:1670:A:H2'	30:0:1671:U:O4'	2.16	0.45
30:0:1759:A:N3	30:0:1818:C:H2'	2.31	0.45
30:0:1948:G:H2'	30:0:1949:G:O4'	2.16	0.45
30:0:2293:G:C6	30:0:2294:C:C5	3.04	0.45
30:0:2757:A:H2'	30:0:2758:G:O4'	2.16	0.45
30:0:360:A:H2'	30:0:361:C:O4'	2.16	0.45
30:0:400:C:O2'	30:0:401:C:H5'	2.17	0.45
30:0:191:A:N6	30:0:435:A:H62	2.14	0.45
30:0:595:U:H2'	30:0:596:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:793:A:H2'	30:0:794:U:H6	1.81	0.45
29:3:12:PRO:HG2	29:3:13:HIS:CD2	2.49	0.45
31:9:59:C:O5'	31:9:59:C:C6	2.63	0.45
1:A:51:ARG:O	1:A:52:SER:HB2	2.16	0.45
8:H:46:TYR:HA	8:H:47:PRO:HD3	1.81	0.45
20:T:114:SER:OG	20:T:117:ASP:HB2	2.16	0.45
30:0:1178:G:C6	30:0:1179:C:N4	2.84	0.45
30:0:912:A:C4	30:0:1294:A:C2	3.04	0.45
30:0:790:A:H1'	30:0:1710:A:C2'	2.46	0.45
30:0:1819:G:H2'	30:0:1820:G:C4'	2.46	0.45
30:0:1964:U:O2	30:0:1964:U:H2'	2.15	0.45
30:0:1970:G:N3	30:0:1970:G:H2'	2.31	0.45
30:0:2005:G:P	30:0:2005:G:H3'	2.55	0.45
30:0:2438:G:H2'	30:0:2439:C:C6	2.51	0.45
30:0:2092:G:H2'	30:0:2613:G:OP1	2.17	0.45
30:0:304:G:O5'	30:0:304:G:H8	2.00	0.45
30:0:734:U:H2'	30:0:736:A:OP2	2.16	0.45
30:0:876:A:C2'	30:0:876:A:N3	2.79	0.45
31:9:29:C:C5	31:9:30:C:C5	3.04	0.45
2:B:254:GLN:HG2	2:B:255:GLY:N	2.30	0.45
13:M:122:GLN:HB2	13:M:127:LYS:HG2	1.98	0.45
13:M:30:GLU:HG2	38:M:8864:HOH:O	2.17	0.45
14:N:144:GLY:O	14:N:147:ILE:HG23	2.15	0.45
17:Q:15:LYS:HG3	30:0:2364:A:O3'	2.16	0.45
18:R:96:VAL:HG13	18:R:106:GLY:HA3	1.98	0.45
25:Y:144:ARG:CZ	38:Y:8916:HOH:O	2.65	0.45
26:Z:70:ARG:O	26:Z:81:CYS:SG	2.74	0.45
30:0:940:G:N3	30:0:1032:A:C2	2.84	0.45
30:0:1524:U:H5''	30:0:1524:U:C6	2.51	0.45
30:0:1547:A:H2'	30:0:1548:U:C6	2.52	0.45
30:0:1940:C:H1'	38:0:9382:HOH:O	2.17	0.45
30:0:2697:A:H2'	30:0:2697:A:N3	2.32	0.45
30:0:2718:C:C6	30:0:2718:C:H5'	2.50	0.45
30:0:2728:C:O5'	30:0:2728:C:H6	1.99	0.45
30:0:420:U:O4'	30:0:1920:C:C4	2.70	0.45
30:0:659:A:H5''	38:0:7082:HOH:O	2.17	0.45
38:C:8558:HOH:O	30:0:751:U:H5'	2.16	0.45
28:2:40:ARG:HG3	28:2:45:ASN:CB	2.45	0.45
29:3:59:ASP:OD1	30:0:2460:A:H5''	2.16	0.45
2:B:162:MET:HE2	2:B:310:ARG:HD3	1.97	0.45
5:E:152:THR:HG21	5:E:165:GLY:HA2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:72:ASN:O	12:L:76:LEU:HG	2.17	0.45
18:R:18:LEU:HB2	18:R:143:VAL:CG1	2.46	0.45
23:W:5:VAL:HG11	23:W:153:MET:HE1	1.99	0.45
30:0:1151:G:N2	30:0:1214:G:C4	2.85	0.45
9:I:82:THR:HG22	30:0:1168:C:H5''	1.97	0.45
30:0:1149:U:C5	30:0:1215:A:N7	2.84	0.45
30:0:1406:A:H4'	30:0:1407:A:H5''	1.98	0.45
30:0:1434:A:H4'	30:0:1435:U:H5	1.82	0.45
30:0:1523:G:C6	30:0:1524:U:C4	3.05	0.45
30:0:1883:U:H5''	30:0:2013:G:OP2	2.17	0.45
30:0:2475:C:H5'	38:0:3664:HOH:O	2.16	0.45
30:0:418:C:H2'	30:0:419:A:C8	2.52	0.45
30:0:790:A:H8	38:0:6078:HOH:O	1.98	0.45
30:0:960:G:N3	30:0:960:G:C2'	2.79	0.45
31:9:61:C:H2'	31:9:62:A:C8	2.46	0.45
1:A:11:ARG:HD3	38:0:9222:HOH:O	2.16	0.45
1:A:204:GLY:N	30:0:2634:G:OP2	2.49	0.45
6:F:34:ASN:HA	13:M:4:ALA:HB2	1.98	0.45
12:L:57:VAL:O	12:L:57:VAL:HG12	2.17	0.45
13:M:34:GLU:HB3	13:M:38:GLU:HG3	1.99	0.45
14:N:33:ARG:HG3	38:N:8841:HOH:O	2.17	0.45
15:O:27:GLY:O	15:O:31:GLU:HG3	2.17	0.45
1:A:189:VAL:HA	30:0:1845:A:OP1	2.16	0.45
30:0:2385:G:H2'	30:0:2386:U:H6	1.81	0.45
30:0:2515:C:H2'	30:0:2516:G:O4'	2.16	0.45
27:1:16:HIS:HE1	30:0:775:G:OP1	1.99	0.45
30:0:92:G:H2'	30:0:93:C:H6	1.82	0.45
29:3:35:TRP:HZ3	30:0:2432:C:OP1	2.00	0.45
2:B:119:HIS:O	2:B:121:PRO:HD3	2.16	0.45
30:0:1405:U:H4'	30:0:1406:A:H5''	1.98	0.45
30:0:1902:G:O2'	30:0:1903:U:H5'	2.16	0.45
30:0:2361:A:H2'	30:0:2362:A:C8	2.51	0.45
30:0:2887:G:H2'	30:0:2888:U:O4'	2.17	0.45
30:0:342:C:N4	30:0:343:C:H41	2.15	0.45
30:0:343:C:O2'	30:0:344:C:H5'	2.17	0.45
30:0:387:G:C2'	30:0:388:G:H5'	2.46	0.45
30:0:916:A:C6	30:0:917:U:C4	3.05	0.45
31:9:30:C:C2'	31:9:30:C:O2	2.65	0.45
31:9:72:C:O2'	31:9:73:A:H5'	2.15	0.45
2:B:43:GLY:O	2:B:308:LEU:HD12	2.16	0.45
4:D:50:VAL:O	4:D:71:ALA:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:96:ALA:HA	38:F:3111:HOH:O	2.15	0.45
10:J:43:ARG:HD3	38:J:8858:HOH:O	2.17	0.45
30:0:1576:G:C2	30:0:1577:U:C2	3.05	0.45
30:0:1626:A:C2'	30:0:1627:G:H5'	2.46	0.45
30:0:1850:U:H2'	30:0:1851:G:C8	2.52	0.45
30:0:228:C:H2'	30:0:229:G:C5'	2.46	0.45
30:0:281:U:H5	38:0:7575:HOH:O	1.99	0.45
30:0:2842:G:H2'	30:0:2843:A:H5'	1.98	0.45
30:0:862:U:H2'	30:0:863:G:C8	2.52	0.45
30:0:957:A:H8	30:0:957:A:O5'	2.00	0.45
2:B:307:ARG:HG3	2:B:307:ARG:HH11	1.82	0.45
2:B:86:ALA:HA	38:B:9051:HOH:O	2.16	0.45
3:C:95:GLU:HG3	38:C:8669:HOH:O	2.16	0.45
5:E:121:ASP:HB2	38:E:5899:HOH:O	2.16	0.45
5:E:102:VAL:HG11	5:E:148:ILE:HG12	1.98	0.45
21:U:6:CYS:SG	21:U:31:PHE:HA	2.56	0.45
26:Z:35:SER:HB3	26:Z:47:ARG:HB2	1.98	0.45
30:0:1041:U:H2'	30:0:1042:U:C5'	2.46	0.45
30:0:1543:G:N1	30:0:1641:A:OP2	2.36	0.45
30:0:1801:A:C2	30:0:1802:G:C4	3.04	0.45
30:0:1477:C:C5'	30:0:1868:G:H5''	2.47	0.45
30:0:2311:A:O2'	30:0:2312:G:H5'	2.17	0.45
30:0:2511:A:H2'	30:0:2512:U:H6	1.82	0.45
30:0:958:G:H2'	30:0:959:C:H6	1.75	0.45
30:0:969:G:N2	30:0:1000:C:C2	2.85	0.45
31:9:33:U:C6	31:9:43:G:C8	3.05	0.45
3:C:88:SER:O	3:C:91:PRO:HD3	2.17	0.45
13:M:86:GLN:NE2	38:M:8882:HOH:O	2.50	0.45
30:0:1181:A:O2'	30:0:1182:C:H5'	2.17	0.44
30:0:1392:A:C6	30:0:1395:C:C2	3.05	0.44
30:0:1524:U:C5'	30:0:1524:U:H6	2.29	0.44
30:0:1584:C:O2'	30:0:1585:C:H5'	2.17	0.44
30:0:1748:U:C5	30:0:1749:U:C4	3.06	0.44
30:0:2293:G:C6	30:0:2294:C:C4	3.05	0.44
30:0:198:A:C2	30:0:2444:U:H1'	2.53	0.44
30:0:2826:G:O6	30:0:2913:A:N6	2.50	0.44
30:0:283:U:H5''	30:0:284:C:OP2	2.17	0.44
30:0:339:A:C6	30:0:342:C:N3	2.85	0.44
30:0:581:G:H5'	38:0:7663:HOH:O	2.17	0.44
30:0:163:U:O3'	30:0:896:C:H4'	2.16	0.44
31:9:107:C:O2'	31:9:108:C:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:3:A:OP2	31:9:25:G:N2	2.50	0.44
1:A:164:ARG:NH1	1:A:164:ARG:HB3	2.31	0.44
4:D:128:LEU:HD23	4:D:129:ASP:N	2.32	0.44
5:E:153:ARG:NH1	30:0:2778:A:C1'	2.81	0.44
8:H:83:GLU:HA	38:H:243:HOH:O	2.18	0.44
10:J:107:ASN:HD21	10:J:109:TYR:HB2	1.82	0.44
16:P:81:LYS:HE3	30:0:1813:U:O2'	2.18	0.44
18:R:34:GLU:HG2	18:R:46:TYR:OH	2.17	0.44
23:W:48:VAL:HG12	23:W:52:VAL:HB	1.98	0.44
26:Z:47:ARG:O	26:Z:51:ALA:HB2	2.16	0.44
30:0:1246:A:O2'	30:0:1247:A:H3'	2.17	0.44
30:0:1362:U:H2'	30:0:1363:G:C8	2.52	0.44
30:0:1434:A:H2'	30:0:1436:C:C5	2.52	0.44
30:0:440:C:O5'	30:0:440:C:H6	2.00	0.44
18:R:98:ASN:ND2	30:0:500:G:H21	2.12	0.44
30:0:711:G:C2'	30:0:712:C:H5'	2.47	0.44
2:B:51:VAL:HG13	2:B:53:LEU:HD13	1.98	0.44
3:C:129:HIS:HD2	3:C:165:ASP:OD2	2.01	0.44
3:C:60:SER:HA	38:C:8575:HOH:O	2.17	0.44
10:J:15:ARG:HG2	10:J:16:ASP:OD1	2.17	0.44
12:L:41:HIS:CD2	30:0:926:A:O2'	2.69	0.44
13:M:76:ARG:HG3	38:M:8827:HOH:O	2.17	0.44
14:N:1:ALA:HB2	31:9:14:G:O2'	2.18	0.44
20:T:81:LYS:HD2	20:T:87:VAL:HG11	1.98	0.44
23:W:10:GLU:O	23:W:13:MET:HB3	2.18	0.44
30:0:1069:C:H2'	30:0:1070:A:O4'	2.18	0.44
30:0:1132:A:H2'	30:0:1133:A:C8	2.52	0.44
30:0:1202:A:C2'	30:0:1203:G:H5'	2.48	0.44
30:0:1391:G:N2	30:0:1434:A:H5''	2.32	0.44
30:0:1649:G:H1'	38:0:5049:HOH:O	2.17	0.44
30:0:1680:C:H2'	30:0:1681:G:O4'	2.17	0.44
30:0:1701:A:H5''	30:0:1702:U:H3'	1.99	0.44
30:0:2276:U:H2'	30:0:2277:U:C6	2.52	0.44
29:3:10:TYR:CD1	30:0:2408:A:H1'	2.52	0.44
30:0:372:A:O2'	30:0:373:G:H5'	2.17	0.44
30:0:57:C:H42	30:0:89:G:H1	1.64	0.44
30:0:729:C:C2	30:0:743:G:C2	3.05	0.44
30:0:877:G:N7	30:0:885:G:C5	2.85	0.44
9:I:130:LEU:HD21	30:0:1167:G:C4'	2.46	0.44
11:K:86:THR:HG22	11:K:87:ARG:N	2.32	0.44
13:M:71:SER:OG	13:M:72:ALA:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:59:PHE:O	18:R:63:ASN:HB3	2.18	0.44
22:V:12:THR:CG2	22:V:15:GLU:H	2.30	0.44
2:B:244:PRO:HB3	30:0:1234:U:N3	2.32	0.44
30:0:1415:G:C2'	30:0:1416:G:H5'	2.47	0.44
30:0:1556:G:O2'	30:0:1557:G:H5'	2.17	0.44
30:0:2507:G:H2'	30:0:2510:C:H42	1.81	0.44
30:0:2509:A:OP2	30:0:2510:C:H5	2.00	0.44
30:0:2775:A:N6	30:0:2799:A:C8	2.86	0.44
30:0:2911:C:H2'	30:0:2912:C:H6	1.82	0.44
30:0:625:U:H5'	38:0:3177:HOH:O	2.16	0.44
29:3:5:ARG:HD2	29:3:21:GLU:HG2	1.98	0.44
4:D:153:THR:O	4:D:156:ARG:HB2	2.16	0.44
5:E:20:ILE:O	5:E:30:THR:HA	2.17	0.44
8:H:14:LYS:HG3	38:H:183:HOH:O	2.17	0.44
12:L:22:ARG:HG2	38:0:3223:HOH:O	2.15	0.44
19:S:11:THR:H	19:S:14:ALA:HB3	1.81	0.44
25:Y:182:PHE:HD2	25:Y:200:THR:O	2.00	0.44
25:Y:189:ASN:HD22	25:Y:189:ASN:C	2.21	0.44
26:Z:69:ASP:O	26:Z:71:VAL:N	2.45	0.44
30:0:1043:C:H2'	38:0:3185:HOH:O	2.18	0.44
18:R:80:TYR:O	30:0:2050:G:H5''	2.16	0.44
30:0:2345:A:C3'	30:0:2346:C:H6	2.23	0.44
23:W:5:VAL:HG11	23:W:153:MET:CE	2.48	0.44
30:0:1112:G:H1	30:0:1251:C:H42	1.65	0.44
30:0:1330:A:H2	38:0:4652:HOH:O	2.00	0.44
30:0:1519:U:O2'	30:0:1520:G:H5'	2.16	0.44
30:0:1706:G:C6	30:0:1707:G:N1	2.86	0.44
30:0:1711:A:H2'	30:0:1712:A:H5'	1.99	0.44
30:0:1762:C:H2'	30:0:1763:C:H6	1.82	0.44
1:A:233:THR:HB	30:0:1942:A:H5''	1.99	0.44
30:0:2005:G:OP2	30:0:2006:C:C5'	2.66	0.44
30:0:1016:U:O2'	30:0:2303:A:N7	2.40	0.44
30:0:2377:U:O2'	30:0:2378:U:H5'	2.17	0.44
30:0:2457:U:H1'	38:0:7515:HOH:O	2.17	0.44
30:0:2552:C:C6	30:0:2577:A:N7	2.85	0.44
30:0:2781:U:H2'	30:0:2782:G:C5'	2.48	0.44
30:0:2834:G:H2'	30:0:2835:C:O5'	2.17	0.44
30:0:2872:U:C2	30:0:2873:C:C6	3.05	0.44
30:0:2854:A:C6	30:0:2905:A:N1	2.86	0.44
30:0:569:A:H5''	30:0:587:A:N1	2.32	0.44
30:0:821:U:H2'	30:0:822:C:H6	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:40:HIS:HE1	30:0:949:U:O2'	2.01	0.44
27:1:20:ARG:HB2	38:1:513:HOH:O	2.18	0.44
23:W:129:LYS:CD	31:9:87:U:H2'	2.47	0.44
3:C:6:TYR:N	3:C:6:TYR:CD1	2.86	0.44
5:E:69:ILE:HA	5:E:72:MET:CE	2.48	0.44
8:H:8:MET:CE	30:0:2494:G:H4'	2.48	0.44
9:I:87:PRO:HG2	30:0:1181:A:O4'	2.18	0.44
13:M:66:SER:HB3	13:M:128:TRP:NE1	2.32	0.44
20:T:97:ARG:NH2	30:0:309:C:OP1	2.51	0.44
25:Y:99:ALA:HB2	25:Y:233:TYR:CE2	2.52	0.44
30:0:1309:U:C2'	30:0:1310:U:H5'	2.48	0.44
25:Y:204:ARG:NH2	30:0:1324:G:N2	2.65	0.44
30:0:1427:A:C2'	30:0:1428:C:H5'	2.47	0.44
19:S:55:GLN:CD	30:0:1446:U:H2'	2.37	0.44
1:A:192:VAL:HG23	30:0:1882:C:OP1	2.17	0.44
30:0:2250:G:N1	30:0:2251:G:N3	2.66	0.44
2:B:5:ARG:NH1	30:0:2547:C:OP2	2.51	0.44
30:0:2541:U:H5'	30:0:2611:G:O6	2.18	0.44
30:0:2566:A:C2	30:0:2696:G:O4'	2.71	0.44
38:T:2151:HOH:O	30:0:317:A:H5'	2.17	0.44
30:0:929:A:H8	30:0:929:A:O5'	2.01	0.44
2:B:241:PRO:HB3	30:0:2609:G:N3	2.33	0.44
4:D:62:ASP:HA	38:D:4233:HOH:O	2.18	0.44
4:D:86:THR:O	4:D:89:PRO:HD2	2.18	0.44
21:U:45:GLU:HB2	21:U:48:ASN:ND2	2.32	0.44
30:0:1202:A:H2'	30:0:1203:G:H5'	2.00	0.44
30:0:157:G:H3'	38:0:3945:HOH:O	2.18	0.44
30:0:1789:G:H2'	30:0:1790:C:O5'	2.17	0.44
30:0:1950:G:H2'	30:0:1951:G:C8	2.53	0.44
30:0:1986:G:C6	30:0:1987:C:N4	2.86	0.44
30:0:2061:C:H2'	30:0:2062:A:H5'	1.99	0.44
30:0:2104:C:O2	30:0:2485:A:N1	2.50	0.44
30:0:304:G:H1'	30:0:347:A:N6	2.32	0.44
30:0:582:U:H2'	30:0:583:C:C6	2.53	0.44
30:0:703:G:C6	30:0:704:C:C4	3.06	0.44
30:0:821:U:O2'	30:0:822:C:H5'	2.18	0.44
30:0:868:G:C4	30:0:887:G:C8	3.06	0.44
31:9:26:C:H2'	31:9:27:C:H6	1.79	0.44
31:9:31:C:C2	31:9:50:G:C2	3.05	0.44
31:9:81:C:C2'	31:9:82:U:H5'	2.48	0.44
1:A:103:VAL:HA	1:A:104:PRO:HD3	1.89	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:MET:SD	30:0:875:A:C2	3.11	0.44
2:B:195:ARG:HE	2:B:323:LEU:HD13	1.83	0.44
8:H:59:GLN:HE21	8:H:129:ARG:HE	1.65	0.44
8:H:87:LYS:HG3	8:H:140:TYR:HD1	1.83	0.44
8:H:66:GLU:HA	38:H:239:HOH:O	2.17	0.44
13:M:80:GLY:O	13:M:81:ARG:HB2	2.18	0.44
14:N:47:LEU:HA	14:N:47:LEU:HD13	1.86	0.44
16:P:13:VAL:HG11	16:P:40:VAL:CG1	2.48	0.44
20:T:19:ARG:HD3	20:T:67:LEU:O	2.18	0.44
30:0:1522:A:H2'	30:0:1523:G:C5'	2.48	0.44
16:P:54:LYS:HB2	30:0:1717:A:H5''	1.98	0.44
30:0:1937:U:O2'	30:0:1938:G:H5'	2.18	0.44
30:0:2250:G:C2	30:0:2251:G:C4	3.06	0.44
29:3:10:TYR:CE2	30:0:2382:A:H1'	2.53	0.44
30:0:2431:C:H2'	30:0:2432:C:C6	2.53	0.44
5:E:90:HIS:CE1	30:0:2694:A:H5''	2.53	0.44
30:0:2729:C:O2'	30:0:2730:G:H5'	2.18	0.44
30:0:483:C:H2'	30:0:484:A:O4'	2.18	0.44
30:0:727:G:C2	30:0:728:C:C2	3.06	0.44
1:A:182:ARG:HB3	38:0:5133:HOH:O	2.18	0.44
2:B:279:THR:HG22	2:B:280:VAL:N	2.33	0.44
2:B:54:VAL:HB	38:B:9083:HOH:O	2.17	0.44
8:H:39:LYS:O	30:0:969:G:H4'	2.18	0.44
10:J:75:PRO:HD3	10:J:136:SER:OG	2.18	0.44
16:P:88:GLN:HB3	38:P:185:HOH:O	2.16	0.44
17:Q:25:PRO:HA	17:Q:26:PRO:HD3	1.78	0.44
30:0:1166:A:C6	30:0:1167:G:C5	3.06	0.43
30:0:1167:G:O2'	30:0:1168:C:H5'	2.18	0.43
30:0:1185:U:C5'	38:0:7447:HOH:O	2.59	0.43
30:0:634:G:O2'	30:0:1358:A:OP1	2.31	0.43
30:0:1421:C:O2'	30:0:1422:U:H5'	2.18	0.43
30:0:1544:U:H2'	30:0:1545:C:H6	1.82	0.43
30:0:1592:G:O2'	30:0:1593:C:O4'	2.36	0.43
30:0:1642:A:N7	30:0:1643:C:C4	2.86	0.43
30:0:175:G:O2'	30:0:176:U:OP2	2.36	0.43
30:0:2090:G:H2'	30:0:2091:G:C8	2.53	0.43
30:0:2435:U:H4'	38:0:9269:HOH:O	2.17	0.43
30:0:2851:G:O2'	30:0:2852:A:H5'	2.17	0.43
30:0:324:G:C6	30:0:325:U:C5	3.06	0.43
30:0:293:A:C5	30:0:360:A:C2	3.06	0.43
30:0:39:G:O2'	30:0:40:C:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:533:U:H3'	38:0:3742:HOH:O	2.18	0.43
30:0:838:C:H4'	38:0:9187:HOH:O	2.18	0.43
31:9:74:G:O2'	31:9:75:G:H5'	2.18	0.43
3:C:174:ILE:CD1	30:0:338:C:H4'	2.48	0.43
4:D:103:ASN:ND2	4:D:133:ASN:HA	2.33	0.43
13:M:104:ARG:HG3	38:M:8866:HOH:O	2.18	0.43
14:N:12:ARG:HD3	14:N:18:THR:OG1	2.18	0.43
23:W:119:HIS:HE1	38:0:9568:HOH:O	2.00	0.43
25:Y:182:PHE:CG	25:Y:202:ALA:HB2	2.53	0.43
26:Z:45:VAL:O	26:Z:49:ARG:HG3	2.18	0.43
30:0:1130:U:C2'	30:0:1131:G:H5'	2.48	0.43
30:0:117:A:H2'	30:0:118:G:C8	2.53	0.43
30:0:1706:G:H1'	30:0:1712:A:N6	2.30	0.43
30:0:1916:C:C2	30:0:1924:A:C2	3.06	0.43
30:0:2135:A:O4'	30:0:2243:C:N4	2.51	0.43
30:0:2871:G:C4	30:0:2887:G:N2	2.86	0.43
30:0:692:A:N6	30:0:693:A:C2	2.86	0.43
30:0:827:A:H2'	30:0:828:G:O4'	2.18	0.43
31:9:2:U:OP2	31:9:3:A:H5'	2.18	0.43
1:A:215:ILE:HG22	1:A:227:ASP:O	2.18	0.43
1:A:94:LEU:HD12	1:A:98:GLU:CB	2.48	0.43
2:B:84:LEU:HD23	2:B:142:LEU:HD23	2.00	0.43
2:B:202:VAL:HA	2:B:310:ARG:O	2.18	0.43
3:C:193:LEU:HD12	3:C:211:ASP:O	2.18	0.43
4:D:10:PHE:CG	4:D:11:HIS:N	2.86	0.43
13:M:65:VAL:HG21	13:M:105:ALA:HB2	2.00	0.43
23:W:115:THR:HG23	38:W:5420:HOH:O	2.18	0.43
23:W:142:ASP:HB3	23:W:145:GLY:H	1.83	0.43
23:W:13:MET:HE2	23:W:17:ILE:HG22	2.00	0.43
24:X:39:LYS:HE2	30:0:2834:G:OP1	2.17	0.43
26:Z:61:HIS:O	26:Z:69:ASP:HA	2.17	0.43
30:0:1210:G:C2	30:0:1211:G:C8	3.06	0.43
30:0:1298:U:H2'	30:0:1299:G:C8	2.53	0.43
30:0:1363:G:H2'	30:0:1364:G:C8	2.54	0.43
30:0:1816:C:H2'	30:0:1817:U:O4'	2.17	0.43
30:0:1949:G:N2	30:0:1964:U:C2	2.87	0.43
30:0:2112:A:H2'	30:0:2113:G:C8	2.53	0.43
30:0:219:G:O5'	30:0:220:C:H5''	2.18	0.43
30:0:2277:U:H1'	30:0:2469:A:N3	2.33	0.43
30:0:2429:A:C4'	38:0:7716:HOH:O	2.66	0.43
30:0:2594:C:O2'	30:0:2595:U:H5'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1815:A:H4'	30:0:2751:C:O4'	2.19	0.43
30:0:2793:A:N6	38:0:5853:HOH:O	2.50	0.43
30:0:2847:G:C2'	30:0:2848:G:H5'	2.48	0.43
30:0:385:C:O5'	30:0:385:C:H6	2.02	0.43
30:0:665:A:C6	30:0:666:A:C6	3.06	0.43
30:0:820:G:H3'	30:0:820:G:N3	2.33	0.43
1:A:38:ILE:HB	1:A:82:VAL:O	2.18	0.43
3:C:44:GLN:HA	38:C:8605:HOH:O	2.18	0.43
3:C:47:GLY:HA2	3:C:92:PRO:HB2	2.00	0.43
4:D:75:LEU:HD22	4:D:79:MET:HB3	2.00	0.43
20:T:14:ALA:HA	20:T:15:PRO:HD3	1.90	0.43
25:Y:154:ARG:HH21	30:0:1293:U:H5'	1.83	0.43
30:0:152:A:O2'	30:0:153:C:H5'	2.18	0.43
30:0:1537:C:H2'	30:0:1538:C:H6	1.83	0.43
30:0:1878:G:O2'	30:0:1879:U:OP2	2.36	0.43
30:0:1980:U:O2	30:0:2008:U:H4'	2.18	0.43
30:0:234:A:H4'	30:0:437:A:O4'	2.18	0.43
30:0:36:C:H1'	38:0:3051:HOH:O	2.17	0.43
30:0:41:G:H8	30:0:41:G:O5'	2.00	0.43
31:9:115:C:C4	31:9:116:C:C5	3.06	0.43
3:C:6:TYR:HD1	3:C:6:TYR:N	2.17	0.43
5:E:126:ILE:HA	5:E:131:LEU:CD2	2.47	0.43
5:E:84:MET:SD	38:E:3134:HOH:O	2.61	0.43
5:E:91:PHE:HA	5:E:92:PRO:HD3	1.89	0.43
11:K:4:LEU:HD22	11:K:116:GLU:HB3	2.00	0.43
14:N:139:TRP:CE3	14:N:139:TRP:HA	2.53	0.43
30:0:1024:G:C6	30:0:1025:C:C4	3.07	0.43
30:0:148:A:O2'	30:0:149:G:H5'	2.19	0.43
30:0:1503:U:H2'	30:0:1504:A:O4'	2.19	0.43
30:0:1520:G:C2	30:0:1521:C:C2	3.07	0.43
30:0:2070:G:H2'	30:0:2072:G:OP1	2.18	0.43
30:0:2354:A:H5'	30:0:2355:G:N7	2.33	0.43
30:0:2361:A:H5'	38:0:9191:HOH:O	2.19	0.43
30:0:2429:A:H4'	38:0:7716:HOH:O	2.16	0.43
30:0:2445:U:H2'	30:0:2446:G:C8	2.54	0.43
30:0:2451:G:N3	30:0:2451:G:H2'	2.32	0.43
30:0:2531:U:H2'	30:0:2532:A:O4'	2.19	0.43
30:0:2748:G:H1'	38:0:7881:HOH:O	2.18	0.43
30:0:2768:A:H3'	30:0:2768:A:N3	2.33	0.43
30:0:772:G:H2'	30:0:773:A:O4'	2.18	0.43
31:9:39:U:O2'	31:9:42:C:H5	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:154:VAL:HA	2:B:155:PRO:HD3	1.88	0.43
3:C:39:GLN:O	3:C:43:LYS:HD3	2.18	0.43
9:I:73:LEU:HD12	9:I:107:LYS:NZ	2.33	0.43
16:P:8:ARG:HG3	38:P:188:HOH:O	2.17	0.43
23:W:6:GLN:HB2	23:W:26:ILE:CD1	2.48	0.43
30:0:1167:G:C2	30:0:1168:C:C2	3.06	0.43
30:0:1175:G:N3	30:0:1193:A:C6	2.86	0.43
30:0:1275:C:C2'	30:0:1276:U:H5'	2.49	0.43
30:0:1284:G:O2'	30:0:1285:U:H5'	2.18	0.43
30:0:1421:C:C2	30:0:1444:G:N2	2.87	0.43
30:0:1985:U:C2	30:0:1996:U:O4'	2.72	0.43
30:0:2429:A:N6	38:0:3326:HOH:O	2.51	0.43
30:0:2569:A:H2'	30:0:2570:G:O5'	2.19	0.43
30:0:2668:G:H2'	30:0:2669:U:H6	1.81	0.43
30:0:2692:G:N2	30:0:2701:G:C8	2.87	0.43
30:0:2886:C:O2'	30:0:2887:G:H5'	2.18	0.43
30:0:629:A:C2	30:0:2074:A:C2	3.07	0.43
29:3:59:ASP:HB3	29:3:63:LYS:HZ1	1.83	0.43
29:3:67:LEU:CD1	29:3:69:TYR:HE1	2.31	0.43
31:9:108:C:H2'	31:9:109:G:H8	1.82	0.43
31:9:65:A:C4	31:9:113:C:C4	3.07	0.43
31:9:5:G:O2'	31:9:6:C:H5'	2.18	0.43
1:A:71:PRO:O	1:A:160:ALA:HB2	2.18	0.43
4:D:104:PHE:CE2	4:D:132:VAL:HB	2.54	0.43
4:D:128:LEU:HB2	38:D:6007:HOH:O	2.18	0.43
5:E:107:PHE:CE2	5:E:108:LEU:HD13	2.54	0.43
6:F:60:VAL:O	6:F:62:HIS:N	2.52	0.43
10:J:70:PHE:HE1	30:0:2676:C:C4'	2.32	0.43
13:M:164:THR:HB	38:M:8820:HOH:O	2.17	0.43
14:N:77:ASN:OD1	14:N:79:PRO:HD2	2.18	0.43
14:N:32:PRO:HD2	14:N:99:GLU:O	2.18	0.43
17:Q:11:ARG:NH2	30:0:2363:G:C5'	2.81	0.43
26:Z:55:SER:HA	38:0:7562:HOH:O	2.19	0.43
30:0:102:A:C6	30:0:103:C:C4	3.06	0.43
30:0:1178:G:C5	30:0:1179:C:C4	3.07	0.43
30:0:1333:U:H2'	30:0:1334:C:C6	2.53	0.43
30:0:1519:U:H1'	38:0:3898:HOH:O	2.18	0.43
30:0:1602:C:H5'	38:0:6467:HOH:O	2.18	0.43
30:0:1552:G:C6	30:0:1634:G:C6	3.07	0.43
30:0:1665:G:C2	30:0:1666:C:C6	3.07	0.43
13:M:29:GLN:OE1	30:0:2244:A:H5''	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2473:U:H2'	30:0:2476:C:H5	1.84	0.43
30:0:2507:G:H22	30:0:2512:U:H5''	1.84	0.43
30:0:1705:C:O2	30:0:2735:U:C5'	2.65	0.43
30:0:273:G:H2'	30:0:274:G:O4'	2.18	0.43
30:0:2803:C:H2'	30:0:2804:C:C6	2.54	0.43
2:B:27:ASN:HD21	30:0:2807:U:P	2.41	0.43
30:0:284:C:OP2	30:0:284:C:H6	2.01	0.43
30:0:2855:G:C2	30:0:2904:U:C2	3.06	0.43
30:0:624:U:O4	30:0:628:1MA:H8	2.01	0.43
26:Z:41:ARG:HD2	30:0:820:G:H22	1.83	0.43
30:0:85:C:H3'	30:0:86:A:H2'	2.01	0.43
30:0:877:G:H3'	38:0:3106:HOH:O	2.19	0.43
31:9:111:U:O2'	31:9:112:U:H5'	2.19	0.43
13:M:70:GLY:HA3	13:M:73:ARG:HH21	1.77	0.43
14:N:91:ARG:O	14:N:94:GLU:HB2	2.19	0.43
30:0:1159:G:C6	30:0:1160:G:C4	3.07	0.43
30:0:1202:A:H2'	30:0:1203:G:O4'	2.19	0.43
30:0:1255:A:H2'	30:0:1256:C:O5'	2.18	0.43
30:0:1703:G:C2	30:0:1716:A:C4	3.06	0.43
30:0:1788:U:C2	30:0:1805:G:C2	3.07	0.43
30:0:2510:C:H42	30:0:2564:G:H22	1.66	0.43
30:0:2094:G:C2	30:0:2652:U:O2	2.71	0.43
30:0:2727:A:C6	30:0:2756:U:N3	2.87	0.43
30:0:2780:C:C4	30:0:2781:U:C4	3.06	0.43
30:0:2812:A:H2	30:0:2814:A:H62	1.63	0.43
30:0:432:G:C2	30:0:433:C:C6	3.07	0.43
30:0:79:G:H22	30:0:97:G:H1'	1.82	0.43
30:0:816:G:C6	30:0:817:G:N1	2.87	0.43
29:3:22:VAL:HG12	29:3:90:PHE:HE2	1.83	0.43
14:N:65:ASP:HB3	38:N:8820:HOH:O	2.19	0.43
16:P:58:SER:HB3	38:0:5593:HOH:O	2.18	0.43
21:U:6:CYS:HB2	21:U:13:ILE:CG1	2.49	0.43
25:Y:144:ARG:HB3	38:0:4369:HOH:O	2.18	0.43
1:A:167:LYS:CE	26:Z:50:VAL:HG13	2.42	0.43
30:0:1399:A:H2'	30:0:1400:C:C6	2.54	0.43
30:0:1667:A:H2'	30:0:1668:U:O4'	2.19	0.43
30:0:1697:G:H1'	38:0:7261:HOH:O	2.19	0.43
30:0:1712:A:H2'	30:0:1713:G:O4'	2.19	0.43
30:0:1882:C:H2'	30:0:1883:U:C6	2.53	0.43
30:0:191:A:H61	30:0:435:A:H62	1.67	0.43
30:0:2080:G:H2'	30:0:2081:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2328:U:C4	30:0:2329:C:C5	3.07	0.43
30:0:2332:A:H3'	30:0:2333:G:H8	1.84	0.43
29:3:17:HIS:ND1	30:0:2408:A:O2'	2.48	0.43
29:3:54:LYS:HE3	38:0:3005:HOH:O	2.18	0.43
31:9:11:A:H2	31:9:68:G:N3	2.17	0.43
31:9:39:U:H2'	31:9:40:C:OP1	2.18	0.43
1:A:105:VAL:HG11	1:A:154:ALA:HB1	2.00	0.43
2:B:305:ASP:O	2:B:306:LYS:CB	2.66	0.43
5:E:95:VAL:O	5:E:126:ILE:HD12	2.18	0.43
5:E:7:ILE:HG23	5:E:45:ASP:O	2.19	0.43
10:J:99:GLU:HA	38:J:8871:HOH:O	2.19	0.43
16:P:134:VAL:O	16:P:137:LEU:HB3	2.19	0.43
18:R:18:LEU:HD12	18:R:143:VAL:CG1	2.49	0.43
18:R:39:THR:HB	18:R:42:GLU:CD	2.39	0.43
25:Y:235:GLU:CD	25:Y:235:GLU:N	2.72	0.43
30:0:1192:A:H4'	38:0:4383:HOH:O	2.18	0.43
12:L:6:ARG:HD3	30:0:1299:G:O6	2.18	0.43
30:0:1342:C:H2'	30:0:1343:C:H5'	1.99	0.43
30:0:1383:U:H2'	30:0:1384:C:C6	2.54	0.43
30:0:135:G:C2	30:0:144:A:N3	2.86	0.43
30:0:1504:A:H4'	30:0:1506:U:C5	2.53	0.43
30:0:1600:G:H8	30:0:1600:G:OP2	2.02	0.43
30:0:1933:G:C2'	30:0:1934:A:H5'	2.48	0.43
30:0:2095:A:OP1	30:0:2096:A:H4'	2.19	0.43
30:0:2293:G:C5	30:0:2294:C:C5	3.07	0.43
30:0:2476:C:H2'	30:0:2476:C:O2	2.19	0.43
30:0:2779:G:N7	30:0:2790:C:C2	2.86	0.43
30:0:2896:A:H2'	30:0:2896:A:N3	2.34	0.43
30:0:393:G:C2	30:0:394:G:C4	3.06	0.43
30:0:435:A:O2'	30:0:436:A:H5'	2.19	0.43
30:0:67:A:H5''	30:0:69:A:C8	2.54	0.43
30:0:699:C:C2	30:0:744:G:N2	2.87	0.43
30:0:793:A:C2	30:0:822:C:C2	3.06	0.43
30:0:816:G:H8	30:0:816:G:O5'	2.02	0.43
31:9:11:A:H4'	31:9:13:A:C8	2.54	0.43
4:D:12:GLU:O	4:D:15:GLU:HG2	2.18	0.43
6:F:58:GLU:HB3	13:M:8:ILE:HG23	2.01	0.43
13:M:48:LYS:HE3	13:M:52:GLN:NE2	2.28	0.43
19:S:57:THR:C	19:S:59:ASP:H	2.21	0.43
20:T:28:SER:HA	20:T:97:ARG:HD3	1.99	0.43
1:A:72:GLU:HG2	26:Z:100:GLY:HA3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1287:A:H8	38:0:7887:HOH:O	2.02	0.42
30:0:248:A:H5'	30:0:249:G:OP2	2.19	0.42
30:0:349:U:O5'	30:0:349:U:H6	2.02	0.42
30:0:577:G:C2	30:0:581:G:C6	3.07	0.42
30:0:729:C:C2	30:0:743:G:N2	2.87	0.42
30:0:877:G:N7	30:0:885:G:C6	2.87	0.42
30:0:970:U:H2'	38:0:6308:HOH:O	2.18	0.42
31:9:110:G:C6	31:9:111:U:C5	3.07	0.42
31:9:16:G:C2	31:9:66:G:O6	2.72	0.42
1:A:23:TYR:HB2	30:0:1872:C:C5	2.54	0.42
1:A:81:GLN:H	1:A:92:ASN:ND2	2.17	0.42
3:C:156:LEU:O	3:C:160:LEU:HG	2.19	0.42
4:D:67:ASP:HA	4:D:68:PRO:HD3	1.92	0.42
5:E:81:GLU:O	5:E:172:PRO:HD3	2.19	0.42
13:M:42:ARG:HA	13:M:43:PRO:HD3	1.86	0.42
15:O:57:THR:O	15:O:111:VAL:HG23	2.19	0.42
19:S:42:GLU:O	19:S:46:ASP:HA	2.19	0.42
21:U:34:SER:HB3	38:0:3126:HOH:O	2.17	0.42
30:0:1183:C:N3	30:0:1184:C:N4	2.67	0.42
30:0:1184:C:O2'	30:0:1185:U:OP2	2.32	0.42
24:X:49:ARG:NH1	30:0:1385:G:O3'	2.51	0.42
30:0:1568:G:C2'	30:0:1569:U:H5'	2.49	0.42
30:0:188:C:O5'	30:0:188:C:H6	2.02	0.42
30:0:1970:G:H4'	30:0:1971:G:O5'	2.19	0.42
30:0:1981:A:C6	30:0:2005:G:H4'	2.54	0.42
30:0:2005:G:OP2	30:0:2006:C:H5''	2.19	0.42
30:0:2512:U:H4'	30:0:2514:U:O4	2.19	0.42
30:0:2531:U:H4'	38:0:9596:HOH:O	2.17	0.42
30:0:2600:A:H2'	30:0:2601:A:O4'	2.19	0.42
30:0:2853:U:C4	30:0:2906:A:N6	2.87	0.42
30:0:726:C:C2	30:0:727:G:C8	3.07	0.42
30:0:95:A:H5''	30:0:97:G:O4'	2.19	0.42
27:1:44:LYS:HG2	30:0:148:A:H5''	2.01	0.42
3:C:24:THR:HG23	3:C:25:PRO:HD2	2.02	0.42
4:D:137:PRO:O	31:9:30:C:OP1	2.37	0.42
13:M:112:LEU:HB3	13:M:133:LEU:HB3	2.02	0.42
23:W:11:VAL:O	23:W:12:ASN:HB2	2.19	0.42
24:X:43:VAL:HG12	24:X:44:ASP:N	2.34	0.42
30:0:107:U:H2'	30:0:108:U:H5'	2.01	0.42
30:0:1115:U:H5''	30:0:1140:C:O2'	2.20	0.42
30:0:111:C:H2'	30:0:112:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1474:C:O2'	30:0:1475:G:H5'	2.18	0.42
30:0:2248:C:O2'	30:0:2249:G:H5'	2.19	0.42
30:0:2374:G:H2'	30:0:2375:A:C8	2.53	0.42
30:0:314:G:N2	30:0:317:A:C8	2.87	0.42
30:0:354:A:H2'	30:0:355:C:C6	2.52	0.42
30:0:752:G:H2'	30:0:753:U:O4'	2.19	0.42
26:Z:34:SER:HB3	30:0:797:A:H4'	2.00	0.42
30:0:830:G:O2'	30:0:831:U:H5'	2.19	0.42
4:D:76:ARG:NE	31:9:44:A:O4'	2.52	0.42
3:C:151:GLN:HA	3:C:151:GLN:HE21	1.84	0.42
3:C:194:PHE:HB2	3:C:212:VAL:HG12	2.00	0.42
3:C:46:TYR:CE1	30:0:450:C:H4'	2.54	0.42
5:E:21:THR:HG23	5:E:30:THR:OG1	2.19	0.42
8:H:65:LEU:HA	8:H:65:LEU:HD12	1.80	0.42
30:0:1195:G:N2	30:0:1205:U:C2	2.87	0.42
30:0:1350:U:H5''	38:0:5090:HOH:O	2.20	0.42
30:0:1789:G:C2'	30:0:1790:C:O5'	2.67	0.42
30:0:2362:A:H2'	30:0:2363:G:C8	2.54	0.42
30:0:2502:C:O2'	30:0:2503:A:H5'	2.19	0.42
30:0:2655:U:C4	30:0:2656:G:N7	2.87	0.42
30:0:282:C:O2'	30:0:368:C:N4	2.52	0.42
30:0:2893:C:C2'	30:0:2894:C:H5'	2.49	0.42
30:0:652:G:H2'	30:0:653:U:O4'	2.20	0.42
30:0:877:G:C6	30:0:885:G:C4	3.08	0.42
28:2:22:PRO:HG2	28:2:25:VAL:CG2	2.49	0.42
29:3:80:ARG:HH22	30:0:2381:C:H4'	1.84	0.42
31:9:36:C:C5	31:9:37:C:C4	3.08	0.42
31:9:57:A:N3	31:9:57:A:H5'	2.34	0.42
31:9:65:A:C2'	31:9:66:G:OP2	2.68	0.42
2:B:57:GLU:HA	2:B:58:PRO:HD2	1.85	0.42
2:B:60:SER:HA	2:B:61:PRO:HD3	1.90	0.42
5:E:106:ASN:ND2	5:E:109:GLY:HA2	2.34	0.42
5:E:35:TYR:CD2	5:E:36:PRO:HD2	2.55	0.42
5:E:72:MET:O	5:E:76:VAL:HG22	2.19	0.42
12:L:38:HIS:CD2	12:L:39:GLU:HG3	2.54	0.42
19:S:57:THR:HG22	19:S:58:MET:N	2.34	0.42
20:T:24:ARG:HH21	20:T:39:ASN:ND2	2.17	0.42
26:Z:66:CYS:SG	26:Z:67:GLY:N	2.93	0.42
30:0:1342:C:O2'	30:0:1343:C:H5'	2.18	0.42
30:0:138:U:P	30:0:139:C:H5	2.42	0.42
30:0:161:A:H2'	30:0:162:C:C6	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:165:A:H2'	30:0:166:A:OP1	2.19	0.42
30:0:1754:A:O5'	30:0:1754:A:H8	2.02	0.42
30:0:1757:U:H5	38:0:3214:HOH:O	2.02	0.42
30:0:1848:G:O2'	30:0:1849:G:H5'	2.19	0.42
30:0:1998:G:O2'	30:0:2026:C:H1'	2.20	0.42
30:0:2346:C:O2	30:0:2346:C:H2'	2.18	0.42
29:3:10:TYR:CD2	30:0:2382:A:H1'	2.55	0.42
30:0:2470:A:H2'	30:0:2471:G:O5'	2.19	0.42
30:0:265:U:C2	30:0:266:G:C8	3.07	0.42
30:0:690:G:H1'	30:0:731:U:O2'	2.20	0.42
30:0:776:A:C2	30:0:780:A:C6	3.08	0.42
31:9:22:G:C6	31:9:55:U:C2	3.07	0.42
1:A:223:ARG:HH12	30:0:2270:G:C4'	2.27	0.42
1:A:81:GLN:HB2	1:A:92:ASN:ND2	2.35	0.42
2:B:162:MET:HG3	2:B:310:ARG:NH1	2.35	0.42
2:B:177:HIS:O	2:B:181:ILE:HG13	2.19	0.42
2:B:307:ARG:HG2	2:B:308:LEU:N	2.34	0.42
3:C:211:ASP:HB2	3:C:231:ARG:HH12	1.85	0.42
4:D:88:LEU:HB2	4:D:89:PRO:HD3	2.00	0.42
8:H:91:ARG:NH2	8:H:135:GLN:NE2	2.68	0.42
12:L:10:SER:O	12:L:11:ARG:HB3	2.19	0.42
15:O:105:ASN:HD21	15:O:109:SER:N	2.18	0.42
16:P:10:ALA:HA	16:P:13:VAL:HG12	2.02	0.42
24:X:12:ILE:HB	24:X:70:ILE:CG2	2.49	0.42
26:Z:38:PHE:HB3	26:Z:42:TYR:HD1	1.82	0.42
30:0:1047:U:O5'	30:0:1047:U:H6	2.03	0.42
30:0:1097:A:H2'	30:0:1098:A:C8	2.54	0.42
30:0:1367:A:H2'	30:0:1368:U:O4'	2.20	0.42
30:0:1391:G:H2'	30:0:1392:A:H5'	2.01	0.42
30:0:1573:A:C8	30:0:1574:C:C6	3.08	0.42
30:0:1603:A:H5'	30:0:1605:G:H5'	1.99	0.42
30:0:1643:C:O2'	30:0:1644:C:H5'	2.19	0.42
30:0:1680:C:H5'	30:0:1685:A:N6	2.34	0.42
30:0:1709:G:C6	30:0:1711:A:C5	3.07	0.42
13:M:191:GLY:O	30:0:175:G:H3'	2.19	0.42
1:A:10:GLY:HA2	30:0:1861:C:O2	2.20	0.42
29:3:33:MET:CG	30:0:1922:A:H2'	2.50	0.42
30:0:221:G:H2'	30:0:222:A:C8	2.55	0.42
30:0:2499:U:H2'	30:0:2500:C:O4'	2.20	0.42
30:0:2805:A:C8	30:0:2806:C:C5	3.07	0.42
30:0:2842:G:C2'	30:0:2843:A:H5'	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:453:A:C4	30:0:479:G:N7	2.87	0.42
30:0:685:C:O2'	30:0:748:C:H5''	2.19	0.42
27:1:37:CYS:SG	27:1:39:PHE:HB2	2.59	0.42
31:9:108:C:H2'	31:9:109:G:C8	2.55	0.42
2:B:48:MET:O	30:0:2719:A:H5'	2.20	0.42
8:H:48:VAL:HG13	38:H:218:HOH:O	2.18	0.42
9:I:133:THR:HG22	9:I:134:ILE:H	1.83	0.42
13:M:185:PRO:HD3	38:0:9800:HOH:O	2.19	0.42
24:X:71:ARG:HD3	38:X:2171:HOH:O	2.20	0.42
30:0:1060:C:H5'	30:0:1060:C:H6	1.85	0.42
30:0:1255:A:C2'	30:0:1256:C:O5'	2.68	0.42
30:0:1523:G:C6	30:0:1524:U:O4	2.73	0.42
30:0:1965:C:H6	30:0:1965:C:O5'	2.02	0.42
30:0:2492:U:C4	30:0:2493:C:C4	3.07	0.42
30:0:2812:A:H2	30:0:2814:A:N7	2.17	0.42
30:0:2864:U:H2'	30:0:2865:G:H5'	2.02	0.42
30:0:462:A:N6	30:0:477:A:C2	2.88	0.42
30:0:583:C:H2'	30:0:584:U:H6	1.85	0.42
30:0:590:A:H2'	30:0:591:A:C5'	2.48	0.42
30:0:669:G:C4	30:0:670:G:C8	3.07	0.42
30:0:795:G:H2'	38:0:9823:HOH:O	2.20	0.42
1:A:26:ASP:HB2	38:0:7291:HOH:O	2.18	0.42
2:B:223:ARG:HG3	2:B:232:TRP:C	2.40	0.42
8:H:59:GLN:HE21	8:H:129:ARG:HG2	1.85	0.42
10:J:116:LEU:HB2	10:J:119:THR:CG2	2.49	0.42
10:J:131:THR:O	10:J:134:GLU:HB2	2.19	0.42
13:M:159:VAL:HG13	13:M:160:PHE:N	2.35	0.42
13:M:70:GLY:HA3	13:M:73:ARG:CZ	2.50	0.42
14:N:169:PRO:O	14:N:172:PHE:HB3	2.20	0.42
20:T:75:GLU:O	20:T:76:ASP:HB2	2.19	0.42
30:0:1241:G:H2'	30:0:1242:A:O4'	2.19	0.42
30:0:1537:C:O2'	30:0:1538:C:H5'	2.18	0.42
30:0:1541:G:O2'	30:0:1542:G:H5'	2.18	0.42
30:0:2256:G:H2'	30:0:2257:G:C5'	2.50	0.42
38:C:8619:HOH:O	30:0:338:C:H5'	2.19	0.42
30:0:451:C:C2'	30:0:452:G:H5'	2.50	0.42
30:0:711:G:N2	30:0:718:C:N1	2.67	0.42
30:0:802:G:N2	30:0:812:A:C4	2.88	0.42
30:0:877:G:C2	30:0:885:G:O4'	2.73	0.42
4:D:104:PHE:N	4:D:104:PHE:CD2	2.88	0.42
13:M:30:GLU:O	13:M:34:GLU:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:92:ASP:OD2	23:W:94:SER:HB2	2.20	0.42
24:X:25:ARG:HD2	38:X:5356:HOH:O	2.19	0.42
26:Z:37:ARG:HG3	26:Z:38:PHE:CD2	2.54	0.42
1:A:160:ALA:CB	26:Z:89:THR:HB	2.49	0.42
30:0:1187:U:O2	30:0:1189:A:H5''	2.20	0.42
30:0:1183:C:H1'	30:0:1192:A:N6	2.35	0.42
30:0:1413:A:H2'	30:0:1414:A:O4'	2.20	0.42
30:0:1819:G:H2'	30:0:1820:G:H5'	2.01	0.42
30:0:1840:A:H4'	30:0:1841:C:O5'	2.20	0.42
30:0:2355:G:N3	30:0:2355:G:C2'	2.83	0.42
30:0:2523:U:O2'	30:0:2524:G:H5'	2.19	0.42
30:0:325:U:H3'	38:0:5512:HOH:O	2.19	0.42
30:0:387:G:O2'	30:0:388:G:H5'	2.20	0.42
30:0:473:A:C2'	30:0:474:C:H5'	2.49	0.42
30:0:485:A:N3	30:0:487:G:H5''	2.34	0.42
31:9:74:G:C2	31:9:75:G:C8	3.08	0.42
31:9:92:G:C6	31:9:93:A:N6	2.88	0.42
1:A:169:PHE:O	1:A:170:VAL:HB	2.20	0.42
2:B:8:LYS:HB3	2:B:218:TRP:O	2.19	0.42
2:B:316:ARG:HB2	30:0:2768:A:C8	2.55	0.42
3:C:87:ARG:NH2	30:0:894:A:C2	2.88	0.42
30:0:1015:C:H2'	30:0:1016:U:H6	1.82	0.42
30:0:2700:G:C2'	30:0:2701:G:H5'	2.49	0.42
30:0:2909:G:N2	30:0:2910:A:C5	2.88	0.42
30:0:293:A:C2	30:0:294:C:C6	3.08	0.42
30:0:59:A:H5''	38:0:4313:HOH:O	2.18	0.42
30:0:67:A:H3'	30:0:67:A:OP2	2.20	0.42
30:0:868:G:H2'	38:0:3039:HOH:O	2.18	0.42
28:2:41:HIS:CE1	30:0:1439:C:H5''	2.54	0.42
29:3:14:CYS:SG	38:3:9063:HOH:O	2.62	0.42
29:3:83:TRP:O	29:3:85:ALA:N	2.53	0.42
31:9:114:G:C6	31:9:115:C:N4	2.88	0.42
5:E:77:THR:OG1	5:E:78:GLU:N	2.50	0.42
8:H:149:VAL:HG13	8:H:150:LYS:N	2.35	0.42
11:K:105:ARG:HD2	38:K:3385:HOH:O	2.19	0.42
16:P:40:VAL:O	16:P:44:VAL:HG23	2.20	0.42
17:Q:27:GLN:HB3	38:9:9083:HOH:O	2.20	0.42
23:W:10:GLU:HB3	38:W:1223:HOH:O	2.20	0.42
24:X:70:ILE:O	24:X:70:ILE:HG23	2.18	0.42
26:Z:61:HIS:CG	26:Z:95:PRO:HG3	2.55	0.42
30:0:1006:A:N3	30:0:2298:C:O2'	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:I:3512:HOH:O	30:0:1163:G:N2	2.53	0.41
30:0:1182:C:H4'	30:0:1192:A:N7	2.35	0.41
30:0:1210:G:C2	30:0:1211:G:N9	2.88	0.41
30:0:1588:G:C6	30:0:1589:G:C6	3.08	0.41
30:0:1624:A:O4'	30:0:1626:A:C8	2.73	0.41
30:0:1789:G:N2	30:0:1790:C:H1'	2.35	0.41
30:0:1919:A:H4'	38:0:4820:HOH:O	2.19	0.41
30:0:2433:A:H2'	30:0:2434:A:C8	2.54	0.41
30:0:2478:U:H2'	30:0:2479:A:H8	1.85	0.41
30:0:2799:A:H5'	30:0:2800:A:P	2.59	0.41
21:U:56:ARG:NH1	30:0:2890:A:C2	2.88	0.41
30:0:314:G:C2	30:0:317:A:C8	3.08	0.41
30:0:335:U:C2'	30:0:336:G:OP1	2.68	0.41
30:0:371:U:H2'	30:0:372:A:H8	1.85	0.41
30:0:628:1MA:H4'	38:0:3136:HOH:O	2.19	0.41
15:O:68:GLY:HA3	30:0:745:G:O6	2.20	0.41
30:0:887:G:H2'	30:0:888:U:C6	2.54	0.41
28:2:48:ASP:O	28:2:49:GLU:HB2	2.20	0.41
29:3:62:THR:CG2	29:3:63:LYS:N	2.83	0.41
2:B:203:ALA:HA	2:B:263:THR:HA	2.02	0.41
2:B:224:LYS:HA	2:B:224:LYS:HD3	1.83	0.41
12:L:35:ARG:HB2	12:L:43:HIS:CD2	2.55	0.41
12:L:73:VAL:HG21	12:L:116:HIS:CE1	2.54	0.41
12:L:53:ARG:N	33:L:8810:CL:CL	2.66	0.41
13:M:89:THR:HA	38:M:8950:HOH:O	2.19	0.41
15:O:39:THR:HB	38:0:4589:HOH:O	2.19	0.41
22:V:39:ALA:C	22:V:41:GLU:H	2.23	0.41
30:0:102:A:C6	30:0:103:C:N4	2.88	0.41
30:0:1163:G:C2	30:0:1184:C:N3	2.87	0.41
30:0:1178:G:H2'	30:0:1179:C:H6	1.79	0.41
30:0:1449:G:H4'	38:0:9213:HOH:O	2.20	0.41
30:0:1507:C:H4'	38:0:3595:HOH:O	2.20	0.41
30:0:1519:U:H6	30:0:1519:U:O5'	2.04	0.41
30:0:1915:U:O2	30:0:1925:G:C2	2.73	0.41
30:0:2004:U:H2'	30:0:2004:U:O2	2.20	0.41
30:0:201:G:H1'	38:0:4539:HOH:O	2.19	0.41
30:0:2020:C:O2'	30:0:2021:C:H5'	2.20	0.41
30:0:2061:C:C2'	30:0:2062:A:H5'	2.51	0.41
30:0:272:A:N1	30:0:369:G:H5''	2.34	0.41
30:0:2912:C:C2'	30:0:2913:A:H5'	2.50	0.41
30:0:412:C:C2'	30:0:413:G:H5'	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:446:G:H3'	38:0:9539:HOH:O	2.20	0.41
30:0:495:A:O4'	30:0:1390:A:H1'	2.20	0.41
27:1:31:LYS:O	27:1:33:VAL:HG23	2.20	0.41
29:3:5:ARG:HA	29:3:22:VAL:HG23	2.02	0.41
31:9:50:G:C6	31:9:51:A:C6	3.08	0.41
31:9:56:A:C3'	31:9:57:A:C5'	2.93	0.41
1:A:199:HIS:CD2	1:A:200:PRO:HD2	2.55	0.41
1:A:51:ARG:NH2	1:A:53:ALA:HB3	2.35	0.41
4:D:76:ARG:CZ	31:9:44:A:C1'	2.98	0.41
9:I:96:SER:H	9:I:99:GLN:CD	2.22	0.41
10:J:19:MET:HE2	10:J:79:PHE:HA	2.02	0.41
11:K:4:LEU:HD23	11:K:4:LEU:HA	1.84	0.41
16:P:94:TRP:CH2	16:P:98:ILE:HG13	2.55	0.41
18:R:99:ALA:HB1	18:R:109:MET:HE2	2.01	0.41
22:V:23:LEU:HD22	22:V:49:LEU:HD23	2.01	0.41
23:W:13:MET:CE	23:W:17:ILE:HG22	2.50	0.41
26:Z:78:ILE:HB	38:Z:8715:HOH:O	2.19	0.41
30:0:1079:A:N1	30:0:2068:G:O2'	2.43	0.41
30:0:1212:C:C5	30:0:1213:C:C5	3.09	0.41
30:0:1303:C:O2	30:0:1353:C:H1'	2.20	0.41
30:0:1419:U:H5'	30:0:1420:C:OP2	2.21	0.41
30:0:1554:C:O2'	30:0:1631:A:H1'	2.19	0.41
30:0:1804:A:H2'	30:0:1805:G:C8	2.55	0.41
30:0:1826:C:O2'	30:0:1827:G:H5'	2.21	0.41
30:0:1878:G:O2'	30:0:1879:U:P	2.78	0.41
30:0:2256:G:C2'	30:0:2257:G:H5'	2.51	0.41
30:0:236:A:H8	30:0:236:A:OP1	2.03	0.41
38:H:216:HOH:O	30:0:2517:A:H2	1.99	0.41
30:0:2474:A:C8	30:0:2621:PSU:H4'	2.55	0.41
30:0:2782:G:O6	30:0:2790:C:H5''	2.19	0.41
30:0:2795:C:O2'	30:0:2796:U:C5'	2.65	0.41
30:0:2799:A:N6	30:0:2801:A:C2	2.89	0.41
30:0:38:G:C2'	30:0:39:G:H5'	2.50	0.41
26:Z:34:SER:HA	30:0:797:A:C5'	2.50	0.41
2:B:211:THR:HG21	38:0:7438:HOH:O	2.20	0.41
2:B:75:GLU:C	2:B:77:PRO:HD3	2.40	0.41
4:D:84:LEU:HD23	4:D:84:LEU:HA	1.92	0.41
5:E:69:ILE:HA	5:E:72:MET:HE3	2.02	0.41
8:H:59:GLN:NE2	8:H:96:GLN:HG2	2.35	0.41
12:L:150:GLN:HB3	38:L:8869:HOH:O	2.19	0.41
21:U:31:PHE:CG	21:U:37:GLU:HG2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:54:ILE:HD11	24:X:85:VAL:HG12	2.03	0.41
25:Y:157:ILE:HD13	38:0:4836:HOH:O	2.20	0.41
30:0:107:U:C2'	30:0:108:U:H5'	2.50	0.41
30:0:1607:A:C5	30:0:1608:G:C8	3.09	0.41
30:0:1757:U:H6	30:0:1757:U:O5'	2.04	0.41
30:0:1769:C:C2'	30:0:1770:U:H5'	2.51	0.41
30:0:1819:G:C2'	30:0:1820:G:H5'	2.50	0.41
30:0:1894:C:N4	30:0:1939:U:H2'	2.34	0.41
30:0:1928:C:C2'	30:0:1929:G:H5'	2.50	0.41
30:0:1942:A:C1'	38:0:9045:HOH:O	2.69	0.41
30:0:1997:A:H2	30:0:2026:C:O2'	2.04	0.41
24:X:23:HIS:HE1	30:0:2044:G:OP1	2.03	0.41
30:0:2710:U:H2'	30:0:2711:U:C6	2.55	0.41
30:0:2723:G:H1'	38:0:4812:HOH:O	2.19	0.41
30:0:2815:G:H4'	30:0:2816:A:OP2	2.20	0.41
30:0:281:U:C2'	30:0:282:C:C5'	2.98	0.41
30:0:517:U:H2'	30:0:518:G:H5'	2.02	0.41
30:0:552:A:H5'	38:0:5878:HOH:O	2.19	0.41
31:9:110:G:C6	31:9:111:U:C4	3.08	0.41
31:9:58:G:C8	31:9:59:C:C4	3.08	0.41
2:B:69:VAL:HA	2:B:70:PRO:HD3	1.77	0.41
5:E:107:PHE:O	5:E:110:GLU:HG3	2.20	0.41
15:O:26:TRP:CE3	15:O:26:TRP:HA	2.55	0.41
19:S:17:ASP:HB3	19:S:23:LYS:HB2	2.01	0.41
26:Z:34:SER:HA	30:0:797:A:H5'	2.02	0.41
30:0:1063:G:O5'	30:0:2307:A:H1'	2.21	0.41
30:0:10:U:O4	30:0:532:A:OP2	2.38	0.41
30:0:1271:A:H2'	30:0:1272:C:H6	1.84	0.41
30:0:1423:C:O2'	30:0:1424:A:H5'	2.20	0.41
30:0:1882:C:H2'	30:0:1883:U:H6	1.86	0.41
30:0:1898:G:H2'	30:0:1899:C:C6	2.55	0.41
1:A:212:PRO:HA	30:0:1943:C:O4'	2.20	0.41
11:K:66:ARG:NH1	30:0:1992:U:H3'	2.35	0.41
30:0:2470:A:C2'	30:0:2471:G:O5'	2.68	0.41
30:0:2511:A:H2'	30:0:2512:U:C6	2.56	0.41
30:0:2854:A:N6	30:0:2905:A:N6	2.69	0.41
30:0:343:C:H1'	38:0:5552:HOH:O	2.19	0.41
30:0:594:C:C4	30:0:595:U:C4	3.08	0.41
30:0:910:C:H2'	30:0:911:G:O4'	2.21	0.41
2:B:222:LYS:HG3	30:0:2038:A:H5''	2.01	0.41
2:B:320:GLN:HE21	2:B:321:PRO:HD3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:5:ILE:HG12	3:C:139:VAL:CG1	2.50	0.41
6:F:26:THR:HB	6:F:102:GLY:HA3	2.02	0.41
7:G:23:ILE:O	7:G:27:ILE:HG13	2.20	0.41
8:H:165:ARG:HD2	38:H:241:HOH:O	2.21	0.41
10:J:54:VAL:HG11	10:J:138:THR:HG21	2.02	0.41
10:J:76:ASP:HA	38:J:8863:HOH:O	2.20	0.41
14:N:132:ASN:O	14:N:135:VAL:HG12	2.21	0.41
19:S:51:GLN:HE21	19:S:53:ASN:HD21	1.67	0.41
21:U:5:GLU:HG2	21:U:6:CYS:N	2.36	0.41
25:Y:130:ARG:HB2	25:Y:142:SER:O	2.20	0.41
25:Y:152:LYS:CB	25:Y:160:LYS:HG3	2.51	0.41
25:Y:189:ASN:HD22	25:Y:191:ASP:N	2.19	0.41
30:0:1278:A:O2'	30:0:1279:U:C2	2.65	0.41
30:0:1540:G:C4	30:0:1541:G:C8	3.09	0.41
30:0:1666:C:C2'	30:0:1667:A:H5'	2.32	0.41
30:0:165:A:C2'	30:0:166:A:OP1	2.67	0.41
30:0:1679:C:O2	30:0:1685:A:C2	2.73	0.41
30:0:2057:U:O5'	30:0:2057:U:H6	2.03	0.41
30:0:2255:A:H2'	30:0:2256:G:O4'	2.20	0.41
30:0:2692:G:N2	30:0:2701:G:C5	2.88	0.41
30:0:307:G:C2	30:0:309:C:C4	3.08	0.41
31:9:60:C:O2	31:9:60:C:H2'	2.19	0.41
1:A:70:ALA:HA	1:A:71:PRO:HD3	1.82	0.41
2:B:241:PRO:HD2	38:B:9125:HOH:O	2.20	0.41
18:R:9:ASP:HA	18:R:10:PRO:HD2	1.90	0.41
19:S:52:VAL:HG22	19:S:66:VAL:HG13	2.03	0.41
23:W:122:ARG:NH2	38:0:5254:HOH:O	2.52	0.41
30:0:1012:A:H8	30:0:1012:A:O5'	2.04	0.41
30:0:1191:A:O5'	30:0:1191:A:C8	2.74	0.41
30:0:1196:C:H2'	30:0:1197:G:H5'	2.02	0.41
30:0:1438:G:N3	30:0:1438:G:H2'	2.35	0.41
30:0:1544:U:O2'	30:0:1545:C:H5'	2.20	0.41
30:0:1798:C:OP2	30:0:1799:G:H5''	2.20	0.41
21:U:42:LEU:HB3	30:0:1810:C:O4'	2.21	0.41
30:0:213:G:O2'	30:0:214:U:OP2	2.39	0.41
30:0:2325:U:C2	30:0:2326:C:C6	3.09	0.41
30:0:2383:G:C6	30:0:2384:U:C4	3.08	0.41
30:0:2668:G:N2	30:0:2669:U:C2	2.88	0.41
30:0:268:U:O4	30:0:269:G:N1	2.54	0.41
30:0:2668:G:O4'	30:0:2827:A:C2	2.73	0.41
30:0:393:G:C6	30:0:394:G:C6	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:631:A:C6	30:0:2074:A:H5'	2.56	0.41
30:0:677:C:H6	30:0:677:C:O5'	2.03	0.41
30:0:69:A:C3'	30:0:69:A:C8	3.04	0.41
30:0:812:A:H1'	38:0:3946:HOH:O	2.20	0.41
30:0:862:U:O2'	30:0:863:G:H5'	2.20	0.41
30:0:870:G:C3'	30:0:871:G:H5''	2.51	0.41
29:3:91:GLN:O	29:3:92:GLU:HB2	2.21	0.41
8:H:89:THR:O	8:H:137:PHE:HD2	2.04	0.41
21:U:17:THR:HG21	38:U:2221:HOH:O	2.21	0.41
26:Z:70:ARG:HB2	26:Z:81:CYS:HG	1.86	0.41
30:0:1173:A:H2'	30:0:1177:A:H62	1.85	0.41
30:0:1209:C:O2'	30:0:1210:G:H5'	2.20	0.41
30:0:1621:G:H2'	30:0:1622:G:H8	1.86	0.41
30:0:1774:G:C2'	30:0:1775:A:H5'	2.51	0.41
30:0:1803:C:H2'	30:0:1804:A:C8	2.56	0.41
30:0:189:A:H2	30:0:205:U:O2	2.04	0.41
30:0:1913:C:H2'	30:0:1914:C:C6	2.54	0.41
1:A:232:ARG:CZ	30:0:1939:U:H4'	2.50	0.41
30:0:1977:U:OP1	30:0:1977:U:H3'	2.20	0.41
30:0:2039:A:H2'	30:0:2040:C:C6	2.56	0.41
30:0:2324:G:H2'	30:0:2325:U:C6	2.56	0.41
30:0:241:A:C2	30:0:378:A:H4'	2.55	0.41
30:0:2700:G:H2'	30:0:2701:G:O5'	2.21	0.41
30:0:383:A:H2'	30:0:384:G:O4'	2.21	0.41
23:W:43:GLY:HA3	30:0:945:U:O2'	2.20	0.41
31:9:82:U:H2'	31:9:83:G:C8	2.56	0.41
1:A:199:HIS:HE1	30:0:1881:A:OP1	2.04	0.41
1:A:47:HIS:HD2	30:0:1654:U:O2'	2.03	0.41
2:B:195:ARG:HG2	2:B:323:LEU:HD22	2.03	0.41
4:D:20:LYS:HG2	4:D:133:ASN:HB3	2.02	0.41
8:H:91:ARG:NH1	8:H:138:THR:OG1	2.53	0.41
10:J:107:ASN:HA	10:J:108:PRO:HD2	1.98	0.41
14:N:83:LEU:HD13	14:N:175:LEU:HD23	2.03	0.41
16:P:89:ASN:HA	38:P:165:HOH:O	2.20	0.41
18:R:114:VAL:HG13	18:R:114:VAL:O	2.20	0.41
30:0:51:G:C2	30:0:111:C:C2	3.08	0.41
30:0:1193:A:C2	30:0:1194:A:N6	2.89	0.41
30:0:1089:G:H1'	30:0:1290:G:N2	2.36	0.41
30:0:1476:A:H1'	30:0:1867:G:O2'	2.21	0.41
30:0:1596:U:O2'	30:0:1598:A:N7	2.46	0.41
30:0:1973:A:C8	30:0:1973:A:H5'	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:20:G:H2'	30:0:21:G:O5'	2.21	0.41
30:0:2453:G:H2'	30:0:2454:C:C6	2.55	0.41
30:0:2599:A:C6	30:0:2600:A:N1	2.89	0.41
30:0:2695:C:N4	30:0:2701:G:N2	2.69	0.41
30:0:2801:A:C4	30:0:2802:C:C5	3.08	0.41
21:U:56:ARG:NH1	30:0:2890:A:C4	2.89	0.41
30:0:844:A:C6	30:0:882:A:C6	3.09	0.41
31:9:29:C:C6	31:9:30:C:C6	3.08	0.41
1:A:171:LYS:HB2	30:0:820:G:C6	2.55	0.41
5:E:119:HIS:O	5:E:140:ALA:HB1	2.21	0.41
5:E:145:ALA:HB1	5:E:168:ILE:CD1	2.49	0.41
5:E:20:ILE:HD12	5:E:33:LEU:HD12	2.03	0.41
6:F:61:MET:O	6:F:64:PRO:HD2	2.21	0.41
19:S:73:ASP:OD1	19:S:76:GLU:HG3	2.21	0.41
26:Z:47:ARG:HD2	38:Z:8718:HOH:O	2.20	0.41
30:0:1024:G:C5	30:0:1025:C:C4	3.09	0.41
23:W:120:PRO:HG2	30:0:1095:U:O2	2.20	0.41
30:0:1168:C:C2'	30:0:1169:U:H5'	2.51	0.41
30:0:1207:A:H5'	30:0:1208:C:OP2	2.21	0.41
30:0:1226:G:C2	30:0:1227:C:C6	3.08	0.41
30:0:1339:G:C5	30:0:1340:G:C6	3.09	0.41
30:0:1362:U:H2'	30:0:1363:G:H8	1.86	0.41
30:0:1416:G:C2'	30:0:1417:G:H5'	2.51	0.41
30:0:1543:G:H2'	30:0:1544:U:C5	2.56	0.41
30:0:1553:C:H6	30:0:1553:C:O5'	2.04	0.41
30:0:1619:G:H2'	30:0:1620:C:O4'	2.21	0.41
30:0:1748:U:C6	30:0:1749:U:C5	3.09	0.41
30:0:2366:C:P	38:0:6939:HOH:O	2.79	0.41
30:0:265:U:C4	30:0:266:G:N7	2.89	0.41
16:P:61:ARG:NH2	30:0:2737:C:OP2	2.40	0.41
30:0:279:C:H2'	30:0:280:C:H5'	2.01	0.41
30:0:61:G:C2	30:0:62:C:C2	3.09	0.41
2:B:74:ILE:HG13	38:B:9076:HOH:O	2.20	0.41
4:D:36:ASN:HA	38:D:7500:HOH:O	2.20	0.41
5:E:15:GLN:HG2	5:E:16:ASP:N	2.36	0.41
14:N:73:ALA:HB1	14:N:74:PRO:CD	2.51	0.41
17:Q:41:LEU:HB3	17:Q:52:PHE:CZ	2.56	0.41
25:Y:152:LYS:HB3	25:Y:160:LYS:HG3	2.02	0.41
30:0:1195:G:N1	30:0:1205:U:N3	2.69	0.41
30:0:1208:C:H2'	30:0:1208:C:O2	2.19	0.41
30:0:1103:C:C2	30:0:1241:G:N2	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:123:U:O2'	30:0:124:C:H5'	2.21	0.41
30:0:1591:A:H5'	30:0:1603:A:H61	1.86	0.41
30:0:1634:G:C4	30:0:1635:U:C5	3.08	0.41
30:0:2016:U:H2'	30:0:2017:U:O4'	2.21	0.41
30:0:2098:C:O5'	30:0:2098:C:H6	2.04	0.41
30:0:2269:C:C4	30:0:2270:G:C5	3.08	0.41
30:0:23:G:H1'	30:0:520:A:N6	2.35	0.41
30:0:2526:C:H5'	30:0:2526:C:C6	2.56	0.41
30:0:2617:G:H5''	38:0:3896:HOH:O	2.20	0.41
38:B:9106:HOH:O	30:0:2818:A:H2	2.04	0.41
30:0:282:C:O2	30:0:282:C:C2'	2.62	0.41
30:0:714:U:O4'	30:0:716:G:C2	2.74	0.41
30:0:736:A:H5''	38:0:4253:HOH:O	2.21	0.41
30:0:965:A:H2'	30:0:965:A:N3	2.36	0.41
31:9:110:G:H2'	31:9:110:G:N3	2.35	0.41
31:9:14:G:C5'	31:9:14:G:H8	2.13	0.41
1:A:37:VAL:HG13	38:A:9088:HOH:O	2.21	0.41
2:B:288:GLY:HA2	30:0:2898:G:H4'	2.02	0.41
5:E:81:GLU:HA	5:E:133:VAL:O	2.21	0.41
5:E:23:GLU:HG2	5:E:28:SER:CB	2.51	0.41
13:M:68:ARG:HB2	38:M:8932:HOH:O	2.19	0.41
18:R:130:MET:HG3	38:0:7551:HOH:O	2.21	0.41
23:W:132:VAL:HG21	23:W:140:LYS:O	2.21	0.41
30:0:1170:U:O2	30:0:1172:G:H8	2.04	0.40
30:0:1177:A:C6	30:0:1178:G:C5	3.09	0.40
30:0:1175:G:C5	30:0:1193:A:C2	3.10	0.40
28:2:42:TRP:HZ2	30:0:1438:G:H1'	1.87	0.40
30:0:1832:G:N3	30:0:1833:U:C6	2.89	0.40
30:0:2330:U:H4'	30:0:2331:C:OP1	2.20	0.40
30:0:2414:A:N1	30:0:2415:A:C6	2.90	0.40
6:F:38:LYS:HE3	30:0:244:C:OP2	2.21	0.40
30:0:257:G:N2	30:0:258:G:C4	2.89	0.40
30:0:2635:A:H2'	30:0:2636:C:H5'	1.98	0.40
30:0:2692:G:N2	30:0:2701:G:C4	2.88	0.40
30:0:797:A:H2'	30:0:798:G:O4'	2.21	0.40
29:3:86:GLY:HA2	38:3:9032:HOH:O	2.21	0.40
3:C:118:THR:HG21	3:C:233:THR:HB	2.03	0.40
4:D:28:GLY:CA	4:D:69:ILE:HG23	2.51	0.40
13:M:72:ALA:HB3	38:M:8950:HOH:O	2.21	0.40
13:M:75:ARG:HG3	38:M:8868:HOH:O	2.20	0.40
14:N:110:THR:HA	14:N:111:PRO:HD3	1.98	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:11:THR:CG2	30:0:1444:G:H5''	2.50	0.40
23:W:48:VAL:HG12	23:W:48:VAL:O	2.21	0.40
23:W:4:LEU:CD2	23:W:54:PHE:HB3	2.51	0.40
25:Y:125:LYS:HB2	25:Y:126:PRO:HD2	2.03	0.40
30:0:1634:G:C6	30:0:1635:U:C4	3.10	0.40
30:0:1681:G:H5''	30:0:1682:A:H5'	2.03	0.40
30:0:1774:G:H2'	30:0:1775:A:C5'	2.51	0.40
30:0:2121:G:C2'	30:0:2122:C:H5'	2.51	0.40
30:0:2245:C:O5'	30:0:2245:C:H6	2.04	0.40
30:0:2300:A:H4'	30:0:2301:A:N3	2.37	0.40
30:0:2335:C:N3	30:0:2350:G:C2	2.89	0.40
30:0:2501:G:H1	30:0:2519:C:N4	2.18	0.40
30:0:2831:C:C2'	30:0:2832:C:C5'	2.93	0.40
30:0:2834:G:C2'	30:0:2835:C:O5'	2.69	0.40
30:0:312:U:O2	30:0:320:G:C2	2.75	0.40
30:0:366:U:H2'	30:0:367:G:O4'	2.20	0.40
30:0:534:C:H2'	30:0:2083:A:C2	2.57	0.40
30:0:594:C:H2'	30:0:595:U:C6	2.56	0.40
30:0:596:C:H6	30:0:596:C:O5'	2.03	0.40
30:0:69:A:C5'	30:0:69:A:C8	2.98	0.40
30:0:962:C:H2'	30:0:963:C:H5'	2.03	0.40
3:C:206:ASN:HB2	30:0:329:A:OP2	2.20	0.40
6:F:48:VAL:CG2	6:F:74:PHE:HB3	2.51	0.40
13:M:113:ARG:NH1	13:M:155:GLN:HB2	2.36	0.40
15:O:32:ARG:HD3	15:O:32:ARG:O	2.22	0.40
24:X:26:ALA:HB3	24:X:63:ARG:HG3	2.03	0.40
30:0:1133:A:H2'	30:0:1134:G:H5'	2.03	0.40
30:0:1325:G:O2'	30:0:1326:C:H5'	2.21	0.40
30:0:1474:C:C6	30:0:1474:C:C5'	2.94	0.40
30:0:1521:C:O2'	30:0:1522:A:H5'	2.22	0.40
30:0:1613:C:C6	30:0:1613:C:H3'	2.57	0.40
30:0:2311:A:H3'	38:0:7660:HOH:O	2.20	0.40
30:0:2325:U:H5''	30:0:2417:C:O2'	2.22	0.40
30:0:238:C:H4'	30:0:287:C:OP1	2.22	0.40
30:0:2493:C:C2'	30:0:2493:C:O2	2.67	0.40
30:0:2510:C:H42	30:0:2564:G:N2	2.19	0.40
2:B:5:ARG:NH2	30:0:2548:C:OP2	2.55	0.40
30:0:249:G:O2'	30:0:266:G:H5'	2.21	0.40
30:0:462:A:H2'	38:0:4853:HOH:O	2.21	0.40
30:0:568:G:H21	30:0:590:A:H62	1.69	0.40
30:0:603:A:H4'	30:0:604:G:O5'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:822:C:H2'	30:0:823:U:H6	1.86	0.40
29:3:39:GLN:O	29:3:52:PHE:HE1	2.04	0.40
2:B:188:HIS:ND1	2:B:188:HIS:N	2.69	0.40
2:B:277:GLU:N	2:B:278:PRO:CD	2.84	0.40
6:F:50:VAL:HG11	6:F:60:VAL:HG11	2.03	0.40
13:M:46:LEU:O	13:M:50:ARG:HG3	2.21	0.40
22:V:12:THR:HG23	22:V:15:GLU:H	1.86	0.40
24:X:43:VAL:HG11	24:X:82:GLU:HA	2.04	0.40
30:0:1102:C:H5	38:0:3479:HOH:O	2.04	0.40
30:0:1159:G:C2	30:0:1209:C:N3	2.89	0.40
30:0:1520:G:C6	30:0:1521:C:N4	2.89	0.40
30:0:192:A:N6	30:0:194:A:C2	2.89	0.40
30:0:1979:G:H1'	38:0:3061:HOH:O	2.21	0.40
30:0:2102:G:N2	30:0:2103:A:N1	2.69	0.40
30:0:2532:A:OP2	30:0:2532:A:H8	2.05	0.40
30:0:2672:C:H2'	30:0:2673:U:C6	2.53	0.40
31:9:81:C:O2'	31:9:82:U:H5'	2.21	0.40
31:9:89:C:O2'	31:9:90:G:H5'	2.22	0.40
1:A:33:GLU:CD	1:A:33:GLU:N	2.75	0.40
2:B:73:VAL:HG21	2:B:284:PHE:HZ	1.86	0.40
3:C:100:LEU:HD22	30:0:751:U:H5''	2.03	0.40
4:D:14:ARG:HD3	31:9:56:A:O2'	2.22	0.40
5:E:23:GLU:HG2	5:E:28:SER:HB3	2.03	0.40
7:G:19:GLU:HG2	7:G:66:LEU:HD13	2.03	0.40
8:H:91:ARG:H	8:H:91:ARG:HG2	1.43	0.40
15:O:96:VAL:HG13	15:O:100:GLN:OE1	2.21	0.40
15:O:47:ARG:NH1	15:O:47:ARG:HG3	2.36	0.40
15:O:49:GLU:OE1	15:O:72:LYS:HG3	2.22	0.40
25:Y:132:ASP:OD1	25:Y:135:LYS:HD2	2.20	0.40
30:0:1016:U:H2'	30:0:1017:U:O4'	2.21	0.40
28:2:41:HIS:HE1	30:0:1439:C:OP1	2.05	0.40
30:0:146:U:C4	30:0:147:G:C6	3.09	0.40
30:0:1525:G:OP1	30:0:1525:G:H4'	2.21	0.40
30:0:1557:G:H2'	30:0:1558:C:C6	2.57	0.40
30:0:2004:U:H5''	30:0:2005:G:C8	2.57	0.40
30:0:2273:C:O2'	30:0:2274:A:H5'	2.22	0.40
30:0:295:C:H2'	30:0:296:G:O4'	2.22	0.40
30:0:37:A:H2'	30:0:38:G:H8	1.84	0.40
25:Y:229:LEU:O	30:0:552:A:H5''	2.22	0.40
30:0:766:A:HO2'	30:0:767:A:H8	1.68	0.40
30:0:920:C:H5'	30:0:921:G:N3	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:17:HIS:CG	30:0:2409:C:H4'	2.57	0.40
31:9:2:U:OP2	31:9:2:U:H4'	2.22	0.40
1:A:20:SER:C	1:A:22:ARG:H	2.25	0.40
2:B:201:ASP:N	2:B:312:ARG:O	2.53	0.40
3:C:104:ASP:O	3:C:108:GLN:HG3	2.22	0.40
3:C:1:MET:HG2	3:C:2:GLN:N	2.34	0.40
4:D:135:VAL:HG22	4:D:136:ARG:N	2.36	0.40
5:E:84:MET:HA	5:E:167:TYR:O	2.22	0.40
6:F:59:ILE:CD1	30:0:263:U:C2	3.04	0.40
14:N:127:LEU:HD12	14:N:127:LEU:HA	1.93	0.40
15:O:32:ARG:NE	15:O:32:ARG:HA	2.35	0.40
16:P:13:VAL:HG21	16:P:41:ARG:HG2	2.03	0.40
16:P:78:GLY:O	30:0:1813:U:H4'	2.22	0.40
20:T:26:THR:HA	20:T:39:ASN:HB3	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	235/240 (98%)	200 (85%)	30 (13%)	5 (2%)	8	36
2	B	335/338 (99%)	305 (91%)	23 (7%)	7 (2%)	8	36
3	C	244/246 (99%)	216 (88%)	26 (11%)	2 (1%)	21	61
4	D	134/177 (76%)	105 (78%)	23 (17%)	6 (4%)	3	16
5	E	170/178 (96%)	158 (93%)	11 (6%)	1 (1%)	27	67
6	F	117/120 (98%)	97 (83%)	16 (14%)	4 (3%)	4	22
7	G	25/348 (7%)	22 (88%)	3 (12%)	0	100	100
8	H	156/177 (88%)	139 (89%)	16 (10%)	1 (1%)	27	67
9	I	68/162 (42%)	49 (72%)	16 (24%)	3 (4%)	3	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	140/145 (97%)	128 (91%)	10 (7%)	2 (1%)	12	47
11	K	130/132 (98%)	120 (92%)	9 (7%)	1 (1%)	21	61
12	L	141/165 (86%)	116 (82%)	22 (16%)	3 (2%)	8	36
13	M	192/196 (98%)	171 (89%)	17 (9%)	4 (2%)	8	36
14	N	184/187 (98%)	163 (89%)	17 (9%)	4 (2%)	7	34
15	O	113/116 (97%)	106 (94%)	7 (6%)	0	100	100
16	P	141/149 (95%)	133 (94%)	8 (6%)	0	100	100
17	Q	93/96 (97%)	86 (92%)	5 (5%)	2 (2%)	7	34
18	R	148/155 (96%)	138 (93%)	9 (6%)	1 (1%)	24	64
19	S	79/85 (93%)	75 (95%)	4 (5%)	0	100	100
20	T	117/120 (98%)	108 (92%)	9 (8%)	0	100	100
21	U	51/67 (76%)	44 (86%)	6 (12%)	1 (2%)	8	37
22	V	63/71 (89%)	58 (92%)	4 (6%)	1 (2%)	11	43
23	W	152/154 (99%)	142 (93%)	9 (6%)	1 (1%)	24	64
24	X	80/92 (87%)	72 (90%)	6 (8%)	2 (2%)	6	31
25	Y	140/241 (58%)	132 (94%)	7 (5%)	1 (1%)	24	64
26	Z	71/116 (61%)	55 (78%)	12 (17%)	4 (6%)	2	11
27	1	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
28	2	42/50 (84%)	41 (98%)	1 (2%)	0	100	100
29	3	90/92 (98%)	64 (71%)	17 (19%)	9 (10%)	0	3
All	All	3705/4472 (83%)	3292 (89%)	348 (9%)	65 (2%)	9	40

All (65) Ramachandran outliers are listed below:

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

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

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

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	179/182 (98%)	170 (95%)	9 (5%)	27	65
2	B	282/283 (100%)	263 (93%)	19 (7%)	18	52
3	C	193/193 (100%)	180 (93%)	13 (7%)	18	52
4	D	117/148 (79%)	110 (94%)	7 (6%)	21	57
5	E	152/156 (97%)	146 (96%)	6 (4%)	35	73
6	F	93/94 (99%)	92 (99%)	1 (1%)	76	92
7	G	27/282 (10%)	25 (93%)	2 (7%)	15	47
8	H	134/145 (92%)	124 (92%)	10 (8%)	15	47
9	I	58/130 (45%)	57 (98%)	1 (2%)	63	88
10	J	118/121 (98%)	109 (92%)	9 (8%)	14	46
11	K	106/106 (100%)	103 (97%)	3 (3%)	47	80
12	L	113/127 (89%)	106 (94%)	7 (6%)	20	56
13	M	158/160 (99%)	147 (93%)	11 (7%)	16	50
14	N	149/150 (99%)	146 (98%)	3 (2%)	58	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	O	93/94 (99%)	93 (100%)	0	100	100
16	P	113/117 (97%)	111 (98%)	2 (2%)	62	87
17	Q	79/80 (99%)	74 (94%)	5 (6%)	20	55
18	R	117/122 (96%)	113 (97%)	4 (3%)	40	76
19	S	71/74 (96%)	70 (99%)	1 (1%)	69	90
20	T	105/106 (99%)	98 (93%)	7 (7%)	18	52
21	U	44/53 (83%)	43 (98%)	1 (2%)	53	84
22	V	51/57 (90%)	51 (100%)	0	100	100
23	W	130/130 (100%)	126 (97%)	4 (3%)	43	78
24	X	66/74 (89%)	61 (92%)	5 (8%)	14	46
25	Y	120/196 (61%)	117 (98%)	3 (2%)	50	82
26	Z	60/94 (64%)	60 (100%)	0	100	100
27	1	46/47 (98%)	46 (100%)	0	100	100
28	2	42/46 (91%)	41 (98%)	1 (2%)	52	83
29	3	79/79 (100%)	73 (92%)	6 (8%)	14	46
All	All	3095/3646 (85%)	2955 (96%)	140 (4%)	30	69

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

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

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

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

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

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

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

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

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

### 5.3.3 RNA

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

All (262) RNA backbone outliers are listed below:

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

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

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

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

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

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

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

All (24) RNA pucker outliers are listed below:

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

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

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

5 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
30	OMU	0	2587	30,35	14,22,23	0.98	1 (7%)	18,31,34	3.68	2 (11%)
30	OMG	0	2588	30	19,26,27	1.10	2 (10%)	22,38,41	2.45	4 (18%)
30	UR3	0	2619	30	13,22,23	0.74	0	15,32,35	0.66	0
30	PSU	0	2621	30	16,21,22	1.66	3 (18%)	20,30,33	5.36	4 (20%)
30	1MA	0	628	30,35	16,25,26	1.06	1 (6%)	12,37,40	1.25	1 (8%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	OMU	0	2587	30,35	-	0/5/27/28	0/2/2/2
30	OMG	0	2588	30	-	0/5/27/28	0/3/3/3
30	UR3	0	2619	30	-	0/3/25/26	0/2/2/2
30	PSU	0	2621	30	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	1MA	0	628	30,35	-	0/3/25/26	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	0	2621	PSU	C5-C1'	-5.10	1.47	1.52
30	0	2588	OMG	C8-N7	-2.09	1.30	1.34
30	0	2621	PSU	C4-N3	2.59	1.37	1.33
30	0	2621	PSU	C2-N1	2.59	1.43	1.38
30	0	2587	OMU	C4-N3	2.63	1.37	1.33
30	0	628	1MA	C6-N6	2.93	1.34	1.27
30	0	2588	OMG	C6-N1	3.60	1.39	1.33

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	0	2621	PSU	N1-C2-N3	-17.02	114.73	128.41
30	0	2588	OMG	C5-C6-N1	-8.28	111.69	123.47
30	0	2621	PSU	C5-C4-N3	-8.09	114.94	125.36
30	0	628	1MA	C2-N3-C4	-3.80	110.71	116.51
30	0	2587	OMU	C5-C4-N3	-3.72	114.53	123.17
30	0	2588	OMG	C2-N3-C4	-2.91	111.76	115.16
30	0	2588	OMG	N3-C2-N1	-2.40	123.89	127.41
30	0	2621	PSU	C6-N1-C2	2.77	119.80	115.36
30	0	2588	OMG	C6-N1-C2	6.27	125.08	116.06
30	0	2621	PSU	C4-N3-C2	14.12	127.16	115.14
30	0	2587	OMU	C4-N3-C2	15.00	127.05	114.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	237/240 (98%)	-0.60	1 (0%) 92 78	29, 65, 98, 115	0
2	B	337/338 (99%)	-0.73	0 100 100	31, 59, 87, 97	0
3	C	246/246 (100%)	-0.82	0 100 100	23, 47, 69, 80	0
4	D	140/177 (79%)	0.45	15 (10%) 6 2	74, 109, 132, 140	0
5	E	172/178 (96%)	-0.64	0 100 100	50, 74, 97, 103	0
6	F	119/120 (99%)	-0.30	1 (0%) 86 64	50, 73, 106, 113	0
7	G	29/348 (8%)	0.08	0 100 100	75, 96, 105, 109	0
8	H	160/177 (90%)	-0.49	0 100 100	48, 67, 99, 109	0
9	I	70/162 (43%)	1.80	29 (41%) 0 0	134, 152, 167, 169	0
10	J	142/145 (97%)	-0.79	1 (0%) 87 68	40, 58, 75, 97	0
11	K	132/132 (100%)	-0.87	0 100 100	39, 55, 81, 86	0
12	L	145/165 (87%)	-0.24	1 (0%) 87 68	35, 72, 113, 129	0
13	M	194/196 (98%)	-0.51	8 (4%) 37 15	31, 46, 99, 106	0
14	N	186/187 (99%)	-0.33	0 100 100	60, 80, 126, 132	0
15	O	115/116 (99%)	-0.86	0 100 100	43, 56, 74, 80	0
16	P	143/149 (95%)	-0.75	0 100 100	40, 59, 79, 85	0
17	Q	95/96 (98%)	-0.71	0 100 100	44, 56, 72, 88	0
18	R	150/155 (96%)	-0.83	0 100 100	33, 49, 70, 83	0
19	S	81/85 (95%)	-0.67	1 (1%) 79 53	40, 62, 82, 92	0
20	T	119/120 (99%)	-0.55	0 100 100	40, 59, 87, 116	0
21	U	53/67 (79%)	2.66	32 (60%) 0 0	107, 117, 125, 126	0
22	V	65/71 (91%)	-0.02	4 (6%) 20 7	47, 74, 118, 123	0
23	W	154/154 (100%)	-0.69	0 100 100	39, 54, 73, 87	0
24	X	82/92 (89%)	-0.45	1 (1%) 79 53	46, 65, 94, 108	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
25	Y	142/241 (58%)	-0.88	0 100 100	30, 49, 71, 92	0
26	Z	73/116 (62%)	3.62	45 (61%) 0 0	98, 116, 126, 130	0
27	1	56/57 (98%)	-0.78	0 100 100	28, 36, 43, 48	0
28	2	46/50 (92%)	-0.57	1 (2%) 62 33	31, 66, 97, 104	0
29	3	92/92 (100%)	4.21	71 (77%) 0 0	104, 119, 130, 134	0
30	0	2749/2923 (94%)	-0.83	2 (0%) 95 89	23, 51, 96, 175	0
31	9	122/122 (100%)	-0.97	1 (0%) 86 64	45, 75, 103, 154	0
All	All	6646/7517 (88%)	-0.53	214 (3%) 47 20	23, 57, 116, 175	0

All (214) RSRZ outliers are listed below:

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

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

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

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

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

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

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
30	OMG	0	2588	24/25	0.98	0.13	39,41,42,45	0
30	UR3	0	2619	21/22	0.98	0.14	39,43,45,48	0
30	1MA	0	628	23/24	0.98	0.14	31,36,38,38	0
30	PSU	0	2621	20/21	0.98	0.18	40,43,44,44	0
30	OMU	0	2587	21/22	0.98	0.12	41,44,50,50	0

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

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

median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
34	SR	0	9006	1/1	0.31	0.83	180,180,180,180	0
35	NA	0	8557	1/1	0.41	0.08	59,59,59,59	0
34	SR	0	9004	1/1	0.44	1.01	200,200,200,200	0
34	SR	0	8985	1/1	0.45	0.12	182,182,182,182	0
35	NA	0	8567	1/1	0.50	0.30	68,68,68,68	0
35	NA	0	8563	1/1	0.53	0.68	65,65,65,65	0
34	SR	0	8971	1/1	0.54	0.11	170,170,170,170	0
34	SR	0	8997	1/1	0.54	0.83	194,194,194,194	0
33	CL	J	8802	1/1	0.54	0.08	76,76,76,76	0
34	SR	0	9001	1/1	0.55	0.08	166,166,166,166	0
34	SR	0	8959	1/1	0.56	0.28	200,200,200,200	0
34	SR	0	8974	1/1	0.57	0.14	164,164,164,164	0
34	SR	0	8957	1/1	0.57	0.73	200,200,200,200	0
34	SR	0	8979	1/1	0.61	0.18	198,198,198,198	0
35	NA	0	8553	1/1	0.62	0.33	70,70,70,70	0
35	NA	0	8528	1/1	0.63	0.91	83,83,83,83	0
34	SR	0	8986	1/1	0.63	0.45	200,200,200,200	0
34	SR	0	8975	1/1	0.64	0.11	171,171,171,171	0
34	SR	0	8962	1/1	0.67	0.08	179,179,179,179	0
34	SR	0	8977	1/1	0.72	0.11	181,181,181,181	0
32	MG	0	8091	1/1	0.73	0.07	58,58,58,58	0
37	CD	U	8701	1/1	0.74	0.35	200,200,200,200	0
34	SR	0	8998	1/1	0.75	0.30	184,184,184,184	0
34	SR	0	8922	1/1	0.75	0.29	169,169,169,169	0
34	SR	9	8980	1/1	0.75	0.14	182,182,182,182	0
36	K	0	8401	1/1	0.75	0.15	156,156,156,156	0
34	SR	0	8919	1/1	0.76	0.32	200,200,200,200	0
34	SR	0	8960	1/1	0.76	0.05	152,152,152,152	0
34	SR	0	8982	1/1	0.78	1.88	200,200,200,200	0
33	CL	0	8814	1/1	0.78	0.18	72,72,72,72	0
34	SR	0	8969	1/1	0.78	0.31	192,192,192,192	0
32	MG	0	8063	1/1	0.78	0.22	86,86,86,86	0
35	NA	0	8518	1/1	0.79	0.26	75,75,75,75	0
35	NA	0	8559	1/1	0.79	0.46	122,122,122,122	0
34	SR	0	8973	1/1	0.80	0.14	112,112,112,112	0
34	SR	0	8944	1/1	0.80	0.08	165,165,165,165	0
34	SR	0	8967	1/1	0.81	0.05	133,133,133,133	0
35	NA	0	8566	1/1	0.81	0.32	62,62,62,62	0
34	SR	0	8988	1/1	0.81	0.13	170,170,170,170	0
35	NA	0	8571	1/1	0.82	0.17	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
34	SR	0	9007	1/1	0.82	0.24	179,179,179,179	0
35	NA	0	8556	1/1	0.82	0.44	63,63,63,63	0
34	SR	0	8968	1/1	0.82	0.15	177,177,177,177	0
34	SR	3	8932	1/1	0.82	0.09	158,158,158,158	0
35	NA	9	8572	1/1	0.82	0.17	71,71,71,71	0
35	NA	0	8573	1/1	0.82	0.28	55,55,55,55	0
34	SR	0	8947	1/1	0.83	0.30	194,194,194,194	0
35	NA	0	8535	1/1	0.83	0.20	64,64,64,64	0
32	MG	A	8051	1/1	0.83	0.22	101,101,101,101	0
34	SR	0	8931	1/1	0.83	0.07	110,110,110,110	0
33	CL	0	8815	1/1	0.83	0.09	87,87,87,87	0
35	NA	0	8541	1/1	0.83	0.24	54,54,54,54	0
34	SR	0	9002	1/1	0.83	0.06	157,157,157,157	0
34	SR	0	8946	1/1	0.85	0.12	123,123,123,123	0
34	SR	0	8955	1/1	0.85	0.17	200,200,200,200	0
35	NA	0	8548	1/1	0.85	0.12	68,68,68,68	0
35	NA	0	8515	1/1	0.86	0.15	44,44,44,44	0
32	MG	0	8081	1/1	0.86	0.32	80,80,80,80	0
35	NA	0	8564	1/1	0.86	0.34	57,57,57,57	0
35	NA	0	8546	1/1	0.86	0.47	80,80,80,80	0
34	SR	A	8993	1/1	0.86	0.08	159,159,159,159	0
37	CD	Z	8703	1/1	0.86	0.28	200,200,200,200	0
35	NA	0	8507	1/1	0.86	0.16	32,32,32,32	0
34	SR	0	8989	1/1	0.86	0.18	200,200,200,200	0
32	MG	2	8060	1/1	0.86	0.10	35,35,35,35	0
35	NA	0	8525	1/1	0.87	0.25	85,85,85,85	0
32	MG	0	8093	1/1	0.87	0.05	28,28,28,28	0
34	SR	B	8987	1/1	0.87	0.39	200,200,200,200	0
34	SR	0	8953	1/1	0.88	0.07	200,200,200,200	0
35	NA	0	8562	1/1	0.88	0.53	89,89,89,89	0
35	NA	0	8530	1/1	0.88	0.37	49,49,49,49	0
34	SR	0	8942	1/1	0.88	0.07	130,130,130,130	0
34	SR	0	8915	1/1	0.88	0.07	118,118,118,118	0
34	SR	0	8964	1/1	0.88	0.08	129,129,129,129	0
34	SR	0	8939	1/1	0.88	0.08	152,152,152,152	0
35	NA	0	8545	1/1	0.88	0.24	33,33,33,33	0
34	SR	0	8991	1/1	0.88	0.35	193,193,193,193	0
33	CL	3	8804	1/1	0.89	0.19	120,120,120,120	0
32	MG	0	8071	1/1	0.89	0.13	31,31,31,31	0
37	CD	3	8704	1/1	0.89	0.71	200,200,200,200	0
35	NA	0	8570	1/1	0.89	0.07	25,25,25,25	0
34	SR	0	8928	1/1	0.89	0.09	146,146,146,146	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
35	NA	0	8549	1/1	0.90	0.17	77,77,77,77	0
32	MG	0	8047	1/1	0.90	0.15	67,67,67,67	0
34	SR	0	8976	1/1	0.90	0.23	197,197,197,197	0
35	NA	0	8522	1/1	0.90	0.21	45,45,45,45	0
32	MG	B	8042	1/1	0.90	0.08	56,56,56,56	0
32	MG	0	8036	1/1	0.90	0.05	37,37,37,37	0
32	MG	0	8069	1/1	0.90	0.19	55,55,55,55	0
35	NA	0	8552	1/1	0.90	0.26	58,58,58,58	0
34	SR	0	8981	1/1	0.91	0.13	157,157,157,157	0
32	MG	0	8052	1/1	0.91	0.04	51,51,51,51	0
35	NA	0	8505	1/1	0.91	1.13	53,53,53,53	0
34	SR	0	8965	1/1	0.91	0.07	127,127,127,127	0
34	SR	9	9003	1/1	0.91	0.09	177,177,177,177	0
34	SR	0	8956	1/1	0.91	0.05	151,151,151,151	0
32	MG	0	8032	1/1	0.91	0.05	27,27,27,27	0
32	MG	0	8050	1/1	0.91	0.08	52,52,52,52	0
34	SR	3	8999	1/1	0.91	0.28	172,172,172,172	0
32	MG	0	8075	1/1	0.92	0.09	83,83,83,83	0
34	SR	F	9005	1/1	0.92	0.09	131,131,131,131	0
32	MG	0	8049	1/1	0.92	0.38	74,74,74,74	0
35	NA	0	8565	1/1	0.92	0.94	70,70,70,70	0
34	SR	0	8984	1/1	0.92	0.07	105,105,105,105	0
35	NA	0	8509	1/1	0.92	0.14	54,54,54,54	0
34	SR	0	9000	1/1	0.92	0.31	200,200,200,200	0
32	MG	0	8068	1/1	0.92	0.11	49,49,49,49	0
32	MG	K	8054	1/1	0.92	0.15	40,40,40,40	0
32	MG	0	8046	1/1	0.92	0.13	26,26,26,26	0
35	NA	0	8519	1/1	0.92	0.27	51,51,51,51	0
34	SR	0	8937	1/1	0.93	0.17	100,100,100,100	0
32	MG	0	8016	1/1	0.93	0.22	48,48,48,48	0
32	MG	0	8010	1/1	0.93	0.17	24,24,24,24	0
34	SR	0	8994	1/1	0.93	0.24	200,200,200,200	0
35	NA	0	8511	1/1	0.93	0.09	48,48,48,48	0
33	CL	L	8810	1/1	0.93	0.10	64,64,64,64	0
35	NA	0	8521	1/1	0.93	0.20	53,53,53,53	0
32	MG	0	8039	1/1	0.94	0.18	71,71,71,71	0
35	NA	0	8547	1/1	0.94	0.67	47,47,47,47	0
33	CL	J	8821	1/1	0.94	0.11	66,66,66,66	0
35	NA	0	8560	1/1	0.94	0.76	74,74,74,74	0
34	SR	0	8970	1/1	0.94	0.04	131,131,131,131	0
35	NA	J	8538	1/1	0.94	0.08	49,49,49,49	0
34	SR	0	8910	1/1	0.94	0.08	99,99,99,99	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
32	MG	0	8037	1/1	0.94	0.17	76,76,76,76	0
32	MG	0	8088	1/1	0.94	0.16	35,35,35,35	0
32	MG	0	8033	1/1	0.94	0.13	40,40,40,40	0
35	NA	0	8544	1/1	0.94	0.11	41,41,41,41	0
33	CL	N	8807	1/1	0.94	0.35	99,99,99,99	0
35	NA	R	8532	1/1	0.94	0.14	37,37,37,37	0
34	SR	0	8916	1/1	0.94	0.10	114,114,114,114	0
33	CL	Y	8820	1/1	0.94	0.11	47,47,47,47	0
34	SR	0	8927	1/1	0.94	0.20	196,196,196,196	0
35	NA	0	8506	1/1	0.95	0.51	58,58,58,58	0
35	NA	0	8526	1/1	0.95	0.13	33,33,33,33	0
34	SR	0	8983	1/1	0.95	0.27	191,191,191,191	0
33	CL	K	8812	1/1	0.95	0.07	48,48,48,48	0
34	SR	0	8914	1/1	0.95	0.20	105,105,105,105	0
35	NA	0	8508	1/1	0.95	0.56	61,61,61,61	0
32	MG	0	8082	1/1	0.95	0.12	66,66,66,66	0
32	MG	0	8065	1/1	0.95	0.12	50,50,50,50	0
33	CL	0	8803	1/1	0.95	0.14	69,69,69,69	0
33	CL	R	8806	1/1	0.95	0.11	47,47,47,47	0
32	MG	0	8062	1/1	0.95	0.20	57,57,57,57	0
35	NA	0	8504	1/1	0.95	0.09	27,27,27,27	0
34	SR	0	8945	1/1	0.95	0.06	107,107,107,107	0
32	MG	0	8080	1/1	0.95	0.28	68,68,68,68	0
33	CL	0	8822	1/1	0.95	0.60	97,97,97,97	0
35	NA	0	8501	1/1	0.96	0.14	43,43,43,43	0
35	NA	0	8561	1/1	0.96	0.36	57,57,57,57	0
35	NA	0	8554	1/1	0.96	0.55	65,65,65,65	0
35	NA	Q	8540	1/1	0.96	0.11	67,67,67,67	0
32	MG	0	8004	1/1	0.96	0.18	21,21,21,21	0
33	CL	0	8817	1/1	0.96	0.20	69,69,69,69	0
33	CL	0	8816	1/1	0.96	0.39	94,94,94,94	0
34	SR	0	8917	1/1	0.96	0.10	109,109,109,109	0
32	MG	B	8043	1/1	0.96	0.11	53,53,53,53	0
34	SR	0	8972	1/1	0.96	0.10	150,150,150,150	0
34	SR	0	8943	1/1	0.96	0.09	72,72,72,72	0
35	NA	S	8510	1/1	0.96	0.04	26,26,26,26	0
35	NA	0	8527	1/1	0.96	0.15	54,54,54,54	0
32	MG	0	8041	1/1	0.96	0.31	36,36,36,36	0
34	SR	0	8990	1/1	0.96	0.15	125,125,125,125	0
35	NA	0	8513	1/1	0.96	0.34	66,66,66,66	0
35	NA	0	8533	1/1	0.96	0.08	53,53,53,53	0
33	CL	J	8801	1/1	0.96	0.13	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
34	SR	0	8996	1/1	0.96	0.22	199,199,199,199	0
32	MG	3	8090	1/1	0.96	0.12	80,80,80,80	0
35	NA	M	8539	1/1	0.96	0.09	32,32,32,32	0
35	NA	0	8574	1/1	0.96	0.35	54,54,54,54	0
35	NA	0	8516	1/1	0.96	0.08	20,20,20,20	0
32	MG	0	8035	1/1	0.96	0.10	61,61,61,61	0
32	MG	0	8040	1/1	0.96	0.21	54,54,54,54	0
34	SR	A	8929	1/1	0.96	0.04	117,117,117,117	0
34	SR	0	8948	1/1	0.97	0.08	103,103,103,103	0
35	NA	0	8536	1/1	0.97	0.06	40,40,40,40	0
32	MG	0	8020	1/1	0.97	0.14	29,29,29,29	0
34	SR	0	8995	1/1	0.97	0.14	140,140,140,140	0
32	MG	0	8055	1/1	0.97	0.10	45,45,45,45	0
32	MG	0	8089	1/1	0.97	0.17	59,59,59,59	0
35	NA	0	8550	1/1	0.97	0.27	47,47,47,47	0
32	MG	0	8029	1/1	0.97	0.07	68,68,68,68	0
32	MG	0	8025	1/1	0.97	0.10	30,30,30,30	0
34	SR	0	8924	1/1	0.97	0.17	133,133,133,133	0
32	MG	0	8064	1/1	0.97	0.06	33,33,33,33	0
32	MG	Y	8086	1/1	0.97	0.06	37,37,37,37	0
33	CL	A	8809	1/1	0.97	0.35	100,100,100,100	0
32	MG	T	8057	1/1	0.97	0.04	63,63,63,63	0
34	SR	0	8920	1/1	0.97	0.05	106,106,106,106	0
35	NA	0	8529	1/1	0.97	0.18	41,41,41,41	0
35	NA	0	8534	1/1	0.97	0.18	37,37,37,37	0
32	MG	0	8083	1/1	0.97	0.12	71,71,71,71	0
32	MG	0	8027	1/1	0.97	0.12	26,26,26,26	0
32	MG	0	8067	1/1	0.98	0.13	32,32,32,32	0
32	MG	0	8021	1/1	0.98	0.11	25,25,25,25	0
34	SR	0	8940	1/1	0.98	0.11	77,77,77,77	0
34	SR	0	8963	1/1	0.98	0.05	123,123,123,123	0
32	MG	0	8078	1/1	0.98	0.23	51,51,51,51	0
34	SR	0	8926	1/1	0.98	0.09	109,109,109,109	0
34	SR	S	8961	1/1	0.98	0.05	126,126,126,126	0
32	MG	0	8002	1/1	0.98	0.08	29,29,29,29	0
35	NA	0	8555	1/1	0.98	0.34	50,50,50,50	0
32	MG	0	8018	1/1	0.98	0.14	34,34,34,34	0
32	MG	0	8092	1/1	0.98	0.02	44,44,44,44	0
32	MG	0	8005	1/1	0.98	0.22	34,34,34,34	0
35	NA	R	8575	1/1	0.98	0.34	89,89,89,89	0
32	MG	0	8024	1/1	0.98	0.12	96,96,96,96	0
35	NA	0	8551	1/1	0.98	0.15	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
34	SR	0	8908	1/1	0.98	0.13	77,77,77,77	0
32	MG	0	8053	1/1	0.98	0.05	45,45,45,45	0
32	MG	0	8014	1/1	0.98	0.19	21,21,21,21	0
32	MG	0	8009	1/1	0.98	0.21	24,24,24,24	0
32	MG	0	8087	1/1	0.98	0.09	26,26,26,26	0
34	SR	0	8936	1/1	0.98	0.08	87,87,87,87	0
32	MG	0	8034	1/1	0.98	0.13	53,53,53,53	0
34	SR	0	8901	1/1	0.98	0.14	63,63,63,63	0
32	MG	0	8006	1/1	0.98	0.13	20,20,20,20	0
34	SR	B	8950	1/1	0.98	0.16	113,113,113,113	0
34	SR	0	8958	1/1	0.98	0.07	114,114,114,114	0
34	SR	0	8921	1/1	0.98	0.09	75,75,75,75	0
37	CD	O	8705	1/1	0.98	0.08	93,93,93,93	0
34	SR	0	8923	1/1	0.98	0.12	85,85,85,85	0
36	K	M	8402	1/1	0.98	0.11	60,60,60,60	0
34	SR	0	8992	1/1	0.98	0.08	130,130,130,130	0
35	NA	0	8568	1/1	0.98	0.10	38,38,38,38	0
34	SR	0	8951	1/1	0.98	0.09	139,139,139,139	0
34	SR	0	8938	1/1	0.98	0.07	164,164,164,164	0
34	SR	0	8941	1/1	0.98	0.18	122,122,122,122	0
32	MG	0	8073	1/1	0.98	0.06	51,51,51,51	0
35	NA	0	8542	1/1	0.98	0.16	51,51,51,51	0
34	SR	0	8935	1/1	0.98	0.09	87,87,87,87	0
35	NA	0	8520	1/1	0.98	0.10	39,39,39,39	0
35	NA	0	8558	1/1	0.98	0.22	44,44,44,44	0
32	MG	0	8023	1/1	0.98	0.18	24,24,24,24	0
34	SR	0	8911	1/1	0.98	0.06	79,79,79,79	0
32	MG	0	8017	1/1	0.98	0.10	20,20,20,20	0
32	MG	0	8066	1/1	0.98	0.31	75,75,75,75	0
34	SR	0	8909	1/1	0.98	0.13	89,89,89,89	0
34	SR	0	8918	1/1	0.99	0.09	71,71,71,71	0
32	MG	0	8019	1/1	0.99	0.15	23,23,23,23	0
32	MG	0	8038	1/1	0.99	0.05	61,61,61,61	0
32	MG	0	8084	1/1	0.99	0.14	24,24,24,24	0
32	MG	0	8072	1/1	0.99	0.08	47,47,47,47	0
32	MG	0	8030	1/1	0.99	0.34	86,86,86,86	0
32	MG	0	8070	1/1	0.99	0.10	40,40,40,40	0
32	MG	0	8077	1/1	0.99	0.10	43,43,43,43	0
32	MG	0	8045	1/1	0.99	0.10	24,24,24,24	0
32	MG	0	8044	1/1	0.99	0.14	52,52,52,52	0
35	NA	0	8512	1/1	0.99	0.08	36,36,36,36	0
32	MG	0	8056	1/1	0.99	0.08	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
34	SR	0	8905	1/1	0.99	0.23	62,62,62,62	0
32	MG	0	8085	1/1	0.99	0.12	67,67,67,67	0
34	SR	0	9008	1/1	0.99	0.17	97,97,97,97	0
32	MG	0	8012	1/1	0.99	0.14	15,15,15,15	0
34	SR	0	8902	1/1	0.99	0.16	67,67,67,67	0
34	SR	0	8966	1/1	0.99	0.07	97,97,97,97	0
32	MG	0	8061	1/1	0.99	0.18	19,19,19,19	0
35	NA	0	8524	1/1	0.99	0.40	54,54,54,54	0
32	MG	0	8048	1/1	0.99	0.21	20,20,20,20	0
32	MG	0	8058	1/1	0.99	0.06	22,22,22,22	0
33	CL	B	8819	1/1	0.99	0.15	59,59,59,59	0
33	CL	M	8818	1/1	0.99	0.05	39,39,39,39	0
33	CL	0	8813	1/1	0.99	0.03	46,46,46,46	0
34	SR	A	8930	1/1	0.99	0.07	125,125,125,125	0
32	MG	0	8013	1/1	0.99	0.04	24,24,24,24	0
32	MG	0	8031	1/1	0.99	0.23	52,52,52,52	0
32	MG	0	8001	1/1	0.99	0.12	26,26,26,26	0
32	MG	0	8079	1/1	0.99	0.11	36,36,36,36	0
35	NA	0	8502	1/1	0.99	0.05	56,56,56,56	0
34	SR	0	8934	1/1	0.99	0.09	99,99,99,99	0
34	SR	1	8913	1/1	0.99	0.11	100,100,100,100	0
32	MG	0	8022	1/1	0.99	0.12	17,17,17,17	0
35	NA	0	8569	1/1	0.99	0.20	67,67,67,67	0
32	MG	0	8003	1/1	0.99	0.17	22,22,22,22	0
35	NA	0	8517	1/1	0.99	0.15	21,21,21,21	0
32	MG	0	8015	1/1	0.99	0.13	25,25,25,25	0
34	SR	0	8933	1/1	0.99	0.07	126,126,126,126	0
35	NA	0	8523	1/1	0.99	0.11	51,51,51,51	0
34	SR	0	8949	1/1	0.99	0.05	102,102,102,102	0
35	NA	0	8514	1/1	0.99	0.19	17,17,17,17	0
32	MG	9	8074	1/1	0.99	0.05	63,63,63,63	0
35	NA	9	8543	1/1	0.99	0.11	38,38,38,38	0
33	CL	0	8811	1/1	0.99	0.38	79,79,79,79	0
35	NA	C	8503	1/1	0.99	0.17	45,45,45,45	0
32	MG	0	8008	1/1	0.99	0.14	26,26,26,26	0
33	CL	O	8808	1/1	0.99	0.11	87,87,87,87	0
32	MG	0	8076	1/1	0.99	0.11	27,27,27,27	0
32	MG	0	8059	1/1	0.99	0.12	53,53,53,53	0
35	NA	0	8531	1/1	0.99	0.10	15,15,15,15	0
33	CL	0	8805	1/1	0.99	0.14	70,70,70,70	0
34	SR	0	8925	1/1	0.99	0.15	94,94,94,94	0
34	SR	0	8906	1/1	1.00	0.20	64,64,64,64	0

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

## 6.5 Other polymers [i](#)

There are no such residues in this entry.