



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:56 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

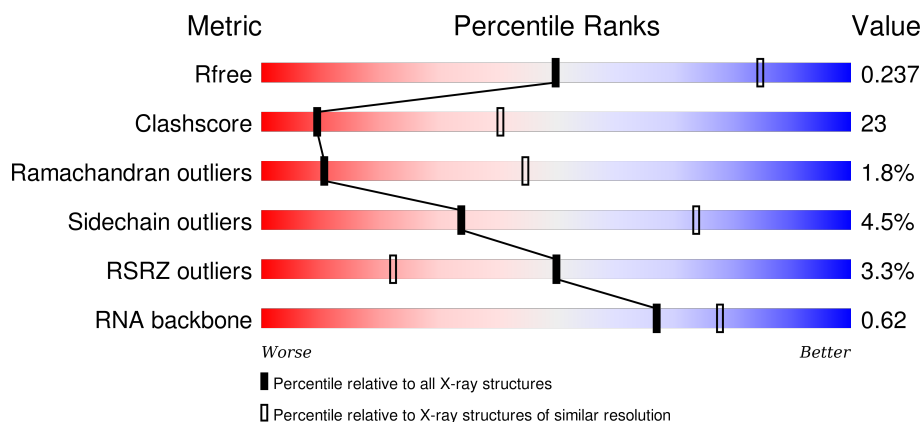
1 Overall quality at a glance

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}	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)
RNA backbone	2183	1036 (3.40-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	<div> <div>62%</div> <div>33%</div> <div>..</div> </div>
2	B	338	<div> <div>58%</div> <div>37%</div> <div>.</div> </div>
3	C	246	<div> <div>68%</div> <div>27%</div> <div>5%</div> </div>
4	D	177	<div> <div>9%</div> <div>42%</div> <div>35%</div> <div>..</div> <div>21%</div> </div>

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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
32	MG	0	8009	-	-	-	X
32	MG	0	8011	-	-	-	X
32	MG	0	8014	-	-	-	X
32	MG	0	8016	-	-	-	X
32	MG	0	8044	-	-	-	X
32	MG	A	8051	-	-	-	X
34	NA	0	8513	-	-	-	X
34	NA	0	8519	-	-	-	X
34	NA	0	8521	-	-	-	X
34	NA	0	8522	-	-	-	X
34	NA	0	8528	-	-	-	X
34	NA	0	8530	-	-	-	X
34	NA	0	8535	-	-	-	X
34	NA	0	8545	-	-	-	X
34	NA	0	8546	-	-	-	X
34	NA	0	8550	-	-	-	X
34	NA	0	8552	-	-	-	X
34	NA	0	8553	-	-	-	X
34	NA	0	8555	-	-	-	X
34	NA	0	8556	-	-	-	X
34	NA	0	8558	-	-	-	X
34	NA	0	8559	-	-	-	X
34	NA	0	8560	-	-	-	X
34	NA	0	8562	-	-	-	X
34	NA	0	8564	-	-	-	X
34	NA	0	8567	-	-	-	X
34	NA	0	8569	-	-	-	X
34	NA	0	8571	-	-	-	X
34	NA	R	8575	-	-	-	X
35	CL	0	8805	-	-	-	X
35	CL	0	8811	-	-	-	X
35	CL	0	8816	-	-	-	X
35	CL	3	8804	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	CL	B	8819	-	-	X	-
35	CL	M	8818	-	-	X	-
36	SR	0	8904	-	-	-	X
36	SR	0	8947	-	-	-	X
36	SR	0	8957	-	-	-	X
36	SR	0	8969	-	-	-	X
36	SR	B	8987	-	-	-	X
37	CD	3	8704	-	-	-	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	S	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	Y	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	9	1	Total	Mg	0	0
			1	1		
32	3	1	Total	Mg	0	0
			1	1		

- Molecule 33 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
33	0	1	Total K 1 1	0	0
33	M	1	Total K 1 1	0	0

- Molecule 34 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
34	0	66	Total Na 66 66	0	0
34	J	1	Total Na 1 1	0	0
34	Q	1	Total Na 1 1	0	0
34	C	1	Total Na 1 1	0	0
34	R	2	Total Na 2 2	0	0
34	9	2	Total Na 2 2	0	0
34	S	1	Total Na 1 1	0	0
34	M	1	Total Na 1 1	0	0

- Molecule 35 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

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

- Molecule 36 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
36	0	93	Total Sr 93 93	0	0
36	1	2	Total Sr 2 2	0	0
36	B	2	Total Sr 2 2	0	0
36	3	2	Total Sr 2 2	0	0
36	A	3	Total Sr 3 3	0	0
36	R	1	Total Sr 1 1	0	0
36	9	3	Total Sr 3 3	0	0
36	S	1	Total Sr 1 1	0	0
36	F	1	Total Sr 1 1	0	0

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

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

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

- Molecule 38 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	0	5897	Total 5897	O 5897	0	0
38	9	154	Total 154	O 154	0	0
38	A	121	Total 121	O 121	0	0
38	B	145	Total 145	O 145	0	0
38	C	166	Total 166	O 166	0	0
38	D	46	Total 46	O 46	0	0
38	E	43	Total 43	O 43	0	0
38	F	31	Total 31	O 31	0	0
38	G	17	Total 17	O 17	0	0
38	H	72	Total 72	O 72	0	0
38	I	5	Total 5	O 5	0	0
38	J	52	Total 52	O 52	0	0
38	K	52	Total 52	O 52	0	0
38	L	81	Total 81	O 81	0	0
38	M	133	Total 133	O 133	0	0
38	N	56	Total 56	O 56	0	0
38	O	41	Total 41	O 41	0	0

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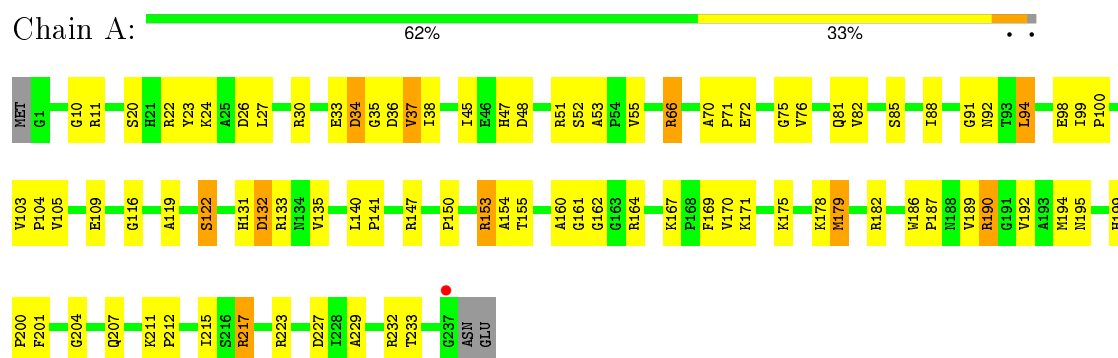
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	P	63	Total 63	O 63	0	0
38	Q	52	Total 52	O 52	0	0
38	R	75	Total 75	O 75	0	0
38	S	37	Total 37	O 37	0	0
38	T	40	Total 40	O 40	0	0
38	U	28	Total 28	O 28	0	0
38	V	15	Total 15	O 15	0	0
38	W	69	Total 69	O 69	0	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

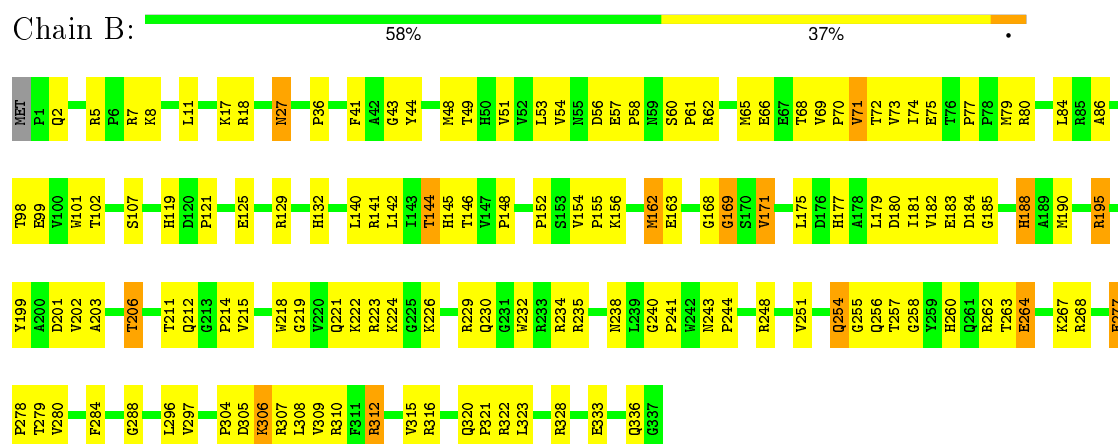
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

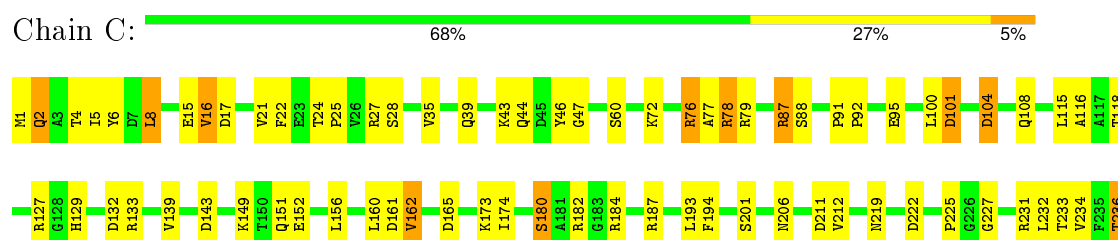
• Molecule 1: 50S ribosomal protein L2P



• Molecule 2: 50S ribosomal protein L3P

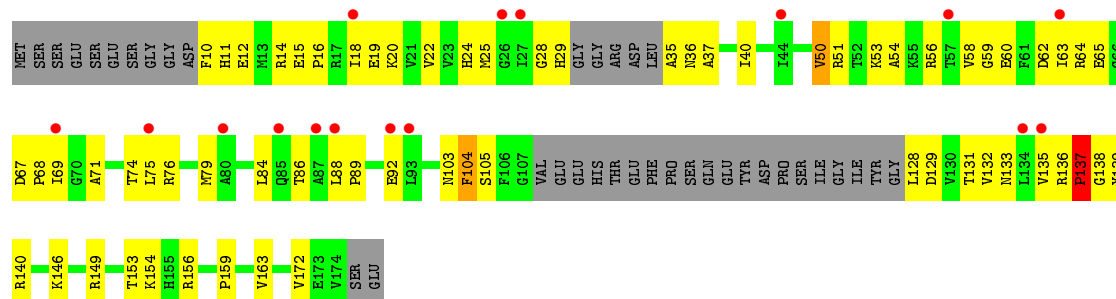
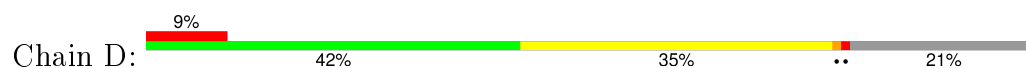


• Molecule 3: 50S ribosomal protein L4P

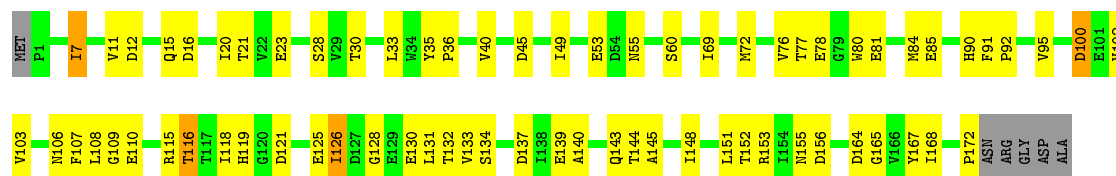




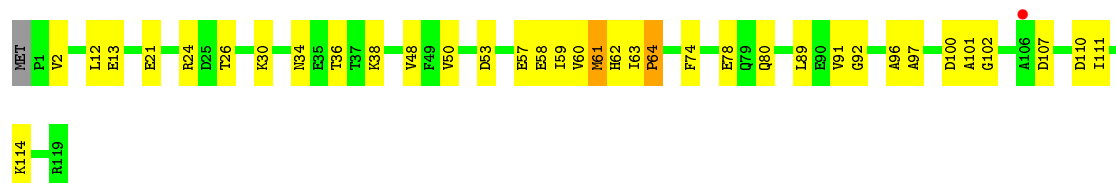
- Molecule 4: 50S ribosomal protein L5P



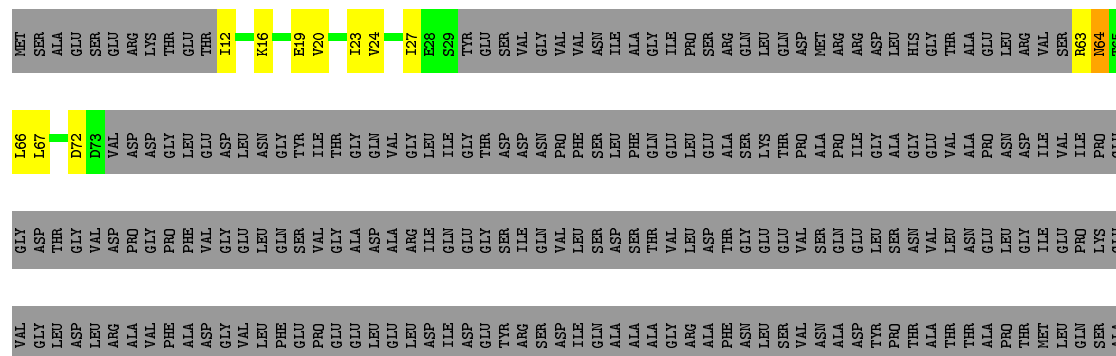
- Molecule 5: 50S ribosomal protein L6P

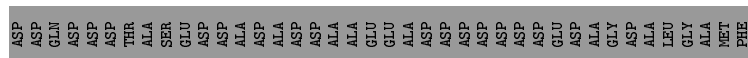


- Molecule 6: 50S ribosomal protein L7Ae

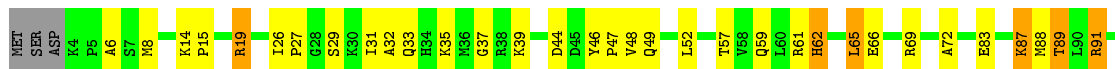


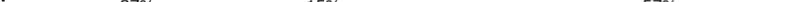
- Molecule 7: 50S ribosomal protein L10E

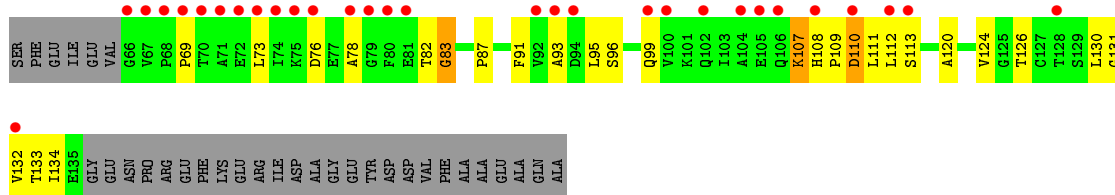
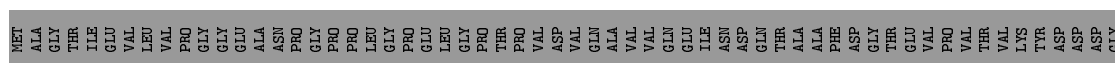


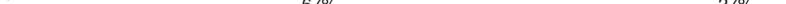


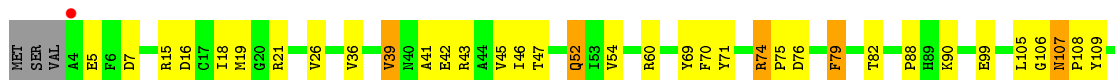
Chain H: 57% 28% 5% 10%

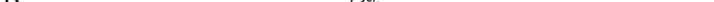


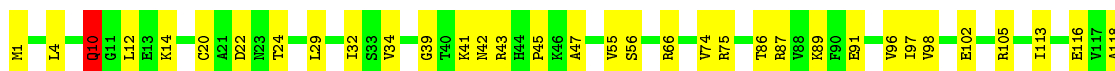
Chain I: 

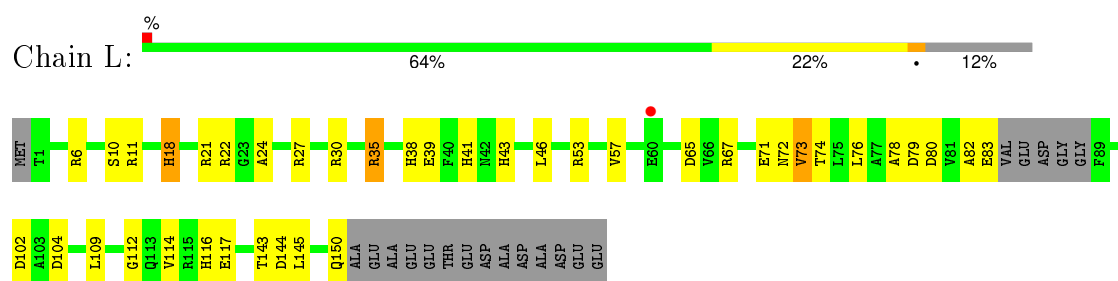


Chain J:  67% 27% . .

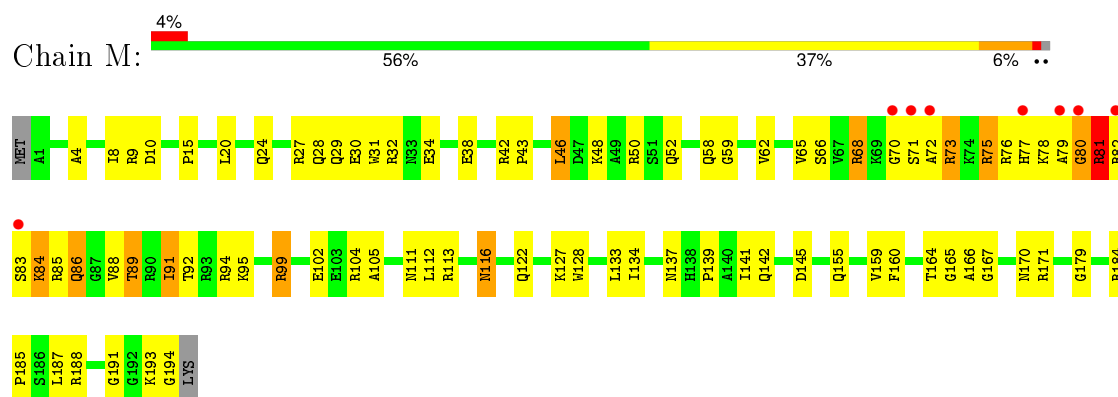


Chain K:  72% 27%

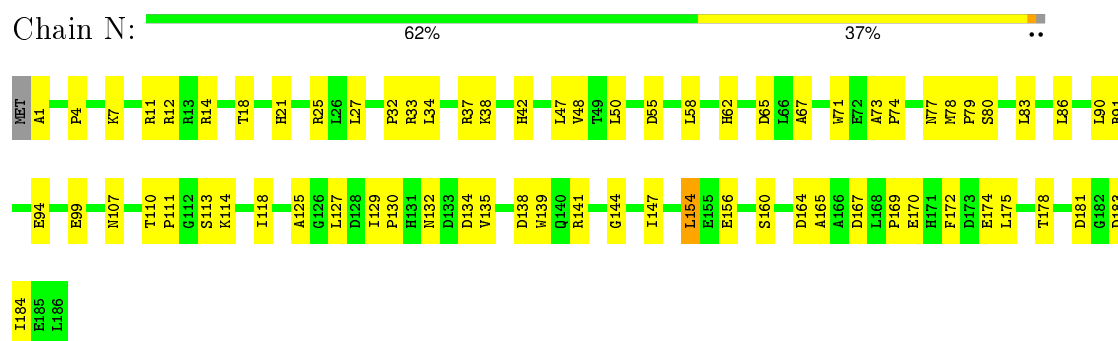




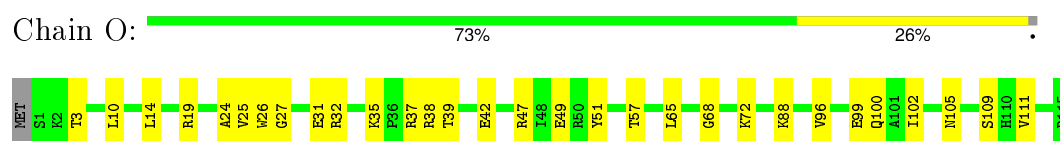
- Molecule 13: 50S ribosomal protein L15e



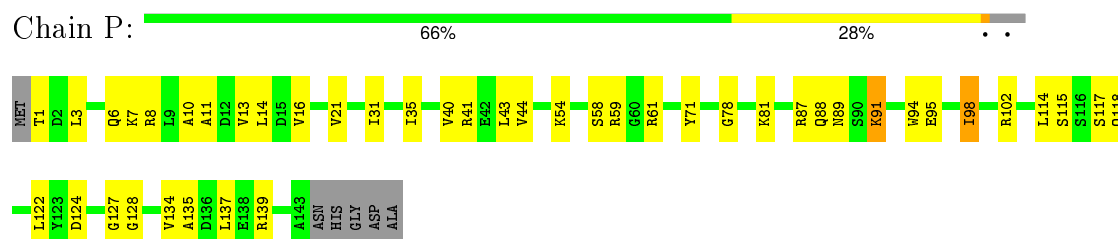
- Molecule 14: 50S ribosomal protein L18P



- Molecule 15: 50S ribosomal protein L18e



- Molecule 16: 50S ribosomal protein L19e



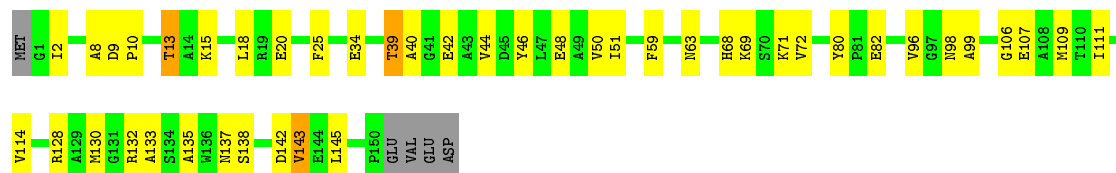
- Molecule 17: 50S ribosomal protein L21e

Chain Q:  69% 27% ..



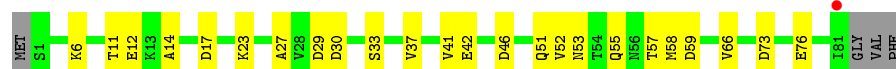
- Molecule 18: 50S ribosomal protein L22P

Chain R:  68% 26% . .



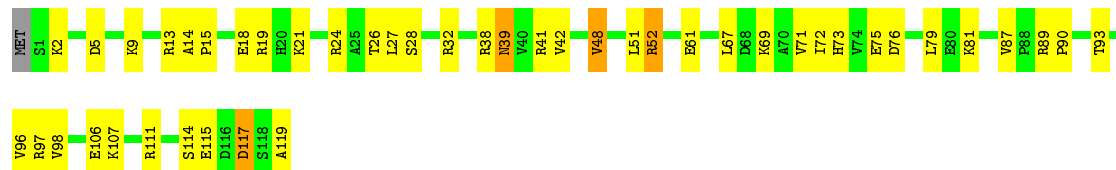
- Molecule 19: 50S ribosomal protein L23P

Chain S:  67% 28% 5%




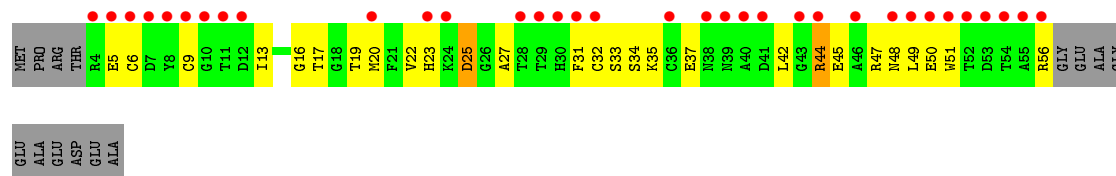
- Molecule 20: 50S ribosomal protein L24P

Chain T:  62% 34% ..



- Molecule 21: 50S ribosomal protein L24e

Chain U:  39% 51% 37% 21%

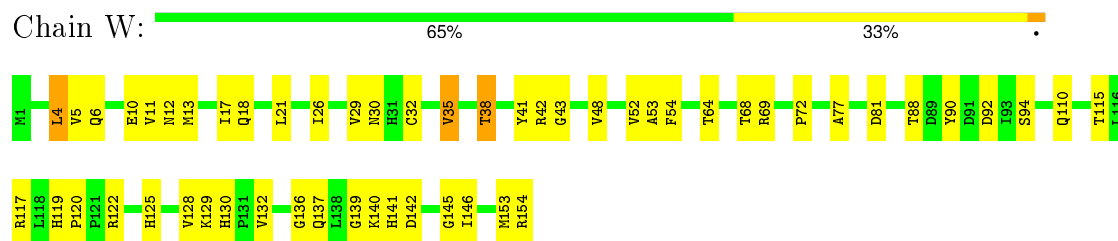


- Molecule 22: 50S ribosomal protein L29P

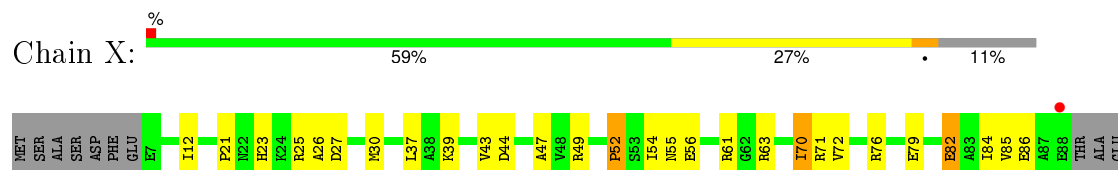
Chain V:  6% 62% 28% 8%



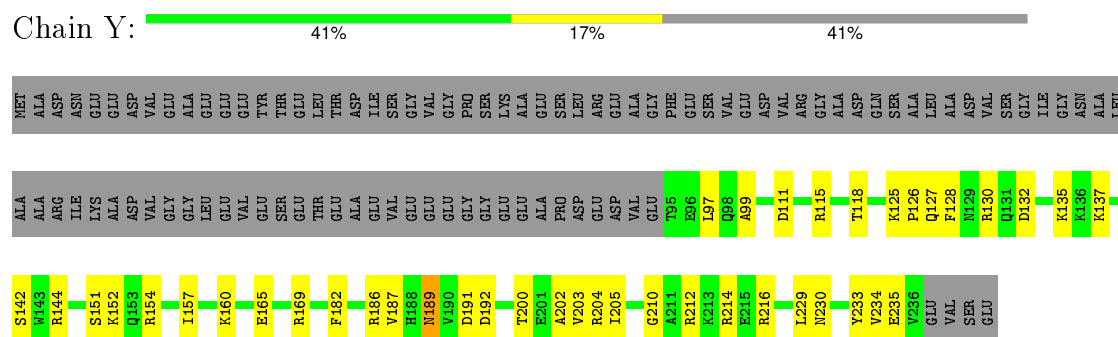
- Molecule 23: 50S ribosomal protein L30P



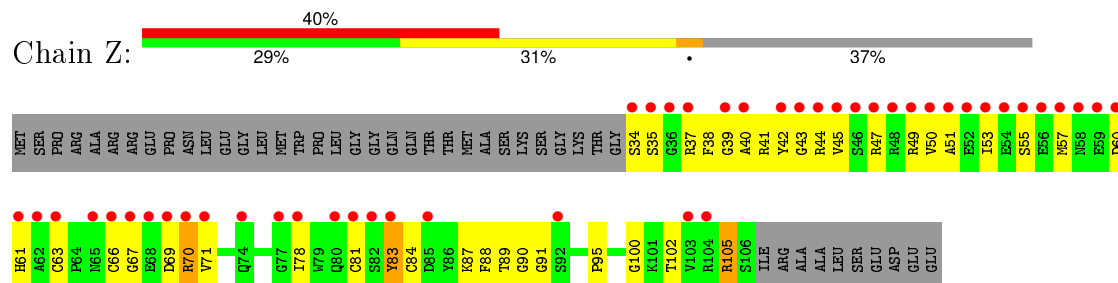
- Molecule 24: 50S ribosomal protein L31e



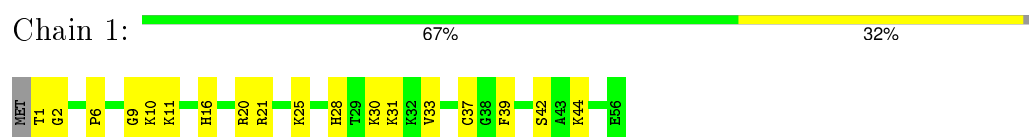
- Molecule 25: 50S ribosomal protein L32e



- Molecule 26: 50S ribosomal protein L37Ae

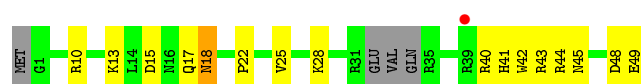


- Molecule 27: 50S ribosomal protein L37e

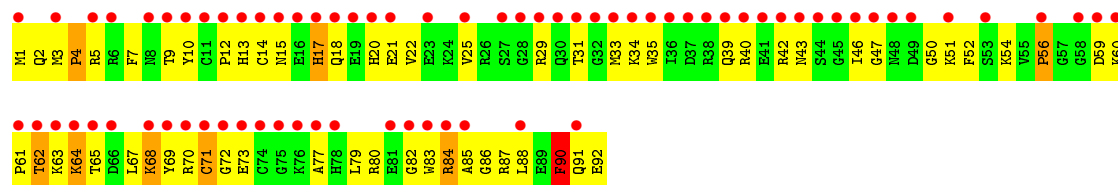
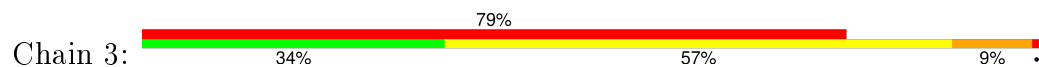


- Molecule 28: 50S ribosomal protein L39e

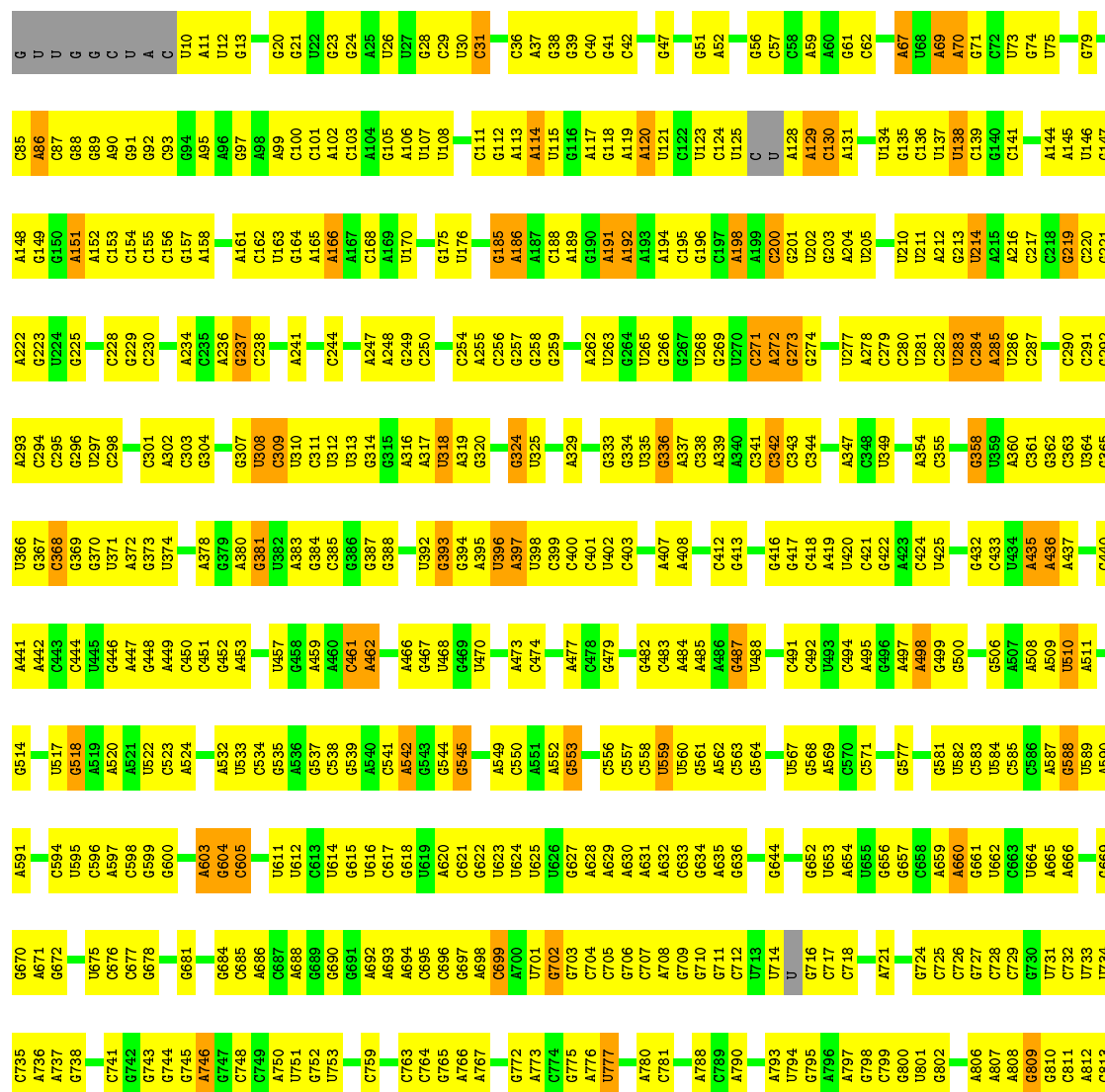




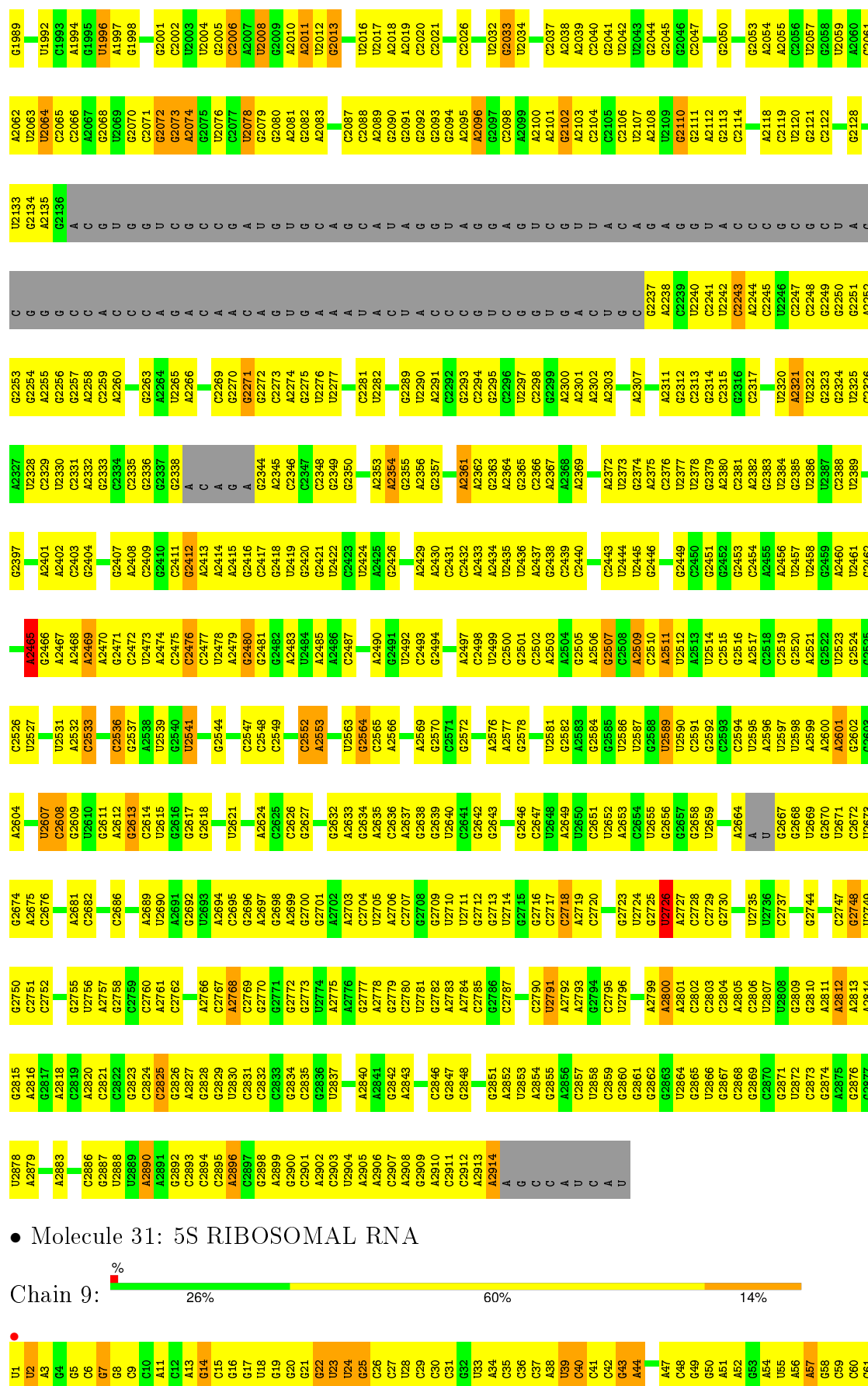
- Molecule 29: 50S ribosomal protein L44E



- Molecule 30: 23S RIBOSOMAL RNA



A1924	C1856	A1778	C1705	G1823	G1555	G1475	U1405	U1333	C1251	G1186	G1112	G1025	G964	G887	G814
G1925	A1857	A1778	G1706	A1624	G1556	A1476	A1406	U1334	C1255	U1187	U1115	U1026	A965	U888	U815
G1926	A1858	C1787	G1707	U1625	G1557	A1477	A1407	C1334	C1256	A1188	U1116	U1028	U966	U889	G816
A1927	A1859	C1787	G1708	A1626	C1558	U1478	U1408	G1337	C1260	A1189	A1117	U1029	G968	C890	G817
G1928	U1860	G1788	G1709	G1627	U1559	G1484	G1410	U1338	G1260	G1190	A1118	U1030	G969	A818	A819
G1929	C1861	G1789	A1710	A1830	U1561	A1485	G1411	G1339	U1264	A1192	G1119	G1031	U970	A820	G820
A1930	C1862	C1790	A1711	A1631	C1562	A1485	A1413	G1340	U1264	A1193	G1120	A1032	G	U821	U821
A1931	G1863	U1791	A1712	A1632	C1563	G1490	A1414	A1341	G1265	A1194	U1121	G1041	U	C822	C822
G1932	C1864	A1796	A1713	C1633	C1564	G1490	A1415	A1342	U1266	G1195	C1127	U1042	G	U823	U823
G1933	A1865	A1797	A1716	G1634	C1566	C1495	G1416	C1343	C1267	C1196	C1127	C1043	U	G824	G824
A1934	A1866	C1798	G1717	U1635	G1567	A1496	G1417	C1344	C1268	G1197	U1128	C1043	C	U825	U825
G1935	G1867	C1799	G1718	U1635	G1568	G1497	U1418	G1344	G1269	U1198	C1129	C1044	C	U826	U826
G1936	G1868	G1800	G1719	A1641	U1569	G1497	U1419	U1350	U1270	A1199	U1130	G1045	G	U827	U827
U1937	A1871	G1801	G1720	A1642	U1570	U1500	C1420	G1351	U1271	A1200	U1131	U1046	C	U828	U828
G1938	C1872	A1802	U1722	C1643	A1572	U1500	C1421	A1352	C1271	G1131	A1132	U1047	C	A829	A829
U1939	G1873	G1803	G1723	U1644	A1573	U1503	C1422	C1353	C1272	A1201	A1133	U1047	C	G830	G830
A1940	C1874	A1804	U1724	C1645	C1574	A1504	C1423	G1354	C1273	A1202	A1133	U1047	U	U831	U831
A1941	U1875	A1805	C1725	G1646	G1575	U1505	A1424	A1355	C1275	G1203	G1134	G1052	C	G910	G910
A1942	A1876	G1806	G1725	G1647	G1576	U1506	G1425	U1356	U1276	U1205	G1137	G1053	C	A912	A912
C1943	C1877	U1807	G1730	G1648	U1577	C1507	G1426	A1358	U1277	U1206	G1138	G1054	G	A913	A913
G1947	U1878	C1808	C1731	A1653	C1578	U1511	C1428	U1359	U1278	A1207	U1139	U1056	A	A916	A916
G1948	U1879	G1809	A1732	C1654	C1578	G1512	C1428	C1360	U1279	G1208	C1140	A1057	A	U917	U917
G1949	C1880	C1810	A1733	G1655	U1583	G1513	U1429	U1361	G1284	G1209	U1149	A1058	G	C838	C838
G1950	A1881	A1811	C1734	A1656	C1584	C1514	G1430	U1362	U1285	G1210	A1150	A1059	G	U840	U840
G1951	C1882	G1812	C1735	C1657	C1585	G1514	A1434	G1363	U1285	G1211	C1151	C1060	A	A841	A841
U	U1883	U1813	A1736	C1662	C1586	A1515	U1435	G1364	U1286	C1212	G1151	C1061	G	C920	C920
A	C1884	C1814	A1737	G1663	U1587	U1516	A1436	C1365	A1287	C1213	C1152	U1062	U	G921	G921
A	A1885	A1815	U1741	A1664	C1588	C1517	C1436	C1366	U1288	G1214	A1154	G1063	C	A923	A923
C	A1886	A1816	A1742	G1665	G1589	A1518	A1437	C1367	U1289	A1215	A1155	G1064	C	G924	G924
U	C1887	C1817	G1743	C1666	A1590	C1519	C1438	U1368	G1290	G1216	C1156	U1066	G	C925	C925
A	A1889	A1818	G1744	A1667	A1591	G1520	C1439	A1369	A1291	G1217	C1157	A1067	C	A926	A926
U	U1890	C1819	G1745	U1668	C1592	C1521	U1440	G1370	G1292	U1218	G1158	C1068	A	U927	U927
G	C1891	G1820	U1748	G1669	C1593	G1523	G1441	U1371	U1293	U1219	G1159	A1070	C	C928	C928
C	U1825	U1749	U1748	U1671	G1595	U1524	A1443	A1372	A1294	U1220	G1160	G1071	A	A929	A929
C	G1826	C1827	G1752	C1875	U1596	G1525	G1444	C1377	U1298	G1224	A1161	G1072	C999	G938	G938
C	C1827	G1828	C1753	G1676	A1597	A1526	G1445	G1378	G1299	C1225	G1162	A1073	C1000	A939	A939
U1964	G1902	A1829	C1754	U1677	U1598	A1527	U1446	U1379	G1300	C1226	U1163	A1074	U1003	G940	G940
C1965	U1903	C1830	A1755	A1678	U1599	A1528	U1447	U1380	G1300	G1227	U1164	G1074	C1004	U941	U941
U1966	U1904	U1831	G1756	C1679	G1600	G1529	A1448	A1381	C1303	C1228	G1165	A1075	C1005	U942	U942
U1967	U1905	G1832	U1757	C1680	G1601	G1530	G1449	G1382	U1304	C1229	G1166	C1080	A1006	U943	U943
A1968	U1906	U1833	U1758	C1681	C1602	A1533	C1450	U1383	C1305	C1230	C1167	A1081	A1007	U944	U944
A1969	U1907	C1834	A1759	G1682	A1603	A1534	C1451	C1384	U1309	U1234	U1169	C1087	C1008	C945	C945
G1970	U1908	U1835	G1760	G1683	G1604	C1537	G1452	G1385	U1309	G1235	U1170	G1087	U1009	U947	U947
U1971	A1909	U1836	U1761	A1684	G1605	C1538	U1453	G1389	U1310	A1236	A1171	A1088	C1010	G948	G948
G1972	A1910	C1837	C1762	A1685	A1606	U1540	U1454	A1390	G1311	U1237	G1172	C1089	C1011	U949	U949
A1973	C1910	C1841	C1763	C1686	A1607	G1541	C1461	A1391	G1312	C1238	A1173	A1090	A1012	G950	G950
G1974	C1911	C1842	C1764	C1687	G1608	G1542	C1462	A1392	U1313	G1239	A1174	U1095	A1013	A951	A951
U1977	C1912	C1843	G1765	C1688	C1613	G1543	C1463	A1393	G1315	G1241	G1175	U1096	A1014	G952	G952
U1978	C1913	A1844	U1766	A1691	G1614	G1544	U1463	C1394	G1316	A1242	C1176	A1097	C1015	G953	G953
G1979	C1914	C1845	U1767	C1692	A1615	U1545	C1464	C1395	G1317	G1243	U1177	A1098	U1016	U956	U956
U1980	C1915	C1846	C1769	G1697	A1616	C1546	C1465	C1396	G1324	U1244	G1178	C1102	U1017	G957	G957
A1981	U1918	G1849	U1770	C1617	A1617	U1547	C1466	C1397	G1325	C1245	C1179	G1102	U1018	A957	A957
U1982	U1919	U1850	U1771	C1618	C1618	U1548	C1467	G1398	G1326	G1246	U1180	C1103	C1019	G958	G958
C1983	C1920	G1851	G1772	A1701	G1619	U1549	A1470	A1399	G1327	A1247	C1182	C1104	A1020	C959	C959
U1986	G1986	U1921	G1773	U1702	C1620	G1552	A1471	A1399	G1328	A1248	C1183	U1109	G1021	G960	G960
C1987	A1922	C1854	G1774	G1703	C1621	C1553	C1472	A1400	G1329	A1249	C1184	U1110	A1022	A961	A961
C1988	G1923	G1855	A1775	G1704	G1622	C1554	C1474	G1401	A1330	C1250	U1185	U1111	G1024	C963	C963



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
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4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	212.41Å 299.52Å 574.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.81 – 3.00 85.66 – 2.40	Depositor EDS
% Data completeness (in resolution range)	77.8 (49.81-3.00) 77.4 (85.66-2.40)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 2.40Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.180 , 0.247 0.178 , 0.237	Depositor DCC
R_{free} test set	3540 reflections (1.27%)	DCC
Wilson B-factor (Å ²)	52.9	Xtriage
Anisotropy	0.446	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 82.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 667115 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	99120	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

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

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	1	0	0	0	0
33	M	1	0	0	0	0
34	0	66	0	0	0	0
34	9	2	0	0	0	0
34	C	1	0	0	0	0
34	J	1	0	0	0	0
34	M	1	0	0	0	0
34	Q	1	0	0	0	0
34	R	2	0	0	0	0
34	S	1	0	0	0	0
35	0	9	0	0	2	0
35	3	1	0	0	3	0
35	A	1	0	0	1	0
35	B	1	0	0	2	0
35	J	3	0	0	2	0
35	K	1	0	0	0	0
35	L	1	0	0	1	0
35	M	1	0	0	2	0
35	N	1	0	0	0	0
35	O	1	0	0	0	0
35	R	1	0	0	0	0
35	Y	1	0	0	0	0
36	0	93	0	0	0	0
36	1	2	0	0	0	0
36	3	2	0	0	0	0
36	9	3	0	0	0	0
36	A	3	0	0	0	0
36	B	2	0	0	0	0
36	F	1	0	0	0	0
36	R	1	0	0	0	0
36	S	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	35:3:8804: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
21:U:51:TRP:HD1	30:0:2865:G:HO2'	1.07	0.96
30:0:2717:C:C2'	30:0:2718:C:H5''	1.95	0.96
30:0:1118:A:H3'	30:0:1118:A:C8	1.99	0.96
30:0:1305:C:H5'	38:0:9833:HOH:O	1.66	0.96
30:0:1209:C:H2'	30:0:1210:G:H8	1.31	0.95
31:9:29:C:H2'	31:9:30:C:H5'	1.49	0.95
30:0:2717: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
30:0:871:G:C5'	30:0:871:G:H8	1.81	0.93
30:0:2321:A:H2	30:0:2378:U:H3	1.12	0.93
3:C:127:ARG:NH2	3:C:225:PRO:HG2	1.82	0.93
30:0:2748:G:H2'	38:0:7523:HOH:O	1.68	0.93
30:0:559:U:H6	30:0:559:U:H5'	1.34	0.92
31:9:54:A:C2'	31:9:55:U:H5'	1.99	0.92
30:0:1116:U:H3	30:0:1246:A:H62	1.17	0.92
30:0:2586:U:H3	30:0:2592:G:H22	1.18	0.91
30:0:2710:U:H1'	38:0:7601:HOH:O	1.69	0.91
30:0:2649:A:H3'	38:0:9829:HOH:O	1.70	0.91
30:0:1856:C:H1'	38:0:5846:HOH:O	1.70	0.91
30:0:1835:U:H5	30:0:1840:A:N7	1.68	0.91
30:0:1170:U:H2'	30:0:1172:G:OP2	1.71	0.91
30:0:1595:G:O2'	30:0:1596:U:H5'	1.71	0.91
30:0:2769:C:C2'	30:0:2770:G:H5'	2.01	0.90
8:H:49:GLN:HE21	8:H:140:TYR:HE2	1.18	0.90
30:0:870:G:H2'	30:0:871:G:H5''	1.51	0.90
13:M:58:GLN:HE22	30:0:259:G:H21	1.13	0.90
10:J:52:GLN:HE22	30:0:1119:G:H2'	1.37	0.90
30:0:963:C:H2'	30:0:964:G:C8	2.05	0.90
23:W:4:LEU:HD13	23:W:52:VAL:HG21	1.51	0.90
30:0:615:G:H1'	38:0:5221:HOH:O	1.72	0.90
30:0:1835:U:H2'	38:0:3618:HOH:O	1.72	0.90
30:0:625:U:H5''	30:0:1044:C:N4	1.87	0.89
30:0:969:G:H1	30:0:999:C:N4	1.71	0.89
30:0:1701:A:H4'	30:0:1702:U:H5''	1.55	0.89
16:P:115:SER:H	16:P:118:GLN:HE21	0.89	0.89
10:J:52:GLN:NE2	30:0:1119:G:H2'	1.88	0.88
13:M:73:ARG:NH2	30:0:2263:G:H5''	1.87	0.88
1:A:199:HIS:HD2	1:A:201:PHE:H	1.21	0.88
28:2:43:ARG:HH22	30:0:1684:A:H1'	1.37	0.87
30:0:542:A:H5'	30:0:542:A:H8	1.39	0.87
30:0:2502: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
31:9:56:A:H2'	31:9:57:A:H5''	1.57	0.86
30:0:506:G:H22	30:0:509:A:C5'	1.87	0.86
30:0:2637:A:H4'	38:0:6039:HOH:O	1.75	0.86
30:0:506:G:H22	30:0:509:A:H5''	1.40	0.86
30:0:2908:A:H2'	30:0:2909:G:O4'	1.75	0.86
30:0:2248:C:H3'	38:0:5403:HOH:O	1.76	0.86
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
30:0:969:G:H1	30:0:999:C:H42	1.24	0.86
30:0:553:G:H3'	38:0:4066:HOH:O	1.76	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
30:0:2505:G:O2'	30:0:2506:A:H5'	1.76	0.85
30:0:2421:G:H1'	38:0:7004:HOH:O	1.75	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
11:K:39:GLY:HA2	38:0:5187:HOH:O	1.75	0.84
30:0:1080:C:H4'	30:0:1081:A:OP1	1.76	0.84
23:W:137:GLN:HE21	23:W:141:HIS:HE1	1.23	0.83
16:P:115:SER:N	16:P:118:GLN:HE21	1.74	0.83
31:9:73:A:H2'	31:9:74:G:H8	1.43	0.83
30:0:2717:C:H2'	30:0:2718:C:H5''	1.59	0.83
30:0:12:U:H2'	30:0:13:G:H5'	1.57	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)
31:9:14:G:C8	31:9:14:G:H5'	2.14	0.83
30:0:2896:A:H5''	38:0:6075:HOH:O	1.77	0.83
30:0:271:C:H41	30:0:378:A:H2	1.22	0.82
30:0:1644:C:H2'	30:0:1645:U:H6	1.44	0.82
30:0:810:G:H2'	30:0:811:C:C6	2.13	0.82
30:0:2437:A:H2'	30:0:2438:G:C8	2.14	0.82
22:V:12:THR:HG22	22:V:15:GLU:HG3	1.60	0.82
30:0:236:A:C4'	30:0:237:G:H5'	2.09	0.82
30:0:1205:U:C2'	30:0:1206:U:C5'	2.57	0.82
30:0:1206:U:H5'	30:0:1206:U:H6	1.43	0.82
4:D:25:MET:SD	4:D:40:ILE:HD11	2.19	0.82
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
30:0:2502:C:C2'	30:0:2503:A:H5'	2.10	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
30:0:1116:U:O2'	30:0:1118:A:H2	1.62	0.81
13:M:134:ILE:HG23	13:M:141:ILE:HD13	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
31:9:59:C:H2'	31:9:60:C:C6	2.16	0.80
30:0:2467:A:H3'	38:0:5416:HOH:O	1.82	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
1:A:167:LYS:HE2	26:Z:50:VAL:HG13	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:55:GLN:NE2	30:0:1446:U:H2'	1.97	0.79
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	35: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
30:0:282:C:H1'	30:0:368:C:H41	1.46	0.79
30:0:282:C:H1'	30:0:368:C:N4	1.98	0.79
30:0:2604:A:H4'	38:0:7586:HOH:O	1.83	0.79
30:0:2783:A:H3'	38:0:5197:HOH:O	1.82	0.78
30:0:2769:C:O2'	30:0:2770:G:H5'	1.84	0.78
30:0:1829:A:H2'	30:0:1830:C:H5'	1.65	0.78
30:0:2533:C:H5'	30:0:2533:C:H6	1.47	0.78
31:9:55:U:H5''	38:9:9146:HOH:O	1.82	0.78
30:0:2906:A:H5'	30:0:2907:C:O4'	1.83	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
13:M:70:GLY:HA3	13:M:73:ARG:NH2	1.99	0.78
10:J:74:ARG:HB3	10:J:74:ARG:HH11	1.48	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
30:0:2237:G:H1'	38:0:4824:HOH:O	1.83	0.78
31:9:56:A:C3'	31:9:57:A:H5''	2.12	0.78
30:0:297:U:H2'	30:0:298:C:H6	1.49	0.78
30:0:1189:A:H1'	30:0:1209:C:O4'	1.84	0.77
13:M:171:ARG:HD3	30:0:156:C:C5'	2.07	0.77
30:0:1617:C:C4	30:0:1643:C:H4'	2.19	0.77
30:0:1426:C:H2'	38:0:9600:HOH:O	1.83	0.77
30:0:1741:U:H5'	30:0:1742:A:OP1	1.83	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
30:0:2769:C:H2'	30:0:2770:G:O4'	1.82	0.77
4:D:105:SER:OG	30:0:2338:G:H1'	1.83	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
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
30:0:2335: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
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
30:0:960:G:N3	30:0:960:G:H3'	2.00	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
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
13:M:88:VAL:HG21	30:0:2122:C:O2'	1.86	0.75
26:Z:63:CYS:SG	26:Z:81:CYS:HB2	2.26	0.75
30:0:564:G:H1'	38:0:6290:HOH:O	1.85	0.75
2:B:18:ARG:HE	2:B:256:GLN:HE21	1.31	0.75
30:0:2083:A:H3'	38:0:7559:HOH:O	1.86	0.75
30:0:1434:A:HO2'	30:0:1435:U:H6	1.32	0.75
30:0:1189: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:OP1	30:0:1524:U:H4'	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
30:0:279:C:O2'	30:0:280:C:H5'	1.87	0.74
30:0:1787:C:O2'	30:0:1788:U:H5'	1.87	0.74
30:0:635:A:H2'	30:0:636:G:H5''	1.68	0.74
1:A:223:ARG:NH2	30:0:2271:G:H5'	2.02	0.74
30:0:1972:U:H2'	30:0:1973:A:C5'	2.18	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
30:0:694:A:C2'	30:0:695:C:H5'	2.18	0.74
30:0:2831:C:C2'	30:0:2832:C:H5'	2.18	0.74
1:A:47:HIS:CD2	30:0:1654:U:H2'	2.22	0.74
30:0:629:A:H4'	38:0:4498:HOH:O	1.88	0.74
30:0:1185:U:H5'	38:0:7447:HOH:O	1.88	0.73
21:U:44:ARG:HD3	21:U:49:LEU:HD11	1.70	0.73
30:0:2703:A:H2'	30:0:2704:C:H6	1.52	0.73
30:0:2100:A:H5'	38:0:7373:HOH:O	1.88	0.73
29:3:68:LYS:CD	29:3:70:ARG:HH21	2.01	0.73
30:0:2011:A:H5''	38:0:4388:HOH:O	1.87	0.73
30:0:1603: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
31:9:1:U:H4'	31:9:3:A:OP1	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
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
31:9:3:A:N6	31:9:22:G:H1'	2.03	0.73
30:0:2505:G:C2'	30:0:2506:A:H5'	2.19	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
30:0:69:A:H5'	30:0:69:A:H8	1.54	0.73
30:0:871:G:C8	30:0:871:G:C5'	2.63	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
38:B:9106:HOH:O	30:0:2672:C:H1'	1.87	0.72
30:0:2635:A:O2'	30:0:2636:C:H5'	1.88	0.72
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
30:0:1625:U:H6	30:0:1625:U:H3'	1.54	0.72
13:M:99:ARG:HD2	13:M:167:GLY:HA2	1.71	0.72
30:0:1733:A:C6	30:0:1734:C:C2	2.77	0.72
13:M:79:ALA:HB1	38:0:4442:HOH:O	1.89	0.72
1:A:48:ASP:HB3	38:A:9085:HOH:O	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:76:ARG:HB2	13:M:88:VAL:HG13	1.72	0.72
4:D:58:VAL:HB	4:D:62:ASP:HB3	1.72	0.72
30:0:2467:A:H1'	38:0:9049:HOH:O	1.89	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
30:0:2898:G:O2'	30:0:2899:A:H5'	1.89	0.72
30:0:2831:C:O2'	30:0:2832:C:H5'	1.88	0.72
30:0:1316:G:H5''	38:0:5285:HOH:O	1.88	0.72
30:0:272:A:H5'	30:0:273:G:OP2	1.90	0.72
30:0:1178:G:H2'	30:0:1179:C:C6	2.25	0.72
30:0:1713:G:H1'	38:0:5039:HOH:O	1.89	0.72
30:0:2297:U:H1'	38:0:5144:HOH:O	1.88	0.72
30:0:2253:G:H2'	30:0:2254:G:H8	1.55	0.72
30:0:595:U:O2'	30:0:596:C:H5'	1.90	0.71
31:9:26:C:O2'	31:9:27:C:H5'	1.91	0.71
30:0:603:A:H5''	30:0:604:G:OP1	1.89	0.71
30:0:958:G:H2'	30:0:959:C:C6	2.24	0.71
30:0:1979:G:H3'	38:0:3283:HOH:O	1.88	0.71
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
30:0:2321:A:H2	30:0:2378:U:N3	1.88	0.71
25:Y:187:VAL:HG23	25:Y:192:ASP:CB	2.21	0.71
27:1:25:LYS:HD2	28:2:49:GLU:H	1.55	0.71
23:W:125:HIS:CE1	30:0:1097:A:H5''	2.25	0.71
30:0:1801:A:H3'	38:0:7596:HOH:O	1.90	0.71
30:0:2769:C:H2'	30:0:2770:G:C5'	2.20	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
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
14:N:33:ARG:HH21	14:N:48:VAL:HG11	1.55	0.71
30:0:920:C:H4'	30:0:921:G:C2	2.26	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
30:0:2717:C:C2'	30:0:2718:C:C5'	2.68	0.70
30:0:1972:U:H2'	30:0:1973:A:H5'	1.73	0.70
22:V:57:LYS:HA	22:V:60:GLN:HE21	1.57	0.70
30:0:2312:G:H2'	30:0:2313:C:H5'	1.72	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
30:0:1596:U:H2'	30:0:1598:A:OP2	1.90	0.70
14:N:4:PRO:HB2	30:0:1010:C:H4'	1.73	0.70
30:0:1829:A:C2'	30:0:1830:C:H5'	2.21	0.70
13:M:164:THR:HG22	13:M:166:ALA:H	1.57	0.70
30:0:2539:U:H1'	38:0:7770:HOH:O	1.90	0.70
1:A:223:ARG:HH12	30:0:2270:G:H4'	1.55	0.70
38:C:8565:HOH:O	20:T:2:LYS:HE3	1.92	0.70
14:N:11:ARG:HD3	31:9:114:G:O6	1.90	0.70
29:3:40:ARG:HA	29:3:52:PHE:CE1	2.26	0.70
30:0:1226:G:H2'	30:0:1227:C:H6	1.57	0.70
31:9:59:C:O5'	31:9:59:C:H6	1.74	0.69
30:0:1589: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
10:J:70:PHE:CD1	30:0:2676:C:H4'	2.27	0.69
30:0:714:U:H4'	38:0:5705:HOH:O	1.93	0.69
7:G:64:ASN:N	7:G:64:ASN:HD22	1.90	0.69
1:A:135:VAL:HG11	1:A:147:ARG:NH2	2.07	0.69
30:0:2404:G:H5''	38:0:5177:HOH:O	1.91	0.69
8:H:168:VAL:HG13	38:H:218:HOH:O	1.91	0.69
30:0:2667:G:H1'	30:0:2914:A:N3	2.08	0.69
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
14:N:37:ARG:NH1	31:9:6:C:C5'	2.50	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
30:0:735:C:H2'	30:0:736:A:O4'	1.93	0.69
3:C:76:ARG:HB3	3:C:76:ARG:HH11	1.57	0.69
2:B:258:GLY:H	2:B:260:HIS:CE1	2.10	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
18:R:128:ARG:NH2	30:0:2054:A:N3	2.41	0.69
13:M:81:ARG:HD2	13:M:85:ARG:HG3	1.74	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
21:U:56:ARG:HB2	30:0:2890:A:C8	2.27	0.68
30:0:2795:C:O2'	30:0:2796:U:H5'	1.93	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
30:0:2635:A:C2'	30:0:2636:C:H5'	2.23	0.68
30:0:2111:G:H1'	38:0:9052:HOH:O	1.94	0.68
23:W:137:GLN:HE21	23:W:141:HIS:CE1	2.10	0.68
2:B:264:GLU:HG2	2:B:267:LYS:CE	2.19	0.68
30:0:2637: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
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
2:B:267:LYS:HD3	38:B:8996:HOH:O	1.93	0.68
26:Z:42:TYR:CA	30:0:1829:A:H61	2.07	0.68
30:0:685:C:O2	30:0:748:C:H4'	1.94	0.68
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
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
29:3:90:PHE:HD1	29:3:90:PHE:H	1.42	0.67
30:0:1625:U:C6	30:0:1625:U:H3'	2.29	0.67
3:C:76:ARG:NH1	3:C:76:ARG:HB3	2.09	0.67
18:R:98:ASN:HD21	30:0:500:G:H21	1.40	0.67
10:J:39:VAL:HG22	10:J:106:GLY:O	1.94	0.67
13:M:95:LYS:HE2	30:0:157:G:H4'	1.76	0.67
30:0:1118:A:C8	30:0:1119:G:H5''	2.29	0.67
13:M:70:GLY:HA2	30:0:2263:G:H4'	1.76	0.67
21:U:42:LEU:HD22	30:0:1810:C:H1'	1.76	0.67
30:0:1813:U:H2'	38:0:6701:HOH:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
30:0:1528:A:H2'	30:0:1529:G:O4'	1.95	0.67
30:0:2524:G:H5''	38:0:4698:HOH:O	1.94	0.67
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
13:M:73:ARG:HH22	30:0:2263:G:H5''	1.58	0.67
28:2:28:LYS:HE2	30:0:86:A:H1'	1.77	0.67
30:0:2894:C:O2'	30:0:2895:C:H5'	1.95	0.67
21:U:19:THR:HG22	21:U:20:MET:H	1.59	0.67
31:9:76:G:C3'	31:9:77:A:H5''	2.23	0.67
30:0:370:G:O2'	30:0:371:U:H5'	1.93	0.67
30:0:119:A:H2'	30:0:120:A:H5''	1.77	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
30:0:810:G:H2'	30:0:811:C:H6	1.56	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
11:K:20:CYS:HB2	11:K:29:LEU:HG	1.77	0.67
10:J:75:PRO:HG2	10:J:105:LEU:HD21	1.77	0.67
29:3:60:LYS:HG3	29:3:61:PRO:HD2	1.77	0.67
30:0:256:C:H2'	30:0:257:G:O4'	1.95	0.67
16:P:59:ARG:HD3	38:0:6249:HOH:O	1.95	0.66
1:A:135:VAL:HG21	1:A:147:ARG:HB3	1.77	0.66
30:0:596:C:H2'	30:0:597:A:C8	2.29	0.66
30:0:2785:C:H5'	38:0:7694:HOH:O	1.95	0.66
14:N:33:ARG:NH2	14:N:48:VAL:HG11	2.10	0.66
29:3:68:LYS:HD3	29:3:70:ARG:NH2	2.07	0.66
30:0:468:U:H3'	38:0:7549:HOH:O	1.93	0.66
15:O:14:LEU:HD23	15:O:102:ILE:HD11	1.77	0.66
30:0:869:G:H1'	38:0:3302:HOH:O	1.95	0.66
30:0:1041:U:H2'	30:0:1042:U:H5'	1.78	0.66
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
30:0:1942: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
30:0:123:U:H5'	38:0:6635:HOH:O	1.96	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
30:0:1167: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
30:0:318:U:H5'	30:0:339:A:C2	2.31	0.66
30:0:2032:U:H2'	30:0:2033:G:C5'	2.26	0.66
31:9:7:G:H5'	38:9:9102:HOH:O	1.95	0.66
30:0:2760:C:H5''	38:0:5294:HOH:O	1.95	0.66
2:B:27:ASN:H	2:B:27:ASN:HD22	1.44	0.66
30:0:1063:G:H5''	38:0:9856:HOH:O	1.94	0.66
30:0:704:C:H2'	30:0:705:C:H6	1.60	0.66
30:0:559:U:C6	30:0:559:U:H5'	2.23	0.66
30:0:2533:C:C6	30:0:2533:C:H5'	2.31	0.66
30:0:921:G:H4'	30:0:924:G:N1	2.11	0.66
3:C:184:ARG:NH2	30:0:450:C:OP1	2.29	0.66
30:0:1603:A:H5'	30:0:1605:G:C4'	2.26	0.65
30:0:1249:U:H2'	30:0:1250:C:C6	2.30	0.65
30:0:449:A:H3'	38:0:6214:HOH:O	1.95	0.65
30:0:559:U:H6	30:0:559:U:C5'	2.09	0.65
26:Z:44:ARG:NH2	30:0:1771:U:H5'	2.09	0.65
14:N:80:SER:HB2	38:N:8833:HOH:O	1.95	0.65
30:0:2851:G:H2'	30:0:2902:A:H61	1.60	0.65
20:T:9:LYS:HE3	20:T:13:ARG:NH1	2.12	0.65
12:L:143:THR:HG22	12:L:144:ASP:H	1.61	0.65
2:B:179:LEU:O	2:B:183:GLU:HG2	1.96	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
38:D:7597:HOH:O	31:9:56:A:H2	1.79	0.65
30:0:2707:C:H2'	30:0:2707:C:O2	1.96	0.65
21:U:56:ARG:HD2	30:0:2890:A:C1'	2.25	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
9:I:110:ASP:O	30:0:1163:G:H5'	1.95	0.65
30:0:1666:C:C2'	30:0:1667:A:H5''	2.27	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
30:0:2597:U:H2'	30:0:2598:U:H5'	1.77	0.65
30:0:213:G:N2	30:0:225:G:H2'	2.11	0.65
30:0:1132:A:N6	30:0:1229:C:H2'	2.12	0.65
30:0:416:G:H5''	38:0:7402:HOH:O	1.96	0.65
30:0:1061:C:H3'	38:0:5051:HOH:O	1.97	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
2:B:238:ASN:HD22	2:B:240:GLY:N	1.90	0.65
38:O:1484:HOH:O	30:0:710:G:H1'	1.97	0.65
30:0:42:C:H1'	38:0:4645:HOH:O	1.97	0.65
30:0:290:C:O2'	30:0:291:C:H5'	1.96	0.65
30:0:812:A:H2'	30:0:813:C:C6	2.31	0.65
16:P:81:LYS:O	30:0:1761:U:H5'	1.97	0.65
30:0:2119:C:O2'	30:0:2120:U:H5'	1.97	0.65
30:0:696:C:O2'	30:0:697:G:H5'	1.97	0.64
31:9:61:C:H2'	31:9:62:A:H8	1.62	0.64
30:0:2892:G:C6	30:0:2893:C:C4	2.85	0.64
30:0:1586:G:O2'	30:0:1587:U:H5'	1.97	0.64
30:0:1377:C:H5'	30:0:1377:C:C6	2.33	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
30:0:1422:U:H2'	30:0:1423:C:C6	2.32	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
21:U:56:ARG:HD2	30:0:2890:A:C8	2.33	0.64
30:0:1972:U:C2'	30:0:1973:A:H5''	2.27	0.64
30:0:1819:G:H5'	38:0:4680:HOH:O	1.96	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
30:0:693:A:H2'	30:0:694:A:C8	2.33	0.64
30:0:281:U:H2'	30:0:282:C:O4'	1.98	0.64
2:B:312:ARG:HD3	2:B:315:VAL:HG13	1.80	0.64
27:1:9:GLY:HA2	30:0:1687:C:O2	1.98	0.64
30:0:2768:A:O2'	30:0:2769:C:H5'	1.97	0.64
5:E:143:GLN:HE22	30:0:2779:G:H21	1.44	0.64
26:Z:70:ARG:HH11	26:Z:83:TYR:HD1	1.46	0.64
30:0:1706:G:H1'	30:0:1712:A:H61	1.61	0.64
23:W:6:GLN:HB2	23:W:26:ILE:HD11	1.79	0.64
5:E:20:ILE:HD11	5:E:40:VAL:HG11	1.79	0.64
27:1:21:ARG:HD2	27:1:37:CYS:SG	2.38	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:169:ARG:HD2	30:0:1328:A:OP1	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:154:ARG:HH22	30:0:1071:G:H4'	1.63	0.64
14:N:86:LEU:HD12	14:N:125:ALA:HB2	1.78	0.64
3:C:16:VAL:HG12	3:C:17:ASP:H	1.62	0.64
30:0:459:A:H5''	38:0:9055:HOH:O	1.96	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
30:0:541:C:H2'	30:0:542:A:H5'	1.77	0.63
3:C:236:THR:HG21	38:C:8571:HOH:O	1.97	0.63
3:C:132:ASP:O	3:C:133:ARG:HG3	1.98	0.63
18:R:40:ALA:O	18:R:44:VAL:HG23	1.99	0.63
30:0:2867:G:H2'	30:0:2868:C:C6	2.33	0.63
11:K:98:VAL:CG1	11:K:102:GLU:HA	2.28	0.63
31:9:17:G:O2'	31:9:18:U:H5'	1.97	0.63
30:0:1116:U:O2'	30:0:1118:A:C2	2.40	0.63
30:0:541:C:O2'	30:0:542:A:H5''	1.97	0.63
17:Q:26:PRO:O	17:Q:30:VAL:HG23	1.97	0.63
8:H:19:ARG:HH12	30:0:1008:C:H5''	1.63	0.63
30:0:2727:A:H2'	30:0:2728:C:H5'	1.80	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:164:THR:HG22	13:M:166:ALA:N	2.13	0.63
13:M:66:SER:HB3	13:M:128:TRP:CD1	2.33	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
30:0:2659:U:H5''	38:0:4112:HOH:O	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
26:Z:38:PHE:HB3	26:Z:42:TYR:CD1	2.33	0.63
1:A:211:LYS:HB3	1:A:212:PRO:HD2	1.79	0.63
30:0:90:A:H2'	30:0:91:G:O4'	1.98	0.63
30:0:1985:U:H1'	38:0:4497:HOH:O	1.98	0.63
14:N:37:ARG:HH12	31:9:6:C:C5'	1.95	0.63
30:0:1644:C:H2'	30:0:1645:U:C6	2.31	0.63
30:0:2824:C:H5''	30:0:2825:C:H5'	1.80	0.63
30:0:1149:U:H5''	30:0:1151:G:O4'	1.98	0.63
30:0:2675:A:H1'	30:0:2813:A:C2	2.34	0.63
14:N:164:ASP:OD1	14:N:167:ASP:HA	1.98	0.63
30:0:2291:A:H8	38:0:6453:HOH:O	1.81	0.63
30:0:2766:A:O2'	30:0:2767:C:H5'	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:2:GLN:HB3	29:3:91:GLN:CD	2.19	0.63
29:3:59:ASP:HB3	29:3:63:LYS:NZ	2.13	0.63
2:B:280:VAL:HG13	2:B:333:GLU:O	1.99	0.63
22:V:42:ASN:HB3	38:V:7247:HOH:O	1.98	0.63
4:D:131:THR:HG21	30:0:2348:C:H1'	1.79	0.63
30:0:2250:G:H2'	30:0:2251:G:O4'	1.99	0.63
30:0:279:C:C2'	30:0:280:C:H5'	2.29	0.63
28:2:41:HIS:HB3	28:2:44:ARG:HB2	1.80	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
11:K:74:VAL:CG1	11:K:113:ILE:HG12	2.29	0.63
30:0:956:G:C8	38:0:9387:HOH:O	2.50	0.63
30:0:630:A:H5''	38:0:4722:HOH:O	1.99	0.63
26:Z:41:ARG:HD2	30:0:1830:C:O2	1.98	0.62
30:0:2349:G:H2'	30:0:2350:G:H8	1.62	0.62
30:0:1165:G:H21	30:0:1173:A:C5'	2.12	0.62
20:T:72:ILE:HD13	20:T:93:THR:HG22	1.81	0.62
27:1:2:GLY:O	27:1:6:PRO:HG2	1.99	0.62
12:L:57:VAL:HG21	30:0:2443:C:H5'	1.80	0.62
26:Z:34:SER:HB2	38:0:7481:HOH:O	1.99	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
21:U:49:LEU:HD12	38:U:3805:HOH:O	1.99	0.62
30:0:1889:C:H2'	30:0:1890:U:O4'	2.00	0.62
30:0:1878:G:H1'	38:0:6097:HOH:O	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
30:0:1351:G:H5'	38:0:3619:HOH:O	1.99	0.62
30:0:1477:C:H5'	30:0:1868:G:C5'	2.29	0.62
5:E:153:ARG:HH12	30:0:2778:A:H1'	1.65	0.62
30:0:229:G:O2'	30:0:230:C:H5'	2.00	0.62
30:0:790:A:H1'	30:0:1710:A:O2'	1.99	0.62
8:H:15:PRO:HG3	30:0:1053:G:OP1	2.00	0.62
20:T:61:GLU:HG2	38:T:3851:HOH:O	1.99	0.62
29:3:68:LYS:NZ	30:0:2436:U:H5'	2.14	0.62
30:0:1226:G:H5'	38:0:4509:HOH:O	1.98	0.62
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
30:0:920:C:H4'	30:0:921:G:N2	2.14	0.62
26:Z:53:ILE:O	26:Z:57:MET:HB2	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:51:TYR:CE2	30:0:721:A:H5''	2.35	0.62
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
30:0:630:A:H5'	38:0:9372:HOH:O	1.98	0.62
30:0:1752:G:H2'	38:0:7531:HOH:O	2.00	0.62
30:0:303:C:O2'	30:0:304:G:H5'	2.00	0.62
17:Q:14:LEU:HD21	17:Q:43:ILE:HD12	1.82	0.62
30:0:1279:U:C2'	30:0:1279:U:O2	2.48	0.61
30:0:236:A:H4'	30:0:237:G:C5'	2.17	0.61
3:C:129:HIS:CE1	3:C:231:ARG:HA	2.35	0.61
31:9:91:C:H1'	38:9:9149:HOH:O	1.98	0.61
30:0:2439:C:H5'	38:0:5449:HOH:O	1.99	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
30:0:1131:G:H1'	38:0:3907:HOH:O	1.99	0.61
30:0:2775:A:C6	30:0:2799:A:C8	2.88	0.61
23:W:64:THR:O	23:W:68:THR:HG22	2.00	0.61
9:I:130:LEU:CD2	30:0:1167:G:H4'	2.29	0.61
30:0:1477:C:O2'	30:0:1478:U:H5'	1.99	0.61
30:0:825:U:H5''	30:0:826:U:OP1	2.00	0.61
22:V:55:ARG:O	22:V:59:ILE:HG12	2.01	0.61
30:0:2576:A:H2'	38:0:7732:HOH:O	2.00	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
23:W:52:VAL:HG22	23:W:53:ALA:H	1.63	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
2:B:262:ARG:HG3	30:0:2716:G:H5'	1.83	0.61
13:M:75:ARG:NH2	13:M:78:LYS:HE2	2.16	0.61
30:0:301:C:O2'	30:0:302:A:H5'	2.00	0.61
7:G:12:ILE:HG23	38:0:5418:HOH:O	1.98	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
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
2:B:336:GLN:O	30:0:2862:G:H4'	2.00	0.61
1:A:20:SER:HB3	30:0:1872:C:H5	1.65	0.61
12:L:67:ARG:HB2	12:L:112:GLY:HA3	1.83	0.61
9:I:130:LEU:HD21	30:0:1167:G:H4'	1.81	0.61
30:0:2526:C:H3'	30:0:2526:C:H6	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:705:C:H2'	30:0:705:C:O2	1.99	0.61
23:W:13:MET:HE1	23:W:18:GLN:HA	1.81	0.61
31:9:20:G:H3'	38:9:9057:HOH:O	2.00	0.61
30:0:877:G:C5'	30:0:878:G:OP1	2.46	0.61
22:V:12:THR:HG22	22:V:15:GLU:CG	2.31	0.61
30:0:228:C:H2'	30:0:229:G:H5'	1.80	0.61
30:0:1774:G:O2'	30:0:1775:A: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
30:0:1676:G:O2'	30:0:1677:U:H5'	2.01	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
30:0:283:U:C5	30:0:284:C:C4	2.88	0.61
30:0:1398:G:H2'	30:0:1399:A:H8	1.64	0.61
31:9:39:U:HO2'	31:9:42:C:H5	1.48	0.61
30:0:807:A:H2'	30:0:808:A:C8	2.36	0.61
30:0:558:C:H2'	30:0:559:U:H5'	1.81	0.61
30:0:1701:A:H4'	30:0:1702:U:C5'	2.30	0.61
11:K:10:GLN:N	11:K:10:GLN:HE21	1.96	0.61
8:H:174:LEU:HD21	30:0:1220:U:H4'	1.82	0.61
10:J:47:THR:HB	38:0:4807:HOH:O	2.01	0.60
1:A:140:LEU:HB3	1:A:141:PRO:HD2	1.83	0.60
38:3:9025:HOH:O	30:0:2468:A:H5'	2.00	0.60
30:0:1878:G:HO2'	30:0:1879:U:H6	1.42	0.60
30:0:31:C:H4'	38:0:7408:HOH:O	2.00	0.60
30:0:1175:G:H1'	30:0:1193:A:C2'	2.31	0.60
29:3:9:THR:HG23	29:3:20:HIS:ND1	2.15	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
30:0:1697: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
2:B:102:THR:HG23	2:B:182:VAL:HG12	1.81	0.60
30:0:282:C:O2'	30:0:283:U:C5'	2.49	0.60
30:0:2312:G:C2'	30:0:2313:C:H5'	2.30	0.60
11:K:74:VAL:HG12	11:K:75:ARG:HG3	1.83	0.60
30:0:2872:U:H2'	30:0:2873:C:O4'	2.02	0.60
30:0:2071:C:H5'	38:0:9540:HOH:O	2.00	0.60
30:0:38:G:O2'	30:0:39:G:H5'	2.02	0.60
30:0:1201:C:H5''	38:0:6211:HOH:O	2.00	0.60
26:Z:84:CYS:HB3	30:0:1604:G:N2	2.15	0.60
25:Y:126:PRO:HG2	25:Y:128:PHE:CE1	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1495:C:H1'	30:0:1573:A:H1'	1.83	0.60
30:0:407:A:H3'	38:0:4438:HOH:O	2.01	0.60
30:0:1205:U:O2'	30:0:1206:U:H5''	2.01	0.60
30:0:2420:G:C2'	30:0:2421:G:H5'	2.30	0.60
20:T:48:VAL:HG22	20:T:97:ARG:O	2.01	0.60
30:0:1972:U:C2'	30:0:1973:A:C5'	2.80	0.60
30:0:1398:G:O2'	30:0:1399:A:H5'	2.02	0.60
11:K:74:VAL:HG13	11:K:113:ILE:HG12	1.82	0.60
2:B:72:THR:HB	38:B:9076:HOH:O	2.02	0.60
30:0:947:U:H2'	30:0:948:G:C8	2.36	0.60
30:0:1407:A:O2'	30:0:1408:U:H3'	2.01	0.60
30:0:51:G:H1'	38:0:9033:HOH:O	2.01	0.60
31:9:18:U:H2'	31:9:19:G:C8	2.37	0.60
30:0:146:U:C2'	30:0:147:G:H5'	2.31	0.60
13:M:102:GLU:OE1	13:M:164:THR:HG21	2.01	0.60
30:0:2893:C:O2'	30:0:2894:C:H5'	2.01	0.60
16:P:41:ARG:HH22	30:0:1500:U:P	2.24	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
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
8:H:72:ALA:HB2	8:H:156:ALA:HB2	1.81	0.60
29:3:31:THR:OG1	29:3:34:LYS:HD3	2.01	0.60
30:0:2353:A:H4'	30:0:2354:A:O5'	2.01	0.60
31:9:3:A:C6	31:9:22:G:H1'	2.36	0.60
31:9:26:C:H2'	31:9:27:C:C6	2.36	0.60
31:9:29:C:H2'	31:9:30:C:C5'	2.28	0.60
35:B:8819:CL:CL	38:B:8997:HOH:O	2.54	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
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
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
30:0:567:U:H5''	38:0:5254:HOH:O	2.02	0.60
6:F:58:GLU:CD	13:M:27:ARG:HH22	2.05	0.60
29:3:43:ASN:HB2	29:3:52:PHE:CE1	2.36	0.60
30:0:947:U:H2'	30:0:948:G:H8	1.65	0.60
30:0:74:G:H2'	30:0:75:U:C6	2.37	0.60
2:B:235:ARG:HD3	30:0:2091:G:H5''	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1878:G:O2'	30:0:1879:U:C6	2.50	0.59
30:0:324:G:O2'	30:0:325:U:H5'	2.02	0.59
30:0:319:A:H4'	30:0:338:C:C4	2.37	0.59
31:9:63:C:O2'	31:9:64:C:H5'	2.01	0.59
16:P:91:LYS:O	16:P:95:GLU:HG3	2.02	0.59
13:M:82:ARG:HH22	13:M:85:ARG:HH21	1.49	0.59
27:1:20:ARG:HG2	30:0:111:C:O2'	2.01	0.59
31:9:65:A:N6	31:9:112:U:C6	2.71	0.59
30:0:2686:C:C2	30:0:2709:G:N2	2.70	0.59
30:0:1590:A:H1'	30:0:1606:A:C2	2.36	0.59
11:K:130:MET:SD	21:U:25:ASP:O	2.60	0.59
30:0:2718:C:H6	30:0:2718:C:H5'	1.67	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
1:A:94:LEU:HG	1:A:99:ILE:HD11	1.84	0.59
30:0:2820:A:H2'	30:0:2821:C:C6	2.36	0.59
30:0:2403:C:H5'	38:0:6001:HOH:O	2.01	0.59
2:B:156:LYS:HB3	30:0:2846:C:H4'	1.84	0.59
14:N:86:LEU:O	14:N:90:LEU:HG	2.02	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
12:L:79:ASP:HB3	38:L:8859:HOH:O	2.03	0.59
30:0:2831:C:H2'	30:0:2832:C:H5'	1.82	0.59
30:0:1585:C:H2'	30:0:1586:G:C8	2.37	0.59
30:0:652:G:C2	30:0:653:U:H1'	2.37	0.59
2:B:62:ARG:HG2	2:B:65:MET:HE3	1.85	0.59
30:0:2874:G:H3'	38:0:9586:HOH:O	2.02	0.59
30:0:2809:G:H2'	30:0:2810:G:C8	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
6:F:13:GLU:OE2	6:F:78:GLU:HG2	2.01	0.59
4:D:58:VAL:HG12	4:D:60:GLU:HG2	1.83	0.59
38:B:8993:HOH:O	30:0:2549:C:H1'	2.03	0.59
8:H:37:GLY:HA3	8:H:87:LYS:HA	1.85	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
30:0:1380:U:C4	30:0:2748:G:C4	2.91	0.59
30:0:542:A:H5'	30:0:542:A:C8	2.29	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:155:ARG:NH1	30:0:2503:A:H5"	2.18	0.59
2:B:215:VAL:HB	38:B:9089:HOH:O	2.02	0.59
30:0:2065:C:O2'	30:0:2066:C:H5'	2.02	0.59
30:0:590:A:H2'	30:0:591:A:H5'	1.83	0.59
31:9:54:A:C2	31:9:55:U:C2	2.91	0.59
18:R:39:THR:HG23	18:R:107:GLU:O	2.03	0.59
11:K:41:LYS:HA	30:0:2582:G:O3'	2.03	0.59
30:0:1972:U:H2'	30:0:1973:A:H5"	1.83	0.59
30:0:921:G:H4'	30:0:924:G:C6	2.37	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
16:P:7:LYS:HD3	16:P:21:VAL:HG22	1.85	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
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
24:X:37:LEU:HD13	24:X:85:VAL:HG21	1.84	0.59
30:0:281:U:C2'	30:0:282:C:H5'	2.33	0.59
30:0:255:A:H2'	30:0:256:C:H6	1.67	0.59
13:M:137:ASN:ND2	30:0:145:A:H4'	2.18	0.59
6:F:30:LYS:HB2	6:F:97:ALA:HB3	1.84	0.59
10:J:69:TYR:CE1	30:0:2081:A:H4'	2.38	0.59
10:J:88:PRO:HD3	30:0:1104:C:H4'	1.85	0.59
30:0:2563:U:H2'	30:0:2565:C:O5'	2.02	0.58
30:0:2826:G:C6	30:0:2913:A:C6	2.90	0.58
26:Z:40:ALA:HA	30:0:1773:G:C8	2.38	0.58
30:0:925:C:H3'	38:0:3826:HOH:O	2.02	0.58
30:0:1568:G:O2'	30:0:1569:U:H5'	2.03	0.58
30:0:2724:U:H2'	30:0:2725:G:O4'	2.03	0.58
29:3:47:GLY:HA2	30:0:2121:G:C4'	2.25	0.58
30:0:2825:C:H4'	30:0:2826:G:O5'	2.03	0.58
25:Y:169:ARG:HD3	30:0:1328:A:C8	2.38	0.58
2:B:297:VAL:HB	38:B:9076:HOH:O	2.03	0.58
30:0:1245:C:O5'	30:0:1245:C:H6	1.85	0.58
8:H:98:LEU:HD11	8:H:127:ALA:HB2	1.85	0.58
2:B:243:ASN:HB3	38:0:6624:HOH:O	2.02	0.58
30:0:28:G:H1'	38:0:4650:HOH:O	2.03	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
30:0:2467:A:H5"	38:0:4285:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:34:SER:HA	30:0:797:A:H4'	1.83	0.58
4:D:28:GLY:HA2	4:D:69:ILE:HG23	1.85	0.58
30:0:951:A:C2'	30:0:952:G:H5'	2.33	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
30:0:1290:G:H4'	38:0:7465:HOH:O	2.02	0.58
3:C:79:ARG:O	3:C:87:ARG:HG2	2.04	0.58
30:0:1186:C:H42	30:0:1190:G:H22	1.48	0.58
20:T:52:ARG:HD2	30:0:317:A:H5''	1.85	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
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
30:0:1711:A:C2'	30:0:1712:A:H5'	2.33	0.58
3:C:182:ARG:HH12	30:0:450:C:H3'	1.67	0.58
25:Y:234:VAL:HG12	25:Y:235:GLU:H	1.66	0.58
12:L:18:HIS:HD2	30:0:902:G:N7	2.01	0.58
30:0:1520:G:C6	30:0:1521:C:C4	2.92	0.58
26:Z:70:ARG:HB2	26:Z:81:CYS:SG	2.44	0.58
10:J:127:ILE:HG22	35:J:8801:CL:CL	2.40	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
30:0:1503:U:C2'	30:0:1504:A:H5'	2.34	0.58
31:9:39:U:H1'	31:9:44:A:N6	2.19	0.58
5:E:100:ASP:HB3	38:E:2789:HOH:O	2.02	0.58
2:B:162:MET:HG3	2:B:310:ARG:HD3	1.84	0.58
30:0:164:G:H3'	38:0:3636:HOH:O	2.03	0.58
2:B:267:LYS:HA	38:B:8996:HOH:O	2.04	0.58
31:9:54:A:C2	31:9:55:U:N3	2.72	0.58
30:0:2505:G:H2'	30:0:2506:A:H5'	1.86	0.58
26:Z:42:TYR:HA	30:0:1829:A:N6	2.16	0.58
30:0:1662:C:H2'	30:0:1663:G:O4'	2.03	0.58
30:0:951:A:O2'	30:0:952:G:H5'	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
30:0:2624: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
17:Q:11:ARG:NH2	30:0:2363:G:H5''	2.19	0.58
30:0:544:G:H2'	30:0:545:G:H5''	1.85	0.58
30:0:2511:A:H2'	30:0:2512:U:O4'	2.03	0.58
30:0:625:U:H3'	38:0:3244:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1634:G:H2'	30:0:1635:U:C6	2.38	0.58
30:0:1973:A:H5'	30:0:1973:A:H8	1.69	0.58
30:0:1585:C:H2'	30:0:1586:G:H8	1.68	0.58
30:0:2581:U:H1'	38:0:4452:HOH:O	2.03	0.58
22:V:1:THR:HG23	22:V:2:VAL:H	1.69	0.58
30:0:412:C:O2'	30:0:413:G:H5'	2.02	0.58
8:H:172:GLU:HB2	38:H:248:HOH:O	2.04	0.58
30:0:1160:G:H5'	30:0:1161:A:H5'	0.78	0.58
30:0:1041:U:C2'	30:0:1042:U:H5'	2.34	0.58
30:0:51:G:O2'	30:0:52:A:H5'	2.03	0.58
30:0:2812:A:N7	38:0:7497:HOH:O	2.32	0.58
30:0:1300:G:H1'	38:0:4652:HOH:O	2.03	0.58
30:0:12:U:C2'	30:0:13:G:H5'	2.32	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
4:D:76:ARG:CZ	31:9:44:A:H1'	2.34	0.57
30:0:1057:A:H1'	30:0:2492:U:O2'	2.03	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
15:O:10:LEU:HD13	15:O:99:GLU:HG3	1.84	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
30:0:2705:U:H2'	30:0:2706:A:H8	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
30:0:821:U:H3'	38:0:3764:HOH:O	2.03	0.57
14:N:48:VAL:HG13	14:N:55:ASP:HB3	1.86	0.57
30:0:1216:G:H2'	30:0:1217:G:O4'	2.03	0.57
1:A:53:ALA:HB2	1:A:122:SER:OG	2.05	0.57
30:0:590:A:C2'	30:0:591:A:H5'	2.33	0.57
26:Z:90:GLY:HA3	26:Z:95:PRO:O	2.04	0.57
30:0:1342:C:C2'	30:0:1343:C:H5'	2.34	0.57
30:0:1256:C:H6	38:0:7140:HOH:O	1.87	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
3:C:236:THR:HG22	3:C:239:ALA:N	2.15	0.57
30:0:1503:U:O2'	30:0:1504:A:H5'	2.04	0.57
30:0:916:A:C2	30:0:928:G:C4	2.93	0.57
20:T:18:GLU:O	20:T:21:LYS:HG2	2.03	0.57
30:0:694:A:H2'	30:0:695:C:C5'	2.27	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:14:LYS:CB	11:K:45:PRO:HG2	2.35	0.57
30:0:1552:G:H2'	30:0:1553:C:C6	2.40	0.57
30:0:1883:U:C2'	30:0:1884:G:H5'	2.34	0.57
29:3:51:LYS:HG3	29:3:52:PHE:CD2	2.40	0.57
30:0:1555:G:H4'	30:0:1630:A:H2	1.69	0.57
30:0:727:G:H3'	30:0:728:C:H6	1.68	0.57
30:0:544:G:C2'	30:0:545:G:H5''	2.35	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
30:0:1819:G:H2'	30:0:1820:G:H4'	1.85	0.57
30:0:1754:A:H5''	38:0:9757:HOH:O	2.04	0.57
3:C:8:LEU:HD11	3:C:143:ASP:O	2.04	0.57
30:0:2240:U:O2'	30:0:2241:C:H5'	2.04	0.57
30:0:2078:U:O2'	30:0:2079:G:H5'	2.05	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
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
30:0:1577:U:O2'	30:0:1578:C:H5'	2.05	0.57
24:X:43:VAL:HG22	24:X:76:ARG:NH1	2.20	0.57
30:0:2001:G:O2'	30:0:2002:C:H5'	2.04	0.57
15:O:19:ARG:NH1	30:0:1276:U:H3'	2.19	0.57
30:0:138:U:OP2	30:0:139:C:C5	2.58	0.57
30:0:371:U:O2'	30:0:372:A:H5'	2.05	0.57
30:0:2010:A:H2'	38:0:5933:HOH:O	2.03	0.57
14:N:160:SER:CB	31:9:51:A:H5'	2.34	0.57
5:E:153:ARG:NH1	30:0:2778:A:H1'	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
2:B:214:PRO:HD2	38:B:8989:HOH:O	2.05	0.57
1:A:153:ARG:HD3	38:A:9011:HOH:O	2.04	0.57
30:0:403:C:H3'	38:0:6286:HOH:O	2.05	0.57
30:0:1718:G:O2'	30:0:1719:G:H5'	2.04	0.57
26:Z:45:VAL:HG13	26:Z:49:ARG:HE	1.70	0.57
18:R:68:HIS:O	30:0:2842:G:H5'	2.05	0.57
30:0:1182:C:H1'	30:0:1192:A:H8	1.69	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
1:A:190:ARG:HD2	30:0:1884:G:O6	2.03	0.57
31:9:23:U:H2'	31:9:24:U:H4'	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:41:PHE:CZ	2:B:79:MET:HG3	2.40	0.57
31:9:64:C:C2'	31:9:65:A:H5'	2.35	0.57
30:0:2407:G:O2'	30:0:2408:A:H5'	2.05	0.57
30:0:1971:G:H5'	38:0:7053:HOH:O	2.05	0.57
24:X:30:MET:HE1	24:X:55:ASN:HA	1.86	0.57
30:0:2769:C:C2'	30:0:2770:G:C5'	2.78	0.56
30:0:1079:A:OP2	30:0:1080:C:N4	2.36	0.56
30:0:2251:G:H2'	30:0:2252:A:H8	1.70	0.56
30:0:407: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
30:0:312:U:O2'	30:0:313:U:H5'	2.05	0.56
30:0:10:U:C4	30:0:532:A:C8	2.94	0.56
31:9:54:A:HO2'	31:9:55:U:H5'	1.67	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
30:0:2700:G:H3'	38:0:3575:HOH:O	2.05	0.56
30:0:2698:G:H2'	30:0:2699:A:O4'	2.05	0.56
30:0:1020:A:H2'	30:0:1021:G:C8	2.40	0.56
11:K:32:ILE:HD11	11:K:56:SER:HB2	1.86	0.56
30:0:2265:U:H2'	30:0:2266:A:C8	2.40	0.56
30:0:1183:C:N4	30:0:1184:C:H41	2.03	0.56
30:0:695:C:O2'	30:0:696:C:H5'	2.04	0.56
30:0:280:C:H2'	30:0:281:U:O4'	2.06	0.56
30:0:1616:A:H5'	30:0:1617:C:OP1	2.05	0.56
28:2:40:ARG:HG3	28:2:45:ASN:HB2	1.85	0.56
14:N:141:ARG:NH2	31:9:48:C:H4'	2.21	0.56
30:0:2011:A:H5'	30:0:2013:G:H1'	1.87	0.56
14:N:48:VAL:CG1	14:N:55:ASP:HB3	2.35	0.56
11:K:98:VAL:HG13	11:K:102:GLU:HA	1.85	0.56
30:0:947:U:O2'	30:0:948:G:H5'	2.05	0.56
29:3:34:LYS:HB3	38:3:9001:HOH:O	2.05	0.56
30:0:1948:G:O2'	30:0:1949:G:H5'	2.05	0.56
23:W:38:THR:O	23:W:42:ARG:HB2	2.04	0.56
30:0:1928:C:H2'	30:0:1929:G:O4'	2.05	0.56
13:M:171:ARG:NH2	30:0:189:A:OP1	2.38	0.56
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
2:B:17:LYS:O	2:B:260:HIS:HD2	1.88	0.56
30:0:1735:C:H2'	30:0:1736:A:C8	2.40	0.56
30:0:2659:U:H3'	38:0:4379:HOH:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:33:U:H2'	38:9:9068:HOH:O	2.04	0.56
17:Q:45:PRO:O	30:0:2365:G:H4'	2.06	0.56
30:0:162:C:H2'	30:0:163:U:H5'	1.87	0.56
13:M:68:ARG:HG3	30:0:1469:C:OP1	2.05	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
30:0:2289:G:O2'	30:0:2290:U:H5'	2.06	0.56
30:0:26:U:H5	38:0:3099:HOH:O	1.89	0.56
30:0:1904:A:H2'	30:0:1905:U:O4'	2.05	0.56
29:3:65:THR:HG23	35:3:8804:CL:CL	2.43	0.56
30:0:2502:C:H2'	30:0:2503:A:C5'	2.34	0.56
30:0:1434:A:O2'	30:0:1435:U:H2'	2.05	0.56
2:B:223:ARG:HD3	35:B:8819:CL:CL	2.43	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
30:0:473: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
31:9:54:A:H2'	31:9:55:U:H5'	1.82	0.56
30:0:138:U:OP2	30:0:139:C:H5	1.88	0.56
26:Z:34:SER:HA	30:0:797:A:C4'	2.36	0.56
29:3:18:GLN:HB3	38:3:9013:HOH:O	2.06	0.56
30:0:2595:U:O2'	30:0:2596:A:H5'	2.05	0.56
30:0:1127:C:C5	30:0:1128:U:C4	2.94	0.56
25:Y:165:GLU:HB3	38:0:6689:HOH:O	2.05	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
2:B:199:TYR:HE2	2:B:268:ARG:HB2	1.71	0.56
30:0:2514:U:OP1	30:0:2572:G:H1'	2.04	0.56
13:M:24:GLN:HE22	13:M:27:ARG:HH11	1.53	0.56
21:U:56:ARG:HD2	30:0:2890:A:H1'	1.87	0.56
21:U:44:ARG:HD3	21:U:49:LEU:CD1	2.35	0.56
30:0:1292:G:HO2'	30:0:1293:U:H6	1.52	0.56
30:0:2241:C:O2'	30:0:2242:U:H5'	2.05	0.56
30:0:473:A:O2'	30:0:890:C:H5'	2.05	0.56
13:M:94:ARG:HD2	30:0:158:A:OP2	2.06	0.56
27:1:28:HIS:HE1	30:0:776:A:OP1	1.88	0.56
3:C:4:THR:HA	3:C:15:GLU:HB3	1.88	0.56
1:A:27:LEU:HD21	1:A:55:VAL:HG21	1.88	0.56
31:9:18:U:H2'	31:9:19:G:H8	1.71	0.56
30:0:1679:C:H5'	38:0:9332:HOH:O	2.06	0.56
30:0:1788:U:C2	30:0:1805:G:N2	2.73	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2673:U:C4	30:0:2674:G:C6	2.94	0.56
15:O:47:ARG:HG3	15:O:47:ARG:HH11	1.71	0.56
30:0:1181:A:H2'	30:0:1182:C:O4'	2.06	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
21:U:23:HIS:CD2	21:U:27:ALA:HB3	2.40	0.56
31:9:49:G:H2'	31:9:50:G:O4'	2.06	0.56
30:0:2314:G:H2'	30:0:2315:C:H5'	1.87	0.56
3:C:174:ILE:HD11	30:0:338:C:H4'	1.89	0.56
30:0:1020:A:H2'	30:0:1021:G:H8	1.71	0.56
30:0:660:A:H4'	30:0:661:G:O5'	2.06	0.56
25:Y:142:SER:HB2	38:Y:8902:HOH:O	2.05	0.56
12:L:41:HIS:HD2	30:0:926:A:O2'	1.89	0.56
2:B:68:THR:HG21	21:U:16:GLY:HA3	1.87	0.56
30:0:1116:U:H3	30:0:1246:A:N6	1.96	0.55
30:0:558:C:C2'	30:0:559:U:C5'	2.68	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
30:0:339:A:H2'	38:0:4203:HOH:O	2.06	0.55
30:0:2325:U:O2'	30:0:2411:C:H1'	2.06	0.55
30:0:2271:G:N3	30:0:2271:G:H2'	2.20	0.55
30:0:2852:A:H5''	38:0:5199:HOH:O	2.05	0.55
29:3:33:MET:HG2	30:0:1922:A:H2'	1.88	0.55
25:Y:99:ALA:HB2	25:Y:233:TYR:CZ	2.42	0.55
30:0:858:U:H2'	30:0:859:C:H6	1.71	0.55
30:0:684:G:H5''	38:0:4053:HOH:O	2.06	0.55
5:E:49:ILE:HD11	5:E:69:ILE:HD12	1.88	0.55
30:0:1613:C:H2'	30:0:1614:G:O4'	2.06	0.55
30:0:1183:C:H41	30:0:1192:A:H5'	1.72	0.55
30:0:1172:G:H1'	38:0:4940:HOH:O	2.05	0.55
23:W:52:VAL:HG22	23:W:53:ALA:N	2.20	0.55
30:0:1165:G:H21	30:0:1173:A:H5''	1.72	0.55
30:0:735:C:C6	30:0:736:A:C8	2.94	0.55
30:0:2113:G:C6	30:0:2114:C:C4	2.94	0.55
30:0:1512:G:O2'	30:0:1513:C:H5'	2.05	0.55
3:C:115:LEU:HD21	3:C:243:VAL:HG13	1.86	0.55
26:Z:44:ARG:HB2	30:0:1886:A:O2'	2.05	0.55
25:Y:210:GLY:HA2	38:0:5285:HOH:O	2.06	0.55
30:0:920:C:H5'	30:0:921:G:C4	2.41	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1:MET:HG2	3:C:2:GLN:H	1.72	0.55
30:0:1625:U:C6	30:0:1625:U:C3'	2.85	0.55
29:3:59:ASP:HB3	29:3:63:LYS:HZ3	1.72	0.55
30:0:2250:G:N2	30:0:2251:G:H1'	2.21	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
2:B:229:ARG:NH2	30:0:1753:C:O2	2.39	0.55
30:0:310:U:H2'	30:0:311:C:C6	2.41	0.55
3:C:21:VAL:HG13	38:C:8594:HOH:O	2.05	0.55
30:0:1562:C:N4	38:0:5836:HOH:O	2.38	0.55
29:3:47:GLY:CA	30:0:2121:G:H4'	2.29	0.55
26:Z:63:CYS:SG	26:Z:81:CYS:CB	2.94	0.55
30:0:956:G:H3'	38:0:9387:HOH:O	2.06	0.55
30:0:1909:A:H2'	30:0:1910:A:C8	2.42	0.55
3:C:149:LYS:HB2	3:C:152:GLU:HG3	1.89	0.55
10:J:19:MET:HE1	10:J:132:LEU:HD21	1.87	0.55
38:Y:8879:HOH:O	30:0:1355:A:H5''	2.06	0.55
3:C:162:VAL:HG22	3:C:232:LEU:HD21	1.87	0.55
30:0:545:G:C5'	30:0:545:G:C8	2.81	0.55
30:0:822:C:C2	30:0:823:U:C5	2.94	0.55
30:0:212:A:O4'	30:0:214:U:C6	2.59	0.55
30:0:1736:A:H1'	38:0:7566:HOH:O	2.07	0.55
2:B:36:PRO:HA	2:B:168:GLY:CA	2.36	0.55
30:0:835:U:H3'	38:0:9381:HOH:O	2.06	0.55
30:0:571:C:O5'	30:0:571:C:H6	1.90	0.55
30:0:1691:A:H5''	38:0:3140:HOH:O	2.06	0.55
23:W:119:HIS:HD2	23:W:120:PRO:O	1.89	0.55
29:3:90:PHE:CD1	29:3:90:PHE:N	2.75	0.55
30:0:696:C:HO2'	30:0:697:G:H5'	1.71	0.55
31:9:59:C:C2	31:9:60:C:C5	2.94	0.55
30:0:401:C:H2'	30:0:402:U:H6	1.72	0.55
30:0:2868:C:H1'	38:0:7107:HOH:O	2.07	0.55
2:B:102:THR:HG21	2:B:182:VAL:O	2.07	0.55
13:M:111:ASN:HB2	38:M:8852:HOH:O	2.07	0.55
4:D:140:ARG:HG3	4:D:140:ARG:HH11	1.72	0.55
30:0:2274:A:H2'	30:0:2275:G:C8	2.42	0.55
30:0:1156:C:O2'	30:0:1157:C:H5'	2.07	0.55
30:0:1166:A:C6	30:0:1181:A:C2	2.95	0.55
30:0:1175:G:H2'	30:0:1176:C:C6	2.42	0.55
13:M:70:GLY:CA	30:0:2263:G:H4'	2.37	0.55
28:2:43:ARG:HH22	30:0:1684:A:C1'	2.16	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1200:A:N1	30:0:1201:C:C2	2.75	0.55
30:0:291:C:H2'	30:0:292:G:O4'	2.07	0.55
5:E:132:THR:HB	38:E:2227:HOH:O	2.06	0.55
30:0:130:C:O2'	30:0:131:A:N7	2.39	0.55
19:S:37:VAL:O	19:S:41:VAL:HG23	2.05	0.55
30:0:2790:C:HO2'	30:0:2791:U:H6	1.55	0.55
30:0:2689:A:C2'	30:0:2690:U:H5'	2.37	0.55
30:0:1849:G:H1'	30:0:2011:A:N1	2.22	0.55
30:0:1905:U:H2'	30:0:1906:C:H6	1.72	0.55
5:E:118:ILE:HG23	5:E:144:THR:HG21	1.89	0.55
30:0:2584:G:H4'	38:0:7102:HOH:O	2.07	0.55
5:E:53:GLU:HB3	5:E:55:ASN:ND2	2.21	0.55
30:0:777:U:OP2	30:0:777:U:H4'	2.07	0.55
30:0:820:G:H5'	30:0:821:U:C5'	2.37	0.54
30:0:2782:G:N2	30:0:2783:A:N6	2.55	0.54
30:0:1377:C:H6	30:0:1377:C:C5'	2.20	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
3:C:132:ASP:HB2	3:C:161:ASP:HB3	1.89	0.54
30:0:1903:U:O2'	30:0:1904:A:N7	2.40	0.54
3:C:2:GLN:HB3	38:C:8581:HOH:O	2.07	0.54
30:0:1909:A:N1	30:0:2128:G:H1'	2.22	0.54
30:0:690:G:H4'	30:0:741:C:O2	2.06	0.54
30:0:941:G:C5	30:0:942:U:C4	2.95	0.54
30:0:960:G:H8	38:0:5945:HOH:O	1.89	0.54
30:0:363:C:O2'	30:0:364:U:H5'	2.07	0.54
31:9:58:G:N7	31:9:59:C:C4	2.75	0.54
30:0:814:G:H2'	30:0:815:U:O4'	2.07	0.54
2:B:232:TRP:CZ3	30:0:2614:C:H5''	2.41	0.54
30:0:1593:C:H1'	38:0:6083:HOH:O	2.06	0.54
29:3:12:PRO:HG2	29:3:13:HIS:HD2	1.71	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
30:0:1175: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
2:B:41:PHE:CE1	2:B:79:MET:HG3	2.43	0.54
27:1:28:HIS:HD2	27:1:30:LYS:H	1.53	0.54
14:N:114:LYS:O	14:N:118:ILE:HG13	2.07	0.54
30:0:2869:G:H5'	38:0:5457:HOH:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1015:C:H4'	38:0:6566:HOH:O	2.06	0.54
14:N:130:PRO:HA	38:N:8837:HOH:O	2.06	0.54
2:B:140:LEU:HA	38:B:9051:HOH:O	2.05	0.54
9:I:78:ALA:HB2	9:I:95:LEU:HD21	1.89	0.54
31:9:27:C:H2'	31:9:28:U:O4'	2.08	0.54
13:M:59:GLY:HA3	13:M:141:ILE:HD12	1.90	0.54
30:0:1447:U:OP1	30:0:1506:U:N3	2.39	0.54
30:0:2281:C:C2'	30:0:2282:U:H5'	2.38	0.54
30:0:1876:C:H4'	30:0:1877:G:OP2	2.08	0.54
6:F:2:VAL:HG22	6:F:57:GLU:OE1	2.08	0.54
5:E:85:GLU:HG2	5:E:130:GLU:HG2	1.89	0.54
9:I:87:PRO:HD2	30:0:1180:U:H1'	1.89	0.54
15:O:19:ARG:HH22	30:0:1278:A:P	2.31	0.54
13:M:99:ARG:HE	13:M:170:ASN:ND2	1.96	0.54
31:9:36:C:C5	31:9:37:C:C5	2.96	0.54
1:A:223:ARG:NH1	30:0:2270:G:H4'	2.22	0.54
1:A:192:VAL:CG1	1:A:207:GLN:HB3	2.38	0.54
30:0:2477:C:O2'	30:0:2478:U:H5'	2.07	0.54
12:L:143:THR:HG22	12:L:144:ASP:N	2.22	0.54
9:I:91:PHE:CD2	9:I:131:GLY:HA2	2.42	0.54
30:0:1139:U:H2'	30:0:1140:C:H6	1.72	0.54
30:0:236:A:H4'	30:0:237:G:OP1	2.08	0.54
1:A:195:ASN:ND2	30:0:877:G:C8	2.76	0.54
30:0:2321:A:C4	30:0:2323:G:C8	2.95	0.54
30:0:963:C:O2	30:0:1005:A:N1	2.40	0.54
30:0:2831:C:H3'	38:0:7197:HOH:O	2.07	0.54
30:0:710:G:O2'	30:0:711:G:H5'	2.08	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
30:0:1697: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
30:0:312:U:C2	30:0:320:G:N2	2.76	0.54
30:0:2107:U:O2'	30:0:2108:A:H5'	2.07	0.54
17:Q:19:ARG:HH21	31:9:11:A:P	2.30	0.54
30:0:960:G:N3	30:0:960:G:C3'	2.71	0.54
30:0:1617:C:C5	30:0:1643:C:H4'	2.42	0.54
30:0:2892:G:C5	30:0:2893:C:C5	2.95	0.54
30:0:2078:U:H2'	30:0:2079:G:C8	2.42	0.54
30:0:661:G:C5	30:0:686:A:C2	2.96	0.54
30:0:461:C:N3	30:0:479:G:H5'	2.22	0.54
30:0:706:G:HO2'	30:0:707:C:H6	1.53	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:623:U:O2'	30:0:624:U:H5'	2.08	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
31:9:30:C:O2	31:9:30:C:H2'	2.08	0.54
30:0:2256:G:O2'	30:0:2257:G:H5'	2.08	0.54
30:0:1676:G:H1'	38:0:9441:HOH:O	2.08	0.54
2:B:62:ARG:HA	2:B:65:MET:HE3	1.88	0.54
30:0:2670:G:O2'	30:0:2671:U:H5'	2.08	0.54
18:R:99:ALA:HB1	18:R:109:MET:CE	2.37	0.54
30:0:2045:G:H5''	38:0:7204:HOH:O	2.06	0.54
30:0:1850:U:H2'	30:0:1851:G:H8	1.73	0.54
5:E:116:THR:HG22	5:E:151:LEU:HD22	1.90	0.54
4:D:135:VAL:HG21	4:D:139:TYR:CD1	2.43	0.54
27:1:16:HIS:HD2	30:0:470:U:O2'	1.91	0.54
15:O:19:ARG:HH11	30:0:1276:U:H3'	1.73	0.54
30:0:2908:A:H8	30:0:2908:A:O5'	1.91	0.54
30:0:1625:U:H5''	38:0:5995:HOH:O	2.07	0.54
13:M:164:THR:CG2	13:M:165:GLY:N	2.70	0.54
30:0:334:G:C4	30:0:335:U:C6	2.96	0.54
30:0:2787:C:H5	38:0:4605:HOH:O	1.90	0.54
30:0:2487:C:H5	38:0:4858:HOH:O	1.91	0.54
30:0:541:C:C2'	30:0:542:A:C5'	2.78	0.54
30:0:2831:C:H2'	30:0:2832:C:C5'	2.38	0.54
30:0:853:C:H2'	30:0:854:G:O4'	2.08	0.54
31:9:23:U:C2'	31:9:24:U:H4'	2.38	0.54
28:2:13:LYS:O	28:2:17:GLN:HG3	2.07	0.54
2:B:238:ASN:ND2	2:B:240:GLY:H	1.92	0.53
30:0:2599:A:H5''	38:0:3367:HOH:O	2.08	0.53
30:0:338:C:H5''	38:0:3793:HOH:O	2.07	0.53
1:A:179:MET:HG2	1:A:186:TRP:HB2	1.91	0.53
25:Y:97:LEU:HA	25:Y:234:VAL:O	2.08	0.53
30:0:2106:C:H2'	30:0:2107:U:C6	2.43	0.53
30:0:30:U:H5''	38:0:5777:HOH:O	2.08	0.53
14:N:132:ASN:HD22	30:0:2413:A:H4'	1.72	0.53
8:H:99:ARG:NH1	30:0:1055:G:OP2	2.41	0.53
30:0:1525:G:H5'	30:0:1526:A:OP2	2.08	0.53
30:0:354:A:H2'	30:0:355:C:H6	1.73	0.53
30:0:1453:G:H2'	30:0:1454:U:O4'	2.07	0.53
9:I:111:LEU:HD23	30:0:1163:G:H4'	1.90	0.53
30:0:2563:U:O2'	30:0:2564:G:H3'	2.08	0.53
30:0:2321:A:C5	30:0:2323:G:C8	2.96	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2769:C:H2'	30:0:2770:G:C4'	2.37	0.53
16:P:7:LYS:HD3	16:P:21:VAL:CG2	2.38	0.53
30:0:2553:A:N3	30:0:2553:A:H2'	2.23	0.53
15:O:105:ASN:HD21	15:O:109:SER:H	1.56	0.53
30:0:2379:G:N3	30:0:2418:G:H2'	2.22	0.53
30:0:1268:C:H2'	30:0:1269:G:H8	1.73	0.53
31:9:73:A:H61	31:9:108:C:H42	1.57	0.53
2:B:212:GLN:HA	30:0:1733:A:H4'	1.89	0.53
30:0:1226:G:C4	30:0:1227:C:C5	2.96	0.53
1:A:33:GLU:O	1:A:34:ASP:HB2	2.08	0.53
23:W:35:VAL:HG23	23:W:41:TYR:CD2	2.43	0.53
18:R:25:PHE:HB3	38:R:8914:HOH:O	2.07	0.53
30:0:1311:G:C2	30:0:1312:G:C8	2.97	0.53
30:0:421:C:H2'	30:0:422:G:H8	1.74	0.53
30:0:2465:A:H5'	38:0:6910:HOH:O	2.07	0.53
30:0:2703:A:H2'	30:0:2704:C:C6	2.40	0.53
31:9:114:G:H2'	31:9:115:C:C6	2.43	0.53
30:0:869:G:OP2	30:0:869:G:C8	2.62	0.53
1:A:20:SER:HB3	30:0:1872:C:C5	2.44	0.53
30:0:1754:A:H2'	30:0:1755:A:O4'	2.09	0.53
30:0:491:C:O2'	30:0:492:C:H5'	2.09	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
8:H:49:GLN:HG3	8:H:140:TYR:CE2	2.43	0.53
30:0:2831:C:C2	30:0:2910:A:C2	2.96	0.53
30:0:1741:U:C4	30:0:2033:G:C8	2.96	0.53
30:0:718:C:C2'	30:0:718:C:O2	2.55	0.53
30:0:597:A:O2'	30:0:598:C:H5'	2.08	0.53
30:0:2895:C:H2'	38:0:9579:HOH:O	2.08	0.53
30:0:213:G:H22	30:0:225:G:H2'	1.72	0.53
30:0:2119:C:C2'	30:0:2120:U:H5'	2.38	0.53
30:0:549:A:C2	30:0:550:C:C2	2.97	0.53
30:0:1271:A:H2'	30:0:1272:C:C6	2.43	0.53
30:0:1762:C:O2'	30:0:1763:C:H5'	2.08	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
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
30:0:2321:A:H2'	30:0:2321:A:N3	2.24	0.53
21:U:56:ARG:CD	30:0:2890:A:H1'	2.38	0.53
30:0:2078:U:H2'	30:0:2079:G:H8	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:466:A:H2'	30:0:467:G:O4'	2.08	0.53
30:0:2501:G:H1	30:0:2519:C:H42	1.56	0.53
30:0:535:G:C5	30:0:2063:U:C4	2.96	0.53
11:K:89:LYS:HA	38:K:7064:HOH:O	2.08	0.53
8:H:69:ARG:HD3	38:H:239:HOH:O	2.08	0.53
30:0:2321:A:H4'	30:0:2322:U:OP1	2.08	0.53
30:0:1806:G:C5	30:0:1807:U:C5	2.97	0.53
30:0:1972:U:O2'	30:0:1973:A:H5''	2.09	0.53
30:0:1706:G:C6	30:0:1707:G:C6	2.97	0.53
14:N:11:ARG:HG3	14:N:14:ARG:NH1	2.23	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
2:B:305:ASP:O	2:B:306:LYS:HB2	2.09	0.53
30:0:561:G:N3	30:0:562:A:C8	2.77	0.53
30:0:398:U:H2'	30:0:399:C:C6	2.44	0.53
30:0:1167:G:H2'	30:0:1168:C:H6	1.71	0.53
30:0:191:A:H61	30:0:435:A:N6	2.06	0.53
30:0:2864:U:C2'	30:0:2865:G:H5'	2.38	0.53
1:A:199:HIS:HD2	1:A:201:PHE:N	2.00	0.53
11:K:41:LYS:O	11:K:42:ASN:HB2	2.09	0.53
30:0:69:A:H2'	30:0:70:A:OP2	2.09	0.53
30:0:2613:G:O2'	30:0:2614:C:H5'	2.09	0.53
30:0:735:C:C5	30:0:736:A:C5	2.97	0.53
10:J:39:VAL:HG22	10:J:107:ASN:HA	1.91	0.53
1:A:164:ARG:HB3	1:A:164:ARG:HH11	1.73	0.53
25:Y:154:ARG:NH2	30:0:1071:G:H4'	2.23	0.53
30:0:2250:G:C2	30:0:2251:G:H1'	2.44	0.53
13:M:179:GLY:O	30:0:399:C:H5'	2.08	0.53
23:W:154:ARG:NH1	30:0:588:G:O6	2.40	0.53
22:V:44:GLY:O	22:V:48:GLU:HG2	2.08	0.53
30:0:1769:C:O2'	30:0:1770:U:H5'	2.09	0.53
2:B:141:ARG:HD2	2:B:163:GLU:OE2	2.08	0.53
14:N:154:LEU:C	14:N:156:GLU:H	2.11	0.53
30:0:424:C:H2'	30:0:425:U:C6	2.44	0.53
13:M:187:LEU:CD2	13:M:194:GLY:HA3	2.38	0.53
30:0:1158:G:C2'	30:0:1159:G:H5'	2.39	0.53
16:P:115:SER:OG	16:P:118:GLN:HG3	2.08	0.53
30:0:2336:G:H2'	38:0:6275:HOH:O	2.09	0.53
30:0:334:G:H2'	30:0:335:U:O4'	2.08	0.53
30:0:1922:A:N1	30:0:2449:G:O2'	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:62:ARG:HA	2:B:65:MET:CE	2.38	0.53
30:0:1913:C:H2'	30:0:1914:C:H6	1.73	0.53
8:H:6:ALA:HA	8:H:61:ARG:HH12	1.74	0.53
30:0:1968:A:H2'	30:0:1969:A:C8	2.44	0.53
10:J:41:ALA:HB3	38:J:8863:HOH:O	2.09	0.53
30:0:1844:C:O2'	30:0:1845:A:H5'	2.08	0.53
30:0:74:G:H1	30:0:103:C:H42	1.55	0.53
14:N:38:LYS:HE2	14:N:107:ASN:ND2	2.24	0.53
9:I:108:HIS:H	9:I:109:PRO:HD2	1.74	0.53
30:0:2642:G:H2'	30:0:2643:G:O4'	2.09	0.53
30:0:1188:A:C6	30:0:1189:A:C6	2.97	0.52
31:9:20:G:O2'	31:9:21:G:H5'	2.09	0.52
30:0:1244:U:H4'	30:0:1246:A:O4'	2.09	0.52
31:9:58:G:C6	31:9:59:C:C2	2.97	0.52
30:0:2037:C:H3'	38:0:6684:HOH:O	2.09	0.52
31:9:37:C:O2	31:9:47:A:H1'	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
30:0:1014:A:H2'	30:0:1015:C:H5'	1.90	0.52
8:H:159:LYS:HG2	30:0:2519:C:O2	2.09	0.52
1:A:105:VAL:HG13	1:A:155:THR:O	2.09	0.52
30:0:488:U:H2'	38:0:3993:HOH:O	2.08	0.52
30:0:216:A:O2'	30:0:217:C:H5'	2.09	0.52
30:0:1451:C:H5'	30:0:1505:U:C5	2.44	0.52
30:0:2719:A:H2'	30:0:2720:C:H5'	1.90	0.52
23:W:4:LEU:HD22	23:W:54:PHE:HB3	1.90	0.52
30:0:675:U:H2'	30:0:676:C:H5'	1.90	0.52
30:0:1164:U:H5	38:0:6024:HOH:O	1.91	0.52
15:O:25:VAL:HG13	30:0:709:G:O3'	2.10	0.52
31:9:1:U:C4'	31:9:3:A:OP1	2.58	0.52
13:M:73:ARG:HH21	30:0:2263:G:H5''	1.70	0.52
30:0:1684:A:O2'	30:0:1685:A:H5''	2.10	0.52
13:M:24:GLN:NE2	13:M:27:ARG:HH11	2.07	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
19:S:33:SER:O	19:S:37:VAL:HG23	2.10	0.52
30:0:622:G:O2'	30:0:623:U:H5'	2.10	0.52
30:0:1557:G:O2'	30:0:1558:C:H5'	2.09	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:126:ILE:HA	5:E:131:LEU:HD23	1.91	0.52
30:0:2320:U:H4'	30:0:2321:A:O4'	2.09	0.52
20:T:26:THR:HG23	20:T:97:ARG:HG3	1.90	0.52
30:0:2783:A:O2'	30:0:2784:A:H5'	2.09	0.52
30:0:249:G:N2	30:0:250:C:C2	2.77	0.52
30:0:40:C:H6	30:0:40:C:O5'	1.93	0.52
28:2:49:GLU:HB2	38:2:131:HOH:O	2.08	0.52
11:K:66:ARG:HH12	30:0:1992:U:H3'	1.75	0.52
31:9:38:A:C2	31:9:39:U:C4	2.97	0.52
30:0:2407:G:H2'	30:0:2408:A:O4'	2.09	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
30:0:24:G:N2	30:0:518:G:H1'	2.24	0.52
23:W:130:HIS:NE2	31:9:88:G:OP1	2.42	0.52
30:0:1359:U:O5'	30:0:1360:C:H5''	2.10	0.52
30:0:204:A:C2'	30:0:205:U:H5'	2.39	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
13:M:81:ARG:HB3	13:M:86:GLN:HG2	1.91	0.52
30:0:1590:A:C2	30:0:1606:A:H1'	2.44	0.52
30:0:916:A:C2	30:0:928:G:N3	2.78	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
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
18:R:132:ARG:HH22	30:0:2055:A:H4'	1.74	0.52
31:9:49:G:O2'	31:9:50:G:H5'	2.08	0.52
5:E:153:ARG:HH12	30:0:2778:A:C1'	2.22	0.52
30:0:1139:U:H2'	30:0:1140:C:C6	2.45	0.52
30:0:1649:G:H1'	38:0:5498:HOH:O	2.09	0.52
4:D:18:ILE:HD13	4:D:84:LEU:HD12	1.91	0.52
20:T:106:GLU:HG3	38:T:4913:HOH:O	2.09	0.52
1:A:66:ARG:HH11	1:A:66:ARG:HB2	1.74	0.52
18:R:111:ILE:HG23	18:R:145:LEU:HD11	1.90	0.52
30:0:1087:G:O2'	35:0:8822:CL:CL	2.55	0.52
30:0:1886:A:H4'	38:0:9333:HOH:O	2.09	0.52
31:9:58:G:C5	31:9:59:C:C2	2.98	0.52
28:2:18:ASN:HD21	28:2:40:ARG:HB3	1.74	0.52
30:0:1890:U:H4'	30:0:2010:A:C6	2.44	0.52
2:B:223:ARG:HG3	2:B:232:TRP:O	2.10	0.52
30:0:2526:C:C6	30:0:2526:C:C3'	2.93	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:228:C:C2'	30:0:229:G:H5'	2.40	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
30:0:1052:G:H2'	30:0:1052:G:N3	2.24	0.52
25:Y:132:ASP:OD2	30:0:621:C:H5'	2.10	0.52
38:I:1549:HOH:O	30:0:1180:U:H1'	2.10	0.52
30:0:506:G:N2	30:0:509:A:H5''	2.18	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
30:0:595: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
18:R:18:LEU:HB2	18:R:143:VAL:HG13	1.91	0.52
31:9:34:A:H2'	31:9:35:C:O4'	2.10	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
30:0:615: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
6:F:91:VAL:HG12	6:F:92:GLY:N	2.20	0.52
30:0:2672:C:H2'	30:0:2673:U:H6	1.74	0.52
7:G:63:ARG:O	7:G:67:LEU:HG	2.10	0.52
2:B:243:ASN:HB2	30:0:2607:U:OP2	2.10	0.52
30:0:599:G:H2'	30:0:600:G:H8	1.74	0.52
12:L:73:VAL:HG23	12:L:74:THR:H	1.75	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
30:0:308:U:C4	30:0:342:C:H1'	2.45	0.52
30:0:818:A:C6	30:0:819:A:N1	2.78	0.52
30:0:1504:A:H5'	38:0:4396:HOH:O	2.10	0.52
30:0:1422:U:H2'	30:0:1423:C:H6	1.72	0.52
30:0:2088:C:H2'	30:0:2089:A:C8	2.44	0.52
30:0:1154:A:H2'	30:0:1155:G:C8	2.44	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
30:0:818:A:C6	30:0:819:A:C2	2.98	0.51
24:X:49:ARG:HD3	24:X:84:ILE:HG12	1.92	0.51
30:0:2872:U:H2'	30:0:2873:C:H6	1.76	0.51
30:0:1743:G:H2'	30:0:1744:G:O4'	2.10	0.51
30:0:1309:U:O2'	30:0:1310:U:H5'	2.10	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)
12:L:78:ALA:HB3	38:L:8860:HOH:O	2.11	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
30:0:1395:C:H2'	30:0:1396:C:C6	2.46	0.51
30:0:2900:G:H2'	30:0:2901:C:O4'	2.10	0.51
14:N:7:LYS:HE3	17:Q:21:ARG:O	2.09	0.51
30:0:395:A:H2'	30:0:397:A:H62	1.74	0.51
30:0:2498:C:O2'	30:0:2499:U:H5'	2.10	0.51
2:B:144:THR:HB	38:B:9096:HOH:O	2.10	0.51
17:Q:87:THR:HB	38:Q:1295:HOH:O	2.10	0.51
30:0:1667:A:H8	30:0:1667:A:H5'	1.75	0.51
30:0:20:G:H5''	30:0:510:U:O4	2.09	0.51
30:0:1992:U:H2'	30:0:1994:A:OP2	2.10	0.51
25:Y:205:ILE:HB	25:Y:230:ASN:HD21	1.75	0.51
30:0:2544:G:H5'	38:0:3418:HOH:O	2.10	0.51
30:0:1641:A:H2'	30:0:1642:A:C5'	2.40	0.51
30:0:2032:U:H2'	30:0:2033:G:H5''	1.92	0.51
30:0:2614:C:O2'	30:0:2615:U:H5'	2.10	0.51
29:3:54:LYS:HE2	30:0:2468:A:C8	2.45	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
31:9:56:A:H3'	31:9:57:A:H5''	1.89	0.51
30:0:1395:C:H2'	30:0:1396:C:H6	1.76	0.51
15:O:65:LEU:HD13	30:0:746:A:C6	2.45	0.51
1:A:175:LYS:HE2	35:A:8809:CL:CL	2.48	0.51
10:J:21:ARG:HH21	30:0:1244:U:H5''	1.76	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
30:0:2846:C:H3'	38:0:7070:HOH:O	2.11	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
30:0:702:G:C2	30:0:703:G:C8	2.98	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
17:Q:7:LEU:HD12	30:0:2424:U:H1'	1.93	0.51
11:K:91:GLU:HG3	38:U:151:HOH:O	2.11	0.51
5:E:137:ASP:OD1	5:E:139:GLU:HB2	2.11	0.51
30:0:2032:U:H2'	30:0:2033:G:H5'	1.93	0.51
30:0:37:A:H2'	30:0:38:G:C8	2.46	0.51
24:X:56:GLU:HG2	30:0:1400:C:H4'	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:40:ARG:HA	29:3:52:PHE:HE1	1.73	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
30:0:1019:C:O2'	30:0:1020:A:H5'	2.11	0.51
29:3:83:TRP:NE1	30:0:2380:A:H2	2.09	0.51
30:0:2719:A:C2'	30:0:2720:C:H5'	2.41	0.51
8:H:114:ASP:HA	38:H:204:HOH:O	2.11	0.51
30:0:128:A:O2'	30:0:129:A:H5'	2.10	0.51
17:Q:94:GLN:O	17:Q:95:GLU:HB2	2.11	0.51
30:0:633:C:O2'	30:0:634:G:H5'	2.10	0.51
15:O:37:ARG:HD2	30:0:656:G:OP2	2.11	0.51
20:T:32:ARG:NH1	20:T:38:ARG:NH1	2.58	0.51
30:0:822:C:N3	30:0:823:U:C5	2.79	0.51
6:F:91:VAL:HG11	30:0:262:A:OP2	2.10	0.51
30:0:2689:A:H2'	30:0:2690:U:H5'	1.92	0.51
7:G:64:ASN:HD22	7:G:64:ASN:H	1.58	0.51
26:Z:78:ILE:HD12	38:Z:8715:HOH:O	2.11	0.51
26:Z:53:ILE:HG23	38:Z:8719:HOH:O	2.10	0.51
6:F:36:THR:HG23	6:F:97:ALA:HB2	1.93	0.51
13:M:28:GLN:O	13:M:32:ARG:HG3	2.10	0.51
30:0:727:G:H3'	30:0:728:C:C6	2.45	0.51
3:C:149:LYS:HE3	38:0:4023:HOH:O	2.10	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
3:C:219:ASN:O	3:C:222:ASP:HB2	2.11	0.51
30:0:1236:A:O2'	30:0:1237:U:H5'	2.11	0.51
30:0:2456:A:O2'	30:0:2457:U:H5'	2.10	0.51
30:0:2712:G:C5'	38:0:5187:HOH:O	2.58	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
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
25:Y:127:GLN:HA	38:Y:8909:HOH:O	2.11	0.51
30:0:523:C:H2'	30:0:524:A:C8	2.46	0.51
24:X:61:ARG:O	30:0:2744:G:H5''	2.11	0.51
30:0:1186:C:N4	30:0:1187:U:C4	2.79	0.51
29:3:22:VAL:HG12	29:3:90:PHE:CE2	2.46	0.51
16:P:118:GLN:O	16:P:122:LEU:HG	2.11	0.51
30:0:39:G:C2	30:0:444:C:C2	2.99	0.51
30:0:2526:C:O2'	30:0:2527:U:H5'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:255:A:H2'	30:0:256:C:C6	2.46	0.51
30:0:1819:G:H2'	30:0:1820:G:C5'	2.41	0.51
2:B:80:ARG:HB2	2:B:145:HIS:CE1	2.45	0.51
30:0:1568:G:H2'	30:0:1569:U:O4'	2.10	0.51
30:0:617:C:H2'	30:0:618:G:O4'	2.11	0.51
8:H:31:ILE:HD11	8:H:65:LEU:HB3	1.93	0.51
9:I:83:GLY:HA3	30:0:1168:C:H5'	1.93	0.50
30:0:553:G:O4'	30:0:1325:G:H5'	2.10	0.50
30:0:1642:A:C8	30:0:1643:C:C5	2.99	0.50
22:V:12:THR:HG23	22:V:14:ALA:H	1.76	0.50
30:0:1805:G:O2'	30:0:1806:G:H5'	2.11	0.50
30:0:1226:G:C5	30:0:1227:C:C5	2.99	0.50
11:K:97:ILE:HG22	11:K:98:VAL:N	2.25	0.50
7:G:20:VAL:O	7:G:24:VAL:HG23	2.11	0.50
30:0:2587:OMU:H2'	30:0:2589:U:H5''	1.93	0.50
30:0:1511:U:O2'	30:0:1512:G:H5'	2.11	0.50
30:0:560:U:H2'	30:0:561:G:H8	1.75	0.50
26:Z:102:THR:HG23	26:Z:105:ARG:HD2	1.93	0.50
2:B:71:VAL:HG21	2:B:296:LEU:HB3	1.92	0.50
30:0:1796:A:H8	30:0:1796:A:O5'	1.94	0.50
30:0:1441:G:O2'	30:0:1442:A:H5'	2.11	0.50
30:0:1167:G:N2	30:0:1180:U:C2	2.79	0.50
3:C:127:ARG:HH21	3:C:225:PRO:HG2	1.71	0.50
30:0:2847:G:O2'	30:0:2848:G:H5'	2.11	0.50
30:0:2672:C:C2	30:0:2673:U:C6	3.00	0.50
25:Y:210:GLY:N	30:0:1313:A:H5''	2.27	0.50
30:0:2087:C:O2'	30:0:2088:C:H5'	2.11	0.50
30:0:134:U:O2	30:0:145:A:C2	2.63	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
30:0:2899:A:O2'	30:0:2900:G:H5'	2.12	0.50
30:0:1216:G:N2	30:0:1217:G:H1'	2.26	0.50
30:0:1735:C:H2'	30:0:1736:A:H8	1.75	0.50
27:1:16:HIS:CD2	30:0:470:U:O2'	2.64	0.50
30:0:1087:G:H4'	30:0:1088:A:OP1	2.12	0.50
30:0:523:C:H2'	30:0:524:A:H8	1.76	0.50
30:0:1461:U:H2'	30:0:1462:C:C6	2.46	0.50
30:0:876:A:N3	30:0:876:A:H2'	2.26	0.50
29:3:29:ARG:HA	38:3:9012:HOH:O	2.11	0.50
5:E:7:ILE:HG13	5:E:11:VAL:HB	1.93	0.50
2:B:248:ARG:O	2:B:251:VAL:HG22	2.11	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
30:0:2564:G:OP2	30:0:2565:C:H5''	2.11	0.50
30:0:1522:A:H2'	30:0:1523:G:H5'	1.92	0.50
30:0:1474:C:H6	30:0:1474:C:C5'	2.17	0.50
30:0:40:C:H2'	30:0:41:G:C8	2.46	0.50
30:0:2635:A:HO2'	30:0:2636:C:H5'	1.76	0.50
10:J:107:ASN:C	10:J:107:ASN:HD22	2.15	0.50
29:3:10:TYR:CE1	30:0:2408:A:H1'	2.46	0.50
29:3:10:TYR:HB2	29:3:17:HIS:HE1	1.76	0.50
30:0:1463:U:H2'	30:0:1464:C:C6	2.47	0.50
12:L:65:ASP:HA	12:L:109:LEU:O	2.11	0.50
30:0:1811:A:C2	30:0:2752:C:H1'	2.46	0.50
30:0:1187:U:O2'	30:0:1189:A:H2	1.94	0.50
13:M:71:SER:HB2	13:M:92:THR:CG2	2.35	0.50
2:B:235:ARG:HH11	30:0:2092:G:P	2.33	0.50
30:0:1149:U:C5	30:0:1215:A:C5	3.00	0.50
7:G:16:LYS:O	7:G:20:VAL:HG23	2.11	0.50
30:0:73:U:H2'	30:0:74:G:C8	2.46	0.50
30:0:1015:C:O5'	30:0:1015:C:H6	1.94	0.50
17:Q:95:GLU:HA	30:0:949:U:H4'	1.94	0.50
30:0:105:G:O2'	30:0:106:A:H5'	2.11	0.50
14:N:37:ARG:NH1	31:9:6:C:OP1	2.44	0.50
30:0:2506:A:C1'	38:0:6031:HOH:O	2.58	0.50
16:P:114:LEU:HD22	16:P:118:GLN:HB3	1.93	0.50
30:0:372:A:C2	30:0:373:G:C4	2.99	0.50
30:0:819:A:C4	30:0:821:U:C5	3.00	0.50
30:0:119:A:H2'	30:0:120:A:C5'	2.42	0.50
30:0:2295:G:N3	30:0:2361:A:C2	2.80	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
30:0:2344:G:N3	30:0:2344:G:H2'	2.26	0.50
8:H:59:GLN:NE2	8:H:129:ARG:HE	2.10	0.50
30:0:929:A:H5''	38:0:7060:HOH:O	2.11	0.50
38:B:8995:HOH:O	30:0:2093:G:H5''	2.11	0.50
16:P:135:ALA:O	16:P:139:ARG:HG3	2.11	0.50
30:0:451:C:O2'	30:0:452:G:H5'	2.12	0.50
29:3:3:MET:O	29:3:90:PHE:HA	2.11	0.50
30:0:1666:C:H42	30:0:1667:A:N6	2.10	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
30:0:2823:G:O2'	30:0:2824:C:H5'	2.12	0.50
30:0:10:U:O4	30:0:532:A:H8	1.95	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
30:0:2803:C:H2'	30:0:2804:C:H6	1.77	0.50
30:0:79:G:N2	30:0:97:G:H1'	2.26	0.50
30:0:1705:C:O2	30:0:2735:U:H5''	2.11	0.50
30:0:282:C:O2'	30:0:283:U:C4'	2.60	0.50
22:V:56:ILE:O	22:V:60:GLN:HG3	2.12	0.50
13:M:77:HIS:CE1	13:M:86:GLN:HG2	2.47	0.50
13:M:82:ARG:HH22	13:M:85:ARG:NH2	2.08	0.50
30:0:1878:G:C4'	38:0:6097:HOH:O	2.60	0.50
31:9:23:U:H2'	31:9:23:U:O2	2.12	0.50
30:0:74:G:H1	30:0:103:C:N4	2.10	0.50
29:3:10:TYR:HB2	29:3:17:HIS:CE1	2.47	0.50
14:N:38:LYS:HE2	14:N:107:ASN:HD21	1.75	0.50
1:A:100:PRO:HG2	1:A:103:VAL:HG21	1.94	0.50
30:0:764:C:H2'	30:0:765:G:O4'	2.12	0.50
30:0:59:A:C5'	38:0:4313:HOH:O	2.60	0.50
3:C:22:PHE:HA	3:C:116:ALA:HA	1.94	0.50
29:3:3:MET:SD	29:3:88:LEU:HD23	2.52	0.50
1:A:141:PRO:HG2	30:0:1855:G:O6	2.12	0.50
30:0:814:G:H2'	30:0:815:U:H6	1.77	0.50
20:T:71:VAL:HG11	20:T:90:PRO:CB	2.38	0.50
2:B:18:ARG:HG3	2:B:256:GLN:HG3	1.93	0.50
30:0:2253:G:O2'	30:0:2254:G:H5'	2.11	0.50
23:W:6:GLN:CB	23:W:26:ILE:HD11	2.40	0.50
31:9:42:C:H5'	31:9:43:G:OP2	2.12	0.50
12:L:24:ALA:HB2	12:L:30:ARG:HE	1.76	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
23:W:130:HIS:O	23:W:136:GLY:HA3	2.12	0.50
3:C:101:ASP:HB2	30:0:750:A:O3'	2.12	0.50
13:M:145:ASP:HB2	38:M:8865:HOH:O	2.11	0.50
24:X:26:ALA:HB2	24:X:63:ARG:HA	1.93	0.50
31:9:28:U:O2	31:9:57:A:N6	2.44	0.49
13:M:159:VAL:CG1	35:M:8818:CL:CL	2.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1165:G:H21	30:0:1173:A:H5'	1.74	0.49
4:D:58:VAL:CG1	4:D:60:GLU:HG2	2.41	0.49
30:0:952:G:N3	30:0:2302:A:H2'	2.26	0.49
31:9:39:U:H1'	31:9:44:A:H61	1.77	0.49
30:0:47:G:N3	30:0:114:A:C2	2.80	0.49
30:0:1268:C:H2'	30:0:1269:G:C8	2.46	0.49
30:0:2854:A:C6	30:0:2905:A:C6	3.00	0.49
2:B:66:GLU:OE1	2:B:328:ARG:HD2	2.12	0.49
30:0:1933:G:O2'	30:0:1934:A:H5'	2.12	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
16:P:87:ARG:HG2	38:0:5919:HOH:O	2.10	0.49
31:9:55:U:H4'	31:9:56:A:H8	1.71	0.49
30:0:1226:G:H2'	30:0:1227:C:C6	2.44	0.49
30:0:1662:C:H6	30:0:1662:C:O5'	1.94	0.49
29:3:60:LYS:C	29:3:62:THR:H	2.15	0.49
30:0:589:U:H2'	30:0:590:A:H8	1.76	0.49
30:0:134:U:C2	30:0:145:A:C2	2.99	0.49
30:0:1902:G:N2	30:0:1936:C:C2	2.80	0.49
8:H:32:ALA:HB3	8:H:69:ARG:HH12	1.77	0.49
18:R:18:LEU:O	18:R:142:ASP:HA	2.12	0.49
4:D:35:ALA:HB2	38:D:5576:HOH:O	2.11	0.49
30:0:873:G:N2	38:0:9173:HOH:O	2.43	0.49
16:P:98:ILE:HD12	16:P:102:ARG:NE	2.27	0.49
30:0:1194:A:C2	30:0:1206:U:H1'	2.47	0.49
30:0:400:C:H2'	30:0:401:C:C6	2.47	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
30:0:1800:G:H2'	30:0:1801:A:H8	1.77	0.49
30:0:316:A:N3	30:0:336:G:O2'	2.41	0.49
30:0:2291:A:N3	30:0:2291:A:H2'	2.28	0.49
25:Y:212:ARG:HB2	30:0:1315:G:C4	2.47	0.49
11:K:34:VAL:HB	38:K:7169:HOH:O	2.12	0.49
30:0:2617:G:C2	30:0:2618:G:C8	3.00	0.49
10:J:131:THR:HG22	10:J:134:GLU:H	1.77	0.49
30:0:1206:U:C5'	30:0:1206:U:H6	2.21	0.49
30:0:816:G:H5'	30:0:1598:A:H4'	1.94	0.49
30:0:814:G:H2'	30:0:815:U:C6	2.47	0.49
1:A:47:HIS:CD2	30:0:1654:U:C2'	2.92	0.49
25:Y:115:ARG:NH2	30:0:1266:U:H4'	2.27	0.49
2:B:215:VAL:O	2:B:219:GLY:HA2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:60:ASP:HB3	26:Z:69:ASP:HB3	1.92	0.49
30:0:1255:A:H1'	38:0:7741:HOH:O	2.11	0.49
30:0:2133:U:H4'	30:0:2134:G:H5'	1.93	0.49
30:0:1947:G:N2	30:0:1966:U:N3	2.60	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
30:0:1381:A:N3	30:0:1382:G:H1'	2.28	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
30:0:2632:G:H2'	30:0:2633:A:C8	2.46	0.49
30:0:2632:G:C6	30:0:2633:A:N6	2.81	0.49
30:0:1339:G:C6	30:0:1340:G:N1	2.81	0.49
30:0:36:C:C2	30:0:447:A:C2	3.00	0.49
6:F:110:ASP:O	6:F:114:LYS:HG3	2.12	0.49
30:0:1559:A:HO2'	30:0:1561:U:H5	1.60	0.49
30:0:1787:C:O4'	30:0:2883:A:H1'	2.11	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
2:B:304:PRO:HD2	2:B:307:ARG:HE	1.78	0.49
30:0:1555:G:H4'	30:0:1630:A:C2	2.47	0.49
30:0:2118:A:H5'	38:0:3996:HOH:O	2.13	0.49
30:0:1370:G:H5''	38:0:5497:HOH:O	2.12	0.49
14:N:58:LEU:HD12	14:N:58:LEU:N	2.27	0.49
30:0:494:C:H1'	30:0:498:A:N6	2.27	0.49
30:0:2366:C:O5'	30:0:2366:C:H6	1.95	0.49
30:0:1189:A:O2'	30:0:1208:C:H2'	2.12	0.49
14:N:37:ARG:HH11	14:N:37:ARG:HG3	1.77	0.49
30:0:1682:A:O2'	30:0:1683:G:H5''	2.12	0.49
30:0:2335:C:C2	30:0:2350:G:C2	3.01	0.49
30:0:1174:A:C5	30:0:1201:C:H4'	2.47	0.49
8:H:27:PRO:HD3	8:H:123:ILE:CG2	2.43	0.49
30:0:29:C:O2'	30:0:30:U:H5'	2.12	0.49
30:0:1517:C:O2	30:0:1670:A:C2	2.66	0.49
20:T:107:LYS:HD2	30:0:97:G:C2	2.47	0.49
10:J:130:VAL:HG12	10:J:131:THR:H	1.78	0.49
30:0:1871:U:O4'	30:0:1873:G:C8	2.66	0.49
30:0:1626:A:O2'	30:0:1627:G:H5'	2.13	0.49
18:R:71:LYS:HE2	30:0:2831:C:O3'	2.13	0.49
30:0:1226:G:N3	30:0:1227:C:C6	2.81	0.49
30:0:2478:U:H2'	30:0:2479:A:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:316:A:H1'	30:0:336:G:N3	2.27	0.49
29:3:33:MET:HG2	30:0:1922:A:C2'	2.42	0.49
2:B:307:ARG:HD2	38:B:9123:HOH:O	2.12	0.49
29:3:12:PRO:HB3	30:0:2382:A:O2'	2.12	0.49
30:0:549:A:C6	30:0:550:C:C4	3.00	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
30:0:285:A:H2'	30:0:286:U:O4'	2.13	0.49
30:0:862:U:H2'	30:0:863:G:H8	1.77	0.49
30:0:889:C:H4'	38:0:6368:HOH:O	2.13	0.49
30:0:1183:C:N4	30:0:1184:C:N4	2.60	0.49
26:Z:47:ARG:HH22	30:0:1771:U:H1'	1.77	0.49
30:0:2326:C:H4'	30:0:2412:G:H4'	1.94	0.49
1:A:109:GLU:HG2	1:A:116:GLY:N	2.25	0.49
30:0:1706:G:C5	30:0:1707:G:C6	3.00	0.49
30:0:2826:G:H1'	30:0:2914:A:N6	2.28	0.49
30:0:1760:G:H5'	30:0:1818:C:O2'	2.12	0.49
30:0:1583:U:O2'	30:0:1584:C:H5'	2.13	0.49
30:0:1921:A:C6	30:0:1922:A:C2	3.00	0.49
31:9:110:G:N2	31:9:111:U:H1'	2.28	0.49
2:B:162:MET:CE	2:B:308:LEU:HD21	2.42	0.49
30:0:447:A:O2'	30:0:448:G:H5'	2.13	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
30:0:1116:U:C2	30:0:1246:A:N6	2.81	0.49
31:9:105:A:H2'	31:9:106:U:O4'	2.12	0.49
14:N:25:ARG:HB3	30:0:2415:A:C2	2.47	0.49
30:0:717:C:H2'	30:0:718:C:H6	1.78	0.49
30:0:2269:C:H2'	30:0:2270:G:O4'	2.12	0.49
25:Y:235:GLU:CD	25:Y:235:GLU:H	2.16	0.49
30:0:1343:C:H2'	30:0:1344:G:O5'	2.12	0.49
30:0:731:U:O2'	30:0:732:C:H5'	2.13	0.49
30:0:1453:G:C2	30:0:1675:C:C2	3.00	0.49
1:A:36:ASP:HB2	1:A:85:SER:H	1.77	0.49
30:0:2103:A:N3	30:0:2103:A:H2'	2.28	0.49
29:3:1:MET:HG2	29:3:87:ARG:O	2.11	0.49
30:0:1119:G:H22	30:0:1246:A:H2	1.46	0.49
31:9:60:C:O2'	31:9:61:C:H5'	2.13	0.49
30:0:271:C:N4	30:0:378:A:H2	2.01	0.49
20:T:69:LYS:O	20:T:71:VAL:HG23	2.13	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
27:1:21:ARG:HD2	27:1:39:PHE:HB2	1.95	0.49
30:0:1351:G:H1'	38:0:4648:HOH:O	2.13	0.49
30:0:2536:C:H6	38:0:4998:HOH:O	1.95	0.49
31:9:8:G:C6	31:9:9:C:C4	3.00	0.49
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
14:N:178:THR:O	14:N:181:ASP:HB3	2.13	0.49
30:0:191:A:H2'	30:0:237:G:O6	2.12	0.48
29:3:88:LEU:HB3	29:3:90:PHE:CE1	2.48	0.48
6:F:63:ILE:HB	6:F:64:PRO:CD	2.37	0.48
30:0:1644:C:C2	30:0:1645:U:C5	3.01	0.48
30:0:2297:U:H2'	30:0:2298:C:H6	1.78	0.48
13:M:52:GLN:OE1	13:M:116:ASN:HB3	2.13	0.48
30:0:1063:G:H4'	30:0:2307:A:H1'	1.95	0.48
30:0:1586:G:C2'	30:0:1587:U:H5'	2.43	0.48
30:0:419:A:H1'	30:0:1921:A:C2	2.48	0.48
3:C:173:LYS:HE3	30:0:1311:G:O6	2.12	0.48
30:0:788:A:H4'	38:0:7005:HOH:O	2.12	0.48
30:0:1240:G:H1'	38:0:9360:HOH:O	2.12	0.48
30:0:2639:G:C5	30:0:2640:U:C5	3.01	0.48
25:Y:137:LYS:HD2	38:0:7590:HOH:O	2.11	0.48
4:D:92:GLU:HB2	38:D:3862:HOH:O	2.13	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
30:0:2864:U:O2'	30:0:2865:G:H5'	2.14	0.48
20:T:28:SER:O	20:T:32:ARG:HG3	2.14	0.48
13:M:134:ILE:CG2	13:M:141:ILE:HD13	2.36	0.48
21:U:19:THR:HG22	21:U:20:MET:N	2.28	0.48
11:K:98:VAL:HG11	11:K:102:GLU:HA	1.94	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
30:0:106:A:C6	30:0:107:U:C4	3.00	0.48
30:0:1916:C:O2'	30:0:1917:G:H5'	2.14	0.48
30:0:1765:G:O2'	30:0:1766:U:H5'	2.12	0.48
30:0:2713:G:O2'	30:0:2714:U:H5'	2.12	0.48
30:0:1066:U:H2'	30:0:1067:A:C8	2.48	0.48
30:0:2646:G:C4	30:0:2647:C:C5	3.02	0.48
31:9:3:A:H2	31:9:21:G:N3	2.12	0.48
30:0:1883:U:H2'	30:0:1884:G:H5'	1.94	0.48
30:0:2898:G:H1'	38:0:7555:HOH:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:595:U:O4'	35:0:8817:CL:CL	2.69	0.48
30:0:2526:C:C6	30:0:2526:C:H3'	2.47	0.48
30:0:2827:A:C2	30:0:2914:A:C2	3.01	0.48
30:0:334:G:C5	30:0:335:U:C5	3.00	0.48
16:P:124:ASP:O	30:0:801:U:H4'	2.13	0.48
30:0:1832:G:C2	30:0:1833:U:C6	3.00	0.48
8:H:52:LEU:HD13	8:H:153:PHE:HB3	1.95	0.48
30:0:681:G:N3	30:0:681:G:H5'	2.28	0.48
30:0:2480:G:O2'	30:0:2481:G:H5'	2.13	0.48
8:H:35:LYS:HE3	30:0:968:G:H1'	1.95	0.48
26:Z:42:TYR:H	30:0:1829:A:H61	1.61	0.48
30:0:1632:A:C3'	30:0:1633:C:H5'	2.43	0.48
30:0:120:A:H2'	30:0:120:A:N3	2.29	0.48
30:0:2700:G:H2'	30:0:2701:G:C5'	2.43	0.48
30:0:1015:C:H2'	30:0:1016:U:C6	2.48	0.48
30:0:1557:G:H2'	30:0:1558:C:H6	1.78	0.48
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
29:3:64:LYS:HE2	38:0:7638:HOH:O	2.12	0.48
30:0:2505:G:C2'	30:0:2506:A:C5'	2.91	0.48
20:T:27:LEU:HB2	20:T:32:ARG:HG2	1.95	0.48
11:K:43:ARG:NH1	30:0:2712:G:OP1	2.46	0.48
4:D:37:ALA:O	4:D:40:ILE:HG12	2.13	0.48
30:0:1634:G:H2'	30:0:1635:U:H6	1.76	0.48
30:0:1434:A:O2'	30:0:1435:U:H6	1.92	0.48
30:0:2672:C:H2'	30:0:2673:U:O4'	2.14	0.48
18:R:132:ARG:HG2	18:R:133:ALA:N	2.27	0.48
30:0:2255:A:C2	30:0:2256:G:C4	3.02	0.48
30:0:677:C:H2'	30:0:678:G:H8	1.77	0.48
30:0:2772:G:O2'	30:0:2773:G:H5'	2.13	0.48
30:0:707:C:C2	30:0:708:A:C8	3.02	0.48
30:0:2755:G:H1'	38:0:4651:HOH:O	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
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
30:0:1496:A:H5'	30:0:1572:A:H1'	1.94	0.48
30:0:222:A:H2'	30:0:223:G:O4'	2.13	0.48
30:0:100:C:C4	30:0:101:C:C5	3.01	0.48
19:S:6:LYS:HB2	19:S:27:ALA:O	2.13	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
30:0:200:C:H6	38:0:3433:HOH:O	1.96	0.48
5:E:139:GLU:OE2	30:0:2781:U:H1'	2.13	0.48
29:3:43:ASN:HB2	29:3:52:PHE:CD1	2.48	0.48
30:0:2598:U:O2	30:0:2600:A:C8	2.66	0.48
2:B:36:PRO:HG3	2:B:169:GLY:H	1.77	0.48
30:0:2133:U:H4'	30:0:2134:G:C5'	2.44	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
30:0:2617:G:H4'	38:0:4487:HOH:O	2.13	0.48
10:J:60:ARG:HD3	10:J:71:TYR:CE1	2.47	0.48
15:O:88:LYS:HB3	38:O:7061:HOH:O	2.13	0.48
4:D:51:ARG:HH11	4:D:68:PRO:HB3	1.78	0.48
30:0:611:U:H2'	30:0:612:U:C6	2.48	0.48
30:0:1520:G:H2'	30:0:1521:C:C6	2.49	0.48
30:0:2569:A:O5'	30:0:2569:A:H8	1.96	0.48
27:1:25:LYS:CD	28:2:49:GLU:H	2.25	0.48
18:R:138:SER:HB2	38:0:5570:HOH:O	2.14	0.48
30:0:705:C:C2'	30:0:705:C:O2	2.62	0.48
30:0:2707:C:C2'	30:0:2707:C:O2	2.59	0.48
23:W:26:ILE:HB	38:W:5420:HOH:O	2.14	0.48
30:0:1878:G:C2	30:0:1879:U:C2	3.02	0.48
30:0:31:C:H2'	38:0:7668:HOH:O	2.13	0.48
30:0:627:G:H2'	30:0:2071:C:C4	2.49	0.48
30:0:1908:G:N1	30:0:1930:A:OP2	2.46	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
13:M:139:PRO:HA	13:M:142:GLN:HB2	1.95	0.48
30:0:1224:G:H2'	30:0:1225:C:C6	2.48	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
30:0:2717:C:H2'	30:0:2718:C:H5'	1.93	0.48
29:3:40:ARG:C	29:3:42:ARG:H	2.16	0.48
30:0:1063:G:H8	38:0:9856:HOH:O	1.96	0.48
30:0:808:A:C5	30:0:809:G:H1'	2.48	0.48
30:0:2354:A:C2	30:0:2367:A:C8	3.02	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
16:P:11:ALA:HB1	16:P:16:VAL:O	2.14	0.48
30:0:1023:C:O2'	30:0:1024:G:H5'	2.14	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
28:2:10:ARG:NH2	30:0:121:U:OP2	2.44	0.48
1:A:162:GLY:N	26:Z:91:GLY:HA2	2.29	0.48
9:I:133:THR:HG22	9:I:134:ILE:N	2.28	0.48
23:W:117:ARG:HH22	30:0:1264:U:P	2.36	0.48
30:0:1029:U:O2'	30:0:1273:C:OP1	2.27	0.48
30:0:1204:C:H2'	30:0:1205:U:O4'	2.14	0.48
30:0:2505:G:H2'	30:0:2506:A:C5'	2.43	0.48
30:0:69:A:C2'	30:0:70:A:OP2	2.62	0.48
30:0:1177:A:N3	30:0:1177:A:H2'	2.28	0.48
30:0:2254:G:C2	30:0:2255:A:C8	3.01	0.48
30:0:920:C:C4'	30:0:921:G:C2	2.95	0.48
30:0:2777:G:O2'	30:0:2778:A:H5'	2.13	0.48
31:9:39:U:C2'	31:9:40:C:OP1	2.62	0.48
30:0:2281:C:H5	38:0:3756:HOH:O	1.97	0.48
30:0:2587:OMU:H5	38:0:7464:HOH:O	2.13	0.48
30:0:763:C:O2'	30:0:764:C:H5'	2.14	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
30:0:842:C:H4'	38:0:3427:HOH:O	2.13	0.48
1:A:71:PRO:HG2	1:A:91:GLY:HA2	1.95	0.48
30:0:432:G:H5''	38:0:6860:HOH:O	2.12	0.48
30:0:1186:C:C4	30:0:1187:U:C4	3.02	0.48
6:F:58:GLU:HA	6:F:61:MET:SD	2.54	0.48
14:N:4:PRO:HG3	31:9:69:U:OP1	2.13	0.48
29:3:51:LYS:HG3	29:3:52:PHE:HD2	1.76	0.48
11:K:1:MET:N	30:0:2686:C:O2'	2.38	0.48
29:3:83:TRP:HB2	38:0:5759:HOH:O	2.14	0.48
2:B:226:LYS:HG2	2:B:230:GLN:HE21	1.78	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
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
13:M:9:ARG:HD2	30:0:380:A:OP2	2.14	0.48
30:0:870:G:H2'	30:0:871:G:C5'	2.34	0.47
30:0:1188:A:C5	30:0:1189:A:C2	3.02	0.47
30:0:625:U:H5''	30:0:1044:C:H42	1.71	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
29:3:50:GLY:CA	30:0:170:U:H1'	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2598:U:O2	30:0:2600:A:H8	1.96	0.47
3:C:162:VAL:HG13	3:C:162:VAL:O	2.13	0.47
9:I:69:PRO:HA	30:0:1164:U:OP1	2.14	0.47
18:R:15:LYS:HE3	38:R:8976:HOH:O	2.14	0.47
30:0:1745:G:H5'	38:0:4312:HOH:O	2.14	0.47
30:0:1471:A:H2'	30:0:1472:C:C6	2.48	0.47
30:0:2458:U:H3'	38:0:3241:HOH:O	2.13	0.47
30:0:1337:G:C5	30:0:1338:U:C5	3.02	0.47
30:0:1337:G:C6	30:0:1338:U:C4	3.01	0.47
30:0:151:A:H2'	30:0:152:A:O4'	2.14	0.47
30:0:2474:A:N7	30:0:2621:PSU:H4'	2.29	0.47
30:0:2474:A:H5'	30:0:2476:C:O5'	2.14	0.47
30:0:968:G:O2'	30:0:969:G:H5'	2.14	0.47
30:0:373:G:O2'	30:0:374:U:H5'	2.14	0.47
1:A:27:LEU:HD21	1:A:55:VAL:CG2	2.44	0.47
30:0:2855:G:C2	30:0:2904:U:N3	2.82	0.47
2:B:84:LEU:O	2:B:99:GLU:HA	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
30:0:2087:C:H2'	30:0:2088:C:H6	1.80	0.47
26:Z:40:ALA:HA	30:0:1773:G:H8	1.79	0.47
30:0:834:G:H3'	30:0:835:U:H4'	1.97	0.47
30:0:361:C:H2'	30:0:362:G:O4'	2.13	0.47
25:Y:234:VAL:HG12	25:Y:235:GLU:N	2.28	0.47
30:0:1947:G:OP1	30:0:1971:G:N7	2.47	0.47
11:K:132:VAL:HG11	21:U:22:VAL:HG22	1.96	0.47
30:0:1275:C:H2'	30:0:1276:U:H5'	1.96	0.47
22:V:12:THR:CG2	22:V:15:GLU:HG3	2.40	0.47
21:U:56:ARG:HB2	30:0:2890:A:N7	2.29	0.47
30:0:1389:G:N2	30:0:1391:G:H3'	2.29	0.47
2:B:201:ASP:CB	2:B:312:ARG:HD2	2.42	0.47
30:0:407:A:H5'	38:0:6000:HOH:O	2.14	0.47
2:B:74:ILE:HD13	2:B:309:VAL:HG21	1.95	0.47
24:X:85:VAL:HG12	24:X:86:GLU:N	2.29	0.47
30:0:2724:U:H6	30:0:2724:U:O5'	1.96	0.47
2:B:162:MET:HE1	2:B:308:LEU:HD21	1.96	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
30:0:681:G:N3	30:0:681:G:H2'	2.30	0.47
1:A:70:ALA:HB1	26:Z:89:THR:HG21	1.97	0.47
30:0:2857:C:H1'	38:0:5328:HOH:O	2.15	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
30:0:965:A:H5'	30:0:966:U:OP2	2.14	0.47
30:0:699:C:C2	30:0:744:G:C2	3.03	0.47
30:0:1619:G:H2'	30:0:1620:C:C6	2.49	0.47
30:0:1210:G:N2	30:0:1211:G:H1'	2.29	0.47
29:3:88:LEU:CD2	35:3:8804:CL:CL	2.86	0.47
30:0:558:C:HO2'	30:0:559:U:H5''	1.78	0.47
29:3:68:LYS:HG2	29:3:77:ALA:CB	2.44	0.47
31:9:73:A:H61	31:9:108:C:N4	2.13	0.47
30:0:371:U:C4	30:0:372:A:N7	2.83	0.47
30:0:820:G:O2'	30:0:856:G:H4'	2.14	0.47
30:0:1503:U:H2'	30:0:1504:A:C5'	2.45	0.47
28:2:15:ASP:O	28:2:18:ASN:HB2	2.15	0.47
30:0:2781:U:C2'	30:0:2782:G:H5'	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
30:0:1226:G:C4	30:0:1227:C:C6	3.02	0.47
31:9:39:U:H3	31:9:42:C:H5''	1.79	0.47
17:Q:11:ARG:HD3	38:0:6238:HOH:O	2.13	0.47
30:0:2265:U:H2'	30:0:2266:A:H8	1.80	0.47
8:H:59:GLN:HE22	8:H:96:GLN:HG2	1.79	0.47
30:0:699:C:C6	30:0:744:G:N3	2.82	0.47
30:0:287:C:H6	30:0:287:C:O5'	1.97	0.47
11:K:118:ALA:HA	11:K:125:ALA:HB2	1.96	0.47
31:9:5:G:C2'	31:9:6:C:H5'	2.45	0.47
30:0:1667:A:H5'	30:0:1667:A:C8	2.50	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
29:3:9:THR:HG23	29:3:20:HIS:CE1	2.49	0.47
30:0:2375:A:H2'	30:0:2376:C:C6	2.50	0.47
20:T:71:VAL:CG1	20:T:90:PRO:HB3	2.40	0.47
7:G:64:ASN:ND2	7:G:64:ASN:N	2.62	0.47
1:A:135:VAL:HA	1:A:150:PRO:HD3	1.96	0.47
30:0:1760:G:C5	30:0:1761:U:C4	3.03	0.47
30:0:2597:U:C2'	30:0:2598:U:H5'	2.45	0.47
2:B:234:ARG:NH2	30:0:2039:A:OP2	2.47	0.47
11:K:97:ILE:HG22	11:K:98:VAL:H	1.79	0.47
26:Z:34:SER:CA	30:0:797:A:H4'	2.44	0.47
30:0:731:U:H2'	30:0:732:C:C6	2.50	0.47
30:0:724:G:O2'	30:0:725:C:H5'	2.15	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
30:0:1858:A:H2'	30:0:1859:A:C8	2.50	0.47
23:W:21:LEU:HD21	23:W:48:VAL:HG11	1.96	0.47
20:T:51:LEU:HD11	20:T:97:ARG:HB2	1.97	0.47
14:N:71:TRP:HZ2	38:N:8833:HOH:O	1.97	0.47
30:0:2781:U:H2'	30:0:2782:G:H5'	1.95	0.47
30:0:711:G:O2'	30:0:712:C:H5'	2.15	0.47
10:J:39:VAL:CG2	10:J:107:ASN:HA	2.44	0.47
25:Y:151:SER:HB3	25:Y:154:ARG:HB3	1.97	0.47
8:H:123:ILE:HD12	8:H:123:ILE:N	2.30	0.47
30:0:2727:A:C2'	30:0:2728:C:H5'	2.45	0.47
30:0:790:A:H1'	30:0:1710:A:H2'	1.97	0.47
16:P:13:VAL:HG13	16:P:14:LEU:N	2.29	0.47
1:A:94:LEU:HG	1:A:99:ILE:CD1	2.44	0.47
8:H:6:ALA:HB3	30:0:2521:A:OP2	2.14	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
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
30:0:2858:U:H2'	30:0:2859:C:C6	2.49	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
30:0:1333:U:H2'	30:0:1334:C:H6	1.80	0.47
30:0:1988:C:H2'	30:0:1989:G:O4'	2.15	0.47
23:W:77:ALA:HB3	38:W:5763:HOH:O	2.14	0.47
2:B:171:VAL:O	2:B:175:LEU:HB2	2.15	0.47
30:0:2837:U:H2'	38:0:6824:HOH:O	2.15	0.47
23:W:129:LYS:HE3	31:9:87:U:H2'	1.97	0.47
30:0:1168:C:H2'	30:0:1169:U:H5'	1.96	0.47
31:9:22:G:N7	31:9:55:U:C6	2.82	0.47
30:0:1446:U:H4'	30:0:1447:U:OP2	2.14	0.47
23:W:128:VAL:HG22	30:0:1098:A:OP1	2.15	0.47
30:0:2460:A:C2	30:0:2461:U:C2	3.02	0.47
30:0:835:U:H5''	38:0:9381:HOH:O	2.14	0.47
30:0:800:G:H8	30:0:800:G:O5'	1.98	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
30:0:2059:U:H1'	38:0:4439:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1857:A:N6	30:0:2247:C:H1'	2.30	0.47
16:P:3:LEU:HA	16:P:6:GLN:OE1	2.14	0.47
22:V:64:GLY:O	22:V:65:ASP:HB2	2.15	0.47
1:A:171:LYS:HB2	30:0:820:G:C5	2.50	0.47
16:P:1:THR:O	30:0:1396:C:H1'	2.15	0.47
30:0:1889:C:O2'	30:0:1890:U:H5'	2.15	0.47
2:B:212:GLN:HB2	2:B:257:THR:OG1	2.15	0.47
30:0:292:G:H2'	30:0:358:G:N2	2.30	0.47
30:0:2490:A:H5''	38:0:7023:HOH:O	2.15	0.47
22:V:1:THR:HG23	22:V:2:VAL:N	2.29	0.47
30:0:561:G:H2'	30:0:562:A:H8	1.79	0.47
30:0:2858:U:H2'	30:0:2859:C:H6	1.80	0.47
23:W:72:PRO:HG2	38:W:5763:HOH:O	2.15	0.47
30:0:2878:U:H2'	30:0:2879:A:O4'	2.14	0.47
6:F:21:GLU:O	6:F:24:ARG:HG2	2.15	0.47
18:R:69:LYS:HB2	18:R:72:VAL:HG23	1.97	0.47
30:0:249:G:O2'	30:0:250:C:H5'	2.15	0.47
30:0:1806:G:C4	30:0:1807:U:C6	3.03	0.47
23:W:125:HIS:CE1	30:0:1097:A:C5'	2.95	0.47
30:0:2301:A:H5''	30:0:2302:A:H5'	1.96	0.47
16:P:41:ARG:NH2	30:0:1500:U:OP2	2.47	0.47
30:0:1056:U:H2'	30:0:1057:A:O4'	2.14	0.47
30:0:1928:C:O2'	30:0:1929:G:H5'	2.15	0.47
13:M:193:LYS:HB3	30:0:392:U:C5'	2.45	0.47
17:Q:34:ASP:O	17:Q:37:GLU:HB2	2.15	0.47
14:N:170:GLU:O	14:N:174:GLU:HG3	2.14	0.47
30:0:1159:G:H1	30:0:1208:C:H42	1.63	0.46
31:9:54:A:C2'	31:9:55:U:C5'	2.85	0.46
30:0:137:U:OP1	30:0:259:G:O2'	2.33	0.46
30:0:1942:A:O2'	30:0:1943:C:H5'	2.15	0.46
30:0:40:C:H5'	38:0:3836:HOH:O	2.14	0.46
30:0:1177:A:N1	30:0:1178:G:C4	2.82	0.46
30:0:1760:G:C6	30:0:1761:U:C4	3.03	0.46
4:D:22:VAL:HG21	30:0:2348:C:C5'	2.45	0.46
30:0:806:A:H2'	30:0:807:A:O4'	2.15	0.46
16:P:13:VAL:HG13	16:P:14:LEU:H	1.80	0.46
30:0:589:U:H2'	30:0:590:A:C8	2.50	0.46
24:X:30:MET:HG2	30:0:1384:C:H5'	1.96	0.46
30:0:2379:G:H4'	30:0:2380:A:C5'	2.45	0.46
30:0:737:A:H2'	30:0:738:G:C8	2.49	0.46
19:S:6:LYS:HE3	19:S:29:ASP:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2019:A:H2'	30:0:2020:C:C6	2.49	0.46
30:0:1854:C:H2'	30:0:1875:A:H61	1.80	0.46
13:M:184:ARG:HG3	13:M:185:PRO:HA	1.97	0.46
30:0:2388:C:O2'	30:0:2389:U:H5'	2.14	0.46
26:Z:70:ARG:NH1	26:Z:83:TYR:HD1	2.11	0.46
30:0:61:G:C6	30:0:86:A:N6	2.83	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
30:0:154:C:O2'	30:0:155:C:H5'	2.14	0.46
2:B:162:MET:CE	2:B:310:ARG:HD3	2.45	0.46
29:3:79:LEU:HD12	30:0:2456:A:C2	2.50	0.46
30:0:1925:G:O2'	30:0:1926:G:H5'	2.15	0.46
21:U:47:ARG:HG3	38:U:4381:HOH:O	2.15	0.46
30:0:11:A:N3	30:0:11:A:H2'	2.30	0.46
10:J:42:GLU:HG2	10:J:43:ARG:N	2.30	0.46
30:0:1409:G:C2	30:0:1410:G:C8	3.03	0.46
27:1:10:LYS:HG3	38:1:2979:HOH:O	2.14	0.46
30:0:400:C:H2'	30:0:401:C:H6	1.80	0.46
13:M:92:THR:HB	30:0:401:C:O2'	2.15	0.46
29:3:67:LEU:HD13	29:3:69:TYR:HE1	1.81	0.46
30:0:604:G:H4'	30:0:605:C:O5'	2.15	0.46
30:0:1398:G:H4'	38:0:6650:HOH:O	2.15	0.46
30:0:214:U:H5'	38:0:6117:HOH:O	2.15	0.46
30:0:2658:G:C2	30:0:2659:U:C6	3.03	0.46
12:L:38:HIS:O	30:0:926:A:H1'	2.15	0.46
30:0:1016:U:H1'	38:0:3652:HOH:O	2.15	0.46
30:0:1790:C:H2'	30:0:1791:U:H6	1.80	0.46
1:A:88:ILE:HD13	1:A:100:PRO:HD3	1.97	0.46
30:0:432:G:C2	30:0:433:C:C5	3.02	0.46
30:0:1825:U:O2'	30:0:1826:C:H5'	2.15	0.46
38:W:7804:HOH:O	30:0:1286:A:H5''	2.15	0.46
30:0:168:C:H6	30:0:168:C:O5'	1.98	0.46
30:0:2871:G:C6	30:0:2887:G:N1	2.83	0.46
30:0:2259:C:C2	30:0:2260:A:C8	3.04	0.46
30:0:1415:G:O2'	30:0:1416:G:H5'	2.15	0.46
2:B:5:ARG:HD2	2:B:8:LYS:NZ	2.31	0.46
29:3:64:LYS:HD3	29:3:82:GLY:O	2.14	0.46
31:9:3:A:H2'	38:9:9044:HOH:O	2.14	0.46
30:0:1603:A:C5'	30:0:1605:G:C5'	2.91	0.46
4:D:138:GLY:HA2	31:9:29:C:O3'	2.15	0.46
30:0:247:A:C2	30:0:265:U:C2	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:440:C:C4	30:0:441:A:C6	3.04	0.46
30:0:1806:G:H2'	30:0:1807:U:H6	1.78	0.46
30:0:959:C:H1'	30:0:961:A:C6	2.50	0.46
30:0:10:U:C4	30:0:532:A:N7	2.84	0.46
30:0:732:C:O2'	30:0:733:U:H5'	2.14	0.46
30:0:2520:G:O2'	30:0:2521:A:H5'	2.16	0.46
30:0:128:A:O2'	30:0:129:A:C5'	2.64	0.46
1:A:36:ASP:CB	1:A:85:SER:HB2	2.45	0.46
30:0:100:C:H2'	30:0:101:C:H6	1.81	0.46
30:0:1484:G:H2'	38:0:9110:HOH:O	2.16	0.46
3:C:72:LYS:HG2	3:C:77:ALA:HA	1.96	0.46
27:1:42:SER:HB3	30:0:1473:U:C1'	2.45	0.46
10:J:90:LYS:HB2	35:J:8802:CL:CL	2.53	0.46
23:W:81:ASP:OD1	23:W:92:ASP:HB2	2.16	0.46
30:0:364:U:H2'	30:0:365:G:O4'	2.15	0.46
30:0:815:U:H5	38:0:7423:HOH:O	1.98	0.46
30:0:2004:U:H4'	38:0:5274:HOH:O	2.14	0.46
1:A:212:PRO:HB2	38:0:4344:HOH:O	2.16	0.46
30:0:1477:C:C5'	30:0:1868:G:C5'	2.94	0.46
30:0:2911:C:O2'	30:0:2912:C:H5'	2.15	0.46
30:0:2355:G:N3	30:0:2355:G:H2'	2.31	0.46
30:0:1590:A:C2	30:0:1606:A:C1'	2.99	0.46
2:B:199:TYR:CE2	2:B:268:ARG:HB2	2.49	0.46
30:0:780:A:H2'	30:0:781:C:C6	2.50	0.46
30:0:1626:A:H2'	30:0:1627:G:C5'	2.45	0.46
30:0:2356:A:H2'	30:0:2357:G:O4'	2.16	0.46
9:I:87:PRO:HD3	38:0:7103:HOH:O	2.14	0.46
30:0:1524:U:H5''	30:0:1524:U:H6	1.81	0.46
30:0:307:G:N2	30:0:309:C:C2	2.84	0.46
30:0:39:G:O6	30:0:441:A:C2	2.68	0.46
30:0:1215:A:O3'	30:0:1216:G:H4'	2.16	0.46
23:W:68:THR:HG23	23:W:69:ARG:H	1.81	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
8:H:6:ALA:HA	8:H:61:ARG:NH1	2.30	0.46
30:0:396:U:O2'	30:0:397:A:P	2.73	0.46
10:J:130:VAL:HG12	10:J:131:THR:N	2.31	0.46
4:D:64:ARG:HB3	4:D:67:ASP:OD2	2.15	0.46
14:N:147:ILE:HD12	38:9:9091:HOH:O	2.15	0.46
30:0:2626:C:H2'	30:0:2627:G:C8	2.51	0.46
18:R:48:GLU:HA	18:R:51:ILE:HD12	1.98	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
30:0:1829:A:H2'	30:0:1830:C:C5'	2.41	0.46
6:F:89:LEU:HD21	30:0:262:A:C6	2.51	0.46
30:0:1200:A:H3'	38:0:5722:HOH:O	2.15	0.46
30:0:2100:A:C5'	38:0:7373:HOH:O	2.57	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
30:0:662:U:H1'	30:0:748:C:H1'	1.98	0.46
15:O:51:TYR:CD2	30:0:721:A:H5''	2.51	0.46
30:0:2314:G:O2'	30:0:2315:C:H5'	2.15	0.46
30:0:1773:G:H2'	30:0:1774:G:H5'	1.98	0.46
24:X:43:VAL:HG12	24:X:47:ALA:HB3	1.98	0.46
30:0:421:C:H2'	30:0:422:G:C8	2.50	0.46
30:0:2397:G:N2	38:0:6910:HOH:O	2.49	0.46
30:0:497:A:H5''	38:0:3588:HOH:O	2.16	0.46
30:0:1427:A:O2'	30:0:1428:C:H5'	2.16	0.46
9:I:112:LEU:CD1	30:0:1162:G:H1'	2.45	0.46
30:0:2017:U:O2'	30:0:2018:A:C8	2.53	0.46
14:N:42:HIS:HB3	14:N:62:HIS:HE1	1.80	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
30:0:969:G:N1	30:0:999:C:N4	2.53	0.46
30:0:282:C:HO2'	30:0:368:C:N4	2.13	0.46
30:0:2326:C:H4'	30:0:2412:G:C4'	2.46	0.46
30:0:920:C:H5''	30:0:921:G:O5'	2.16	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
18:R:135:ALA:HB1	18:R:137:ASN:ND2	2.29	0.46
30:0:567:U:C5'	38:0:5254:HOH:O	2.62	0.46
9:I:124:VAL:C	9:I:126:THR:H	2.18	0.46
30:0:1497:G:H4'	30:0:1627:G:O2'	2.16	0.46
30:0:2612:A:H4'	38:0:3676:HOH:O	2.15	0.46
30:0:2401:A:H2'	30:0:2402:A:C8	2.51	0.46
30:0:277:U:O2'	30:0:278:A:H5'	2.16	0.46
30:0:1157:C:H2'	30:0:1158:G:H8	1.80	0.46
20:T:48:VAL:HG23	20:T:98:VAL:HA	1.97	0.46
31:9:47:A:C2	31:9:48:C:C2	3.03	0.46
30:0:735:C:C5	30:0:736:A:C4	3.03	0.46
30:0:2038:A:C2	30:0:2039:A:C5	3.04	0.46
19:S:12:GLU:OE1	30:0:1444:G:H4'	2.15	0.46
26:Z:34:SER:CB	30:0:797:A:H4'	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:15:C:N4	31:9:16:G:C6	2.84	0.46
15:O:38:ARG:HD3	30:0:654:A:OP2	2.16	0.46
30:0:2241:C:H2'	30:0:2242:U:C6	2.50	0.46
30:0:1790:C:H2'	30:0:1791:U:C6	2.51	0.46
30:0:562:A:H2'	30:0:563:C:O4'	2.15	0.46
30:0:488:U:C2'	38:0:3993:HOH:O	2.64	0.46
30:0:2456:A:H1'	38:0:6579:HOH:O	2.16	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
23:W:29:VAL:O	23:W:30:ASN:HB2	2.16	0.46
30:0:1058:A:H2'	30:0:1060:C:H5''	1.97	0.46
30:0:897:A:H2'	30:0:899:C:C5	2.50	0.46
30:0:1812:G:H4'	30:0:1814:G:O4'	2.15	0.46
30:0:1119:G:N2	30:0:1246:A:H2	2.04	0.46
30:0:2831:C:C2	30:0:2910:A:N1	2.84	0.46
29:3:20:HIS:CE1	29:3:71:CYS:SG	3.09	0.46
30:0:1504:A:C5'	38:0:4396:HOH:O	2.63	0.46
30:0:2011:A:H5'	30:0:2013:G:C1'	2.46	0.46
30:0:1707:G:H1'	30:0:1711:A:N6	2.31	0.46
13:M:164:THR:HG22	13:M:165:GLY:N	2.30	0.46
30:0:2694:A:H3'	30:0:2695:C:H6	1.81	0.46
30:0:212:A:H5'	30:0:214:U:H1'	1.98	0.46
30:0:1902:G:H2'	30:0:1903:U:O4'	2.16	0.46
13:M:94:ARG:NH2	30:0:175:G:O6	2.49	0.46
30:0:1512:G:H4'	38:0:4618:HOH:O	2.15	0.46
25:Y:214:ARG:HH12	25:Y:230:ASN:ND2	2.13	0.46
30:0:1236:A:C2'	30:0:1237:U:H5'	2.46	0.46
30:0:1809:G:H2'	30:0:1811:A:OP2	2.16	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
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
30:0:56:G:H1'	38:0:5300:HOH:O	2.16	0.45
13:M:133:LEU:O	13:M:134:ILE:HD13	2.16	0.45
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
30:0:1864:C:H2'	30:0:1865:A:O4'	2.16	0.45
4:D:63:ILE:HG13	4:D:64:ARG:N	2.32	0.45
30:0:1490:G:H4'	30:0:1533:A:OP1	2.16	0.45
3:C:35:VAL:HG21	3:C:227:GLY:HA2	1.98	0.45
17:Q:64:GLU:HG3	17:Q:74:ASP:CG	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:103:VAL:HG22	5:E:115:ARG:HB3	1.96	0.45
9:I:83:GLY:H	30:0:1168:C:C5'	2.28	0.45
30:0:369:G:O2'	30:0:370:G:H5'	2.16	0.45
30:0:1503:U:H2'	30:0:1504:A:H5'	1.98	0.45
30:0:1400:C:C2'	30:0:1401:G:H5'	2.46	0.45
15:O:32:ARG:HH21	15:O:35:LYS:NZ	2.14	0.45
30:0:1444:G:C6	30:0:1445:G:C5	3.05	0.45
2:B:320:GLN:HA	2:B:321:PRO:HD3	1.83	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:94:LEU:N	1:A:94:LEU:HD23	2.31	0.45
1:A:186:TRP:CG	1:A:187:PRO:HA	2.50	0.45
30:0:2812:A:C2	30:0:2814:A:N7	2.85	0.45
30:0:2134:G:N2	30:0:2242:U:C2	2.85	0.45
30:0:1908:G:H1'	30:0:1931:A:N6	2.31	0.45
30:0:1831:U:H2'	30:0:1832:G:H5'	1.98	0.45
8:H:157:TYR:CD1	8:H:157:TYR:C	2.89	0.45
11:K:132:VAL:HG21	21:U:22:VAL:HG13	1.97	0.45
30:0:743:G:O2'	30:0:744:G:H5'	2.16	0.45
30:0:1987:C:O2'	30:0:1988:C:H5'	2.16	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
1:A:35:GLY:O	1:A:37:VAL:HG22	2.17	0.45
30:0:1074:G:H4'	30:0:1260:G:C6	2.52	0.45
30:0:2577:A:H8	38:0:9606:HOH:O	1.99	0.45
30:0:1362:U:O2'	30:0:1363:G:H5'	2.17	0.45
9:I:113:SER:HA	30:0:1186:C:H5'	1.98	0.45
30:0:191:A:N6	30:0:435:A:H62	2.14	0.45
30:0:1116:U:N3	30:0:1246:A:N6	2.60	0.45
30:0:1603:A:H5'	30:0:1605:G:C5'	2.46	0.45
31:9:59:C:O5'	31:9:59:C:C6	2.63	0.45
30:0:400:C:O2'	30:0:401:C:H5'	2.17	0.45
30:0:793:A:H2'	30:0:794:U:H6	1.81	0.45
30:0:595:U:H2'	30:0:596:C:C6	2.52	0.45
30:0:1213:C:O2'	30:0:1214:G:H5'	2.17	0.45
30:0:1759:A:N3	30:0:1818:C:H2'	2.31	0.45
1:A:51:ARG:O	1:A:52:SER:HB2	2.16	0.45
30:0:154:C:H2'	30:0:155:C:H6	1.82	0.45
30:0:360:A:H2'	30:0:361:C:O4'	2.16	0.45
29:3:12:PRO:HG2	29:3:13:HIS:CD2	2.49	0.45
30:0:1948:G:H2'	30:0:1949:G:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1670:A:H2'	30:0:1671:U:O4'	2.16	0.45
30:0:99:A:C8	30:0:100:C:C5	3.05	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
30:0:2293:G:C6	30:0:2294:C:C5	3.04	0.45
30:0:2757:A:H2'	30:0:2758:G:O4'	2.16	0.45
31:9:29:C:C5	31:9:30:C:C5	3.04	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
26:Z:70:ARG:O	26:Z:81:CYS:SG	2.74	0.45
30:0:1178:G:C6	30:0:1179:C:N4	2.84	0.45
30:0:2092:G:H2'	30:0:2613:G:OP1	2.17	0.45
30:0:734:U:H2'	30:0:736:A:OP2	2.16	0.45
30:0:1819:G:H2'	30:0:1820:G:C4'	2.46	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
30:0:304:G:O5'	30:0:304:G:H8	2.00	0.45
30:0:1970:G:N3	30:0:1970:G:H2'	2.31	0.45
30:0:1964:U:O2	30:0:1964:U:H2'	2.15	0.45
30:0:876:A:N3	30:0:876:A:C2'	2.79	0.45
14:N:144:GLY:O	14:N:147:ILE:HG23	2.15	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
13:M:122:GLN:HB2	13:M:127:LYS:HG2	1.98	0.45
17:Q:15:LYS:HG3	30:0:2364:A:O3'	2.16	0.45
13:M:30:GLU:HG2	38:M:8864:HOH:O	2.17	0.45
2:B:254:GLN:HG2	2:B:255:GLY:N	2.30	0.45
30:0:1524:U:H5''	30:0:1524:U:C6	2.51	0.45
30:0:2718:C:C6	30:0:2718:C:H5'	2.50	0.45
28:2:40:ARG:HG3	28:2:45:ASN:CB	2.45	0.45
29:3:59:ASP:OD1	30:0:2460:A:H5''	2.16	0.45
30:0:2728:C:O5'	30:0:2728:C:H6	1.99	0.45
2:B:162:MET:HE2	2:B:310:ARG:HD3	1.97	0.45
23:W:5:VAL:HG11	23:W:153:MET:HE1	1.99	0.45
18:R:18:LEU:HB2	18:R:143:VAL:CG1	2.46	0.45
30:0:940:G:N3	30:0:1032:A:C2	2.84	0.45
5:E:152:THR:HG21	5:E:165:GLY:HA2	1.99	0.45
30:0:2697:A:H2'	30:0:2697:A:N3	2.32	0.45
30:0:420:U:O4'	30:0:1920:C:C4	2.70	0.45
38:C:8558:HOH:O	30:0:751:U:H5'	2.16	0.45
30:0:1940:C:H1'	38:0:9382:HOH:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:659:A:H5''	38:0:7082:HOH:O	2.17	0.45
12:L:72:ASN:O	12:L:76:LEU:HG	2.17	0.45
30:0:1547:A:H2'	30:0:1548:U:C6	2.52	0.45
9:I:82:THR:HG22	30:0:1168:C:H5''	1.97	0.45
30:0:960:G:N3	30:0:960:G:C2'	2.79	0.45
30:0:1523:G:C6	30:0:1524:U:C4	3.05	0.45
31:9:61:C:H2'	31:9:62:A:C8	2.46	0.45
30:0:1434:A:H4'	30:0:1435:U:H5	1.82	0.45
30:0:1883:U:H5''	30:0:2013:G:OP2	2.17	0.45
1:A:204:GLY:N	30:0:2634:G:OP2	2.49	0.45
14:N:33:ARG:HG3	38:N:8841:HOH:O	2.17	0.45
30:0:1149:U:C5	30:0:1215:A:N7	2.84	0.45
30:0:1151:G:N2	30:0:1214:G:C4	2.85	0.45
12:L:57:VAL:O	12:L:57:VAL:HG12	2.17	0.45
30:0:418:C:H2'	30:0:419:A:C8	2.52	0.45
30:0:790:A:H8	38:0:6078:HOH:O	1.98	0.45
30:0:1406:A:H4'	30:0:1407:A:H5''	1.98	0.45
13:M:34:GLU:HB3	13:M:38:GLU:HG3	1.99	0.45
15:O:27:GLY:O	15:O:31:GLU:HG3	2.17	0.45
1:A:11:ARG:HD3	38:0:9222:HOH:O	2.16	0.45
6:F:34:ASN:HA	13:M:4:ALA:HB2	1.98	0.45
30:0:2475:C:H5'	38:0:3664:HOH:O	2.16	0.45
1:A:189:VAL:HA	30:0:1845:A:OP1	2.16	0.45
2:B:119:HIS:O	2:B:121:PRO:HD3	2.16	0.45
27:1:16:HIS:HE1	30:0:775:G:OP1	1.99	0.45
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
29:3:35:TRP:HZ3	30:0:2432:C:OP1	2.00	0.45
30:0:92:G:H2'	30:0:93:C:H6	1.82	0.45
31:9:30:C:C2'	31:9:30:C:O2	2.65	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
31:9:72:C:O2'	31:9:73:A:H5'	2.15	0.45
30:0:1405:U:H4'	30:0:1406:A:H5''	1.98	0.45
2:B:43:GLY:O	2:B:308:LEU:HD12	2.16	0.45
30:0:2361:A:H2'	30:0:2362:A:C8	2.51	0.45
30:0:916:A:C6	30:0:917:U:C4	3.05	0.45
30:0:1902:G:O2'	30:0:1903:U:H5'	2.16	0.45
10:J:43:ARG:HD3	38:J:8858:HOH:O	2.17	0.45
30:0:2887:G:H2'	30:0:2888:U:O4'	2.17	0.45
6:F:96:ALA:HA	38:F:3111:HOH:O	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:50:VAL:O	4:D:71:ALA:HA	2.17	0.45
30:0:387:G:C2'	30:0:388:G:H5'	2.46	0.45
26:Z:35:SER:HB3	26:Z:47:ARG:HB2	1.98	0.45
30:0:281:U:H5	38:0:7575:HOH:O	1.99	0.45
30:0:228:C:H2'	30:0:229:G:C5'	2.46	0.45
2:B:307:ARG:HG3	2:B:307:ARG:HH11	1.82	0.45
30:0:1576:G:C2	30:0:1577:U:C2	3.05	0.45
21:U:6:CYS:SG	21:U:31:PHE:HA	2.56	0.45
30:0:2842:G:H2'	30:0:2843:A:H5'	1.98	0.45
2:B:86:ALA:HA	38:B:9051:HOH:O	2.16	0.45
30:0:1850:U:H2'	30:0:1851:G:C8	2.52	0.45
30:0:1626:A:C2'	30:0:1627:G:H5'	2.46	0.45
30:0:862:U:H2'	30:0:863:G:C8	2.52	0.45
5:E:102:VAL:HG11	5:E:148:ILE:HG12	1.98	0.45
30:0:957:A:H8	30:0:957:A:O5'	2.00	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
30:0:2511:A:H2'	30:0:2512:U:H6	1.82	0.45
30:0:969:G:N2	30:0:1000:C:C2	2.85	0.45
30:0:1543:G:N1	30:0:1641:A:OP2	2.36	0.45
30:0:958:G:H2'	30:0:959:C:H6	1.75	0.45
30:0:1477:C:C5'	30:0:1868:G:H5''	2.47	0.45
30:0:1801:A:C2	30:0:1802:G:C4	3.04	0.45
30:0:2311:A:O2'	30:0:2312:G:H5'	2.17	0.45
13:M:86:GLN:NE2	38:M:8882:HOH:O	2.50	0.45
30:0:1041:U:H2'	30:0:1042:U:C5'	2.46	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
30:0:1181:A:O2'	30:0:1182:C:H5'	2.17	0.44
31:9:3:A:OP2	31:9:25:G:N2	2.50	0.44
30:0:1524:U:C5'	30:0:1524:U:H6	2.29	0.44
26:Z:47:ARG:O	26:Z:51:ALA:HB2	2.16	0.44
23:W:48:VAL:HG12	23:W:52:VAL:HB	1.98	0.44
30:0:339:A:C6	30:0:342:C:N3	2.85	0.44
31:9:107:C:O2'	31:9:108:C:H5'	2.17	0.44
30:0:283:U:H5''	30:0:284:C:OP2	2.17	0.44
30:0:1392:A:C6	30:0:1395:C:C2	3.05	0.44
30:0:2826:G:O6	30:0:2913:A:N6	2.50	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
1:A:164:ARG:NH1	1:A:164:ARG:HB3	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
5:E:153:ARG:NH1	30:0:2778:A:C1'	2.81	0.44
18:R:34:GLU:HG2	18:R:46:TYR:OH	2.17	0.44
30:0:163:U:O3'	30:0:896:C:H4'	2.16	0.44
30:0:2293:G:C6	30:0:2294:C:C4	3.05	0.44
30:0:581:G:H5'	38:0:7663:HOH:O	2.17	0.44
8:H:83:GLU:HA	38:H:243:HOH:O	2.18	0.44
30:0:198:A:C2	30:0:2444:U:H1'	2.53	0.44
4:D:128:LEU:HD23	4:D:129:ASP:N	2.32	0.44
30:0:1246:A:O2'	30:0:1247:A:H3'	2.17	0.44
14:N:1:ALA:HB2	31:9:14:G:O2'	2.18	0.44
13:M:76:ARG:HG3	38:M:8827:HOH:O	2.17	0.44
3:C:129:HIS:HD2	3:C:165:ASP:OD2	2.01	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
30:0:711:G:C2'	30:0:712:C:H5'	2.47	0.44
18:R:98:ASN:ND2	30:0:500:G:H21	2.12	0.44
23:W:10:GLU:O	23:W:13:MET:HB3	2.18	0.44
12:L:41:HIS:CD2	30:0:926:A:O2'	2.69	0.44
30:0:1362:U:H2'	30:0:1363:G:C8	2.52	0.44
10:J:15:ARG:HG2	10:J:16:ASP:OD1	2.17	0.44
2:B:51:VAL:HG13	2:B:53:LEU:HD13	1.98	0.44
20:T:81:LYS:HD2	20:T:87:VAL:HG11	1.98	0.44
3:C:60:SER:HA	38:C:8575:HOH:O	2.17	0.44
9:I:130:LEU:HD21	30:0:1167:G:C4'	2.46	0.44
30:0:877:G:N7	30:0:885:G:C5	2.85	0.44
30:0:1701:A:H5''	30:0:1702:U:H3'	1.99	0.44
30:0:1680:C:H2'	30:0:1681:G:O4'	2.17	0.44
13:M:71:SER:OG	13:M:72:ALA:N	2.51	0.44
30:0:372:A:O2'	30:0:373:G:H5'	2.17	0.44
22:V:12:THR:CG2	22:V:15:GLU:H	2.30	0.44
30:0:2276:U:H2'	30:0:2277:U:C6	2.52	0.44
30:0:1391:G:N2	30:0:1434:A:H5''	2.32	0.44
30:0:1202:A:C2'	30:0:1203:G:H5'	2.48	0.44
30:0:1132:A:H2'	30:0:1133:A:C8	2.52	0.44
29:3:10:TYR:CD1	30:0:2408:A:H1'	2.52	0.44
30:0:1649:G:H1'	38:0:5049:HOH:O	2.17	0.44
30:0:729:C:C2	30:0:743:G:C2	3.05	0.44
30:0:1069:C:H2'	30:0:1070:A:O4'	2.18	0.44
18:R:59:PHE:O	18:R:63:ASN:HB3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:86:THR:HG22	11:K:87:ARG:N	2.32	0.44
30:0:57:C:H42	30:0:89:G:H1	1.64	0.44
29:3:5:ARG:HD2	29:3:21:GLU:HG2	1.98	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
30:0:625:U:H5'	38:0:3177:HOH:O	2.16	0.44
30:0:2911:C:H2'	30:0:2912:C:H6	1.82	0.44
19:S:11:THR:H	19:S:14:ALA:HB3	1.81	0.44
5:E:20:ILE:O	5:E:30:THR:HA	2.17	0.44
30:0:2775:A:N6	30:0:2799:A:C8	2.86	0.44
26:Z:69:ASP:O	26:Z:71:VAL:N	2.45	0.44
30:0:1556:G:O2'	30:0:1557:G:H5'	2.17	0.44
30:0:1415:G:C2'	30:0:1416:G:H5'	2.47	0.44
12:L:22:ARG:HG2	38:0:3223:HOH:O	2.15	0.44
2:B:244:PRO:HB3	30:0:1234:U:N3	2.32	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
8:H:14:LYS:HG3	38:H:183:HOH:O	2.17	0.44
4:D:153:THR:O	4:D:156:ARG:HB2	2.16	0.44
30:0:2345:A:C3'	30:0:2346:C:H6	2.23	0.44
30:0:1043:C:H2'	38:0:3185:HOH:O	2.18	0.44
23:W:5:VAL:HG11	23:W:153:MET:CE	2.48	0.44
18:R:80:TYR:O	30:0:2050:G:H5''	2.16	0.44
9:I:87:PRO:HG2	30:0:1181:A:O4'	2.18	0.44
30:0:1519:U:O2'	30:0:1520:G:H5'	2.16	0.44
30:0:2377:U:O2'	30:0:2378:U:H5'	2.17	0.44
30:0:2005:G:OP2	30:0:2006:C:C5'	2.66	0.44
20:T:97:ARG:NH2	30:0:309:C:OP1	2.51	0.44
30:0:821:U:H2'	30:0:822:C:H6	1.81	0.44
30:0:2781:U:H2'	30:0:2782:G:C5'	2.48	0.44
1:A:233:THR:HB	30:0:1942:A:H5''	1.99	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
13:M:66:SER:HB3	13:M:128:TRP:NE1	2.32	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
27:1:20:ARG:HB2	38:1:513:HOH:O	2.18	0.44
30:0:1330:A:H2	38:0:4652:HOH:O	2.00	0.44
25:Y:99:ALA:HB2	25:Y:233:TYR:CE2	2.52	0.44
5:E:69:ILE:HA	5:E:72:MET:CE	2.48	0.44
30:0:1016:U:O2'	30:0:2303:A:N7	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1762:C:H2'	30:0:1763:C:H6	1.82	0.44
17:Q:40:HIS:HE1	30:0:949:U:O2'	2.01	0.44
30:0:2457:U:H1'	38:0:7515:HOH:O	2.17	0.44
30:0:2854:A:C6	30:0:2905:A:N1	2.86	0.44
23:W:129:LYS:CD	31:9:87:U:H2'	2.47	0.44
30:0:2552:C:C6	30:0:2577:A:N7	2.85	0.44
8:H:8:MET:CE	30:0:2494:G:H4'	2.48	0.44
3:C:6:TYR:N	3:C:6:TYR:CD1	2.86	0.44
30:0:569:A:H5''	30:0:587:A:N1	2.32	0.44
30:0:1112:G:H1	30:0:1251:C:H42	1.65	0.44
38:T:2151:HOH:O	30:0:317:A:H5'	2.17	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
4:D:62:ASP:HA	38:D:4233:HOH:O	2.18	0.44
30:0:2250:G:N1	30:0:2251:G:N3	2.66	0.44
30:0:1309:U:C2'	30:0:1310:U:H5'	2.48	0.44
30:0:929:A:H8	30:0:929:A:O5'	2.01	0.44
2:B:5:ARG:NH1	30:0:2547:C:OP2	2.51	0.44
30:0:1427:A:C2'	30:0:1428:C:H5'	2.47	0.44
21:U:45:GLU:HB2	21:U:48:ASN:ND2	2.32	0.44
30:0:2541:U:H5'	30:0:2611:G:O6	2.18	0.44
2:B:241:PRO:HB3	30:0:2609:G:N3	2.33	0.44
4:D:86:THR:O	4:D:89:PRO:HD2	2.18	0.44
30:0:2566:A:C2	30:0:2696:G:O4'	2.71	0.44
25:Y:204:ARG:NH2	30:0:1324:G:N2	2.65	0.44
31:9:26:C:H2'	31:9:27:C:H6	1.79	0.44
8:H:87:LYS:HG3	8:H:140:TYR:HD1	1.83	0.44
30:0:821:U:O2'	30:0:822:C:H5'	2.18	0.44
30:0:1202:A:H2'	30:0:1203:G:H5'	2.00	0.44
13:M:80:GLY:O	13:M:81:ARG:HB2	2.18	0.44
30:0:157:G:H3'	38:0:3945:HOH:O	2.18	0.44
30:0:703:G:C6	30:0:704:C:C4	3.06	0.44
31:9:31:C:C2	31:9:50:G:C2	3.05	0.44
30:0:304:G:H1'	30:0:347:A:N6	2.32	0.44
16:P:13:VAL:HG11	16:P:40:VAL:CG1	2.48	0.44
30:0:1789:G:H2'	30:0:1790:C:O5'	2.17	0.44
8:H:66:GLU:HA	38:H:239:HOH:O	2.17	0.44
8:H:59:GLN:HE21	8:H:129:ARG:HE	1.65	0.44
1:A:103:VAL:HA	1:A:104:PRO:HD3	1.89	0.44
30:0:1986:G:C6	30:0:1987:C:N4	2.86	0.44
2:B:195:ARG:HE	2:B:323:LEU:HD13	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:47:LEU:HA	14:N:47:LEU:HD13	1.86	0.44
20:T:19:ARG:HD3	20:T:67:LEU:O	2.18	0.44
30:0:582:U:H2'	30:0:583:C:C6	2.53	0.44
30:0:2061:C:H2'	30:0:2062:A:H5'	1.99	0.44
30:0:1950:G:H2'	30:0:1951:G:C8	2.53	0.44
1:A:194:MET:SD	30:0:875:A:C2	3.11	0.44
30:0:868:G:C4	30:0:887:G:C8	3.06	0.44
31:9:81:C:C2'	31:9:82:U:H5'	2.48	0.44
30:0:2104:C:O2	30:0:2485:A:N1	2.50	0.44
30:0:1522:A:H2'	30:0:1523:G:C5'	2.48	0.44
8:H:39:LYS:O	30:0:969:G:H4'	2.18	0.44
16:P:88:GLN:HB3	38:P:185:HOH:O	2.16	0.44
5:E:90:HIS:CE1	30:0:2694:A:H5''	2.53	0.44
10:J:75:PRO:HD3	10:J:136:SER:OG	2.18	0.44
17:Q:25:PRO:HA	17:Q:26:PRO:HD3	1.78	0.44
2:B:279:THR:HG22	2:B:280:VAL:N	2.33	0.44
30:0:2250:G:C2	30:0:2251:G:C4	3.06	0.44
30:0:727:G:C2	30:0:728:C:C2	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
2:B:54:VAL:HB	38:B:9083:HOH:O	2.17	0.44
30:0:1937:U:O2'	30:0:1938:G:H5'	2.18	0.44
30:0:483:C:H2'	30:0:484:A:O4'	2.18	0.44
30:0:2729:C:O2'	30:0:2730:G:H5'	2.18	0.44
1:A:182:ARG:HB3	38:0:5133:HOH:O	2.18	0.44
16:P:54:LYS:HB2	30:0:1717:A:H5''	1.98	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
31:9:74:G:O2'	31:9:75:G:H5'	2.18	0.43
30:0:1544:U:H2'	30:0:1545:C:H6	1.82	0.43
30:0:1642:A:N7	30:0:1643:C:C4	2.86	0.43
30:0:39:G:O2'	30:0:40:C:H5'	2.18	0.43
30:0:2090:G:H2'	30:0:2091:G:C8	2.53	0.43
30:0:1592:G:O2'	30:0:1593:C:O4'	2.36	0.43
30:0:2851:G:O2'	30:0:2852:A:H5'	2.17	0.43
30:0:1421:C:O2'	30:0:1422:U:H5'	2.18	0.43
30:0:324:G:C6	30:0:325:U:C5	3.06	0.43
3:C:174:ILE:CD1	30:0:338:C:H4'	2.48	0.43
30:0:293:A:C5	30:0:360:A:C2	3.06	0.43
26:Z:45:VAL:O	26:Z:49:ARG:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:175:G:O2'	30:0:176:U:OP2	2.36	0.43
23:W:119:HIS:HE1	38:0:9568:HOH:O	2.00	0.43
30:0:634:G:O2'	30:0:1358:A:OP1	2.31	0.43
25:Y:182:PHE:CG	25:Y:202:ALA:HB2	2.53	0.43
30:0:838:C:H4'	38:0:9187:HOH:O	2.18	0.43
30:0:2435:U:H4'	38:0:9269:HOH:O	2.17	0.43
14:N:12:ARG:HD3	14:N:18:THR:OG1	2.18	0.43
4:D:103:ASN:ND2	4:D:133:ASN:HA	2.33	0.43
30:0:533:U:H3'	38:0:3742:HOH:O	2.18	0.43
13:M:104:ARG:HG3	38:M:8866:HOH:O	2.18	0.43
31:9:2:U:OP2	31:9:3:A:H5'	2.18	0.43
30:0:692:A:N6	30:0:693:A:C2	2.86	0.43
3:C:193:LEU:HD12	3:C:211:ASP:O	2.18	0.43
30:0:1706:G:H1'	30:0:1712:A:N6	2.30	0.43
23:W:115:THR:HG23	38:W:5420:HOH:O	2.18	0.43
30:0:1130:U:C2'	30:0:1131:G:H5'	2.48	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
23:W:142:ASP:HB3	23:W:145:GLY:H	1.83	0.43
1:A:94:LEU:HD12	1:A:98:GLU:CB	2.48	0.43
2:B:202:VAL:HA	2:B:310:ARG:O	2.18	0.43
26:Z:61:HIS:O	26:Z:69:ASP:HA	2.17	0.43
2:B:84:LEU:HD23	2:B:142:LEU:HD23	2.00	0.43
30:0:1916:C:C2	30:0:1924:A:C2	3.06	0.43
30:0:2871:G:C4	30:0:2887:G:N2	2.86	0.43
13:M:65:VAL:HG21	13:M:105:ALA:HB2	2.00	0.43
30:0:827:A:H2'	30:0:828:G:O4'	2.18	0.43
30:0:2135:A:O4'	30:0:2243:C:N4	2.51	0.43
4:D:10:PHE:CG	4:D:11:HIS:N	2.86	0.43
30:0:117:A:H2'	30:0:118:G:C8	2.53	0.43
1:A:215:ILE:HG22	1:A:227:ASP:O	2.18	0.43
30:0:1210:G:C2	30:0:1211:G:C8	3.06	0.43
30:0:820:G:N3	30:0:820:G:H3'	2.33	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
30:0:2277:U:H1'	30:0:2469:A:N3	2.33	0.43
25:Y:154:ARG:HH21	30:0:1293:U:H5'	1.83	0.43
30:0:1949:G:N2	30:0:1964:U:C2	2.87	0.43
30:0:2594:C:O2'	30:0:2595:U:H5'	2.19	0.43
30:0:2112:A:H2'	30:0:2113:G:C8	2.53	0.43
30:0:1363:G:H2'	30:0:1364:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:385:C:O5'	30:0:385:C:H6	2.02	0.43
1:A:38:ILE:HB	1:A:82:VAL:O	2.18	0.43
30:0:665:A:C6	30:0:666:A:C6	3.06	0.43
30:0:2429:A:C4'	38:0:7716:HOH:O	2.66	0.43
30:0:219:G:O5'	30:0:220:C:H5''	2.18	0.43
4:D:75:LEU:HD22	4:D:79:MET:HB3	2.00	0.43
3:C:47:GLY:HA2	3:C:92:PRO:HB2	2.00	0.43
20:T:14:ALA:HA	20:T:15:PRO:HD3	1.90	0.43
30:0:1298:U:H2'	30:0:1299:G:C8	2.53	0.43
3:C:44:GLN:HA	38:C:8605:HOH:O	2.18	0.43
30:0:1815:A:H4'	30:0:2751:C:O4'	2.19	0.43
30:0:1816:C:H2'	30:0:1817:U:O4'	2.17	0.43
30:0:41: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
5:E:91:PHE:HA	5:E:92:PRO:HD3	1.89	0.43
30:0:1878:G:O2'	30:0:1879:U:OP2	2.36	0.43
5:E:126:ILE:HA	5:E:131:LEU:CD2	2.47	0.43
30:0:36:C:H1'	38:0:3051:HOH:O	2.17	0.43
30:0:152:A:O2'	30:0:153:C:H5'	2.18	0.43
3:C:6:TYR:HD1	3:C:6:TYR:N	2.17	0.43
14:N:139:TRP:CE3	14:N:139:TRP:HA	2.53	0.43
30:0:234:A:H4'	30:0:437:A:O4'	2.18	0.43
30:0:1980:U:O2	30:0:2008:U:H4'	2.18	0.43
11:K:4:LEU:HD22	11:K:116:GLU:HB3	2.00	0.43
30:0:1537:C:H2'	30:0:1538:C:H6	1.83	0.43
5:E:84:MET:SD	38:E:3134:HOH:O	2.61	0.43
30:0:1520:G:C2	30:0:1521:C:C2	3.07	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
30:0:1503:U:H2'	30:0:1504:A:O4'	2.19	0.43
3:C:39:GLN:O	3:C:43:LYS:HD3	2.18	0.43
23:W:6:GLN:HB2	23:W:26:ILE:CD1	2.48	0.43
31:9:39:U:O2'	31:9:42:C:H5	2.01	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
30:0:1024:G:C6	30:0:1025:C:C4	3.07	0.43
30:0:2429:A:H4'	38:0:7716:HOH:O	2.16	0.43
30:0:2451:G:N3	30:0:2451:G:H2'	2.32	0.43
30:0:148:A:O2'	30:0:149:G:H5'	2.19	0.43
16:P:8:ARG:HG3	38:P:188:HOH:O	2.17	0.43
30:0:772:G:H2'	30:0:773:A:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:73:LEU:HD12	9:I:107:LYS:NZ	2.33	0.43
30:0:2070:G:H2'	30:0:2072:G:OP1	2.18	0.43
30:0:2531:U:H2'	30:0:2532:A:O4'	2.19	0.43
30:0:2445:U:H2'	30:0:2446:G:C8	2.54	0.43
2:B:154:VAL:HA	2:B:155:PRO:HD3	1.88	0.43
30:0:1167:G:C2	30:0:1168:C:C2	3.06	0.43
30:0:1275:C:C2'	30:0:1276:U:H5'	2.49	0.43
31:9:5:G:O2'	31:9:6:C:H5'	2.18	0.43
30:0:1175:G:N3	30:0:1193:A:C6	2.86	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
30:0:2569:A:H2'	30:0:2570:G:O5'	2.19	0.43
10:J:70:PHE:HE1	30:0:2676:C:C4'	2.32	0.43
30:0:629:A:C2	30:0:2074:A:C2	3.07	0.43
13:M:164:THR:HB	38:M:8820:HOH:O	2.17	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
29:3:59:ASP:HB3	29:3:63:LYS:HZ1	1.83	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
31:9:65:A:C4	31:9:113:C:C4	3.07	0.43
17:Q:11:ARG:NH2	30:0:2363:G:C5'	2.81	0.43
5:E:107:PHE:CE2	5:E:108:LEU:HD13	2.54	0.43
30:0:1284:G:O2'	30:0:1285:U:H5'	2.18	0.43
14:N:77:ASN:OD1	14:N:79:PRO:HD2	2.18	0.43
1:A:71:PRO:O	1:A:160:ALA:HB2	2.18	0.43
30:0:2886:C:O2'	30:0:2887:G:H5'	2.18	0.43
4:D:128:LEU:HB2	38:D:6007:HOH:O	2.18	0.43
30:0:2429:A:N6	38:0:3326:HOH:O	2.51	0.43
26:Z:55:SER:HA	38:0:7562:HOH:O	2.19	0.43
4:D:104:PHE:CE2	4:D:132:VAL:HB	2.54	0.43
6:F:60:VAL:O	6:F:62:HIS:N	2.52	0.43
14:N:32:PRO:HD2	14:N:99:GLU:O	2.18	0.43
30:0:2507:G:H22	30:0:2512:U:H5''	1.84	0.43
30:0:1519:U:H1'	38:0:3898:HOH:O	2.18	0.43
30:0:1665:G:C2	30:0:1666:C:C6	3.07	0.43
30:0:877:G:H3'	38:0:3106:HOH:O	2.19	0.43
13:M:70:GLY:HA3	13:M:73:ARG:HH21	1.77	0.43
30:0:273:G:H2'	30:0:274:G:O4'	2.18	0.43
30:0:284:C:OP2	30:0:284:C:H6	2.01	0.43
26:Z:41:ARG:HD2	30:0:820:G:H22	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1552:G:C6	30:0:1634:G:C6	3.07	0.43
30:0:1178:G:C5	30:0:1179:C:C4	3.07	0.43
30:0:85:C:H3'	30:0:86:A:H2'	2.01	0.43
2:B:27:ASN:HD21	30:0:2807:U:P	2.41	0.43
30:0:102:A:C6	30:0:103:C:C4	3.06	0.43
31:9:111:U:O2'	31:9:112:U:H5'	2.19	0.43
30:0:624:U:O4	30:0:628:1MA:H8	2.01	0.43
30:0:2803:C:H2'	30:0:2804:C:C6	2.54	0.43
30:0:1705:C:O2	30:0:2735:U:C5'	2.65	0.43
30:0:2855:G:C2	30:0:2904:U:C2	3.06	0.43
30:0:2473:U:H2'	30:0:2476:C:H5	1.84	0.43
30:0:1333:U:H2'	30:0:1334:C:C6	2.53	0.43
13:M:29:GLN:OE1	30:0:2244:A:H5''	2.18	0.43
14:N:91:ARG:O	14:N:94:GLU:HB2	2.19	0.43
30:0:1602:C:H5'	38:0:6467:HOH:O	2.18	0.43
30:0:1159:G:C6	30:0:1160:G:C4	3.07	0.43
29:3:22:VAL:HG12	29:3:90:PHE:HE2	1.83	0.43
30:0:2510:C:H42	30:0:2564:G:H22	1.66	0.43
30:0:816:G:C6	30:0:817:G:N1	2.87	0.43
1:A:167:LYS:CE	26:Z:50:VAL:HG13	2.42	0.43
30:0:2780:C:C4	30:0:2781:U:C4	3.06	0.43
30:0:1788:U:C2	30:0:1805:G:C2	3.07	0.43
30:0:2094:G:C2	30:0:2652:U:O2	2.71	0.43
30:0:1202:A:H2'	30:0:1203:G:O4'	2.19	0.43
30:0:2727:A:C6	30:0:2756:U:N3	2.87	0.43
30:0:2812:A:H2	30:0:2814:A:H62	1.63	0.43
30:0:1255:A:H2'	30:0:1256:C:O5'	2.18	0.43
21:U:6:CYS:HB2	21:U:13:ILE:CG1	2.49	0.43
30:0:79:G:H22	30:0:97:G:H1'	1.82	0.43
30:0:432:G:C2	30:0:433:C:C6	3.07	0.43
25:Y:144:ARG:HB3	38:0:4369:HOH:O	2.18	0.43
16:P:58:SER:HB3	38:0:5593:HOH:O	2.18	0.43
14:N:65:ASP:HB3	38:N:8820:HOH:O	2.19	0.43
30:0:1703:G:C2	30:0:1716:A:C4	3.06	0.43
30:0:191:A:H61	30:0:435:A:H62	1.67	0.43
31:9:11:A:H2	31:9:68:G:N3	2.17	0.43
30:0:1667:A:H2'	30:0:1668:U:O4'	2.19	0.43
18:R:39:THR:HB	18:R:42:GLU:CD	2.39	0.43
30:0:1882:C:H2'	30:0:1883:U:C6	2.53	0.43
30:0:1712:A:H2'	30:0:1713:G:O4'	2.19	0.43
30:0:1399:A:H2'	30:0:1400:C:C6	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
29:3:54:LYS:HE3	38:0:3005:HOH:O	2.18	0.43
31:9:39:U:H2'	31:9:40:C:OP1	2.18	0.43
30:0:1697:G:H1'	38:0:7261:HOH:O	2.19	0.43
30:0:2080:G:H2'	30:0:2081:A:C8	2.54	0.43
25:Y:235:GLU:CD	25:Y:235:GLU:N	2.72	0.43
29:3:17:HIS:ND1	30:0:2408:A:O2'	2.48	0.43
2:B:305:ASP:O	2:B:306:LYS:CB	2.66	0.43
1:A:105:VAL:HG11	1:A:154:ALA:HB1	2.00	0.43
5:E:95:VAL:O	5:E:126:ILE:HD12	2.18	0.43
18:R:18:LEU:HD12	18:R:143:VAL:CG1	2.49	0.43
5:E:7:ILE:HG23	5:E:45:ASP:O	2.19	0.43
30:0:2332:A:H3'	30:0:2333:G:H8	1.84	0.43
16:P:134:VAL:O	16:P:137:LEU:HB3	2.19	0.43
10:J:99:GLU:HA	38:J:8871:HOH:O	2.19	0.43
30:0:1192:A:H4'	38:0:4383:HOH:O	2.18	0.43
30:0:435:A:O2'	30:0:436:A:H5'	2.19	0.43
31:9:11:A:H4'	31:9:13:A:C8	2.54	0.43
30:0:816:G:O5'	30:0:816:G:H8	2.02	0.43
6:F:58:GLU:HB3	13:M:8:ILE:HG23	2.01	0.43
20:T:28:SER:HA	20:T:97:ARG:HD3	1.99	0.43
30:0:2896:A:N3	30:0:2896:A:H2'	2.34	0.43
30:0:793:A:C2	30:0:822:C:C2	3.06	0.43
30:0:1504:A:H4'	30:0:1506:U:C5	2.53	0.43
30:0:2779:G:N7	30:0:2790:C:C2	2.86	0.43
30:0:67:A:H5''	30:0:69:A:C8	2.54	0.43
13:M:48:LYS:HE3	13:M:52:GLN:NE2	2.28	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
30:0:1933:G:C2'	30:0:1934:A:H5'	2.48	0.43
30:0:2476:C:H2'	30:0:2476:C:O2	2.19	0.43
30:0:699:C:C2	30:0:744:G:N2	2.87	0.43
30:0:2293:G:C5	30:0:2294:C:C5	3.07	0.43
12:L:6:ARG:HD3	30:0:1299:G:O6	2.18	0.43
4:D:12:GLU:O	4:D:15:GLU:HG2	2.18	0.43
30:0:1600:G:H8	30:0:1600:G:OP2	2.02	0.43
30:0:393:G:C2	30:0:394:G:C4	3.06	0.43
1:A:72:GLU:HG2	26:Z:100:GLY:HA3	2.01	0.43
30:0:135:G:C2	30:0:144:A:N3	2.86	0.43
30:0:2095:A:OP1	30:0:2096:A:H4'	2.19	0.43
19:S:57:THR:C	19:S:59:ASP:H	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:877:G:N7	30:0:885:G:C6	2.87	0.42
30:0:248:A:H5'	30:0:249:G:OP2	2.19	0.42
1:A:23:TYR:HB2	30:0:1872:C:C5	2.54	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
13:M:42:ARG:HA	13:M:43:PRO:HD3	1.86	0.42
4:D:67:ASP:HA	4:D:68:PRO:HD3	1.92	0.42
30:0:729:C:C2	30:0:743:G:N2	2.87	0.42
30:0:577:G:C2	30:0:581:G:C6	3.07	0.42
21:U:34:SER:HB3	38:0:3126:HOH:O	2.17	0.42
30:0:1287:A:H8	38:0:7887:HOH:O	2.02	0.42
30:0:349:U:O5'	30:0:349:U:H6	2.02	0.42
15:O:57:THR:O	15:O:111:VAL:HG23	2.19	0.42
1:A:81:GLN:H	1:A:92:ASN:ND2	2.17	0.42
30:0:970:U:H2'	38:0:6308:HOH:O	2.18	0.42
19:S:42:GLU:O	19:S:46:ASP:HA	2.19	0.42
3:C:156:LEU:O	3:C:160:LEU:HG	2.19	0.42
5:E:81:GLU:O	5:E:172:PRO:HD3	2.19	0.42
30:0:1183:C:N3	30:0:1184:C:N4	2.67	0.42
30:0:1184:C:O2'	30:0:1185:U:OP2	2.32	0.42
30:0:2512:U:H4'	30:0:2514:U:O4	2.19	0.42
4:D:137:PRO:O	31:9:30:C:OP1	2.37	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
13:M:112:LEU:HB3	13:M:133:LEU:HB3	2.02	0.42
30:0:2853:U:C4	30:0:2906:A:N6	2.87	0.42
30:0:2600:A:H2'	30:0:2601:A:O4'	2.19	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
30:0:726:C:C2	30:0:727:G:C8	3.07	0.42
24:X:43:VAL:HG12	24:X:44:ASP:N	2.34	0.42
30:0:1970:G:H4'	30:0:1971:G:O5'	2.19	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
30:0:2531:U:H4'	38:0:9596:HOH:O	2.17	0.42
30:0:188:C:O5'	30:0:188:C:H6	2.02	0.42
23:W:11:VAL:O	23:W:12:ASN:HB2	2.19	0.42
3:C:24:THR:HG23	3:C:25:PRO:HD2	2.02	0.42
30:0:2248:C:O2'	30:0:2249:G:H5'	2.19	0.42
30:0:314:G:N2	30:0:317:A:C8	2.87	0.42
30:0:1474:C:O2'	30:0:1475:G:H5'	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2374:G:H2'	30:0:2375:A:C8	2.53	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
26:Z:34:SER:HB3	30:0:797:A:H4'	2.00	0.42
4:D:76:ARG:NE	31:9:44:A:O4'	2.52	0.42
30:0:111:C:H2'	30:0:112:G:O4'	2.19	0.42
30:0:1115:U:H5''	30:0:1140:C:O2'	2.20	0.42
30:0:354:A:H2'	30:0:355:C:C6	2.52	0.42
8:H:65:LEU:HA	8:H:65:LEU:HD12	1.80	0.42
30:0:107:U:H2'	30:0:108:U:H5'	2.01	0.42
3:C:151:GLN:HA	3:C:151:GLN:HE21	1.84	0.42
30:0:830:G:O2'	30:0:831:U:H5'	2.19	0.42
30:0:752:G:H2'	30:0:753:U:O4'	2.19	0.42
3:C:194:PHE:HB2	3:C:212:VAL:HG12	2.00	0.42
30:0:1195:G:N2	30:0:1205:U:C2	2.87	0.42
31:9:57:A:N3	31:9:57:A:H5'	2.34	0.42
30:0:877:G:C6	30:0:885:G:C4	3.08	0.42
30:0:2502:C:O2'	30:0:2503:A:H5'	2.19	0.42
20:T:24:ARG:HH21	20:T:39:ASN:ND2	2.17	0.42
30:0:282:C:O2'	30:0:368:C:N4	2.52	0.42
31:9:36:C:C5	31:9:37:C:C4	3.08	0.42
30:0:2893:C:C2'	30:0:2894:C:H5'	2.49	0.42
28:2:22:PRO:HG2	28:2:25:VAL:CG2	2.49	0.42
31:9:65:A:C2'	31:9:66:G:OP2	2.68	0.42
30:0:652:G:H2'	30:0:653:U:O4'	2.20	0.42
30:0:2362:A:H2'	30:0:2363:G:C8	2.54	0.42
12:L:38:HIS:CD2	12:L:39:GLU:HG3	2.54	0.42
5:E:72:MET:O	5:E:76:VAL:HG22	2.19	0.42
30:0:1789:G:C2'	30:0:1790:C:O5'	2.67	0.42
19:S:57:THR:HG22	19:S:58:MET:N	2.34	0.42
26:Z:66:CYS:SG	26:Z:67:GLY:N	2.93	0.42
2:B:57:GLU:HA	2:B:58:PRO:HD2	1.85	0.42
5:E:35:TYR:CD2	5:E:36:PRO:HD2	2.55	0.42
5:E:106:ASN:ND2	5:E:109:GLY:HA2	2.34	0.42
30:0:2655:U:C4	30:0:2656:G:N7	2.87	0.42
29:3:80:ARG:HH22	30:0:2381:C:H4'	1.84	0.42
30:0:1350:U:H5''	38:0:5090:HOH:O	2.20	0.42
2:B:60:SER:HA	2:B:61:PRO:HD3	1.90	0.42
31:9:22:G:C6	31:9:55:U:C2	3.07	0.42
3:C:211:ASP:HB2	3:C:231:ARG:HH12	1.85	0.42
30:0:138:U:P	30:0:139:C:H5	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2346:C:O2	30:0:2346:C:H2'	2.18	0.42
26:Z:38:PHE:HB3	26:Z:42:TYR:HD1	1.82	0.42
8:H:91:ARG:NH2	8:H:135:GLN:NE2	2.68	0.42
30:0:265:U:C2	30:0:266:G:C8	3.07	0.42
1:A:223:ARG:HH12	30:0:2270:G:C4'	2.27	0.42
30:0:1848:G:O2'	30:0:1849:G:H5'	2.19	0.42
30:0:2470:A:H2'	30:0:2471:G:O5'	2.19	0.42
16:P:10:ALA:HA	16:P:13:VAL:HG12	2.02	0.42
2:B:162:MET:HG3	2:B:310:ARG:NH1	2.35	0.42
2:B:307:ARG:HG2	2:B:308:LEU:N	2.34	0.42
30:0:1342:C:O2'	30:0:1343:C:H5'	2.18	0.42
30:0:1754:A:O5'	30:0:1754:A:H8	2.02	0.42
29:3:10:TYR:CD2	30:0:2382:A:H1'	2.55	0.42
30:0:161:A:H2'	30:0:162:C:C6	2.53	0.42
30:0:776:A:C2	30:0:780:A:C6	3.08	0.42
30:0:690:G:H1'	30:0:731:U:O2'	2.20	0.42
15:O:105:ASN:HD21	15:O:109:SER:N	2.18	0.42
12:L:10:SER:O	12:L:11:ARG:HB3	2.19	0.42
4:D:88:LEU:HB2	4:D:89:PRO:HD3	2.00	0.42
1:A:81:GLN:HB2	1:A:92:ASN:ND2	2.35	0.42
30:0:1757:U:H5	38:0:3214:HOH:O	2.02	0.42
24:X:12:ILE:HB	24:X:70:ILE:CG2	2.49	0.42
30:0:1998:G:O2'	30:0:2026:C:H1'	2.20	0.42
30:0:165:A:H2'	30:0:166:A:OP1	2.19	0.42
2:B:177:HIS:O	2:B:181:ILE:HG13	2.19	0.42
30:0:1603:A:H5'	30:0:1605:G:H5'	1.99	0.42
30:0:1680:C:H5'	30:0:1685:A:N6	2.34	0.42
31:9:108:C:H2'	31:9:109:G:C8	2.55	0.42
30:0:1643:C:O2'	30:0:1644:C:H5'	2.19	0.42
30:0:1391:G:H2'	30:0:1392:A:H5'	2.01	0.42
30:0:1709:G:C6	30:0:1711:A:C5	3.07	0.42
30:0:1097:A:H2'	30:0:1098:A:C8	2.54	0.42
8:H:48:VAL:HG13	38:H:218:HOH:O	2.18	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
29:3:33:MET:CG	30:0:1922:A:H2'	2.50	0.42
24:X:71:ARG:HD3	38:X:2171:HOH:O	2.20	0.42
30:0:1573:A:C8	30:0:1574:C:C6	3.08	0.42
30:0:2842:G:C2'	30:0:2843:A:H5'	2.50	0.42
13:M:191:GLY:O	30:0:175:G:H3'	2.19	0.42
30:0:453:A:C4	30:0:479:G:N7	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:48:MET:O	30:0:2719:A:H5'	2.20	0.42
30:0:2499:U:H2'	30:0:2500:C:O4'	2.20	0.42
30:0:221:G:H2'	30:0:222:A:C8	2.55	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
30:0:1047:U:O5'	30:0:1047:U:H6	2.03	0.42
30:0:2805:A:C8	30:0:2806:C:C5	3.07	0.42
1:A:10:GLY:HA2	30:0:1861:C:O2	2.20	0.42
30:0:1367:A:H2'	30:0:1368:U:O4'	2.20	0.42
30:0:1523:G:C6	30:0:1524:U:O4	2.73	0.42
30:0:2864:U:H2'	30:0:2865:G:H5'	2.02	0.42
13:M:70:GLY:HA3	13:M:73:ARG:CZ	2.50	0.42
13:M:159:VAL:HG13	13:M:160:PHE:N	2.35	0.42
2:B:223:ARG:HG3	2:B:232:TRP:C	2.40	0.42
30:0:590:A:H2'	30:0:591:A:C5'	2.48	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
30:0:1255:A:C2'	30:0:1256:C:O5'	2.68	0.42
10:J:116:LEU:HB2	10:J:119:THR:CG2	2.49	0.42
8:H:59:GLN:HE21	8:H:129:ARG:HG2	1.85	0.42
10:J:131:THR:O	10:J:134:GLU:HB2	2.19	0.42
30:0:1060:C:H5'	30:0:1060:C:H6	1.85	0.42
30:0:583:C:H2'	30:0:584:U:H6	1.85	0.42
30:0:462:A:N6	30:0:477:A:C2	2.88	0.42
30:0:1965:C:H6	30:0:1965:C:O5'	2.02	0.42
20:T:75:GLU:O	20:T:76:ASP:HB2	2.19	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
14:N:169:PRO:O	14:N:172:PHE:HB3	2.20	0.42
30:0:1241:G:H2'	30:0:1242:A:O4'	2.19	0.42
30:0:877:G:C2	30:0:885:G:O4'	2.73	0.42
26:Z:37:ARG:HG3	26:Z:38:PHE:CD2	2.54	0.42
30:0:711:G:N2	30:0:718:C:N1	2.67	0.42
30:0:2256:G:H2'	30:0:2257:G:C5'	2.50	0.42
30:0:802:G:N2	30:0:812:A:C4	2.88	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
1:A:160:ALA:CB	26:Z:89:THR:HB	2.49	0.42
23:W:92:ASP:OD2	23:W:94:SER:HB2	2.20	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)
30:0:1537:C:O2'	30:0:1538:C:H5'	2.18	0.42
4:D:104:PHE:N	4:D:104:PHE:CD2	2.88	0.42
24:X:25:ARG:HD2	38:X:5356:HOH:O	2.19	0.42
30:0:1541:G:O2'	30:0:1542:G:H5'	2.18	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
30:0:1840:A:H4'	30:0:1841:C:O5'	2.20	0.42
2:B:316:ARG:HB2	30:0:2768:A:C8	2.55	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
30:0:2523:U:O2'	30:0:2524:G:H5'	2.19	0.42
30:0:1819:G:H2'	30:0:1820:G:H5'	2.01	0.42
30:0:2355:G:N3	30:0:2355:G:C2'	2.83	0.42
30:0:325:U:H3'	38:0:5512:HOH:O	2.19	0.42
3:C:87:ARG:NH2	30:0:894:A:C2	2.88	0.42
30:0:473:A:C2'	30:0:474:C:H5'	2.49	0.42
2:B:8:LYS:HB3	2:B:218:TRP:O	2.19	0.42
30:0:387:G:O2'	30:0:388:G:H5'	2.20	0.42
30:0:485:A:N3	30:0:487:G:H5''	2.34	0.42
30:0:1413:A:H2'	30:0:1414:A:O4'	2.20	0.42
1:A:169:PHE:O	1:A:170:VAL:HB	2.20	0.42
30:0:2909:G:N2	30:0:2910:A:C5	2.88	0.42
28:2:41:HIS:CE1	30:0:1439:C:H5''	2.54	0.42
30:0:67:A:H3'	30:0:67:A:OP2	2.20	0.42
31:9:114:G:C6	31:9:115:C:N4	2.88	0.42
30:0:2700:G:C2'	30:0:2701:G:H5'	2.49	0.42
23:W:10:GLU:HB3	38:W:1223:HOH:O	2.20	0.42
16:P:40:VAL:O	16:P:44:VAL:HG23	2.20	0.42
30:0:293:A:C2	30:0:294:C:C6	3.08	0.42
26:Z:61:HIS:CG	26:Z:95:PRO:HG3	2.55	0.42
30:0:1015:C:H2'	30:0:1016:U:H6	1.82	0.42
29:3:83:TRP:O	29:3:85:ALA:N	2.53	0.42
30:0:59:A:H5''	38:0:4313:HOH:O	2.18	0.42
17:Q:27:GLN:HB3	38:9:9083:HOH:O	2.20	0.42
30:0:868:G:H2'	38:0:3039:HOH:O	2.18	0.42
24:X:70:ILE:O	24:X:70:ILE:HG23	2.18	0.42
29:3:14:CYS:SG	38:3:9063:HOH:O	2.62	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
5:E:77:THR:OG1	5:E:78:GLU:N	2.50	0.42
38:I:3512:HOH:O	30:0:1163:G:N2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
13:M:89:THR:HA	38:M:8950:HOH:O	2.19	0.41
30:0:314:G:C2	30:0:317:A:C8	3.08	0.41
30:0:371:U:H2'	30:0:372:A:H8	1.85	0.41
21:U:56:ARG:NH1	30:0:2890:A:C2	2.88	0.41
30:0:1006:A:N3	30:0:2298:C:O2'	2.45	0.41
28:2:48:ASP:O	28:2:49:GLU:HB2	2.20	0.41
30:0:2478:U:H2'	30:0:2479:A:H8	1.85	0.41
30:0:335:U:C2'	30:0:336:G:OP1	2.68	0.41
29:3:62:THR:CG2	29:3:63:LYS:N	2.83	0.41
22:V:39:ALA:C	22:V:41:GLU:H	2.23	0.41
30:0:2799:A:H5'	30:0:2800:A:P	2.59	0.41
30:0:628:1MA:H4'	38:0:3136:HOH:O	2.19	0.41
30:0:1789:G:N2	30:0:1790:C:H1'	2.35	0.41
12:L:73:VAL:HG21	12:L:116:HIS:CE1	2.54	0.41
30:0:2433:A:H2'	30:0:2434:A:C8	2.54	0.41
30:0:1624:A:O4'	30:0:1626:A:C8	2.73	0.41
30:0:887:G:H2'	30:0:888:U:C6	2.54	0.41
30:0:1919:A:H4'	38:0:4820:HOH:O	2.19	0.41
15:O:39:THR:HB	38:0:4589:HOH:O	2.19	0.41
2:B:224:LYS:HA	2:B:224:LYS:HD3	1.83	0.41
2:B:203:ALA:HA	2:B:263:THR:HA	2.02	0.41
15:O:68:GLY:HA3	30:0:745:G:O6	2.20	0.41
12:L:53:ARG:N	35:L:8810:CL:CL	2.66	0.41
12:L:35:ARG:HB2	12:L:43:HIS:CD2	2.55	0.41
30:0:1163:G:C2	30:0:1184:C:N3	2.87	0.41
29:3:5:ARG:HA	29:3:22:VAL:HG23	2.02	0.41
31:9:56:A:C3'	31:9:57:A:C5'	2.93	0.41
30:0:1519:U:H6	30:0:1519:U:O5'	2.04	0.41
1:A:199:HIS:CD2	1:A:200:PRO:HD2	2.55	0.41
30:0:2004:U:H2'	30:0:2004:U:O2	2.20	0.41
30:0:272:A:N1	30:0:369:G:H5''	2.34	0.41
30:0:1178:G:H2'	30:0:1179:C:H6	1.79	0.41
30:0:2912:C:C2'	30:0:2913:A:H5'	2.50	0.41
26:Z:78:ILE:HB	38:Z:8715:HOH:O	2.19	0.41
1:A:51:ARG:NH2	1:A:53:ALA:HB3	2.35	0.41
31:9:50:G:C6	31:9:51:A:C6	3.08	0.41
23:W:13:MET:CE	23:W:17:ILE:HG22	2.50	0.41
4:D:76:ARG:CZ	31:9:44:A:C1'	2.98	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:102:A:C6	30:0:103:C:N4	2.88	0.41
30:0:412:C:C2'	30:0:413:G:H5'	2.50	0.41
10:J:19:MET:HE2	10:J:79:PHE:HA	2.02	0.41
18:R:99:ALA:HB1	18:R:109:MET:HE2	2.01	0.41
16:P:94:TRP:CH2	16:P:98:ILE:HG13	2.55	0.41
30:0:2020:C:O2'	30:0:2021:C:H5'	2.20	0.41
30:0:1915:U:O2	30:0:1925:G:C2	2.73	0.41
30:0:2061:C:C2'	30:0:2062:A:H5'	2.51	0.41
11:K:4:LEU:HD23	11:K:4:LEU:HA	1.84	0.41
22:V:23:LEU:HD22	22:V:49:LEU:HD23	2.01	0.41
30:0:201:G:H1'	38:0:4539:HOH:O	2.19	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
30:0:1507:C:H4'	38:0:3595:HOH:O	2.20	0.41
9:I:96:SER:H	9:I:99:GLN:CD	2.22	0.41
30:0:1449:G:H4'	38:0:9213:HOH:O	2.20	0.41
30:0:446:G:H3'	38:0:9539:HOH:O	2.20	0.41
30:0:236:A:H8	30:0:236:A:OP1	2.03	0.41
30:0:1079:A:N1	30:0:2068:G:O2'	2.43	0.41
30:0:2782:G:O6	30:0:2790:C:H5''	2.19	0.41
30:0:38:G:C2'	30:0:39:G:H5'	2.50	0.41
30:0:1804:A:H2'	30:0:1805:G:C8	2.55	0.41
30:0:2256:G:C2'	30:0:2257:G:H5'	2.51	0.41
30:0:2795:C:O2'	30:0:2796:U:C5'	2.65	0.41
30:0:1212:C:C5	30:0:1213:C:C5	3.09	0.41
26:Z:34:SER:HA	30:0:797:A:C5'	2.50	0.41
30:0:1878:G:O2'	30:0:1879:U:P	2.78	0.41
30:0:2799:A:N6	30:0:2801:A:C2	2.89	0.41
24:X:54:ILE:HD11	24:X:85:VAL:HG12	2.03	0.41
21:U:31:PHE:CG	21:U:37:GLU:HG2	2.55	0.41
5:E:69:ILE:HA	5:E:72:MET:HE3	2.02	0.41
4:D:84:LEU:HD23	4:D:84:LEU:HA	1.92	0.41
8:H:59:GLN:NE2	8:H:96:GLN:HG2	2.35	0.41
30:0:2474:A:C8	30:0:2621:PSU:H4'	2.55	0.41
30:0:1826:C:O2'	30:0:1827:G:H5'	2.21	0.41
30:0:1554:C:O2'	30:0:1631:A:H1'	2.19	0.41
12:L:150:GLN:HB3	38:L:8869:HOH:O	2.19	0.41
2:B:75:GLU:C	2:B:77:PRO:HD3	2.40	0.41
2:B:211:THR:HG21	38:0:7438:HOH:O	2.20	0.41
25:Y:157:ILE:HD13	38:0:4836:HOH:O	2.20	0.41
38:H:216:HOH:O	30:0:2517:A:H2	1.99	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1419:U:H5'	30:0:1420:C:OP2	2.21	0.41
30:0:1303:C:O2	30:0:1353:C:H1'	2.20	0.41
31:9:58:G:C8	31:9:59:C:C4	3.08	0.41
30:0:2710:U:H2'	30:0:2711:U:C6	2.55	0.41
30:0:281:U:C2'	30:0:282:C:C5'	2.98	0.41
30:0:2723:G:H1'	38:0:4812:HOH:O	2.19	0.41
30:0:1942:A:C1'	38:0:9045:HOH:O	2.69	0.41
30:0:1819:G:C2'	30:0:1820:G:H5'	2.50	0.41
26:Z:34:SER:HA	30:0:797:A:H5'	2.02	0.41
31:9:110:G:C6	31:9:111:U:C4	3.08	0.41
30:0:1928:C:C2'	30:0:1929:G:H5'	2.50	0.41
5:E:107:PHE:O	5:E:110:GLU:HG3	2.20	0.41
30:0:1769:C:C2'	30:0:1770:U:H5'	2.51	0.41
30:0:517:U:H2'	30:0:518:G:H5'	2.02	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
30:0:1997:A:H2	30:0:2026:C:O2'	2.04	0.41
30:0:552:A:H5'	38:0:5878:HOH:O	2.19	0.41
15:O:26:TRP:HA	15:O:26:TRP:CE3	2.55	0.41
30:0:1894:C:N4	30:0:1939:U:H2'	2.34	0.41
2:B:69:VAL:HA	2:B:70:PRO:HD3	1.77	0.41
24:X:23:HIS:HE1	30:0:2044:G:OP1	2.03	0.41
19:S:17:ASP:HB3	19:S:23:LYS:HB2	2.01	0.41
30:0:2815:G:H4'	30:0:2816:A:OP2	2.20	0.41
30:0:2511:A:H2'	30:0:2512:U:C6	2.56	0.41
30:0:343:C:H1'	38:0:5552:HOH:O	2.19	0.41
1:A:212:PRO:HA	30:0:1943:C:O4'	2.20	0.41
30:0:1882:C:H2'	30:0:1883:U:H6	1.86	0.41
30:0:2470:A:C2'	30:0:2471:G:O5'	2.68	0.41
30:0:594:C:C4	30:0:595:U:C4	3.08	0.41
3:C:5:ILE:HG12	3:C:139:VAL:CG1	2.50	0.41
30:0:1063:G:O5'	30:0:2307:A:H1'	2.21	0.41
2:B:222:LYS:HG3	30:0:2038:A:H5''	2.01	0.41
30:0:1423:C:O2'	30:0:1424:A:H5'	2.20	0.41
11:K:66:ARG:NH1	30:0:1992:U:H3'	2.35	0.41
2:B:320:GLN:HE21	2:B:321:PRO:HD3	1.84	0.41
21:U:5:GLU:HG2	21:U:6:CYS:N	2.36	0.41
30:0:10:U:O4	30:0:532:A:OP2	2.38	0.41
25:Y:130:ARG:HB2	25:Y:142:SER:O	2.20	0.41
14:N:132:ASN:O	14:N:135:VAL:HG12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1271:A:H2'	30:0:1272:C:H6	1.84	0.41
10:J:76:ASP:HA	38:J:8863:HOH:O	2.20	0.41
30:0:2854:A:N6	30:0:2905:A:N6	2.69	0.41
25:Y:189:ASN:HD22	25:Y:191:ASP:N	2.19	0.41
30:0:910:C:H2'	30:0:911:G:O4'	2.21	0.41
25:Y:152:LYS:CB	25:Y:160:LYS:HG3	2.51	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
30:0:1898:G:H2'	30:0:1899:C:C6	2.55	0.41
10:J:54:VAL:HG11	10:J:138:THR:HG21	2.02	0.41
6:F:26:THR:HB	6:F:102:GLY:HA3	2.02	0.41
19:S:51:GLN:HE21	19:S:53:ASN:HD21	1.67	0.41
30:0:1278:A:O2'	30:0:1279:U:C2	2.65	0.41
30:0:1666:C:C2'	30:0:1667:A:H5'	2.32	0.41
31:9:60:C:O2	31:9:60:C:H2'	2.19	0.41
30:0:1679:C:O2	30:0:1685:A:C2	2.73	0.41
30:0:307:G:C2	30:0:309:C:C4	3.08	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
23:W:122:ARG:NH2	38:0:5254:HOH:O	2.52	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
30:0:165:A:C2'	30:0:166:A:OP1	2.67	0.41
30:0:1540:G:C4	30:0:1541:G:C8	3.09	0.41
30:0:2057:U:O5'	30:0:2057:U:H6	2.03	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
30:0:870:G:C3'	30:0:871:G:H5''	2.51	0.41
30:0:1191:A:O5'	30:0:1191:A:C8	2.74	0.41
29:3:91:GLN:O	29:3:92:GLU:HB2	2.21	0.41
30:0:1544:U:O2'	30:0:1545:C:H5'	2.20	0.41
30:0:2325:U:C2	30:0:2326:C:C6	3.09	0.41
26:Z:70:ARG:HB2	26:Z:81:CYS:HG	1.86	0.41
30:0:69:A:C3'	30:0:69:A:C8	3.04	0.41
30:0:631:A:C6	30:0:2074:A:H5'	2.56	0.41
30:0:1196:C:H2'	30:0:1197:G:H5'	2.02	0.41
30:0:2668:G:N2	30:0:2669:U:C2	2.88	0.41
30:0:2668:G:O4'	30:0:2827:A:C2	2.73	0.41
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
30:0:812:A:H1'	38:0:3946:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:677:C:H6	30:0:677:C:O5'	2.03	0.41
30:0:862:U:O2'	30:0:863:G:H5'	2.20	0.41
30:0:393:G:C6	30:0:394:G:C6	3.09	0.41
30:0:1012:A:H8	30:0:1012:A:O5'	2.04	0.41
8:H:89:THR:O	8:H:137:PHE:HD2	2.04	0.41
30:0:1798:C:OP2	30:0:1799:G:H5''	2.20	0.41
30:0:1438:G:N3	30:0:1438:G:H2'	2.35	0.41
21:U:17:THR:HG21	38:U:2221:HOH:O	2.21	0.41
30:0:2383:G:C6	30:0:2384:U:C4	3.08	0.41
30:0:268:U:O4	30:0:269:G:N1	2.54	0.41
30:0:1209:C:O2'	30:0:1210:G:H5'	2.20	0.41
30:0:189:A:H2	30:0:205:U:O2	2.04	0.41
1:A:199:HIS:HE1	30:0:1881:A:OP1	2.04	0.41
30:0:241:A:C2	30:0:378:A:H4'	2.55	0.41
30:0:2324:G:H2'	30:0:2325:U:C6	2.56	0.41
8:H:91:ARG:NH1	8:H:138:THR:OG1	2.53	0.41
30:0:1803:C:H2'	30:0:1804:A:C8	2.56	0.41
30:0:1173:A:H2'	30:0:1177:A:H62	1.85	0.41
1:A:47:HIS:HD2	30:0:1654:U:O2'	2.03	0.41
10:J:107:ASN:HA	10:J:108:PRO:HD2	1.98	0.41
30:0:2700:G:H2'	30:0:2701:G:O5'	2.21	0.41
30:0:2039:A:H2'	30:0:2040:C:C6	2.56	0.41
30:0:1774:G:C2'	30:0:1775:A:H5'	2.51	0.41
30:0:1913:C:H2'	30:0:1914:C:C6	2.54	0.41
2:B:195:ARG:HG2	2:B:323:LEU:HD22	2.03	0.41
31:9:82:U:H2'	31:9:83:G:C8	2.56	0.41
4:D:20:LYS:HG2	4:D:133:ASN:HB3	2.02	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
18:R:114:VAL:HG13	18:R:114:VAL:O	2.20	0.41
23:W:43:GLY:HA3	30:0:945:U:O2'	2.20	0.41
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
30:0:383:A:H2'	30:0:384:G:O4'	2.21	0.41
30:0:1621:G:H2'	30:0:1622:G:H8	1.86	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
30:0:1193:A:C2	30:0:1194:A:N6	2.89	0.41
31:9:29:C:C6	31:9:30:C:C6	3.08	0.41
26:Z:47:ARG:HD2	38:Z:8718:HOH:O	2.20	0.41
30:0:1596:U:O2'	30:0:1598:A:N7	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:61:MET:O	6:F:64:PRO:HD2	2.21	0.41
30:0:279:C:H2'	30:0:280:C:H5'	2.01	0.41
30:0:1543:G:H2'	30:0:1544:U:C5	2.56	0.41
1:A:171:LYS:HB2	30:0:820:G:C6	2.55	0.41
21:U:56:ARG:NH1	30:0:2890:A:C4	2.89	0.41
30:0:265:U:C4	30:0:266:G:N7	2.89	0.41
30:0:1553:C:H6	30:0:1553:C:O5'	2.04	0.41
30:0:1973:A:C8	30:0:1973:A:H5'	2.53	0.41
30:0:20:G:H2'	30:0:21:G:O5'	2.21	0.41
30:0:1226:G:C2	30:0:1227:C:C6	3.08	0.41
30:0:61:G:C2	30:0:62:C:C2	3.09	0.41
30:0:2695:C:N4	30:0:2701:G:N2	2.69	0.41
30:0:2599:A:C6	30:0:2600:A:N1	2.89	0.41
30:0:1476:A:H1'	30:0:1867:G:O2'	2.21	0.41
5:E:20:ILE:HD12	5:E:33:LEU:HD12	2.03	0.41
30:0:1748:U:C6	30:0:1749:U:C5	3.09	0.41
30:0:2801:A:C4	30:0:2802:C:C5	3.08	0.41
30:0:51:G:C2	30:0:111:C:C2	3.08	0.41
2:B:74:ILE:HG13	38:B:9076:HOH:O	2.20	0.41
5:E:145:ALA:HB1	5:E:168:ILE:CD1	2.49	0.41
30:0:1089:G:H1'	30:0:1290:G:N2	2.36	0.41
23:W:120:PRO:HG2	30:0:1095:U:O2	2.20	0.41
30:0:1339:G:C5	30:0:1340:G:C6	3.09	0.41
30:0:2366:C:P	38:0:6939:HOH:O	2.79	0.41
30:0:1024:G:C5	30:0:1025:C:C4	3.09	0.41
30:0:1619:G:H2'	30:0:1620:C:O4'	2.21	0.41
30:0:1416:G:C2'	30:0:1417:G:H5'	2.51	0.41
30:0:1362:U:H2'	30:0:1363:G:H8	1.86	0.41
25:Y:152:LYS:HB3	25:Y:160:LYS:HG3	2.02	0.41
5:E:119:HIS:O	5:E:140:ALA:HB1	2.21	0.41
19:S:73:ASP:OD1	19:S:76:GLU:HG3	2.21	0.41
30:0:844:A:C6	30:0:882:A:C6	3.09	0.41
30:0:2453:G:H2'	30:0:2454:C:C6	2.55	0.41
5:E:15:GLN:HG2	5:E:16:ASP:N	2.36	0.41
4:D:36:ASN:HA	38:D:7500:HOH:O	2.20	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
16:P:61:ARG:NH2	30:0:2737:C:OP2	2.40	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
30:0:1195:G:N1	30:0:1205:U:N3	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:14:G:C5'	31:9:14:G:H8	2.13	0.41
30:0:1591:A:H5'	30:0:1603:A:H61	1.86	0.41
13:M:68:ARG:HB2	38:M:8932:HOH:O	2.19	0.41
30:0:282:C:O2	30:0:282:C:C2'	2.62	0.41
30:0:1634:G:C4	30:0:1635:U:C5	3.08	0.41
30:0:714:U:O4'	30:0:716:G:C2	2.74	0.41
30:0:2269:C:C4	30:0:2270:G:C5	3.08	0.41
38:B:9106:HOH:O	30:0:2818:A:H2	2.04	0.41
2:B:288:GLY:HA2	30:0:2898:G:H4'	2.02	0.41
30:0:2526:C:H5'	30:0:2526:C:C6	2.56	0.41
30:0:736:A:H5''	38:0:4253:HOH:O	2.21	0.41
30:0:123:U:O2'	30:0:124:C:H5'	2.21	0.41
31:9:110:G:H2'	31:9:110:G:N3	2.35	0.41
30:0:2617:G:H5''	38:0:3896:HOH:O	2.20	0.41
30:0:965:A:H2'	30:0:965:A:N3	2.36	0.41
30:0:2016:U:H2'	30:0:2017:U:O4'	2.21	0.41
1:A:37:VAL:HG13	38:A:9088:HOH:O	2.21	0.41
5:E:81:GLU:HA	5:E:133:VAL:O	2.21	0.41
18:R:130:MET:HG3	38:0:7551:HOH:O	2.21	0.41
30:0:2098:C:O5'	30:0:2098:C:H6	2.04	0.41
5:E:23:GLU:HG2	5:E:28:SER:CB	2.51	0.41
23:W:132:VAL:HG21	23:W:140:LYS:O	2.21	0.41
30:0:23:G:H1'	30:0:520:A:N6	2.35	0.41
30:0:1175:G:C5	30:0:1193:A:C2	3.10	0.40
30:0:1170:U:O2	30:0:1172:G:H8	2.04	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
13:M:72:ALA:HB3	38:M:8950:HOH:O	2.21	0.40
30:0:2414:A:N1	30:0:2415:A:C6	2.90	0.40
30:0:1177:A:C6	30:0:1178:G:C5	3.09	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
30:0:257:G:N2	30:0:258:G:C4	2.89	0.40
30:0:2330:U:H4'	30:0:2331:C:OP1	2.20	0.40
14:N:110:THR:HA	14:N:111:PRO:HD3	1.98	0.40
19:S:11:THR:CG2	30:0:1444:G:H5''	2.50	0.40
30:0:797:A:H2'	30:0:798:G:O4'	2.21	0.40
4:D:28:GLY:CA	4:D:69:ILE:HG23	2.51	0.40
13:M:75:ARG:HG3	38:M:8868:HOH:O	2.20	0.40
25:Y:125:LYS:HB2	25:Y:126:PRO:HD2	2.03	0.40
3:C:118:THR:HG21	3:C:233:THR:HB	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1832:G:N3	30:0:1833:U:C6	2.89	0.40
28:2:42:TRP:HZ2	30:0:1438:G:H1'	1.87	0.40
6:F:38:LYS:HE3	30:0:244:C:OP2	2.21	0.40
29:3:86:GLY:HA2	38:3:9032:HOH:O	2.21	0.40
30:0:2121:G:C2'	30:0:2122:C:H5'	2.51	0.40
30:0:962:C:H2'	30:0:963:C:H5'	2.03	0.40
30:0:1681:G:H5''	30:0:1682:A:H5'	2.03	0.40
30:0:2831:C:C2'	30:0:2832:C:C5'	2.93	0.40
30:0:2335:C:N3	30:0:2350:G:C2	2.89	0.40
30:0:1634:G:C6	30:0:1635:U:C4	3.10	0.40
30:0:534:C:H2'	30:0:2083:A:C2	2.57	0.40
30:0:69:A:C5'	30:0:69:A:C8	2.98	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
15:O:32:ARG:HD3	15:O:32:ARG:O	2.22	0.40
30:0:2300:A:H4'	30:0:2301:A:N3	2.37	0.40
30:0:1774:G:H2'	30:0:1775:A:C5'	2.51	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
30:0:2501:G:H1	30:0:2519:C:N4	2.18	0.40
24:X:26:ALA:HB3	24:X:63:ARG:HG3	2.03	0.40
13:M:113:ARG:NH1	13:M:155:GLN:HB2	2.36	0.40
30:0:2245:C:H6	30:0:2245:C:O5'	2.04	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
30:0:366:U:H2'	30:0:367:G:O4'	2.20	0.40
30:0:2510:C:H42	30:0:2564:G:N2	2.19	0.40
30:0:1521:C:O2'	30:0:1522:A:H5'	2.22	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
22:V:12:THR:HG23	22:V:15:GLU:H	1.86	0.40
30:0:822:C:H2'	30:0:823:U:H6	1.86	0.40
30:0:2325:U:H5''	30:0:2417:C:O2'	2.22	0.40
30:0:603:A:H4'	30:0:604:G:O5'	2.22	0.40
30:0:249:G:O2'	30:0:266:G:H5'	2.21	0.40
30:0:2311:A:H3'	38:0:7660:HOH:O	2.20	0.40
29:3:39:GLN:O	29:3:52:PHE:HE1	2.04	0.40
30:0:1133:A:H2'	30:0:1134:G:H5'	2.03	0.40
2:B:188:HIS:ND1	2:B:188:HIS:N	2.69	0.40
30:0:568:G:H21	30:0:590:A:H62	1.69	0.40
30:0:2493:C:C2'	30:0:2493:C:O2	2.67	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:43:VAL:HG11	24:X:82:GLU:HA	2.04	0.40
30:0:1613:C:C6	30:0:1613:C:H3'	2.57	0.40
30:0:238:C:H4'	30:0:287:C:OP1	2.22	0.40
2:B:5:ARG:NH2	30:0:2548:C:OP2	2.55	0.40
6:F:50:VAL:HG11	6:F:60:VAL:HG11	2.03	0.40
30:0:462:A:H2'	38:0:4853:HOH:O	2.21	0.40
13:M:46:LEU:O	13:M:50:ARG:HG3	2.21	0.40
2:B:277:GLU:N	2:B:278:PRO:CD	2.84	0.40
30:0:1159:G:C2	30:0:1209:C:N3	2.89	0.40
4:D:14:ARG:HD3	31:9:56:A:O2'	2.22	0.40
30:0:1520:G:C6	30:0:1521:C:N4	2.89	0.40
8:H:91:ARG:H	8:H:91:ARG:HG2	1.43	0.40
30:0:2672:C:H2'	30:0:2673:U:C6	2.53	0.40
30:0:1979:G:H1'	38:0:3061:HOH:O	2.21	0.40
1:A:33:GLU:CD	1:A:33:GLU:N	2.75	0.40
15:O:47:ARG:NH1	15:O:47:ARG:HG3	2.36	0.40
25:Y:132:ASP:OD1	25:Y:135:LYS:HD2	2.20	0.40
30:0:2102:G:N2	30:0:2103:A:N1	2.69	0.40
3:C:100:LEU:HD22	30:0:751:U:H5''	2.03	0.40
31:9:81:C:O2'	31:9:82:U:H5'	2.21	0.40
30:0:2532:A:OP2	30:0:2532:A:H8	2.05	0.40
5:E:23:GLU:HG2	5:E:28:SER:HB3	2.03	0.40
2:B:73:VAL:HG21	2:B:284:PHE:HZ	1.86	0.40
31:9:89:C:O2'	31:9:90:G:H5'	2.22	0.40
30:0:192:A:N6	30:0:194:A:C2	2.89	0.40
30:0:1102:C:H5	38:0:3479:HOH:O	2.04	0.40
15:O:96:VAL:HG13	15:O:100:GLN:OE1	2.21	0.40
15:O:49:GLU:OE1	15:O:72:LYS:HG3	2.22	0.40
7:G:19:GLU:HG2	7:G:66:LEU:HD13	2.03	0.40
31:9:2:U:OP2	31:9:2:U:H4'	2.22	0.40
30:0:2004:U:H5''	30:0:2005:G:C8	2.57	0.40
20:T:26:THR:HA	20:T:39:ASN:HB3	2.03	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
30:0:37:A:H2'	30:0:38:G:H8	1.84	0.40
2:B:201:ASP:N	2:B:312:ARG:O	2.53	0.40
30:0:920:C:H5'	30:0:921:G:N3	2.37	0.40
15:O:32:ARG:NE	15:O:32:ARG:HA	2.35	0.40
16:P:78:GLY:O	30:0:1813:U:H4'	2.22	0.40
1:A:20:SER:C	1:A:22:ARG:H	2.25	0.40
16:P:13:VAL:HG21	16:P:41:ARG:HG2	2.03	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
3:C:1:MET:HG2	3:C:2:GLN:N	2.34	0.40
30:0:2273:C:O2'	30:0:2274:A:H5'	2.22	0.40
30:0:1016:U:H2'	30:0:1017:U:O4'	2.21	0.40
4:D:135:VAL:HG22	4:D:136:ARG:N	2.36	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
5:E:84:MET:HA	5:E:167:TYR:O	2.22	0.40
25:Y:229:LEU:O	30:0:552:A:H5''	2.22	0.40
14:N:127:LEU:HD12	14:N:127:LEU:HA	1.93	0.40
3:C:104:ASP:O	3:C:108:GLN:HG3	2.22	0.40
30:0:766:A:HO2'	30:0:767:A:H8	1.68	0.40
30:0:295:C:H2'	30:0:296:G:O4'	2.22	0.40
6:F:59:ILE:CD1	30:0:263:U:C2	3.04	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%)	9	40
2	B	335/338 (99%)	305 (91%)	23 (7%)	7 (2%)	9	40
3	C	244/246 (99%)	216 (88%)	26 (11%)	2 (1%)	24	66
4	D	134/177 (76%)	105 (78%)	23 (17%)	6 (4%)	3	18
5	E	170/178 (96%)	158 (93%)	11 (6%)	1 (1%)	30	72
6	F	117/120 (98%)	97 (83%)	16 (14%)	4 (3%)	5	25
7	G	25/348 (7%)	22 (88%)	3 (12%)	0	100	100
8	H	156/177 (88%)	139 (89%)	16 (10%)	1 (1%)	30	72
9	I	68/162 (42%)	49 (72%)	16 (24%)	3 (4%)	3	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	140/145 (97%)	128 (91%)	10 (7%)	2 (1%)	14	51
11	K	130/132 (98%)	120 (92%)	9 (7%)	1 (1%)	24	66
12	L	141/165 (86%)	116 (82%)	22 (16%)	3 (2%)	9	40
13	M	192/196 (98%)	171 (89%)	17 (9%)	4 (2%)	9	40
14	N	184/187 (98%)	163 (89%)	17 (9%)	4 (2%)	8	38
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%)	8	38
18	R	148/155 (96%)	138 (93%)	9 (6%)	1 (1%)	26	70
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%)	9	41
22	V	63/71 (89%)	58 (92%)	4 (6%)	1 (2%)	12	48
23	W	152/154 (99%)	142 (93%)	9 (6%)	1 (1%)	26	70
24	X	80/92 (87%)	72 (90%)	6 (8%)	2 (2%)	7	34
25	Y	140/241 (58%)	132 (94%)	7 (5%)	1 (1%)	26	70
26	Z	71/116 (61%)	55 (78%)	12 (17%)	4 (6%)	2	13
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%)	1	3
All	All	3705/4472 (83%)	3292 (89%)	348 (9%)	65 (2%)	11	45

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%)	30	70
2	B	282/283 (100%)	263 (93%)	19 (7%)	20	57
3	C	193/193 (100%)	180 (93%)	13 (7%)	20	57
4	D	117/148 (79%)	110 (94%)	7 (6%)	24	62
5	E	152/156 (97%)	146 (96%)	6 (4%)	39	77
6	F	93/94 (99%)	92 (99%)	1 (1%)	80	94
7	G	27/282 (10%)	25 (93%)	2 (7%)	17	52
8	H	134/145 (92%)	124 (92%)	10 (8%)	17	51
9	I	58/130 (45%)	57 (98%)	1 (2%)	68	91
10	J	118/121 (98%)	109 (92%)	9 (8%)	16	51
11	K	106/106 (100%)	103 (97%)	3 (3%)	51	84
12	L	113/127 (89%)	106 (94%)	7 (6%)	23	60
13	M	158/160 (99%)	147 (93%)	11 (7%)	19	55
14	N	149/150 (99%)	146 (98%)	3 (2%)	63	89

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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%)	66	91
17	Q	79/80 (99%)	74 (94%)	5 (6%)	22	60
18	R	117/122 (96%)	113 (97%)	4 (3%)	44	81
19	S	71/74 (96%)	70 (99%)	1 (1%)	74	93
20	T	105/106 (99%)	98 (93%)	7 (7%)	20	57
21	U	44/53 (83%)	43 (98%)	1 (2%)	58	87
22	V	51/57 (90%)	51 (100%)	0	100	100
23	W	130/130 (100%)	126 (97%)	4 (3%)	47	83
24	X	66/74 (89%)	61 (92%)	5 (8%)	16	51
25	Y	120/196 (61%)	117 (98%)	3 (2%)	55	86
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%)	57	87
29	3	79/79 (100%)	73 (92%)	6 (8%)	16	51
All	All	3095/3646 (85%)	2955 (96%)	140 (4%)	34	74

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	30,34	12,22,23	0.99	1 (8%)	19,31,34	3.14	2 (10%)
30	OMG	0	2588	30	17,26,27	1.07	1 (5%)	21,38,41	2.52	3 (14%)
30	UR3	0	2619	30	12,22,23	0.73	0	16,32,35	0.72	0
30	PSU	0	2621	30	13,21,22	1.66	2 (15%)	18,30,33	6.08	4 (22%)
30	1MA	0	628	30,34	14,25,26	1.00	1 (7%)	15,37,40	1.10	1 (6%)

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	30,34	-	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	30,34	-	0/3/25/26	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	0	2621	PSU	C5-C1'	-5.07	1.47	1.52
30	0	2621	PSU	C4-N3	2.47	1.37	1.33
30	0	2587	OMU	C4-N3	2.51	1.37	1.33
30	0	628	1MA	C6-N6	2.71	1.34	1.29
30	0	2588	OMG	C6-N1	3.45	1.39	1.33

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	0	2621	PSU	N1-C2-N3	-21.32	114.73	128.33
30	0	2588	OMG	C5-C6-N1	-8.70	111.69	123.59
30	0	628	1MA	C2-N3-C4	-3.68	110.71	116.40
30	0	2587	OMU	C5-C4-N3	-3.35	114.53	123.12
30	0	2588	OMG	N3-C2-N1	-2.33	123.89	127.44
30	0	2621	PSU	O4'-C1'-C2'	2.17	106.94	104.73
30	0	2621	PSU	C6-N1-C2	2.69	119.80	115.47
30	0	2588	OMG	C6-N1-C2	6.59	125.08	115.94
30	0	2587	OMU	C4-N3-C2	13.03	127.05	114.14
30	0	2621	PSU	C4-N3-C2	13.78	127.16	115.25

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	237/240 (98%)	-0.59	1 (0%) 93 80	29, 65, 98, 115	0
2	B	337/338 (99%)	-0.72	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%)	0.49	16 (11%) 7 2	74, 109, 132, 140	0
5	E	172/178 (96%)	-0.63	0 100 100	50, 74, 97, 103	0
6	F	119/120 (99%)	-0.29	1 (0%) 87 67	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%)	-0.48	0 100 100	48, 67, 99, 109	0
9	I	70/162 (43%)	1.87	30 (42%) 0 0	134, 152, 167, 169	0
10	J	142/145 (97%)	-0.79	1 (0%) 89 70	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%)	-0.23	1 (0%) 89 70	35, 72, 113, 129	0
13	M	194/196 (98%)	-0.50	8 (4%) 41 16	31, 46, 99, 106	0
14	N	186/187 (99%)	-0.31	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%)	-0.74	0 100 100	40, 59, 79, 85	0
17	Q	95/96 (98%)	-0.70	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%) 81 55	40, 62, 82, 92	0
20	T	119/120 (99%)	-0.54	0 100 100	40, 59, 87, 116	0
21	U	53/67 (79%)	2.76	34 (64%) 0 0	107, 117, 125, 126	0
22	V	65/71 (91%)	-0.01	4 (6%) 24 9	47, 74, 118, 123	0
23	W	154/154 (100%)	-0.67	0 100 100	39, 54, 73, 87	0
24	X	82/92 (89%)	-0.44	1 (1%) 81 55	46, 65, 94, 108	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	Y	142/241 (58%)	-0.88	0 100 100	30, 49, 71, 92	0
26	Z	73/116 (62%)	3.71	46 (63%) 0 0	98, 116, 126, 130	0
27	1	56/57 (98%)	-0.77	0 100 100	28, 36, 43, 48	0
28	2	46/50 (92%)	-0.57	1 (2%) 65 35	31, 66, 97, 104	0
29	3	92/92 (100%)	4.35	73 (79%) 0 0	104, 119, 130, 134	0
30	0	2749/2923 (94%)	-0.82	2 (0%) 95 90	23, 51, 96, 175	0
31	9	122/122 (100%)	-0.97	1 (0%) 87 67	45, 75, 103, 154	0
All	All	6646/7517 (88%)	-0.52	221 (3%) 50 22	23, 57, 116, 175	0

All (221) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
26	Z	46	SER	17.6
26	Z	58	ASN	13.0
29	3	39	GLN	12.5
26	Z	36	GLY	11.7
29	3	34	LYS	11.6
29	3	38	ARG	11.2
29	3	35	TRP	11.1
26	Z	55	SER	10.9
29	3	41	GLU	10.6
26	Z	35	SER	10.1
29	3	37	ASP	10.1
26	Z	50	VAL	9.9
29	3	42	ARG	9.4
29	3	33	MET	9.3
29	3	20	HIS	9.2
26	Z	43	GLY	9.0
29	3	36	ILE	8.6
29	3	82	GLY	8.3
26	Z	59	GLU	8.1
26	Z	69	ASP	8.0
29	3	19	GLU	7.8
29	3	31	THR	7.7
21	U	54	THR	7.6
13	M	71	SER	7.5
29	3	14	CYS	7.4
26	Z	49	ARG	7.4
29	3	11	CYS	7.3
13	M	70	GLY	7.2

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Mol	Chain	Res	Type	RSRZ
29	3	15	ASN	7.2
29	3	32	GLY	6.9
29	3	40	ARG	6.9
26	Z	44	ARG	6.5
26	Z	53	ILE	6.3
26	Z	54	GLU	6.3
26	Z	34	SER	6.3
21	U	46	ALA	6.2
29	3	43	ASN	6.2
29	3	71	CYS	6.2
29	3	62	THR	6.1
26	Z	42	TYR	5.9
29	3	56	PRO	5.8
26	Z	48	ARG	5.7
21	U	9	CYS	5.6
26	Z	57	MET	5.6
21	U	11	THR	5.6
29	3	16	GLU	5.5
29	3	78	HIS	5.5
13	M	80	GLY	5.5
26	Z	47	ARG	5.5
29	3	48	ASN	5.4
21	U	39	ASN	5.3
29	3	51	LYS	5.2
26	Z	77	GLY	5.2
26	Z	82	SER	5.1
9	I	74	ILE	5.1
29	3	47	GLY	5.1
26	Z	45	VAL	5.1
26	Z	60	ASP	5.1
29	3	44	SER	5.0
26	Z	81	CYS	5.0
26	Z	67	GLY	4.9
29	3	12	PRO	4.9
29	3	18	GLN	4.8
29	3	81	GLU	4.8
21	U	55	ALA	4.7
26	Z	51	ALA	4.7
26	Z	56	GLU	4.6
29	3	21	GLU	4.6
9	I	93	ALA	4.6
29	3	85	ALA	4.5

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Mol	Chain	Res	Type	RSRZ
29	3	28	GLY	4.5
9	I	71	ALA	4.5
21	U	32	CYS	4.4
21	U	40	ALA	4.4
29	3	27	SER	4.4
29	3	30	GLN	4.3
29	3	53	SER	4.3
9	I	92	VAL	4.3
29	3	59	ASP	4.3
29	3	74	CYS	4.2
29	3	13	HIS	4.2
1	A	237	GLY	4.2
9	I	106	GLN	4.2
4	D	57	THR	4.2
9	I	66	GLY	4.2
21	U	53	ASP	4.2
21	U	12	ASP	4.1
21	U	5	GLU	4.1
29	3	23	GLU	4.1
9	I	100	VAL	4.1
21	U	6	CYS	4.1
29	3	10	TYR	4.0
29	3	76	LYS	4.0
21	U	48	ASN	4.0
26	Z	63	CYS	3.9
29	3	29	ARG	3.9
9	I	102	GLN	3.9
29	3	75	GLY	3.9
9	I	70	THR	3.8
29	3	84	ARG	3.8
22	V	1	THR	3.7
31	9	1	U	3.7
21	U	52	THR	3.7
26	Z	71	VAL	3.7
29	3	45	GLY	3.6
29	3	60	LYS	3.6
21	U	10	GLY	3.6
9	I	67	VAL	3.6
29	3	77	ALA	3.6
9	I	112	LEU	3.6
29	3	9	THR	3.4
21	U	36	CYS	3.4

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Mol	Chain	Res	Type	RSRZ
29	3	61	PRO	3.4
29	3	91	GLN	3.4
9	I	78	ALA	3.3
26	Z	61	HIS	3.3
9	I	104	ALA	3.3
21	U	29	THR	3.3
29	3	25	VAL	3.3
4	D	18	ILE	3.3
9	I	72	GLU	3.3
21	U	56	ARG	3.3
9	I	99	GLN	3.3
21	U	31	PHE	3.3
4	D	88	LEU	3.3
29	3	83	TRP	3.3
29	3	58	GLY	3.3
4	D	69	ILE	3.2
29	3	17	HIS	3.2
22	V	38	GLY	3.2
29	3	69	TYR	3.2
29	3	63	LYS	3.2
29	3	72	GLY	3.2
26	Z	52	GLU	3.2
26	Z	80	GLN	3.2
9	I	132	VAL	3.1
9	I	76	ASP	3.1
21	U	28	THR	3.0
26	Z	68	GLU	3.0
9	I	73	LEU	3.0
26	Z	65	ASN	3.0
29	3	64	LYS	3.0
9	I	110	ASP	3.0
24	X	88	GLU	3.0
26	Z	104	ARG	3.0
26	Z	40	ALA	2.9
26	Z	39	GLY	2.9
22	V	40	PRO	2.9
4	D	92	GLU	2.9
22	V	39	ALA	2.9
26	Z	70	ARG	2.9
29	3	73	GLU	2.9
21	U	30	HIS	2.9
9	I	128	THR	2.8

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Mol	Chain	Res	Type	RSRZ
21	U	51	TRP	2.8
21	U	24	LYS	2.8
4	D	63	ILE	2.8
29	3	70	ARG	2.8
13	M	79	ALA	2.8
21	U	8	TYR	2.8
13	M	82	ARG	2.8
29	3	6	ARG	2.7
30	0	1198	U	2.7
29	3	49	ASP	2.7
26	Z	37	ARG	2.7
29	3	8	ASN	2.7
29	3	1	MET	2.7
21	U	43	GLY	2.7
21	U	4	ARG	2.7
10	J	4	ALA	2.6
4	D	26	GLY	2.6
26	Z	83	TYR	2.6
4	D	44	ILE	2.6
9	I	68	PRO	2.6
29	3	65	THR	2.6
29	3	68	LYS	2.5
9	I	105	GLU	2.5
26	Z	92	SER	2.5
29	3	3	MET	2.5
4	D	93	LEU	2.5
26	Z	62	ALA	2.5
13	M	72	ALA	2.5
21	U	7	ASP	2.4
21	U	49	LEU	2.4
9	I	75	LYS	2.4
26	Z	78	ILE	2.4
4	D	87	ALA	2.4
9	I	108	HIS	2.4
21	U	23	HIS	2.4
30	0	1172	G	2.4
9	I	79	GLY	2.4
29	3	46	ILE	2.3
9	I	113	SER	2.3
21	U	41	ASP	2.3
19	S	81	ILE	2.3
12	L	60	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
9	I	94	ASP	2.3
9	I	81	GLU	2.3
29	3	88	LEU	2.3
4	D	135	VAL	2.3
9	I	80	PHE	2.2
26	Z	85	ASP	2.2
4	D	80	ALA	2.2
26	Z	74	GLN	2.2
4	D	85	GLN	2.1
26	Z	103	VAL	2.1
26	Z	66	CYS	2.1
28	2	39	ARG	2.1
21	U	50	GLU	2.1
4	D	27	ILE	2.1
21	U	44	ARG	2.1
21	U	20	MET	2.1
13	M	77	HIS	2.1
9	I	69	PRO	2.1
6	F	106	ALA	2.1
29	3	66	ASP	2.1
4	D	134	LEU	2.1
13	M	83	SER	2.1
29	3	5	ARG	2.0
4	D	75	LEU	2.0
21	U	38	ASN	2.0

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	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	0.15	-	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
34	NA	0	8559	1/1	0.79	0.45	33.62	122,122,122,122	0
34	NA	0	8528	1/1	0.64	0.91	31.75	83,83,83,83	0
34	NA	0	8562	1/1	0.88	0.53	29.60	89,89,89,89	0
36	SR	0	8957	1/1	0.56	0.75	22.57	200,200,200,200	0
34	NA	0	8545	1/1	0.88	0.24	19.26	33,33,33,33	0
34	NA	0	8564	1/1	0.86	0.35	13.61	57,57,57,57	0
35	CL	0	8816	1/1	0.96	0.39	12.34	94,94,94,94	0
36	SR	0	8947	1/1	0.83	0.30	10.53	194,194,194,194	0
34	NA	R	8575	1/1	0.98	0.34	10.32	89,89,89,89	0
34	NA	0	8530	1/1	0.88	0.36	8.58	49,49,49,49	0
34	NA	0	8546	1/1	0.86	0.48	8.53	80,80,80,80	0
36	SR	0	8969	1/1	0.78	0.30	8.16	192,192,192,192	0
34	NA	0	8553	1/1	0.63	0.32	8.15	70,70,70,70	0
34	NA	0	8535	1/1	0.83	0.20	7.84	64,64,64,64	0
36	SR	B	8987	1/1	0.87	0.39	7.69	200,200,200,200	0
34	NA	0	8513	1/1	0.96	0.34	7.62	66,66,66,66	0
34	NA	0	8567	1/1	0.51	0.30	7.25	68,68,68,68	0
32	MG	0	8016	1/1	0.93	0.21	6.97	48,48,48,48	0
34	NA	0	8519	1/1	0.92	0.26	6.82	51,51,51,51	0
34	NA	0	8550	1/1	0.96	0.28	6.15	47,47,47,47	0
34	NA	0	8556	1/1	0.81	0.45	5.38	63,63,63,63	0
34	NA	0	8555	1/1	0.98	0.34	5.04	50,50,50,50	0
32	MG	0	8014	1/1	0.98	0.19	4.75	21,21,21,21	0
34	NA	0	8552	1/1	0.90	0.26	4.61	58,58,58,58	0
34	NA	0	8521	1/1	0.93	0.21	4.17	53,53,53,53	0
34	NA	0	8558	1/1	0.98	0.21	3.42	44,44,44,44	0
34	NA	0	8571	1/1	0.82	0.17	3.27	46,46,46,46	0
32	MG	0	8011	1/1	1.00	0.21	3.02	24,24,24,24	0
34	NA	0	8522	1/1	0.90	0.21	2.97	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	CL	0	8811	1/1	0.99	0.37	2.88	79,79,79,79	0
32	MG	0	8009	1/1	0.98	0.21	2.69	24,24,24,24	0
36	SR	0	8904	1/1	1.00	0.17	2.50	58,58,58,58	0
35	CL	0	8805	1/1	0.99	0.14	2.38	70,70,70,70	0
32	MG	0	8044	1/1	0.99	0.14	2.28	52,52,52,52	0
32	MG	A	8051	1/1	0.84	0.22	2.09	101,101,101,101	0
34	NA	0	8569	1/1	0.99	0.21	2.06	67,67,67,67	0
32	MG	0	8008	1/1	0.99	0.14	1.74	26,26,26,26	0
32	MG	0	8004	1/1	0.96	0.18	1.74	21,21,21,21	0
32	MG	0	8003	1/1	0.99	0.17	1.61	22,22,22,22	0
34	NA	0	8517	1/1	0.99	0.15	1.54	21,21,21,21	0
32	MG	0	8015	1/1	0.99	0.13	1.28	25,25,25,25	0
32	MG	0	8088	1/1	0.94	0.16	1.25	35,35,35,35	0
36	SR	0	8903	1/1	1.00	0.13	1.24	46,46,46,46	0
34	NA	0	8507	1/1	0.86	0.16	1.23	32,32,32,32	0
32	MG	0	8085	1/1	0.99	0.12	1.22	67,67,67,67	0
32	MG	0	8062	1/1	0.95	0.20	1.22	57,57,57,57	0
36	SR	0	8902	1/1	0.99	0.16	1.03	67,67,67,67	0
34	NA	0	8534	1/1	0.97	0.18	0.99	37,37,37,37	0
34	NA	0	8537	1/1	1.00	0.17	0.91	29,29,29,29	0
32	MG	0	8010	1/1	0.93	0.17	0.91	24,24,24,24	0
34	NA	0	8560	1/1	0.94	0.79	0.89	74,74,74,74	0
32	MG	0	8084	1/1	0.99	0.14	0.72	24,24,24,24	0
32	MG	0	8065	1/1	0.95	0.12	0.57	50,50,50,50	0
36	SR	0	8975	1/1	0.64	0.11	0.52	171,171,171,171	0
36	SR	0	8985	1/1	0.44	0.12	0.50	182,182,182,182	0
34	NA	0	8515	1/1	0.87	0.15	0.06	44,44,44,44	0
37	CD	3	8704	1/1	0.90	0.71	-0.04	200,200,200,200	0
32	MG	0	8080	1/1	0.95	0.30	-0.13	68,68,68,68	0
35	CL	B	8819	1/1	0.99	0.15	-0.16	59,59,59,59	0
36	SR	0	8923	1/1	0.98	0.12	-0.25	85,85,85,85	0
32	MG	0	8006	1/1	0.98	0.13	-0.34	20,20,20,20	0
37	CD	1	8702	1/1	1.00	0.13	-0.35	61,61,61,61	0
32	MG	0	8021	1/1	0.98	0.11	-0.43	25,25,25,25	0
32	MG	0	8028	1/1	1.00	0.13	-0.47	19,19,19,19	0
34	NA	0	8557	1/1	0.40	0.08	-0.52	59,59,59,59	0
32	MG	0	8047	1/1	0.90	0.15	-0.57	67,67,67,67	0
32	MG	0	8045	1/1	0.99	0.10	-0.63	24,24,24,24	0
34	NA	0	8523	1/1	0.99	0.11	-0.66	51,51,51,51	0
34	NA	0	8542	1/1	0.98	0.17	-0.70	51,51,51,51	0
34	NA	Q	8540	1/1	0.96	0.11	-0.70	67,67,67,67	0
35	CL	J	8821	1/1	0.94	0.12	-0.72	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
33	K	M	8402	1/1	0.98	0.11	-0.79	60,60,60,60	0
32	MG	0	8034	1/1	0.98	0.13	-0.90	53,53,53,53	0
36	SR	0	8943	1/1	0.96	0.09	-0.94	72,72,72,72	0
36	SR	0	8972	1/1	0.96	0.10	-1.00	150,150,150,150	0
32	MG	B	8043	1/1	0.96	0.11	-1.21	53,53,53,53	0
32	MG	0	8001	1/1	0.99	0.13	-1.26	26,26,26,26	0
36	SR	0	8964	1/1	0.88	0.08	-1.32	129,129,129,129	0
36	SR	0	8944	1/1	0.80	0.08	-1.42	165,165,165,165	0
34	NA	J	8538	1/1	0.94	0.08	-1.42	49,49,49,49	0
32	MG	0	8012	1/1	0.99	0.15	-1.50	15,15,15,15	0
36	SR	3	8932	1/1	0.82	0.08	-1.51	158,158,158,158	0
35	CL	O	8808	1/1	0.99	0.10	-1.53	87,87,87,87	0
37	CD	U	8701	1/1	0.74	0.35	-1.61	200,200,200,200	0
32	MG	0	8058	1/1	0.99	0.06	-1.74	22,22,22,22	0
34	NA	M	8539	1/1	0.96	0.09	-1.85	32,32,32,32	0
36	SR	A	8930	1/1	0.99	0.07	-2.06	125,125,125,125	0
37	CD	Z	8703	1/1	0.86	0.28	-2.09	200,200,200,200	0
36	SR	0	8936	1/1	0.98	0.08	-2.17	87,87,87,87	0
34	NA	0	8533	1/1	0.96	0.08	-2.19	53,53,53,53	0
34	NA	0	8504	1/1	0.95	0.10	-2.27	27,27,27,27	0
36	SR	0	8984	1/1	0.91	0.07	-2.34	105,105,105,105	0
36	SR	A	8929	1/1	0.96	0.04	-2.47	117,117,117,117	0
36	SR	0	9001	1/1	0.55	0.08	-2.53	166,166,166,166	0
32	MG	T	8057	1/1	0.97	0.04	-2.71	63,63,63,63	0
34	NA	0	8568	1/1	0.99	0.10	-2.75	38,38,38,38	0
35	CL	K	8812	1/1	0.95	0.07	-2.82	48,48,48,48	0
35	CL	3	8804	1/1	0.90	0.19	-2.98	120,120,120,120	0
32	MG	0	8025	1/1	0.97	0.10	-3.14	30,30,30,30	0
36	SR	0	8910	1/1	0.94	0.08	-3.23	99,99,99,99	0
36	SR	0	8992	1/1	0.98	0.08	-3.40	130,130,130,130	0
32	MG	0	8052	1/1	0.91	0.04	-3.67	51,51,51,51	0
36	SR	0	8948	1/1	0.97	0.08	-3.90	103,103,103,103	0
32	MG	Y	8086	1/1	0.97	0.06	-4.07	37,37,37,37	0
35	CL	M	8818	1/1	0.99	0.05	-4.17	39,39,39,39	0
32	MG	0	8087	1/1	0.98	0.09	-4.79	26,26,26,26	0
32	MG	0	8050	1/1	0.91	0.08	-4.90	52,52,52,52	0
32	MG	0	8072	1/1	0.99	0.08	-5.76	47,47,47,47	0
32	MG	0	8002	1/1	0.98	0.08	-6.07	29,29,29,29	0
32	MG	0	8013	1/1	0.99	0.04	-7.18	24,24,24,24	0
36	SR	0	8945	1/1	0.95	0.06	-8.05	107,107,107,107	0
36	SR	0	8949	1/1	0.99	0.05	-11.90	102,102,102,102	0
36	SR	0	8982	1/1	0.78	1.84	-	200,200,200,200	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	0	8026	1/1	1.00	0.04	-	27,27,27,27	0
36	SR	0	8908	1/1	0.98	0.13	-	77,77,77,77	0
36	SR	0	8914	1/1	0.95	0.20	-	105,105,105,105	0
36	SR	0	8990	1/1	0.96	0.15	-	125,125,125,125	0
36	SR	0	8968	1/1	0.82	0.15	-	177,177,177,177	0
34	NA	S	8510	1/1	0.96	0.04	-	26,26,26,26	0
34	NA	0	8544	1/1	0.94	0.11	-	41,41,41,41	0
32	MG	0	8033	1/1	0.94	0.13	-	40,40,40,40	0
36	SR	0	8973	1/1	0.80	0.14	-	112,112,112,112	0
36	SR	0	8965	1/1	0.91	0.07	-	127,127,127,127	0
34	NA	0	8514	1/1	0.99	0.19	-	17,17,17,17	0
36	SR	0	8931	1/1	0.83	0.07	-	110,110,110,110	0
36	SR	1	8952	1/1	1.00	0.12	-	72,72,72,72	0
34	NA	0	8563	1/1	0.52	0.67	-	65,65,65,65	0
36	SR	0	8988	1/1	0.81	0.14	-	170,170,170,170	0
32	MG	0	8019	1/1	0.99	0.15	-	23,23,23,23	0
36	SR	0	8924	1/1	0.97	0.17	-	133,133,133,133	0
34	NA	0	8529	1/1	0.98	0.18	-	41,41,41,41	0
36	SR	0	8907	1/1	1.00	0.12	-	40,40,40,40	0
32	MG	0	8056	1/1	0.99	0.09	-	75,75,75,75	0
36	SR	0	8905	1/1	0.99	0.23	-	62,62,62,62	0
34	NA	0	8524	1/1	0.99	0.39	-	54,54,54,54	0
34	NA	0	8518	1/1	0.79	0.26	-	75,75,75,75	0
36	SR	1	8913	1/1	0.99	0.11	-	100,100,100,100	0
34	NA	0	8520	1/1	0.98	0.10	-	39,39,39,39	0
32	MG	0	8023	1/1	0.98	0.18	-	24,24,24,24	0
34	NA	0	8548	1/1	0.85	0.13	-	68,68,68,68	0
35	CL	0	8817	1/1	0.96	0.19	-	69,69,69,69	0
32	MG	0	8066	1/1	0.98	0.31	-	75,75,75,75	0
32	MG	0	8031	1/1	0.99	0.23	-	52,52,52,52	0
36	SR	0	8909	1/1	0.98	0.13	-	89,89,89,89	0
32	MG	0	8079	1/1	1.00	0.11	-	36,36,36,36	0
36	SR	0	8911	1/1	0.98	0.06	-	79,79,79,79	0
36	SR	0	8953	1/1	0.89	0.07	-	200,200,200,200	0
34	NA	0	8566	1/1	0.81	0.33	-	62,62,62,62	0
36	SR	0	9000	1/1	0.93	0.32	-	200,200,200,200	0
36	SR	0	8974	1/1	0.57	0.14	-	164,164,164,164	0
34	NA	C	8503	1/1	0.98	0.17	-	45,45,45,45	0
34	NA	0	8551	1/1	0.98	0.15	-	55,55,55,55	0
34	NA	0	8554	1/1	0.96	0.55	-	65,65,65,65	0
34	NA	0	8526	1/1	0.95	0.13	-	33,33,33,33	0
36	SR	0	8983	1/1	0.95	0.28	-	191,191,191,191	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
36	SR	0	8921	1/1	0.98	0.09	-	75,75,75,75	0
34	NA	0	8516	1/1	0.96	0.08	-	20,20,20,20	0
32	MG	0	8036	1/1	0.90	0.05	-	37,37,37,37	0
36	SR	0	8956	1/1	0.91	0.05	-	151,151,151,151	0
36	SR	9	9003	1/1	0.90	0.09	-	177,177,177,177	0
36	SR	0	8954	1/1	1.00	0.12	-	103,103,103,103	0
34	NA	0	8549	1/1	0.90	0.17	-	77,77,77,77	0
32	MG	0	8038	1/1	0.99	0.05	-	61,61,61,61	0
34	NA	0	8509	1/1	0.92	0.14	-	54,54,54,54	0
37	CD	O	8705	1/1	0.98	0.08	-	93,93,93,93	0
32	MG	0	8070	1/1	0.99	0.10	-	40,40,40,40	0
36	SR	0	8996	1/1	0.96	0.21	-	199,199,199,199	0
36	SR	0	8920	1/1	0.97	0.05	-	106,106,106,106	0
34	NA	0	8541	1/1	0.83	0.24	-	54,54,54,54	0
35	CL	Y	8820	1/1	0.94	0.11	-	47,47,47,47	0
36	SR	0	8997	1/1	0.54	0.85	-	194,194,194,194	0
32	MG	K	8054	1/1	0.92	0.15	-	40,40,40,40	0
36	SR	0	8979	1/1	0.61	0.18	-	198,198,198,198	0
32	MG	2	8060	1/1	0.86	0.10	-	35,35,35,35	0
32	MG	0	8082	1/1	0.95	0.12	-	66,66,66,66	0
32	MG	0	8089	1/1	0.97	0.17	-	59,59,59,59	0
36	SR	0	8998	1/1	0.76	0.31	-	184,184,184,184	0
34	NA	9	8572	1/1	0.82	0.17	-	71,71,71,71	0
36	SR	9	8978	1/1	1.00	0.07	-	125,125,125,125	0
35	CL	0	8813	1/1	0.99	0.03	-	46,46,46,46	0
32	MG	0	8024	1/1	0.98	0.12	-	96,96,96,96	0
36	SR	0	8933	1/1	0.99	0.07	-	126,126,126,126	0
36	SR	0	8939	1/1	0.88	0.08	-	152,152,152,152	0
36	SR	B	8950	1/1	0.98	0.15	-	113,113,113,113	0
36	SR	0	8916	1/1	0.94	0.10	-	114,114,114,114	0
34	NA	0	8502	1/1	0.99	0.05	-	56,56,56,56	0
36	SR	0	8934	1/1	0.99	0.09	-	99,99,99,99	0
36	SR	0	8922	1/1	0.75	0.29	-	169,169,169,169	0
32	MG	0	8017	1/1	0.98	0.11	-	20,20,20,20	0
36	SR	0	8901	1/1	0.98	0.14	-	63,63,63,63	0
36	SR	0	8958	1/1	0.98	0.07	-	114,114,114,114	0
36	SR	S	8961	1/1	0.98	0.05	-	126,126,126,126	0
32	MG	0	8029	1/1	0.97	0.07	-	68,68,68,68	0
36	SR	0	8989	1/1	0.86	0.19	-	200,200,200,200	0
32	MG	0	8078	1/1	0.98	0.23	-	51,51,51,51	0
32	MG	0	8068	1/1	0.92	0.11	-	49,49,49,49	0
32	MG	9	8074	1/1	0.99	0.05	-	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	0	8037	1/1	0.94	0.16	-	76,76,76,76	0
32	MG	0	8076	1/1	0.99	0.10	-	27,27,27,27	0
35	CL	A	8809	1/1	0.97	0.34	-	100,100,100,100	0
36	SR	0	8942	1/1	0.88	0.07	-	130,130,130,130	0
32	MG	3	8090	1/1	0.96	0.12	-	80,80,80,80	0
32	MG	0	8059	1/1	0.99	0.12	-	53,53,53,53	0
32	MG	0	8020	1/1	0.97	0.14	-	29,29,29,29	0
32	MG	0	8063	1/1	0.79	0.23	-	86,86,86,86	0
32	MG	0	8067	1/1	0.98	0.14	-	32,32,32,32	0
36	SR	0	8960	1/1	0.76	0.05	-	152,152,152,152	0
36	SR	3	8999	1/1	0.91	0.28	-	172,172,172,172	0
35	CL	0	8815	1/1	0.84	0.09	-	87,87,87,87	0
32	MG	0	8030	1/1	0.99	0.34	-	86,86,86,86	0
36	SR	0	8940	1/1	0.98	0.11	-	77,77,77,77	0
32	MG	0	8077	1/1	0.99	0.10	-	43,43,43,43	0
36	SR	0	8963	1/1	0.98	0.06	-	123,123,123,123	0
34	NA	0	8547	1/1	0.94	0.68	-	47,47,47,47	0
36	SR	0	8962	1/1	0.67	0.08	-	179,179,179,179	0
36	SR	F	9005	1/1	0.92	0.09	-	131,131,131,131	0
32	MG	0	8005	1/1	0.98	0.22	-	34,34,34,34	0
36	SR	R	8912	1/1	1.00	0.12	-	86,86,86,86	0
34	NA	0	8511	1/1	0.93	0.10	-	48,48,48,48	0
36	SR	0	9008	1/1	0.99	0.17	-	97,97,97,97	0
32	MG	0	8048	1/1	0.99	0.21	-	20,20,20,20	0
32	MG	0	8075	1/1	0.91	0.09	-	83,83,83,83	0
36	SR	0	8971	1/1	0.55	0.10	-	170,170,170,170	0
33	K	0	8401	1/1	0.75	0.14	-	156,156,156,156	0
36	SR	0	9006	1/1	0.31	0.83	-	180,180,180,180	0
32	MG	0	8053	1/1	0.98	0.05	-	45,45,45,45	0
36	SR	0	8976	1/1	0.91	0.24	-	197,197,197,197	0
36	SR	0	9004	1/1	0.45	1.04	-	200,200,200,200	0
32	MG	0	8081	1/1	0.86	0.32	-	80,80,80,80	0
34	NA	0	8561	1/1	0.96	0.36	-	57,57,57,57	0
36	SR	0	8986	1/1	0.62	0.47	-	200,200,200,200	0
36	SR	0	8955	1/1	0.85	0.18	-	200,200,200,200	0
36	SR	0	8928	1/1	0.89	0.09	-	146,146,146,146	0
34	NA	0	8505	1/1	0.90	1.17	-	53,53,53,53	0
32	MG	0	8073	1/1	0.98	0.06	-	51,51,51,51	0
32	MG	0	8055	1/1	0.97	0.10	-	45,45,45,45	0
36	SR	0	8938	1/1	0.98	0.07	-	164,164,164,164	0
32	MG	0	8039	1/1	0.94	0.18	-	71,71,71,71	0
36	SR	0	8981	1/1	0.91	0.14	-	157,157,157,157	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
36	SR	0	8951	1/1	0.98	0.08	-	139,139,139,139	0
32	MG	0	8092	1/1	0.98	0.02	-	44,44,44,44	0
35	CL	N	8807	1/1	0.94	0.35	-	99,99,99,99	0
32	MG	B	8042	1/1	0.90	0.08	-	56,56,56,56	0
34	NA	0	8570	1/1	0.88	0.07	-	25,25,25,25	0
32	MG	0	8022	1/1	0.99	0.12	-	17,17,17,17	0
34	NA	0	8531	1/1	0.99	0.10	-	15,15,15,15	0
36	SR	0	8994	1/1	0.93	0.24	-	200,200,200,200	0
34	NA	0	8527	1/1	0.96	0.15	-	54,54,54,54	0
36	SR	0	8937	1/1	0.93	0.17	-	100,100,100,100	0
36	SR	0	8970	1/1	0.94	0.04	-	131,131,131,131	0
32	MG	0	8041	1/1	0.96	0.31	-	36,36,36,36	0
34	NA	9	8543	1/1	0.99	0.12	-	38,38,38,38	0
32	MG	0	8027	1/1	0.97	0.12	-	26,26,26,26	0
34	NA	0	8508	1/1	0.95	0.56	-	61,61,61,61	0
35	CL	0	8803	1/1	0.95	0.14	-	69,69,69,69	0
35	CL	J	8801	1/1	0.96	0.13	-	71,71,71,71	0
36	SR	0	8918	1/1	0.98	0.10	-	71,71,71,71	0
34	NA	0	8506	1/1	0.95	0.53	-	58,58,58,58	0
36	SR	0	8926	1/1	0.98	0.09	-	109,109,109,109	0
34	NA	0	8525	1/1	0.86	0.26	-	85,85,85,85	0
32	MG	0	8064	1/1	0.97	0.06	-	33,33,33,33	0
34	NA	0	8512	1/1	0.99	0.08	-	36,36,36,36	0
36	SR	0	8959	1/1	0.56	0.29	-	200,200,200,200	0
35	CL	R	8806	1/1	0.95	0.11	-	47,47,47,47	0
32	MG	0	8018	1/1	0.98	0.14	-	34,34,34,34	0
34	NA	0	8573	1/1	0.82	0.27	-	55,55,55,55	0
36	SR	0	8967	1/1	0.81	0.05	-	133,133,133,133	0
36	SR	0	9007	1/1	0.82	0.23	-	179,179,179,179	0
35	CL	0	8822	1/1	0.95	0.60	-	97,97,97,97	0
36	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	CL	0	8814	1/1	0.78	0.18	-	72,72,72,72	0
36	SR	0	8919	1/1	0.75	0.32	-	200,200,200,200	0
35	CL	J	8802	1/1	0.54	0.08	-	76,76,76,76	0
32	MG	0	8046	1/1	0.92	0.13	-	26,26,26,26	0
36	SR	A	8993	1/1	0.86	0.08	-	159,159,159,159	0
32	MG	0	8083	1/1	0.97	0.12	-	71,71,71,71	0
36	SR	0	8917	1/1	0.96	0.10	-	109,109,109,109	0
32	MG	0	8093	1/1	0.87	0.06	-	28,28,28,28	0
32	MG	0	8032	1/1	0.91	0.05	-	27,27,27,27	0
36	SR	0	8977	1/1	0.72	0.12	-	181,181,181,181	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
36	SR	9	8980	1/1	0.75	0.14	-	182,182,182,182	0
32	MG	0	8049	1/1	0.92	0.38	-	74,74,74,74	0
35	CL	L	8810	1/1	0.93	0.09	-	64,64,64,64	0
34	NA	0	8565	1/1	0.92	0.95	-	70,70,70,70	0
36	SR	0	8915	1/1	0.87	0.07	-	118,118,118,118	0
36	SR	0	8946	1/1	0.85	0.12	-	123,123,123,123	0
36	SR	0	8906	1/1	1.00	0.20	-	64,64,64,64	0
32	MG	0	8071	1/1	0.89	0.13	-	31,31,31,31	0
34	NA	0	8536	1/1	0.97	0.07	-	40,40,40,40	0
36	SR	0	8995	1/1	0.97	0.14	-	140,140,140,140	0
32	MG	0	8040	1/1	0.96	0.21	-	54,54,54,54	0
32	MG	0	8091	1/1	0.73	0.07	-	58,58,58,58	0
36	SR	0	8941	1/1	0.98	0.18	-	122,122,122,122	0
36	SR	0	9002	1/1	0.84	0.06	-	157,157,157,157	0
32	MG	0	8069	1/1	0.90	0.19	-	55,55,55,55	0
32	MG	0	8007	1/1	1.00	0.19	-	18,18,18,18	0
36	SR	0	8935	1/1	0.98	0.09	-	87,87,87,87	0
34	NA	0	8501	1/1	0.96	0.14	-	43,43,43,43	0
34	NA	0	8574	1/1	0.96	0.35	-	54,54,54,54	0
34	NA	R	8532	1/1	0.94	0.13	-	37,37,37,37	0
32	MG	0	8035	1/1	0.96	0.10	-	61,61,61,61	0
36	SR	0	8991	1/1	0.88	0.34	-	193,193,193,193	0
36	SR	0	8927	1/1	0.94	0.20	-	196,196,196,196	0
36	SR	0	8925	1/1	0.99	0.15	-	94,94,94,94	0

6.5 Other polymers [i](#)

There are no such residues in this entry.