



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 25, 2020 – 05:31 PM BST

PDB ID : 3CCS
Title : Structure of Anisomycin resistant 50S Ribosomal Subunit: 23S rRNA mutation G2482A
Authors : Blaha, G.; Gurel, G.
Deposited on : 2008-02-26
Resolution : 2.95 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13

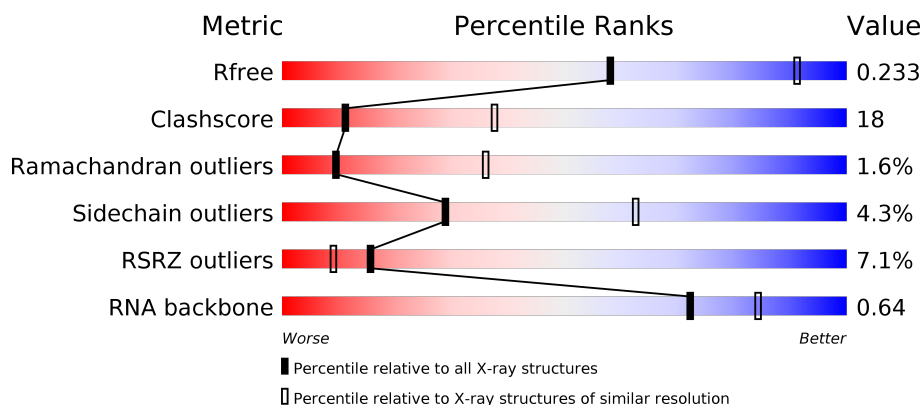
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)
RNA backbone	3102	1065 (3.22-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	240	<div> <div>3%</div> <div>66%</div> <div>28%</div> <div>• •</div> </div>
2	B	338	<div> <div>62%</div> <div>33%</div> <div>•</div> </div>
3	C	246	<div> <div>73%</div> <div>24%</div> <div>•</div> </div>
4	D	177	<div> <div>29%</div> <div>51%</div> <div>25%</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
33	CL	0	8812	-	-	X	-
33	CL	Y	8820	-	-	X	-
34	SR	0	8982	-	-	-	X
34	SR	0	9004	-	-	-	X
34	SR	0	9006	-	-	-	X
34	SR	0	9007	-	-	-	X
35	NA	0	8528	-	-	-	X
37	CD	3	8704	-	-	-	X
37	CD	Z	8703	-	-	-	X

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 99121 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	0	2754	Total	C	N	O	P	0	0	0
			59019	26349	10873	19052	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	86	Total	Mg	0	0
			86	86		
32	9	1	Total	Mg	0	0
			1	1		
32	K	1	Total	Mg	0	0
			1	1		
32	B	1	Total	Mg	0	0
			1	1		
32	A	2	Total	Mg	0	0
			2	2		
32	T	1	Total	Mg	0	0
			1	1		
32	Y	1	Total	Mg	0	0
			1	1		

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
33	0	10	Total Cl 10 10	0	0
33	J	3	Total Cl 3 3	0	0
33	B	1	Total Cl 1 1	0	0
33	A	1	Total Cl 1 1	0	0
33	N	1	Total Cl 1 1	0	0
33	O	1	Total Cl 1 1	0	0
33	R	1	Total Cl 1 1	0	0
33	Y	1	Total Cl 1 1	0	0
33	L	1	Total Cl 1 1	0	0
33	3	1	Total Cl 1 1	0	0
33	M	1	Total Cl 1 1	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
34	0	92	Total Sr 92 92	0	0
34	1	2	Total Sr 2 2	0	0
34	H	1	Total Sr 1 1	0	0
34	B	2	Total Sr 2 2	0	0
34	3	2	Total Sr 2 2	0	0
34	A	2	Total Sr 2 2	0	0
34	R	1	Total Sr 1 1	0	0
34	9	3	Total Sr 3 3	0	0
34	L	1	Total Sr 1 1	0	0

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	0	65	Total 65	Na 65	0	0
35	J	1	Total 1	Na 1	0	0
35	Q	1	Total 1	Na 1	0	0
35	H	1	Total 1	Na 1	0	0
35	B	1	Total 1	Na 1	0	0
35	C	1	Total 1	Na 1	0	0
35	R	1	Total 1	Na 1	0	0
35	9	2	Total 2	Na 2	0	0
35	S	1	Total 1	Na 1	0	0
35	M	1	Total 1	Na 1	0	0

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

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

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

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

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	Z	1	Total 1	Cd 1	0	0
37	1	1	Total 1	Cd 1	0	0
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	A	119	Total 119	O 119	0	0
38	B	152	Total 152	O 152	0	0
38	C	185	Total 185	O 185	0	0
38	D	42	Total 42	O 42	0	0
38	E	43	Total 43	O 43	0	0
38	F	26	Total 26	O 26	0	0
38	G	19	Total 19	O 19	0	0
38	H	65	Total 65	O 65	0	0
38	I	8	Total 8	O 8	0	0
38	J	53	Total 53	O 53	0	0
38	K	58	Total 58	O 58	0	0
38	L	85	Total 85	O 85	0	0
38	M	127	Total 127	O 127	0	0
38	N	59	Total 59	O 59	0	0
38	O	39	Total 39	O 39	0	0

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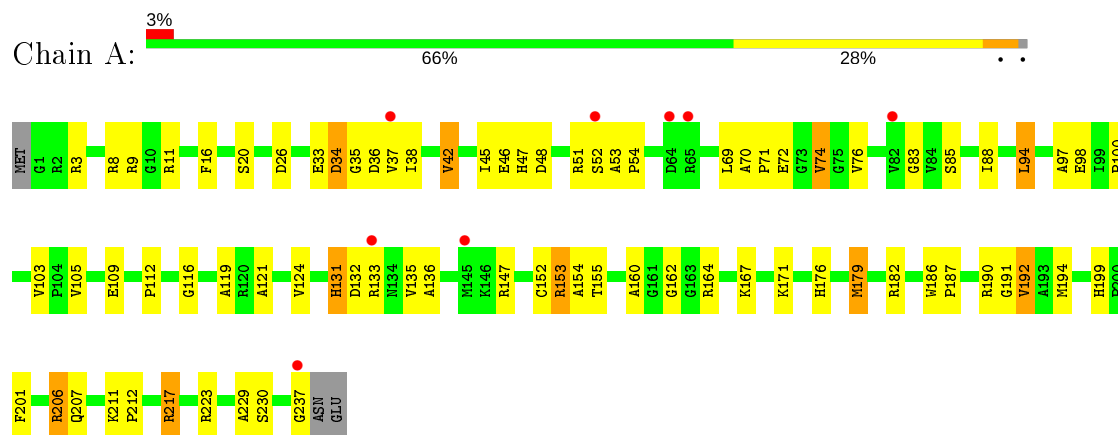
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	P	67	Total 67	O 67	0	0
38	Q	48	Total 48	O 48	0	0
38	R	77	Total 77	O 77	0	0
38	S	30	Total 30	O 30	0	0
38	T	36	Total 36	O 36	0	0
38	U	28	Total 28	O 28	0	0
38	V	13	Total 13	O 13	0	0
38	W	67	Total 67	O 67	0	0
38	X	21	Total 21	O 21	0	0
38	Y	100	Total 100	O 100	0	0
38	Z	31	Total 31	O 31	0	0
38	1	59	Total 59	O 59	0	0
38	2	43	Total 43	O 43	0	0
38	3	70	Total 70	O 70	0	0
38	0	5904	Total 5904	O 5904	0	0
38	9	149	Total 149	O 149	0	0

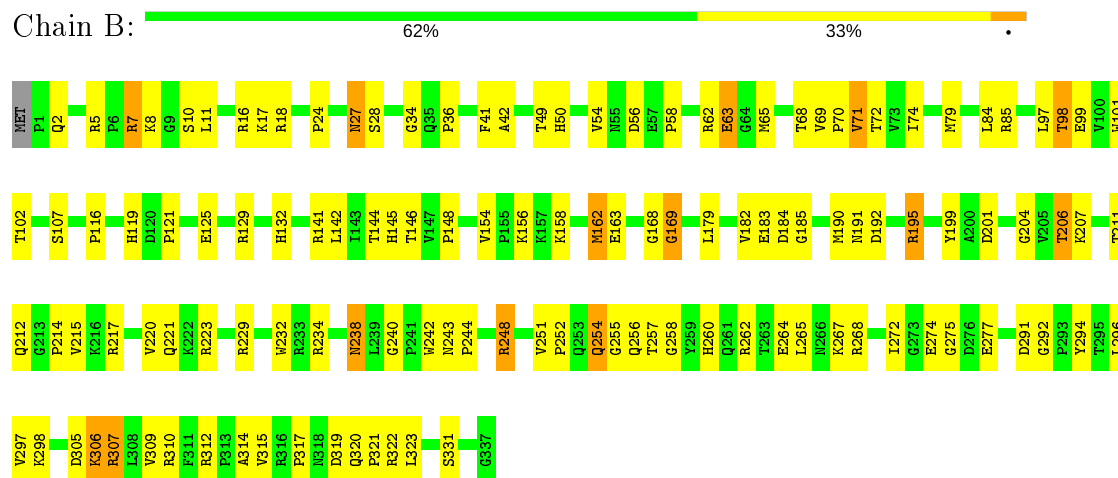
3 Residue-property plots

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

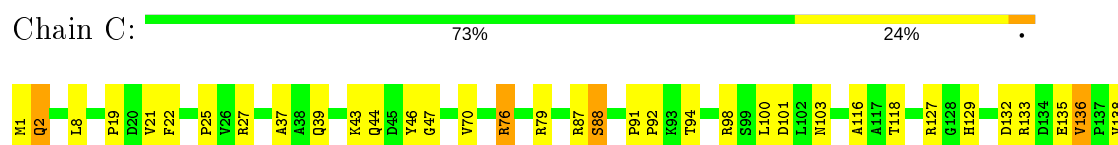
• Molecule 1: 50S ribosomal protein L2P



• Molecule 2: 50S ribosomal protein L3P

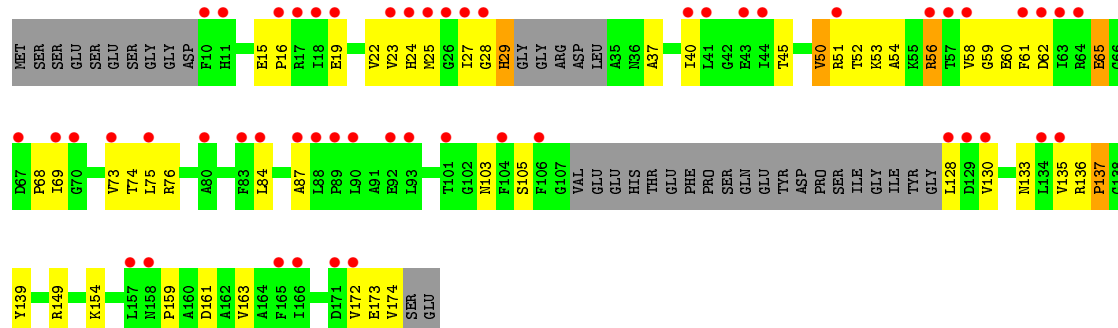


• Molecule 3: 50S ribosomal protein L4P

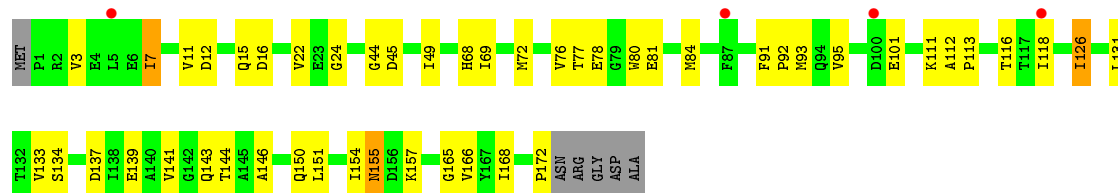




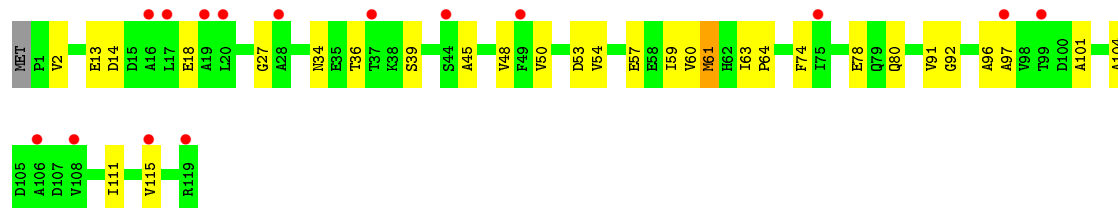
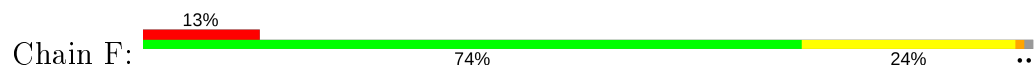
• Molecule 4: 50S ribosomal protein L5P



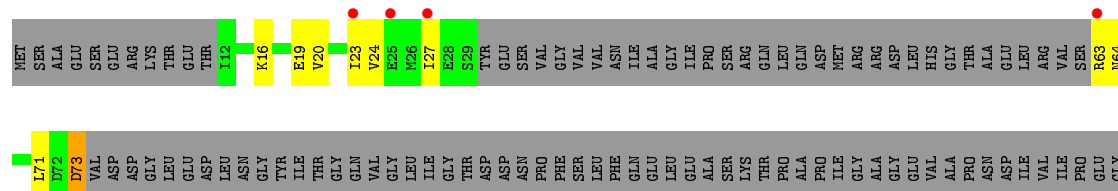
• Molecule 5: 50S ribosomal protein L6P



• Molecule 6: 50S ribosomal protein L7Ae

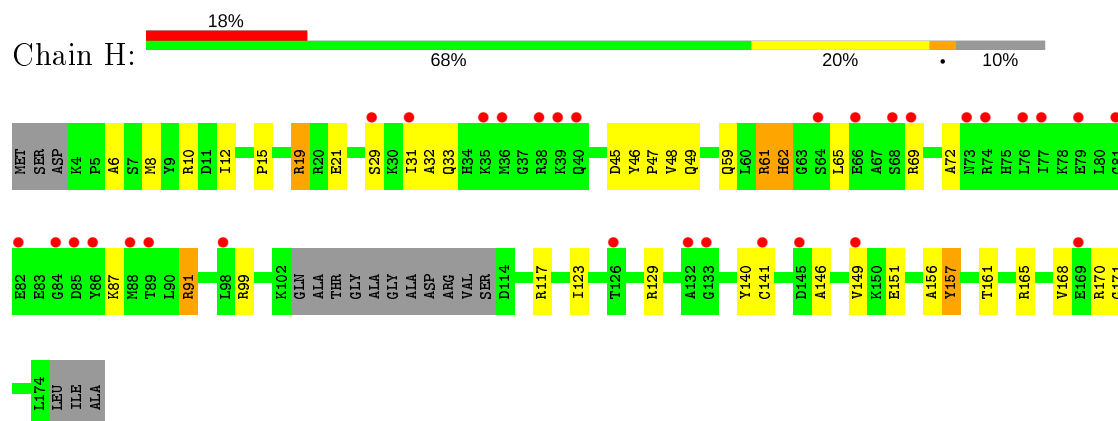


• Molecule 7: 50S ribosomal protein L10E

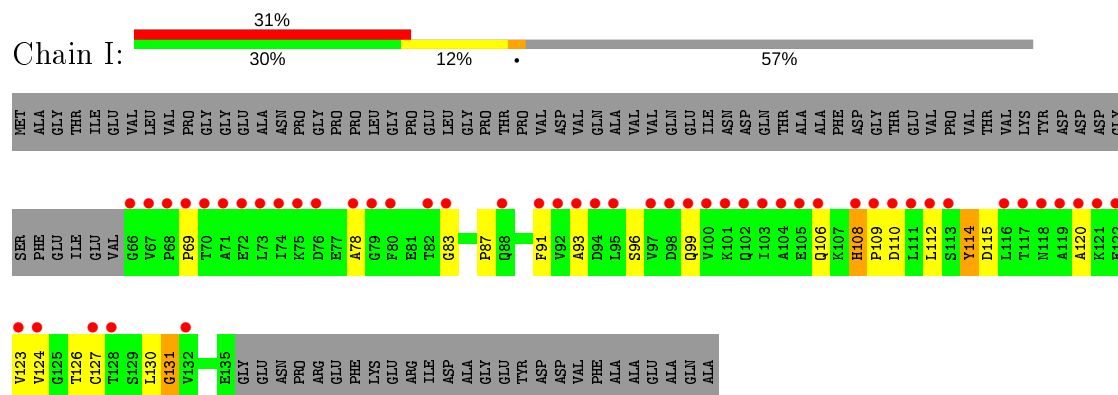


ASP	GLN	ASP	GLY	ASN	GLY	ASP	GLY	THR	ASP
ASP	ASP	ALA	ASP	ALA	LEU	ASP	LEU	GLY	THR
ASP	ASP	LYS	ASP	LYS	LEU	ASP	ARG	ASP	PRO
THR	THR	LEU	LEU	LEU	ALA	VAL	ALA	GLY	GLY
SER	SER	ALA	ALA	ALA	ILE	VAL	VAL	GLU	GLU
GLU	GLU	GLN	GLN	ASP	GLU	PHE	GLN	LEU	LEU
ASP	ASP	ALA	ALA	ASP	GLU	GLY	GLY	VAL	VAL
ASP	ASP	ALA	ILE	GLU	ILE	VAL	GLU	GLY	GLY
ASP	ALA	ASP	GLU	ASP	PRO	PHE	GLN	SER	GLN
ALA	ALA	PRO	ASP	GLY	VAL	GLU	GLU	VAL	ALA
ALA	ALA	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ALA
GLU	GLU	PRO	PRO	PRO	ASP	LEU	LEU	ASP	ASP
GLU	ALA	ASP	LEU	LEU	LEU	ARG	ILE	GLY	GLY
ALA	ALA	VAL	VAL	VAL	SER	ILE	ASP	VAL	ALA
ASP	ASP	SER	LYS	LYS	ASP	ASP	ASP	VAL	GLN
ASP	ASP	ALA	ALA	ALA	THR	GLY	GLY	LEU	GLY
ASP	ASP	ASP	ASP	ASP	ILE	ILE	ILE	SER	SER
ASP	ASP	ALA	ALA	ALA	GLN	GLN	GLN	GLN	GLN
GLU	GLU	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
ASP	ASP	ARG	ARG	ARG	ARG	ILE	ILE	LEU	LEU
GLY	GLY	LEU	LEU	LEU	ALA	ALA	ALA	SER	SER
ASP	ASP	ALA	ALA	ALA	SER	ALA	ALA	THR	THR
LEU	LEU	GLN	GLN	GLN	ILE	GLY	GLY	VAL	VAL
GLY	GLY	ASP	ASP	ASP	ASP	ARG	ARG	ASP	ASP
ALA	ALA	ASP	ASP	ASP	GLU	ASP	PHE	THR	THR
PHE	PHE	GLU	GLU	GLU	GLU	SER	LEU	GLY	GLY
		ALA	ALA	ALA	ALA	LEU	VAL	VAL	VAL
		LEU	LEU	LEU	LEU	ASN	ASN	SER	SER
		PRO	PRO	PRO	PRO	GLN	GLN	GLN	GLN
		THR	THR	THR	THR	THR	THR	THR	THR
		ASN	ASN	ASN	ASN	THR	THR	THR	THR
		GLU	GLU	GLU	GLU	ALA	ALA	ALA	ALA
		SER	SER	SER	SER	VAL	VAL	VAL	VAL
		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
		THR	THR	THR	THR	THR	THR	THR	THR
		GLY	GLY	GLY	GLY	THR	THR	THR	THR
		VAL	VAL	VAL	VAL	THR	THR	THR	THR
		GLN	GLN	GLN	GLN	THR	THR	THR	THR
		ASP	ASP	ASP	ASP	THR	THR	THR	THR
		THR	THR	THR	THR	THR	THR	THR	THR
		GLY	GLY	GLY	GLY	THR	THR	THR	THR
		VAL	VAL	VAL	VAL	THR	THR	THR	THR
		GLU	GLU	GLU	GLU	THR	THR	THR	THR
		SER	SER	SER	SER	THR	THR	THR	THR
		ASP	ASP	ASP	ASP	THR	THR	THR	THR
		THR	THR	THR	THR	THR	THR	THR	THR
		GLY	GLY	GLY	GLY	THR	THR	THR	THR
		VAL	VAL	VAL	VAL	THR	THR	THR	THR
		GLN	GLN	GLN	GLN	THR	THR	THR	THR
		ASP	ASP	ASP	ASP	THR	THR	THR	THR
		THR	THR	THR	THR	THR	THR	THR	THR
		GLY	GLY	GLY	GLY	THR	THR	THR	THR
		VAL	VAL	VAL	VAL	THR	THR	THR	THR
		GLU	GLU	GLU	GLU	THR	THR	THR	THR
		SER	SER	SER	SER	THR	THR	THR	THR
		ASP	ASP	ASP	ASP	THR	THR	THR	THR
		THR	THR	THR	THR	THR	THR	THR	THR
		GLY	GLY	GLY	GLY	THR	THR	THR	THR
		VAL	VAL	VAL	VAL	THR	THR	THR	THR
		GLN	GLN	GLN	GLN	THR	THR	THR	THR
		ASP	ASP	ASP	ASP	THR	THR	THR	THR
		THR	THR	THR	THR	THR	THR	THR	THR
		GLY	GLY	GLY	GLY	THR	THR	THR	THR
		VAL	VAL	VAL	VAL	THR	THR	THR	THR

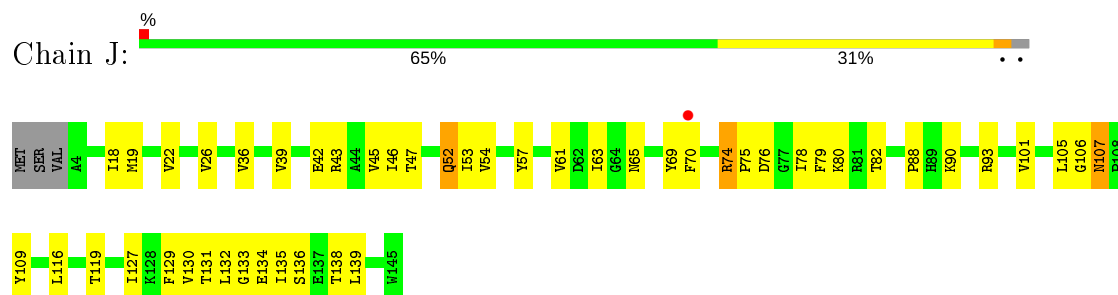
- Molecule 8: 50S ribosomal protein L10e



- Molecule 9: 50S ribosomal protein L11P

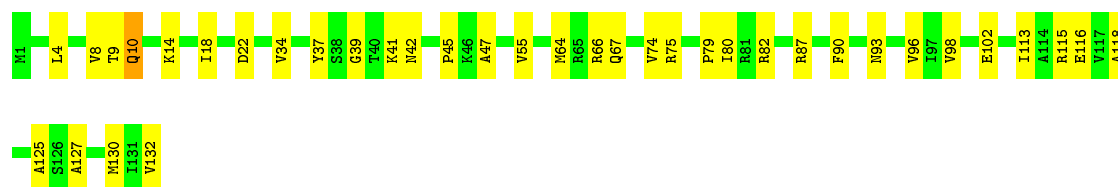


- Molecule 10: 50S ribosomal protein L13P



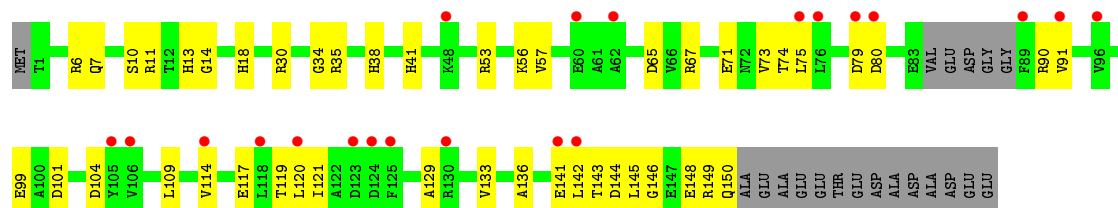
- Molecule 11: 50S ribosomal protein L14P

Chain K:  72% 27%



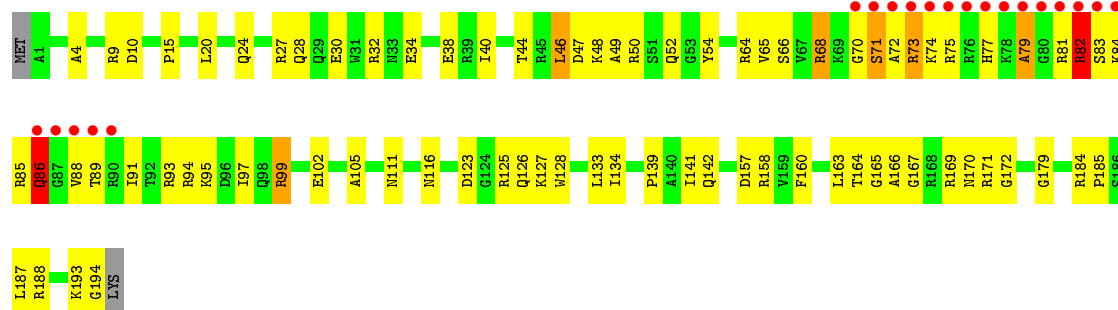
- Molecule 12: 50S ribosomal protein L15P

Chain L:  13% 60% 28% 12%



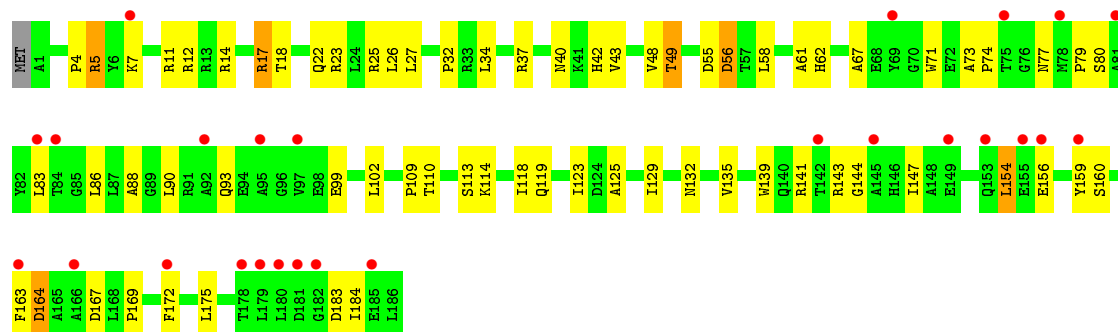
- Molecule 13: 50S ribosomal protein L15e

Chain M:  10% 58% 37%




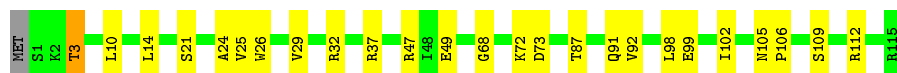
- Molecule 14: 50S ribosomal protein L18P

Chain N:  14% 63% 33%



- Molecule 15: 50S ribosomal protein L18e

Chain O:  78% 21% ..




- Molecule 16: 50S ribosomal protein L19e

Chain P:  70% 23% . .



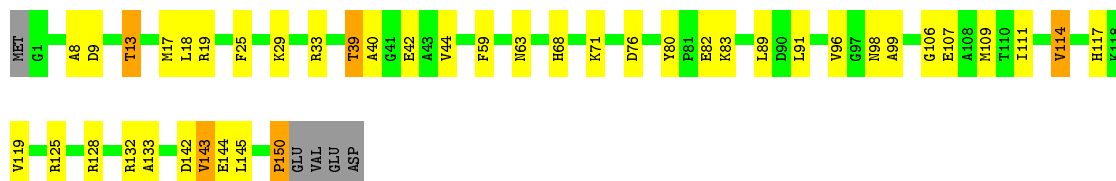
- Molecule 17: 50S ribosomal protein L21e

Chain Q:  73% 25% ..



- Molecule 18: 50S ribosomal protein L22P

Chain R:  70% 24% . .



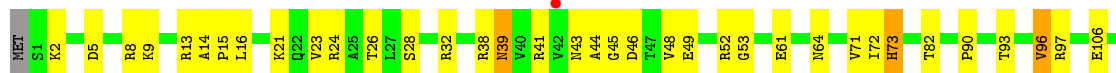
- Molecule 19: 50S ribosomal protein L23P

Chain S:  72% 24% 5%



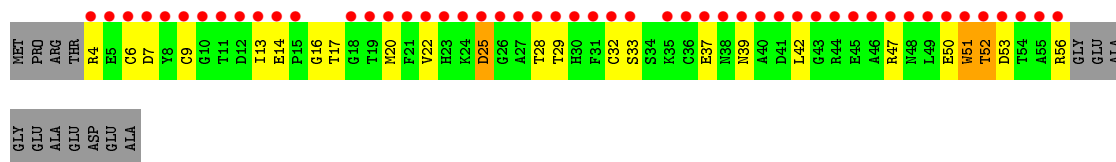
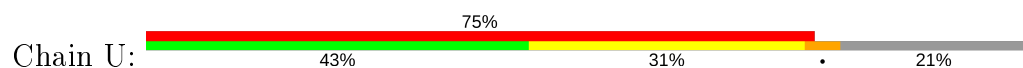
- Molecule 20: 50S ribosomal protein L24P

Chain T:  68% 29% . .

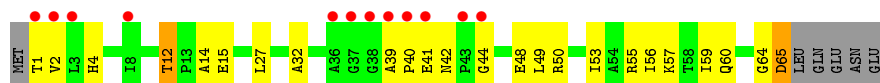




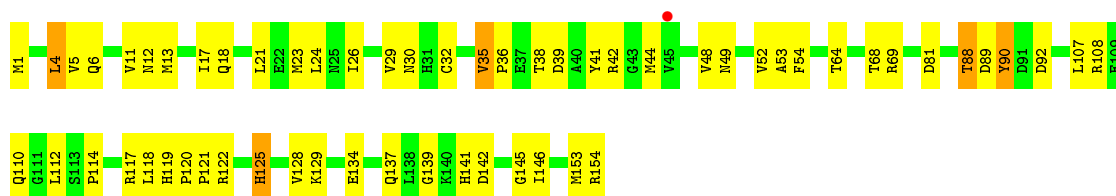
- Molecule 21: 50S ribosomal protein L24e



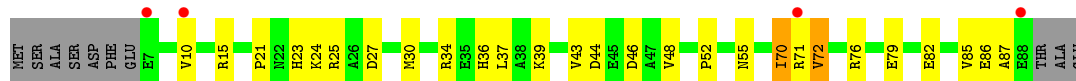
- Molecule 22: 50S ribosomal protein L29P



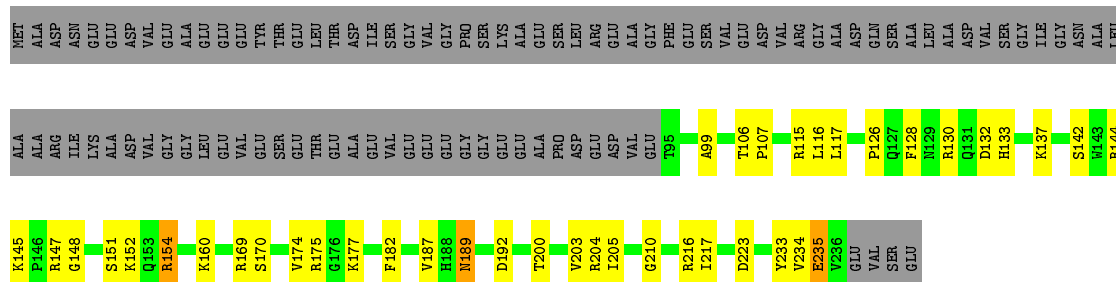
- Molecule 23: 50S ribosomal protein L30P



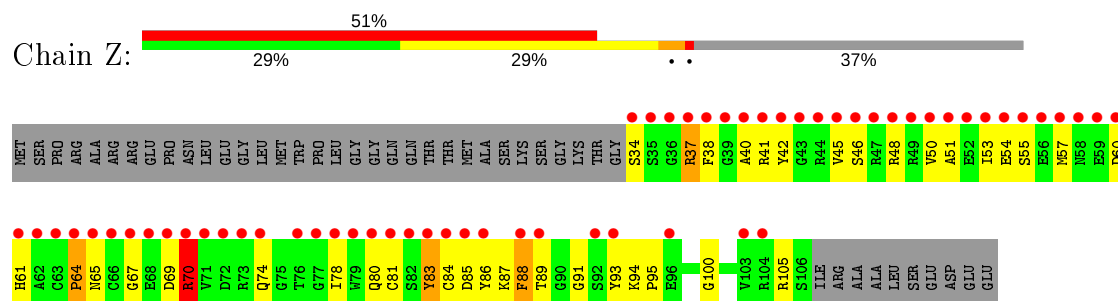
- Molecule 24: 50S ribosomal protein L31e



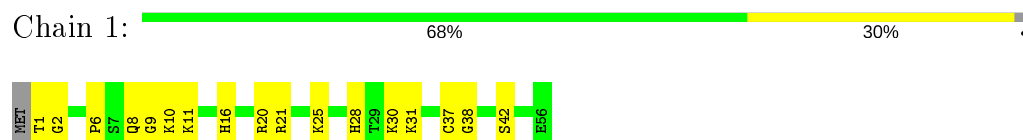
- Molecule 25: 50S ribosomal protein L32e



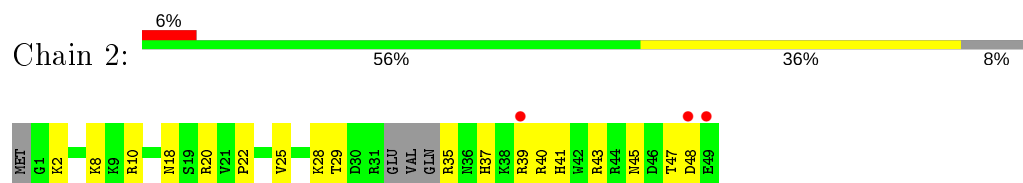
- Molecule 26: 50S ribosomal protein L37Ae



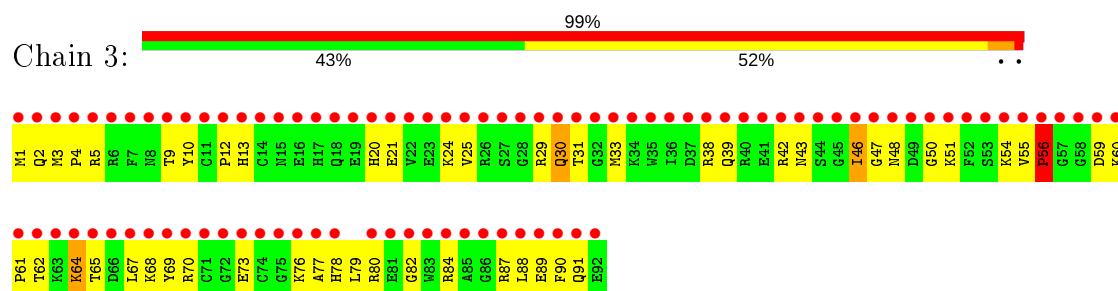
- Molecule 27: 50S ribosomal protein L37e



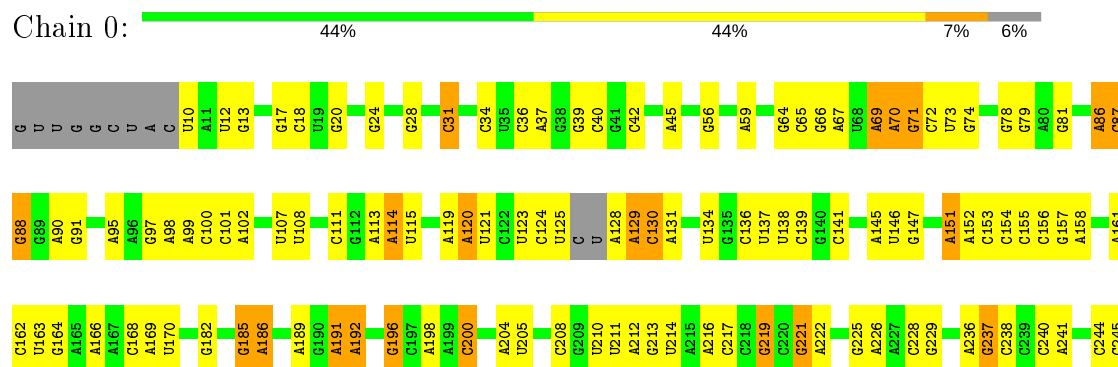
- Molecule 28: 50S ribosomal protein L39e



- Molecule 29: 50S ribosomal protein L44E

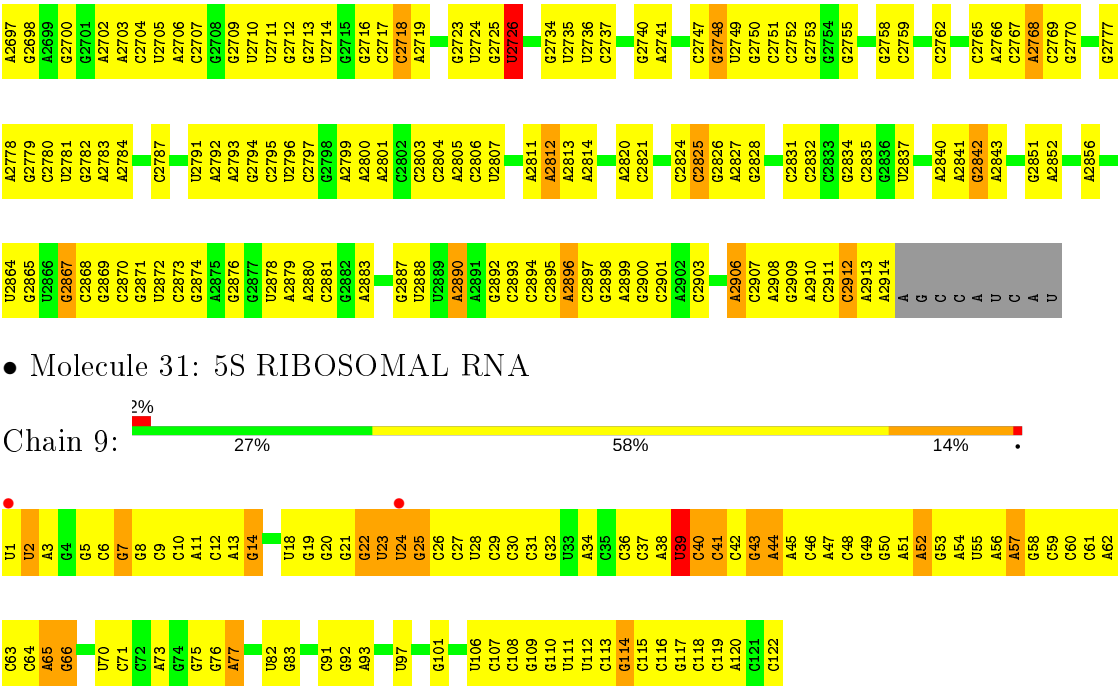


- Molecule 30: 23S RIBOSOMAL RNA



G1398	U1314	G1226	G1162	G1059	A	G902	G814	C717	G644	C558	U481	U392	G315	G246
A1399	G1315	C1229	G1163	C1080	G	U903	U815	C718	U645	U559	G482	G393	A316	A247
U1405	A1317	A1230	G1165	C1081	A	U904	G816	C719	U646	U560	C483	G394	A317	A248
A1406	A1318		G1166	G	G	C905	G817		U647	G561	A485	U396	U318	G249
A1407		U1234	G1167	U1066	A	A912	A818	G724		A562	A486	A397	A319	C250
U1408	A1321	G1235	C1168	A1067			A819	C725	G652	C563	U486	U398	G320	C254
G1409	G1322	A1236	U1168		U	G918	G820	C726	U653	G564	G487	C399	G324	A255
G1410		U1237	U1169	U1072	C	U919	U821	G727	U654	A565	U488	A407	U325	A256
	G1325	G1238	A1170	A1073	G	C920	A820	C728		A566	G496	A408	U328	G257
A1413	C1326	G1239	G1171	G1074	G	G921	A821		U655	U567	G497	U409	U329	G258
G1419	G1327		A1172	G1075	C	A922	U822	U734	G656	C571	G498	A410	A329	G259
C1420	A1328	A1242	A1173	G1076	A	A923	A827	C735	G657		G499	U409	U328	
C1421		C1243	G1175	U1077	C	G924	G834	A736	U658	C571	G500	A411	C330	
C1422	C1332	U1244	C1176	A1081	A	C925	U835	C737	A660	U582	G500	C412	G333	U263
C1423	U1333	C1245	A1177		C999	A926	G836	G738		C583	G661	G413	G334	U264
A1424	C1334	A1246	U1180	G1084	G1000	U932	U840	G744	U662	U584	A507	G416	U335	U265
G1425	C1335	A1247	A1181	C1085	U1003	C933		G745	C663	C585	A508	G417	G336	C271
C1426	U1336	U1248	A1182	A1086	U1004		U840	A746	U664	C586	A509	C418	A337	A272
A1427	G1337	C1250	U1183	A1087	G1004	A939	A844	G747		C587	U510	A419	C338	G273
C1428	U1338		C1184	A1088	U1005	G940	U845	C748	G669	U588	A511	U420	A339	G274
U1429	G1339	C1254	U1185	U1095	A1006	G941	A846	C749	G670	U589	G512	C421	G275	C276
G1430	G1340	A1255	C1186	U1096	A1007	A942	C849	U751	A671	A590	A513		C342	
	A1341		U1187	U1097	C1008	U943	U850		G672	A591	G514	C424	C343	
A1434	C1342	G1260	A1188	A1098	U1009	A944	C851	C759	G677	G592	U517	U425	C344	C279
C1435	G1343	U1266	A1189	G1099	C1010	G945	U852	G760	G678	A593	G518	C440	G345	C280
C1436	A1344	C1267	G1190	U1100	A1011	U946	C853	A761		C594	U595	A441	U346	U281
A1345	U1345	A1268	A1191	G1100	C1012	U947	G854	C762	G681	C596	A521	A442	C348	C283
C1439	U1346	G1268	A1192	C1015	A1013	U948	U855	C763	A682	A597	U522	C443	C284	C284
U1440	U1347	G1269	A1193	U1016	A1014	U949	G856	C764	G683	C598	U524	C444	A352	A285
G1441		U1270	A1194	U1017	C1015	G950	A857	G765	G684	C599	A524	U445	C353	U286
A1442	U1350		G1197	G1110	U1017	G952	U858		G685	G600	U526	G446	C287	
	G1351	C1273	U1198	U1116	A1018	G953	A867	G775	A686		U527	A447	G358	A288
U1446	A1352	A1278	A1199	A1117	C1019	G954	G868	A776	C687	A603	U527	G448	U359	G289
U1447	C1353	U1279	A1200	A1118	G1021	A957	C869	C777	A688	G604	C580	A449	A360	C290
	U1359	A1280	C1201	G1119	A1022		G870	U779			U611	C450	C361	C291
C1451	C1360		A1202	C1117	G1021	G960	U872		A693	U612	G531	C451	C362	C292
G1452	G1361	A1287	G1203	U1128	U1025	A961	C879	A790	A694	C363	U613	C452	A293	A293
U1454	U1362	U1288	C1204	G1129	C1026	C962	U872	A791	C695	C364	U533	C453	U364	C294
C1455	G1363	C1289	U1205	U1130	G1027	C963	A875	G792	C696	C365	C534	U454	C295	C295
C1456	G1364		U1206	G1131	U1027	A964	A876	A793	G697	G615	G535	A459	U366	G296
U1457	C1365	A1294	U1207	A1132	U1028	A965	G877		C698	U616	A536	A459	G367	U297
		G1295	C1208	A1133	U1029	G965	C878	A797	C699	C368	G537	A460	C298	C298
U1461	A1372	A1296	C1209	G1135	G1039	G969	C879		A700	G369	U619	C461	U299	G299
C1462		G1299	U1210	U1136	U1042	U970	C880	G800	U701	A620	G539	A462	U300	U300
	A1375	G1300	G1213	G1137	C1043	G	C881	U801	G702	C621	U620	A463	U371	C301
C1469	G1376		A1214	U1137	C1044	U	A882	G802	G703	G622	C541	G464	A372	A302
A1470	C1377	U1304	A1215	G1151	G1044	G	U883	C803	C704	U623	A542	U465	G373	C303
C1471	A1378	C1305	G1216		G1045	U	G884	C804	C705	U624	U624	A466	U374	G304
U1472	A1379	U1306	G1217	G1154	C1051	C	G885	G805	G706	U625	G544	G467	G375	A305
U1473		A1307	U1218	A1154	C1051	C	U886	A806	C707	C546	G545	U468	C376	A306
C1474	C1384	A1307	U1218	G1155	G1052	G	U888	A807	A708	A628	C546	G469	C377	G307
	U1308	U1219	C1157	C1156	G1053	C	A894	A808	G709	A629	U470	U470	A378	U308
	G1309	U1220	U1221	C1157	G1054	C		G809	G710	A471	G471	A472	G380	C309
A1477	A1393	U1310	G1221	C1157	G1055	U	A894	C810	G711	A632	C550	A473	U310	U310
U1478	C1394	G1311	G1222	G1158	G1055	C	G898	C811		C633	G553		G381	C311
C1395	G1311	G1311	G1222	G1158	U1056	U		C811	U714	G634	U			U312
C1396	G1312	G1312	G1224	U1057	A1057	C	C899	A812		A473	G553		G381	C311
A1482	A1313	A1313	G1225	A1151	A1057	C		A813		A479	G557	C480	U313	U314





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	212.24Å 299.19Å 575.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.95 85.59 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.95) 91.7 (85.59-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 2.40Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.179 , 0.238 0.177 , 0.233	Depositor DCC
R_{free} test set	6547 reflections (0.98%)	wwPDB-VP
Wilson B-factor (Å ²)	62.1	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 79.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	99121	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.64	0/2408
2	B	0.34	0/2690	0.64	0/3652
3	C	0.39	0/1885	0.65	0/2552
4	D	0.33	0/1111	0.57	0/1498
5	E	0.34	0/1382	0.56	0/1880
6	F	0.35	0/901	0.57	0/1224
7	G	0.32	0/241	0.47	0/324
8	H	0.33	0/1302	0.62	0/1743
9	I	0.32	0/526	0.54	0/716
10	J	0.39	0/1136	0.61	0/1530
11	K	0.37	0/1004	0.66	0/1351
12	L	0.34	0/1130	0.61	0/1509
13	M	0.40	0/1582	0.63	0/2116
14	N	0.32	0/1474	0.61	0/1999
15	O	0.37	0/874	0.62	0/1181
16	P	0.34	0/1147	0.53	0/1528
17	Q	0.33	0/749	0.64	0/1005
18	R	1.27	7/1172 (0.6%)	1.10	6/1578 (0.4%)
19	S	0.36	0/648	0.59	0/875
20	T	0.34	0/958	0.66	0/1289
21	U	0.45	0/417	0.60	0/562
22	V	0.34	0/502	0.53	0/675
23	W	0.38	0/1219	0.65	0/1655
24	X	0.36	0/664	0.61	0/895
25	Y	0.38	0/1146	0.62	0/1536
26	Z	0.43	0/584	0.63	0/781
27	1	0.47	0/438	0.64	0/578
28	2	0.36	0/401	0.61	0/529
29	3	0.46	0/771	0.60	0/1024
30	0	0.42	0/65956	0.68	7/102865 (0.0%)
31	9	0.32	0/2904	0.67	1/4526 (0.0%)
All	All	0.42	7/98700 (0.0%)	0.67	14/147584 (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
18	R	1	0
23	W	0	1
30	0	0	34
All	All	1	35

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	R	150	PRO	CB-CG	27.15	2.85	1.50
18	R	150	PRO	CA-C	-18.51	1.15	1.52
18	R	150	PRO	CG-CD	13.84	1.96	1.50
18	R	150	PRO	C-O	11.87	1.47	1.23
18	R	150	PRO	N-CA	11.57	1.67	1.47
18	R	150	PRO	N-CD	10.73	1.62	1.47
18	R	150	PRO	CA-CB	7.84	1.69	1.53

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	R	150	PRO	CB-CA-C	-22.43	55.92	112.00
18	R	150	PRO	N-CA-C	-19.45	61.53	112.10
18	R	150	PRO	CA-N-CD	12.27	128.88	111.70
18	R	150	PRO	N-CA-CB	10.98	116.47	103.30
18	R	150	PRO	CA-C-O	-8.27	100.34	120.20
18	R	150	PRO	CA-CB-CG	-6.08	92.45	104.00
30	0	871	G	C5'-C4'-O4'	-5.70	102.26	109.10
30	0	1504	A	C1'-O4'-C4'	-5.64	105.39	109.90
30	0	1942	A	C5'-C4'-C3'	5.59	124.94	116.00
30	0	1971	G	N9-C1'-C2'	5.38	121.00	114.00
30	0	1819	G	C5'-C4'-C3'	5.29	124.46	116.00
30	0	2726	U	N1-C1'-C2'	5.20	120.75	114.00
30	0	2313	C	O4'-C4'-C3'	-5.12	98.88	104.00
31	9	39	U	N1-C1'-C2'	5.09	120.62	114.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
18	R	150	PRO	CA

All (35) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
30	0	1039	G	Sidechain
30	0	1236	A	Sidechain
30	0	1260	G	Sidechain
30	0	1430	G	Sidechain
30	0	1524	U	Sidechain
30	0	1599	U	Sidechain
30	0	1736	A	Sidechain
30	0	1741	U	Sidechain
30	0	1777	G	Sidechain
30	0	1819	G	Sidechain
30	0	1829	A	Sidechain
30	0	1878	G	Sidechain
30	0	196	G	Sidechain
30	0	1993	C	Sidechain
30	0	221	G	Sidechain
30	0	2316	G	Sidechain
30	0	2473	U	Sidechain
30	0	2493	C	Sidechain
30	0	2503	A	Sidechain
30	0	2552	C	Sidechain
30	0	2599	A	Sidechain
30	0	2630	G	Sidechain
30	0	2673	U	Sidechain
30	0	2726	U	Sidechain
30	0	2842	G	Sidechain
30	0	324	G	Sidechain
30	0	333	G	Sidechain
30	0	470	U	Sidechain
30	0	471	G	Sidechain
30	0	482	G	Sidechain
30	0	506	G	Sidechain
30	0	518	G	Sidechain
30	0	619	U	Sidechain
30	0	888	U	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	85	0
2	B	2625	0	2533	108	0
3	C	1860	0	1813	63	0
4	D	1094	0	1085	37	0
5	E	1357	0	1266	39	0
6	F	890	0	843	19	0
7	G	240	0	231	8	0
8	H	1282	0	1292	33	0
9	I	519	0	500	14	0
10	J	1120	0	1098	44	0
11	K	994	0	1027	34	0
12	L	1118	0	1076	38	0
13	M	1558	0	1573	95	0
14	N	1445	0	1401	73	0
15	O	865	0	873	22	0
16	P	1136	0	1123	34	0
17	Q	735	0	729	28	0
18	R	1149	0	1122	41	0
19	S	641	0	605	15	0
20	T	950	0	924	36	0
21	U	410	0	368	26	0
22	V	499	0	511	21	0
23	W	1196	0	1137	58	0
24	X	654	0	653	20	0
25	Y	1130	0	1133	39	0
26	Z	573	0	535	50	0
27	1	431	0	426	21	0
28	2	396	0	413	21	0
29	3	755	0	732	57	0
30	0	59019	0	29809	1661	0
31	9	2599	0	1325	127	0
32	0	86	0	0	0	0
32	9	1	0	0	0	0
32	A	2	0	0	0	0
32	B	1	0	0	0	0
32	K	1	0	0	0	0
32	T	1	0	0	0	0
32	Y	1	0	0	0	0
33	0	10	0	0	3	0
33	3	1	0	0	1	0
33	A	1	0	0	0	0
33	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	J	3	0	0	2	0
33	L	1	0	0	0	0
33	M	1	0	0	0	0
33	N	1	0	0	0	0
33	O	1	0	0	0	0
33	R	1	0	0	0	0
33	Y	1	0	0	2	0
34	0	92	0	0	0	0
34	1	2	0	0	0	0
34	3	2	0	0	0	0
34	9	3	0	0	0	0
34	A	2	0	0	0	0
34	B	2	0	0	0	0
34	F	1	0	0	0	0
34	H	1	0	0	0	0
34	L	1	0	0	0	0
34	R	1	0	0	0	0
34	S	1	0	0	0	0
35	0	65	0	0	0	0
35	9	2	0	0	0	0
35	B	1	0	0	0	0
35	C	1	0	0	0	0
35	H	1	0	0	0	0
35	J	1	0	0	0	0
35	M	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	1	0	0	0	0
35	S	1	0	0	0	0
36	0	1	0	0	0	0
36	M	1	0	0	0	0
37	1	1	0	0	0	0
37	3	1	0	0	0	0
37	O	1	0	0	0	0
37	U	1	0	0	0	0
37	Z	1	0	0	0	0
38	0	5904	0	0	251	0
38	1	59	0	0	3	0
38	2	43	0	0	2	0
38	3	70	0	0	3	0
38	9	149	0	0	10	0
38	A	119	0	0	7	0
38	B	152	0	0	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	C	185	0	0	18	0
38	D	42	0	0	4	0
38	E	43	0	0	1	0
38	F	26	0	0	1	0
38	G	19	0	0	1	0
38	H	65	0	0	4	0
38	I	8	0	0	1	0
38	J	53	0	0	1	0
38	K	58	0	0	3	0
38	L	85	0	0	9	0
38	M	127	0	0	13	0
38	N	59	0	0	2	0
38	O	39	0	0	2	0
38	P	67	0	0	3	0
38	Q	48	0	0	1	0
38	R	77	0	0	2	0
38	S	30	0	0	2	0
38	T	36	0	0	3	0
38	U	28	0	0	4	0
38	V	13	0	0	2	0
38	W	67	0	0	3	0
38	X	21	0	0	2	0
38	Y	100	0	0	5	0
38	Z	31	0	0	7	0
All	All	99121	0	59922	2675	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 18.

All (2675) 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)
18:R:150:PRO:CG	18:R:150:PRO:CD	1.96	1.41
30:0:871:G:C8	30:0:871:G:H5'	1.77	1.19
10:J:82:THR:HG23	30:0:1242:A:H5'	1.23	1.16
30:0:1165:G:H1'	30:0:1174:A:H1'	1.17	1.14
31:9:56:A:H2'	31:9:57:A:H5''	1.19	1.13
30:0:1559:A:H1'	38:0:5849:HOH:O	1.45	1.13
30:0:1160:G:C5'	30:0:1161:A:H5'	1.78	1.13
31:9:29:C:H2'	31:9:30:C:H5'	1.32	1.10
15:O:3:THR:HG22	30:0:656:G:H5'	1.19	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:171:ARG:HD3	30:0:156:C:H5''	1.28	1.09
30:0:1160:G:H5'	30:0:1161:A:C5'	1.80	1.09
30:0:871:G:H8	30:0:871:G:H5'	0.99	1.08
10:J:52:GLN:HE22	30:0:1119:G:H2'	1.17	1.08
18:R:150:PRO:CG	18:R:150:PRO:C	2.22	1.07
10:J:52:GLN:NE2	30:0:1119:G:H2'	1.69	1.07
31:9:76:G:H3'	31:9:77:A:H5''	1.33	1.05
30:0:545:G:H8	30:0:545:G:H5'	1.22	1.05
14:N:37:ARG:NH1	31:9:6:C:H5''	1.71	1.03
30:0:1603:A:H5'	30:0:1605:G:O4'	1.60	1.02
30:0:1641:A:H2'	30:0:1642:A:H5'	1.44	0.99
21:U:56:ARG:HD2	30:0:2890:A:C8	1.98	0.98
30:0:1666:C:O2'	30:0:1667:A:H5''	1.63	0.98
26:Z:60:ASP:HB3	26:Z:69:ASP:HB3	1.43	0.98
11:K:10:GLN:H	11:K:10:GLN:HE21	0.99	0.97
30:0:1979:G:H2'	38:0:9283:HOH:O	1.65	0.97
30:0:381:G:H5''	38:0:4317:HOH:O	1.64	0.96
30:0:871:G:H8	30:0:871:G:C5'	1.78	0.96
30:0:1165:G:H21	30:0:1173:A:H5''	1.30	0.96
13:M:70:GLY:HA3	13:M:73:ARG:NH2	1.80	0.96
17:Q:15:LYS:HD3	30:0:2364:A:H5''	1.47	0.96
16:P:59:ARG:HH22	16:P:66:GLN:HE22	1.05	0.95
31:9:56:A:C2'	31:9:57:A:H5''	1.95	0.95
30:0:1474:C:H6	30:0:1474:C:H5'	1.30	0.95
31:9:14:G:H5'	31:9:14:G:H8	1.32	0.94
18:R:8:ALA:HB1	18:R:13:THR:HG21	1.50	0.94
30:0:236:A:H4'	30:0:237:G:H5'	1.49	0.94
2:B:264:GLU:HG2	2:B:267:LYS:HE3	1.50	0.94
30:0:1165:G:H21	30:0:1173:A:C5'	1.81	0.93
16:P:115:SER:H	16:P:118:GLN:HE21	1.11	0.93
30:0:2505:G:H2'	30:0:2506:A:H5'	1.50	0.93
30:0:2717:C:C2'	30:0:2718:C:H5''	1.99	0.93
30:0:2502:C:H2'	30:0:2503:A:H5'	1.52	0.92
23:W:108:ARG:HH21	23:W:114:PRO:HG2	1.35	0.92
1:A:211:LYS:HB3	1:A:212:PRO:HD2	1.52	0.91
3:C:27:ARG:HG2	3:C:27:ARG:HH11	1.36	0.91
30:0:2321:A:H2	30:0:2378:U:H3	1.14	0.91
15:O:3:THR:CG2	30:0:656:G:H5'	2.00	0.91
30:0:2710:U:H1'	38:0:7613:HOH:O	1.71	0.90
30:0:282:C:O2'	30:0:283:U:H5'	1.71	0.90
30:0:1118:A:H62	30:0:1244:U:H3	1.14	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:236:THR:HG22	3:C:239:ALA:H	1.35	0.90
30:0:2506:A:HO2'	30:0:2507:G:H8	0.90	0.90
29:3:60:LYS:HG3	29:3:61:PRO:HD2	1.53	0.90
30:0:2812:A:H2	30:0:2814:A:H62	1.19	0.90
30:0:1116:U:O2'	30:0:1118:A:H2	1.54	0.90
30:0:545:G:C8	30:0:545:G:H5'	2.06	0.89
30:0:2321:A:H8	30:0:2322:U:HO2'	1.13	0.89
30:0:2502:C:C2'	30:0:2503:A:H5'	2.03	0.89
30:0:870:G:H2'	30:0:871:G:H5''	1.53	0.88
33:Y:8820:CL:CL	38:0:4953:HOH:O	2.27	0.88
30:0:1119:G:H22	30:0:1246:A:H2	1.16	0.88
30:0:2700:G:H3'	38:0:3569:HOH:O	1.73	0.88
23:W:137:GLN:HE21	23:W:141:HIS:HE1	1.20	0.88
31:9:92:G:H2'	31:9:93:A:C8	2.07	0.88
13:M:79:ALA:HB3	13:M:81:ARG:HH12	1.38	0.88
30:0:1118:A:H3'	30:0:1118:A:C8	2.08	0.88
30:0:1206:U:H6	30:0:1206:U:H5'	1.39	0.88
15:O:47:ARG:HG3	15:O:47:ARG:HH11	1.35	0.88
30:0:506:G:H22	30:0:509:A:C5'	1.85	0.87
30:0:1474:C:C6	30:0:1474:C:H5'	2.10	0.87
30:0:1835:U:H5	30:0:1840:A:N7	1.73	0.87
30:0:542:A:H5'	30:0:542:A:H8	1.39	0.87
30:0:1118:A:H3'	30:0:1118:A:H8	1.39	0.87
30:0:2321:A:H4'	30:0:2322:U:OP1	1.73	0.87
30:0:363:C:H1'	38:0:5273:HOH:O	1.75	0.86
30:0:1278:A:H4'	30:0:1279:U:C4	2.10	0.86
30:0:2505:G:C2'	30:0:2506:A:H5'	2.04	0.86
1:A:70:ALA:HB1	26:Z:89:THR:HG21	1.57	0.86
30:0:1701:A:H4'	30:0:1702:U:H5''	1.55	0.86
13:M:70:GLY:HA2	30:0:2263:G:H4'	1.59	0.85
23:W:6:GLN:HB2	23:W:26:ILE:HD11	1.58	0.85
30:0:506:G:H22	30:0:509:A:H5''	1.42	0.85
30:0:1205:U:H2'	30:0:1206:U:H5'	1.58	0.85
30:0:1641:A:C2'	30:0:1642:A:H5'	2.06	0.85
26:Z:70:ARG:NH1	26:Z:83:TYR:HB2	1.91	0.85
30:0:2717:C:H2'	30:0:2718:C:H5''	1.59	0.85
30:0:1666:C:H2'	30:0:1667:A:H5'	1.58	0.84
30:0:2717:C:O2'	30:0:2718:C:H5''	1.76	0.84
29:3:68:LYS:HE2	30:0:2436:U:H5'	1.60	0.84
30:0:2637:A:H4'	38:0:4923:HOH:O	1.78	0.83
30:0:2043:U:H3'	38:0:6696:HOH:O	1.76	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:217:ARG:HG3	2:B:257:THR:HG22	1.58	0.83
23:W:125:HIS:NE2	30:0:1097:A:H5''	1.93	0.83
30:0:2010:A:H2'	38:0:5942:HOH:O	1.77	0.83
1:A:167:LYS:HE2	26:Z:50:VAL:HG13	1.61	0.83
30:0:380:A:H2'	38:0:7216:HOH:O	1.77	0.83
29:3:64:LYS:HA	29:3:84:ARG:HA	1.57	0.83
13:M:68:ARG:NH2	13:M:73:ARG:HD3	1.94	0.83
11:K:10:GLN:H	11:K:10:GLN:NE2	1.77	0.83
11:K:39:GLY:HA2	38:0:5215:HOH:O	1.76	0.83
30:0:2454:C:H5''	38:0:7719:HOH:O	1.79	0.82
2:B:36:PRO:HA	2:B:168:GLY:HA3	1.61	0.82
30:0:1189:A:H1'	30:0:1209:C:O4'	1.79	0.82
30:0:1667:A:H8	30:0:1667:A:H5'	1.44	0.82
13:M:27:ARG:HH22	13:M:44:THR:HG23	1.44	0.82
30:0:541:C:C2'	30:0:542:A:H5''	2.09	0.82
30:0:541:C:H2'	30:0:542:A:C5'	2.08	0.82
30:0:1300:G:H1'	38:0:4678:HOH:O	1.80	0.81
29:3:31:THR:O	30:0:1923:G:H4'	1.79	0.81
30:0:1184:C:H1'	38:0:7461:HOH:O	1.80	0.81
11:K:10:GLN:N	11:K:10:GLN:HE21	1.79	0.81
20:T:71:VAL:HG11	20:T:90:PRO:HB3	1.62	0.81
30:0:2769:C:O2'	30:0:2770:G:H5'	1.81	0.81
30:0:2005:G:H3'	30:0:2005:G:OP2	1.80	0.81
30:0:559:U:H5'	30:0:559:U:H6	1.45	0.81
31:9:29:C:C2'	31:9:30:C:H5'	2.08	0.81
3:C:139:VAL:HG13	38:C:8658:HOH:O	1.79	0.81
30:0:1174:A:C6	30:0:1201:C:H4'	2.14	0.81
8:H:59:GLN:HE21	8:H:129:ARG:HE	1.25	0.81
18:R:39:THR:HG22	18:R:42:GLU:H	1.46	0.81
30:0:1205:U:H2'	30:0:1206:U:C5'	2.10	0.81
30:0:1119:G:N2	30:0:1246:A:C2	2.47	0.81
30:0:681:G:H5'	30:0:681:G:N3	1.96	0.81
30:0:1641:A:H2'	30:0:1642:A:C5'	2.09	0.81
30:0:1801:A:H3'	38:0:7607:HOH:O	1.81	0.80
28:2:43:ARG:HH22	30:0:1684:A:H1'	1.47	0.80
30:0:2748:G:H2'	38:0:7534:HOH:O	1.81	0.80
30:0:1593:C:H1'	38:0:6089:HOH:O	1.80	0.80
28:2:41:HIS:H	28:2:45:ASN:HD22	1.27	0.80
20:T:9:LYS:HE3	20:T:13:ARG:NH1	1.96	0.80
15:O:3:THR:HG22	30:0:656:G:C5'	2.09	0.80
25:Y:115:ARG:NH2	30:0:1266:U:H4'	1.97	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2783:A:H3'	38:0:5225:HOH:O	1.81	0.80
31:9:39:U:H1'	31:9:44:A:H61	1.45	0.80
30:0:1603:A:H5''	30:0:1605:G:H5'	1.63	0.80
31:9:14:G:H5'	31:9:14:G:C8	2.16	0.80
9:I:112:LEU:HD11	30:0:1162:G:H1'	1.63	0.80
18:R:99:ALA:HB1	18:R:109:MET:HE1	1.62	0.80
30:0:586:C:H5''	38:0:7275:HOH:O	1.81	0.80
22:V:12:THR:HG22	22:V:15:GLU:HG3	1.63	0.79
13:M:27:ARG:NH2	13:M:44:THR:HG23	1.96	0.79
6:F:91:VAL:HG12	6:F:92:GLY:H	1.46	0.79
38:N:8842:HOH:O	31:9:49:G:H5''	1.83	0.79
10:J:82:THR:CG2	30:0:1242:A:H5'	2.09	0.79
30:0:2419:U:H5''	30:0:2420:G:H5'	1.65	0.79
30:0:2586:U:H3	30:0:2592:G:H22	1.28	0.79
30:0:1183:C:H2'	38:0:6224:HOH:O	1.82	0.79
30:0:255:A:H2'	30:0:256:C:H6	1.48	0.79
3:C:1:MET:HG2	3:C:2:GLN:H	1.47	0.78
30:0:2635:A:O2'	30:0:2636:C:H5'	1.82	0.78
30:0:308:U:H5'	30:0:309:C:OP1	1.82	0.78
30:0:659:A:H5''	38:0:7089:HOH:O	1.83	0.78
2:B:320:GLN:HE21	2:B:321:PRO:HD2	1.48	0.78
30:0:123:U:H5'	38:0:6637:HOH:O	1.82	0.78
30:0:1372:A:H3'	38:0:7180:HOH:O	1.81	0.78
30:0:2485:A:H3'	38:0:5838:HOH:O	1.82	0.78
4:D:154:LYS:HD2	4:D:154:LYS:H	1.48	0.78
13:M:99:ARG:HE	13:M:170:ASN:HD22	1.31	0.78
13:M:134:ILE:HG23	13:M:141:ILE:HD13	1.66	0.78
16:P:59:ARG:NH2	16:P:66:GLN:HE22	1.80	0.78
30:0:960:G:H4'	38:0:7423:HOH:O	1.83	0.78
30:0:1595:G:O2'	30:0:1596:U:H5'	1.84	0.78
30:0:2291:A:C8	30:0:2309:C:H5'	2.19	0.78
8:H:59:GLN:NE2	8:H:129:ARG:HE	1.82	0.78
30:0:2469:A:H1'	38:0:3229:HOH:O	1.83	0.77
30:0:541:C:H2'	30:0:542:A:H5''	1.65	0.77
30:0:871:G:C8	30:0:871:G:C5'	2.58	0.77
30:0:1189:A:H3'	38:0:7669:HOH:O	1.83	0.77
30:0:2420:G:O2'	30:0:2421:G:H5'	1.85	0.77
30:0:1116:U:H3	30:0:1246:A:H62	1.33	0.77
30:0:558:C:C2'	30:0:559:U:H5''	2.14	0.77
30:0:564:G:H1'	38:0:6295:HOH:O	1.84	0.77
30:0:2769:C:C2'	30:0:2770:G:H5'	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:558:C:O2'	30:0:559:U:H5''	1.85	0.77
30:0:1632:A:H2'	30:0:1633:C:H5'	1.67	0.76
30:0:1973:A:H5'	30:0:1973:A:H8	1.48	0.76
30:0:2703:A:H2'	30:0:2704:C:H6	1.50	0.76
30:0:283:U:H5	30:0:284:C:C4	2.02	0.76
30:0:1175:G:H1'	30:0:1193:A:H2'	1.65	0.76
31:9:1:U:H4'	31:9:3:A:OP1	1.84	0.76
30:0:2468:A:H3'	38:0:5449:HOH:O	1.84	0.76
2:B:221:GLN:HE22	11:K:42:ASN:HD22	1.33	0.76
24:X:37:LEU:HD13	24:X:85:VAL:HG21	1.68	0.76
30:0:2506:A:O2'	30:0:2507:G:H8	1.68	0.76
38:C:8633:HOH:O	30:0:338:C:H5''	1.86	0.76
30:0:969:G:H1	30:0:999:C:H42	1.34	0.76
13:M:71:SER:HB3	30:0:2264:A:OP1	1.85	0.75
30:0:899:C:H5'	38:0:3190:HOH:O	1.85	0.75
4:D:105:SER:OG	30:0:2338:G:H1'	1.85	0.75
10:J:75:PRO:HG2	10:J:105:LEU:HD21	1.66	0.75
30:0:2505:G:H2'	30:0:2506:A:C5'	2.17	0.75
30:0:282:C:H1'	30:0:368:C:N4	2.01	0.75
14:N:132:ASN:HD22	30:0:2413:A:H4'	1.52	0.75
30:0:1170:U:H2'	30:0:1172:G:OP2	1.87	0.75
30:0:2908:A:H2'	30:0:2909:G:O4'	1.87	0.74
26:Z:70:ARG:HB2	26:Z:70:ARG:HH11	1.51	0.74
30:0:1741:U:O2'	30:0:2723:G:H4'	1.87	0.74
30:0:544:G:H2'	30:0:545:G:H5''	1.68	0.74
24:X:76:ARG:HH11	24:X:76:ARG:HG3	1.52	0.74
3:C:218:VAL:HG12	38:C:8637:HOH:O	1.87	0.74
22:V:57:LYS:HA	22:V:60:GLN:HE21	1.52	0.74
30:0:1834:C:H2'	30:0:1840:A:N6	2.02	0.74
33:0:8813:CL:CL	38:0:4678:HOH:O	2.43	0.74
30:0:2781:U:C2'	30:0:2782:G:H5'	2.18	0.74
23:W:4:LEU:HD23	23:W:54:PHE:HB3	1.69	0.74
30:0:2793:A:H1'	38:0:6312:HOH:O	1.88	0.74
14:N:11:ARG:HD3	31:9:114:G:O6	1.88	0.74
25:Y:235:GLU:H	25:Y:235:GLU:CD	1.92	0.73
3:C:140:VAL:HB	38:C:8660:HOH:O	1.86	0.73
4:D:22:VAL:HG22	4:D:74:THR:HG22	1.70	0.73
18:R:98:ASN:HD21	30:0:500:G:H21	1.36	0.73
30:0:1525:G:H5'	30:0:1526:A:OP2	1.89	0.73
30:0:2578:G:H5'	30:0:2578:G:H8	1.52	0.73
31:9:92:G:H2'	31:9:93:A:H8	1.50	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:56:ASP:HB2	2:B:322:ARG:HE	1.52	0.73
21:U:56:ARG:HH11	21:U:56:ARG:HG3	1.54	0.73
30:0:2748:G:H1'	38:0:7889:HOH:O	1.88	0.73
11:K:14:LYS:HB2	11:K:45:PRO:HG2	1.70	0.73
30:0:1279:U:O2	30:0:1279:U:H2'	1.89	0.72
30:0:2768:A:O2'	30:0:2769:C:H5'	1.89	0.72
30:0:619:U:H3'	38:0:3270:HOH:O	1.88	0.72
30:0:2524:G:H21	30:0:2526:C:N4	1.85	0.72
30:0:2871:G:H2'	30:0:2872:U:H6	1.54	0.72
14:N:37:ARG:HH12	31:9:6:C:H5''	1.55	0.72
30:0:271:C:H41	30:0:378:A:H2	1.33	0.72
30:0:558:C:H2'	30:0:559:U:C5'	2.20	0.72
30:0:1921:A:O2'	30:0:1922:A:H5'	1.89	0.72
30:0:2766:A:H5'	38:0:9565:HOH:O	1.88	0.72
2:B:179:LEU:O	2:B:183:GLU:HG2	1.89	0.72
30:0:1166:A:P	30:0:1174:A:H4'	2.29	0.72
31:9:29:C:H2'	31:9:30:C:C5'	2.17	0.72
30:0:2533:C:H5'	30:0:2533:C:H6	1.53	0.72
30:0:877:G:H5'	30:0:878:G:OP1	1.89	0.72
30:0:2712:G:H5'	38:0:5215:HOH:O	1.90	0.72
30:0:544:G:C2'	30:0:545:G:H5''	2.20	0.72
30:0:836:G:H5''	38:0:9285:HOH:O	1.89	0.72
13:M:15:PRO:HA	13:M:20:LEU:HD23	1.70	0.72
13:M:79:ALA:H	13:M:81:ARG:HH22	1.37	0.72
29:3:2:GLN:O	30:0:2320:U:H2'	1.90	0.71
31:9:54:A:O2'	31:9:55:U:H5'	1.89	0.71
2:B:145:HIS:HD2	2:B:146:THR:O	1.73	0.71
13:M:66:SER:HB3	13:M:128:TRP:CD1	2.24	0.71
14:N:159:TYR:HE1	31:9:50:G:H5''	1.55	0.71
30:0:281:U:H2'	30:0:282:C:O4'	1.90	0.71
30:0:702:G:O2'	30:0:703:G:H5'	1.90	0.71
14:N:67:ALA:HA	14:N:71:TRP:HB3	1.72	0.71
30:0:2534:C:H1'	38:0:3477:HOH:O	1.91	0.71
30:0:821:U:H3'	38:0:3759:HOH:O	1.90	0.71
30:0:2426:G:H1'	38:0:6075:HOH:O	1.90	0.71
30:0:1165:G:N2	30:0:1173:A:C5'	2.53	0.71
30:0:221:G:H5''	38:0:5725:HOH:O	1.90	0.71
38:I:6825:HOH:O	30:0:1166:A:H2	1.73	0.71
30:0:1835:U:C5	30:0:1840:A:N7	2.57	0.71
2:B:307:ARG:HH11	2:B:307:ARG:HG3	1.55	0.71
30:0:1132:A:N6	30:0:1229:C:H2'	2.06	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1589:G:N2	30:0:1605:G:H1'	2.05	0.71
30:0:1979:G:H3'	38:0:3282:HOH:O	1.88	0.71
14:N:5:ARG:HB2	14:N:5:ARG:HH11	1.56	0.71
30:0:2487:C:H5	38:0:4880:HOH:O	1.73	0.70
30:0:2514:U:OP1	30:0:2572:G:H1'	1.90	0.70
14:N:143:ARG:HH21	14:N:169:PRO:HB2	1.56	0.70
30:0:2505:G:O2'	30:0:2506:A:H5'	1.90	0.70
14:N:17:ARG:HB3	14:N:17:ARG:HH11	1.55	0.70
30:0:1666:C:H2'	30:0:1667:A:C5'	2.21	0.70
11:K:98:VAL:CG1	11:K:102:GLU:HA	2.20	0.70
26:Z:70:ARG:HH12	26:Z:83:TYR:HB2	1.55	0.70
17:Q:11:ARG:NH2	30:0:2297:U:H4'	2.07	0.70
30:0:1189:A:H1'	30:0:1209:C:C1'	2.21	0.70
30:0:1209:C:H2'	30:0:1210:G:H8	1.57	0.70
18:R:132:ARG:NH2	30:0:2055:A:H4'	2.06	0.70
30:0:2237:G:H1'	30:0:2238:A:C8	2.27	0.70
13:M:188:ARG:HD3	30:0:155:C:OP2	1.92	0.70
26:Z:80:GLN:HG3	26:Z:81:CYS:H	1.56	0.70
30:0:31:C:H2'	38:0:7677:HOH:O	1.90	0.70
38:Q:6286:HOH:O	30:0:1019:C:H5'	1.91	0.69
30:0:2251:G:H2'	30:0:2252:A:C8	2.27	0.69
3:C:127:ARG:NH2	3:C:225:PRO:HG2	2.07	0.69
30:0:138:U:H5''	30:0:139:C:OP2	1.93	0.69
30:0:1451:C:H5'	30:0:1505:U:C5	2.27	0.69
30:0:1562:C:O2	30:0:1562:C:H2'	1.91	0.69
30:0:42:C:H3'	38:0:4166:HOH:O	1.92	0.69
2:B:36:PRO:HG3	2:B:169:GLY:H	1.57	0.69
5:E:143:GLN:HE21	30:0:2780:C:H1'	1.57	0.69
1:A:94:LEU:HD12	1:A:98:GLU:HB2	1.74	0.69
9:I:91:PHE:HD2	9:I:131:GLY:HA2	1.55	0.69
14:N:49:THR:HB	14:N:58:LEU:HD11	1.74	0.69
30:0:1666:C:C2'	30:0:1667:A:C5'	2.70	0.69
30:0:2102:G:H4'	38:0:5631:HOH:O	1.92	0.69
30:0:2102:G:N2	30:0:2103:A:N1	2.40	0.69
30:0:2871:G:H2'	30:0:2872:U:C6	2.28	0.69
30:0:287:C:H42	30:0:365:G:H1	1.41	0.69
30:0:407:A:H2'	30:0:408:A:C8	2.28	0.69
30:0:961:A:H4'	38:0:6759:HOH:O	1.91	0.69
4:D:28:GLY:HA2	4:D:69:ILE:HG23	1.72	0.69
13:M:79:ALA:HB3	13:M:81:ARG:NH1	2.06	0.69
14:N:141:ARG:HH21	31:9:48:C:H4'	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:26:VAL:HG13	10:J:36:VAL:HG11	1.75	0.69
2:B:206:THR:HG21	30:0:2716:G:H5''	1.73	0.69
31:9:39:U:H3'	31:9:40:C:H5''	1.75	0.69
12:L:91:VAL:HG13	12:L:120:LEU:HD23	1.75	0.69
30:0:2511:A:H2'	30:0:2512:U:O4'	1.93	0.69
30:0:2781:U:H2'	30:0:2782:G:H5'	1.73	0.69
2:B:18:ARG:HE	2:B:256:GLN:HE21	1.41	0.69
30:0:1589:G:H22	30:0:1605:G:H1'	1.55	0.69
30:0:969:G:H1	30:0:999:C:N4	1.91	0.69
13:M:68:ARG:HD3	13:M:68:ARG:O	1.93	0.69
30:0:317:A:H5'	38:0:3761:HOH:O	1.91	0.68
4:D:51:ARG:HH11	4:D:68:PRO:HB3	1.59	0.68
10:J:18:ILE:HD13	30:0:1244:U:OP1	1.92	0.68
22:V:50:ARG:HH12	30:0:56:G:H5''	1.58	0.68
30:0:1474:C:C5'	30:0:1474:C:H6	2.06	0.68
30:0:2781:U:O2'	30:0:2782:G:H5'	1.93	0.68
30:0:870:G:C2'	30:0:871:G:H5''	2.22	0.68
14:N:40:ASN:ND2	31:9:28:U:H5''	2.08	0.68
16:P:59:ARG:HH22	16:P:66:GLN:NE2	1.87	0.68
29:3:59:ASP:HA	30:0:2460:A:H5''	1.74	0.68
30:0:962:C:H2'	30:0:963:C:H5'	1.74	0.68
2:B:254:GLN:HG3	38:0:9697:HOH:O	1.92	0.68
13:M:99:ARG:HD2	13:M:167:GLY:HA2	1.75	0.68
30:0:255:A:H2'	30:0:256:C:C6	2.29	0.68
30:0:390:G:H5'	38:0:7539:HOH:O	1.94	0.68
28:2:35:ARG:HB2	38:2:2691:HOH:O	1.92	0.68
10:J:131:THR:HB	10:J:134:GLU:HG3	1.75	0.68
30:0:1527:A:H1'	30:0:1528:A:C8	2.28	0.68
30:0:1634:G:H2'	30:0:1635:U:H6	1.57	0.68
30:0:1702:U:H1'	38:0:5758:HOH:O	1.93	0.68
30:0:283:U:H5	30:0:284:C:N3	1.91	0.68
12:L:6:ARG:HD3	30:0:1299:G:O6	1.94	0.68
13:M:171:ARG:CD	30:0:156:C:H5''	2.15	0.68
30:0:2374:G:H2'	30:0:2375:A:C8	2.29	0.68
30:0:440:C:H2'	30:0:441:A:C8	2.29	0.68
13:M:83:SER:HA	38:M:8877:HOH:O	1.94	0.68
24:X:25:ARG:HD2	38:X:5356:HOH:O	1.91	0.68
26:Z:70:ARG:HB3	38:Z:8728:HOH:O	1.93	0.68
30:0:1666:C:C2'	30:0:1667:A:H5''	2.23	0.67
27:1:8:GLN:HE22	27:1:11:LYS:NZ	1.93	0.67
2:B:264:GLU:CG	2:B:267:LYS:HE3	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1158:G:C2'	30:0:1159:G:H5'	2.24	0.67
8:H:72:ALA:HB2	8:H:156:ALA:HB2	1.75	0.67
23:W:137:GLN:HE21	23:W:141:HIS:CE1	2.08	0.67
10:J:90:LYS:HB2	33:J:8802:CL:CL	2.31	0.67
30:0:1634:G:H2'	30:0:1635:U:C6	2.29	0.67
23:W:88:THR:HG23	23:W:110:GLN:HB3	1.76	0.67
31:9:24:U:H3'	31:9:25:G:H5'	1.75	0.67
6:F:63:ILE:HB	6:F:64:PRO:HD3	1.74	0.67
30:0:283:U:C5	30:0:284:C:C4	2.83	0.67
20:T:2:LYS:HG2	30:0:447:A:OP1	1.95	0.67
30:0:1632:A:C2'	30:0:1633:C:H5'	2.24	0.67
30:0:1762:C:O2'	30:0:1763:C:H5'	1.95	0.67
30:0:735:C:C5	30:0:736:A:C4	2.82	0.67
31:9:91:C:H1'	38:9:9143:HOH:O	1.95	0.67
30:0:1268:C:H2'	30:0:1269:G:H8	1.59	0.67
30:0:541:C:H2'	30:0:542:A:H5'	1.75	0.67
30:0:221:G:H2'	30:0:222:A:C8	2.30	0.67
30:0:603:A:H5''	30:0:604:G:OP1	1.94	0.67
14:N:7:LYS:HE3	17:Q:21:ARG:O	1.95	0.67
18:R:150:PRO:O	18:R:150:PRO:CG	2.42	0.67
1:A:72:GLU:HG2	26:Z:100:GLY:HA3	1.76	0.67
9:I:96:SER:H	9:I:99:GLN:NE2	1.93	0.66
25:Y:187:VAL:HG23	25:Y:192:ASP:HB3	1.77	0.66
30:0:2073:G:OP2	30:0:2490:A:H5'	1.95	0.66
30:0:506:G:H22	30:0:509:A:H5'	1.60	0.66
30:0:613:C:H2'	30:0:614:U:H6	1.61	0.66
12:L:121:ILE:HG12	12:L:141:GLU:HB2	1.78	0.66
23:W:44:MET:CE	30:0:944:G:H21	2.09	0.66
30:0:2488:A:C2	38:0:7265:HOH:O	2.48	0.66
30:0:451:C:O2'	30:0:452:G:H5'	1.95	0.66
11:K:18:ILE:HG22	11:K:93:ASN:HB2	1.77	0.66
30:0:1158:G:O2'	30:0:1159:G:H5'	1.96	0.66
18:R:18:LEU:HB2	18:R:143:VAL:HG13	1.76	0.66
30:0:849:C:H1'	38:0:6602:HOH:O	1.95	0.66
31:9:55:U:H4'	31:9:56:A:C8	2.31	0.66
22:V:50:ARG:NH1	30:0:56:G:H5''	2.10	0.66
25:Y:169:ARG:HD2	30:0:1328:A:OP1	1.96	0.66
30:0:2461:U:O2	30:0:2466:G:H1'	1.96	0.66
30:0:2321:A:C2	30:0:2378:U:N3	2.57	0.66
30:0:735:C:H2'	30:0:736:A:O4'	1.96	0.66
30:0:558:C:H2'	30:0:559:U:H5'	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:32:ALA:HB3	8:H:69:ARG:HH12	1.61	0.66
9:I:87:PRO:HD2	30:0:1180:U:H1'	1.77	0.66
2:B:162:MET:HG3	2:B:310:ARG:NH1	2.10	0.65
9:I:110:ASP:O	30:0:1163:G:H5'	1.96	0.65
3:C:233:THR:HG22	3:C:234:VAL:H	1.61	0.65
4:D:103:ASN:HD22	4:D:133:ASN:HA	1.60	0.65
4:D:103:ASN:ND2	4:D:133:ASN:HA	2.11	0.65
21:U:56:ARG:NE	30:0:2890:A:H1'	2.11	0.65
30:0:567:U:H5''	38:0:5280:HOH:O	1.97	0.65
30:0:635:A:H2'	30:0:636:G:H5''	1.77	0.65
30:0:1477:C:H5'	30:0:1868:G:C5'	2.26	0.65
30:0:1940:C:H1'	38:0:9376:HOH:O	1.96	0.65
30:0:1950:G:H2'	30:0:1951:G:C8	2.32	0.65
30:0:625:U:H5''	30:0:1044:C:N4	2.11	0.65
30:0:1925:G:O2'	30:0:1926:G:H5'	1.96	0.65
25:Y:187:VAL:HG23	25:Y:192:ASP:CB	2.27	0.65
5:E:139:GLU:OE2	30:0:2781:U:H1'	1.97	0.65
30:0:2869:G:H2'	30:0:2870:C:C6	2.31	0.65
30:0:1165:G:H1'	30:0:1174:A:C1'	2.11	0.65
14:N:144:GLY:O	14:N:147:ILE:HG22	1.97	0.65
22:V:39:ALA:N	22:V:40:PRO:HD2	2.12	0.65
30:0:1972:U:H2'	30:0:1973:A:C5'	2.27	0.65
30:0:2458:U:H3'	38:0:3239:HOH:O	1.96	0.64
17:Q:19:ARG:HH21	31:9:11:A:P	2.19	0.64
23:W:21:LEU:HD21	23:W:48:VAL:HG11	1.78	0.64
30:0:1165:G:H21	30:0:1173:A:H5'	1.63	0.64
30:0:128:A:O2'	30:0:129:A:H5'	1.97	0.64
30:0:2672:C:O2'	30:0:2673:U:H5'	1.97	0.64
30:0:2896:A:H5''	38:0:6082:HOH:O	1.96	0.64
30:0:583:C:H2'	30:0:584:U:H6	1.62	0.64
30:0:125:U:H2'	38:0:3755:HOH:O	1.97	0.64
30:0:369:G:O2'	30:0:370:G:H5'	1.98	0.64
30:0:660:A:H4'	30:0:661:G:O5'	1.98	0.64
30:0:69:A:H5'	30:0:69:A:C8	2.32	0.64
11:K:74:VAL:HG11	11:K:113:ILE:HG12	1.79	0.64
30:0:200:C:H2'	38:0:3428:HOH:O	1.96	0.64
30:0:2488:A:H2	38:0:7265:HOH:O	1.81	0.64
2:B:312:ARG:HD3	2:B:315:VAL:HG13	1.79	0.64
30:0:1167:G:H2'	30:0:1168:C:O4'	1.98	0.64
19:S:17:ASP:HB3	19:S:23:LYS:HB2	1.79	0.64
31:9:36:C:H5'	38:9:9047:HOH:O	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:70:GLY:CA	30:0:2263:G:H4'	2.28	0.64
30:0:285:A:H2'	30:0:286:U:O4'	1.97	0.64
30:0:1119:G:N2	30:0:1246:A:H2	1.89	0.64
30:0:2781:U:H2'	30:0:2782:G:C5'	2.27	0.64
30:0:1181:A:H2'	30:0:1182:C:H5'	1.78	0.64
30:0:441:A:H1'	30:0:442:A:N7	2.13	0.64
31:9:5:G:O2'	31:9:6:C:H5'	1.97	0.64
15:O:47:ARG:HG3	15:O:47:ARG:NH1	2.12	0.64
30:0:1213:C:O2'	30:0:1214:G:H5'	1.98	0.64
30:0:2436:U:H2'	30:0:2437:A:C8	2.33	0.64
30:0:2878:U:H5''	38:0:4165:HOH:O	1.98	0.64
30:0:2887:G:H2'	30:0:2888:U:C6	2.32	0.64
18:R:132:ARG:HH21	30:0:2055:A:H4'	1.61	0.64
30:0:2377:U:O2'	30:0:2378:U:H5'	1.98	0.63
30:0:2613:G:O2'	30:0:2614:C:H5'	1.99	0.63
31:9:24:U:H3'	31:9:25:G:C5'	2.28	0.63
12:L:143:THR:HG22	12:L:144:ASP:H	1.62	0.63
30:0:2281:C:C2'	30:0:2282:U:H5'	2.28	0.63
30:0:2831:C:C2'	30:0:2832:C:H5'	2.28	0.63
30:0:585:C:H5''	38:0:4864:HOH:O	1.98	0.63
3:C:162:VAL:HG22	3:C:232:LEU:HD21	1.81	0.63
14:N:141:ARG:NH2	31:9:48:C:H4'	2.13	0.63
21:U:4:ARG:O	21:U:13:ILE:HG22	1.98	0.63
30:0:1170:U:H1'	30:0:1172:G:N7	2.13	0.63
30:0:281:U:O2'	30:0:282:C:H5'	1.97	0.63
30:0:2869:G:H5'	38:0:5487:HOH:O	1.97	0.63
13:M:99:ARG:HE	13:M:170:ASN:ND2	1.96	0.63
30:0:1204:C:H1'	38:0:4741:HOH:O	1.98	0.63
30:0:1268:C:H2'	30:0:1269:G:C8	2.34	0.63
30:0:1904:A:C2	30:0:1905:U:H1'	2.34	0.63
30:0:2336:G:H2'	38:0:6280:HOH:O	1.98	0.63
30:0:2868:C:H1'	38:0:7114:HOH:O	1.97	0.63
13:M:81:ARG:HB3	13:M:85:ARG:HB2	1.80	0.63
30:0:820:G:H5'	30:0:821:U:H5'	1.80	0.63
29:3:55:VAL:HB	29:3:56:PRO:HD2	1.81	0.63
2:B:262:ARG:HG3	30:0:2716:G:H5'	1.79	0.63
3:C:174:ILE:CD1	30:0:338:C:H4'	2.29	0.63
30:0:1528:A:H2'	30:0:1529:G:O4'	1.98	0.63
30:0:2321:A:H8	30:0:2322:U:O2'	1.80	0.63
30:0:2831:C:H2'	30:0:2832:C:H5'	1.79	0.63
30:0:424:C:H2'	30:0:425:U:H6	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1950:G:H2'	30:0:1951:G:H8	1.64	0.63
30:0:2401:A:H2'	30:0:2402:A:C8	2.34	0.63
30:0:280:C:H2'	30:0:281:U:O4'	1.99	0.63
31:9:36:C:C5	31:9:37:C:C5	2.87	0.63
31:9:2:U:OP2	31:9:3:A:H5'	1.99	0.63
4:D:25:MET:SD	4:D:40:ILE:HD11	2.39	0.63
30:0:558:C:C2'	30:0:559:U:C5'	2.77	0.62
18:R:9:ASP:O	18:R:13:THR:HB	1.99	0.62
30:0:2594:C:O2'	30:0:2595:U:H5'	1.99	0.62
30:0:2827:A:H2'	30:0:2828:G:O4'	1.99	0.62
30:0:2894:C:O2'	30:0:2895:C:H5'	1.99	0.62
13:M:179:GLY:O	30:0:399:C:H5'	1.98	0.62
30:0:834:G:H4'	30:0:835:U:OP2	1.99	0.62
2:B:238:ASN:HD22	2:B:240:GLY:H	1.45	0.62
2:B:272:ILE:HG22	38:B:9132:HOH:O	2.00	0.62
12:L:79:ASP:HB3	38:L:9022:HOH:O	1.98	0.62
18:R:39:THR:HG23	18:R:107:GLU:O	1.99	0.62
30:0:1829:A:H2'	30:0:1830:C:H5'	1.81	0.62
11:K:66:ARG:HH22	30:0:1994:A:P	2.21	0.62
30:0:2505:G:C2'	30:0:2506:A:C5'	2.76	0.62
30:0:308:U:C4	30:0:342:C:H1'	2.34	0.62
30:0:1797:A:H4'	30:0:1798:C:C5	2.33	0.62
30:0:249:G:O2'	30:0:250:C:H5'	1.99	0.62
30:0:256:C:H2'	30:0:257:G:O4'	2.00	0.62
15:O:10:LEU:HD13	15:O:99:GLU:HG3	1.82	0.62
30:0:506:G:N2	30:0:509:A:H5''	2.14	0.62
25:Y:204:ARG:HH22	30:0:553:G:P	2.22	0.62
30:0:1087:G:H4'	30:0:1088:A:OP1	2.00	0.62
30:0:1230:A:OP1	30:0:1230:A:H8	1.83	0.62
17:Q:11:ARG:HH21	30:0:2297:U:H4'	1.62	0.62
30:0:2705:U:H2'	30:0:2706:A:C8	2.35	0.62
23:W:48:VAL:HG12	23:W:52:VAL:HB	1.81	0.62
30:0:418:C:H5	38:0:5765:HOH:O	1.82	0.62
30:0:1625:U:H5''	38:0:6005:HOH:O	2.00	0.62
30:0:2248:C:H3'	38:0:5435:HOH:O	1.98	0.62
17:Q:27:GLN:HE21	31:9:8:G:C5'	2.11	0.62
1:A:47:HIS:CD2	30:0:1654:U:H2'	2.35	0.62
13:M:24:GLN:HE21	13:M:27:ARG:HH11	1.48	0.62
30:0:1165:G:N2	30:0:1173:A:H5''	2.09	0.62
30:0:303:C:O2'	30:0:304:G:H5'	2.00	0.62
15:O:37:ARG:HD2	30:0:656:G:OP2	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1477:C:H5'	30:0:1868:G:H5'	1.81	0.62
30:0:289:G:O2'	30:0:290:C:H5'	1.98	0.62
8:H:168:VAL:HG13	38:H:9006:HOH:O	2.00	0.62
13:M:79:ALA:H	13:M:81:ARG:NH2	1.96	0.62
23:W:44:MET:HE2	30:0:944:G:H21	1.63	0.61
31:9:110:G:C6	31:9:111:U:C5	2.88	0.61
30:0:545:G:H8	30:0:545:G:C5'	2.08	0.61
30:0:807:A:O2'	30:0:808:A:H5'	1.99	0.61
19:S:52:VAL:HG22	19:S:66:VAL:HG22	1.82	0.61
25:Y:126:PRO:HG2	25:Y:128:PHE:CE1	2.34	0.61
3:C:27:ARG:NH1	3:C:27:ARG:HG2	2.12	0.61
10:J:75:PRO:HG2	10:J:105:LEU:CD2	2.31	0.61
12:L:90:ARG:HA	12:L:119:THR:HB	1.82	0.61
14:N:83:LEU:HD13	14:N:175:LEU:HD23	1.82	0.61
20:T:9:LYS:HD2	38:0:3744:HOH:O	2.00	0.61
30:0:1596:U:H2'	30:0:1598:A:OP2	2.00	0.61
30:0:2102:G:N2	30:0:2104:C:C2	2.69	0.61
30:0:39:G:N2	30:0:444:C:C2	2.68	0.61
28:2:41:HIS:HE1	30:0:1439:C:H5''	1.65	0.61
31:9:107:C:O2'	31:9:108:C:H5'	2.00	0.61
30:0:1245:C:O5'	30:0:1245:C:H6	1.84	0.61
3:C:129:HIS:CE1	3:C:231:ARG:HA	2.35	0.61
30:0:1015:C:H2'	30:0:1016:U:H6	1.64	0.61
13:M:102:GLU:OE1	13:M:164:THR:HG21	2.00	0.61
30:0:138:U:OP2	30:0:139:C:H5	1.84	0.61
30:0:2502:C:H2'	30:0:2503:A:C5'	2.29	0.61
30:0:2717:C:H2'	30:0:2718:C:C5'	2.30	0.61
3:C:236:THR:HG22	3:C:239:ALA:N	2.12	0.61
3:C:1:MET:HG2	3:C:2:GLN:N	2.15	0.61
26:Z:40:ALA:HA	30:0:1773:G:C8	2.35	0.61
30:0:24:G:N2	30:0:518:G:H1'	2.16	0.61
30:0:559:U:H5'	30:0:559:U:C6	2.32	0.61
29:3:60:LYS:CG	29:3:61:PRO:HD2	2.29	0.61
4:D:173:GLU:HG3	4:D:174:VAL:HG23	1.83	0.61
30:0:272:A:H5'	30:0:273:G:OP2	2.01	0.61
30:0:2766:A:O2'	30:0:2767:C:H5'	2.00	0.61
30:0:424:C:H2'	30:0:425:U:C6	2.35	0.61
30:0:735:C:H5	30:0:736:A:C4	2.18	0.61
16:P:98:ILE:HD12	16:P:102:ARG:NE	2.16	0.61
26:Z:78:ILE:HD12	38:Z:8714:HOH:O	2.01	0.61
30:0:1015:C:H2'	30:0:1016:U:C6	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:657:G:H2'	30:0:658:C:H6	1.64	0.61
30:0:946:C:H2'	30:0:947:U:H6	1.65	0.61
29:3:4:PRO:HA	29:3:91:GLN:HB2	1.82	0.61
30:0:1741:U:H5'	30:0:1742:A:OP1	2.01	0.60
27:1:8:GLN:HE22	27:1:11:LYS:HZ2	1.49	0.60
30:0:1165:G:N2	30:0:1173:A:H5'	2.15	0.60
30:0:1972:U:H2'	30:0:1973:A:H5'	1.83	0.60
30:0:2769:C:H2'	30:0:2770:G:H5'	1.82	0.60
15:O:32:ARG:HD3	15:O:32:ARG:O	2.01	0.60
30:0:1181:A:C2'	30:0:1182:C:H5'	2.30	0.60
28:2:10:ARG:NH2	30:0:121:U:OP2	2.34	0.60
30:0:1603:A:C5'	30:0:1605:G:H5'	2.29	0.60
2:B:207:LYS:HG3	30:0:2717:C:OP1	2.01	0.60
5:E:154:ILE:HD11	5:E:157:LYS:HE2	1.83	0.60
30:0:1183:C:N4	30:0:1184:C:H41	1.98	0.60
30:0:1603:A:C5'	30:0:1605:G:O4'	2.45	0.60
30:0:1622:G:H2'	30:0:1623:C:H5'	1.83	0.60
30:0:192:A:H5'	38:0:7634:HOH:O	1.99	0.60
30:0:2281:C:H2'	30:0:2282:U:H5'	1.83	0.60
30:0:2102:G:C8	30:0:2538:A:O4'	2.54	0.60
30:0:272:A:H3'	38:0:7522:HOH:O	2.00	0.60
31:9:20:G:O2'	31:9:21:G:H5'	2.02	0.60
31:9:76:G:C3'	31:9:77:A:H5''	2.21	0.60
8:H:29:SER:HA	8:H:62:HIS:HD2	1.66	0.60
30:0:396:U:H3'	38:0:3920:HOH:O	2.00	0.60
30:0:851:C:O2	30:0:2022:A:H2	1.85	0.60
29:3:25:VAL:HG22	29:3:68:LYS:HG3	1.84	0.60
10:J:107:ASN:HD22	10:J:109:TYR:H	1.48	0.60
13:M:84:LYS:HA	29:3:46:ILE:O	2.01	0.60
18:R:96:VAL:HG13	18:R:106:GLY:HA3	1.84	0.60
30:0:182:G:H5'	38:0:5152:HOH:O	2.01	0.60
30:0:2659:U:H5''	38:0:4122:HOH:O	2.02	0.60
30:0:282:C:O2'	30:0:283:U:C5'	2.48	0.60
30:0:333:G:O2'	30:0:334:G:H5'	2.01	0.60
30:0:946:C:H2'	30:0:947:U:C6	2.35	0.60
29:3:3:MET:SD	29:3:88:LEU:HD11	2.41	0.60
13:M:77:HIS:HB2	13:M:81:ARG:HH21	1.66	0.60
30:0:228:C:H2'	30:0:229:G:H5'	1.82	0.60
5:E:24:GLY:HA3	5:E:76:VAL:HB	1.82	0.60
16:P:115:SER:N	16:P:118:GLN:HE21	1.92	0.60
30:0:671:A:O2'	30:0:672:G:H2'	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:90:A:H2'	30:0:91:G:O4'	2.01	0.60
30:0:2793:A:H2'	38:0:4488:HOH:O	2.02	0.60
30:0:293:A:O2'	30:0:294:C:H5'	2.02	0.60
1:A:217:ARG:HG2	1:A:229:ALA:HB2	1.84	0.60
19:S:33:SER:O	19:S:37:VAL:HG23	2.02	0.60
23:W:6:GLN:CB	23:W:26:ILE:HD11	2.30	0.60
30:0:1183:C:H42	30:0:1184:C:H41	1.50	0.60
30:0:2769:C:H2'	30:0:2770:G:C5'	2.31	0.60
3:C:184:ARG:NH2	30:0:450:C:OP1	2.29	0.60
30:0:453:A:H5''	38:0:3254:HOH:O	2.02	0.60
26:Z:37:ARG:HB2	30:0:819:A:C4'	2.32	0.60
26:Z:53:ILE:O	26:Z:57:MET:HB2	2.02	0.60
27:1:9:GLY:HA2	30:0:1687:C:O2	2.02	0.59
1:A:35:GLY:O	1:A:36:ASP:HB3	2.02	0.59
11:K:4:LEU:HD22	11:K:116:GLU:HB3	1.83	0.59
21:U:39:ASN:HB3	38:U:3805:HOH:O	2.02	0.59
30:0:2812:A:H1'	38:0:5773:HOH:O	2.01	0.59
31:9:63:C:O2'	31:9:64:C:H5'	2.02	0.59
2:B:154:VAL:CG1	2:B:156:LYS:HG2	2.31	0.59
2:B:258:GLY:H	2:B:260:HIS:CE1	2.20	0.59
30:0:1058:A:H2'	30:0:1060:C:H5''	1.83	0.59
30:0:1819:G:H2'	30:0:1820:G:H4'	1.82	0.59
30:0:1973:A:H5'	30:0:1973:A:C8	2.35	0.59
27:1:10:LYS:HG3	38:1:2979:HOH:O	2.01	0.59
27:1:1:THR:HB	38:0:7134:HOH:O	2.02	0.59
14:N:159:TYR:CE1	31:9:50:G:H5''	2.37	0.59
30:0:2321:A:H2	30:0:2378:U:N3	1.92	0.59
30:0:2472:C:O2'	30:0:2634:G:H4'	2.02	0.59
30:0:747:G:H5'	38:0:4947:HOH:O	2.02	0.59
31:9:39:U:H1'	31:9:44:A:N6	2.15	0.59
30:0:247:A:H2'	38:0:3921:HOH:O	2.02	0.59
30:0:2498:C:O2'	30:0:2499:U:H5'	2.03	0.59
30:0:2670:G:O2'	30:0:2671:U:H5'	2.02	0.59
30:0:2689:A:H2'	30:0:2690:U:H5'	1.85	0.59
9:I:112:LEU:CD1	30:0:1162:G:H1'	2.32	0.59
3:C:174:ILE:HD11	30:0:338:C:H4'	1.85	0.59
13:M:9:ARG:HD2	30:0:380:A:OP2	2.02	0.59
30:0:468:U:H3'	38:0:7561:HOH:O	2.03	0.59
29:3:51:LYS:HB3	30:0:219:G:O2'	2.03	0.59
17:Q:11:ARG:NH2	30:0:2363:G:H4'	2.18	0.59
18:R:17:MET:HE3	18:R:19:ARG:NH2	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:6:CYS:SG	21:U:32:CYS:HB3	2.43	0.59
26:Z:64:PRO:HB2	26:Z:86:TYR:CE2	2.38	0.59
30:0:1201:C:H5''	38:0:6132:HOH:O	2.02	0.59
30:0:1904:A:H2'	30:0:1905:U:O4'	2.02	0.59
30:0:1116:U:HO2'	30:0:1118:A:H2	0.72	0.59
30:0:1377:C:H6	30:0:1377:C:H5'	1.67	0.59
30:0:214:U:H5'	38:0:6123:HOH:O	2.01	0.59
17:Q:26:PRO:O	17:Q:30:VAL:HG22	2.02	0.59
30:0:1187:U:H2'	38:0:6882:HOH:O	2.02	0.59
30:0:1634:G:H3'	38:0:3889:HOH:O	2.02	0.59
30:0:2250:G:H2'	30:0:2251:G:O4'	2.03	0.59
30:0:319:A:H4'	30:0:338:C:C4	2.38	0.59
4:D:62:ASP:HA	38:D:4233:HOH:O	2.03	0.59
15:O:25:VAL:HG12	30:0:709:G:O2'	2.03	0.59
30:0:827:A:H1'	38:0:6196:HOH:O	2.02	0.59
30:0:1118:A:C8	30:0:1118:A:C3'	2.74	0.58
30:0:1175:G:H1'	30:0:1193:A:C2'	2.31	0.58
29:3:3:MET:O	29:3:90:PHE:HA	2.03	0.58
2:B:68:THR:HG21	21:U:16:GLY:HA3	1.85	0.58
18:R:40:ALA:O	18:R:44:VAL:HG23	2.03	0.58
20:T:48:VAL:HG11	20:T:96:VAL:HG13	1.85	0.58
30:0:1603:A:H5'	30:0:1605:G:C4'	2.33	0.58
30:0:2353:A:H4'	30:0:2354:A:O5'	2.02	0.58
30:0:542:A:H5'	30:0:542:A:C8	2.29	0.58
2:B:195:ARG:HE	2:B:323:LEU:HD13	1.68	0.58
30:0:1393:A:H2'	30:0:1394:C:C6	2.38	0.58
30:0:1929:G:H1'	38:0:5153:HOH:O	2.03	0.58
30:0:482:G:H4'	30:0:508:A:N1	2.18	0.58
30:0:669:G:O2'	30:0:670:G:H5'	2.03	0.58
30:0:918:G:H5''	38:0:9099:HOH:O	2.01	0.58
31:9:54:A:C2'	31:9:55:U:H5'	2.33	0.58
2:B:256:GLN:HG2	38:B:9129:HOH:O	2.03	0.58
4:D:25:MET:HE3	4:D:37:ALA:HB1	1.84	0.58
30:0:1127:C:C5	30:0:1128:U:C4	2.91	0.58
30:0:1161:A:O5'	30:0:1161:A:H8	1.85	0.58
30:0:657:G:H2'	30:0:658:C:C6	2.38	0.58
1:A:199:HIS:CD2	1:A:201:PHE:H	2.21	0.58
12:L:30:ARG:HD2	30:0:164:G:H5''	1.85	0.58
30:0:812:A:H2'	30:0:813:C:C6	2.38	0.58
30:0:962:C:H2'	30:0:963:C:C5'	2.33	0.58
2:B:307:ARG:NH1	2:B:307:ARG:HG3	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:2:GLN:HB3	38:C:8594:HOH:O	2.04	0.58
12:L:133:VAL:HA	38:L:9035:HOH:O	2.04	0.58
13:M:68:ARG:HH21	13:M:73:ARG:HD3	1.65	0.58
30:0:2256:G:O2'	30:0:2257:G:H5'	2.04	0.58
30:0:2878:U:H2'	30:0:2879:A:O4'	2.02	0.58
30:0:2900:G:H2'	30:0:2901:C:O4'	2.03	0.58
30:0:416:G:H3'	38:0:9910:HOH:O	2.02	0.58
30:0:696:C:O2'	30:0:697:G:H5'	2.03	0.58
30:0:69:A:H5'	30:0:69:A:H8	1.69	0.58
30:0:814:G:H4'	38:0:3124:HOH:O	2.03	0.58
30:0:858:U:H5	38:0:5421:HOH:O	1.86	0.58
2:B:41:PHE:CZ	2:B:79:MET:HG3	2.39	0.58
7:G:64:ASN:N	7:G:64:ASN:HD22	1.99	0.58
12:L:80:ASP:HB2	12:L:90:ARG:O	2.03	0.58
13:M:157:ASP:HB3	13:M:160:PHE:HD1	1.68	0.58
30:0:2276:U:H1'	38:0:9608:HOH:O	2.04	0.58
30:0:244:C:H6	30:0:244:C:O5'	1.87	0.58
30:0:541:C:O2'	30:0:542:A:H5''	2.03	0.58
28:2:41:HIS:CD2	28:2:43:ARG:H	2.22	0.58
2:B:125:GLU:O	2:B:129:ARG:HG3	2.03	0.58
3:C:236:THR:HA	38:C:8660:HOH:O	2.04	0.58
25:Y:133:HIS:HD2	38:Y:8886:HOH:O	1.85	0.58
30:0:1221:G:H8	38:0:5971:HOH:O	1.87	0.58
13:M:81:ARG:HG3	30:0:161:A:OP1	2.04	0.58
30:0:1819:G:H2'	30:0:1820:G:C5'	2.34	0.58
30:0:2064:U:H5'	30:0:2652:U:H4'	1.86	0.58
31:9:1:U:C4'	31:9:3:A:OP1	2.52	0.58
1:A:109:GLU:HG2	1:A:116:GLY:H	1.69	0.58
13:M:30:GLU:O	13:M:34:GLU:HG3	2.04	0.58
29:3:60:LYS:HB2	30:0:2460:A:OP1	2.04	0.58
31:9:64:C:C2'	31:9:65:A:H5'	2.33	0.58
30:0:1205:U:C2'	30:0:1206:U:C5'	2.81	0.58
30:0:2867:G:H2'	30:0:2868:C:C6	2.39	0.58
30:0:316:A:N3	30:0:336:G:O2'	2.35	0.58
13:M:28:GLN:O	13:M:32:ARG:HG3	2.02	0.58
22:V:1:THR:HG23	22:V:2:VAL:H	1.69	0.58
23:W:64:THR:O	23:W:68:THR:HG22	2.04	0.58
30:0:1829:A:C2'	30:0:1830:C:H5'	2.34	0.57
5:E:143:GLN:NE2	30:0:2779:G:H21	2.01	0.57
18:R:71:LYS:HE2	30:0:2831:C:O3'	2.04	0.57
31:9:12:C:H5'	31:9:70:U:O4'	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:25:PRO:HG2	38:C:8522:HOH:O	2.03	0.57
26:Z:80:GLN:HG3	26:Z:81:CYS:N	2.20	0.57
30:0:1626:A:H2'	30:0:1627:G:C5'	2.35	0.57
30:0:1664:A:H8	30:0:1664:A:OP1	1.87	0.57
30:0:2499:U:H2'	30:0:2500:C:H6	1.69	0.57
30:0:553:G:H5'	38:0:3481:HOH:O	2.04	0.57
30:0:695:C:O2'	30:0:696:C:H5'	2.04	0.57
31:9:108:C:H2'	31:9:109:G:C8	2.38	0.57
30:0:1197:G:H1'	30:0:1203:G:N2	2.19	0.57
12:L:14:GLY:O	30:0:1295:G:H5''	2.04	0.57
30:0:1494:A:C4	30:0:1495:C:C5	2.93	0.57
4:D:58:VAL:HB	4:D:62:ASP:HB2	1.86	0.57
30:0:1395:C:H2'	30:0:1396:C:C6	2.39	0.57
30:0:2269:C:C2'	30:0:2270:G:H5'	2.34	0.57
30:0:544:G:C3'	30:0:545:G:H5''	2.35	0.57
30:0:558:C:H2'	30:0:559:U:H5''	1.81	0.57
29:3:69:TYR:HD1	29:3:78:HIS:O	1.87	0.57
31:9:49:G:O2'	31:9:50:G:H5'	2.05	0.57
16:P:81:LYS:O	30:0:1761:U:H5'	2.04	0.57
19:S:55:GLN:NE2	30:0:1446:U:H2'	2.19	0.57
20:T:26:THR:HA	20:T:39:ASN:HB3	1.86	0.57
30:0:2563:U:H2'	30:0:2565:C:O5'	2.04	0.57
30:0:2840:A:H3'	38:0:7638:HOH:O	2.04	0.57
30:0:318:U:H5'	30:0:339:A:C2	2.39	0.57
1:A:192:VAL:CG1	1:A:207:GLN:HB3	2.34	0.57
30:0:1919:A:H4'	38:0:4844:HOH:O	2.04	0.57
30:0:2300:A:H4'	30:0:2301:A:O5'	2.05	0.57
19:S:51:GLN:HE21	19:S:53:ASN:HD21	1.52	0.57
30:0:1165:G:O3'	30:0:1174:A:H4'	2.04	0.57
30:0:1201:C:H2'	30:0:1202:A:H5'	1.85	0.57
30:0:957:A:H8	30:0:957:A:O5'	1.88	0.57
5:E:81:GLU:HG2	5:E:134:SER:HB3	1.85	0.57
9:I:126:THR:O	9:I:130:LEU:HG	2.03	0.57
25:Y:130:ARG:HD2	38:Y:8857:HOH:O	2.04	0.57
30:0:2531:U:O2'	30:0:2532:A:H5'	2.05	0.57
3:C:101:ASP:HB2	30:0:750:A:O3'	2.05	0.57
31:9:114:G:H2'	31:9:115:C:C6	2.39	0.57
8:H:146:ALA:O	8:H:149:VAL:HG12	2.04	0.57
14:N:4:PRO:HD2	38:0:6759:HOH:O	2.04	0.57
30:0:1200:A:H3'	38:0:5738:HOH:O	2.05	0.57
30:0:1482:A:H1'	38:0:9425:HOH:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2032:U:H2'	30:0:2033:G:C5'	2.35	0.57
4:D:65:GLU:HA	38:D:6752:HOH:O	2.05	0.57
5:E:69:ILE:HA	5:E:72:MET:HE3	1.86	0.57
15:O:73:ASP:HA	15:O:92:VAL:O	2.05	0.57
20:T:53:GLY:HA3	38:T:6384:HOH:O	2.04	0.57
23:W:81:ASP:OD1	23:W:92:ASP:HB2	2.05	0.57
30:0:1697:G:H4'	38:0:9342:HOH:O	2.05	0.57
30:0:2437:A:H2'	30:0:2438:G:C8	2.40	0.57
30:0:2768:A:H2'	30:0:2769:C:O4'	2.05	0.57
30:0:2831:C:H2'	30:0:2832:C:C5'	2.35	0.57
29:3:25:VAL:HG12	38:0:9267:HOH:O	2.04	0.57
2:B:102:THR:HG23	2:B:182:VAL:HG12	1.85	0.57
23:W:137:GLN:NE2	23:W:141:HIS:HE1	1.99	0.57
30:0:1202:A:H2'	30:0:1203:G:C5'	2.34	0.56
30:0:1748:U:C5	30:0:1749:U:C5	2.92	0.56
30:0:2324:G:H1'	38:0:6095:HOH:O	2.04	0.56
30:0:589:U:H2'	30:0:590:A:H8	1.69	0.56
2:B:307:ARG:HB3	38:B:9126:HOH:O	2.04	0.56
30:0:1511:U:O2'	30:0:1512:G:H5'	2.05	0.56
30:0:2032:U:O2'	30:0:2033:G:H5''	2.04	0.56
30:0:2758:G:H2'	30:0:2759:C:C6	2.40	0.56
30:0:2824:C:O3'	30:0:2825:C:H6	1.88	0.56
2:B:229:ARG:HD2	38:0:9111:HOH:O	2.04	0.56
2:B:297:VAL:HB	38:B:9075:HOH:O	2.03	0.56
3:C:214:THR:HG23	38:C:8649:HOH:O	2.04	0.56
4:D:135:VAL:HG21	4:D:139:TYR:CD1	2.39	0.56
22:V:39:ALA:H	22:V:40:PRO:HD2	1.69	0.56
26:Z:45:VAL:HA	26:Z:48:ARG:HB3	1.87	0.56
30:0:1206:U:C5'	30:0:1206:U:H6	2.14	0.56
2:B:244:PRO:HB3	30:0:1234:U:N3	2.20	0.56
30:0:1426:C:H2'	38:0:9592:HOH:O	2.04	0.56
30:0:962:C:C2'	30:0:963:C:H5'	2.35	0.56
31:9:38:A:H2'	31:9:39:U:C6	2.41	0.56
2:B:212:GLN:HB2	2:B:257:THR:HG21	1.87	0.56
3:C:138:VAL:HG11	3:C:160:LEU:HD13	1.87	0.56
30:0:594:C:O2'	30:0:595:U:H5'	2.05	0.56
30:0:708:A:H2'	30:0:709:G:O4'	2.05	0.56
31:9:18:U:H2'	31:9:19:G:C8	2.40	0.56
3:C:88:SER:HB3	3:C:91:PRO:HB3	1.87	0.56
8:H:49:GLN:HG3	8:H:140:TYR:CE2	2.40	0.56
8:H:31:ILE:HD11	8:H:65:LEU:HD23	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:61:ALA:HB3	14:N:88:ALA:HB2	1.88	0.56
21:U:56:ARG:HD2	30:0:2890:A:N9	2.20	0.56
24:X:71:ARG:HD3	38:X:2171:HOH:O	2.04	0.56
30:0:1202:A:C2'	30:0:1203:G:H5'	2.35	0.56
30:0:1236:A:C2'	30:0:1237:U:H5'	2.36	0.56
30:0:28:G:H1'	38:0:4676:HOH:O	2.04	0.56
30:0:31:C:H4'	38:0:7417:HOH:O	2.04	0.56
30:0:1523:G:H2'	30:0:1524:U:C6	2.41	0.56
30:0:2248:C:H2'	30:0:2249:G:H8	1.70	0.56
30:0:2703:A:H2'	30:0:2704:C:C6	2.37	0.56
30:0:941:G:C5	30:0:942:U:C4	2.94	0.56
29:3:67:LEU:HD21	29:3:88:LEU:HD21	1.86	0.56
5:E:93:MET:HE1	5:E:165:GLY:N	2.21	0.56
30:0:1559:A:OP2	30:0:1559:A:H8	1.87	0.56
38:B:9106:HOH:O	30:0:2672:C:H1'	2.05	0.56
14:N:58:LEU:N	14:N:58:LEU:HD12	2.20	0.56
20:T:61:GLU:HG2	38:T:3851:HOH:O	2.06	0.56
22:V:55:ARG:O	22:V:59:ILE:HG12	2.06	0.56
26:Z:37:ARG:HD3	26:Z:37:ARG:H	1.71	0.56
30:0:1342:C:C2'	30:0:1343:C:H5'	2.35	0.56
30:0:1504:A:H5'	38:0:4410:HOH:O	2.06	0.56
30:0:711:G:C2	30:0:718:C:C2	2.93	0.56
31:9:52:A:O2'	31:9:53:G:H5'	2.06	0.56
13:M:24:GLN:HE21	13:M:27:ARG:NH1	2.03	0.56
30:0:119:A:H2'	30:0:120:A:H5''	1.87	0.56
30:0:1537:C:H1'	38:0:6573:HOH:O	2.05	0.56
30:0:1574:C:H2'	30:0:1575:C:H6	1.70	0.56
30:0:2559:C:H4'	38:0:7245:HOH:O	2.06	0.56
19:S:37:VAL:O	19:S:41:VAL:HG23	2.04	0.56
21:U:56:ARG:NH1	21:U:56:ARG:HG3	2.18	0.56
26:Z:51:ALA:O	26:Z:55:SER:HB2	2.05	0.56
30:0:1202:A:H2'	30:0:1203:G:O4'	2.06	0.56
30:0:1574:C:H2'	30:0:1575:C:C6	2.41	0.56
30:0:1622:G:C2'	30:0:1623:C:H5'	2.36	0.56
30:0:1850:U:O4'	30:0:1941:A:C2	2.59	0.56
10:J:70:PHE:CE1	30:0:2676:C:H4'	2.40	0.56
30:0:2795:C:O2'	30:0:2796:U:H5'	2.05	0.56
30:0:2897:C:O2'	30:0:2898:G:H5'	2.06	0.56
28:2:41:HIS:CE1	30:0:1439:C:H5''	2.41	0.56
19:S:51:GLN:NE2	19:S:53:ASN:HD21	2.04	0.56
30:0:1060:C:H6	30:0:1060:C:H5'	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1159:G:H21	30:0:1189:A:H8	1.53	0.56
30:0:1778:A:H2'	30:0:1779:A:H5'	1.87	0.56
30:0:2004:U:H2'	30:0:2004:U:O2	2.05	0.56
30:0:2291:A:N9	30:0:2309:C:H5'	2.21	0.56
30:0:290:C:O2'	30:0:291:C:H5'	2.05	0.56
30:0:2316:G:H4'	38:0:6075:HOH:O	2.06	0.55
30:0:2906:A:H5'	30:0:2907:C:O4'	2.07	0.55
29:3:12:PRO:HD3	38:3:9032:HOH:O	2.05	0.55
1:A:112:PRO:HD3	1:A:152:CYS:SG	2.46	0.55
8:H:59:GLN:HE21	8:H:129:ARG:NE	2.01	0.55
26:Z:34:SER:HA	30:0:797:A:H4'	1.88	0.55
30:0:1594:C:O2'	30:0:1607:A:H4'	2.07	0.55
24:X:23:HIS:HE1	30:0:2044:G:OP1	1.89	0.55
30:0:299:U:C2	30:0:300:U:C6	2.95	0.55
30:0:304:G:H1'	30:0:347:A:N6	2.21	0.55
30:0:485:A:N3	30:0:487:G:H5''	2.20	0.55
30:0:595:U:O2'	30:0:596:C:H5'	2.05	0.55
3:C:46:TYR:CE2	3:C:98:ARG:NH1	2.75	0.55
13:M:77:HIS:HB2	13:M:81:ARG:HE	1.72	0.55
14:N:49:THR:HG22	14:N:56:ASP:HB3	1.88	0.55
22:V:42:ASN:HB3	38:V:7247:HOH:O	2.06	0.55
30:0:1972:U:C2'	30:0:1973:A:H5''	2.36	0.55
30:0:2718:C:H6	30:0:2718:C:H5'	1.71	0.55
30:0:2887:G:H2'	30:0:2888:U:O4'	2.07	0.55
12:L:30:ARG:HD3	30:0:164:G:H4'	1.87	0.55
30:0:12:U:H2'	30:0:13:G:H5'	1.88	0.55
30:0:1361:C:H2'	30:0:1362:U:H6	1.72	0.55
22:V:4:HIS:HB3	38:V:6622:HOH:O	2.06	0.55
26:Z:81:CYS:O	26:Z:85:ASP:HA	2.05	0.55
30:0:136:C:H2'	30:0:137:U:O4'	2.07	0.55
30:0:1809:G:H1'	38:0:7682:HOH:O	2.06	0.55
30:0:1913:C:H2'	30:0:1914:C:C6	2.41	0.55
30:0:536:A:H3'	38:0:5040:HOH:O	2.06	0.55
30:0:699:C:C2	30:0:744:G:C2	2.95	0.55
29:3:2:GLN:HA	29:3:89:GLU:O	2.07	0.55
1:A:211:LYS:HB3	1:A:212:PRO:CD	2.32	0.55
13:M:82:ARG:H	13:M:82:ARG:HD3	1.72	0.55
23:W:38:THR:HG22	23:W:39:ASP:H	1.72	0.55
30:0:1342:C:O2'	30:0:1343:C:H5'	2.06	0.55
30:0:1762:C:H2'	30:0:1763:C:H6	1.71	0.55
30:0:2451:G:H8	38:0:5174:HOH:O	1.90	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2812:A:C2	30:0:2814:A:N6	2.71	0.55
29:3:48:ASN:O	30:0:170:U:H4'	2.07	0.55
1:A:54:PRO:HG2	1:A:160:ALA:HB3	1.89	0.55
1:A:88:ILE:HD13	1:A:100:PRO:HD3	1.88	0.55
13:M:164:THR:HG22	13:M:166:ALA:H	1.71	0.55
14:N:17:ARG:NH1	14:N:17:ARG:HB3	2.21	0.55
12:L:56:LYS:HE3	30:0:2443:C:H1'	1.89	0.55
30:0:2480:G:H3'	38:0:4182:HOH:O	2.07	0.55
30:0:876:A:N3	30:0:876:A:H2'	2.22	0.55
2:B:74:ILE:HD13	2:B:309:VAL:HG21	1.89	0.55
8:H:29:SER:HA	8:H:62:HIS:CD2	2.41	0.55
30:0:1174:A:C5	30:0:1201:C:H4'	2.41	0.55
30:0:1202:A:C8	30:0:1203:G:C8	2.95	0.55
30:0:1204:C:H2'	30:0:1205:U:O4'	2.06	0.55
30:0:1236:A:O2'	30:0:1237:U:H5'	2.07	0.55
30:0:1667:A:C8	30:0:1667:A:H5'	2.34	0.55
30:0:2240:U:O2'	30:0:2241:C:H5'	2.06	0.55
6:F:59:ILE:CD1	30:0:263:U:C2	2.90	0.55
30:0:945:U:H2'	30:0:946:C:C6	2.42	0.55
18:R:114:VAL:HA	18:R:144:GLU:O	2.06	0.55
30:0:154:C:H2'	30:0:155:C:H6	1.72	0.55
30:0:2416:G:H2'	30:0:2417:C:C6	2.42	0.55
31:9:59:C:H4'	38:9:9127:HOH:O	2.06	0.55
19:S:57:THR:HG22	19:S:58:MET:N	2.21	0.55
25:Y:182:PHE:HD2	25:Y:200:THR:O	1.89	0.55
30:0:2102:G:N3	30:0:2103:A:C6	2.75	0.55
30:0:807:A:H2'	30:0:808:A:C8	2.41	0.55
1:A:192:VAL:HG12	38:A:9012:HOH:O	2.06	0.55
2:B:41:PHE:HA	2:B:79:MET:HE2	1.89	0.55
22:V:64:GLY:O	22:V:65:ASP:HB2	2.07	0.55
30:0:1377:C:H5'	30:0:1377:C:C6	2.42	0.54
1:A:237:GLY:O	30:0:1939:U:H5''	2.06	0.54
30:0:204:A:H2'	30:0:205:U:H5'	1.89	0.54
30:0:2869:G:H2'	30:0:2870:C:H6	1.73	0.54
30:0:368:C:H2'	30:0:369:G:H5'	1.88	0.54
3:C:188:ARG:HD3	38:C:8571:HOH:O	2.07	0.54
11:K:74:VAL:CG1	11:K:113:ILE:HG12	2.37	0.54
16:P:54:LYS:HB2	30:0:1717:A:H5''	1.90	0.54
30:0:1878:G:C4'	38:0:6104:HOH:O	2.55	0.54
3:C:233:THR:HG22	3:C:234:VAL:N	2.21	0.54
26:Z:46:SER:O	26:Z:50:VAL:HB	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1183:C:N3	30:0:1184:C:N4	2.55	0.54
30:0:1334:C:O2'	30:0:1335:C:H5'	2.07	0.54
30:0:2372:A:H2'	30:0:2373:U:C6	2.43	0.54
30:0:2872:U:H2'	30:0:2873:C:H6	1.73	0.54
30:0:963:C:O2	30:0:1005:A:N1	2.39	0.54
18:R:150:PRO:CG	18:R:150:PRO:CB	2.85	0.54
30:0:1188:A:C5	30:0:1189:A:C2	2.95	0.54
30:0:1902:G:N2	30:0:1936:C:C2	2.75	0.54
30:0:561:G:H2'	30:0:562:A:H8	1.73	0.54
2:B:201:ASP:HB2	2:B:312:ARG:HD2	1.88	0.54
25:Y:169:ARG:NE	33:Y:8820:CL:CL	2.73	0.54
30:0:1969:A:O2'	30:0:1970:G:H5'	2.08	0.54
20:T:52:ARG:HD2	30:0:317:A:H5''	1.90	0.54
30:0:951:A:C2'	30:0:952:G:H5'	2.37	0.54
25:Y:216:ARG:HD2	38:Y:8874:HOH:O	2.06	0.54
18:R:80:TYR:O	30:0:2050:G:H5''	2.08	0.54
30:0:2102:G:C2	30:0:2103:A:C6	2.95	0.54
30:0:314:G:N2	30:0:317:A:C8	2.75	0.54
30:0:703:G:O2'	30:0:704:C:H5'	2.07	0.54
4:D:76:ARG:NE	31:9:44:A:O4'	2.41	0.54
1:A:199:HIS:HD2	1:A:201:PHE:H	1.55	0.54
14:N:43:VAL:CG1	14:N:118:ILE:HD11	2.38	0.54
14:N:5:ARG:HB2	14:N:5:ARG:NH1	2.21	0.54
30:0:2321:A:H2'	30:0:2321:A:N3	2.22	0.54
29:3:79:LEU:HD13	30:0:2457:U:H1'	1.88	0.54
30:0:255:A:C5	30:0:256:C:C5	2.96	0.54
27:1:42:SER:HB2	38:1:354:HOH:O	2.08	0.54
31:9:55:U:H4'	31:9:56:A:H8	1.73	0.54
1:A:211:LYS:HG2	38:0:7019:HOH:O	2.08	0.54
6:F:2:VAL:HG22	6:F:57:GLU:OE1	2.06	0.54
7:G:20:VAL:O	7:G:24:VAL:HG23	2.07	0.54
15:O:14:LEU:HG	15:O:102:ILE:HD11	1.89	0.54
16:P:115:SER:H	16:P:118:GLN:NE2	1.92	0.54
18:R:18:LEU:HB2	18:R:143:VAL:CG1	2.36	0.54
30:0:120:A:H2'	30:0:120:A:N3	2.22	0.54
30:0:535:G:C5	30:0:2063:U:C4	2.95	0.54
27:1:1:THR:HA	38:0:9360:HOH:O	2.07	0.54
12:L:18:HIS:HD2	30:0:902:G:N7	2.05	0.54
12:L:41:HIS:CD2	12:L:41:HIS:H	2.25	0.54
30:0:1130:U:H2'	30:0:1131:G:O4'	2.08	0.54
30:0:1202:A:O2'	30:0:1203:G:H5'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2326:C:H4'	30:0:2412:G:C4'	2.38	0.54
30:0:2589:U:H2'	30:0:2590:U:C6	2.42	0.54
30:0:2638:G:H5'	38:0:4923:HOH:O	2.07	0.54
1:A:176:HIS:CD2	30:0:857:A:H4'	2.43	0.54
1:A:190:ARG:HD2	30:0:1884:G:O6	2.08	0.54
10:J:39:VAL:HG13	10:J:106:GLY:O	2.08	0.54
23:W:26:ILE:HB	38:W:5420:HOH:O	2.06	0.54
14:N:4:PRO:HB2	30:0:1010:C:H4'	1.89	0.54
30:0:1163:G:H1	30:0:1184:C:N4	2.06	0.54
30:0:1176:C:H5	38:0:5727:HOH:O	1.91	0.54
30:0:1714:C:O2'	30:0:1715:C:H5'	2.08	0.54
30:0:2344:G:H8	38:0:6641:HOH:O	1.91	0.54
1:A:179:MET:HG2	1:A:186:TRP:HB2	1.89	0.54
2:B:98:THR:HG22	2:B:99:GLU:H	1.73	0.54
3:C:237:GLU:HA	38:C:8643:HOH:O	2.08	0.54
11:K:82:ARG:NH2	11:K:115:ARG:HG2	2.22	0.54
14:N:147:ILE:HD11	31:9:49:G:O3'	2.07	0.54
8:H:15:PRO:HG3	30:0:1053:G:OP1	2.08	0.53
30:0:1706:G:C6	30:0:1707:G:C6	2.96	0.53
30:0:2335:C:H2'	30:0:2336:G:C8	2.43	0.53
29:3:33:MET:SD	30:0:2450:C:H4'	2.48	0.53
3:C:135:GLU:HB3	38:C:8586:HOH:O	2.08	0.53
6:F:53:ASP:OD1	6:F:80:GLN:HB2	2.08	0.53
6:F:96:ALA:HA	38:F:3111:HOH:O	2.08	0.53
14:N:37:ARG:NH1	31:9:6:C:C5'	2.60	0.53
14:N:67:ALA:HA	14:N:71:TRP:CB	2.37	0.53
21:U:33:SER:O	21:U:37:GLU:HG3	2.08	0.53
30:0:1379:A:H1'	38:0:9690:HOH:O	2.08	0.53
30:0:1506:U:H6	30:0:1506:U:H5'	1.73	0.53
29:3:48:ASN:HB3	30:0:170:U:H5'	1.91	0.53
30:0:2347:C:H2'	30:0:2348:C:H6	1.73	0.53
30:0:2712:G:H1'	38:0:5829:HOH:O	2.08	0.53
30:0:480:C:H4'	38:0:7715:HOH:O	2.08	0.53
30:0:962:C:H5''	38:0:4907:HOH:O	2.06	0.53
21:U:51:TRP:HA	21:U:56:ARG:HE	1.72	0.53
30:0:2546:U:H4'	38:0:6160:HOH:O	2.09	0.53
30:0:311:C:H2'	30:0:312:U:C6	2.43	0.53
1:A:36:ASP:HB2	1:A:85:SER:H	1.73	0.53
3:C:180:SER:HB2	38:C:8656:HOH:O	2.06	0.53
10:J:107:ASN:HD21	10:J:109:TYR:HB2	1.74	0.53
11:K:98:VAL:HG13	11:K:102:GLU:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:88:THR:HG22	23:W:89:ASP:H	1.74	0.53
30:0:185:G:H4'	30:0:186:A:OP1	2.08	0.53
17:Q:40:HIS:HE1	30:0:949:U:O2'	1.91	0.53
31:9:117:G:H2'	31:9:118:C:C6	2.44	0.53
31:9:13:A:O2'	31:9:14:G:H5''	2.09	0.53
31:9:39:U:H3'	31:9:40:C:C5'	2.39	0.53
31:9:60:C:O2'	31:9:61:C:H5'	2.08	0.53
14:N:55:ASP:OD2	31:9:7:G:H4'	2.08	0.53
1:A:109:GLU:HG2	1:A:116:GLY:N	2.23	0.53
1:A:47:HIS:HD2	30:0:1654:U:H2'	1.72	0.53
24:X:43:VAL:HG11	24:X:82:GLU:HA	1.89	0.53
30:0:1205:U:H2'	30:0:1206:U:H5''	1.88	0.53
30:0:2265:U:H2'	30:0:2266:A:C8	2.43	0.53
31:9:64:C:H2'	31:9:65:A:H5'	1.90	0.53
13:M:164:THR:HG22	13:M:166:ALA:N	2.23	0.53
30:0:1014:A:H5''	31:9:101:G:O2'	2.09	0.53
30:0:1269:G:H2'	30:0:1270:U:C6	2.44	0.53
30:0:1523:G:C6	30:0:1524:U:O4	2.62	0.53
30:0:1553:C:H2'	30:0:1554:C:H6	1.74	0.53
30:0:2112:A:C8	38:0:6930:HOH:O	2.54	0.53
30:0:363:C:O2'	30:0:364:U:H5'	2.09	0.53
30:0:517:U:H2'	30:0:518:G:H5'	1.90	0.53
6:F:13:GLU:OE2	6:F:78:GLU:HG2	2.09	0.53
30:0:10:U:O4	30:0:532:A:OP2	2.27	0.53
13:M:68:ARG:HG3	30:0:1469:C:OP1	2.09	0.53
30:0:2371:G:H5'	38:0:5000:HOH:O	2.07	0.53
18:R:39:THR:HB	18:R:42:GLU:HG3	1.91	0.53
30:0:2578:G:C8	30:0:2578:G:H5'	2.40	0.53
30:0:734:U:O2'	30:0:736:A:N7	2.35	0.53
31:9:39:U:H3	31:9:42:C:H5''	1.72	0.53
31:9:76:G:H3'	31:9:77:A:C5'	2.23	0.53
2:B:102:THR:HG21	2:B:182:VAL:O	2.09	0.53
16:P:134:VAL:O	16:P:137:LEU:HB3	2.09	0.53
30:0:1224:G:H2'	30:0:1225:C:C6	2.43	0.53
30:0:1940:C:H4'	38:0:7336:HOH:O	2.08	0.53
30:0:312:U:C2	30:0:320:G:N2	2.77	0.53
30:0:454:U:C2	38:0:9033:HOH:O	2.53	0.53
14:N:132:ASN:O	14:N:135:VAL:HG12	2.09	0.53
30:0:10:U:C4	30:0:532:A:C8	2.97	0.53
30:0:1515:A:H2'	30:0:1516:U:C6	2.43	0.53
30:0:279:C:O2'	30:0:280:C:H5'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:821:U:H2'	30:0:822:C:H6	1.73	0.53
29:3:70:ARG:HA	29:3:77:ALA:HB2	1.91	0.53
2:B:199:TYR:HE2	2:B:268:ARG:HB2	1.74	0.53
2:B:62:ARG:HA	2:B:65:MET:CE	2.39	0.53
14:N:160:SER:CB	31:9:51:A:H5'	2.39	0.53
14:N:42:HIS:HB3	14:N:62:HIS:HE1	1.73	0.53
23:W:13:MET:HE1	23:W:18:GLN:HA	1.90	0.53
25:Y:152:LYS:HB3	25:Y:160:LYS:HG3	1.91	0.53
30:0:2438:G:H2'	30:0:2439:C:O4'	2.09	0.52
2:B:211:THR:HG23	30:0:2840:A:OP1	2.08	0.52
30:0:72:C:H5'	38:0:5876:HOH:O	2.10	0.52
30:0:853:C:H3'	38:0:4548:HOH:O	2.08	0.52
1:A:51:ARG:NH2	1:A:53:ALA:HB3	2.25	0.52
26:Z:61:HIS:HB3	38:Z:8710:HOH:O	2.07	0.52
25:Y:154:ARG:HH22	30:0:1071:G:H4'	1.74	0.52
30:0:1180:U:H2'	30:0:1181:A:O4'	2.10	0.52
30:0:1201:C:H6	38:0:5738:HOH:O	1.93	0.52
30:0:2506:A:N6	30:0:2511:A:O2'	2.42	0.52
30:0:2748:G:H5'	38:0:7534:HOH:O	2.08	0.52
27:1:2:GLY:O	27:1:6:PRO:HG2	2.09	0.52
1:A:33:GLU:O	1:A:34:ASP:HB2	2.09	0.52
3:C:94:THR:HG22	38:C:8687:HOH:O	2.09	0.52
9:I:108:HIS:H	9:I:109:PRO:HD2	1.74	0.52
24:X:30:MET:HE1	24:X:55:ASN:HA	1.91	0.52
30:0:1311:G:C2	30:0:1312:G:C8	2.96	0.52
30:0:1441:G:O2'	30:0:1442:A:H5'	2.09	0.52
30:0:2499:U:H2'	30:0:2500:C:C6	2.44	0.52
30:0:705:C:H2'	30:0:705:C:O2	2.08	0.52
30:0:960:G:H2'	30:0:960:G:N3	2.23	0.52
2:B:298:LYS:HD3	38:B:9095:HOH:O	2.08	0.52
12:L:145:LEU:O	12:L:148:GLU:HG3	2.09	0.52
14:N:32:PRO:HD2	14:N:99:GLU:O	2.10	0.52
17:Q:21:ARG:HH12	30:0:2353:A:H1'	1.74	0.52
23:W:68:THR:HG23	23:W:69:ARG:HG2	1.91	0.52
30:0:1928:C:H2'	30:0:1929:G:O4'	2.09	0.52
30:0:2295:G:N3	30:0:2361:A:C2	2.77	0.52
30:0:2864:U:O2'	30:0:2865:G:H5'	2.09	0.52
30:0:324:G:O2'	30:0:325:U:H5'	2.09	0.52
30:0:506:G:N2	30:0:509:A:C5'	2.66	0.52
2:B:18:ARG:HE	2:B:256:GLN:NE2	2.06	0.52
13:M:73:ARG:HD2	13:M:73:ARG:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:12:ARG:HD3	14:N:18:THR:OG1	2.10	0.52
30:0:107:U:H2'	30:0:108:U:H5'	1.92	0.52
30:0:1375:A:C2'	30:0:1376:G:H5'	2.39	0.52
30:0:2032:U:H2'	30:0:2033:G:H5'	1.91	0.52
30:0:2831:C:O2'	30:0:2832:C:H5'	2.10	0.52
31:9:56:A:C3'	31:9:57:A:H5''	2.39	0.52
1:A:94:LEU:N	1:A:94:LEU:HD23	2.24	0.52
4:D:58:VAL:CG1	4:D:60:GLU:HG2	2.40	0.52
5:E:80:TRP:O	5:E:134:SER:HA	2.10	0.52
20:T:28:SER:O	20:T:32:ARG:HG3	2.10	0.52
23:W:38:THR:O	23:W:42:ARG:HB2	2.09	0.52
30:0:297:U:H2'	30:0:298:C:C6	2.43	0.52
5:E:118:ILE:HG23	5:E:144:THR:HG21	1.92	0.52
21:U:6:CYS:SG	21:U:13:ILE:HD12	2.49	0.52
23:W:52:VAL:HG22	23:W:53:ALA:H	1.75	0.52
30:0:1183:C:O2	30:0:1183:C:H2'	2.08	0.52
30:0:1182:C:H1'	30:0:1192:A:H8	1.74	0.52
30:0:1269:G:H2'	30:0:1270:U:H6	1.75	0.52
30:0:1667:A:H2'	30:0:1668:U:C6	2.44	0.52
30:0:2326:C:H4'	30:0:2412:G:H4'	1.91	0.52
30:0:64:G:H2'	30:0:65:C:O4'	2.10	0.52
30:0:694:A:H2'	30:0:695:C:H5'	1.90	0.52
2:B:49:THR:HG21	2:B:331:SER:O	2.10	0.52
3:C:70:VAL:HG21	30:0:1361:C:H5'	1.91	0.52
4:D:128:LEU:HB2	38:D:6007:HOH:O	2.10	0.52
13:M:77:HIS:CE1	13:M:86:GLN:HG3	2.44	0.52
13:M:91:ILE:HG12	38:0:7539:HOH:O	2.10	0.52
20:T:9:LYS:HE3	20:T:13:ARG:CZ	2.40	0.52
30:0:101:C:H2'	30:0:102:A:C8	2.45	0.52
30:0:1845:A:O2'	30:0:1846:U:H5'	2.10	0.52
30:0:1972:U:H2'	30:0:1973:A:H5''	1.90	0.52
30:0:1992:U:H2'	30:0:1994:A:OP2	2.10	0.52
30:0:2111:G:H1'	38:0:9051:HOH:O	2.09	0.52
30:0:2420:G:C2'	30:0:2421:G:H5'	2.39	0.52
30:0:2584:G:H4'	38:0:7109:HOH:O	2.08	0.52
30:0:2689:A:C2'	30:0:2690:U:H5'	2.40	0.52
30:0:506:G:N2	30:0:508:A:H3'	2.25	0.52
30:0:952:G:N3	30:0:2302:A:H2'	2.25	0.52
13:M:46:LEU:HG	38:M:8918:HOH:O	2.08	0.52
13:M:89:THR:HA	38:M:8851:HOH:O	2.10	0.52
30:0:553:G:O4'	30:0:1325:G:H5'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:208:C:H3'	38:0:6388:HOH:O	2.10	0.52
30:0:2549:C:O2'	30:0:2550:U:H5'	2.09	0.52
29:3:51:LYS:HA	29:3:54:LYS:HD2	1.92	0.52
1:A:100:PRO:HG2	1:A:103:VAL:HG21	1.91	0.52
30:0:293:A:C4	30:0:360:A:C2	2.98	0.52
30:0:365:G:C6	30:0:366:U:C4	2.98	0.52
30:0:541:C:C2'	30:0:542:A:C5'	2.75	0.52
31:9:18:U:H2'	31:9:19:G:H8	1.74	0.52
7:G:27:ILE:HD13	7:G:71:LEU:HD23	1.92	0.52
11:K:118:ALA:HA	11:K:125:ALA:HB2	1.91	0.52
11:K:8:VAL:HG13	11:K:80:ILE:HG22	1.91	0.52
14:N:119:GLN:O	14:N:123:ILE:HG13	2.10	0.52
14:N:11:ARG:HG3	14:N:14:ARG:NH1	2.24	0.52
18:R:119:VAL:HG21	18:R:142:ASP:CG	2.31	0.52
23:W:4:LEU:HD22	23:W:52:VAL:HG21	1.91	0.52
23:W:4:LEU:O	23:W:32:CYS:HA	2.10	0.52
30:0:1189:A:H1'	30:0:1209:C:H1'	1.92	0.51
30:0:1495:C:H1'	30:0:1573:A:H1'	1.93	0.51
30:0:2526:C:O2'	30:0:2527:U:H5'	2.10	0.51
30:0:523:C:H2'	30:0:524:A:C8	2.45	0.51
30:0:960:G:N3	30:0:960:G:C2'	2.73	0.51
29:3:64:LYS:HD2	30:0:2459:G:OP2	2.11	0.51
2:B:214:PRO:HD2	38:0:9078:HOH:O	2.10	0.51
26:Z:42:TYR:HA	30:0:1829:A:H61	1.74	0.51
3:C:226:GLY:HA3	30:0:1308:A:O4'	2.10	0.51
30:0:1682:A:O2'	30:0:1683:G:H5''	2.10	0.51
29:3:42:ARG:NH1	30:0:396:U:H5'	2.25	0.51
31:9:22:G:H5'	31:9:23:U:OP1	2.10	0.51
14:N:4:PRO:CB	30:0:1010:C:H4'	2.40	0.51
17:Q:45:PRO:O	30:0:2365:G:H4'	2.10	0.51
30:0:1185:U:H5'	38:0:7461:HOH:O	2.10	0.51
30:0:1805:G:O2'	30:0:1806:G:H5'	2.10	0.51
30:0:2004:U:H4'	38:0:5299:HOH:O	2.09	0.51
30:0:2344:G:N3	30:0:2344:G:H2'	2.24	0.51
30:0:78:G:C6	30:0:79:G:C6	2.99	0.51
5:E:22:VAL:O	5:E:76:VAL:HG11	2.10	0.51
11:K:41:LYS:HA	30:0:2582:G:O3'	2.11	0.51
14:N:102:LEU:HD13	14:N:119:GLN:HB2	1.92	0.51
22:V:44:GLY:O	22:V:48:GLU:HG2	2.10	0.51
30:0:2088:C:H1'	30:0:2841:A:N1	2.25	0.51
30:0:2239:C:H2'	30:0:2240:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2269:C:O2'	30:0:2270:G:H5'	2.10	0.51
30:0:255:A:C4	30:0:256:C:C6	2.98	0.51
30:0:2769:C:C2'	30:0:2770:G:C5'	2.88	0.51
5:E:143:GLN:NE2	30:0:2780:C:H1'	2.26	0.51
30:0:282:C:C2'	30:0:283:U:H5'	2.40	0.51
13:M:81:ARG:HG2	38:M:8926:HOH:O	2.11	0.51
15:O:105:ASN:HD21	15:O:109:SER:H	1.58	0.51
30:0:1361:C:H2'	30:0:1362:U:C6	2.45	0.51
30:0:1563:G:H4'	38:0:4227:HOH:O	2.10	0.51
30:0:1788:U:C2	30:0:1805:G:N2	2.79	0.51
30:0:2269:C:H2'	30:0:2270:G:O4'	2.09	0.51
28:2:2:LYS:HG3	30:0:1486:A:C5	2.45	0.51
3:C:150:THR:HA	3:C:203:ALA:O	2.11	0.51
8:H:141:CYS:HB2	38:H:8991:HOH:O	2.10	0.51
30:0:1061:C:H1'	30:0:2283:G:O6	2.10	0.51
30:0:1304:U:H2'	30:0:1305:C:C6	2.46	0.51
30:0:2851:G:O2'	30:0:2852:A:H5'	2.11	0.51
30:0:343:C:O2'	30:0:344:C:H5'	2.11	0.51
30:0:466:A:H2'	30:0:467:G:O4'	2.10	0.51
30:0:646:G:H2'	30:0:647:U:C6	2.46	0.51
1:A:97:ALA:HA	1:A:131:HIS:NE2	2.26	0.51
22:V:12:THR:HG23	22:V:14:ALA:H	1.75	0.51
26:Z:37:ARG:HB2	30:0:819:A:H4'	1.92	0.51
30:0:1855:G:H4'	30:0:1856:C:O5'	2.10	0.51
30:0:1878:G:H1'	38:0:6104:HOH:O	2.11	0.51
30:0:2099:A:H2	38:0:3918:HOH:O	1.93	0.51
30:0:2507:G:H2'	30:0:2510:C:H42	1.75	0.51
30:0:2899:A:O2'	30:0:2900:G:H5'	2.10	0.51
30:0:42:C:H1'	38:0:4670:HOH:O	2.09	0.51
31:9:117:G:H2'	31:9:118:C:H6	1.75	0.51
31:9:3:A:OP2	31:9:25:G:N2	2.43	0.51
31:9:45:A:C5	31:9:46:C:C5	2.98	0.51
3:C:21:VAL:HG13	38:C:8606:HOH:O	2.09	0.51
13:M:24:GLN:NE2	13:M:27:ARG:NH1	2.58	0.51
13:M:86:GLN:HE22	30:0:2274:A:H1'	1.74	0.51
14:N:163:PHE:HB3	38:N:8829:HOH:O	2.11	0.51
21:U:47:ARG:HG3	38:U:4381:HOH:O	2.10	0.51
22:V:56:ILE:O	22:V:60:GLN:HG3	2.10	0.51
24:X:76:ARG:NH1	24:X:76:ARG:HG3	2.24	0.51
30:0:1020:A:H1'	38:0:7218:HOH:O	2.11	0.51
30:0:1056:U:H2'	30:0:1057:A:O4'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:124:C:H3'	38:0:7649:HOH:O	2.10	0.51
30:0:1581:A:C5	30:0:1582:C:C5	2.99	0.51
30:0:1626:A:O2'	30:0:1627:G:H5'	2.10	0.51
30:0:2354:A:H5'	30:0:2355:G:N7	2.26	0.51
30:0:2842:G:H2'	30:0:2843:A:H5'	1.92	0.51
30:0:703:G:H2'	30:0:704:C:H6	1.76	0.51
2:B:162:MET:HG3	2:B:310:ARG:HH11	1.75	0.51
5:E:133:VAL:HG12	5:E:141:VAL:HG13	1.93	0.51
5:E:137:ASP:O	5:E:141:VAL:HG23	2.10	0.51
6:F:39:SER:OG	6:F:45:ALA:HB2	2.11	0.51
10:J:70:PHE:CD1	30:0:2676:C:H4'	2.46	0.51
14:N:114:LYS:O	14:N:118:ILE:HG13	2.10	0.51
30:0:1279:U:O2	30:0:1279:U:C2'	2.58	0.51
30:0:1562:C:O2	30:0:1562:C:C2'	2.59	0.51
30:0:1701:A:H5''	30:0:1702:U:H3'	1.93	0.51
29:3:10:TYR:HD1	30:0:2408:A:HO2'	1.52	0.51
30:0:615:G:H2'	30:0:616:U:C6	2.46	0.51
30:0:920:C:H5'	30:0:921:G:C4	2.46	0.51
1:A:132:ASP:CG	1:A:133:ARG:H	2.14	0.51
1:A:223:ARG:HG3	38:A:9021:HOH:O	2.11	0.51
3:C:76:ARG:NH2	30:0:1363:G:OP1	2.44	0.51
17:Q:25:PRO:HB2	38:9:9082:HOH:O	2.11	0.51
30:0:1202:A:H2'	30:0:1203:G:H5'	1.92	0.51
30:0:1218:U:H2'	30:0:1219:U:C6	2.46	0.51
30:0:168:C:O5'	30:0:168:C:H6	1.92	0.51
30:0:1972:U:C2'	30:0:1973:A:C5'	2.89	0.51
30:0:2345:A:H3'	30:0:2346:C:C6	2.45	0.51
30:0:255:A:C5	30:0:256:C:C4	2.99	0.51
1:A:207:GLN:HA	38:A:8981:HOH:O	2.10	0.51
5:E:116:THR:HG22	5:E:151:LEU:HD22	1.92	0.51
17:Q:28:ARG:HG2	38:9:9082:HOH:O	2.11	0.51
20:T:71:VAL:HG11	20:T:90:PRO:CB	2.38	0.51
30:0:1626:A:C2'	30:0:1627:G:H5'	2.41	0.50
17:Q:11:ARG:HH22	30:0:2363:G:C5'	2.24	0.50
30:0:291:C:H2'	30:0:292:G:O4'	2.11	0.50
30:0:407:A:H5'	38:0:6009:HOH:O	2.11	0.50
6:F:34:ASN:HA	13:M:4:ALA:HB2	1.93	0.50
14:N:164:ASP:OD1	14:N:167:ASP:HA	2.11	0.50
20:T:72:ILE:HD13	20:T:93:THR:HG22	1.92	0.50
26:Z:80:GLN:CG	26:Z:81:CYS:H	2.22	0.50
30:0:1213:C:C2'	30:0:1214:G:H5'	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:151:A:H2'	30:0:152:A:O4'	2.11	0.50
30:0:2506:A:O2'	30:0:2507:G:C8	2.49	0.50
33:0:8812:CL:CL	38:0:5117:HOH:O	2.57	0.50
1:A:179:MET:HG2	1:A:186:TRP:CB	2.41	0.50
2:B:320:GLN:HE21	2:B:321:PRO:CD	2.20	0.50
2:B:72:THR:HB	38:B:9075:HOH:O	2.10	0.50
3:C:46:TYR:CE1	30:0:450:C:H4'	2.45	0.50
30:0:1589:G:H4'	38:0:6843:HOH:O	2.10	0.50
30:0:1934:A:C8	30:0:1935:C:C5	3.00	0.50
30:0:2758:G:H2'	30:0:2759:C:H6	1.76	0.50
30:0:396:U:O2'	30:0:397:A:P	2.70	0.50
2:B:238:ASN:HD22	2:B:240:GLY:N	2.10	0.50
30:0:99:A:C8	30:0:100:C:C5	2.99	0.50
30:0:1189:A:O2'	30:0:1208:C:H2'	2.12	0.50
25:Y:115:ARG:HH22	30:0:1266:U:H4'	1.72	0.50
38:C:8676:HOH:O	30:0:2100:A:H5'	2.12	0.50
30:0:2533:C:C6	30:0:2533:C:H5'	2.42	0.50
30:0:2724:U:H2'	30:0:2725:G:O4'	2.12	0.50
30:0:2896:A:N3	30:0:2896:A:H2'	2.26	0.50
30:0:549:A:O2'	30:0:550:C:H5'	2.11	0.50
3:C:47:GLY:HA2	3:C:92:PRO:HB2	1.93	0.50
5:E:81:GLU:O	5:E:172:PRO:HD3	2.12	0.50
13:M:139:PRO:HA	13:M:142:GLN:HB2	1.93	0.50
21:U:9:CYS:HB2	38:U:6796:HOH:O	2.12	0.50
23:W:5:VAL:HG22	23:W:32:CYS:HB2	1.94	0.50
1:A:162:GLY:N	26:Z:91:GLY:HA2	2.26	0.50
30:0:1118:A:H8	30:0:1119:G:H5'	1.75	0.50
28:2:8:LYS:NZ	30:0:1677:U:OP2	2.44	0.50
30:0:693:A:H2'	30:0:694:A:C8	2.46	0.50
30:0:920:C:H4'	30:0:921:G:C2	2.46	0.50
1:A:135:VAL:HG21	1:A:147:ARG:HB3	1.94	0.50
30:0:1180:U:O2'	30:0:1181:A:H5'	2.11	0.50
30:0:1183:C:N3	30:0:1184:C:C5	2.79	0.50
16:P:41:ARG:HH22	30:0:1500:U:P	2.34	0.50
30:0:1759:A:N3	30:0:1818:C:H2'	2.27	0.50
30:0:2072:G:C6	30:0:2533:C:H1'	2.47	0.50
30:0:216:A:O2'	30:0:217:C:H5'	2.12	0.50
17:Q:11:ARG:NH1	30:0:2363:G:O3'	2.45	0.50
28:2:22:PRO:HG2	28:2:25:VAL:HG23	1.94	0.50
3:C:197:SER:HB3	38:C:8583:HOH:O	2.12	0.50
13:M:184:ARG:HG3	13:M:185:PRO:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:72:ALA:HB3	38:M:8944:HOH:O	2.12	0.50
30:0:1158:G:H2'	30:0:1159:G:H5'	1.93	0.50
30:0:1395:C:H2'	30:0:1396:C:H6	1.77	0.50
30:0:1494:A:H1'	30:0:1495:C:C6	2.47	0.50
30:0:1819:G:H2'	30:0:1820:G:C4'	2.42	0.50
30:0:2416:G:H2'	30:0:2417:C:H6	1.76	0.50
30:0:2781:U:C2'	30:0:2782:G:C5'	2.89	0.50
30:0:39:G:C2	30:0:444:C:C2	3.00	0.50
30:0:559:U:C5'	30:0:559:U:H6	2.20	0.50
30:0:820:G:H5'	30:0:821:U:C5'	2.41	0.50
2:B:158:LYS:HB2	38:0:4101:HOH:O	2.11	0.50
5:E:11:VAL:HG12	5:E:12:ASP:N	2.27	0.50
6:F:36:THR:HG23	6:F:97:ALA:HB2	1.94	0.50
10:J:75:PRO:HD3	10:J:136:SER:OG	2.12	0.50
23:W:4:LEU:CD2	23:W:54:PHE:HB3	2.39	0.50
10:J:88:PRO:HD3	30:0:1104:C:H4'	1.94	0.50
30:0:1610:G:H2'	30:0:1611:G:O4'	2.12	0.50
30:0:1765:G:H1'	30:0:1780:G:N2	2.26	0.50
30:0:204:A:C2'	30:0:205:U:H5'	2.41	0.50
30:0:2354:A:H5'	30:0:2355:G:C5	2.46	0.50
30:0:2598:U:O2	30:0:2600:A:H8	1.95	0.50
30:0:441:A:C2	30:0:442:A:N6	2.80	0.50
30:0:523:C:H2'	30:0:524:A:H8	1.77	0.50
31:9:61:C:H2'	31:9:62:A:H8	1.76	0.50
10:J:82:THR:HG23	30:0:1242:A:C5'	2.17	0.50
11:K:34:VAL:HG22	11:K:47:ALA:HB2	1.94	0.50
14:N:160:SER:HB3	31:9:51:A:H5'	1.93	0.50
23:W:121:PRO:CA	23:W:153:MET:HG2	2.42	0.50
30:0:1160:G:H5'	30:0:1161:A:H5'	0.83	0.50
30:0:1226:G:H5'	38:0:4526:HOH:O	2.11	0.50
30:0:1398:G:H2'	30:0:1399:A:C8	2.47	0.50
30:0:1947:G:H2'	30:0:1948:G:H8	1.77	0.50
30:0:2269:C:H2'	30:0:2270:G:C5'	2.42	0.50
30:0:2330:U:H4'	30:0:2331:C:OP1	2.11	0.50
27:1:28:HIS:HE1	30:0:776:A:OP1	1.95	0.50
30:0:932:U:H2'	30:0:933:C:C6	2.47	0.50
31:9:58:G:C8	31:9:59:C:C5	3.00	0.50
10:J:22:VAL:O	10:J:26:VAL:HG23	2.12	0.50
10:J:76:ASP:HA	38:J:8863:HOH:O	2.11	0.50
14:N:169:PRO:O	14:N:172:PHE:HB3	2.12	0.50
30:0:1365:C:H4'	38:0:4606:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1541:G:O2'	30:0:1542:G:H5'	2.11	0.49
30:0:1791:U:O2'	30:0:1792:C:H5'	2.12	0.49
30:0:2502:C:O2'	30:0:2503:A:H5'	2.12	0.49
30:0:299:U:N3	30:0:300:U:C5	2.80	0.49
30:0:88:G:H5'	30:0:88:G:H8	1.76	0.49
27:1:28:HIS:HD2	27:1:30:LYS:H	1.58	0.49
30:0:1188:A:C6	30:0:1189:A:C6	3.00	0.49
13:M:94:ARG:HD2	30:0:158:A:OP2	2.11	0.49
30:0:1964:U:O2	30:0:1964:U:H2'	2.10	0.49
30:0:249:G:N2	30:0:250:C:C2	2.80	0.49
30:0:2705:U:H2'	30:0:2706:A:H8	1.73	0.49
30:0:951:A:O2'	30:0:952:G:H5'	2.12	0.49
31:9:114:G:H2'	31:9:115:C:H6	1.76	0.49
1:A:153:ARG:HH11	1:A:153:ARG:HB2	1.77	0.49
6:F:48:VAL:HG23	6:F:74:PHE:CB	2.41	0.49
15:O:24:ALA:HB3	30:0:710:G:OP1	2.12	0.49
18:R:117:HIS:HD2	30:0:20:G:H21	1.61	0.49
30:0:2002:C:H2'	30:0:2003:U:H5'	1.94	0.49
30:0:699:C:O2'	30:0:744:G:H1'	2.12	0.49
30:0:876:A:N3	30:0:876:A:C2'	2.75	0.49
31:9:20:G:H3'	38:9:9055:HOH:O	2.12	0.49
4:D:76:ARG:NH1	31:9:42:C:O2	2.45	0.49
31:9:49:G:H2'	31:9:50:G:O4'	2.12	0.49
2:B:24:PRO:HG3	2:B:204:GLY:HA2	1.94	0.49
5:E:15:GLN:HG2	5:E:16:ASP:N	2.28	0.49
11:K:8:VAL:HG12	11:K:9:THR:N	2.26	0.49
18:R:111:ILE:HG23	18:R:145:LEU:HD11	1.94	0.49
30:0:1191:A:H2'	30:0:1193:A:H5'	1.95	0.49
30:0:1453:G:H2'	30:0:1454:U:O4'	2.13	0.49
30:0:2316:G:H8	38:0:5642:HOH:O	1.95	0.49
30:0:816:G:H5'	30:0:1598:A:H4'	1.94	0.49
23:W:11:VAL:HG11	30:0:1086:A:C6	2.48	0.49
23:W:90:TYR:N	23:W:90:TYR:CD1	2.80	0.49
24:X:21:PRO:HG2	24:X:24:LYS:HD3	1.94	0.49
26:Z:38:PHE:HB3	26:Z:42:TYR:HD1	1.78	0.49
30:0:1206:U:C6	30:0:1206:U:H5'	2.31	0.49
30:0:1526:A:H4'	30:0:1527:A:H5'	1.95	0.49
2:B:212:GLN:HA	30:0:1733:A:H4'	1.94	0.49
30:0:1942:A:O2'	30:0:1943:C:H5'	2.11	0.49
30:0:2612:A:H4'	38:0:3666:HOH:O	2.13	0.49
30:0:445:U:O2'	30:0:446:G:H5'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:514:G:OP1	30:0:514:G:H2'	2.12	0.49
29:3:38:ARG:CB	29:3:42:ARG:HH12	2.25	0.49
6:F:50:VAL:HG13	6:F:60:VAL:HG11	1.95	0.49
11:K:22:ASP:HB2	38:K:5264:HOH:O	2.13	0.49
14:N:18:THR:HG21	38:9:9099:HOH:O	2.12	0.49
15:O:25:VAL:HG23	15:O:26:TRP:N	2.27	0.49
23:W:119:HIS:HE1	38:0:9557:HOH:O	1.96	0.49
30:0:1159:G:H2'	30:0:1160:G:O4'	2.11	0.49
30:0:1375:A:H2'	30:0:1376:G:H5'	1.95	0.49
30:0:314:G:C2	30:0:317:A:C8	3.01	0.49
30:0:352:A:H2'	30:0:353:G:C8	2.48	0.49
31:9:7:G:H5'	38:9:9099:HOH:O	2.11	0.49
2:B:199:TYR:CE2	2:B:268:ARG:HB2	2.48	0.49
2:B:28:SER:HB2	30:0:2807:U:OP2	2.13	0.49
11:K:98:VAL:HG11	11:K:102:GLU:HA	1.94	0.49
24:X:43:VAL:HG12	24:X:44:ASP:N	2.27	0.49
8:H:19:ARG:HH12	30:0:1008:C:H5''	1.78	0.49
30:0:128:A:C8	30:0:128:A:H3'	2.47	0.49
29:3:48:ASN:ND2	30:0:169:A:H1'	2.27	0.49
30:0:2135:A:O4'	30:0:2243:C:N4	2.45	0.49
30:0:2265:U:H2'	30:0:2266:A:H8	1.77	0.49
30:0:2820:A:H2'	30:0:2821:C:C6	2.46	0.49
27:1:16:HIS:HD2	30:0:470:U:O2'	1.95	0.49
14:N:77:ASN:OD1	14:N:79:PRO:HD2	2.13	0.49
30:0:1181:A:C2	30:0:1192:A:C8	3.00	0.49
30:0:1209:C:H2'	30:0:1210:G:C8	2.42	0.49
30:0:1572:A:H3'	38:0:4098:HOH:O	2.13	0.49
30:0:1765:G:O2'	30:0:1766:U:H5'	2.12	0.49
30:0:1976:G:H1'	30:0:2005:G:N2	2.28	0.49
30:0:2237:G:H1'	30:0:2238:A:H8	1.77	0.49
30:0:2707:C:H2'	30:0:2707:C:O2	2.13	0.49
30:0:2805:A:C8	30:0:2806:C:C5	3.01	0.49
30:0:661:G:C5	30:0:686:A:C2	3.01	0.49
31:9:52:A:H2'	31:9:53:G:H8	1.76	0.49
7:G:16:LYS:O	7:G:20:VAL:HG23	2.13	0.49
21:U:9:CYS:HA	21:U:52:THR:HG22	1.94	0.49
30:0:1521:C:H2'	30:0:1522:A:H8	1.78	0.49
38:L:9036:HOH:O	30:0:196:G:H2'	2.12	0.49
30:0:2254:G:H1'	38:0:5527:HOH:O	2.12	0.49
30:0:2359:G:H3'	38:0:5674:HOH:O	2.13	0.49
30:0:2635:A:C2'	30:0:2636:C:H5'	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:264:G:H1'	30:0:265:U:H5	1.78	0.49
13:M:133:LEU:O	13:M:134:ILE:HD13	2.13	0.49
30:0:1118:A:C8	30:0:1119:G:H5''	2.47	0.49
30:0:1118:A:N6	30:0:1244:U:H3	1.95	0.49
30:0:1566:C:O2'	30:0:1567:G:H5'	2.12	0.49
30:0:1586:G:O2'	30:0:1587:U:H5'	2.13	0.49
30:0:1913:C:H2'	30:0:1914:C:H6	1.76	0.49
30:0:2289:G:O2'	30:0:2291:A:N6	2.45	0.49
30:0:2911:C:H2'	30:0:2912:C:C6	2.48	0.49
30:0:526:U:H2'	30:0:527:U:C6	2.48	0.49
30:0:727:G:H3'	30:0:728:C:H6	1.78	0.49
29:3:68:LYS:HE3	30:0:2435:U:O2'	2.12	0.49
10:J:19:MET:HE1	10:J:132:LEU:HD21	1.93	0.49
14:N:132:ASN:HD22	30:0:2413:A:C4'	2.25	0.49
19:S:49:VAL:HG13	19:S:66:VAL:HG13	1.95	0.49
26:Z:64:PRO:HB2	26:Z:86:TYR:HE2	1.78	0.49
30:0:10:U:O4	30:0:532:A:H8	1.96	0.48
30:0:146:U:O2'	30:0:147:G:H5'	2.12	0.48
30:0:2269:C:H2'	30:0:2270:G:H5'	1.95	0.48
17:Q:11:ARG:HH22	30:0:2363:G:H5''	1.78	0.48
30:0:59:A:H5'	38:0:4330:HOH:O	2.13	0.48
2:B:7:ARG:HG2	2:B:7:ARG:HH11	1.77	0.48
4:D:23:VAL:HG12	4:D:130:VAL:HG22	1.95	0.48
6:F:91:VAL:HG12	6:F:92:GLY:N	2.22	0.48
25:Y:174:VAL:HG23	25:Y:177:LYS:HD2	1.94	0.48
30:0:1447:U:H3'	30:0:1506:U:O2	2.12	0.48
30:0:1641:A:O2'	30:0:1642:A:H5'	2.13	0.48
30:0:2061:C:C2'	30:0:2062:A:H5'	2.43	0.48
30:0:2073:G:C6	30:0:2489:G:H4'	2.48	0.48
30:0:2710:U:O2'	30:0:2711:U:H5'	2.13	0.48
29:3:5:ARG:O	29:3:21:GLU:HA	2.12	0.48
2:B:71:VAL:HG21	2:B:296:LEU:HB3	1.95	0.48
3:C:236:THR:H	3:C:239:ALA:HB3	1.78	0.48
16:P:64:GLU:HG2	38:P:169:HOH:O	2.13	0.48
21:U:50:GLU:O	21:U:56:ARG:HG2	2.13	0.48
25:Y:235:GLU:CD	25:Y:235:GLU:N	2.65	0.48
30:0:1461:U:H2'	30:0:1462:C:C6	2.48	0.48
30:0:1566:C:H2'	30:0:1567:G:H8	1.78	0.48
30:0:1922:A:N1	30:0:2449:G:O2'	2.46	0.48
30:0:2509:A:H2'	30:0:2510:C:O4'	2.13	0.48
30:0:2512:U:H4'	30:0:2514:U:O4	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2616:G:H1'	38:0:9428:HOH:O	2.12	0.48
30:0:305:A:C5	30:0:329:A:C2	3.02	0.48
30:0:311:C:H2'	30:0:312:U:H6	1.77	0.48
30:0:344:C:H2'	30:0:345:G:O4'	2.12	0.48
30:0:598:C:H2'	30:0:599:G:H8	1.77	0.48
30:0:682:A:H2'	30:0:683:G:O4'	2.13	0.48
1:A:212:PRO:HB2	38:A:8985:HOH:O	2.13	0.48
2:B:49:THR:HG22	2:B:50:HIS:H	1.79	0.48
11:K:74:VAL:HG21	11:K:96:VAL:HG23	1.95	0.48
13:M:164:THR:CG2	13:M:165:GLY:N	2.75	0.48
13:M:70:GLY:HA3	13:M:73:ARG:CZ	2.42	0.48
20:T:8:ARG:NH1	30:0:31:C:OP2	2.46	0.48
25:Y:145:LYS:O	25:Y:147:ARG:HG2	2.13	0.48
30:0:1706:G:C6	30:0:1707:G:N1	2.81	0.48
30:0:2271:G:N3	30:0:2271:G:H2'	2.27	0.48
30:0:370:G:O2'	30:0:371:U:H5'	2.14	0.48
12:L:143:THR:HG22	12:L:144:ASP:N	2.28	0.48
30:0:1188:A:H5'	38:0:7418:HOH:O	2.12	0.48
30:0:1626:A:H2'	30:0:1627:G:H5'	1.96	0.48
30:0:1835:U:H3'	38:0:5569:HOH:O	2.12	0.48
30:0:2511:A:H2'	30:0:2512:U:C6	2.47	0.48
30:0:2626:C:H2'	30:0:2627:G:C8	2.49	0.48
30:0:2651:C:H2'	30:0:2652:U:O4'	2.13	0.48
30:0:2673:U:C4	30:0:2674:G:C6	3.01	0.48
30:0:645:U:O2	30:0:761:A:H2	1.97	0.48
30:0:809:G:H2'	30:0:810:G:H8	1.78	0.48
30:0:816:G:C6	30:0:817:G:N1	2.82	0.48
29:3:64:LYS:HA	29:3:84:ARG:CA	2.38	0.48
13:M:48:LYS:HE3	13:M:52:GLN:HE21	1.78	0.48
18:R:18:LEU:HG	18:R:91:LEU:HD13	1.95	0.48
26:Z:37:ARG:HB2	30:0:819:A:O4'	2.14	0.48
30:0:1187:U:O2'	30:0:1188:A:C8	2.64	0.48
30:0:1684:A:O2'	30:0:1685:A:H5''	2.14	0.48
30:0:1905:U:H2'	30:0:1906:C:H6	1.79	0.48
30:0:2713:G:O2'	30:0:2714:U:H5'	2.13	0.48
30:0:421:C:H4'	30:0:1919:A:C6	2.49	0.48
29:3:64:LYS:HD3	29:3:82:GLY:O	2.13	0.48
11:K:130:MET:SD	21:U:25:ASP:O	2.71	0.48
13:M:74:LYS:O	13:M:88:VAL:HG13	2.13	0.48
14:N:48:VAL:CG1	14:N:55:ASP:HB3	2.43	0.48
20:T:48:VAL:HG12	20:T:49:GLU:N	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:6:GLN:HB2	23:W:26:ILE:CD1	2.36	0.48
26:Z:74:GLN:HG2	26:Z:80:GLN:HB2	1.95	0.48
30:0:1343:C:H2'	30:0:1344:G:O5'	2.12	0.48
30:0:154:C:H2'	30:0:155:C:C6	2.49	0.48
30:0:2608:C:H2'	38:0:3561:HOH:O	2.13	0.48
30:0:696:C:HO2'	30:0:697:G:H5'	1.78	0.48
1:A:171:LYS:HB2	30:0:820:G:C5	2.49	0.48
31:9:23:U:H2'	31:9:23:U:O2	2.14	0.48
2:B:74:ILE:HG13	38:B:9075:HOH:O	2.13	0.48
5:E:101:GLU:HB2	5:E:116:THR:O	2.13	0.48
12:L:65:ASP:HA	12:L:109:LEU:O	2.14	0.48
18:R:33:ARG:NH1	38:R:8944:HOH:O	2.47	0.48
25:Y:170:SER:OG	25:Y:175:ARG:HG3	2.14	0.48
1:A:72:GLU:HG2	26:Z:100:GLY:CA	2.40	0.48
30:0:1168:C:H5	38:0:7488:HOH:O	1.96	0.48
30:0:1422:U:H2'	30:0:1423:C:C6	2.49	0.48
30:0:1632:A:C3'	30:0:1633:C:H5'	2.44	0.48
30:0:228:C:C2'	30:0:229:G:H5'	2.44	0.48
30:0:2524:G:N2	30:0:2526:C:N4	2.57	0.48
30:0:284:C:H4'	30:0:285:A:H8	1.79	0.48
30:0:533:U:H3'	38:0:3736:HOH:O	2.13	0.48
30:0:589:U:H2'	30:0:590:A:C8	2.47	0.48
17:Q:27:GLN:HE21	31:9:8:G:H5''	1.75	0.48
2:B:84:LEU:HD23	2:B:142:LEU:HD23	1.96	0.48
10:J:75:PRO:HB3	10:J:132:LEU:HB3	1.96	0.48
10:J:135:ILE:O	10:J:139:LEU:HG	2.14	0.48
13:M:73:ARG:HH22	30:0:2263:G:H5''	1.77	0.48
23:W:107:LEU:O	23:W:112:LEU:HB2	2.13	0.48
38:2:3526:HOH:O	30:0:1413:A:H5''	2.14	0.48
30:0:1795:G:H2'	30:0:1796:A:O4'	2.13	0.48
30:0:1965:C:H2'	30:0:1966:U:C6	2.49	0.48
30:0:2614:C:O2'	30:0:2615:U:H5'	2.13	0.48
30:0:581:G:O2'	30:0:582:U:H5'	2.13	0.48
31:9:38:A:H2	31:9:43:G:H5''	1.77	0.48
30:0:113:A:C8	30:0:114:A:C8	3.02	0.48
30:0:138:U:OP2	30:0:139:C:C5	2.67	0.48
30:0:1592:G:C4	30:0:1593:C:C5	3.02	0.48
30:0:1706:G:C5	30:0:1707:G:C6	3.02	0.48
30:0:1790:C:H2'	30:0:1791:U:H6	1.79	0.48
30:0:2296:C:H2'	30:0:2297:U:H6	1.79	0.48
4:D:52:THR:HG21	30:0:2346:C:O2'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2842:G:C2'	30:0:2843:A:H5'	2.44	0.48
3:C:206:ASN:HB2	30:0:329:A:OP2	2.13	0.48
30:0:542:A:H2'	30:0:543:G:O4'	2.14	0.48
31:9:5:G:C2'	31:9:6:C:H5'	2.43	0.48
1:A:36:ASP:HA	1:A:83:GLY:HA3	1.96	0.48
2:B:36:PRO:CA	2:B:168:GLY:HA3	2.40	0.48
2:B:24:PRO:CG	2:B:204:GLY:HA2	2.44	0.48
13:M:40:ILE:HG21	13:M:64:ARG:NH2	2.29	0.48
14:N:139:TRP:HA	14:N:139:TRP:CE3	2.49	0.48
20:T:38:ARG:NH1	38:0:6667:HOH:O	2.47	0.48
23:W:134:GLU:OE2	31:9:97:U:H1'	2.14	0.48
24:X:85:VAL:HG12	24:X:86:GLU:N	2.29	0.48
30:0:1735:C:H2'	30:0:1736:A:C8	2.49	0.47
30:0:1878:G:C1'	38:0:6104:HOH:O	2.62	0.47
30:0:2074:A:H2'	38:0:3520:HOH:O	2.13	0.47
30:0:764:C:H2'	30:0:765:G:O4'	2.14	0.47
1:A:36:ASP:O	1:A:38:ILE:N	2.44	0.47
1:A:42:VAL:HG21	1:A:74:VAL:CG1	2.44	0.47
5:E:154:ILE:HD11	5:E:157:LYS:HB2	1.96	0.47
11:K:37:TYR:HB3	38:K:7169:HOH:O	2.14	0.47
14:N:22:GLN:O	14:N:26:LEU:HB2	2.14	0.47
18:R:39:THR:HB	18:R:42:GLU:CG	2.44	0.47
23:W:11:VAL:O	23:W:12:ASN:HB2	2.14	0.47
16:P:102:ARG:NH2	30:0:1596:U:C5	2.82	0.47
30:0:2864:U:C2'	30:0:2865:G:H5'	2.44	0.47
30:0:45:A:N6	30:0:147:G:C4	2.83	0.47
30:0:24:G:H22	30:0:518:G:H1'	1.79	0.47
30:0:844:A:C6	30:0:882:A:C6	3.02	0.47
29:3:38:ARG:HB3	29:3:42:ARG:HH12	1.79	0.47
10:J:107:ASN:ND2	10:J:109:TYR:H	2.11	0.47
30:0:1205:U:C2'	30:0:1206:U:H5''	2.44	0.47
30:0:2241:C:O2'	30:0:2242:U:H5'	2.14	0.47
30:0:1787:C:H4'	30:0:2883:A:O4'	2.14	0.47
30:0:2890:A:H2'	30:0:2890:A:N3	2.29	0.47
30:0:301:C:H2'	30:0:302:A:H8	1.79	0.47
30:0:703:G:H2'	30:0:704:C:C6	2.49	0.47
28:2:29:THR:HG22	30:0:86:A:O4'	2.14	0.47
27:1:20:ARG:HG2	30:0:111:C:O2'	2.14	0.47
31:9:52:A:H2'	31:9:53:G:O4'	2.13	0.47
2:B:41:PHE:HB3	2:B:190:MET:CE	2.44	0.47
2:B:54:VAL:HB	38:B:9084:HOH:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:58:VAL:HG12	4:D:60:GLU:HG2	1.96	0.47
25:Y:187:VAL:HG23	25:Y:192:ASP:HB2	1.96	0.47
26:Z:65:ASN:HD22	26:Z:84:CYS:HB2	1.80	0.47
30:0:1561:U:H5'	38:0:7421:HOH:O	2.13	0.47
30:0:1603:A:H5''	30:0:1604:G:H3'	1.96	0.47
30:0:2032:U:C2'	30:0:2033:G:C5'	2.93	0.47
30:0:2784:A:H8	30:0:2784:A:O5'	1.98	0.47
30:0:95:A:H5''	30:0:97:G:O4'	2.14	0.47
29:3:10:TYR:HE2	30:0:2382:A:H1'	1.80	0.47
31:9:108:C:H2'	31:9:109:G:H8	1.79	0.47
2:B:305:ASP:O	2:B:306:LYS:HB2	2.15	0.47
3:C:153:VAL:O	3:C:157:LEU:HG	2.15	0.47
16:P:55:LYS:HG3	16:P:56:GLY:N	2.29	0.47
20:T:48:VAL:HG13	20:T:97:ARG:O	2.14	0.47
25:Y:106:THR:HG23	25:Y:107:PRO:HD2	1.96	0.47
30:0:1217:G:C2	30:0:1218:U:C2	3.03	0.47
30:0:1942:A:H3'	38:0:7336:HOH:O	2.14	0.47
30:0:2336:G:C2'	38:0:6280:HOH:O	2.60	0.47
30:0:2697:A:H2'	30:0:2698:G:O4'	2.15	0.47
30:0:2908:A:O5'	30:0:2908:A:H8	1.97	0.47
30:0:292:G:H2'	30:0:358:G:N2	2.30	0.47
30:0:599:G:H2'	30:0:600:G:H8	1.79	0.47
30:0:810:G:H2'	30:0:811:C:C6	2.49	0.47
1:A:45:ILE:HG22	26:Z:78:ILE:HG12	1.96	0.47
10:J:54:VAL:HG11	10:J:138:THR:HG21	1.95	0.47
13:M:75:ARG:HB2	38:M:8905:HOH:O	2.14	0.47
20:T:64:ASN:HB3	20:T:73:HIS:HB2	1.96	0.47
23:W:120:PRO:HG2	30:0:1095:U:O2	2.14	0.47
30:0:1181:A:H2'	30:0:1182:C:C5'	2.45	0.47
30:0:1318:A:H4'	30:0:1343:C:H4'	1.96	0.47
30:0:1359:U:C5	30:0:2101:A:C8	3.03	0.47
30:0:2510:C:H5'	30:0:2511:A:OP2	2.13	0.47
30:0:371:U:H2'	30:0:372:A:C8	2.49	0.47
30:0:960:G:H3'	30:0:960:G:N3	2.30	0.47
29:3:46:ILE:HG12	38:0:3138:HOH:O	2.14	0.47
29:3:79:LEU:HB2	38:0:6581:HOH:O	2.14	0.47
1:A:186:TRP:CG	1:A:187:PRO:HA	2.50	0.47
2:B:5:ARG:NH2	30:0:2548:C:OP2	2.47	0.47
5:E:69:ILE:HA	5:E:72:MET:CE	2.44	0.47
6:F:50:VAL:HG21	6:F:63:ILE:HG21	1.97	0.47
10:J:131:THR:HG22	10:J:133:GLY:H	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:65:VAL:HG21	13:M:105:ALA:HB2	1.97	0.47
13:M:91:ILE:HD11	38:M:8830:HOH:O	2.15	0.47
23:W:119:HIS:HD2	23:W:120:PRO:O	1.97	0.47
30:0:1042:U:O2'	30:0:1043:C:H5'	2.15	0.47
30:0:1523:G:C6	30:0:1524:U:C4	3.03	0.47
30:0:2686:C:C2	30:0:2709:G:N2	2.82	0.47
30:0:484:A:N1	30:0:506:G:H4'	2.30	0.47
30:0:512:G:O3'	30:0:513:A:H8	1.97	0.47
30:0:677:C:O2'	30:0:678:G:H5'	2.14	0.47
2:B:98:THR:HG23	30:0:2820:A:OP1	2.15	0.47
18:R:68:HIS:CD2	18:R:76:ASP:HB2	2.50	0.47
23:W:121:PRO:HA	23:W:153:MET:HG2	1.96	0.47
23:W:88:THR:HB	38:W:6679:HOH:O	2.14	0.47
30:0:1173:A:H4'	30:0:1174:A:C8	2.49	0.47
30:0:1769:C:O2'	30:0:1770:U:H5'	2.15	0.47
30:0:1790:C:H2'	30:0:1791:U:C6	2.50	0.47
30:0:1864:C:H2'	30:0:1865:A:O4'	2.14	0.47
30:0:1882:C:H2'	30:0:1883:U:H6	1.80	0.47
30:0:2598:U:O2	30:0:2600:A:C8	2.68	0.47
30:0:282:C:H1'	30:0:368:C:H41	1.78	0.47
29:3:50:GLY:HA3	38:0:9164:HOH:O	2.14	0.47
30:0:1183:C:C2	30:0:1184:C:C5	3.03	0.47
30:0:1187:U:O2'	30:0:1189:A:H2	1.98	0.47
30:0:1377:C:C5'	30:0:1377:C:H6	2.28	0.47
30:0:2134:G:N2	30:0:2242:U:C2	2.83	0.47
30:0:2253:G:H2'	30:0:2254:G:H8	1.80	0.47
30:0:2329:C:O2'	30:0:2330:U:H5'	2.14	0.47
30:0:2383:G:C6	30:0:2384:U:C4	3.03	0.47
30:0:2752:C:O2'	30:0:2753:G:H5'	2.15	0.47
30:0:304:G:H8	30:0:304:G:O5'	1.98	0.47
29:3:24:LYS:HE3	29:3:90:PHE:CE1	2.50	0.47
1:A:121:ALA:O	1:A:124:VAL:HG22	2.14	0.47
3:C:127:ARG:HD3	3:C:129:HIS:HE1	1.80	0.47
17:Q:14:LEU:HD21	17:Q:43:ILE:HD12	1.97	0.47
20:T:24:ARG:HH21	20:T:39:ASN:HD22	1.63	0.47
22:V:39:ALA:N	22:V:40:PRO:CD	2.77	0.47
23:W:29:VAL:O	23:W:30:ASN:HB2	2.13	0.47
30:0:1966:U:O5'	30:0:1966:U:H6	1.98	0.47
30:0:2096:A:H2'	30:0:2539:U:O4'	2.14	0.47
30:0:2769:C:H2'	30:0:2770:G:O4'	2.14	0.47
30:0:371:U:H2'	30:0:372:A:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:36:C:C2	30:0:447:A:C2	3.03	0.47
30:0:447:A:O2'	30:0:448:G:H5'	2.15	0.47
25:Y:137:LYS:HD2	30:0:521:A:H5''	1.97	0.47
8:H:91:ARG:HB2	30:0:1003:U:OP1	2.15	0.47
25:Y:99:ALA:HB2	25:Y:233:TYR:CZ	2.50	0.47
30:0:1878:G:O2'	30:0:1879:U:C5	2.66	0.47
30:0:2604:A:H5'	38:0:5775:HOH:O	2.14	0.47
23:W:154:ARG:NH1	30:0:588:G:O6	2.47	0.47
30:0:613:C:H2'	30:0:614:U:C6	2.46	0.47
30:0:805:G:N2	30:0:807:A:H3'	2.30	0.47
3:C:103:ASN:ND2	30:0:663:C:H5''	2.29	0.47
13:M:111:ASN:HB2	38:M:8849:HOH:O	2.14	0.47
17:Q:11:ARG:CZ	30:0:2363:G:H4'	2.44	0.47
18:R:82:GLU:HG3	18:R:83:LYS:N	2.29	0.47
30:0:1350:U:H4'	38:0:5115:HOH:O	2.15	0.46
30:0:1477:C:C5'	30:0:1868:G:H5''	2.45	0.46
30:0:1477:C:H4'	30:0:1868:G:OP1	2.15	0.46
30:0:1969:A:C2'	30:0:1970:G:H5'	2.45	0.46
3:C:127:ARG:CZ	3:C:225:PRO:HG2	2.44	0.46
5:E:93:MET:HE1	5:E:165:GLY:H	1.79	0.46
5:E:7:ILE:HG23	5:E:45:ASP:O	2.15	0.46
30:0:1116:U:C2	30:0:1246:A:N6	2.83	0.46
30:0:1163:G:N1	30:0:1184:C:N4	2.64	0.46
30:0:1634:G:H2'	38:0:3889:HOH:O	2.15	0.46
30:0:1701:A:H4'	30:0:1702:U:C5'	2.37	0.46
30:0:1838:U:O2'	30:0:2644:C:H5'	2.15	0.46
30:0:1949:G:H22	30:0:1964:U:H1'	1.79	0.46
30:0:629:A:C2	30:0:2074:A:C2	3.03	0.46
30:0:735:C:H3'	30:0:736:A:C8	2.50	0.46
30:0:877:G:C5'	30:0:878:G:OP1	2.62	0.46
30:0:921:G:H4'	30:0:924:G:N1	2.30	0.46
29:3:69:TYR:O	29:3:77:ALA:HA	2.15	0.46
2:B:79:MET:HE1	38:B:9096:HOH:O	2.15	0.46
11:K:34:VAL:HB	38:K:7169:HOH:O	2.15	0.46
16:P:120:ARG:HD2	30:0:1594:C:OP2	2.14	0.46
30:0:1197:G:H1'	30:0:1203:G:C2	2.51	0.46
30:0:130:C:O2'	30:0:131:A:N7	2.46	0.46
30:0:1545:C:H1'	30:0:1641:A:N6	2.29	0.46
30:0:1617:C:C5	30:0:1643:C:H4'	2.50	0.46
30:0:1797:A:O3'	30:0:1798:C:C6	2.69	0.46
30:0:1928:C:C2'	30:0:1929:G:H5'	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2102:G:C2	30:0:2103:A:N6	2.83	0.46
30:0:2256:G:H2'	30:0:2257:G:C5'	2.46	0.46
30:0:2347:C:H2'	30:0:2348:C:C6	2.50	0.46
30:0:2526:C:H5'	30:0:2526:C:C6	2.50	0.46
30:0:530:C:H4'	30:0:612:U:H4'	1.97	0.46
30:0:790:A:H2'	30:0:791:A:O4'	2.16	0.46
3:C:129:HIS:HE1	3:C:231:ARG:HA	1.77	0.46
7:G:63:ARG:N	38:G:2569:HOH:O	2.48	0.46
16:P:87:ARG:HG2	38:P:186:HOH:O	2.15	0.46
18:R:99:ALA:HB1	18:R:109:MET:CE	2.37	0.46
20:T:32:ARG:NH1	20:T:38:ARG:HH12	2.13	0.46
22:V:27:LEU:HA	22:V:49:LEU:HD13	1.98	0.46
30:0:2297:U:H1'	38:0:5172:HOH:O	2.16	0.46
30:0:238:C:H4'	30:0:287:C:OP1	2.16	0.46
30:0:2438:G:H2'	30:0:2439:C:C6	2.50	0.46
30:0:2445:U:H2'	30:0:2446:G:C8	2.51	0.46
30:0:254:C:O2	30:0:254:C:H2'	2.14	0.46
30:0:834:G:C4'	30:0:835:U:OP2	2.61	0.46
27:1:25:LYS:O	27:1:25:LYS:HG2	2.16	0.46
29:3:47:GLY:HA2	30:0:2121:G:H4'	1.97	0.46
4:D:29:HIS:N	4:D:29:HIS:ND1	2.61	0.46
5:E:84:MET:HG2	5:E:168:ILE:HA	1.98	0.46
21:U:13:ILE:HG13	38:U:3194:HOH:O	2.15	0.46
30:0:2434:A:H2'	30:0:2435:U:O4'	2.15	0.46
1:A:171:LYS:HB2	30:0:820:G:C6	2.50	0.46
6:F:111:ILE:O	6:F:115:VAL:HG23	2.15	0.46
10:J:80:LYS:HE3	10:J:101:VAL:O	2.14	0.46
12:L:10:SER:O	12:L:11:ARG:HB3	2.16	0.46
13:M:102:GLU:CD	13:M:164:THR:HG21	2.36	0.46
21:U:56:ARG:HD2	30:0:2890:A:C1'	2.46	0.46
30:0:100:C:H2'	30:0:101:C:H6	1.80	0.46
30:0:101:C:H2'	30:0:102:A:H8	1.80	0.46
30:0:1154:A:H2'	30:0:1155:G:C8	2.50	0.46
30:0:1434:A:H2'	30:0:1436:C:C5	2.51	0.46
30:0:461:C:N3	30:0:479:G:H5'	2.31	0.46
30:0:660:A:N6	30:0:746:A:O4'	2.49	0.46
29:3:1:MET:HG2	29:3:87:ARG:O	2.16	0.46
31:9:14:G:H8	31:9:14:G:C5'	2.16	0.46
30:0:134:U:C2	30:0:145:A:C2	3.04	0.46
30:0:1503:U:H2'	30:0:1504:A:O4'	2.16	0.46
28:2:43:ARG:NH2	30:0:1684:A:H1'	2.25	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:17:G:H2'	30:0:18:C:C6	2.51	0.46
30:0:1878:G:O2'	30:0:1879:U:OP2	2.33	0.46
30:0:365:G:C5	30:0:366:U:C5	3.04	0.46
30:0:517:U:C2'	30:0:518:G:H5'	2.46	0.46
30:0:561:G:O2'	30:0:562:A:H5'	2.15	0.46
27:1:16:HIS:HE1	30:0:775:G:OP1	1.97	0.46
2:B:144:THR:HG22	2:B:145:HIS:N	2.31	0.46
8:H:48:VAL:HA	8:H:170:ARG:O	2.15	0.46
10:J:69:TYR:CE1	30:0:2081:A:H4'	2.50	0.46
14:N:11:ARG:NH1	31:9:8:G:O6	2.48	0.46
16:P:115:SER:OG	16:P:118:GLN:HG3	2.16	0.46
30:0:1526:A:H4'	30:0:1527:A:C5'	2.45	0.46
30:0:1764:C:O2'	30:0:1765:G:H5'	2.15	0.46
30:0:1845:A:C2'	30:0:1846:U:H5'	2.45	0.46
30:0:1871:U:O4'	30:0:1873:G:C8	2.69	0.46
30:0:1894:C:N4	30:0:1939:U:H2'	2.30	0.46
30:0:2537:G:H5''	30:0:2538:A:H5''	1.98	0.46
30:0:2812:A:N7	38:0:7508:HOH:O	2.36	0.46
30:0:241:A:C2	30:0:378:A:H4'	2.51	0.46
26:Z:41:ARG:HH12	30:0:821:U:H4'	1.81	0.46
29:3:30:GLN:HB3	38:3:9051:HOH:O	2.16	0.46
31:9:3:A:H2	31:9:21:G:N3	2.14	0.46
31:9:47:A:C2	31:9:48:C:C2	3.04	0.46
2:B:232:TRP:CZ3	30:0:2614:C:H5''	2.51	0.46
2:B:85:ARG:NH1	38:B:9106:HOH:O	2.47	0.46
12:L:34:GLY:HA2	38:L:9017:HOH:O	2.16	0.46
13:M:47:ASP:CG	13:M:48:LYS:N	2.70	0.46
19:S:43:GLU:HB3	38:S:7106:HOH:O	2.16	0.46
20:T:16:LEU:HB2	30:0:100:C:H4'	1.98	0.46
30:0:1021:G:O2'	30:0:1022:A:H5'	2.16	0.46
30:0:1132:A:H61	30:0:1229:C:H2'	1.80	0.46
30:0:1294:A:H2'	30:0:1295:G:O4'	2.16	0.46
30:0:1346:U:H2'	30:0:1347:U:C6	2.50	0.46
30:0:1634:G:C4	30:0:1635:U:C5	3.03	0.46
1:A:230:SER:HB2	30:0:1852:A:H4'	1.97	0.46
14:N:22:GLN:HG3	30:0:2415:A:C2	2.51	0.46
30:0:2624:A:H1'	38:0:9764:HOH:O	2.14	0.46
3:C:43:LYS:HG2	30:0:449:A:N7	2.31	0.46
30:0:545:G:C8	30:0:545:G:C5'	2.88	0.46
30:0:594:C:C2'	30:0:595:U:H5'	2.46	0.46
25:Y:189:ASN:HA	25:Y:217:ILE:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1012:A:O5'	30:0:1012:A:H8	1.99	0.46
30:0:1166:A:C6	30:0:1181:A:C2	3.04	0.46
30:0:1588:G:C6	30:0:1589:G:N1	2.84	0.46
30:0:1615:A:H4'	38:0:5868:HOH:O	2.16	0.46
30:0:1615:A:H5'	38:0:4181:HOH:O	2.15	0.46
30:0:2017:U:O2'	30:0:2018:A:C8	2.66	0.46
30:0:2276:U:H2'	30:0:2277:U:C6	2.51	0.46
30:0:2488:A:H1'	38:0:9096:HOH:O	2.16	0.46
30:0:372:A:H2'	30:0:373:G:C8	2.51	0.46
30:0:483:C:C4	30:0:484:A:C6	3.04	0.46
30:0:603:A:H4'	30:0:604:G:O5'	2.15	0.46
31:9:65:A:C2'	31:9:66:G:OP2	2.64	0.46
13:M:169:ARG:HD2	38:M:8885:HOH:O	2.16	0.46
38:C:8575:HOH:O	20:T:2:LYS:HE2	2.15	0.46
30:0:1052:G:H2'	30:0:1052:G:N3	2.31	0.45
30:0:1119:G:C5	30:0:1243:C:C4	3.04	0.45
30:0:1029:U:O2'	30:0:1273:C:OP1	2.31	0.45
30:0:1409:G:C2	30:0:1410:G:C8	3.04	0.45
30:0:1520:G:C6	30:0:1521:C:C4	3.05	0.45
30:0:1756:G:H1'	38:0:6244:HOH:O	2.15	0.45
30:0:1890:U:H4'	30:0:2010:A:C6	2.51	0.45
30:0:255:A:C4	30:0:256:C:C5	3.05	0.45
30:0:2740:G:H2'	30:0:2741:A:O4'	2.15	0.45
30:0:71:G:H8	38:0:3908:HOH:O	1.98	0.45
25:Y:151:SER:HB3	25:Y:154:ARG:HB3	1.98	0.45
30:0:1625:U:H4'	38:0:4661:HOH:O	2.15	0.45
30:0:1768:C:H2'	30:0:1769:C:O4'	2.16	0.45
30:0:2057:U:O5'	30:0:2057:U:H6	1.98	0.45
30:0:2717:C:C2'	30:0:2718:C:C5'	2.84	0.45
30:0:293:A:C5	30:0:360:A:C2	3.04	0.45
30:0:633:C:O2'	30:0:634:G:H5'	2.15	0.45
30:0:810:G:H2'	30:0:811:C:H6	1.81	0.45
28:2:28:LYS:O	30:0:87:C:H2'	2.17	0.45
14:N:37:ARG:NH1	31:9:6:C:OP1	2.48	0.45
30:0:1131:G:C6	30:0:1230:A:C4	3.04	0.45
30:0:1310:U:C2'	30:0:1311:G:O5'	2.64	0.45
30:0:1588:G:C6	30:0:1589:G:C6	3.04	0.45
30:0:1730:G:H4'	30:0:1731:C:H6	1.82	0.45
30:0:1856:C:H1'	38:0:5858:HOH:O	2.17	0.45
30:0:1882:C:H2'	30:0:1883:U:C6	2.51	0.45
30:0:1902:G:O2'	30:0:1903:U:H5'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2298:C:O2'	30:0:2299:G:H5'	2.17	0.45
30:0:612:U:H2'	30:0:613:C:C6	2.52	0.45
27:1:11:LYS:HG2	30:0:777:U:O2'	2.17	0.45
29:3:70:ARG:NH2	29:3:77:ALA:HB3	2.31	0.45
31:9:28:U:O2	31:9:57:A:N6	2.50	0.45
17:Q:25:PRO:HA	17:Q:26:PRO:HD3	1.65	0.45
30:0:1342:C:H2'	30:0:1343:C:H5'	1.99	0.45
18:R:128:ARG:NH2	30:0:2054:A:C2	2.84	0.45
30:0:2438:G:H2'	30:0:2439:C:H6	1.81	0.45
30:0:670:G:H2'	30:0:671:A:C8	2.51	0.45
26:Z:34:SER:HA	30:0:797:A:C4'	2.46	0.45
1:A:192:VAL:HG13	1:A:207:GLN:HB3	1.99	0.45
2:B:275:GLY:O	2:B:291:ASP:HA	2.16	0.45
12:L:142:LEU:HG	12:L:146:GLY:HA3	1.99	0.45
13:M:88:VAL:HG13	38:M:8902:HOH:O	2.16	0.45
14:N:34:LEU:HD22	14:N:129:ILE:HD13	1.98	0.45
30:0:1187:U:C2	30:0:1189:A:OP2	2.70	0.45
30:0:1540:G:C4	30:0:1541:G:C8	3.05	0.45
30:0:1613:C:H2'	30:0:1614:G:O4'	2.15	0.45
30:0:169:A:HO2'	30:0:170:U:H6	1.63	0.45
30:0:1758:U:O2'	30:0:1759:A:H5'	2.15	0.45
30:0:2032:U:C2'	30:0:2033:G:H5''	2.46	0.45
30:0:2315:C:H4'	30:0:2425:A:C6	2.51	0.45
29:3:9:THR:HG23	29:3:20:HIS:ND1	2.32	0.45
14:N:40:ASN:HD22	31:9:28:U:H5''	1.82	0.45
3:C:236:THR:CG2	3:C:239:ALA:H	2.17	0.45
11:K:115:ARG:HG3	11:K:116:GLU:N	2.32	0.45
30:0:1016:U:H2'	30:0:1017:U:O4'	2.17	0.45
30:0:1278:A:H4'	30:0:1279:U:C5	2.49	0.45
30:0:1535:G:H2'	30:0:1536:C:C6	2.52	0.45
30:0:1603:A:H5''	30:0:1605:G:C5'	2.39	0.45
30:0:2104:C:O2	30:0:2485:A:N1	2.49	0.45
30:0:2505:G:H3'	38:0:5626:HOH:O	2.17	0.45
30:0:2591:C:H2'	30:0:2592:G:O4'	2.16	0.45
1:A:9:ARG:HG2	1:A:16:PHE:CD2	2.52	0.45
8:H:123:ILE:HD12	8:H:123:ILE:N	2.32	0.45
8:H:165:ARG:HD2	38:H:9029:HOH:O	2.16	0.45
8:H:170:ARG:HD2	38:H:8987:HOH:O	2.15	0.45
10:J:42:GLU:HG2	10:J:43:ARG:HG3	1.98	0.45
12:L:75:LEU:HD21	38:O:7543:HOH:O	2.17	0.45
15:O:87:THR:O	15:O:91:GLN:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:14:GLU:O	21:U:17:THR:HB	2.16	0.45
25:Y:142:SER:HB2	38:Y:8903:HOH:O	2.16	0.45
24:X:30:MET:HG2	30:0:1384:C:H5'	1.98	0.45
30:0:212:A:O4'	30:0:214:U:C6	2.70	0.45
30:0:2321:A:C4	30:0:2323:G:C8	3.05	0.45
30:0:2778:A:C2	30:0:2797:C:O2	2.70	0.45
30:0:352:A:H2'	30:0:353:G:H8	1.79	0.45
2:B:254:GLN:HG2	2:B:255:GLY:N	2.31	0.45
8:H:12:ILE:HG23	8:H:129:ARG:CZ	2.47	0.45
8:H:99:ARG:NH1	30:0:1055:G:OP2	2.50	0.45
21:U:6:CYS:SG	21:U:13:ILE:HB	2.57	0.45
23:W:129:LYS:HE2	30:0:1098:A:O3'	2.17	0.45
30:0:1151:G:H2'	38:0:5008:HOH:O	2.17	0.45
30:0:1346:U:H2'	30:0:1347:U:H6	1.82	0.45
1:A:47:HIS:HD2	30:0:1654:U:C2'	2.30	0.45
30:0:2071:C:H5'	38:0:9532:HOH:O	2.17	0.45
30:0:213:G:N2	30:0:225:G:H2'	2.31	0.45
30:0:2679:G:H2'	30:0:2681:A:OP2	2.17	0.45
30:0:226:A:H1'	30:0:393:G:C5	2.51	0.45
30:0:644:G:H1'	38:0:6390:HOH:O	2.16	0.45
30:0:727:G:C2	30:0:728:C:C2	3.05	0.45
30:0:867:A:H2	30:0:880:C:O2	2.00	0.45
30:0:921:G:H4'	30:0:924:G:C6	2.52	0.45
31:9:26:C:H5''	38:9:9049:HOH:O	2.17	0.45
1:A:105:VAL:CG1	1:A:154:ALA:HB1	2.47	0.45
3:C:170:ASP:OD2	30:0:330:C:H5	2.00	0.45
14:N:110:THR:HB	14:N:113:SER:OG	2.17	0.45
14:N:86:LEU:HD12	14:N:125:ALA:HB2	1.99	0.45
18:R:132:ARG:HG2	18:R:133:ALA:N	2.31	0.45
30:0:113:A:H3'	30:0:114:A:H5''	1.98	0.45
30:0:1755:A:H2'	30:0:1756:G:O4'	2.16	0.45
30:0:2596:A:H2	33:0:8812:CL:CL	2.37	0.45
30:0:2650:U:O2'	30:0:2651:C:H5'	2.16	0.45
30:0:2691:A:H5'	30:0:2693:U:H1'	1.99	0.45
30:0:2735:U:H2'	30:0:2736:U:C6	2.52	0.45
30:0:282:C:H2'	30:0:283:U:O4'	2.16	0.45
30:0:482:G:O4'	30:0:511:A:C2	2.70	0.45
30:0:559:U:H2'	30:0:560:U:O4'	2.17	0.45
25:Y:132:ASP:OD2	30:0:621:C:H5'	2.17	0.45
30:0:941:G:C6	30:0:942:U:C4	3.05	0.45
31:9:82:U:H2'	31:9:83:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:252:PRO:HD2	30:0:2548:C:H5'	1.99	0.45
3:C:27:ARG:CG	3:C:27:ARG:HH11	2.15	0.45
4:D:154:LYS:HD2	4:D:154:LYS:N	2.22	0.45
12:L:136:ALA:HB3	38:L:9035:HOH:O	2.17	0.45
13:M:68:ARG:HD3	13:M:68:ARG:C	2.37	0.45
16:P:91:LYS:O	16:P:95:GLU:HG3	2.17	0.45
30:0:1249:U:H2'	30:0:1250:C:H6	1.82	0.45
25:Y:142:SER:OG	30:0:1331:G:OP2	2.32	0.45
30:0:1878:G:O2'	30:0:1879:U:P	2.74	0.45
30:0:2010:A:C2'	38:0:5942:HOH:O	2.51	0.45
30:0:2252:A:C5	30:0:2253:G:H1'	2.51	0.45
30:0:792:G:O2'	30:0:793:A:H5'	2.16	0.45
2:B:5:ARG:HD2	2:B:8:LYS:HE2	1.99	0.45
3:C:39:GLN:O	3:C:43:LYS:HD3	2.17	0.45
18:R:25:PHE:CE2	18:R:29:LYS:HE2	2.51	0.45
1:A:76:VAL:HG23	26:Z:87:LYS:O	2.17	0.45
30:0:1209:C:C2	30:0:1210:G:C8	3.04	0.44
30:0:1268:C:O2'	30:0:1269:G:H5'	2.16	0.44
30:0:152:A:H2'	30:0:153:C:C6	2.52	0.44
16:P:68:LYS:HE2	30:0:1787:C:OP1	2.16	0.44
30:0:2301:A:H5''	30:0:2302:A:H5'	1.99	0.44
30:0:2335:C:H2'	30:0:2336:G:H8	1.80	0.44
14:N:25:ARG:HG2	30:0:2416:G:O2'	2.17	0.44
30:0:2837:U:H2'	38:0:6825:HOH:O	2.15	0.44
30:0:65:C:O2'	30:0:66:G:H5'	2.16	0.44
30:0:699:C:C2	30:0:744:G:N2	2.85	0.44
30:0:797:A:N6	30:0:816:G:H1'	2.32	0.44
28:2:41:HIS:H	28:2:45:ASN:ND2	2.04	0.44
31:9:1:U:O3'	31:9:3:A:C5'	2.65	0.44
13:M:72:ALA:C	13:M:74:LYS:H	2.20	0.44
15:O:98:LEU:O	15:O:102:ILE:HG13	2.17	0.44
18:R:114:VAL:HG13	18:R:114:VAL:O	2.18	0.44
30:0:1310:U:H2'	30:0:1311:G:O5'	2.17	0.44
30:0:1949:G:N2	30:0:1964:U:H1'	2.32	0.44
30:0:2074:A:H1'	38:0:9875:HOH:O	2.16	0.44
30:0:2250:G:C2	30:0:2251:G:H1'	2.52	0.44
30:0:2493:C:O2	30:0:2493:C:H2'	2.17	0.44
1:A:206:ARG:HH21	30:0:2629:C:N4	2.16	0.44
30:0:2734:G:O2'	30:0:2735:U:H5'	2.17	0.44
30:0:365:G:C5	30:0:366:U:C4	3.05	0.44
30:0:598:C:H2'	30:0:599:G:C8	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:1:U:O3'	31:9:3:A:H5''	2.16	0.44
1:A:51:ARG:C	1:A:53:ALA:H	2.20	0.44
8:H:46:TYR:HA	8:H:47:PRO:HD3	1.81	0.44
18:R:106:GLY:HA2	18:R:109:MET:HE3	1.99	0.44
21:U:42:LEU:O	30:0:1810:C:H5'	2.17	0.44
23:W:35:VAL:HG23	23:W:41:TYR:CD2	2.52	0.44
30:0:1206:U:C3'	30:0:1206:U:C6	3.01	0.44
30:0:1279:U:C5'	30:0:1280:A:OP2	2.65	0.44
30:0:1461:U:H2'	30:0:1462:C:H6	1.83	0.44
30:0:1735:C:O2'	30:0:1736:A:H5'	2.17	0.44
30:0:2004:U:H2'	30:0:2005:G:OP1	2.17	0.44
30:0:2410:G:O2'	30:0:2411:C:H5'	2.18	0.44
30:0:2642:G:H2'	30:0:2643:G:O4'	2.16	0.44
30:0:2777:G:O2'	30:0:2778:A:H5'	2.17	0.44
30:0:307:G:C2	30:0:309:C:C4	3.05	0.44
30:0:40:C:O5'	30:0:40:C:H6	2.01	0.44
30:0:734:U:H2'	30:0:736:A:OP2	2.17	0.44
30:0:970:U:H2'	38:0:6313:HOH:O	2.16	0.44
28:2:22:PRO:HG2	28:2:25:VAL:CG2	2.48	0.44
5:E:3:VAL:HG22	5:E:49:ILE:HB	2.00	0.44
7:G:64:ASN:N	7:G:64:ASN:ND2	2.65	0.44
14:N:11:ARG:HG3	14:N:14:ARG:HH12	1.82	0.44
38:B:9136:HOH:O	21:U:17:THR:HG21	2.16	0.44
23:W:24:LEU:O	23:W:26:ILE:HG22	2.18	0.44
26:Z:65:ASN:HB2	26:Z:84:CYS:SG	2.58	0.44
3:C:226:GLY:HA3	30:0:1308:A:C4'	2.48	0.44
30:0:161:A:H2'	30:0:162:C:C6	2.52	0.44
30:0:1928:C:O2'	30:0:1929:G:H5'	2.17	0.44
13:M:73:ARG:NH2	30:0:2263:G:H5''	2.32	0.44
30:0:2663:U:N3	30:0:2664:A:N6	2.65	0.44
30:0:2755:G:H1'	38:0:4677:HOH:O	2.17	0.44
30:0:664:U:O4	30:0:681:G:H5''	2.16	0.44
30:0:711:G:C2	30:0:718:C:O2	2.70	0.44
4:D:154:LYS:H	4:D:154:LYS:CD	2.24	0.44
4:D:22:VAL:HA	4:D:73:VAL:O	2.17	0.44
5:E:84:MET:HG2	5:E:168:ILE:HD13	1.98	0.44
20:T:71:VAL:HG12	20:T:72:ILE:N	2.32	0.44
30:0:1076:G:C2	30:0:1084:C:C2	3.06	0.44
30:0:1477:C:H5'	30:0:1868:G:H5''	1.98	0.44
30:0:2245:C:H6	30:0:2245:C:O5'	2.00	0.44
31:9:82:U:H2'	31:9:83:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:ARG:HD3	38:0:9221:HOH:O	2.17	0.44
3:C:162:VAL:CG2	3:C:232:LEU:HD21	2.47	0.44
4:D:159:PRO:O	4:D:163:VAL:HG23	2.17	0.44
5:E:95:VAL:HG11	5:E:131:LEU:HD11	1.99	0.44
6:F:48:VAL:HG23	6:F:74:PHE:HB3	1.99	0.44
18:R:125:ARG:HG2	38:R:8942:HOH:O	2.17	0.44
20:T:23:VAL:HG23	20:T:41:ARG:HG3	2.00	0.44
30:0:1028:U:H1'	38:0:3631:HOH:O	2.18	0.44
30:0:1067:A:H5'	38:0:4344:HOH:O	2.18	0.44
30:0:1116:U:C2'	30:0:1118:A:H2	2.28	0.44
10:J:63:ILE:CD1	30:0:1236:A:C8	3.01	0.44
30:0:2119:C:O2'	30:0:2120:U:H5'	2.18	0.44
30:0:2313:C:H4'	38:0:6558:HOH:O	2.18	0.44
30:0:2325:U:O2'	30:0:2411:C:H1'	2.18	0.44
30:0:2887:G:H2'	30:0:2888:U:H6	1.79	0.44
30:0:549:A:C2	30:0:550:C:C2	3.06	0.44
30:0:737:A:H2'	30:0:738:G:O4'	2.18	0.44
30:0:81:G:N3	30:0:98:A:C2	2.85	0.44
1:A:46:GLU:C	26:Z:78:ILE:HD11	2.38	0.44
3:C:37:ALA:HA	3:C:100:LEU:HD12	2.00	0.44
9:I:114:TYR:N	9:I:114:TYR:CD1	2.86	0.44
12:L:129:ALA:O	12:L:133:VAL:HG23	2.17	0.44
13:M:123:ASP:OD1	13:M:126:GLN:HG2	2.18	0.44
13:M:97:ILE:HD13	13:M:127:LYS:HD2	2.00	0.44
14:N:93:GLN:HA	14:N:93:GLN:HE21	1.82	0.44
15:O:49:GLU:OE1	15:O:72:LYS:HG3	2.17	0.44
16:P:18:LYS:O	16:P:21:VAL:HG13	2.18	0.44
19:S:57:THR:CG2	19:S:58:MET:N	2.79	0.44
21:U:7:ASP:HB2	21:U:29:THR:HG23	2.00	0.44
30:0:1014:A:H2'	30:0:1015:C:H5'	1.99	0.44
30:0:1249:U:H2'	30:0:1250:C:C6	2.53	0.44
30:0:912:A:C4	30:0:1294:A:C2	3.05	0.44
16:P:41:ARG:NH2	30:0:1500:U:OP2	2.49	0.44
30:0:1597:A:C4	30:0:1598:A:C8	3.05	0.44
30:0:1883:U:C2'	30:0:1884:G:H5'	2.48	0.44
13:M:171:ARG:NH2	30:0:189:A:OP1	2.50	0.44
30:0:295:C:H2'	30:0:296:G:O4'	2.18	0.44
30:0:462:A:H2'	38:0:4875:HOH:O	2.18	0.44
30:0:615:G:H2'	30:0:616:U:H6	1.83	0.44
30:0:725:C:H2'	30:0:726:C:O5'	2.18	0.44
27:1:1:THR:O	30:0:1836:A:H1'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:62:THR:HG21	30:0:2317:C:H5'	1.98	0.44
4:D:56:ARG:NH2	30:0:2332:A:H5'	2.32	0.44
12:L:149:ARG:O	12:L:150:GLN:HB2	2.17	0.44
17:Q:3:SER:O	17:Q:8:GLU:HG3	2.18	0.44
25:Y:116:LEU:HA	25:Y:116:LEU:HD23	1.80	0.44
30:0:1246:A:C4	30:0:1248:A:C8	3.06	0.44
30:0:1307:A:H2'	30:0:1308:A:C8	2.53	0.44
30:0:1603:A:C5'	30:0:1605:G:C5'	2.96	0.44
30:0:1730:G:H4'	30:0:1731:C:C6	2.52	0.44
30:0:1771:U:O2'	30:0:1773:G:N7	2.50	0.44
30:0:1773:G:C2'	30:0:1774:G:H5'	2.48	0.44
30:0:2105:C:H2'	30:0:2106:C:C6	2.53	0.44
30:0:2128:G:C5	30:0:2129:U:C5	3.06	0.44
30:0:2276:U:O2'	30:0:2277:U:H5'	2.18	0.44
30:0:2457:U:O2'	30:0:2458:U:H5'	2.17	0.44
30:0:2588:OMG:HM23	30:0:2617:G:C2	2.53	0.44
30:0:2793:A:H2'	30:0:2794:G:H5'	2.00	0.44
30:0:368:C:C2'	30:0:369:G:H5'	2.48	0.44
2:B:119:HIS:O	2:B:121:PRO:HD3	2.18	0.44
14:N:73:ALA:HB1	14:N:74:PRO:CD	2.48	0.44
15:O:21:SER:OG	15:O:106:PRO:HB2	2.18	0.44
23:W:122:ARG:NH2	23:W:154:ARG:HG2	2.33	0.44
25:Y:234:VAL:HG12	25:Y:235:GLU:N	2.33	0.44
30:0:1066:U:H2'	30:0:1067:A:C8	2.53	0.44
30:0:1254:C:O2'	30:0:1255:A:H5'	2.18	0.44
13:M:95:LYS:HE2	30:0:157:G:H4'	1.99	0.44
30:0:1657:A:H2'	30:0:1658:A:C8	2.53	0.44
30:0:2072:G:H3'	30:0:2073:G:C5'	2.48	0.44
30:0:2473:U:O2'	30:0:2474:A:H5''	2.18	0.44
30:0:416:G:H2'	38:0:9910:HOH:O	2.16	0.44
30:0:559:U:C6	30:0:559:U:C3'	3.01	0.44
27:1:21:ARG:HD2	27:1:37:CYS:SG	2.57	0.44
1:A:26:ASP:OD2	30:0:1872:C:H4'	2.18	0.44
2:B:242:TRP:CZ2	30:0:2607:U:C4	3.06	0.44
3:C:27:ARG:HD2	38:O:327:HOH:O	2.17	0.44
8:H:157:TYR:HD1	8:H:157:TYR:C	2.21	0.44
14:N:147:ILE:HD11	31:9:50:G:OP1	2.18	0.44
17:Q:62:THR:O	17:Q:64:GLU:HG2	2.18	0.44
30:0:1198:U:C6	30:0:1200:A:OP2	2.71	0.43
30:0:1592:G:H1'	30:0:1593:C:C6	2.53	0.43
30:0:2256:G:C2'	30:0:2257:G:H5'	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:297:U:H2'	30:0:298:C:H6	1.83	0.43
30:0:590:A:H2'	30:0:591:A:O4'	2.18	0.43
30:0:653:U:H2'	30:0:654:A:C8	2.52	0.43
4:D:59:GLY:HA3	38:D:4886:HOH:O	2.17	0.43
12:L:117:GLU:HB3	38:L:9018:HOH:O	2.18	0.43
13:M:102:GLU:OE2	13:M:164:THR:HG21	2.17	0.43
13:M:134:ILE:CG2	13:M:141:ILE:HD13	2.42	0.43
20:T:48:VAL:CG1	20:T:49:GLU:N	2.81	0.43
24:X:72:VAL:HG22	24:X:85:VAL:HG12	2.00	0.43
30:0:1477:C:O2'	30:0:1478:U:H5'	2.17	0.43
30:0:1973:A:H2'	30:0:1974:G:O4'	2.17	0.43
30:0:2387:U:H2'	30:0:2388:C:C6	2.52	0.43
30:0:2543:G:H2'	30:0:2544:G:O4'	2.18	0.43
5:E:111:LYS:HE3	30:0:2690:U:H4'	1.99	0.43
30:0:549:A:C6	30:0:550:C:C4	3.07	0.43
30:0:596:C:H2'	30:0:597:A:C8	2.53	0.43
31:9:64:C:O2'	31:9:65:A:H5'	2.18	0.43
1:A:182:ARG:HG2	1:A:182:ARG:HH11	1.83	0.43
2:B:223:ARG:HG3	2:B:232:TRP:O	2.17	0.43
2:B:305:ASP:O	2:B:306:LYS:CB	2.66	0.43
2:B:41:PHE:HB3	2:B:190:MET:HE2	2.00	0.43
3:C:118:THR:O	3:C:136:VAL:HG13	2.18	0.43
4:D:45:THR:HB	4:D:75:LEU:HD21	1.99	0.43
12:L:41:HIS:CD2	30:0:926:A:O2'	2.71	0.43
16:P:10:ALA:HA	16:P:13:VAL:HG12	2.01	0.43
17:Q:1:PRO:HA	30:0:2299:G:O6	2.18	0.43
19:S:50:GLU:HB3	19:S:67:ARG:NH2	2.33	0.43
20:T:38:ARG:HH11	20:T:38:ARG:HG3	1.83	0.43
30:0:107:U:C2'	30:0:108:U:H5'	2.48	0.43
30:0:1362:U:H5'	38:0:3253:HOH:O	2.18	0.43
30:0:1702:U:H5"	38:0:7207:HOH:O	2.19	0.43
30:0:2321:A:N1	30:0:2378:U:O2	2.52	0.43
25:Y:148:GLY:HA3	30:0:622:G:P	2.59	0.43
1:A:211:LYS:HB2	38:A:9038:HOH:O	2.18	0.43
2:B:18:ARG:HG3	2:B:256:GLN:HG3	2.00	0.43
14:N:67:ALA:CA	14:N:71:TRP:HB3	2.44	0.43
20:T:48:VAL:HG11	20:T:96:VAL:CG1	2.46	0.43
25:Y:144:ARG:NH1	38:Y:8882:HOH:O	2.51	0.43
30:0:1183:C:H41	30:0:1192:A:P	2.42	0.43
2:B:234:ARG:HG3	30:0:1735:C:OP2	2.17	0.43
30:0:1878:G:O2'	30:0:1879:U:C6	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2474:A:H4'	30:0:2475:C:O5'	2.18	0.43
30:0:275:G:N2	30:0:376:C:C2	2.87	0.43
30:0:2834:G:H2'	30:0:2835:C:O5'	2.18	0.43
30:0:496:G:H3'	38:0:7658:HOH:O	2.18	0.43
30:0:853:C:H2'	30:0:854:G:O4'	2.17	0.43
30:0:920:C:H5''	30:0:921:G:O5'	2.18	0.43
2:B:42:ALA:CB	2:B:162:MET:HE3	2.48	0.43
2:B:199:TYR:HE1	2:B:319:ASP:HB2	1.83	0.43
8:H:157:TYR:C	8:H:157:TYR:CD1	2.90	0.43
14:N:154:LEU:C	14:N:156:GLU:H	2.20	0.43
22:V:50:ARG:HH12	30:0:56:G:C5'	2.30	0.43
26:Z:94:LYS:HA	38:Z:8719:HOH:O	2.18	0.43
30:0:1809:G:H2'	30:0:1811:A:OP2	2.19	0.43
30:0:2355:G:H5''	30:0:2356:A:OP2	2.19	0.43
30:0:40:C:H4'	38:0:6993:HOH:O	2.18	0.43
29:3:39:GLN:HG2	29:3:43:ASN:OD1	2.19	0.43
12:L:34:GLY:HA3	12:L:38:HIS:CE1	2.52	0.43
23:W:118:LEU:HD12	23:W:153:MET:HE3	2.00	0.43
23:W:13:MET:HE3	23:W:17:ILE:HG22	1.99	0.43
30:0:1185:U:H2'	30:0:1186:C:C6	2.54	0.43
30:0:1471:A:H2'	30:0:1472:C:C6	2.54	0.43
30:0:2039:A:H2'	30:0:2040:C:C6	2.53	0.43
30:0:2102:G:N2	30:0:2104:C:N3	2.67	0.43
30:0:2346:C:O5'	30:0:2346:C:C6	2.72	0.43
30:0:2718:C:H5'	30:0:2718:C:C6	2.52	0.43
30:0:557:C:O2'	30:0:558:C:H5'	2.19	0.43
6:F:14:ASP:O	6:F:18:GLU:HG3	2.18	0.43
10:J:19:MET:HE2	10:J:79:PHE:HA	2.01	0.43
13:M:49:ALA:C	13:M:54:TYR:HB3	2.38	0.43
14:N:86:LEU:O	14:N:90:LEU:HG	2.19	0.43
20:T:43:ASN:C	20:T:45:GLY:H	2.22	0.43
22:V:49:LEU:O	22:V:53:ILE:HG13	2.18	0.43
30:0:1173:A:H4'	30:0:1174:A:H8	1.83	0.43
30:0:1427:A:C2'	30:0:1428:C:H5'	2.49	0.43
30:0:1566:C:H2'	30:0:1567:G:C8	2.54	0.43
30:0:1773:G:H4'	38:0:3505:HOH:O	2.19	0.43
11:K:66:ARG:NH2	30:0:1994:A:OP1	2.52	0.43
30:0:2103:A:H2'	30:0:2103:A:N3	2.33	0.43
30:0:2379:G:N3	30:0:2418:G:H2'	2.34	0.43
30:0:2564:G:OP2	30:0:2565:C:H5''	2.18	0.43
24:X:15:ARG:NH1	30:0:2896:A:OP1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:328:U:C2	30:0:348:C:H4'	2.53	0.43
30:0:459:A:H4'	38:0:9455:HOH:O	2.17	0.43
20:T:82:THR:HG21	30:0:488:U:O2'	2.19	0.43
30:0:750:A:H2'	30:0:751:U:C6	2.54	0.43
30:0:878:G:H4'	30:0:1835:U:H4'	2.00	0.43
28:2:20:ARG:NH1	28:2:39:ARG:HH21	2.17	0.43
28:2:40:ARG:HG3	28:2:45:ASN:CB	2.48	0.43
31:9:45:A:N7	31:9:46:C:C5	2.87	0.43
1:A:190:ARG:NH2	1:A:207:GLN:OE1	2.52	0.43
1:A:217:ARG:HG2	1:A:229:ALA:CB	2.48	0.43
1:A:51:ARG:HH21	1:A:53:ALA:HB3	1.82	0.43
10:J:107:ASN:HD22	10:J:107:ASN:C	2.22	0.43
25:Y:117:LEU:HB2	25:Y:174:VAL:HG21	1.99	0.43
30:0:119:A:H2'	30:0:120:A:C5'	2.49	0.43
38:M:8865:HOH:O	30:0:2244:A:H1'	2.18	0.43
30:0:2681:A:H4'	30:0:2682:C:OP1	2.19	0.43
30:0:2694:A:H3'	30:0:2695:C:H6	1.84	0.43
30:0:361:C:H2'	30:0:362:G:O4'	2.19	0.43
31:9:110:G:C2	31:9:111:U:C6	3.07	0.43
31:9:110:G:C5	31:9:111:U:C5	3.07	0.43
1:A:192:VAL:O	1:A:207:GLN:HG2	2.18	0.43
3:C:132:ASP:O	3:C:133:ARG:HG3	2.19	0.43
4:D:103:ASN:ND2	4:D:133:ASN:HD22	2.17	0.43
5:E:91:PHE:HE1	30:0:2694:A:H4'	1.83	0.43
14:N:109:PRO:HB3	30:0:2413:A:N7	2.34	0.43
14:N:49:THR:HG22	14:N:56:ASP:CB	2.49	0.43
18:R:59:PHE:O	18:R:63:ASN:HB3	2.18	0.43
23:W:122:ARG:HH11	23:W:122:ARG:HG3	1.84	0.43
26:Z:95:PRO:HD2	38:Z:8719:HOH:O	2.18	0.43
30:0:1099:G:H2'	30:0:1100:G:O4'	2.19	0.43
30:0:1156:C:O2'	30:0:1157:C:H5'	2.19	0.43
9:I:69:PRO:HA	30:0:1164:U:OP1	2.19	0.43
30:0:1592:G:HO2'	30:0:1593:C:H6	1.67	0.43
30:0:1937:U:O2'	30:0:1938:G:H5'	2.18	0.43
26:Z:40:ALA:O	30:0:2018:A:H2	2.02	0.43
30:0:920:C:C5	30:0:2467:A:OP1	2.72	0.43
30:0:2487:C:C5	38:0:4880:HOH:O	2.57	0.43
8:H:6:ALA:HB3	30:0:2521:A:OP2	2.19	0.43
30:0:2523:U:H2'	30:0:2524:G:O4'	2.18	0.43
30:0:2581:U:H1'	38:0:4466:HOH:O	2.17	0.43
2:B:116:PRO:HG3	30:0:2821:C:H4'	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:636:G:H5'	30:0:2059:U:OP2	2.19	0.43
30:0:802:G:H2'	30:0:803:C:C6	2.54	0.43
2:B:215:VAL:HB	38:B:9090:HOH:O	2.19	0.43
8:H:6:ALA:HA	8:H:61:ARG:NH1	2.34	0.43
26:Z:88:PHE:N	26:Z:88:PHE:CD2	2.86	0.43
30:0:1456:C:H2'	30:0:1457:U:C6	2.53	0.43
30:0:1561:U:C5'	38:0:7421:HOH:O	2.67	0.43
30:0:1758:U:H2'	30:0:1759:A:O4'	2.19	0.43
30:0:1923:G:H2'	30:0:1924:A:H8	1.83	0.43
30:0:2252:A:H2'	30:0:2253:G:O4'	2.19	0.43
30:0:236:A:OP1	30:0:236:A:H8	2.02	0.43
24:X:15:ARG:NH2	30:0:2856:A:OP1	2.52	0.43
30:0:301:C:H2'	30:0:302:A:C8	2.54	0.43
30:0:308:U:C4	30:0:342:C:C1'	3.01	0.43
29:3:13:HIS:HD2	29:3:76:LYS:HB3	1.83	0.43
31:9:3:A:N6	31:9:22:G:H1'	2.34	0.43
1:A:230:SER:CB	30:0:1852:A:H4'	2.49	0.43
1:A:48:ASP:HB3	1:A:51:ARG:HG3	2.00	0.43
4:D:136:ARG:HA	4:D:137:PRO:HD3	1.84	0.43
5:E:91:PHE:HA	5:E:92:PRO:HD3	1.86	0.43
10:J:93:ARG:HH11	10:J:93:ARG:HB3	1.84	0.43
16:P:129:GLY:HA2	38:P:153:HOH:O	2.18	0.43
16:P:58:SER:HB3	38:0:5616:HOH:O	2.18	0.43
23:W:122:ARG:NH2	38:0:5280:HOH:O	2.51	0.43
24:X:34:ARG:NH1	24:X:48:VAL:O	2.51	0.43
30:0:1095:U:H2'	30:0:1096:U:O4'	2.18	0.42
30:0:1552:G:C6	30:0:1634:G:C6	3.07	0.42
30:0:1748:U:C5	30:0:1749:U:C4	3.07	0.42
30:0:1882:C:O2'	30:0:2012:U:OP2	2.32	0.42
30:0:2070:G:H2'	30:0:2072:G:OP1	2.19	0.42
30:0:2499:U:H1'	38:0:9433:HOH:O	2.19	0.42
30:0:2553:A:H2'	30:0:2553:A:N3	2.34	0.42
30:0:2587:OMU:H2'	30:0:2589:U:H5''	2.01	0.42
30:0:290:C:C2'	30:0:291:C:H5'	2.49	0.42
30:0:412:C:O2'	30:0:413:G:H5'	2.18	0.42
30:0:612:U:H2'	30:0:613:C:H6	1.84	0.42
31:9:65:A:N6	31:9:112:U:C6	2.86	0.42
2:B:141:ARG:HD2	2:B:163:GLU:OE2	2.19	0.42
10:J:131:THR:HG22	10:J:133:GLY:N	2.34	0.42
12:L:117:GLU:HG3	12:L:117:GLU:O	2.19	0.42
12:L:150:GLN:HB3	38:L:9032:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1562:C:N4	38:0:5849:HOH:O	2.49	0.42
30:0:1878:G:H4'	38:0:6104:HOH:O	2.19	0.42
30:0:1878:G:H5''	38:0:5160:HOH:O	2.18	0.42
30:0:2061:C:H2'	30:0:2062:A:H5'	1.99	0.42
30:0:2415:A:H2'	30:0:2416:G:H5'	2.01	0.42
30:0:271:C:C2	30:0:273:G:O4'	2.73	0.42
30:0:2842:G:H2'	30:0:2843:A:C5'	2.48	0.42
30:0:696:C:H4'	38:0:7268:HOH:O	2.19	0.42
30:0:706:G:N2	30:0:707:C:H41	2.17	0.42
1:A:135:VAL:HG22	1:A:136:ALA:N	2.35	0.42
5:E:146:ALA:O	5:E:150:GLN:HG2	2.19	0.42
15:O:105:ASN:HD21	15:O:109:SER:N	2.17	0.42
15:O:112:ARG:NH2	30:0:719:C:O2'	2.52	0.42
17:Q:64:GLU:HG3	17:Q:74:ASP:OD2	2.18	0.42
30:0:113:A:H3'	30:0:114:A:C5'	2.48	0.42
30:0:1206:U:H3'	30:0:1206:U:C6	2.55	0.42
30:0:128:A:C8	30:0:128:A:C3'	2.99	0.42
30:0:1345:A:H2'	30:0:1346:U:C6	2.54	0.42
30:0:1407:A:O2'	30:0:1408:U:H3'	2.20	0.42
30:0:1544:U:O2'	30:0:1545:C:H5'	2.19	0.42
30:0:1757:U:H6	30:0:1757:U:O5'	2.03	0.42
30:0:2035:C:H6	30:0:2035:C:O5'	2.02	0.42
30:0:276:C:O5'	30:0:276:C:H6	2.02	0.42
30:0:2787:C:H5	38:0:4627:HOH:O	2.02	0.42
27:1:25:LYS:HD2	28:2:48:ASP:HA	2.02	0.42
1:A:8:ARG:HG2	38:A:8978:HOH:O	2.20	0.42
2:B:217:ARG:HG3	2:B:257:THR:CG2	2.41	0.42
2:B:17:LYS:O	2:B:260:HIS:HD2	2.02	0.42
2:B:62:ARG:HA	2:B:65:MET:HE2	2.01	0.42
2:B:8:LYS:HG3	2:B:220:VAL:HG12	2.01	0.42
12:L:11:ARG:O	30:0:903:U:C2	2.72	0.42
13:M:84:LYS:HB2	30:0:170:U:OP1	2.18	0.42
16:P:105:LEU:HD21	16:P:137:LEU:HD11	2.01	0.42
17:Q:2:SER:HA	38:0:6711:HOH:O	2.19	0.42
23:W:142:ASP:HB3	23:W:145:GLY:H	1.83	0.42
30:0:1173:A:C2	30:0:1177:A:C8	3.07	0.42
30:0:1393:A:N1	30:0:1725:C:O2'	2.44	0.42
30:0:1585:C:H2'	30:0:1586:G:H8	1.84	0.42
30:0:1804:A:H2'	30:0:1805:G:C8	2.53	0.42
30:0:1902:G:C2	30:0:1936:C:C2	3.07	0.42
30:0:2709:G:N2	38:0:7613:HOH:O	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2828:G:H8	30:0:2828:G:O5'	2.03	0.42
18:R:68:HIS:O	30:0:2842:G:H5'	2.19	0.42
30:0:707:C:C2	30:0:708:A:C8	3.07	0.42
29:3:3:MET:HA	29:3:4:PRO:HD2	1.86	0.42
1:A:135:VAL:HG11	1:A:147:ARG:NH2	2.34	0.42
1:A:70:ALA:HA	1:A:71:PRO:HD3	1.73	0.42
4:D:50:VAL:HG13	31:9:41:C:O4'	2.19	0.42
4:D:54:ALA:HB2	30:0:2346:C:H5'	2.01	0.42
5:E:126:ILE:HA	5:E:131:LEU:HD23	2.00	0.42
11:K:79:PRO:HB3	11:K:87:ARG:HB3	2.02	0.42
12:L:7:GLN:HB3	12:L:13:HIS:CE1	2.54	0.42
13:M:97:ILE:HG21	13:M:127:LYS:HD2	2.01	0.42
30:0:1321:A:H2'	30:0:1322:G:C8	2.55	0.42
30:0:1420:C:O2	30:0:1420:C:H2'	2.19	0.42
30:0:1933:G:O2'	30:0:1934:A:H5'	2.19	0.42
30:0:2480:G:O2'	30:0:2481:G:H5'	2.19	0.42
30:0:407:A:H3'	38:0:4452:HOH:O	2.19	0.42
30:0:420:U:O4'	30:0:1920:C:C4	2.73	0.42
30:0:727:G:H3'	30:0:728:C:C6	2.54	0.42
30:0:849:C:H2'	30:0:850:U:O4'	2.20	0.42
30:0:939:A:N1	30:0:1027:G:O2'	2.45	0.42
31:9:58:G:H3'	31:9:59:C:C6	2.54	0.42
2:B:310:ARG:HB3	38:B:9121:HOH:O	2.19	0.42
10:J:45:VAL:CG2	10:J:129:PHE:HD1	2.32	0.42
11:K:64:MET:HA	11:K:67:GLN:HE21	1.84	0.42
12:L:53:ARG:NH2	12:L:57:VAL:HG12	2.34	0.42
16:P:103:THR:O	16:P:107:GLU:HG3	2.19	0.42
19:S:6:LYS:HD3	38:S:2519:HOH:O	2.20	0.42
23:W:128:VAL:HG22	30:0:1098:A:OP1	2.19	0.42
30:0:1006:A:H2'	30:0:1007:A:C8	2.55	0.42
13:M:188:ARG:NH1	30:0:154:C:H3'	2.35	0.42
30:0:1559:A:C8	30:0:1559:A:OP2	2.70	0.42
30:0:154:C:O2'	30:0:155:C:H5'	2.18	0.42
2:B:234:ARG:NH2	30:0:2039:A:OP2	2.53	0.42
30:0:273:G:H2'	30:0:274:G:O4'	2.20	0.42
30:0:299:U:C2	30:0:300:U:C5	3.08	0.42
30:0:571:C:H6	30:0:571:C:O5'	2.02	0.42
29:3:29:ARG:HG2	29:3:30:GLN:N	2.35	0.42
2:B:101:TRP:HB2	2:B:119:HIS:CD2	2.54	0.42
2:B:145:HIS:CD2	2:B:146:THR:O	2.63	0.42
2:B:215:VAL:HA	2:B:220:VAL:HG22	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:112:ALA:HA	5:E:113:PRO:HD3	1.77	0.42
5:E:137:ASP:OD1	5:E:139:GLU:HB2	2.19	0.42
8:H:61:ARG:HG3	8:H:61:ARG:HH11	1.85	0.42
30:0:1168:C:C5	30:0:1169:U:C4	3.08	0.42
30:0:137:U:OP1	30:0:259:G:O2'	2.36	0.42
30:0:1454:U:H5''	30:0:1455:C:OP2	2.19	0.42
30:0:17:G:H2'	30:0:18:C:H6	1.84	0.42
1:A:217:ARG:NH2	30:0:1853:C:O2'	2.53	0.42
30:0:1883:U:O2'	30:0:1884:G:H5'	2.19	0.42
30:0:1924:A:H1'	38:0:5731:HOH:O	2.19	0.42
30:0:2274:A:H2'	30:0:2275:G:C8	2.54	0.42
8:H:117:ARG:HH12	30:0:2287:C:N4	2.17	0.42
30:0:2321:A:C5	30:0:2323:G:C8	3.07	0.42
30:0:947:U:O2'	30:0:948:G:H5'	2.20	0.42
2:B:314:ALA:HB3	2:B:317:PRO:HG3	2.02	0.42
13:M:172:GLY:HA2	38:0:9086:HOH:O	2.19	0.42
13:M:46:LEU:HD22	13:M:50:ARG:CD	2.50	0.42
14:N:143:ARG:HG2	14:N:172:PHE:CD2	2.54	0.42
30:0:1188:A:C5	30:0:1189:A:N1	2.88	0.42
30:0:1539:U:O2'	30:0:1540:G:H5'	2.20	0.42
30:0:1576:G:H2'	30:0:1577:U:C6	2.54	0.42
30:0:162:C:H2'	30:0:163:U:H5'	2.02	0.42
30:0:1815:A:H2'	30:0:1816:C:O4'	2.20	0.42
1:A:190:ARG:NH1	30:0:1845:A:OP2	2.53	0.42
30:0:2354:A:C2	30:0:2367:A:C8	3.08	0.42
30:0:2671:U:C2'	30:0:2672:C:O5'	2.68	0.42
30:0:2673:U:O2'	30:0:2674:G:H5'	2.20	0.42
30:0:2690:U:C4	30:0:2691:A:C5	3.07	0.42
30:0:644:G:N3	30:0:644:G:H5'	2.35	0.42
30:0:918:G:C2	30:0:926:A:C2	3.08	0.42
29:3:64:LYS:HB3	29:3:82:GLY:O	2.20	0.42
31:9:116:C:O2'	31:9:117:G:H5'	2.20	0.42
31:9:91:C:H2'	31:9:92:G:O4'	2.18	0.42
2:B:252:PRO:HD3	38:0:9818:HOH:O	2.18	0.42
8:H:151:GLU:HA	8:H:151:GLU:OE1	2.19	0.42
13:M:74:LYS:HB3	38:M:8944:HOH:O	2.20	0.42
19:S:8:PRO:HD2	22:V:32:ALA:HA	2.02	0.42
20:T:106:GLU:HG3	38:T:4913:HOH:O	2.20	0.42
11:K:132:VAL:HG11	21:U:22:VAL:HG22	2.02	0.42
22:V:39:ALA:C	22:V:41:GLU:H	2.22	0.42
24:X:70:ILE:O	24:X:70:ILE:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:42:TYR:HA	30:0:1829:A:N6	2.35	0.42
30:0:1198:U:H2'	30:0:1200:A:OP2	2.20	0.42
30:0:1200:A:H4'	38:0:7330:HOH:O	2.19	0.42
30:0:1474:C:C5'	30:0:1474:C:C6	2.89	0.42
30:0:151:A:H2'	30:0:152:A:C8	2.55	0.42
30:0:1573:A:H2'	30:0:1574:C:O4'	2.20	0.42
30:0:2332:A:H2'	38:0:5623:HOH:O	2.19	0.42
30:0:2458:U:O2'	30:0:2459:G:H5'	2.20	0.42
30:0:2474:A:N7	30:0:2621:PSU:H4'	2.34	0.42
30:0:2893:C:O2'	30:0:2894:C:H5'	2.19	0.42
30:0:710:G:O2'	30:0:711:G:H5'	2.20	0.42
30:0:820:G:O2'	30:0:856:G:H4'	2.20	0.42
28:2:43:ARG:HH22	30:0:1684:A:C1'	2.26	0.42
8:H:10:ARG:HD2	8:H:161:THR:HG21	2.01	0.42
10:J:74:ARG:O	10:J:78:ILE:HG12	2.20	0.42
13:M:187:LEU:HD22	13:M:194:GLY:HA3	2.01	0.42
13:M:48:LYS:HE3	13:M:52:GLN:NE2	2.34	0.42
25:Y:160:LYS:HA	25:Y:160:LYS:HD3	1.87	0.42
25:Y:189:ASN:HD22	25:Y:189:ASN:C	2.23	0.42
10:J:52:GLN:HE21	30:0:1119:G:H5'	1.84	0.42
30:0:1158:G:H2'	30:0:1159:G:C5'	2.50	0.42
30:0:1181:A:N1	30:0:1192:A:O2'	2.45	0.42
30:0:1314:U:H5''	30:0:1316:G:O4'	2.19	0.42
30:0:1538:C:O2'	30:0:1539:U:H5'	2.19	0.42
30:0:1585:C:H2'	30:0:1586:G:C8	2.54	0.42
30:0:1794:G:N2	30:0:1796:A:H3'	2.35	0.42
30:0:191:A:H2'	30:0:237:G:O6	2.20	0.42
30:0:364:U:H2'	30:0:365:G:O4'	2.20	0.42
18:R:98:ASN:ND2	30:0:500:G:H21	2.11	0.42
31:9:29:C:C5	31:9:30:C:C6	3.08	0.42
1:A:94:LEU:HD12	1:A:98:GLU:CB	2.47	0.42
18:R:89:LEU:HA	18:R:89:LEU:HD23	1.82	0.42
20:T:48:VAL:CG1	20:T:96:VAL:HG13	2.50	0.42
23:W:139:GLY:O	23:W:141:HIS:CD2	2.73	0.42
24:X:10:VAL:HG11	24:X:36:HIS:HE1	1.85	0.42
30:0:1135:G:H5'	38:0:5913:HOH:O	2.19	0.41
30:0:1316:G:H5''	38:0:5311:HOH:O	2.20	0.41
30:0:1345:A:H2'	30:0:1346:U:H6	1.85	0.41
30:0:1359:U:C5	30:0:2101:A:H8	2.38	0.41
30:0:1531:U:O2	30:0:1661:A:C2	2.73	0.41
30:0:1734:C:H6	30:0:1734:C:O5'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:SER:HB3	30:0:1872:C:H5	1.85	0.41
6:F:54:VAL:HG13	30:0:263:U:C4	2.55	0.41
30:0:299:U:H2'	30:0:300:U:H6	1.85	0.41
31:9:73:A:N1	31:9:108:C:O2	2.53	0.41
2:B:49:THR:HG22	2:B:331:SER:HB3	2.02	0.41
9:I:91:PHE:CD2	9:I:131:GLY:HA2	2.44	0.41
10:J:42:GLU:HG2	10:J:43:ARG:N	2.34	0.41
23:W:21:LEU:HD21	23:W:48:VAL:CG1	2.48	0.41
26:Z:41:ARG:HD3	38:Z:8717:HOH:O	2.19	0.41
25:Y:154:ARG:NH2	30:0:1071:G:H4'	2.36	0.41
30:0:1333:U:H2'	30:0:1334:C:C6	2.54	0.41
30:0:1405:U:H2'	38:0:6827:HOH:O	2.20	0.41
30:0:1441:G:H1'	38:0:7755:HOH:O	2.19	0.41
30:0:1572:A:C2	30:0:1573:A:C4	3.08	0.41
30:0:1832:G:H5''	38:0:9044:HOH:O	2.19	0.41
30:0:1926:G:C4	30:0:1927:A:C8	3.08	0.41
30:0:1980:U:O2'	30:0:1981:A:H5'	2.20	0.41
30:0:1997:A:C6	30:0:1998:G:C5	3.09	0.41
30:0:257:G:N2	30:0:258:G:C4	2.88	0.41
16:P:61:ARG:NH2	30:0:2737:C:OP2	2.45	0.41
30:0:34:C:H1'	38:0:9175:HOH:O	2.18	0.41
30:0:559:U:C4	30:0:560:U:C4	3.08	0.41
30:0:567:U:H5''	38:0:6387:HOH:O	2.19	0.41
30:0:820:G:N3	30:0:1831:U:H1'	2.35	0.41
31:9:3:A:C8	31:9:26:C:O2	2.72	0.41
1:A:135:VAL:HG11	1:A:147:ARG:HH21	1.85	0.41
11:K:41:LYS:O	11:K:42:ASN:HB2	2.21	0.41
20:T:14:ALA:HA	20:T:15:PRO:HD3	1.89	0.41
20:T:52:ARG:O	30:0:317:A:OP1	2.37	0.41
26:Z:65:ASN:ND2	26:Z:84:CYS:SG	2.91	0.41
30:0:1116:U:C2'	30:0:1118:A:C2	3.04	0.41
30:0:1168:C:C4	30:0:1169:U:C4	3.08	0.41
30:0:1168:C:C5	30:0:1169:U:C5	3.09	0.41
30:0:2675:A:H1'	30:0:2813:A:C2	2.56	0.41
30:0:282:C:O2'	30:0:283:U:C4'	2.69	0.41
30:0:2909:G:H2'	30:0:2910:A:H8	1.85	0.41
30:0:778:C:C4	30:0:779:U:C4	3.08	0.41
30:0:818:A:C6	30:0:819:A:C2	3.07	0.41
28:2:40:ARG:HD2	28:2:47:THR:HG22	2.01	0.41
31:9:119:C:H2'	31:9:120:A:C8	2.55	0.41
31:9:39:U:C2'	31:9:40:C:OP1	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:ARG:NH2	1:A:69:LEU:HD11	2.36	0.41
3:C:19:PRO:HG2	3:C:22:PHE:CE1	2.56	0.41
5:E:101:GLU:HA	5:E:118:ILE:HG13	2.01	0.41
15:O:29:VAL:HG11	15:O:98:LEU:HD21	2.02	0.41
20:T:71:VAL:CG1	20:T:90:PRO:HB3	2.40	0.41
30:0:1015:C:C2	30:0:1016:U:C5	3.09	0.41
30:0:1246:A:C5	30:0:1248:A:C5	3.09	0.41
30:0:1607:A:C4	30:0:1608:G:C8	3.08	0.41
30:0:2011:A:H5'	30:0:2013:G:H1'	2.01	0.41
30:0:2092:G:H5''	30:0:2613:G:OP1	2.21	0.41
30:0:2874:G:H3'	38:0:9578:HOH:O	2.21	0.41
30:0:271:C:N4	30:0:378:A:C2	2.76	0.41
30:0:546:C:O5'	30:0:546:C:H6	2.03	0.41
30:0:820:G:C5'	30:0:821:U:H5'	2.46	0.41
29:3:69:TYR:CE1	29:3:80:ARG:HB2	2.55	0.41
14:N:40:ASN:HD21	31:9:28:U:H5''	1.83	0.41
31:9:31:C:O2'	31:9:32:G:H5'	2.20	0.41
31:9:7:G:C5'	38:9:9099:HOH:O	2.68	0.41
14:N:42:HIS:CB	14:N:62:HIS:HE1	2.33	0.41
30:0:1183:C:O2	30:0:1183:C:C2'	2.68	0.41
30:0:1191:A:H3'	30:0:1191:A:H8	1.84	0.41
23:W:117:ARG:HD3	30:0:1287:A:O4'	2.20	0.41
30:0:932:U:H1'	30:0:1296:A:H1'	2.02	0.41
30:0:1335:C:H2'	30:0:1336:U:C6	2.56	0.41
30:0:1545:C:H2'	30:0:1546:G:O4'	2.20	0.41
30:0:2799:A:N6	30:0:2801:A:C2	2.89	0.41
30:0:293:A:P	30:0:358:G:H22	2.43	0.41
30:0:488:U:H2'	38:0:4003:HOH:O	2.20	0.41
30:0:652:G:H8	38:0:3003:HOH:O	2.03	0.41
29:3:46:ILE:HA	38:0:7897:HOH:O	2.20	0.41
31:9:112:U:H2'	31:9:113:C:H5'	2.02	0.41
31:9:1:U:O3'	31:9:3:A:OP1	2.39	0.41
31:9:9:C:H2'	31:9:10:C:H5'	2.03	0.41
9:I:123:VAL:O	9:I:127:CYS:SG	2.78	0.41
10:J:116:LEU:HB2	10:J:119:THR:HG21	2.02	0.41
13:M:68:ARG:CZ	13:M:73:ARG:HD3	2.51	0.41
16:P:3:LEU:HA	16:P:6:GLN:OE1	2.21	0.41
17:Q:21:ARG:HG2	17:Q:22:GLY:H	1.86	0.41
22:V:12:THR:H	22:V:15:GLU:HB2	1.85	0.41
25:Y:187:VAL:HG13	25:Y:205:ILE:HA	2.02	0.41
12:L:6:ARG:NH1	30:0:1299:G:N7	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1362:U:H2'	30:0:1363:G:C8	2.55	0.41
30:0:1427:A:O2'	30:0:1428:C:H5'	2.21	0.41
30:0:1563:G:H4'	30:0:1564:C:H5'	2.01	0.41
30:0:1757:U:H5	38:0:3211:HOH:O	2.03	0.41
30:0:1903:U:O2'	30:0:1904:A:C8	2.73	0.41
30:0:1915:U:H2'	30:0:1916:C:O4'	2.21	0.41
30:0:2409:C:H5''	38:0:4005:HOH:O	2.20	0.41
30:0:2092:G:H2'	30:0:2613:G:OP1	2.21	0.41
30:0:69:A:H2'	30:0:70:A:OP2	2.20	0.41
30:0:69:A:C2'	30:0:70:A:OP2	2.69	0.41
30:0:822:C:C2	30:0:823:U:C5	3.08	0.41
27:1:16:HIS:CD2	30:0:470:U:O2'	2.72	0.41
28:2:2:LYS:HG3	30:0:1486:A:C4	2.55	0.41
29:3:73:GLU:HB3	38:3:9056:HOH:O	2.21	0.41
1:A:194:MET:CE	1:A:199:HIS:HB2	2.50	0.41
3:C:27:ARG:NH1	3:C:27:ARG:CG	2.79	0.41
7:G:71:LEU:C	7:G:73:ASP:H	2.23	0.41
11:K:34:VAL:CG2	11:K:47:ALA:HB2	2.51	0.41
13:M:77:HIS:CG	13:M:81:ARG:HB2	2.56	0.41
14:N:23:ARG:O	14:N:27:LEU:HG	2.21	0.41
16:P:80:ARG:HG2	16:P:87:ARG:CZ	2.50	0.41
17:Q:16:ASN:HA	17:Q:16:ASN:HD22	1.67	0.41
18:R:17:MET:HE3	18:R:19:ARG:HH21	1.86	0.41
23:W:24:LEU:HD21	23:W:44:MET:SD	2.61	0.41
30:0:1051:C:H2'	30:0:1052:G:O4'	2.20	0.41
30:0:130:C:H2'	38:0:3150:HOH:O	2.21	0.41
30:0:1339:G:C6	30:0:1340:G:N1	2.89	0.41
30:0:186:A:H4'	30:0:186:A:OP1	2.21	0.41
30:0:1947:G:H2'	30:0:1948:G:C8	2.55	0.41
30:0:2872:U:C2	30:0:2873:C:C6	3.08	0.41
30:0:2880:A:H2'	30:0:2881:C:H5'	2.02	0.41
30:0:396:U:H1'	30:0:397:A:OP1	2.20	0.41
30:0:536:A:N1	30:0:2075:G:O2'	2.50	0.41
30:0:964:G:C4	30:0:965:A:C8	3.08	0.41
31:9:70:U:H2'	31:9:71:C:O4'	2.20	0.41
4:D:84:LEU:HA	4:D:87:ALA:HB3	2.02	0.41
5:E:155:ASN:ND2	5:E:155:ASN:H	2.17	0.41
5:E:77:THR:OG1	5:E:78:GLU:N	2.52	0.41
16:P:13:VAL:HG13	16:P:14:LEU:N	2.36	0.41
23:W:23:MET:O	30:0:1025:C:H5'	2.21	0.41
23:W:38:THR:HG22	38:W:3580:HOH:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1215:A:O3'	30:0:1216:G:C4'	2.69	0.41
30:0:1337:G:C6	30:0:1338:U:C4	3.09	0.41
30:0:1682:A:H5''	38:0:9458:HOH:O	2.20	0.41
30:0:240:C:O2	30:0:240:C:H2'	2.20	0.41
30:0:2780:C:C4	30:0:2781:U:C4	3.09	0.41
30:0:2892:G:C6	30:0:2893:C:C4	3.09	0.41
30:0:397:A:H1'	30:0:417:G:H1'	2.03	0.41
30:0:706:G:O2'	30:0:707:C:H6	2.03	0.41
30:0:73:U:O2'	30:0:74:G:H5'	2.21	0.41
30:0:800:G:H2'	30:0:801:U:C6	2.56	0.41
3:C:22:PHE:HA	3:C:116:ALA:HA	2.02	0.41
30:0:99:A:C8	30:0:100:C:C6	3.09	0.41
30:0:1244:U:H4'	30:0:1246:A:O4'	2.21	0.41
30:0:1423:C:O2'	30:0:1424:A:H5'	2.20	0.41
30:0:1523:G:C5	30:0:1524:U:C4	3.08	0.41
30:0:1819:G:C2'	30:0:1820:G:H5'	2.50	0.41
30:0:1834:C:H2'	30:0:1840:A:H62	1.82	0.41
30:0:210:U:O2'	30:0:211:U:H5'	2.21	0.41
30:0:2296:C:H2'	30:0:2297:U:C6	2.56	0.41
2:B:27:ASN:HD21	30:0:2807:U:P	2.43	0.41
30:0:37:A:C2	30:0:446:G:C2	3.09	0.41
30:0:565:A:N6	30:0:593:A:C8	2.88	0.41
29:3:88:LEU:HD22	33:3:8804:CL:CL	2.58	0.41
1:A:45:ILE:HD12	26:Z:89:THR:HG23	2.02	0.41
2:B:274:GLU:HA	2:B:292:GLY:O	2.21	0.41
3:C:44:GLN:HA	38:C:8614:HOH:O	2.21	0.41
4:D:15:GLU:HA	4:D:16:PRO:HD3	1.73	0.41
11:K:75:ARG:HD2	11:K:90:PHE:CD2	2.55	0.41
14:N:48:VAL:HG11	14:N:55:ASP:HB3	2.02	0.41
20:T:32:ARG:NH1	20:T:38:ARG:NH1	2.68	0.41
26:Z:54:GLU:HB3	38:Z:8731:HOH:O	2.21	0.41
30:0:1351:G:H1'	38:0:4673:HOH:O	2.21	0.41
30:0:2345:A:H3'	30:0:2346:C:C5	2.56	0.41
30:0:2438:G:C6	30:0:2439:C:C4	3.08	0.41
31:9:75:G:H1	31:9:106:U:H3	1.69	0.41
2:B:58:PRO:HA	2:B:63:GLU:CD	2.40	0.41
2:B:69:VAL:HA	2:B:70:PRO:HD3	1.82	0.41
3:C:87:ARG:NH2	30:0:894:A:C2	2.89	0.41
6:F:57:GLU:O	6:F:61:MET:HG3	2.21	0.41
10:J:45:VAL:HG21	10:J:129:PHE:CD1	2.56	0.41
12:L:53:ARG:HD2	30:0:2441:U:H4'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1193:A:C2	30:0:1194:A:N6	2.89	0.41
30:0:1419:U:H2'	30:0:1685:A:C2	2.56	0.41
30:0:1769:C:C2'	30:0:1770:U:H5'	2.51	0.41
30:0:2002:C:C2'	30:0:2003:U:H5'	2.50	0.41
30:0:2064:U:H5'	30:0:2652:U:O3'	2.21	0.41
13:M:193:LYS:HB3	30:0:392:U:C5'	2.51	0.41
30:0:407:A:H8	38:0:4452:HOH:O	2.04	0.41
30:0:375:G:C4	30:0:411:A:C6	3.09	0.41
30:0:39:G:C2	30:0:444:C:N3	2.89	0.41
30:0:622:G:O2'	30:0:623:U:H5'	2.21	0.41
30:0:685:C:O2	30:0:748:C:H4'	2.21	0.41
15:O:68:GLY:HA3	30:0:745:G:O6	2.20	0.41
27:1:38:GLY:HA3	38:1:6935:HOH:O	2.20	0.41
4:D:53:LYS:HE3	31:9:40:C:H42	1.85	0.41
1:A:191:GLY:HA2	1:A:194:MET:HE2	2.02	0.41
1:A:33:GLU:CD	1:A:33:GLU:H	2.24	0.41
1:A:47:HIS:CD2	30:0:1654:U:C2'	3.02	0.41
2:B:243:ASN:HA	2:B:244:PRO:C	2.41	0.41
2:B:244:PRO:HG3	2:B:248:ARG:NH2	2.35	0.41
3:C:127:ARG:HD3	3:C:129:HIS:CE1	2.56	0.41
13:M:158:ARG:HB2	13:M:163:LEU:HB2	2.02	0.41
14:N:22:GLN:HG3	30:0:2415:A:H2	1.85	0.41
16:P:81:LYS:HG2	38:0:9540:HOH:O	2.20	0.41
21:U:20:MET:HG3	21:U:28:THR:HG23	2.03	0.41
24:X:43:VAL:HG12	24:X:44:ASP:H	1.84	0.41
25:Y:126:PRO:HG2	25:Y:128:PHE:CZ	2.56	0.41
30:0:1008:C:H2'	30:0:1009:U:C6	2.56	0.40
30:0:1327:G:C6	30:0:1331:G:C6	3.09	0.40
30:0:1656:A:H2'	30:0:1657:A:O4'	2.21	0.40
30:0:2765:C:H2'	30:0:2766:A:C8	2.56	0.40
30:0:375:G:C2	30:0:411:A:C2	3.08	0.40
31:9:14:G:C8	31:9:14:G:C5'	2.95	0.40
4:D:172:VAL:HG12	4:D:173:GLU:N	2.36	0.40
8:H:12:ILE:HG12	8:H:59:GLN:HG3	2.02	0.40
10:J:47:THR:O	10:J:53:ILE:HD11	2.21	0.40
13:M:46:LEU:HD22	13:M:50:ARG:HD2	2.03	0.40
13:M:95:LYS:HA	13:M:170:ASN:HD21	1.86	0.40
19:S:42:GLU:HG2	19:S:49:VAL:HG23	2.03	0.40
26:Z:53:ILE:HG23	26:Z:93:TYR:HB3	2.02	0.40
26:Z:65:ASN:HD22	26:Z:84:CYS:CB	2.33	0.40
30:0:1398:G:H2'	30:0:1399:A:H8	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1531:U:C2	30:0:1661:A:C2	3.10	0.40
30:0:1576:G:H2'	30:0:1577:U:H6	1.87	0.40
30:0:1577:U:O2'	30:0:1578:C:H5'	2.21	0.40
30:0:1589:G:C2	30:0:1605:G:N3	2.89	0.40
30:0:1497:G:H4'	30:0:1627:G:O2'	2.21	0.40
30:0:1626:A:H2'	30:0:1627:G:O4'	2.21	0.40
30:0:1543:G:N1	30:0:1641:A:OP2	2.41	0.40
30:0:1947:G:N2	30:0:1966:U:C2	2.89	0.40
30:0:1972:U:O2'	30:0:1973:A:H5''	2.22	0.40
30:0:2319:C:H2'	30:0:2320:U:H5'	2.03	0.40
30:0:245:C:N4	30:0:246:G:C6	2.89	0.40
30:0:2526:C:H6	30:0:2526:C:H3'	1.86	0.40
30:0:559:U:C6	30:0:559:U:H3'	2.57	0.40
27:1:28:HIS:CE1	27:1:31:LYS:HE2	2.56	0.40
1:A:47:HIS:HA	38:A:9024:HOH:O	2.20	0.40
5:E:139:GLU:OE2	30:0:2781:U:C1'	2.68	0.40
5:E:166:VAL:HB	38:E:6341:HOH:O	2.19	0.40
7:G:19:GLU:O	7:G:23:ILE:HG13	2.21	0.40
10:J:19:MET:HE3	10:J:132:LEU:HD11	2.03	0.40
10:J:127:ILE:HG22	33:J:8801:CL:CL	2.58	0.40
11:K:74:VAL:HG12	11:K:75:ARG:HG3	2.02	0.40
12:L:73:VAL:HG23	12:L:74:THR:H	1.86	0.40
16:P:7:LYS:HD3	16:P:21:VAL:HG22	2.03	0.40
17:Q:80:LYS:HG2	17:Q:82:LYS:HE3	2.02	0.40
23:W:4:LEU:HA	23:W:4:LEU:HD23	1.88	0.40
30:0:1074:G:H4'	30:0:1260:G:C6	2.57	0.40
30:0:1333:U:H2'	30:0:1334:C:H6	1.86	0.40
30:0:1461:U:H1'	38:0:7457:HOH:O	2.21	0.40
30:0:1749:U:O2	30:0:1751:G:C8	2.75	0.40
30:0:1926:G:H2'	30:0:1927:A:H8	1.86	0.40
30:0:2867:G:H2'	30:0:2868:C:H6	1.86	0.40
30:0:372:A:H2'	30:0:373:G:H8	1.86	0.40
30:0:464:G:HO2'	30:0:465:U:P	2.44	0.40
30:0:611:U:O5'	30:0:611:U:H6	2.05	0.40
30:0:727:G:N2	30:0:728:C:H1'	2.36	0.40
31:9:2:U:OP2	31:9:2:U:H4'	2.22	0.40
2:B:148:PRO:HD2	38:B:9047:HOH:O	2.21	0.40
3:C:168:ARG:NH2	3:C:190:ALA:O	2.55	0.40
9:I:120:ALA:O	9:I:124:VAL:HG23	2.21	0.40
9:I:78:ALA:HB1	9:I:93:ALA:CB	2.51	0.40
10:J:57:TYR:O	10:J:61:VAL:HG23	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:117:GLU:HG2	38:L:9025:HOH:O	2.20	0.40
13:M:64:ARG:HD2	38:M:8879:HOH:O	2.21	0.40
13:M:74:LYS:O	13:M:88:VAL:HG22	2.21	0.40
26:Z:65:ASN:CB	26:Z:84:CYS:SG	3.08	0.40
30:0:113:A:OP2	30:0:114:A:H2'	2.21	0.40
25:Y:210:GLY:N	30:0:1313:A:H5''	2.36	0.40
30:0:1936:C:H2'	30:0:1937:U:C6	2.56	0.40
30:0:1982:C:H2'	30:0:1983:C:O4'	2.21	0.40
30:0:2248:C:H2'	30:0:2249:G:C8	2.54	0.40
8:H:8:MET:SD	30:0:2494:G:H4'	2.61	0.40
30:0:2803:C:H2'	30:0:2804:C:H6	1.86	0.40
24:X:39:LYS:HE2	30:0:2834:G:OP1	2.22	0.40
30:0:2826:G:C6	30:0:2913:A:C6	3.10	0.40
31:9:27:C:C4	31:9:28:U:C5	3.09	0.40
1:A:105:VAL:HG13	1:A:155:THR:O	2.21	0.40
2:B:294:TYR:HE2	38:B:9123:HOH:O	2.03	0.40
8:H:91:ARG:O	30:0:1003:U:H4'	2.22	0.40
12:L:56:LYS:NZ	38:L:9036:HOH:O	2.54	0.40
12:L:67:ARG:O	12:L:71:GLU:HG3	2.22	0.40
14:N:58:LEU:HD12	14:N:58:LEU:H	1.85	0.40
16:P:89:ASN:HB3	16:P:92:GLU:HB2	2.03	0.40
30:0:1130:U:H4'	38:0:6109:HOH:O	2.21	0.40
30:0:1135:G:O2'	30:0:1136:U:H5'	2.22	0.40
30:0:1163:G:C2	30:0:1184:C:N3	2.89	0.40
30:0:1191:A:H3'	30:0:1191:A:C8	2.56	0.40
30:0:1397:C:O2'	30:0:1398:G:H5'	2.22	0.40
30:0:1589:G:H5'	38:0:6843:HOH:O	2.20	0.40
30:0:1815:A:H4'	30:0:2751:C:O4'	2.22	0.40
30:0:2321:A:H1'	30:0:2322:U:H3'	2.04	0.40
30:0:2295:G:N3	30:0:2361:A:H2	2.17	0.40
30:0:2694:A:C6	30:0:2702:A:C8	3.09	0.40
30:0:2803:C:C4	30:0:2804:C:C5	3.10	0.40
30:0:506:G:N2	30:0:509:A:H5'	2.31	0.40
30:0:724:G:O2'	30:0:725:C:H5'	2.21	0.40
30:0:763:C:O2'	30:0:764:C:H5'	2.21	0.40
1:A:164:ARG:NH2	30:0:1877:G:OP1	2.53	0.40
1:A:88:ILE:HG22	1:A:88:ILE:O	2.20	0.40
2:B:10:SER:O	2:B:16:ARG:NH1	2.45	0.40
13:M:34:GLU:HB3	13:M:38:GLU:HG3	2.02	0.40
16:P:59:ARG:HD3	38:0:6252:HOH:O	2.22	0.40
20:T:21:LYS:HA	20:T:24:ARG:HD2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:139:GLY:O	23:W:141:HIS:HD2	2.04	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%)	202 (86%)	27 (12%)	6 (3%)	5	24
2	B	335/338 (99%)	309 (92%)	17 (5%)	9 (3%)	5	23
3	C	244/246 (99%)	222 (91%)	20 (8%)	2 (1%)	19	53
4	D	134/177 (76%)	110 (82%)	20 (15%)	4 (3%)	4	20
5	E	170/178 (96%)	157 (92%)	12 (7%)	1 (1%)	25	60
6	F	117/120 (98%)	106 (91%)	7 (6%)	4 (3%)	3	17
7	G	25/348 (7%)	24 (96%)	1 (4%)	0	100	100
8	H	156/177 (88%)	144 (92%)	10 (6%)	2 (1%)	12	41
9	I	68/162 (42%)	52 (76%)	12 (18%)	4 (6%)	1	7
10	J	140/145 (97%)	131 (94%)	8 (6%)	1 (1%)	22	56
11	K	130/132 (98%)	121 (93%)	8 (6%)	1 (1%)	19	53
12	L	141/165 (86%)	120 (85%)	21 (15%)	0	100	100
13	M	192/196 (98%)	179 (93%)	9 (5%)	4 (2%)	7	29
14	N	184/187 (98%)	163 (89%)	17 (9%)	4 (2%)	6	28
15	O	113/116 (97%)	107 (95%)	6 (5%)	0	100	100
16	P	141/149 (95%)	133 (94%)	8 (6%)	0	100	100
17	Q	93/96 (97%)	85 (91%)	7 (8%)	1 (1%)	14	46
18	R	148/155 (96%)	140 (95%)	7 (5%)	1 (1%)	22	56
19	S	79/85 (93%)	74 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	T	117/120 (98%)	107 (92%)	8 (7%)	2 (2%)	9	34
21	U	51/67 (76%)	42 (82%)	8 (16%)	1 (2%)	7	30
22	V	63/71 (89%)	58 (92%)	5 (8%)	0	100	100
23	W	152/154 (99%)	140 (92%)	10 (7%)	2 (1%)	12	41
24	X	80/92 (87%)	74 (92%)	4 (5%)	2 (2%)	5	25
25	Y	140/241 (58%)	137 (98%)	3 (2%)	0	100	100
26	Z	71/116 (61%)	58 (82%)	8 (11%)	5 (7%)	1	4
27	1	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
28	2	42/50 (84%)	39 (93%)	2 (5%)	1 (2%)	6	26
29	3	90/92 (98%)	74 (82%)	13 (14%)	3 (3%)	4	18
All	All	3705/4472 (83%)	3359 (91%)	286 (8%)	60 (2%)	9	36

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	ASP
1	A	37	VAL
1	A	74	VAL
4	D	65	GLU
4	D	137	PRO
8	H	19	ARG
11	K	127	ALA
13	M	82	ARG
14	N	154	LEU
14	N	183	ASP
14	N	184	ILE
26	Z	105	ARG
29	3	64	LYS
2	B	306	LYS
6	F	61	MET
6	F	101	ALA
13	M	71	SER
21	U	51	TRP
24	X	70	ILE
26	Z	70	ARG
2	B	184	ASP
3	C	8	LEU
5	E	44	GLY

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Mol	Chain	Res	Type
6	F	27	GLY
9	I	83	GLY
20	T	44	ALA
23	W	36	PRO
23	W	49	ASN
24	X	87	ALA
26	Z	67	GLY
29	3	46	ILE
2	B	2	GLN
2	B	107	SER
4	D	56	ARG
9	I	106	GLN
13	M	86	GLN
20	T	46	ASP
26	Z	83	TYR
28	2	37	HIS
1	A	52	SER
1	A	119	ALA
2	B	206	THR
3	C	79	ARG
10	J	65	ASN
13	M	79	ALA
18	R	114	VAL
29	3	56	PRO
2	B	63	GLU
6	F	104	ALA
8	H	171	GLY
14	N	164	ASP
4	D	27	ILE
17	Q	48	PRO
2	B	34	GLY
2	B	169	GLY
26	Z	64	PRO
2	B	185	GLY
9	I	108	HIS
9	I	131	GLY
1	A	42	VAL

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%)	171 (96%)	8 (4%)	27	61
2	B	282/283 (100%)	264 (94%)	18 (6%)	17	47
3	C	193/193 (100%)	182 (94%)	11 (6%)	20	52
4	D	117/148 (79%)	110 (94%)	7 (6%)	19	50
5	E	152/156 (97%)	148 (97%)	4 (3%)	46	75
6	F	93/94 (99%)	93 (100%)	0	100	100
7	G	27/282 (10%)	26 (96%)	1 (4%)	34	66
8	H	134/145 (92%)	126 (94%)	8 (6%)	19	50
9	I	58/130 (45%)	56 (97%)	2 (3%)	37	69
10	J	118/121 (98%)	113 (96%)	5 (4%)	30	63
11	K	106/106 (100%)	104 (98%)	2 (2%)	57	81
12	L	113/127 (89%)	108 (96%)	5 (4%)	28	62
13	M	158/160 (99%)	148 (94%)	10 (6%)	18	48
14	N	149/150 (99%)	144 (97%)	5 (3%)	37	69
15	O	93/94 (99%)	92 (99%)	1 (1%)	73	89
16	P	113/117 (97%)	107 (95%)	6 (5%)	22	55
17	Q	79/80 (99%)	78 (99%)	1 (1%)	69	87
18	R	117/122 (96%)	114 (97%)	3 (3%)	46	75
19	S	71/74 (96%)	70 (99%)	1 (1%)	67	86
20	T	105/106 (99%)	99 (94%)	6 (6%)	20	52
21	U	44/53 (83%)	41 (93%)	3 (7%)	16	45
22	V	51/57 (90%)	49 (96%)	2 (4%)	32	65
23	W	130/130 (100%)	124 (95%)	6 (5%)	27	60
24	X	66/74 (89%)	61 (92%)	5 (8%)	13	39
25	Y	120/196 (61%)	115 (96%)	5 (4%)	30	63
26	Z	60/94 (64%)	57 (95%)	3 (5%)	24	57
27	1	46/47 (98%)	46 (100%)	0	100	100
28	2	42/46 (91%)	41 (98%)	1 (2%)	49	77
29	3	79/79 (100%)	76 (96%)	3 (4%)	33	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3095/3646 (85%)	2963 (96%)	132 (4%)	29 62

All (132) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	94	LEU
1	A	131	HIS
1	A	153	ARG
1	A	179	MET
1	A	192	VAL
1	A	206	ARG
1	A	217	ARG
2	B	7	ARG
2	B	11	LEU
2	B	27	ASN
2	B	71	VAL
2	B	97	LEU
2	B	98	THR
2	B	132	HIS
2	B	162	MET
2	B	191	ASN
2	B	192	ASP
2	B	195	ARG
2	B	238	ASN
2	B	248	ARG
2	B	251	VAL
2	B	254	GLN
2	B	265	LEU
2	B	277	GLU
2	B	307	ARG
3	C	2	GLN
3	C	76	ARG
3	C	88	SER
3	C	136	VAL
3	C	187	ARG
3	C	202	THR
3	C	223	LEU
3	C	234	VAL
3	C	236	THR
3	C	237	GLU
3	C	243	VAL

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Mol	Chain	Res	Type
4	D	19	GLU
4	D	24	HIS
4	D	29	HIS
4	D	50	VAL
4	D	61	PHE
4	D	149	ARG
4	D	161	ASP
5	E	7	ILE
5	E	68	HIS
5	E	126	ILE
5	E	155	ASN
7	G	73	ASP
8	H	21	GLU
8	H	33	GLN
8	H	45	ASP
8	H	61	ARG
8	H	62	HIS
8	H	87	LYS
8	H	91	ARG
8	H	157	TYR
9	I	114	TYR
9	I	115	ASP
10	J	46	ILE
10	J	52	GLN
10	J	74	ARG
10	J	107	ASN
10	J	130	VAL
11	K	10	GLN
11	K	55	VAL
12	L	35	ARG
12	L	99	GLU
12	L	101	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	82	ARG
13	M	86	GLN
13	M	93	ARG
13	M	99	ARG

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Mol	Chain	Res	Type
13	M	116	ASN
13	M	125	ARG
14	N	5	ARG
14	N	17	ARG
14	N	49	THR
14	N	56	ASP
14	N	80	SER
15	O	3	THR
16	P	21	VAL
16	P	79	SER
16	P	91	LYS
16	P	94	TRP
16	P	98	ILE
16	P	120	ARG
17	Q	16	ASN
18	R	13	THR
18	R	39	THR
18	R	143	VAL
19	S	30	ASP
20	T	5	ASP
20	T	39	ASN
20	T	73	HIS
20	T	96	VAL
20	T	115	GLU
20	T	117	ASP
21	U	25	ASP
21	U	52	THR
21	U	53	ASP
22	V	12	THR
22	V	65	ASP
23	W	1	MET
23	W	4	LEU
23	W	35	VAL
23	W	88	THR
23	W	125	HIS
23	W	146	ILE
24	X	27	ASP
24	X	46	ASP
24	X	52	PRO
24	X	72	VAL
24	X	79	GLU
25	Y	154	ARG

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Mol	Chain	Res	Type
25	Y	189	ASN
25	Y	203	VAL
25	Y	223	ASP
25	Y	235	GLU
26	Z	37	ARG
26	Z	70	ARG
26	Z	88	PHE
28	2	18	ASN
29	3	30	GLN
29	3	56	PRO
29	3	65	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (80) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	HIS
1	A	199	HIS
2	B	27	ASN
2	B	145	HIS
2	B	221	GLN
2	B	238	ASN
2	B	256	GLN
2	B	260	HIS
2	B	320	GLN
3	C	2	GLN
3	C	73	GLN
3	C	103	ASN
3	C	129	HIS
4	D	103	ASN
5	E	55	ASN
5	E	90	HIS
5	E	143	GLN
5	E	150	GLN
7	G	64	ASN
8	H	59	GLN
9	I	99	GLN
9	I	106	GLN
10	J	52	GLN
10	J	107	ASN
10	J	126	ASN
11	K	10	GLN
11	K	44	HIS

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Mol	Chain	Res	Type
11	K	67	GLN
12	L	18	HIS
12	L	41	HIS
12	L	116	HIS
13	M	24	GLN
13	M	29	GLN
13	M	170	ASN
14	N	40	ASN
14	N	53	ASN
14	N	93	GLN
14	N	107	ASN
14	N	132	ASN
16	P	50	GLN
16	P	66	GLN
16	P	73	HIS
16	P	88	GLN
16	P	118	GLN
17	Q	16	ASN
17	Q	27	GLN
17	Q	40	HIS
18	R	61	GLN
18	R	94	ASN
18	R	98	ASN
18	R	117	HIS
18	R	123	GLN
19	S	7	HIS
19	S	44	GLN
19	S	53	ASN
20	T	39	ASN
21	U	38	ASN
21	U	39	ASN
22	V	34	GLN
22	V	60	GLN
23	W	2	HIS
23	W	12	ASN
23	W	28	HIS
23	W	110	GLN
23	W	119	HIS
23	W	141	HIS
24	X	23	HIS
25	Y	134	HIS
25	Y	149	GLN

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Mol	Chain	Res	Type
25	Y	189	ASN
26	Z	80	GLN
27	1	8	GLN
27	1	16	HIS
27	1	28	HIS
28	2	18	ASN
28	2	41	HIS
28	2	45	ASN
29	3	30	GLN
29	3	48	ASN
29	3	91	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	0	2745/2923 (93%)	250 (9%)	21 (0%)
31	9	121/122 (99%)	19 (15%)	2 (1%)
All	All	2866/3045 (94%)	269 (9%)	23 (0%)

All (269) 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	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

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Mol	Chain	Res	Type
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
30	0	283	U
30	0	284	C
30	0	308	U
30	0	309	C
30	0	318	U
30	0	336	G
30	0	337	A
30	0	358	G
30	0	381	G
30	0	397	A
30	0	409	U
30	0	417	G
30	0	461	C
30	0	473	A
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	581	G
30	0	588	G
30	0	604	G
30	0	620	A
30	0	632	A
30	0	644	G
30	0	660	A
30	0	688	A
30	0	699	C

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Mol	Chain	Res	Type
30	0	701	U
30	0	759	C
30	0	777	U
30	0	809	G
30	0	821	U
30	0	835	U
30	0	840	U
30	0	846	A
30	0	857	A
30	0	858	U
30	0	868	G
30	0	869	G
30	0	872	U
30	0	875	A
30	0	877	G
30	0	878	G
30	0	882	A
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	1029	U
30	0	1045	G
30	0	1059	G
30	0	1060	C
30	0	1072	G
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

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Mol	Chain	Res	Type
30	0	1164	U
30	0	1165	G
30	0	1166	A
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	1216	G
30	0	1234	U
30	0	1238	C
30	0	1239	G
30	0	1242	A
30	0	1279	U
30	0	1289	C
30	0	1331	G
30	0	1342	C
30	0	1353	C
30	0	1360	C
30	0	1377	C
30	0	1378	G
30	0	1407	A
30	0	1474	C
30	0	1485	A
30	0	1488	U
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	1559	A
30	0	1562	C
30	0	1592	G
30	0	1625	U
30	0	1626	A
30	0	1634	G
30	0	1656	A
30	0	1667	A
30	0	1682	A

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Mol	Chain	Res	Type
30	0	1684	A
30	0	1685	A
30	0	1692	C
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	1732	A
30	0	1752	G
30	0	1778	A
30	0	1779	A
30	0	1798	C
30	0	1819	G
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	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

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Mol	Chain	Res	Type
30	0	2103	A
30	0	2110	G
30	0	2243	C
30	0	2258	A
30	0	2271	G
30	0	2272	G
30	0	2291	A
30	0	2317	C
30	0	2321	A
30	0	2322	U
30	0	2354	A
30	0	2361	A
30	0	2369	A
30	0	2422	U
30	0	2462	G
30	0	2469	A
30	0	2476	C
30	0	2483	A
30	0	2507	G
30	0	2509	A
30	0	2511	A
30	0	2513	A
30	0	2533	C
30	0	2537	G
30	0	2541	U
30	0	2553	A
30	0	2564	G
30	0	2570	G
30	0	2589	U
30	0	2601	A
30	0	2602	G
30	0	2608	C
30	0	2613	G
30	0	2634	G
30	0	2637	A
30	0	2638	G
30	0	2649	A
30	0	2664	A
30	0	2676	C
30	0	2681	A
30	0	2682	C
30	0	2718	C

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Mol	Chain	Res	Type
30	0	2719	A
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
30	0	2825	C
30	0	2867	G
30	0	2876	G
30	0	2890	A
30	0	2896	A
30	0	2903	C
30	0	2906	A
30	0	2912	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	34	A
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	66	G
31	9	77	A
31	9	114	G
31	9	122	C

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
30	0	69	A
30	0	129	A
30	0	396	U
30	0	603	A
30	0	644	G
30	0	834	G
30	0	857	A
30	0	871	G
30	0	877	G
30	0	1237	U
30	0	1352	A
30	0	1377	C
30	0	1474	C
30	0	1506	U
30	0	2011	A
30	0	2321	A
30	0	2467	A
30	0	2526	C
30	0	2718	C
30	0	2726	U
30	0	2791	U
31	9	43	G
31	9	65	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
30	PSU	0	2621	30	17,21,22	1.66	3 (17%)	20,30,33	5.46	4 (20%)
30	OMG	0	2588	30	18,26,27	1.03	2 (11%)	20,38,41	2.62	4 (20%)
30	1MA	0	628	30,35	15,25,26	0.77	0	15,37,40	1.42	1 (6%)
30	UR3	0	2619	30	14,22,23	0.76	0	15,32,35	0.55	0
30	OMU	0	2587	30	14,22,23	0.99	1 (7%)	14,31,34	1.17	1 (7%)

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	PSU	0	2621	30	-	0/7/25/26	0/2/2/2
30	OMG	0	2588	30	-	0/5/27/28	0/3/3/3
30	1MA	0	628	30,35	-	0/3/25/26	0/3/3/3
30	UR3	0	2619	30	-	0/5/25/26	0/2/2/2
30	OMU	0	2587	30	-	0/7/27/28	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	0	2621	PSU	C5-C1'	-5.31	1.47	1.52
30	0	2588	OMG	C6-N1	3.28	1.38	1.33
30	0	2621	PSU	C4-N3	2.70	1.37	1.33
30	0	2587	OMU	C4-N3	2.45	1.37	1.33
30	0	2621	PSU	C2-N1	2.35	1.42	1.38
30	0	2588	OMG	C8-N7	-2.19	1.30	1.34

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	0	2621	PSU	N1-C2-N3	-17.30	114.68	128.43
30	0	2621	PSU	C4-N3-C2	14.37	127.28	115.14
30	0	2588	OMG	C5-C6-N1	-8.66	111.59	123.43
30	0	2621	PSU	C5-C4-N3	-8.19	114.81	125.36
30	0	2588	OMG	C6-N1-C2	5.90	125.31	115.93
30	0	628	1MA	C2-N3-C4	-4.66	110.76	116.58
30	0	2587	OMU	C5-C4-N3	-3.89	114.75	123.31
30	0	2588	OMG	C2-N3-C4	-3.15	111.76	115.36
30	0	2621	PSU	C6-N1-C2	2.64	119.72	115.36
30	0	2588	OMG	N3-C2-N1	-2.49	123.90	127.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	0	2621	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	0	2588	OMG	1	0
30	0	2587	OMU	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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%)	-0.14	8 (3%) 45 29	36, 71, 108, 128	0
2	B	337/338 (99%)	-0.45	0 100 100	38, 67, 98, 112	0
3	C	246/246 (100%)	-0.38	0 100 100	32, 56, 80, 91	0
4	D	140/177 (79%)	1.53	52 (37%) 0 0	89, 121, 144, 151	0
5	E	172/178 (96%)	-0.07	4 (2%) 60 43	57, 83, 104, 113	0
6	F	119/120 (99%)	0.50	15 (12%) 3 2	64, 88, 121, 131	0
7	G	29/348 (8%)	1.11	4 (13%) 2 1	92, 107, 116, 118	0
8	H	160/177 (90%)	0.89	31 (19%) 1 0	65, 89, 118, 127	0
9	I	70/162 (43%)	3.64	50 (71%) 0 0	145, 162, 177, 179	0
10	J	142/145 (97%)	-0.38	1 (0%) 87 76	47, 63, 86, 105	0
11	K	132/132 (100%)	-0.38	0 100 100	45, 63, 91, 100	0
12	L	145/165 (87%)	0.55	21 (14%) 2 1	41, 88, 131, 140	0
13	M	194/196 (98%)	0.25	20 (10%) 6 4	37, 53, 115, 122	0
14	N	186/187 (99%)	0.65	26 (13%) 2 1	70, 90, 134, 139	0
15	O	115/116 (99%)	-0.37	0 100 100	46, 64, 81, 87	0
16	P	143/149 (95%)	-0.30	0 100 100	48, 67, 85, 96	0
17	Q	95/96 (98%)	-0.17	1 (1%) 80 65	57, 69, 89, 97	0
18	R	150/155 (96%)	-0.50	0 100 100	39, 56, 79, 95	0
19	S	81/85 (95%)	-0.28	2 (2%) 57 40	52, 70, 89, 104	0
20	T	119/120 (99%)	-0.03	5 (4%) 36 23	48, 67, 95, 125	0
21	U	53/67 (79%)	4.50	50 (94%) 0 0	112, 125, 131, 134	0
22	V	65/71 (91%)	0.92	12 (18%) 1 0	51, 83, 131, 135	0
23	W	154/154 (100%)	-0.34	1 (0%) 89 78	45, 62, 79, 92	0
24	X	82/92 (89%)	0.03	4 (4%) 29 18	54, 72, 95, 109	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	Y	142/241 (58%)	-0.60	0 100 100	30, 53, 78, 97	0
26	Z	73/116 (62%)	7.40	59 (80%) 0 0	111, 130, 139, 142	0
27	1	56/57 (98%)	-0.51	0 100 100	30, 39, 47, 65	0
28	2	46/50 (92%)	-0.22	3 (6%) 18 11	39, 72, 104, 110	0
29	3	92/92 (100%)	8.50	91 (98%) 0 0	123, 135, 142, 148	0
30	0	2749/2923 (94%)	-0.63	10 (0%) 92 84	25, 58, 106, 183	0
31	9	122/122 (100%)	-0.81	2 (1%) 72 55	51, 90, 111, 159	0
All	All	6646/7517 (88%)	-0.00	472 (7%) 16 9	25, 66, 129, 183	0

All (472) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
26	Z	58	ASN	25.7
29	3	39	GLN	21.9
29	3	41	GLU	19.7
29	3	47	GLY	18.8
29	3	35	TRP	18.8
26	Z	35	SER	18.6
26	Z	55	SER	18.4
29	3	32	GLY	18.0
26	Z	46	SER	17.8
26	Z	36	GLY	17.3
13	M	87	GLY	17.0
29	3	44	SER	16.6
29	3	42	ARG	15.8
29	3	45	GLY	15.7
29	3	36	ILE	15.5
29	3	48	ASN	15.4
26	Z	50	VAL	15.4
26	Z	39	GLY	15.1
26	Z	56	GLU	14.9
26	Z	38	PHE	14.7
26	Z	34	SER	14.7
29	3	43	ASN	14.5
26	Z	43	GLY	14.3
26	Z	59	GLU	14.0
29	3	33	MET	13.9
29	3	38	ARG	13.8
29	3	40	ARG	13.5
26	Z	69	ASP	13.3

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Mol	Chain	Res	Type	RSRZ
29	3	82	GLY	13.1
26	Z	82	SER	12.7
29	3	11	CYS	12.7
13	M	80	GLY	12.6
26	Z	42	TYR	12.6
29	3	37	ASP	12.3
29	3	34	LYS	12.3
26	Z	44	ARG	12.0
29	3	62	THR	11.9
26	Z	57	MET	11.7
29	3	56	PRO	11.7
29	3	15	ASN	11.4
26	Z	45	VAL	11.3
29	3	57	GLY	11.1
26	Z	54	GLU	11.0
29	3	20	HIS	10.8
26	Z	68	GLU	10.6
29	3	59	ASP	10.5
29	3	81	GLU	10.5
29	3	55	VAL	10.4
29	3	31	THR	10.1
26	Z	53	ILE	10.1
29	3	51	LYS	10.0
9	I	70	THR	9.9
9	I	104	ALA	9.6
29	3	83	TRP	9.6
9	I	74	ILE	9.6
29	3	30	GLN	9.4
29	3	10	TYR	9.3
29	3	71	CYS	9.2
13	M	83	SER	9.2
29	3	53	SER	9.0
21	U	40	ALA	9.0
13	M	89	THR	8.9
29	3	18	GLN	8.8
29	3	27	SER	8.8
13	M	90	ARG	8.8
29	3	14	CYS	8.7
26	Z	49	ARG	8.6
29	3	19	GLU	8.4
26	Z	77	GLY	8.4
29	3	78	HIS	8.4

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Mol	Chain	Res	Type	RSRZ
21	U	9	CYS	8.3
26	Z	78	ILE	8.3
26	Z	71	VAL	8.2
21	U	31	PHE	8.2
26	Z	60	ASP	8.0
29	3	13	HIS	8.0
21	U	43	GLY	8.0
9	I	128	THR	8.0
29	3	80	ARG	7.9
29	3	61	PRO	7.8
26	Z	48	ARG	7.8
29	3	16	GLU	7.7
29	3	9	THR	7.7
29	3	12	PRO	7.7
26	Z	81	CYS	7.7
13	M	82	ARG	7.7
21	U	36	CYS	7.6
29	3	46	ILE	7.6
29	3	1	MET	7.6
21	U	38	ASN	7.5
21	U	52	THR	7.5
29	3	58	GLY	7.5
26	Z	37	ARG	7.4
29	3	17	HIS	7.3
9	I	106	GLN	7.3
9	I	66	GLY	7.3
21	U	54	THR	7.2
29	3	8	ASN	7.1
4	D	57	THR	7.1
26	Z	52	GLU	7.0
26	Z	61	HIS	7.0
26	Z	79	TRP	7.0
29	3	69	TYR	7.0
22	V	39	ALA	7.0
22	V	1	THR	7.0
21	U	51	TRP	6.9
21	U	41	ASP	6.9
29	3	91	GLN	6.9
9	I	71	ALA	6.8
29	3	77	ALA	6.7
29	3	52	PHE	6.7
26	Z	67	GLY	6.7

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Mol	Chain	Res	Type	RSRZ
29	3	22	VAL	6.7
13	M	70	GLY	6.7
29	3	74	CYS	6.7
21	U	46	ALA	6.6
12	L	60	GLU	6.6
26	Z	62	ALA	6.5
13	M	81	ARG	6.4
26	Z	63	CYS	6.4
26	Z	47	ARG	6.4
29	3	28	GLY	6.3
9	I	113	SER	6.3
29	3	29	ARG	6.2
14	N	166	ALA	6.2
26	Z	51	ALA	6.2
9	I	103	ILE	6.1
9	I	97	VAL	6.1
13	M	74	LYS	6.0
29	3	49	ASP	6.0
26	Z	40	ALA	6.0
4	D	69	ILE	5.9
29	3	92	GLU	5.9
29	3	66	ASP	5.9
13	M	78	LYS	5.8
26	Z	65	ASN	5.8
21	U	30	HIS	5.8
9	I	132	VAL	5.7
4	D	18	ILE	5.7
9	I	100	VAL	5.7
29	3	90	PHE	5.7
21	U	12	ASP	5.7
21	U	19	THR	5.7
26	Z	74	GLN	5.6
29	3	84	ARG	5.6
26	Z	66	CYS	5.6
29	3	76	LYS	5.5
29	3	3	MET	5.5
21	U	53	ASP	5.5
4	D	63	ILE	5.5
26	Z	93	TYR	5.5
21	U	33	SER	5.5
9	I	111	LEU	5.4
21	U	42	LEU	5.4

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Mol	Chain	Res	Type	RSRZ
26	Z	76	THR	5.4
26	Z	88	PHE	5.3
29	3	68	LYS	5.3
26	Z	41	ARG	5.3
26	Z	70	ARG	5.3
4	D	135	VAL	5.3
9	I	117	THR	5.3
21	U	29	THR	5.3
9	I	73	LEU	5.2
29	3	60	LYS	5.2
9	I	109	PRO	5.2
21	U	24	LYS	5.2
31	9	1	U	5.2
29	3	88	LEU	5.1
29	3	7	PHE	5.1
9	I	102	GLN	5.1
19	S	81	ILE	5.1
29	3	85	ALA	5.1
13	M	86	GLN	5.1
4	D	75	LEU	5.0
29	3	86	GLY	5.0
26	Z	89	THR	5.0
21	U	55	ALA	5.0
29	3	5	ARG	5.0
14	N	179	LEU	5.0
29	3	4	PRO	5.0
29	3	23	GLU	5.0
21	U	32	CYS	5.0
26	Z	85	ASP	5.0
13	M	79	ALA	4.9
9	I	72	GLU	4.9
26	Z	80	GLN	4.9
13	M	71	SER	4.9
22	V	43	PRO	4.8
21	U	39	ASN	4.8
29	3	6	ARG	4.8
9	I	108	HIS	4.8
29	3	25	VAL	4.8
29	3	70	ARG	4.8
20	T	119	ALA	4.8
4	D	27	ILE	4.7
29	3	2	GLN	4.7

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Mol	Chain	Res	Type	RSRZ
29	3	50	GLY	4.7
21	U	45	GLU	4.7
9	I	105	GLU	4.7
21	U	47	ARG	4.7
9	I	116	LEU	4.6
21	U	11	THR	4.6
29	3	72	GLY	4.6
4	D	25	MET	4.5
21	U	48	ASN	4.5
29	3	54	LYS	4.5
9	I	118	ASN	4.5
21	U	25	ASP	4.5
22	V	38	GLY	4.5
29	3	64	LYS	4.5
9	I	78	ALA	4.5
9	I	110	ASP	4.5
4	D	40	ILE	4.4
13	M	76	ARG	4.4
4	D	166	ILE	4.4
21	U	28	THR	4.4
4	D	90	LEU	4.4
21	U	6	CYS	4.4
29	3	75	GLY	4.4
21	U	8	TYR	4.3
26	Z	92	SER	4.3
29	3	89	GLU	4.3
22	V	40	PRO	4.3
21	U	13	ILE	4.3
22	V	37	GLY	4.2
9	I	69	PRO	4.2
29	3	65	THR	4.2
29	3	67	LEU	4.2
26	Z	86	TYR	4.2
29	3	73	GLU	4.1
12	L	106	VAL	4.1
7	G	27	ILE	4.1
21	U	4	ARG	4.1
29	3	21	GLU	4.1
9	I	94	ASP	4.1
26	Z	83	TYR	4.1
9	I	67	VAL	4.1
21	U	23	HIS	4.1

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Mol	Chain	Res	Type	RSRZ
4	D	88	LEU	4.1
21	U	10	GLY	4.0
13	M	75	ARG	4.0
13	M	73	ARG	4.0
4	D	26	GLY	4.0
13	M	88	VAL	4.0
26	Z	72	ASP	3.9
24	X	10	VAL	3.9
4	D	84	LEU	3.8
30	0	970	U	3.8
22	V	44	GLY	3.8
4	D	134	LEU	3.8
9	I	93	ALA	3.8
8	H	84	GLY	3.8
29	3	87	ARG	3.8
9	I	98	ASP	3.7
4	D	87	ALA	3.7
8	H	39	LYS	3.7
9	I	112	LEU	3.7
4	D	44	ILE	3.7
7	G	23	ILE	3.7
1	A	237	GLY	3.7
9	I	91	PHE	3.7
9	I	75	LYS	3.6
8	H	82	GLU	3.6
21	U	37	GLU	3.6
29	3	24	LYS	3.6
12	L	105	TYR	3.6
9	I	80	PHE	3.6
9	I	92	VAL	3.6
21	U	5	GLU	3.6
6	F	17	LEU	3.6
30	0	735	C	3.6
6	F	75	ILE	3.6
9	I	119	ALA	3.5
1	A	64	ASP	3.5
8	H	40	GLN	3.5
8	H	66	GLU	3.5
29	3	26	ARG	3.5
9	I	95	LEU	3.5
12	L	48	LYS	3.5
6	F	106	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
26	Z	103	VAL	3.5
4	D	11	HIS	3.4
26	Z	73	ARG	3.4
8	H	133	GLY	3.4
8	H	77	ILE	3.4
29	3	63	LYS	3.4
30	0	1198	U	3.4
9	I	82	THR	3.4
12	L	120	LEU	3.4
4	D	130	VAL	3.4
9	I	68	PRO	3.3
8	H	86	TYR	3.3
13	M	77	HIS	3.2
22	V	2	VAL	3.2
4	D	41	LEU	3.2
4	D	129	ASP	3.2
9	I	88	GLN	3.2
4	D	157	LEU	3.2
1	A	37	VAL	3.2
28	2	49	GLU	3.2
8	H	69	ARG	3.2
9	I	83	GLY	3.1
4	D	93	LEU	3.1
4	D	128	LEU	3.1
26	Z	84	CYS	3.1
28	2	48	ASP	3.1
8	H	81	GLY	3.1
9	I	76	ASP	3.1
9	I	127	CYS	3.1
8	H	36	MET	3.1
13	M	84	LYS	3.1
8	H	35	LYS	3.0
9	I	124	VAL	3.0
1	A	65	ARG	3.0
4	D	165	PHE	3.0
30	0	1172	G	3.0
4	D	104	PHE	3.0
30	0	1177	A	3.0
8	H	38	ARG	3.0
12	L	123	ASP	3.0
9	I	121	LYS	3.0
14	N	155	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
4	D	10	PHE	2.9
8	H	76	LEU	2.9
14	N	78	MET	2.9
21	U	22	VAL	2.9
12	L	96	VAL	2.9
4	D	16	PRO	2.9
8	H	149	VAL	2.9
6	F	99	THR	2.9
6	F	49	PHE	2.9
4	D	17	ARG	2.9
4	D	92	GLU	2.8
30	0	1199	A	2.8
8	H	89	THR	2.8
8	H	88	MET	2.8
12	L	79	ASP	2.8
9	I	101	LYS	2.8
4	D	67	ASP	2.8
4	D	58	VAL	2.8
12	L	142	LEU	2.7
14	N	178	THR	2.7
21	U	44	ARG	2.7
6	F	108	VAL	2.7
14	N	142	THR	2.7
14	N	95	ALA	2.7
4	D	70	GLY	2.7
21	U	20	MET	2.7
14	N	159	TYR	2.7
4	D	23	VAL	2.7
22	V	41	GLU	2.7
24	X	88	GLU	2.7
24	X	71	ARG	2.7
8	H	141	CYS	2.6
4	D	56	ARG	2.6
12	L	125	PHE	2.6
6	F	44	SER	2.6
21	U	49	LEU	2.6
22	V	3	LEU	2.6
14	N	145	ALA	2.6
4	D	83	PHE	2.6
21	U	21	PHE	2.6
14	N	97	VAL	2.6
22	V	8	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
12	L	80	ASP	2.6
14	N	185	GLU	2.6
21	U	56	ARG	2.6
6	F	119	ARG	2.6
4	D	80	ALA	2.6
6	F	20	LEU	2.6
8	H	31	ILE	2.5
4	D	106	PHE	2.5
12	L	130	ARG	2.5
12	L	124	ASP	2.5
5	E	5	LEU	2.5
12	L	91	VAL	2.5
9	I	79	GLY	2.5
9	I	122	GLU	2.5
21	U	35	LYS	2.5
22	V	36	ALA	2.5
4	D	28	GLY	2.5
4	D	89	PRO	2.5
9	I	123	VAL	2.5
26	Z	104	ARG	2.5
19	S	45	TYR	2.5
12	L	76	LEU	2.5
4	D	73	VAL	2.4
20	T	116	ASP	2.4
6	F	19	ALA	2.4
4	D	51	ARG	2.4
14	N	83	LEU	2.4
12	L	114	VAL	2.4
14	N	180	LEU	2.4
4	D	101	THR	2.4
14	N	181	ASP	2.4
8	H	126	THR	2.4
12	L	89	PHE	2.4
14	N	75	THR	2.4
7	G	63	ARG	2.4
20	T	42	VAL	2.4
8	H	145	ASP	2.4
14	N	84	THR	2.4
6	F	28	ALA	2.4
8	H	73	ASN	2.4
12	L	75	LEU	2.4
12	L	118	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
7	G	25	GLU	2.3
9	I	99	GLN	2.3
4	D	171	ASP	2.3
8	H	85	ASP	2.3
4	D	61	PHE	2.3
13	M	72	ALA	2.3
30	0	1170	U	2.3
5	E	118	ILE	2.3
8	H	79	GLU	2.3
8	H	98	LEU	2.3
10	J	70	PHE	2.3
6	F	37	THR	2.3
26	Z	64	PRO	2.3
14	N	153	GLN	2.3
1	A	52	SER	2.3
4	D	64	ARG	2.3
31	9	24	U	2.3
14	N	92	ALA	2.3
30	0	1163	G	2.3
8	H	132	ALA	2.2
9	I	120	ALA	2.2
4	D	172	VAL	2.2
20	T	118	SER	2.2
14	N	156	GLU	2.2
12	L	62	ALA	2.2
1	A	145	MET	2.2
30	0	282	C	2.2
5	E	100	ASP	2.2
5	E	87	PHE	2.2
14	N	172	PHE	2.2
23	W	45	VAL	2.2
4	D	19	GLU	2.2
6	F	97	ALA	2.2
8	H	169	GLU	2.2
14	N	81	ALA	2.2
14	N	163	PHE	2.2
4	D	24	HIS	2.2
4	D	62	ASP	2.1
4	D	158	ASN	2.1
8	H	29	SER	2.1
28	2	39	ARG	2.1
14	N	182	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
21	U	27	ALA	2.1
21	U	15	PRO	2.1
17	Q	20	ASP	2.1
6	F	16	ALA	2.1
4	D	43	GLU	2.1
20	T	112	LEU	2.1
21	U	18	GLY	2.1
6	F	115	VAL	2.1
14	N	149	GLU	2.1
24	X	7	GLU	2.1
21	U	26	GLY	2.1
1	A	133	ARG	2.1
21	U	50	GLU	2.1
30	0	1000	C	2.1
14	N	69	TYR	2.1
26	Z	96	GLU	2.1
21	U	7	ASP	2.0
12	L	141	GLU	2.0
21	U	14	GLU	2.0
8	H	74	ARG	2.0
8	H	64	SER	2.0
8	H	68	SER	2.0
1	A	82	VAL	2.0
14	N	7	LYS	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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
30	PSU	0	2621	20/21	0.98	0.18	39,41,53,53	0
30	OMG	0	2588	24/25	0.98	0.12	41,43,46,50	0
30	1MA	0	628	23/24	0.98	0.14	38,44,47,47	0
30	UR3	0	2619	21/22	0.98	0.13	47,49,51,54	0
30	OMU	0	2587	21/22	0.98	0.11	43,47,50,51	0

6.3 Carbohydrates ⓘ

There are no monosaccharides 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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
33	CL	3	8804	1/1	0.25	0.20	128,128,128,128	0
35	NA	0	8528	1/1	0.51	0.67	76,76,76,76	0
34	SR	0	8979	1/1	0.53	0.19	196,196,196,196	0
34	SR	0	9006	1/1	0.57	0.98	200,200,200,200	0
35	NA	J	8538	1/1	0.58	0.15	78,78,78,78	0
35	NA	0	8563	1/1	0.59	0.12	117,117,117,117	0
32	MG	0	8040	1/1	0.59	0.39	86,86,86,86	0
34	SR	0	8988	1/1	0.61	0.08	173,173,173,173	0
35	NA	0	8570	1/1	0.66	0.09	61,61,61,61	0
35	NA	0	8511	1/1	0.67	0.08	81,81,81,81	0
34	SR	0	8991	1/1	0.67	0.08	180,180,180,180	0
34	SR	0	8982	1/1	0.68	1.93	200,200,200,200	0
34	SR	0	9004	1/1	0.71	0.84	200,200,200,200	0
35	NA	0	8506	1/1	0.72	0.20	83,83,83,83	0
34	SR	0	9001	1/1	0.75	0.13	177,177,177,177	0
32	MG	A	8051	1/1	0.76	0.25	94,94,94,94	0
35	NA	0	8525	1/1	0.77	0.16	75,75,75,75	0
37	CD	Z	8703	1/1	0.78	0.46	200,200,200,200	0
35	NA	B	8552	1/1	0.78	0.28	89,89,89,89	0
37	CD	3	8704	1/1	0.78	0.66	200,200,200,200	0
34	SR	0	8977	1/1	0.80	0.07	200,200,200,200	0
32	MG	0	8089	1/1	0.80	0.25	65,65,65,65	0
34	SR	0	8959	1/1	0.80	0.27	200,200,200,200	0
34	SR	0	9007	1/1	0.80	1.77	200,200,200,200	0
34	SR	0	8938	1/1	0.80	0.08	183,183,183,183	0
34	SR	0	9002	1/1	0.82	0.12	193,193,193,193	0
35	NA	0	8562	1/1	0.83	0.97	82,82,82,82	0
35	NA	0	8535	1/1	0.83	0.29	67,67,67,67	0
34	SR	3	8999	1/1	0.84	0.28	187,187,187,187	0
35	NA	0	8509	1/1	0.84	0.13	69,69,69,69	0
34	SR	0	8962	1/1	0.84	0.09	172,172,172,172	0
32	MG	0	8071	1/1	0.84	0.12	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
33	CL	J	8801	1/1	0.84	0.12	95,95,95,95	0
34	SR	0	8992	1/1	0.84	0.23	159,159,159,159	0
35	NA	0	8502	1/1	0.85	0.12	69,69,69,69	0
35	NA	H	8518	1/1	0.85	0.42	91,91,91,91	0
32	MG	0	8075	1/1	0.85	0.05	55,55,55,55	0
34	SR	0	8951	1/1	0.85	0.10	155,155,155,155	0
34	SR	0	8928	1/1	0.86	0.04	137,137,137,137	0
35	NA	Q	8540	1/1	0.86	0.11	79,79,79,79	0
32	MG	0	8081	1/1	0.86	0.17	88,88,88,88	0
34	SR	0	8985	1/1	0.86	0.06	164,164,164,164	0
34	SR	0	8957	1/1	0.86	0.34	200,200,200,200	0
34	SR	0	8953	1/1	0.86	0.55	200,200,200,200	0
34	SR	0	8994	1/1	0.86	0.48	200,200,200,200	0
35	NA	0	8555	1/1	0.87	0.42	52,52,52,52	0
34	SR	9	8980	1/1	0.87	0.15	183,183,183,183	0
35	NA	0	8560	1/1	0.87	0.56	118,118,118,118	0
34	SR	0	8919	1/1	0.87	0.09	168,168,168,168	0
35	NA	0	8548	1/1	0.88	0.12	56,56,56,56	0
34	SR	0	8989	1/1	0.88	0.20	178,178,178,178	0
35	NA	0	8545	1/1	0.88	0.80	58,58,58,58	0
34	SR	0	8993	1/1	0.89	0.08	167,167,167,167	0
32	MG	0	8056	1/1	0.89	0.06	57,57,57,57	0
34	SR	9	9003	1/1	0.89	0.10	187,187,187,187	0
32	MG	0	8067	1/1	0.89	0.11	35,35,35,35	0
35	NA	0	8508	1/1	0.89	0.47	52,52,52,52	0
32	MG	9	8074	1/1	0.89	0.07	87,87,87,87	0
35	NA	0	8536	1/1	0.90	0.17	64,64,64,64	0
34	SR	0	8976	1/1	0.90	0.29	193,193,193,193	0
35	NA	0	8544	1/1	0.90	0.19	79,79,79,79	0
32	MG	0	8080	1/1	0.90	0.75	83,83,83,83	0
35	NA	0	8551	1/1	0.90	0.46	63,63,63,63	0
32	MG	0	8030	1/1	0.90	0.47	90,90,90,90	0
34	SR	0	8944	1/1	0.90	0.07	172,172,172,172	0
34	SR	3	8932	1/1	0.90	0.23	178,178,178,178	0
34	SR	0	8975	1/1	0.90	0.14	149,149,149,149	0
34	SR	0	8954	1/1	0.91	0.12	108,108,108,108	0
35	NA	0	8565	1/1	0.91	1.10	78,78,78,78	0
34	SR	0	8983	1/1	0.91	0.33	197,197,197,197	0
35	NA	9	8543	1/1	0.91	0.21	61,61,61,61	0
36	K	0	8401	1/1	0.91	0.63	139,139,139,139	0
34	SR	0	8946	1/1	0.91	0.20	137,137,137,137	0
35	NA	0	8522	1/1	0.91	0.14	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
35	NA	0	8566	1/1	0.92	0.30	63,63,63,63	0
34	SR	0	8971	1/1	0.92	0.06	192,192,192,192	0
33	CL	O	8808	1/1	0.92	0.17	86,86,86,86	0
34	SR	0	8996	1/1	0.92	0.52	200,200,200,200	0
34	SR	H	8972	1/1	0.92	0.10	164,164,164,164	0
32	MG	0	8031	1/1	0.92	0.39	83,83,83,83	0
34	SR	L	8969	1/1	0.92	0.29	200,200,200,200	0
36	K	M	8402	1/1	0.92	0.19	87,87,87,87	0
33	CL	0	8805	1/1	0.92	0.17	98,98,98,98	0
35	NA	S	8510	1/1	0.93	0.03	44,44,44,44	0
35	NA	0	8567	1/1	0.93	0.25	78,78,78,78	0
35	NA	0	8547	1/1	0.93	0.99	67,67,67,67	0
34	SR	9	8978	1/1	0.93	0.06	157,157,157,157	0
32	MG	0	8053	1/1	0.93	0.05	63,63,63,63	0
35	NA	0	8526	1/1	0.93	0.15	46,46,46,46	0
33	CL	B	8819	1/1	0.93	0.22	69,69,69,69	0
32	MG	0	8059	1/1	0.93	0.09	51,51,51,51	0
33	CL	0	8815	1/1	0.93	0.22	89,89,89,89	0
35	NA	0	8530	1/1	0.93	0.44	74,74,74,74	0
34	SR	0	8915	1/1	0.93	0.08	126,126,126,126	0
35	NA	0	8542	1/1	0.93	0.53	58,58,58,58	0
34	SR	A	8930	1/1	0.93	0.15	142,142,142,142	0
32	MG	0	8063	1/1	0.93	0.30	116,116,116,116	0
35	NA	0	8553	1/1	0.93	0.28	89,89,89,89	0
35	NA	0	8521	1/1	0.93	0.45	64,64,64,64	0
34	SR	B	8987	1/1	0.93	0.62	200,200,200,200	0
34	SR	0	8997	1/1	0.93	0.15	189,189,189,189	0
33	CL	J	8802	1/1	0.93	0.06	67,67,67,67	0
32	MG	0	8061	1/1	0.93	0.17	36,36,36,36	0
33	CL	N	8807	1/1	0.94	0.22	87,87,87,87	0
35	NA	0	8558	1/1	0.94	0.20	58,58,58,58	0
34	SR	0	8968	1/1	0.94	0.06	177,177,177,177	0
34	SR	0	8922	1/1	0.94	0.17	168,168,168,168	0
34	SR	0	8939	1/1	0.94	0.04	144,144,144,144	0
35	NA	0	8550	1/1	0.94	0.26	71,71,71,71	0
32	MG	0	8066	1/1	0.94	0.18	69,69,69,69	0
35	NA	0	8568	1/1	0.94	0.33	54,54,54,54	0
35	NA	0	8546	1/1	0.94	0.74	94,94,94,94	0
32	MG	0	8055	1/1	0.94	0.06	62,62,62,62	0
35	NA	0	8557	1/1	0.94	0.06	65,65,65,65	0
34	SR	0	8917	1/1	0.94	0.16	114,114,114,114	0
32	MG	0	8019	1/1	0.94	0.19	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
35	NA	0	8569	1/1	0.94	0.18	50,50,50,50	0
35	NA	0	8573	1/1	0.94	0.13	73,73,73,73	0
32	MG	0	8044	1/1	0.94	0.05	58,58,58,58	0
32	MG	0	8082	1/1	0.94	0.23	76,76,76,76	0
32	MG	A	8050	1/1	0.94	0.05	64,64,64,64	0
35	NA	0	8527	1/1	0.94	0.28	72,72,72,72	0
32	MG	0	8028	1/1	0.94	0.17	34,34,34,34	0
32	MG	0	8006	1/1	0.94	0.12	44,44,44,44	0
35	NA	0	8571	1/1	0.94	0.12	79,79,79,79	0
35	NA	0	8564	1/1	0.95	0.43	69,69,69,69	0
35	NA	9	8572	1/1	0.95	0.27	88,88,88,88	0
32	MG	0	8060	1/1	0.95	0.06	53,53,53,53	0
32	MG	0	8091	1/1	0.95	0.11	56,56,56,56	0
34	SR	0	8947	1/1	0.95	0.26	200,200,200,200	0
32	MG	0	8092	1/1	0.95	0.08	76,76,76,76	0
35	NA	0	8519	1/1	0.95	0.15	52,52,52,52	0
34	SR	0	8920	1/1	0.95	0.05	127,127,127,127	0
32	MG	0	8090	1/1	0.95	0.17	97,97,97,97	0
34	SR	0	8965	1/1	0.95	0.06	134,134,134,134	0
32	MG	0	8036	1/1	0.95	0.10	48,48,48,48	0
35	NA	C	8503	1/1	0.95	0.17	46,46,46,46	0
34	SR	A	8929	1/1	0.95	0.11	139,139,139,139	0
35	NA	0	8533	1/1	0.95	0.09	70,70,70,70	0
34	SR	0	8963	1/1	0.95	0.06	133,133,133,133	0
35	NA	0	8537	1/1	0.95	0.15	50,50,50,50	0
37	CD	U	8701	1/1	0.95	0.45	200,200,200,200	0
33	CL	Y	8820	1/1	0.95	0.07	52,52,52,52	0
32	MG	Y	8086	1/1	0.95	0.07	50,50,50,50	0
34	SR	S	8961	1/1	0.95	0.09	128,128,128,128	0
34	SR	0	8943	1/1	0.95	0.13	84,84,84,84	0
34	SR	0	8956	1/1	0.95	0.12	169,169,169,169	0
32	MG	0	8026	1/1	0.95	0.08	50,50,50,50	0
35	NA	0	8574	1/1	0.95	0.58	60,60,60,60	0
34	SR	0	9000	1/1	0.95	0.07	183,183,183,183	0
32	MG	0	8083	1/1	0.95	0.10	55,55,55,55	0
32	MG	0	8020	1/1	0.95	0.16	41,41,41,41	0
32	MG	0	8021	1/1	0.95	0.09	33,33,33,33	0
34	SR	0	8966	1/1	0.96	0.09	105,105,105,105	0
33	CL	J	8821	1/1	0.96	0.10	77,77,77,77	0
33	CL	L	8810	1/1	0.96	0.05	64,64,64,64	0
34	SR	0	8937	1/1	0.96	0.15	113,113,113,113	0
35	NA	0	8514	1/1	0.96	0.29	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
35	NA	0	8529	1/1	0.96	0.11	48,48,48,48	0
34	SR	B	8950	1/1	0.96	0.16	130,130,130,130	0
32	MG	0	8010	1/1	0.96	0.13	72,72,72,72	0
33	CL	0	8816	1/1	0.96	0.43	85,85,85,85	0
32	MG	0	8068	1/1	0.96	0.09	56,56,56,56	0
35	NA	0	8513	1/1	0.96	0.41	68,68,68,68	0
35	NA	0	8561	1/1	0.96	0.31	65,65,65,65	0
32	MG	0	8085	1/1	0.96	0.17	76,76,76,76	0
35	NA	0	8515	1/1	0.96	0.15	32,32,32,32	0
32	MG	0	8064	1/1	0.96	0.18	45,45,45,45	0
34	SR	0	8967	1/1	0.96	0.04	131,131,131,131	0
32	MG	0	8087	1/1	0.96	0.09	38,38,38,38	0
34	SR	0	8908	1/1	0.96	0.11	85,85,85,85	0
34	SR	0	8960	1/1	0.96	0.02	151,151,151,151	0
34	SR	0	8941	1/1	0.96	0.11	114,114,114,114	0
34	SR	0	8955	1/1	0.96	0.07	200,200,200,200	0
34	SR	0	8970	1/1	0.96	0.05	125,125,125,125	0
32	MG	0	8033	1/1	0.96	0.06	63,63,63,63	0
32	MG	0	8039	1/1	0.96	0.19	84,84,84,84	0
34	SR	0	8927	1/1	0.96	0.06	181,181,181,181	0
32	MG	0	8052	1/1	0.96	0.09	44,44,44,44	0
34	SR	0	8933	1/1	0.96	0.04	135,135,135,135	0
32	MG	0	8073	1/1	0.96	0.07	72,72,72,72	0
35	NA	0	8517	1/1	0.96	0.09	38,38,38,38	0
32	MG	0	8093	1/1	0.96	0.06	36,36,36,36	0
35	NA	0	8520	1/1	0.97	0.10	56,56,56,56	0
32	MG	0	8058	1/1	0.97	0.06	18,18,18,18	0
32	MG	0	8047	1/1	0.97	0.31	66,66,66,66	0
32	MG	0	8077	1/1	0.97	0.08	48,48,48,48	0
34	SR	0	8931	1/1	0.97	0.09	111,111,111,111	0
32	MG	B	8042	1/1	0.97	0.07	69,69,69,69	0
32	MG	0	8003	1/1	0.97	0.17	38,38,38,38	0
34	SR	0	8958	1/1	0.97	0.07	116,116,116,116	0
32	MG	0	8002	1/1	0.97	0.10	40,40,40,40	0
33	CL	0	8822	1/1	0.97	0.42	88,88,88,88	0
32	MG	0	8062	1/1	0.97	0.17	56,56,56,56	0
34	SR	0	8942	1/1	0.97	0.09	124,124,124,124	0
32	MG	0	8065	1/1	0.97	0.06	42,42,42,42	0
35	NA	0	8554	1/1	0.97	0.86	69,69,69,69	0
34	SR	0	8974	1/1	0.97	0.06	166,166,166,166	0
33	CL	0	8814	1/1	0.97	0.16	79,79,79,79	0
34	SR	0	8984	1/1	0.97	0.09	119,119,119,119	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
32	MG	0	8041	1/1	0.97	0.16	36,36,36,36	0
32	MG	0	8079	1/1	0.97	0.20	66,66,66,66	0
32	MG	0	8045	1/1	0.97	0.10	31,31,31,31	0
35	NA	0	8524	1/1	0.97	0.69	73,73,73,73	0
35	NA	M	8539	1/1	0.97	0.14	42,42,42,42	0
34	SR	0	8914	1/1	0.98	0.27	133,133,133,133	0
32	MG	0	8038	1/1	0.98	0.08	74,74,74,74	0
32	MG	0	8025	1/1	0.98	0.10	37,37,37,37	0
32	MG	0	8076	1/1	0.98	0.06	40,40,40,40	0
32	MG	0	8069	1/1	0.98	0.10	102,102,102,102	0
35	NA	0	8541	1/1	0.98	0.23	64,64,64,64	0
34	SR	0	8949	1/1	0.98	0.15	117,117,117,117	0
34	SR	0	9008	1/1	0.98	0.14	92,92,92,92	0
35	NA	0	8559	1/1	0.98	0.17	77,77,77,77	0
32	MG	0	8043	1/1	0.98	0.13	52,52,52,52	0
35	NA	0	8549	1/1	0.98	0.85	56,56,56,56	0
34	SR	R	8912	1/1	0.98	0.19	95,95,95,95	0
32	MG	T	8057	1/1	0.98	0.07	65,65,65,65	0
35	NA	0	8534	1/1	0.98	0.13	50,50,50,50	0
32	MG	0	8024	1/1	0.98	0.16	62,62,62,62	0
34	SR	0	8973	1/1	0.98	0.16	146,146,146,146	0
32	MG	0	8072	1/1	0.98	0.06	59,59,59,59	0
34	SR	0	8926	1/1	0.98	0.14	122,122,122,122	0
33	CL	0	8803	1/1	0.98	0.09	60,60,60,60	0
34	SR	F	9005	1/1	0.98	0.07	147,147,147,147	0
33	CL	0	8817	1/1	0.98	0.14	72,72,72,72	0
32	MG	0	8032	1/1	0.98	0.04	52,52,52,52	0
34	SR	0	8945	1/1	0.98	0.09	105,105,105,105	0
32	MG	0	8001	1/1	0.98	0.11	36,36,36,36	0
32	MG	0	8027	1/1	0.98	0.12	47,47,47,47	0
35	NA	0	8505	1/1	0.98	0.66	53,53,53,53	0
32	MG	0	8005	1/1	0.98	0.21	42,42,42,42	0
33	CL	0	8812	1/1	0.98	0.05	61,61,61,61	0
34	SR	0	8986	1/1	0.98	1.04	200,200,200,200	0
32	MG	0	8012	1/1	0.98	0.16	25,25,25,25	0
34	SR	0	8910	1/1	0.98	0.09	108,108,108,108	0
34	SR	0	8995	1/1	0.98	0.19	150,150,150,150	0
34	SR	0	8911	1/1	0.98	0.13	88,88,88,88	0
32	MG	0	8035	1/1	0.98	0.10	66,66,66,66	0
32	MG	0	8078	1/1	0.98	0.26	65,65,65,65	0
35	NA	0	8523	1/1	0.98	0.14	54,54,54,54	0
35	NA	0	8512	1/1	0.98	0.15	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
34	SR	0	8901	1/1	0.99	0.18	66,66,66,66	0
34	SR	0	8990	1/1	0.99	0.14	137,137,137,137	0
34	SR	0	8935	1/1	0.99	0.11	103,103,103,103	0
37	CD	O	8705	1/1	0.99	0.08	100,100,100,100	0
34	SR	0	8934	1/1	0.99	0.13	133,133,133,133	0
32	MG	0	8023	1/1	0.99	0.17	28,28,28,28	0
33	CL	A	8809	1/1	0.99	0.15	104,104,104,104	0
34	SR	0	8998	1/1	0.99	0.18	178,178,178,178	0
34	SR	0	8948	1/1	0.99	0.10	115,115,115,115	0
34	SR	0	8905	1/1	0.99	0.25	72,72,72,72	0
33	CL	0	8811	1/1	0.99	0.20	81,81,81,81	0
32	MG	0	8070	1/1	0.99	0.17	66,66,66,66	0
34	SR	0	8936	1/1	0.99	0.11	95,95,95,95	0
32	MG	0	8088	1/1	0.99	0.10	35,35,35,35	0
35	NA	0	8531	1/1	0.99	0.06	39,39,39,39	0
32	MG	0	8009	1/1	0.99	0.24	34,34,34,34	0
32	MG	0	8013	1/1	0.99	0.06	28,28,28,28	0
35	NA	0	8556	1/1	0.99	0.80	71,71,71,71	0
34	SR	0	8981	1/1	0.99	0.13	161,161,161,161	0
32	MG	0	8007	1/1	0.99	0.18	36,36,36,36	0
32	MG	0	8022	1/1	0.99	0.20	33,33,33,33	0
34	SR	0	8924	1/1	0.99	0.20	124,124,124,124	0
32	MG	0	8046	1/1	0.99	0.10	45,45,45,45	0
34	SR	0	8918	1/1	0.99	0.12	85,85,85,85	0
34	SR	0	8916	1/1	0.99	0.05	105,105,105,105	0
32	MG	0	8018	1/1	0.99	0.24	33,33,33,33	0
32	MG	0	8048	1/1	0.99	0.24	29,29,29,29	0
32	MG	0	8008	1/1	0.99	0.13	31,31,31,31	0
32	MG	0	8014	1/1	0.99	0.17	37,37,37,37	0
33	CL	M	8818	1/1	0.99	0.05	49,49,49,49	0
33	CL	0	8813	1/1	0.99	0.07	60,60,60,60	0
35	NA	0	8516	1/1	0.99	0.19	39,39,39,39	0
32	MG	0	8037	1/1	0.99	0.21	77,77,77,77	0
32	MG	0	8017	1/1	0.99	0.17	40,40,40,40	0
32	MG	0	8049	1/1	0.99	0.23	64,64,64,64	0
32	MG	K	8054	1/1	0.99	0.17	57,57,57,57	0
33	CL	R	8806	1/1	0.99	0.14	58,58,58,58	0
32	MG	0	8016	1/1	0.99	0.17	40,40,40,40	0
35	NA	R	8532	1/1	0.99	0.11	50,50,50,50	0
34	SR	0	8907	1/1	0.99	0.13	63,63,63,63	0
34	SR	0	8925	1/1	0.99	0.13	98,98,98,98	0
34	SR	0	8940	1/1	0.99	0.09	93,93,93,93	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
32	MG	0	8004	1/1	0.99	0.12	29,29,29,29	0
34	SR	1	8913	1/1	0.99	0.06	95,95,95,95	0
32	MG	0	8011	1/1	0.99	0.22	25,25,25,25	0
35	NA	0	8575	1/1	0.99	0.23	103,103,103,103	0
35	NA	0	8507	1/1	0.99	0.24	43,43,43,43	0
32	MG	0	8084	1/1	0.99	0.14	35,35,35,35	0
34	SR	0	8902	1/1	0.99	0.15	68,68,68,68	0
34	SR	0	8964	1/1	0.99	0.12	134,134,134,134	0
34	SR	0	8921	1/1	0.99	0.13	83,83,83,83	0
35	NA	0	8501	1/1	0.99	0.16	39,39,39,39	0
34	SR	0	8906	1/1	1.00	0.21	67,67,67,67	0
35	NA	0	8504	1/1	1.00	0.12	40,40,40,40	0
37	CD	1	8702	1/1	1.00	0.10	61,61,61,61	0
32	MG	0	8029	1/1	1.00	0.13	59,59,59,59	0
34	SR	0	8904	1/1	1.00	0.20	57,57,57,57	0
34	SR	1	8952	1/1	1.00	0.15	90,90,90,90	0
34	SR	0	8909	1/1	1.00	0.14	93,93,93,93	0
34	SR	0	8923	1/1	1.00	0.13	109,109,109,109	0
32	MG	0	8034	1/1	1.00	0.07	50,50,50,50	0
32	MG	0	8015	1/1	1.00	0.13	45,45,45,45	0
34	SR	0	8903	1/1	1.00	0.19	57,57,57,57	0

6.5 Other polymers

There are no such residues in this entry.