



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:32 PM UTC

PDB ID : 3CCR / pdb_00003ccr
Title : Structure of Anisomycin resistant 50S Ribosomal Subunit: 23S rRNA mutation A2488C. Density for anisomycin is visible but not included in the model.
Authors : Blaha, G.; Gurel, G.
Deposited on : 2008-02-26
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

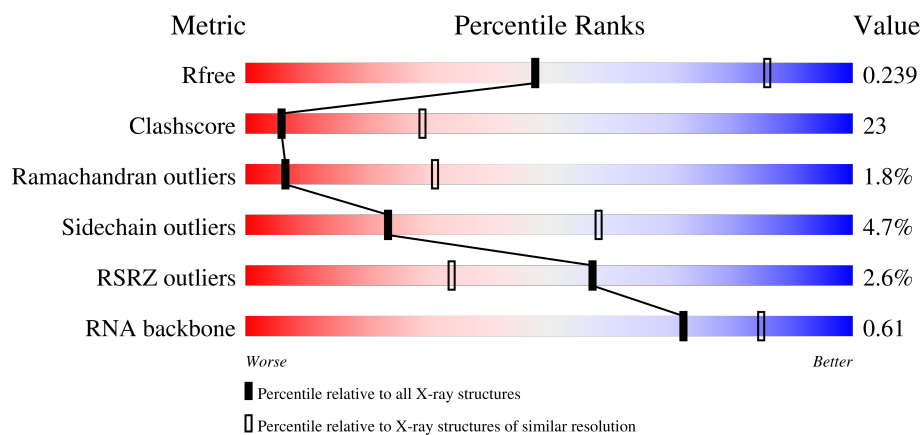
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



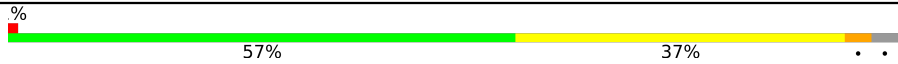
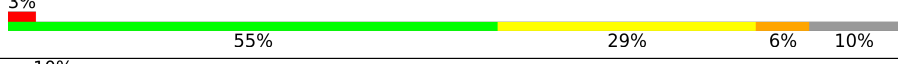
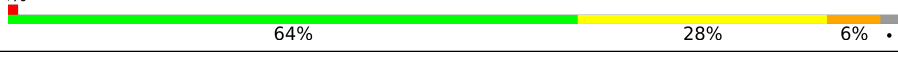
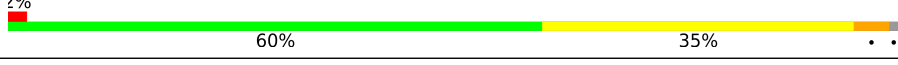
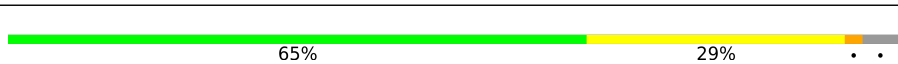
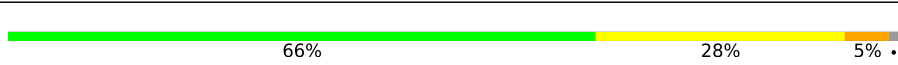
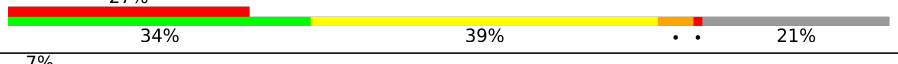
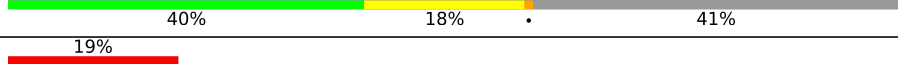
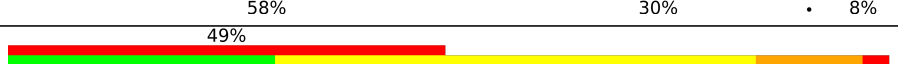
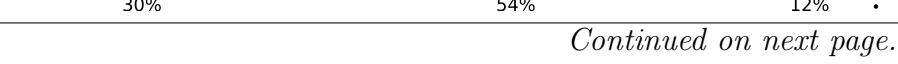
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)
RNA backbone	3983	1109 (3.20-2.80)

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

Mol	Chain	Length	Quality of chain
1	A	240	2% 60% 33% 6%
2	B	338	55% 40% 5%
3	C	246	63% 30% 6%
4	D	177	5% 41% 35% 21%

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

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

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
33	CL	3	8804	-	-	X	-
33	CL	B	8819	-	-	X	-
33	CL	M	8818	-	-	X	-
35	NA	0	8528	-	-	-	X
35	NA	0	8559	-	-	-	X

2 Entry composition [i](#)

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 33 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 34 is STRONTIUM ION (CCD ID: SR) (formula: Sr).

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

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

- Molecule 35 is SODIUM ION (CCD ID: NA) (formula: Na).

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

- Molecule 36 is POTASSIUM ION (CCD ID: K) (formula: K).

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

- Molecule 37 is CADMIUM ION (CCD ID: CD) (formula: Cd).

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

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

- Molecule 38 is water.

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

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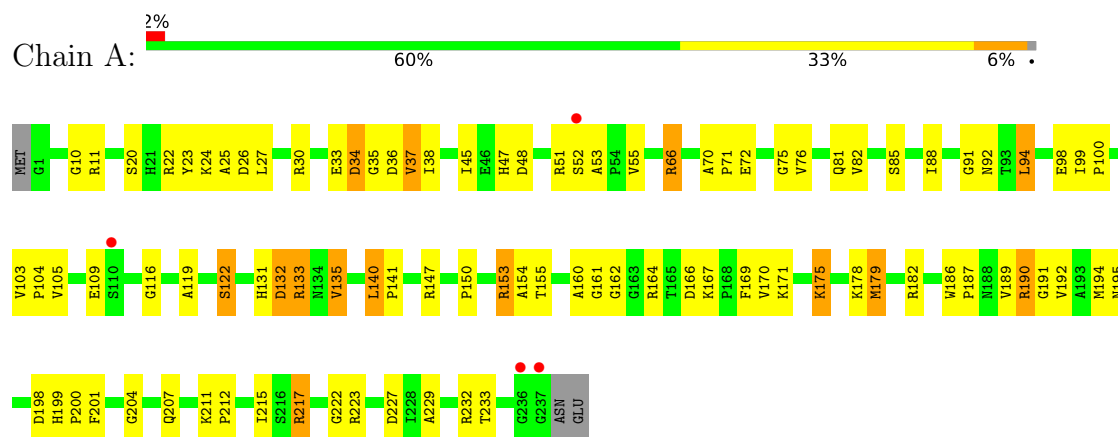
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	R	75	Total 75	O 75	0	0
38	S	37	Total 37	O 37	0	0
38	T	40	Total 40	O 40	0	0
38	U	28	Total 28	O 28	0	0
38	V	15	Total 15	O 15	0	0
38	W	69	Total 69	O 69	0	0
38	X	22	Total 22	O 22	0	0
38	Y	100	Total 100	O 100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

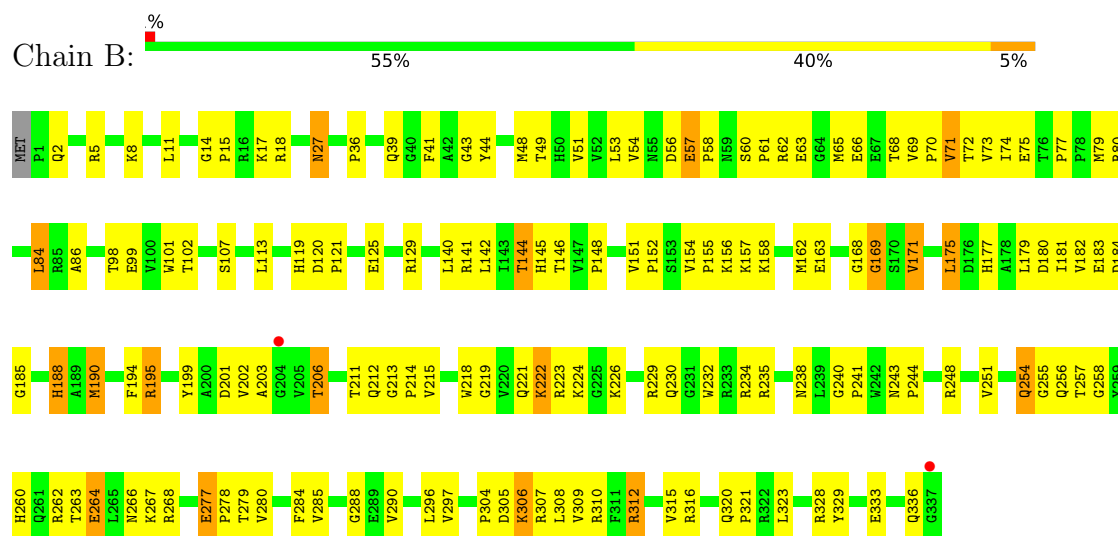
3 Residue-property plots

These plots are drawn for all protein, RNA, 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.

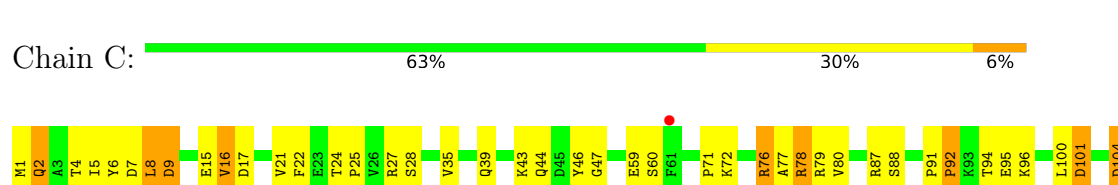
• Molecule 1: 50S ribosomal protein L2P

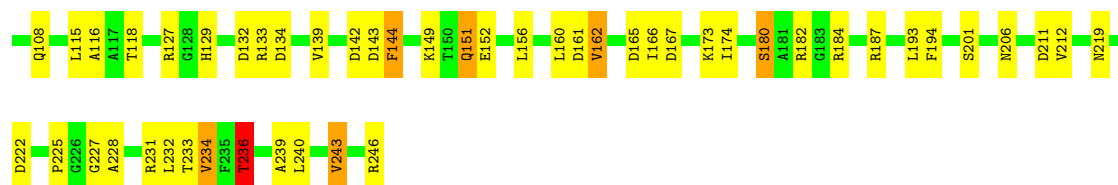


• Molecule 2: 50S ribosomal protein L3P

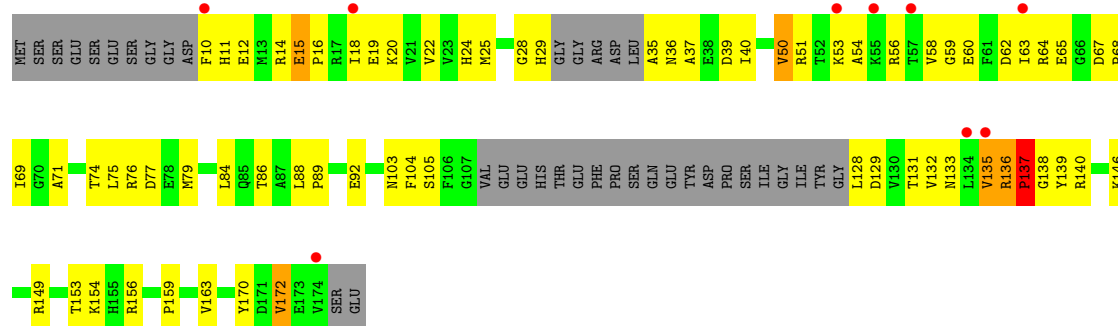
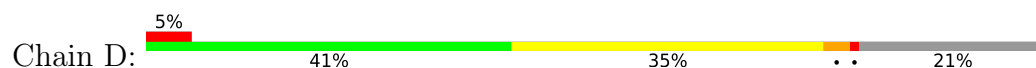


• Molecule 3: 50S ribosomal protein L4P

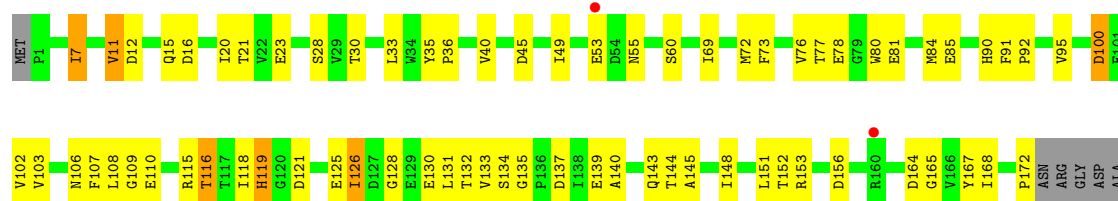




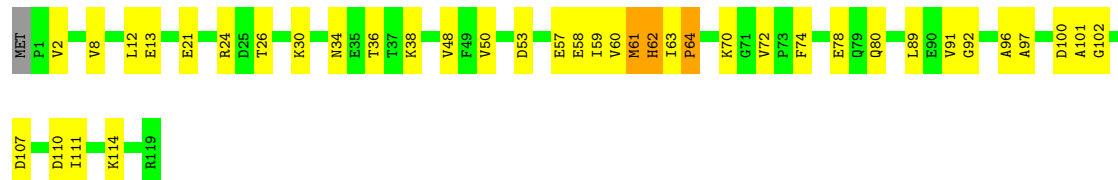
• Molecule 4: 50S ribosomal protein L5P



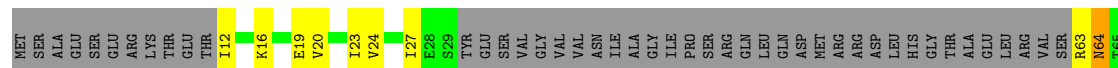
• Molecule 5: 50S ribosomal protein L6P



• Molecule 6: 50S ribosomal protein L7Ae

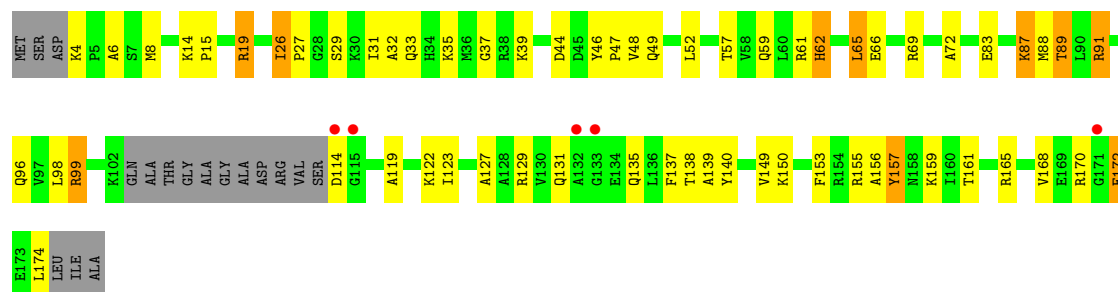


• Molecule 7: 50S ribosomal protein L10E

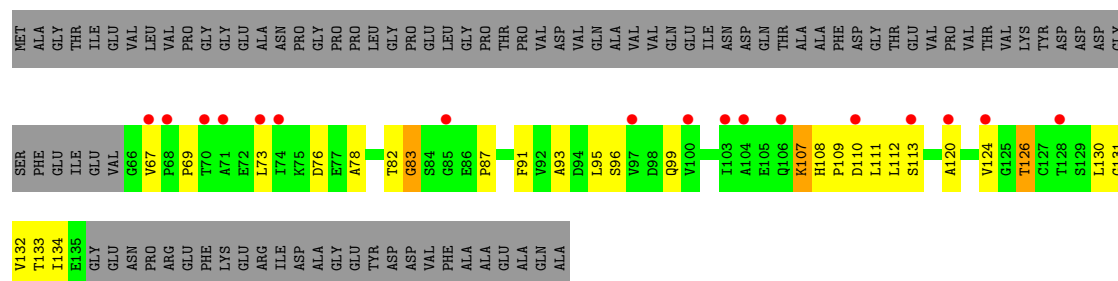




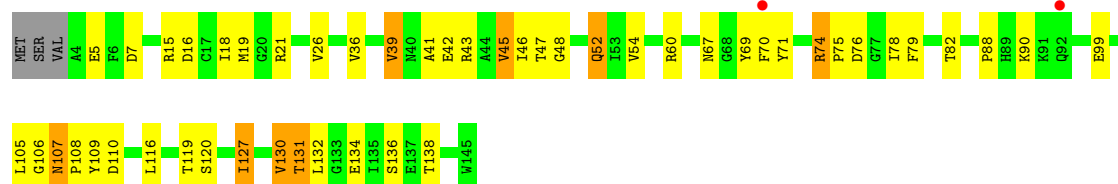
• Molecule 8: 50S ribosomal protein L10e



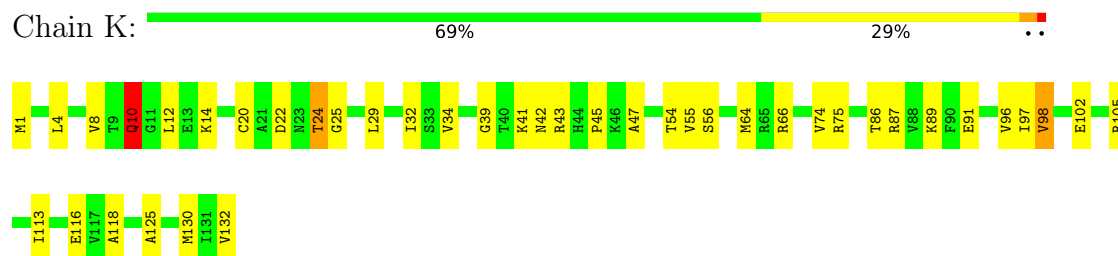
• Molecule 9: 50S ribosomal protein L11P



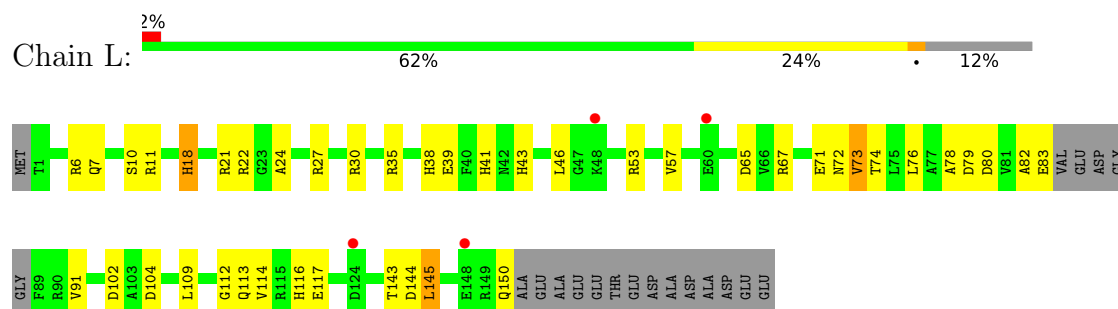
• Molecule 10: 50S ribosomal protein L13P



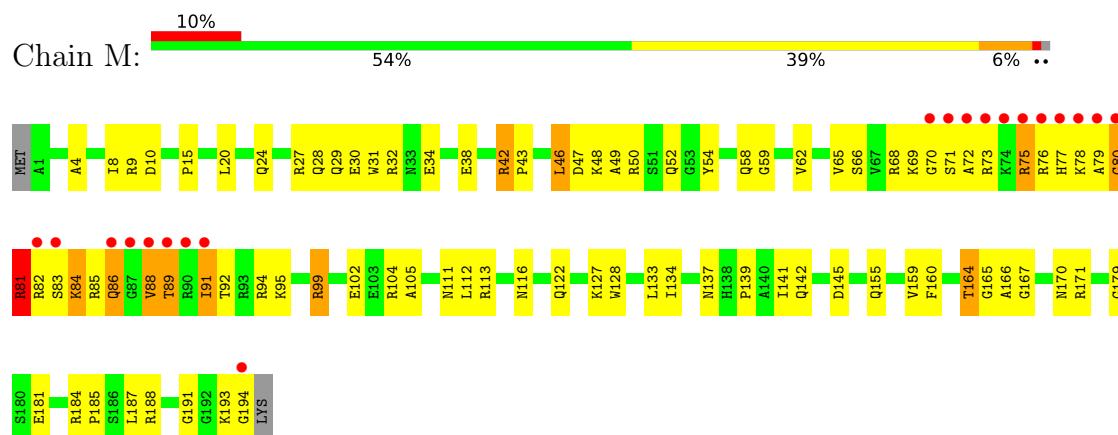
- Molecule 11: 50S ribosomal protein L14P



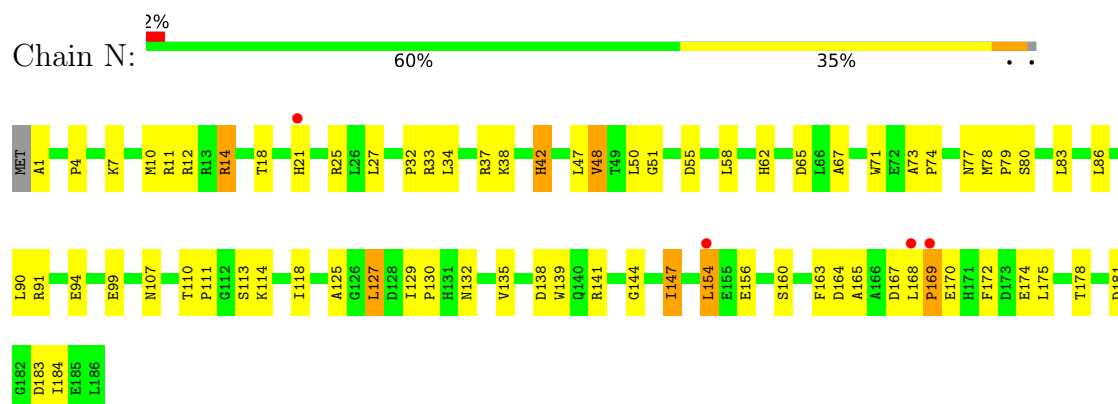
- Molecule 12: 50S ribosomal protein L15P



- Molecule 13: 50S ribosomal protein L15e



- Molecule 14: 50S ribosomal protein L18P



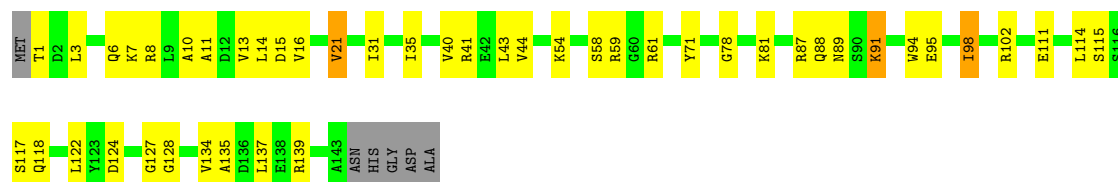
- Molecule 15: 50S ribosomal protein L18e

Chain O:  71% 28% .



- Molecule 16: 50S ribosomal protein L19e

Chain P:  65% 29% . .



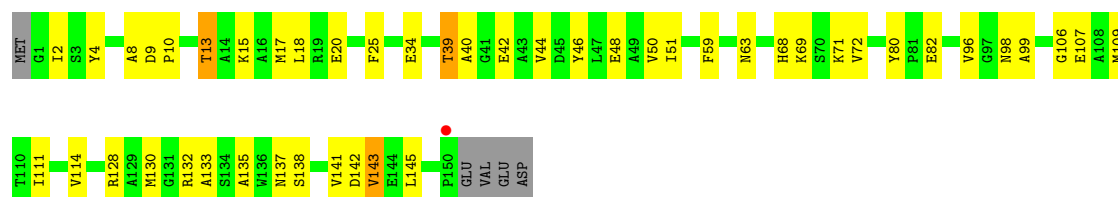
- Molecule 17: 50S ribosomal protein L21e

Chain Q:  66% 28% 5% .



- Molecule 18: 50S ribosomal protein L22P

Chain R:  66% 28% . .



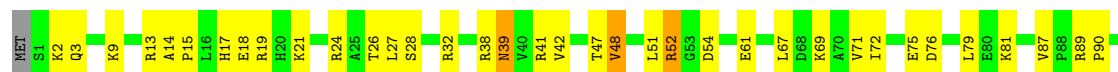
- Molecule 19: 50S ribosomal protein L23P

Chain S:  65% 28% 5% .



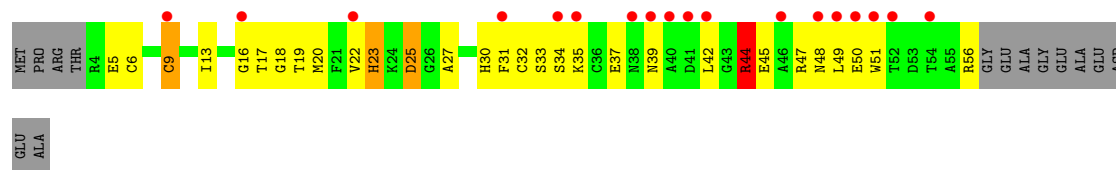
- Molecule 20: 50S ribosomal protein L24P

Chain T:  60% 36% . .

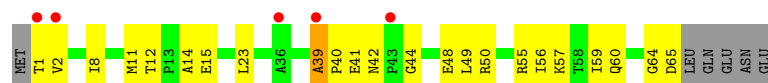




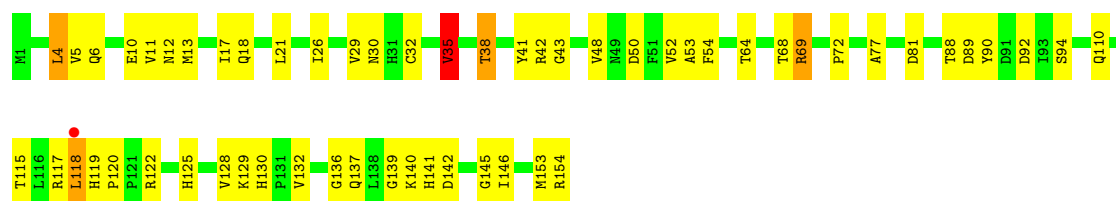
• Molecule 21: 50S ribosomal protein L24e



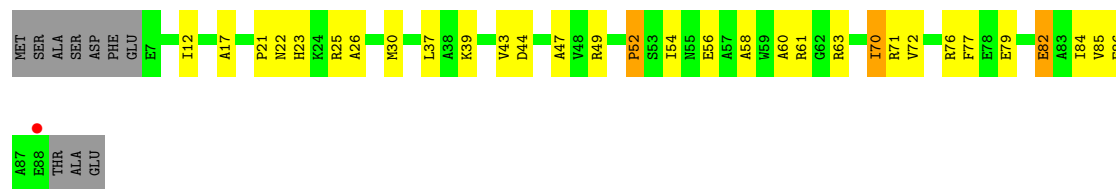
• Molecule 22: 50S ribosomal protein L29P



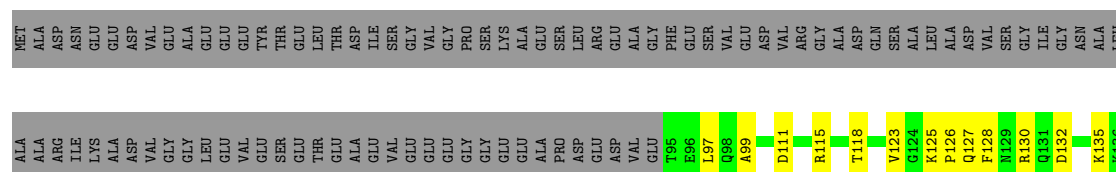
• Molecule 23: 50S ribosomal protein L30P

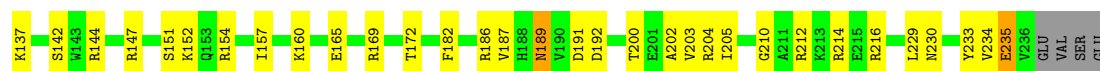


• Molecule 24: 50S ribosomal protein L31e

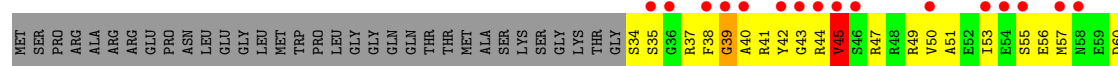
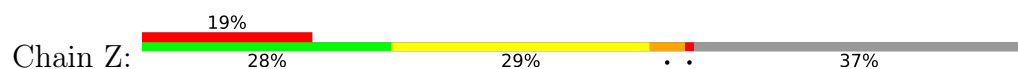


• Molecule 25: 50S ribosomal protein L32e

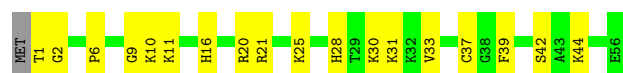




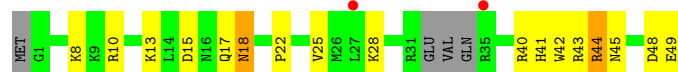
- Molecule 26: 50S ribosomal protein L37Ae



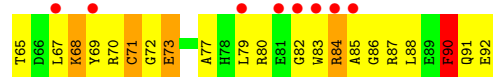
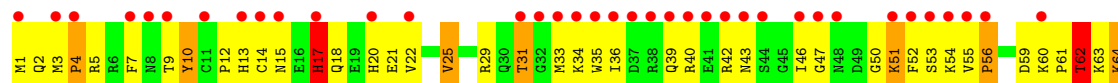
- Molecule 27: 50S ribosomal protein L37e



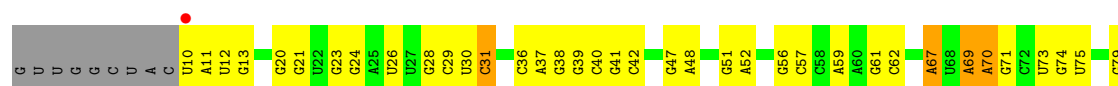
- Molecule 28: 50S ribosomal protein L39e



- Molecule 29: 50S ribosomal protein L44E

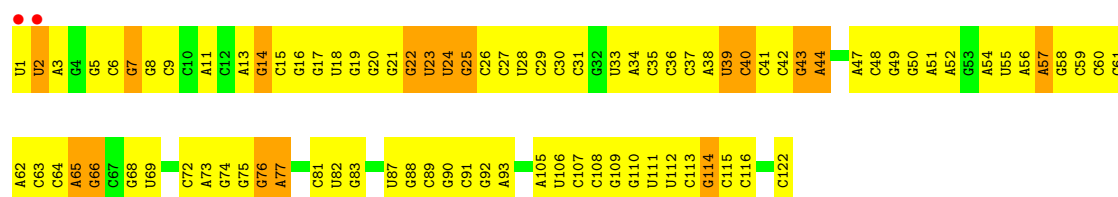


- Molecule 30: 23S RIBOSOMAL RNA



[illegible]





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	212.41Å 299.52Å 574.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.81 – 3.00 49.81 – 3.00	Depositor EDS
% Data completeness (in resolution range)	77.8 (49.81-3.00) 77.8 (49.81-3.00)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 2.40Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.180 , 0.247 0.178 , 0.239	Depositor DCC
R_{free} test set	6547 reflections (0.98%)	wwPDB-VP
Wilson B-factor (Å ²)	52.9	Xtriage
Anisotropy	0.446	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 80.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	99120	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

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

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 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: UR3, CL, OMU, CD, K, PSU, 1MA, MG, NA, OMG, SR

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	0.45	0/1786	1.03	8/2408 (0.3%)
2	B	0.44	0/2690	1.02	17/3652 (0.5%)
3	C	0.49	0/1885	1.02	11/2552 (0.4%)
4	D	0.39	0/1111	1.02	8/1498 (0.5%)
5	E	0.42	0/1382	0.93	5/1880 (0.3%)
6	F	0.41	0/901	0.97	3/1224 (0.2%)
7	G	0.37	0/241	0.81	0/324
8	H	0.41	0/1302	1.00	6/1743 (0.3%)
9	I	0.42	0/526	0.92	3/716 (0.4%)
10	J	0.44	0/1136	0.99	4/1530 (0.3%)
11	K	0.44	0/1004	1.00	3/1351 (0.2%)
12	L	0.39	0/1130	0.93	3/1509 (0.2%)
13	M	0.49	0/1582	0.96	3/2116 (0.1%)
14	N	0.39	0/1474	1.07	8/1999 (0.4%)
15	O	0.46	0/874	0.96	3/1181 (0.3%)
16	P	0.42	0/1147	0.90	1/1528 (0.1%)
17	Q	0.42	0/749	1.08	6/1005 (0.6%)
18	R	0.49	0/1172	0.97	1/1578 (0.1%)
19	S	0.44	0/648	0.92	4/875 (0.5%)
20	T	0.43	0/958	1.03	5/1289 (0.4%)
21	U	0.54	0/417	1.13	5/562 (0.9%)
22	V	0.42	0/502	0.95	0/675
23	W	0.49	0/1219	1.03	4/1655 (0.2%)
24	X	0.47	0/664	1.06	4/895 (0.4%)
25	Y	0.45	0/1146	0.94	2/1536 (0.1%)
26	Z	0.55	0/584	1.05	3/781 (0.4%)
27	1	0.47	0/438	0.87	0/578
28	2	0.45	0/401	0.90	1/529 (0.2%)
29	3	0.63	0/771	1.14	7/1024 (0.7%)
30	0	0.40	0/65954	0.60	9/102862 (0.0%)
31	9	0.40	0/2904	0.58	0/4526
All	All	0.42	0/98698	0.73	137/147581 (0.1%)

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

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

There are no bond length outliers.

All (137) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	3	25	VAL	N-CA-C	9.17	121.79	108.58
14	N	51	GLY	CA-C-N	8.79	128.38	119.24
14	N	51	GLY	C-N-CA	8.79	128.38	119.24
20	T	52	ARG	N-CA-C	8.62	124.73	114.04
4	D	136	ARG	CA-C-N	8.19	130.08	119.84
4	D	136	ARG	C-N-CA	8.19	130.08	119.84
29	3	55	VAL	CA-C-N	7.84	129.65	119.84
29	3	55	VAL	C-N-CA	7.84	129.65	119.84
14	N	48	VAL	N-CA-C	7.54	119.15	108.36
3	C	166	ILE	N-CA-C	-7.43	105.53	112.96
4	D	15	GLU	CA-C-N	7.38	129.07	119.84
4	D	15	GLU	C-N-CA	7.38	129.07	119.84
2	B	158	LYS	CA-C-N	7.38	127.36	119.76
2	B	158	LYS	C-N-CA	7.38	127.36	119.76
6	F	62	HIS	N-CA-C	7.34	119.28	111.28
23	W	69	ARG	N-CA-C	7.10	121.60	113.15
21	U	18	GLY	N-CA-C	6.92	120.04	112.29
24	X	22	ASN	N-CA-C	6.78	119.25	111.11
14	N	169	PRO	N-CA-C	-6.69	106.17	114.20
15	O	43	VAL	N-CA-C	6.60	117.80	108.36
5	E	135	GLY	CA-C-N	6.59	126.04	118.85
5	E	135	GLY	C-N-CA	6.59	126.04	118.85
3	C	134	ASP	N-CA-C	-6.58	104.42	113.18
26	Z	63	CYS	CA-C-N	6.54	128.02	119.84
26	Z	63	CYS	C-N-CA	6.54	128.02	119.84
2	B	120	ASP	CA-C-N	6.52	125.96	118.85
2	B	120	ASP	C-N-CA	6.52	125.96	118.85
8	H	161	THR	N-CA-C	6.51	121.72	113.25
15	O	4	ASN	CA-C-N	6.47	126.23	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	O	4	ASN	C-N-CA	6.47	126.23	119.05
1	A	166	ASP	N-CA-C	6.42	118.28	111.28
14	N	42	HIS	N-CA-C	6.42	117.91	108.86
30	0	1819	G	C5'-C4'-C3'	6.39	125.59	116.00
1	A	133	ARG	N-CA-C	-6.39	106.45	114.56
29	3	31	THR	N-CA-C	6.37	119.04	111.33
24	X	77	PHE	N-CA-C	6.37	116.26	107.73
10	J	48	GLY	N-CA-C	6.36	118.95	111.63
18	R	141	VAL	N-CA-C	6.35	117.62	108.48
14	N	14	ARG	N-CA-C	-6.29	104.35	111.14
1	A	198	ASP	N-CA-C	6.28	120.94	113.28
1	A	135	VAL	N-CA-C	6.25	116.06	108.06
1	A	222	GLY	N-CA-C	-6.24	106.51	114.37
23	W	35	VAL	N-CA-C	6.23	114.68	107.89
11	K	8	VAL	N-CA-C	6.22	117.44	108.48
13	M	69	LYS	N-CA-C	6.16	119.47	110.17
4	D	170	TYR	N-CA-C	6.14	120.11	111.52
24	X	17	ALA	N-CA-C	-6.09	105.82	113.18
1	A	140	LEU	CA-C-N	6.08	126.52	119.47
1	A	140	LEU	C-N-CA	6.08	126.52	119.47
12	L	91	VAL	N-CA-C	5.99	117.31	108.45
4	D	39	ASP	N-CA-C	5.98	118.29	111.11
2	B	39	GLN	N-CA-C	5.97	119.31	112.57
13	M	42	ARG	CA-C-N	5.96	125.90	119.76
13	M	42	ARG	C-N-CA	5.96	125.90	119.76
1	A	25	ALA	N-CA-C	5.94	118.32	108.99
20	T	3	GLN	CA-C-N	5.93	126.08	119.32
20	T	3	GLN	C-N-CA	5.93	126.08	119.32
8	H	26	ILE	CA-C-N	5.91	125.85	119.76
8	H	26	ILE	C-N-CA	5.91	125.85	119.76
20	T	54	ASP	N-CA-C	-5.86	105.63	112.89
26	Z	45	VAL	N-CA-C	5.85	117.29	110.62
14	N	163	PHE	N-CA-C	-5.83	98.38	110.80
2	B	151	VAL	CA-C-N	5.76	125.44	119.05
2	B	151	VAL	C-N-CA	5.76	125.44	119.05
5	E	119	HIS	N-CA-C	5.73	118.09	108.23
10	J	110	ASP	N-CA-C	-5.73	105.06	112.68
23	W	89	ASP	N-CA-C	-5.69	106.94	112.97
3	C	80	VAL	CA-C-N	5.68	126.06	119.47
3	C	80	VAL	C-N-CA	5.68	126.06	119.47
30	0	2726	U	N1-C1'-C2'	5.68	120.52	112.00
19	S	66	VAL	N-CA-C	5.67	116.03	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	Y	147	ARG	N-CA-C	5.67	120.36	113.38
3	C	228	ALA	CA-C-N	5.67	125.57	119.85
3	C	228	ALA	C-N-CA	5.67	125.57	119.85
2	B	222	LYS	N-CA-C	-5.65	102.16	110.52
21	U	9	CYS	N-CA-C	5.65	117.44	111.28
2	B	113	LEU	N-CA-C	5.63	118.86	110.14
11	K	25	GLY	N-CA-C	-5.62	107.34	115.27
3	C	167	ASP	N-CA-C	-5.60	105.70	112.54
9	I	67	VAL	CA-C-N	5.60	126.15	120.38
9	I	67	VAL	C-N-CA	5.60	126.15	120.38
19	S	30	ASP	N-CA-C	5.59	119.58	112.87
30	0	1261	A	N9-C1'-C2'	5.59	120.39	112.00
23	W	118	LEU	N-CA-C	5.54	117.68	110.53
16	P	111	GLU	N-CA-C	-5.53	106.37	114.39
3	C	144	PHE	N-CA-C	-5.52	104.78	112.45
5	E	73	PHE	N-CA-C	-5.50	104.97	110.97
30	0	1504	A	N9-C1'-C2'	5.47	120.20	112.00
29	3	51	LYS	N-CA-C	-5.46	106.11	112.89
14	N	10	MET	N-CA-C	-5.46	102.93	110.35
11	K	54	THR	N-CA-C	-5.45	101.65	110.32
17	Q	68	GLY	N-CA-C	-5.44	101.71	110.95
17	Q	53	HIS	CA-C-N	5.43	126.62	119.84
17	Q	53	HIS	C-N-CA	5.43	126.62	119.84
12	L	145	LEU	N-CA-C	-5.41	105.46	111.36
30	0	1592	G	N9-C1'-C2'	5.40	120.09	112.00
8	H	119	ALA	N-CA-C	5.37	119.46	113.01
25	Y	123	VAL	N-CA-C	5.37	115.51	110.30
19	S	10	VAL	N-CA-C	5.35	115.29	107.37
5	E	11	VAL	N-CA-C	5.35	117.57	109.12
2	B	213	GLY	CA-C-N	5.32	124.95	119.05
2	B	213	GLY	C-N-CA	5.32	124.95	119.05
17	Q	25	PRO	CA-C-N	5.30	124.81	119.19
17	Q	25	PRO	C-N-CA	5.30	124.81	119.19
9	I	126	THR	N-CA-C	-5.29	108.59	114.62
12	L	7	GLN	N-CA-C	5.28	118.98	112.54
21	U	23	HIS	N-CA-C	5.28	116.74	110.19
10	J	45	VAL	N-CA-C	5.26	117.33	108.81
2	B	175	LEU	N-CA-C	-5.22	105.49	111.07
21	U	39	ASN	N-CA-C	-5.22	106.85	113.43
20	T	47	THR	N-CA-C	-5.21	101.66	109.95
29	3	10	TYR	N-CA-C	5.20	117.21	109.25
10	J	67	ASN	N-CA-C	-5.20	105.52	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	Q	56	PHE	N-CA-C	5.20	118.76	112.93
28	2	44	ARG	N-CA-C	5.20	116.64	110.97
3	C	92	PRO	N-CA-C	-5.17	103.07	111.14
4	D	77	ASP	CB-CA-C	-5.17	110.19	117.23
2	B	57	GLU	CA-C-N	5.16	124.78	119.56
2	B	57	GLU	C-N-CA	5.16	124.78	119.56
30	0	1819	G	C2'-C3'-O3'	-5.16	105.97	113.70
30	0	834	G	C2'-C3'-O3'	-5.15	105.97	113.70
30	0	871	G	C5'-C4'-O4'	-5.15	102.08	109.80
21	U	44	ARG	N-CA-C	5.12	121.71	110.80
2	B	266	ASN	N-CA-C	5.11	118.37	111.17
4	D	135	VAL	N-CA-C	5.10	113.92	107.70
30	0	745	G	C2'-C3'-O3'	-5.09	106.06	113.70
29	3	17	HIS	N-CA-C	5.09	117.20	108.90
2	B	157	LYS	N-CA-C	-5.07	107.17	113.55
24	X	60	ALA	N-CA-C	5.06	116.79	111.28
3	C	236	THR	N-CA-C	-5.05	101.63	109.72
8	H	4	LYS	CA-C-N	5.04	124.95	119.85
8	H	4	LYS	C-N-CA	5.04	124.95	119.85
2	B	329	TYR	N-CA-C	5.04	116.58	108.32
6	F	8	VAL	CA-C-N	5.04	125.32	119.93
6	F	8	VAL	C-N-CA	5.04	125.32	119.93
3	C	9	ASP	N-CA-C	-5.04	107.81	114.31
19	S	54	THR	N-CA-C	5.02	117.30	109.52

There are no chirality outliers.

All (20) planarity outliers are listed below:

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

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Mol	Chain	Res	Type	Group
30	0	436	A	Sidechain
30	0	462	A	Sidechain
30	0	518	G	Sidechain
30	0	664	U	Sidechain
30	0	868	G	Sidechain
31	9	76	G	Sidechain
23	W	90	TYR	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1753	0	1766	100	0
2	B	2625	0	2532	133	0
3	C	1860	0	1813	74	0
4	D	1094	0	1085	51	0
5	E	1357	0	1266	56	0
6	F	890	0	843	28	0
7	G	240	0	231	11	0
8	H	1282	0	1292	55	0
9	I	519	0	500	26	0
10	J	1120	0	1098	45	0
11	K	994	0	1027	40	0
12	L	1118	0	1076	30	0
13	M	1558	0	1573	102	0
14	N	1445	0	1401	61	0
15	O	865	0	873	33	0
16	P	1136	0	1123	45	0
17	Q	735	0	729	21	0
18	R	1149	0	1122	39	0
19	S	641	0	605	16	0
20	T	950	0	924	35	0
21	U	410	0	368	39	0
22	V	499	0	511	20	0
23	W	1196	0	1137	55	0
24	X	654	0	653	24	0
25	Y	1130	0	1133	44	0
26	Z	573	0	535	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	1	431	0	426	20	0
28	2	396	0	413	22	0
29	3	755	0	732	95	0
30	0	59018	0	29810	2254	0
31	9	2599	0	1325	160	0
32	0	84	0	0	0	0
32	2	1	0	0	0	0
32	3	1	0	0	0	0
32	9	1	0	0	0	0
32	A	1	0	0	0	0
32	B	2	0	0	0	0
32	K	1	0	0	0	0
32	T	1	0	0	0	0
32	Y	1	0	0	0	0
33	0	9	0	0	2	0
33	3	1	0	0	3	0
33	A	1	0	0	1	0
33	B	1	0	0	2	0
33	J	3	0	0	2	0
33	K	1	0	0	0	0
33	L	1	0	0	1	0
33	M	1	0	0	2	0
33	N	1	0	0	0	0
33	O	1	0	0	0	0
33	R	1	0	0	0	0
33	Y	1	0	0	0	0
34	0	93	0	0	0	0
34	1	2	0	0	0	0
34	3	2	0	0	0	0
34	9	3	0	0	0	0
34	A	3	0	0	0	0
34	B	2	0	0	0	0
34	F	1	0	0	0	0
34	R	1	0	0	0	0
34	S	1	0	0	0	0
35	0	66	0	0	0	0
35	9	2	0	0	0	0
35	C	1	0	0	0	0
35	J	1	0	0	0	0
35	M	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	5897	0	0	323	0
38	1	61	0	0	3	0
38	2	45	0	0	1	0
38	3	76	0	0	7	0
38	9	154	0	0	11	0
38	A	121	0	0	3	0
38	B	145	0	0	20	0
38	C	166	0	0	13	0
38	D	46	0	0	7	0
38	E	43	0	0	4	0
38	F	31	0	0	1	0
38	G	17	0	0	0	0
38	H	72	0	0	10	0
38	I	5	0	0	2	0
38	J	52	0	0	4	0
38	K	52	0	0	3	0
38	L	81	0	0	4	0
38	M	133	0	0	12	0
38	N	56	0	0	6	0
38	O	41	0	0	2	0
38	P	63	0	0	5	0
38	Q	52	0	0	1	0
38	R	75	0	0	2	0
38	S	37	0	0	0	0
38	T	40	0	0	3	0
38	U	28	0	0	5	0
38	V	15	0	0	1	0
38	W	69	0	0	7	0
38	X	22	0	0	4	0
38	Y	100	0	0	5	0
38	Z	28	0	0	5	0
All	All	99120	0	59922	3426	0

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

All (3426) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:3:THR:HG22	30:0:656:G:H5'	1.46	0.95
30:0:545:G:H5'	30:0:545:G:C8	2.01	0.95
38:M:8869:HOH:O	30:0:381:G:H5''	1.67	0.95
26:Z:44:ARG:HH21	30:0:1771:U:H5'	1.31	0.95
30:0:2420:G:O2'	30:0:2421:G:H5'	1.64	0.94
31:9:59:C:H2'	31:9:60:C:H6	1.33	0.94
30:0:1118:A:H62	30:0:1244:U:H3	1.14	0.93
30:0:871:G:H8	30:0:871:G:C5'	1.81	0.93
30:0:2321:A:H2	30:0:2378:U:H3	1.12	0.93
3:C:127:ARG:NH2	3:C:225:PRO:HG2	1.82	0.93
30:0:2748:G:H2'	38:0:7523:HOH:O	1.68	0.93
30:0:559:U:H6	30:0:559:U:H5'	1.34	0.92
31:9:54:A:C2'	31:9:55:U:H5'	1.99	0.92
30:0:1116:U:H3	30:0:1246:A:H62	1.17	0.92
30:0:2586:U:H3	30:0:2592:G:H22	1.18	0.91
30:0:2710:U:H1'	38:0:7601:HOH:O	1.69	0.91
30:0:2649:A:H3'	38:0:9829:HOH:O	1.70	0.91
30:0:1856:C:H1'	38:0:5846:HOH:O	1.70	0.91
30:0:1170:U:H2'	30:0:1172:G:OP2	1.71	0.91
30:0:1835:U:H5	30:0:1840:A:N7	1.68	0.91
30:0:1595:G:O2'	30:0:1596:U:H5'	1.71	0.91
30:0:2506:A:HO2'	30:0:2507:G:H8	0.94	0.91
30:0:2769:C:C2'	30:0:2770:G:H5'	2.01	0.90
8:H:49:GLN:HE21	8:H:140:TYR:HE2	1.18	0.90
30:0:870:G:H2'	30:0:871:G:H5''	1.51	0.90
13:M:58:GLN:HE22	30:0:259:G:H21	1.13	0.90
10:J:52:GLN:HE22	30:0:1119:G:H2'	1.37	0.90
30:0:963:C:H2'	30:0:964:G:C8	2.05	0.90
23:W:4:LEU:HD13	23:W:52:VAL:HG21	1.51	0.90
30:0:615:G:H1'	38:0:5221:HOH:O	1.72	0.90
30:0:1835:U:H2'	38:0:3618:HOH:O	1.72	0.90
30:0:625:U:H5''	30:0:1044:C:N4	1.87	0.89
30:0:969:G:H1	30:0:999:C:N4	1.71	0.89
30:0:1701:A:H4'	30:0:1702:U:H5''	1.55	0.89
16:P:115:SER:H	16:P:118:GLN:HE21	0.89	0.89
10:J:52:GLN:NE2	30:0:1119:G:H2'	1.88	0.88
13:M:73:ARG:NH2	30:0:2263:G:H5''	1.87	0.88
1:A:199:HIS:HD2	1:A:201:PHE:H	1.21	0.88
28:2:43:ARG:HH22	30:0:1684:A:H1'	1.37	0.87
30:0:542:A:H5'	30:0:542:A:H8	1.39	0.87
30:0:814:G:H4'	38:0:3128:HOH:O	1.73	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2502:C:H2'	30:0:2503:A:H5'	1.57	0.87
30:0:1666:C:H2'	30:0:1667:A:H5'	1.55	0.87
30:0:2005:G:H3'	30:0:2005:G:OP2	1.75	0.87
25:Y:187:VAL:HG23	25:Y:192:ASP:HB2	1.57	0.87
30:0:506:G:H22	30:0:509:A:C5'	1.87	0.86
31:9:56:A:H2'	31:9:57:A:H5''	1.57	0.86
30:0:2637:A:H4'	38:0:6039:HOH:O	1.75	0.86
30:0:506:G:H22	30:0:509:A:H5''	1.40	0.86
30:0:2908:A:H2'	30:0:2909:G:O4'	1.75	0.86
30:0:2248:C:H3'	38:0:5403:HOH:O	1.76	0.86
13:M:71:SER:HB2	13:M:92:THR:HG22	1.56	0.86
30:0:2372:A:H2'	30:0:2373:U:C6	2.09	0.86
11:K:10:GLN:HE21	11:K:10:GLN:H	1.18	0.86
30:0:553:G:H3'	38:0:4066:HOH:O	1.76	0.86
30:0:969:G:H1	30:0:999:C:H42	1.24	0.86
16:P:115:SER:H	16:P:118:GLN:NE2	1.73	0.86
6:F:63:ILE:HB	6:F:64:PRO:HD3	1.57	0.86
30:0:1183:C:H2'	38:0:6223:HOH:O	1.75	0.85
13:M:99:ARG:HE	13:M:170:ASN:HD22	1.19	0.85
30:0:558:C:H2'	30:0:559:U:H5''	1.57	0.85
30:0:2419:U:H5''	30:0:2420:G:H5'	1.57	0.85
29:3:20:HIS:CD2	29:3:69:TYR:HB3	2.12	0.85
30:0:2421:G:H1'	38:0:7004:HOH:O	1.75	0.85
30:0:2505:G:O2'	30:0:2506:A:H5'	1.76	0.85
30:0:308:U:H5'	30:0:309:C:OP1	1.75	0.85
30:0:1474:C:H6	30:0:1474:C:H5'	1.40	0.85
30:0:200:C:H2'	38:0:3433:HOH:O	1.75	0.84
30:0:2345:A:H3'	30:0:2346:C:H6	1.43	0.84
30:0:1474:C:H5'	30:0:1474:C:C6	2.13	0.84
30:0:870:G:C2'	30:0:871:G:H5''	2.07	0.84
31:9:13:A:O2'	31:9:14:G:H5''	1.77	0.84
11:K:39:GLY:HA2	38:0:5187:HOH:O	1.75	0.84
30:0:1080:C:H4'	30:0:1081:A:OP1	1.76	0.84
23:W:137:GLN:HE21	23:W:141:HIS:HE1	1.23	0.83
16:P:115:SER:N	16:P:118:GLN:HE21	1.74	0.83
31:9:73:A:H2'	31:9:74:G:H8	1.43	0.83
30:0:12:U:H2'	30:0:13:G:H5'	1.57	0.83
30:0:2717:C:H2'	30:0:2718:C:H5''	1.59	0.83
30:0:558:C:H2'	30:0:559:U:C5'	2.08	0.83
31:9:92:G:H2'	31:9:93:A:C8	2.14	0.83
30:0:2570:G:H5''	38:0:4880:HOH:O	1.78	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:68:ARG:NH2	13:M:73:ARG:HD3	1.94	0.83
30:0:2896:A:H5''	38:0:6075:HOH:O	1.77	0.83
31:9:14:G:H5'	31:9:14:G:C8	2.14	0.83
30:0:271:C:H41	30:0:378:A:H2	1.22	0.82
30:0:1644:C:H2'	30:0:1645:U:H6	1.44	0.82
30:0:810:G:H2'	30:0:811:C:C6	2.13	0.82
30:0:2437:A:H2'	30:0:2438:G:C8	2.14	0.82
22:V:12:THR:HG22	22:V:15:GLU:HG3	1.60	0.82
30:0:236:A:C4'	30:0:237:G:H5'	2.09	0.82
30:0:1205:U:C2'	30:0:1206:U:C5'	2.57	0.82
30:0:1206:U:H5'	30:0:1206:U:H6	1.43	0.82
4:D:25:MET:SD	4:D:40:ILE:HD11	2.19	0.82
3:C:236:THR:HG22	3:C:239:ALA:H	1.44	0.82
15:O:3:THR:CG2	30:0:656:G:H5'	2.09	0.82
30:0:2345:A:H3'	30:0:2346:C:C6	2.15	0.82
30:0:2426:G:H1'	38:0:6068:HOH:O	1.79	0.82
30:0:2502:C:C2'	30:0:2503:A:H5'	2.10	0.82
13:M:134:ILE:HG23	13:M:141:ILE:HD13	1.62	0.81
30:0:1116:U:O2'	30:0:1118:A:H2	1.62	0.81
30:0:1191:A:H2'	30:0:1193:A:H5'	1.62	0.81
30:0:1278:A:H4'	30:0:1279:U:C5	2.15	0.81
30:0:614:U:O2'	30:0:615:G:H5'	1.80	0.81
30:0:2604:A:H5'	38:0:5760:HOH:O	1.79	0.81
26:Z:42:TYR:HA	30:0:1829:A:H61	1.45	0.81
30:0:185:G:H4'	30:0:186:A:OP1	1.78	0.81
14:N:67:ALA:HA	14:N:71:TRP:HB3	1.62	0.81
30:0:282:C:O2'	30:0:283:U:H5'	1.79	0.81
18:R:39:THR:HG22	18:R:42:GLU:H	1.44	0.80
13:M:171:ARG:CD	30:0:156:C:H5''	2.06	0.80
31:9:56:A:C2'	31:9:57:A:H5''	2.11	0.80
30:0:1632:A:H2'	30:0:1633:C:H5'	1.61	0.80
29:3:2:GLN:O	30:0:2320:U:H2'	1.80	0.80
6:F:91:VAL:HG12	6:F:92:GLY:H	1.47	0.80
30:0:1119:G:N2	30:0:1246:A:C2	2.48	0.80
30:0:2467:A:H3'	38:0:5416:HOH:O	1.82	0.80
31:9:59:C:H2'	31:9:60:C:C6	2.16	0.80
30:0:558:C:O2'	30:0:559:U:H5''	1.81	0.80
22:V:50:ARG:NH1	30:0:56:G:H5''	1.95	0.80
30:0:1185:U:H2'	30:0:1186:C:H6	1.46	0.80
11:K:14:LYS:HB2	11:K:45:PRO:HG2	1.63	0.80
23:W:13:MET:HE1	23:W:21:LEU:HD12	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:29:C:C2'	31:9:30:C:H5'	2.12	0.79
1:A:167:LYS:HE2	26:Z:50:VAL:HG13	1.63	0.79
19:S:55:GLN:NE2	30:0:1446:U:H2'	1.97	0.79
21:U:56:ARG:HD2	30:0:2890:A:N9	1.97	0.79
28:2:41:HIS:H	28:2:45:ASN:HD22	1.31	0.79
30:0:1116:U:HO2'	30:0:1118:A:H2	0.80	0.79
30:0:1603:A:H5''	30:0:1605:G:H5'	1.65	0.79
13:M:58:GLN:NE2	30:0:259:G:H21	1.81	0.79
1:A:199:HIS:CD2	1:A:201:PHE:H	2.00	0.79
13:M:159:VAL:HG12	33:M:8818:CL:CL	2.20	0.79
30:0:2506:A:O2'	30:0:2507:G:H8	1.66	0.79
30:0:2717:C:H2'	30:0:2718:C:C5'	2.13	0.79
31:9:73:A:H2'	31:9:74:G:C8	2.17	0.79
30:0:282:C:H1'	30:0:368:C:H41	1.46	0.79
30:0:282:C:H1'	30:0:368:C:N4	1.98	0.79
30:0:2604:A:H4'	38:0:7586:HOH:O	1.83	0.79
30:0:2783:A:H3'	38:0:5197:HOH:O	1.82	0.78
30:0:2769:C:O2'	30:0:2770:G:H5'	1.84	0.78
30:0:1829:A:H2'	30:0:1830:C:H5'	1.65	0.78
30:0:2533:C:H5'	30:0:2533:C:H6	1.47	0.78
30:0:2906:A:H5'	30:0:2907:C:O4'	1.83	0.78
31:9:55:U:H5''	38:9:9146:HOH:O	1.82	0.78
30:0:541:C:C2'	30:0:542:A:H5''	2.13	0.78
30:0:853:C:H3'	38:0:4528:HOH:O	1.83	0.78
2:B:221:GLN:HE22	11:K:42:ASN:HD22	1.32	0.78
10:J:74:ARG:HB3	10:J:74:ARG:HH11	1.48	0.78
13:M:70:GLY:HA3	13:M:73:ARG:NH2	1.99	0.78
30:0:2416:G:H2'	30:0:2417:C:H6	1.49	0.78
30:0:2237:G:H1'	38:0:4824:HOH:O	1.83	0.78
30:0:297:U:H2'	30:0:298:C:H6	1.49	0.78
31:9:56:A:C3'	31:9:57:A:H5''	2.12	0.78
13:M:171:ARG:HD3	30:0:156:C:C5'	2.07	0.77
30:0:1189:A:H1'	30:0:1209:C:O4'	1.84	0.77
30:0:1426:C:H2'	38:0:9600:HOH:O	1.83	0.77
30:0:1617:C:C4	30:0:1643:C:H4'	2.19	0.77
30:0:1741:U:H5'	30:0:1742:A:OP1	1.83	0.77
30:0:603:A:H1'	30:0:605:C:C2	2.19	0.77
30:0:1942:A:H5'	38:0:7329:HOH:O	1.84	0.77
30:0:2440:C:H5''	38:0:3808:HOH:O	1.83	0.77
30:0:1118:A:C8	30:0:1118:A:C3'	2.66	0.77
4:D:105:SER:OG	30:0:2338:G:H1'	1.83	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2769:C:H2'	30:0:2770:G:O4'	1.82	0.77
10:J:70:PHE:CE1	30:0:2676:C:H4'	2.19	0.77
30:0:2578:G:H5'	30:0:2578:G:H8	1.49	0.77
8:H:91:ARG:O	30:0:1003:U:H4'	1.84	0.77
11:K:10:GLN:H	11:K:10:GLN:NE2	1.83	0.76
29:3:64:LYS:HA	29:3:84:ARG:HA	1.67	0.76
30:0:247:A:H2'	38:0:3913:HOH:O	1.85	0.76
30:0:2335:C:H2'	30:0:2336:G:C8	2.20	0.76
30:0:2469:A:H1'	38:0:3231:HOH:O	1.85	0.76
20:T:71:VAL:HG11	20:T:90:PRO:HB3	1.65	0.76
30:0:1205:U:H2'	30:0:1206:U:H5''	1.66	0.76
30:0:1834:C:H2'	30:0:1840:A:H62	1.48	0.76
30:0:1249:U:H2'	30:0:1250:C:H6	1.51	0.76
30:0:136:C:H2'	30:0:137:U:O4'	1.86	0.76
30:0:960:G:H3'	30:0:960:G:N3	2.00	0.76
30:0:1170:U:H1'	30:0:1172:G:N7	2.00	0.76
31:9:36:C:H4'	38:9:9029:HOH:O	1.85	0.76
30:0:1634:G:H3'	38:0:3885:HOH:O	1.85	0.76
30:0:146:U:O2'	30:0:147:G:H5'	1.86	0.76
30:0:541:C:H2'	30:0:542:A:C5'	2.15	0.75
31:9:75:G:H1	31:9:106:U:H3	1.33	0.75
2:B:18:ARG:HE	2:B:256:GLN:HE21	1.31	0.75
13:M:88:VAL:HG21	30:0:2122:C:O2'	1.86	0.75
26:Z:63:CYS:SG	26:Z:81:CYS:HB2	2.26	0.75
30:0:564:G:H1'	38:0:6290:HOH:O	1.85	0.75
30:0:2083:A:H3'	38:0:7559:HOH:O	1.86	0.75
30:0:1434:A:HO2'	30:0:1435:U:H6	1.32	0.75
31:9:54:A:HO2'	31:9:55:U:H5'	1.52	0.75
30:0:297:U:H2'	30:0:298:C:C6	2.21	0.75
30:0:1189:A:H3'	38:0:7661:HOH:O	1.86	0.75
2:B:62:ARG:HA	2:B:65:MET:HE3	1.69	0.75
30:0:281:U:O2'	30:0:282:C:H5'	1.85	0.75
30:0:1524:U:OP1	30:0:1524:U:H4'	1.87	0.75
30:0:40:C:H4'	38:0:6986:HOH:O	1.86	0.75
30:0:1184:C:H1'	38:0:7447:HOH:O	1.86	0.75
30:0:1377:C:H5'	30:0:1377:C:H6	1.52	0.74
30:0:69:A:H5'	30:0:69:A:C8	2.22	0.74
30:0:718:C:O2	30:0:718:C:H2'	1.87	0.74
8:H:44:ASP:HA	8:H:170:ARG:HH12	1.50	0.74
30:0:279:C:O2'	30:0:280:C:H5'	1.87	0.74
30:0:635:A:H2'	30:0:636:G:H5''	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1279:U:O2	30:0:1279:U:H2'	1.85	0.74
30:0:1787:C:O2'	30:0:1788:U:H5'	1.87	0.74
1:A:223:ARG:NH2	30:0:2271:G:H5'	2.02	0.74
30:0:1972:U:H2'	30:0:1973:A:C5'	2.18	0.74
10:J:26:VAL:HG13	10:J:36:VAL:HG11	1.69	0.74
30:0:848:C:H5'	38:0:7257:HOH:O	1.87	0.74
30:0:1589:G:N2	30:0:1605:G:H1'	2.02	0.74
30:0:1165:G:O3'	30:0:1174:A:H4'	1.88	0.74
1:A:47:HIS:CD2	30:0:1654:U:H2'	2.22	0.74
30:0:629:A:H4'	38:0:4498:HOH:O	1.88	0.74
30:0:694:A:C2'	30:0:695:C:H5'	2.18	0.74
30:0:2831:C:C2'	30:0:2832:C:H5'	2.18	0.74
30:0:1185:U:H5'	38:0:7447:HOH:O	1.88	0.73
21:U:44:ARG:HD3	21:U:49:LEU:HD11	1.70	0.73
30:0:2100:A:H5'	38:0:7373:HOH:O	1.88	0.73
30:0:2703:A:H2'	30:0:2704:C:H6	1.52	0.73
29:3:68:LYS:CD	29:3:70:ARG:HH21	2.01	0.73
30:0:2011:A:H5''	38:0:4388:HOH:O	1.87	0.73
30:0:254:C:O2	30:0:254:C:H2'	1.88	0.73
30:0:1603:A:C5'	30:0:1605:G:H5'	2.19	0.73
2:B:18:ARG:HE	2:B:256:GLN:NE2	1.86	0.73
30:0:1855:G:H4'	30:0:1856:C:O5'	1.88	0.73
30:0:2769:C:H2'	30:0:2770:G:H5'	1.69	0.73
31:9:1:U:H4'	31:9:3:A:OP1	1.88	0.73
30:0:137:U:H2'	30:0:139:C:C5	2.23	0.73
2:B:201:ASP:HB2	2:B:312:ARG:HD2	1.70	0.73
30:0:69:A:H5'	30:0:69:A:H8	1.54	0.73
30:0:1589:G:H22	30:0:1605:G:H1'	1.53	0.73
30:0:1835:U:C5	30:0:1840:A:N7	2.53	0.73
30:0:2505:G:C2'	30:0:2506:A:H5'	2.19	0.73
31:9:3:A:N6	31:9:22:G:H1'	2.03	0.73
10:J:47:THR:HG21	30:0:1244:U:H2'	1.69	0.73
30:0:871:G:C8	30:0:871:G:C5'	2.63	0.73
30:0:2064:U:H5'	30:0:2652:U:O3'	1.89	0.73
30:0:2472:C:O2'	30:0:2634:G:H4'	1.89	0.73
38:B:9106:HOH:O	30:0:2672:C:H1'	1.87	0.72
30:0:2635:A:O2'	30:0:2636:C:H5'	1.88	0.72
1:A:109:GLU:HG2	1:A:116:GLY:H	1.53	0.72
30:0:283:U:H5	30:0:284:C:N3	1.87	0.72
30:0:1625:U:H6	30:0:1625:U:H3'	1.54	0.72
30:0:1666:C:H2'	30:0:1667:A:C5'	2.19	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:99:ARG:HD2	13:M:167:GLY:HA2	1.71	0.72
30:0:1733:A:C6	30:0:1734:C:C2	2.77	0.72
1:A:48:ASP:HB3	38:A:9085:HOH:O	1.90	0.72
13:M:79:ALA:HB1	38:0:4442:HOH:O	1.89	0.72
4:D:58:VAL:HB	4:D:62:ASP:HB3	1.72	0.72
13:M:76:ARG:HB2	13:M:88:VAL:HG13	1.72	0.72
18:R:132:ARG:NH2	30:0:2055:A:H4'	2.05	0.72
30:0:1372:A:H3'	38:0:7172:HOH:O	1.88	0.72
30:0:2467:A:H1'	38:0:9049:HOH:O	1.89	0.72
30:0:2898:G:O2'	30:0:2899:A:H5'	1.89	0.72
30:0:1316:G:H5''	38:0:5285:HOH:O	1.88	0.72
30:0:2831:C:O2'	30:0:2832:C:H5'	1.88	0.72
30:0:272:A:H5'	30:0:273:G:OP2	1.90	0.72
30:0:1178:G:H2'	30:0:1179:C:C6	2.25	0.72
30:0:1713:G:H1'	38:0:5039:HOH:O	1.89	0.72
30:0:2297:U:H1'	38:0:5144:HOH:O	1.88	0.72
30:0:2253:G:H2'	30:0:2254:G:H8	1.55	0.72
30:0:595:U:O2'	30:0:596:C:H5'	1.90	0.71
30:0:603:A:H5''	30:0:604:G:OP1	1.89	0.71
31:9:26:C:O2'	31:9:27:C:H5'	1.91	0.71
1:A:191:GLY:HA2	1:A:194:MET:HE3	1.71	0.71
8:H:8:MET:HE3	30:0:2494:G:H4'	1.73	0.71
30:0:958:G:H2'	30:0:959:C:C6	2.24	0.71
30:0:1979:G:H3'	38:0:3283:HOH:O	1.88	0.71
18:R:2:ILE:HG22	30:0:21:G:H4'	1.71	0.71
30:0:1477:C:H5'	30:0:1868:G:H5'	1.72	0.71
23:W:125:HIS:CE1	30:0:1097:A:H5''	2.25	0.71
25:Y:187:VAL:HG23	25:Y:192:ASP:CB	2.21	0.71
27:1:25:LYS:HD2	28:2:49:GLU:H	1.55	0.71
30:0:1801:A:H3'	38:0:7596:HOH:O	1.90	0.71
30:0:2321:A:H2	30:0:2378:U:N3	1.88	0.71
30:0:1197:G:H1'	30:0:1203:G:N2	2.06	0.71
30:0:1398:G:H2'	30:0:1399:A:C8	2.25	0.71
30:0:2769:C:H2'	30:0:2770:G:C5'	2.20	0.71
5:E:143:GLN:NE2	30:0:2779:G:H21	1.89	0.71
14:N:33:ARG:HH21	14:N:48:VAL:HG11	1.55	0.71
26:Z:84:CYS:HB3	30:0:1604:G:H22	1.56	0.71
30:0:920:C:H4'	30:0:921:G:C2	2.26	0.71
30:0:2780:C:H2'	30:0:2781:U:C6	2.26	0.71
21:U:56:ARG:HH11	21:U:56:ARG:HG3	1.56	0.71
31:9:55:U:H4'	31:9:56:A:C8	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:3:MET:HE2	29:3:22:VAL:HG11	1.73	0.71
30:0:1666:C:C2'	30:0:1667:A:C5'	2.69	0.71
3:C:139:VAL:HG13	38:C:8645:HOH:O	1.91	0.70
30:0:1185:U:H2'	30:0:1186:C:C6	2.25	0.70
30:0:2321:A:C2	30:0:2378:U:N3	2.55	0.70
30:0:2524:G:H21	30:0:2526:C:N4	1.88	0.70
3:C:78:ARG:HH11	3:C:78:ARG:HG3	1.56	0.70
30:0:1118:A:N6	30:0:1244:U:H3	1.89	0.70
30:0:2416:G:H2'	30:0:2417:C:C6	2.26	0.70
22:V:57:LYS:HA	22:V:60:GLN:HE21	1.57	0.70
30:0:1972:U:H2'	30:0:1973:A:H5'	1.73	0.70
30:0:2312:G:H2'	30:0:2313:C:H5'	1.72	0.70
30:0:2717:C:C2'	30:0:2718:C:C5'	2.68	0.70
14:N:4:PRO:HB2	30:0:1010:C:H4'	1.73	0.70
26:Z:43:GLY:O	26:Z:47:ARG:HG2	1.91	0.70
30:0:1596:U:H2'	30:0:1598:A:OP2	1.90	0.70
30:0:2565:C:H4'	38:0:4806:HOH:O	1.91	0.70
13:M:164:THR:HG22	13:M:166:ALA:H	1.57	0.70
30:0:1829:A:C2'	30:0:1830:C:H5'	2.21	0.70
30:0:2539:U:H1'	38:0:7770:HOH:O	1.90	0.70
1:A:223:ARG:HH12	30:0:2270:G:H4'	1.55	0.70
38:C:8565:HOH:O	20:T:2:LYS:HE3	1.92	0.70
14:N:11:ARG:HD3	31:9:114:G:O6	1.90	0.70
23:W:5:VAL:HG11	23:W:153:MET:HE1	1.73	0.70
29:3:40:ARG:HA	29:3:52:PHE:CE1	2.26	0.70
30:0:1226:G:H2'	30:0:1227:C:H6	1.57	0.70
31:9:59:C:O5'	31:9:59:C:H6	1.74	0.69
30:0:522:U:O2'	30:0:1366:C:H5'	1.92	0.69
30:0:1589:G:H5'	38:0:6843:HOH:O	1.91	0.69
30:0:2415:A:H2'	30:0:2416:G:H5'	1.74	0.69
1:A:135:VAL:HG11	1:A:147:ARG:NH2	2.07	0.69
7:G:64:ASN:HD22	7:G:64:ASN:N	1.90	0.69
10:J:70:PHE:CD1	30:0:2676:C:H4'	2.27	0.69
30:0:714:U:H4'	38:0:5705:HOH:O	1.93	0.69
30:0:1181:A:C2'	30:0:1182:C:H5'	2.22	0.69
30:0:2404:G:H5''	38:0:5177:HOH:O	1.91	0.69
8:H:168:VAL:HG13	38:H:218:HOH:O	1.91	0.69
30:0:2667:G:H1'	30:0:2914:A:N3	2.08	0.69
26:Z:37:ARG:HB3	38:0:4665:HOH:O	1.91	0.69
29:3:20:HIS:HD2	29:3:69:TYR:HB3	1.56	0.69
14:N:37:ARG:NH1	31:9:6:C:C5'	2.50	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:545:G:H8	30:0:545:G:C5'	1.99	0.69
30:0:1205:U:C2'	30:0:1206:U:H5''	2.23	0.69
2:B:258:GLY:H	2:B:260:HIS:CE1	2.10	0.69
3:C:76:ARG:HB3	3:C:76:ARG:HH11	1.57	0.69
30:0:735:C:H2'	30:0:736:A:O4'	1.93	0.69
15:O:32:ARG:HE	15:O:35:LYS:HD2	1.58	0.69
30:0:1741:U:O2'	30:0:2723:G:H4'	1.91	0.69
30:0:2705:U:H2'	30:0:2706:A:C8	2.28	0.69
13:M:81:ARG:HD2	13:M:85:ARG:HG3	1.74	0.69
18:R:128:ARG:NH2	30:0:2054:A:N3	2.41	0.69
30:0:2827:A:H2'	30:0:2828:G:O4'	1.92	0.69
30:0:596:C:H2'	30:0:597:A:H8	1.58	0.69
21:U:56:ARG:HB2	30:0:2890:A:C8	2.27	0.68
30:0:1632:A:C2'	30:0:1633:C:H5'	2.22	0.68
30:0:2795:C:O2'	30:0:2796:U:H5'	1.93	0.68
11:K:74:VAL:HG21	11:K:96:VAL:HG23	1.75	0.68
18:R:138:SER:HB3	30:0:2053:G:OP1	1.94	0.68
16:P:117:SER:HB3	30:0:1593:C:OP1	1.92	0.68
30:0:1702:U:H5'	38:0:3414:HOH:O	1.92	0.68
26:Z:47:ARG:NH2	30:0:1771:U:H1'	2.08	0.68
30:0:2111:G:H1'	38:0:9052:HOH:O	1.94	0.68
30:0:2635:A:C2'	30:0:2636:C:H5'	2.23	0.68
23:W:137:GLN:HE21	23:W:141:HIS:CE1	2.10	0.68
2:B:264:GLU:HG2	2:B:267:LYS:CE	2.19	0.68
30:0:333:G:O2'	30:0:334:G:H5'	1.94	0.68
30:0:2637:A:H5'	38:0:4897:HOH:O	1.94	0.68
23:W:125:HIS:NE2	30:0:1097:A:H5''	2.09	0.68
29:3:50:GLY:HA3	30:0:170:U:H1'	1.75	0.68
30:0:585:C:H5''	38:0:4840:HOH:O	1.94	0.68
30:0:1197:G:H1'	30:0:1203:G:C2	2.28	0.68
2:B:267:LYS:HD3	38:B:8996:HOH:O	1.93	0.68
26:Z:42:TYR:CA	30:0:1829:A:H61	2.07	0.68
30:0:685:C:O2	30:0:748:C:H4'	1.94	0.68
30:0:1209:C:H2'	30:0:1210:G:C8	2.23	0.68
2:B:206:THR:HG21	30:0:2716:G:H5''	1.76	0.68
10:J:18:ILE:HD13	30:0:1244:U:OP1	1.94	0.68
10:J:74:ARG:HH11	10:J:74:ARG:CB	2.07	0.68
30:0:1151:G:H2'	38:0:5713:HOH:O	1.92	0.68
30:0:2840:A:H3'	38:0:7629:HOH:O	1.94	0.68
3:C:76:ARG:HB3	3:C:76:ARG:NH1	2.09	0.67
10:J:39:VAL:HG22	10:J:106:GLY:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:95:LYS:HE2	30:0:157:G:H4'	1.76	0.67
18:R:98:ASN:HD21	30:0:500:G:H21	1.40	0.67
29:3:90:PHE:HD1	29:3:90:PHE:H	1.42	0.67
30:0:1625:U:H3'	30:0:1625:U:C6	2.29	0.67
13:M:70:GLY:HA2	30:0:2263:G:H4'	1.76	0.67
21:U:42:LEU:HD22	30:0:1810:C:H1'	1.76	0.67
29:3:2:GLN:HB3	29:3:91:GLN:CD	2.19	0.67
30:0:1118:A:C8	30:0:1119:G:H5''	2.29	0.67
30:0:1813:U:H2'	38:0:6701:HOH:O	1.94	0.67
8:H:57:THR:HG23	8:H:131:GLN:HA	1.76	0.67
30:0:541:C:H2'	30:0:542:A:H5''	1.74	0.67
30:0:1528:A:H2'	30:0:1529:G:O4'	1.95	0.67
30:0:2524:G:H5''	38:0:4698:HOH:O	1.94	0.67
13:M:91:ILE:HG23	38:0:7530:HOH:O	1.94	0.67
30:0:1787:C:H4'	30:0:2883:A:O4'	1.94	0.67
13:M:73:ARG:HH22	30:0:2263:G:H5''	1.58	0.67
21:U:19:THR:HG22	21:U:20:MET:H	1.59	0.67
28:2:28:LYS:HE2	30:0:86:A:H1'	1.77	0.67
30:0:2894:C:O2'	30:0:2895:C:H5'	1.95	0.67
30:0:119:A:H2'	30:0:120:A:H5''	1.77	0.67
30:0:370:G:O2'	30:0:371:U:H5'	1.93	0.67
31:9:76:G:C3'	31:9:77:A:H5''	2.23	0.67
12:L:46:LEU:O	30:0:2430:A:H4'	1.95	0.67
30:0:2780:C:H2'	30:0:2781:U:H6	1.59	0.67
30:0:2829:G:N2	30:0:2912:C:C2	2.63	0.67
30:0:1641:A:H2'	30:0:1642:A:H5'	1.77	0.67
4:D:154:LYS:H	4:D:154:LYS:HD2	1.60	0.67
5:E:91:PHE:HE1	30:0:2694:A:H4'	1.58	0.67
10:J:75:PRO:HG2	10:J:105:LEU:HD21	1.77	0.67
11:K:20:CYS:HB2	11:K:29:LEU:HG	1.77	0.67
29:3:60:LYS:HG3	29:3:61:PRO:HD2	1.77	0.67
30:0:256:C:H2'	30:0:257:G:O4'	1.95	0.67
30:0:810:G:H2'	30:0:811:C:H6	1.56	0.67
16:P:59:ARG:HD3	38:0:6249:HOH:O	1.95	0.66
1:A:135:VAL:HG21	1:A:147:ARG:HB3	1.77	0.66
30:0:596:C:H2'	30:0:597:A:C8	2.29	0.66
30:0:2785:C:H5'	38:0:7694:HOH:O	1.95	0.66
14:N:33:ARG:NH2	14:N:48:VAL:HG11	2.10	0.66
10:J:19:MET:HE1	10:J:78:ILE:HG22	1.78	0.66
15:O:14:LEU:HD23	15:O:102:ILE:HD11	1.77	0.66
29:3:68:LYS:HD3	29:3:70:ARG:NH2	2.07	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:468:U:H3'	38:0:7549:HOH:O	1.93	0.66
13:M:48:LYS:HE3	13:M:52:GLN:HE21	1.60	0.66
30:0:869:G:H1'	38:0:3302:HOH:O	1.95	0.66
30:0:1041:U:H2'	30:0:1042:U:H5'	1.78	0.66
11:K:12:LEU:HB2	11:K:47:ALA:HB3	1.77	0.66
30:0:1120:U:H5'	30:0:1121:G:OP2	1.95	0.66
14:N:113:SER:HB2	38:N:8852:HOH:O	1.94	0.66
30:0:123:U:H5'	38:0:6635:HOH:O	1.96	0.66
30:0:1205:U:C2'	30:0:1206:U:H5'	2.18	0.66
30:0:1942:A:H3'	38:0:7329:HOH:O	1.95	0.66
30:0:2329:C:O2'	30:0:2330:U:H5'	1.95	0.66
2:B:27:ASN:HD22	2:B:27:ASN:H	1.44	0.66
28:2:43:ARG:NH2	30:0:1684:A:H1'	2.10	0.66
30:0:318:U:H5'	30:0:339:A:C2	2.31	0.66
30:0:704:C:H2'	30:0:705:C:H6	1.60	0.66
30:0:1063:G:H5''	38:0:9856:HOH:O	1.94	0.66
30:0:1167:G:H2'	30:0:1168:C:C6	2.31	0.66
30:0:2032:U:H2'	30:0:2033:G:C5'	2.26	0.66
30:0:2760:C:H5''	38:0:5294:HOH:O	1.95	0.66
31:9:7:G:H5'	38:9:9102:HOH:O	1.95	0.66
3:C:184:ARG:NH2	30:0:450:C:OP1	2.29	0.66
30:0:559:U:H5'	30:0:559:U:C6	2.23	0.66
30:0:921:G:H4'	30:0:924:G:N1	2.11	0.66
30:0:2533:C:H5'	30:0:2533:C:C6	2.31	0.66
30:0:449:A:H3'	38:0:6214:HOH:O	1.95	0.65
30:0:1249:U:H2'	30:0:1250:C:C6	2.30	0.65
30:0:1603:A:H5'	30:0:1605:G:C4'	2.26	0.65
2:B:179:LEU:O	2:B:183:GLU:HG2	1.96	0.65
12:L:143:THR:HG22	12:L:144:ASP:H	1.61	0.65
14:N:80:SER:HB2	38:N:8833:HOH:O	1.95	0.65
20:T:9:LYS:HE3	20:T:13:ARG:NH1	2.12	0.65
26:Z:44:ARG:NH2	30:0:1771:U:H5'	2.09	0.65
30:0:559:U:H6	30:0:559:U:C5'	2.09	0.65
30:0:2851:G:H2'	30:0:2902:A:H61	1.60	0.65
30:0:368:C:H2'	30:0:369:G:H5'	1.77	0.65
26:Z:78:ILE:HG21	26:Z:87:LYS:HE2	1.78	0.65
31:9:29:C:C5	31:9:30:C:C6	2.84	0.65
38:D:7597:HOH:O	31:9:56:A:H2	1.79	0.65
30:0:2707:C:O2	30:0:2707:C:H2'	1.96	0.65
1:A:122:SER:HB2	1:A:164:ARG:NH1	2.11	0.65
16:P:88:GLN:NE2	30:0:1800:G:H1'	2.10	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:56:ARG:HD2	30:0:2890:A:C1'	2.25	0.65
5:E:91:PHE:CE1	30:0:2694:A:H4'	2.32	0.65
9:I:110:ASP:O	30:0:1163:G:H5'	1.95	0.65
25:Y:115:ARG:HH21	30:0:1266:U:H4'	1.60	0.65
30:0:213:G:N2	30:0:225:G:H2'	2.11	0.65
30:0:416:G:H5''	38:0:7402:HOH:O	1.96	0.65
30:0:696:C:H4'	38:0:7263:HOH:O	1.96	0.65
30:0:1061:C:H3'	38:0:5051:HOH:O	1.97	0.65
30:0:1132:A:N6	30:0:1229:C:H2'	2.12	0.65
30:0:1666:C:C2'	30:0:1667:A:H5''	2.27	0.65
30:0:2597:U:H2'	30:0:2598:U:H5'	1.77	0.65
30:0:1385:G:H1'	38:0:4024:HOH:O	1.97	0.65
2:B:238:ASN:HD22	2:B:240:GLY:N	1.90	0.65
38:O:1484:HOH:O	30:0:710:G:H1'	1.97	0.65
30:0:42:C:H1'	38:0:4645:HOH:O	1.97	0.65
30:0:290:C:O2'	30:0:291:C:H5'	1.96	0.65
30:0:812:A:H2'	30:0:813:C:C6	2.31	0.65
16:P:81:LYS:O	30:0:1761:U:H5'	1.97	0.65
30:0:2119:C:O2'	30:0:2120:U:H5'	1.97	0.65
30:0:696:C:O2'	30:0:697:G:H5'	1.97	0.64
30:0:1586:G:O2'	30:0:1587:U:H5'	1.97	0.64
30:0:2892:G:C6	30:0:2893:C:C4	2.85	0.64
31:9:61:C:H2'	31:9:62:A:H8	1.62	0.64
6:F:58:GLU:CD	13:M:27:ARG:HH22	2.05	0.64
30:0:1377:C:H5'	30:0:1377:C:C6	2.33	0.64
30:0:1422:U:H2'	30:0:1423:C:C6	2.32	0.64
30:0:1735:C:O2'	30:0:1736:A:H5'	1.97	0.64
30:0:1862:C:H1'	38:0:7203:HOH:O	1.96	0.64
1:A:47:HIS:HD2	30:0:1654:U:H2'	1.61	0.64
38:B:8996:HOH:O	30:0:2766:A:H5'	1.97	0.64
30:0:441:A:H1'	30:0:442:A:N7	2.13	0.64
2:B:36:PRO:HA	2:B:168:GLY:HA3	1.78	0.64
21:U:56:ARG:HD2	30:0:2890:A:C8	2.33	0.64
30:0:522:U:HO2'	30:0:1366:C:H5'	1.61	0.64
30:0:671:A:O2'	30:0:672:G:H2'	1.97	0.64
30:0:1819:G:H5'	38:0:4680:HOH:O	1.96	0.64
30:0:1972:U:C2'	30:0:1973:A:H5''	2.27	0.64
2:B:162:MET:HE2	2:B:310:ARG:HD3	1.78	0.64
2:B:312:ARG:HD3	2:B:315:VAL:HG13	1.80	0.64
23:W:13:MET:HE3	23:W:17:ILE:HG22	1.80	0.64
27:1:9:GLY:HA2	30:0:1687:C:O2	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:281:U:H2'	30:0:282:C:O4'	1.98	0.64
30:0:693:A:H2'	30:0:694:A:C8	2.33	0.64
5:E:20:ILE:HD11	5:E:40:VAL:HG11	1.79	0.64
5:E:143:GLN:HE22	30:0:2779:G:H21	1.44	0.64
23:W:6:GLN:HB2	23:W:26:ILE:HD11	1.79	0.64
26:Z:70:ARG:HH11	26:Z:83:TYR:HD1	1.46	0.64
27:1:21:ARG:HD2	27:1:37:CYS:SG	2.38	0.64
30:0:1706:G:H1'	30:0:1712:A:H61	1.61	0.64
30:0:2768:A:O2'	30:0:2769:C:H5'	1.97	0.64
1:A:33:GLU:H	1:A:33:GLU:CD	2.06	0.64
3:C:78:ARG:HG3	3:C:78:ARG:NH1	2.13	0.64
30:0:1181:A:H2'	30:0:1182:C:H5'	1.80	0.64
30:0:1973:A:H2'	30:0:1974:G:O4'	1.96	0.64
30:0:2088:C:H2'	30:0:2089:A:H8	1.62	0.64
25:Y:154:ARG:HH22	30:0:1071:G:H4'	1.63	0.64
25:Y:169:ARG:HD2	30:0:1328:A:OP1	1.98	0.64
3:C:16:VAL:HG12	3:C:17:ASP:H	1.62	0.64
14:N:86:LEU:HD12	14:N:125:ALA:HB2	1.78	0.64
30:0:459:A:H5''	38:0:9055:HOH:O	1.96	0.64
8:H:27:PRO:HD3	8:H:123:ILE:HG22	1.79	0.63
11:K:66:ARG:HH22	30:0:1994:A:P	2.21	0.63
21:U:23:HIS:HD2	21:U:27:ALA:HB3	1.63	0.63
30:0:1748:U:C5	30:0:1749:U:C5	2.85	0.63
3:C:132:ASP:O	3:C:133:ARG:HG3	1.98	0.63
3:C:236:THR:HG21	38:C:8571:HOH:O	1.97	0.63
11:K:98:VAL:CG1	11:K:102:GLU:HA	2.28	0.63
18:R:40:ALA:O	18:R:44:VAL:HG23	1.99	0.63
30:0:541:C:H2'	30:0:542:A:H5'	1.77	0.63
30:0:2867:G:H2'	30:0:2868:C:C6	2.33	0.63
8:H:19:ARG:HH12	30:0:1008:C:H5''	1.63	0.63
17:Q:26:PRO:O	17:Q:30:VAL:HG23	1.97	0.63
30:0:541:C:O2'	30:0:542:A:H5''	1.97	0.63
30:0:1116:U:O2'	30:0:1118:A:C2	2.40	0.63
30:0:2727:A:H2'	30:0:2728:C:H5'	1.80	0.63
31:9:17:G:O2'	31:9:18:U:H5'	1.97	0.63
10:J:19:MET:HE2	10:J:79:PHE:HA	1.80	0.63
13:M:66:SER:HB3	13:M:128:TRP:CD1	2.33	0.63
13:M:164:THR:HG22	13:M:166:ALA:N	2.13	0.63
30:0:1835:U:H3'	38:0:5539:HOH:O	1.97	0.63
30:0:2032:U:O2'	30:0:2033:G:H5''	1.98	0.63
23:W:88:THR:HG22	23:W:110:GLN:HB3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:506:G:H22	30:0:509:A:H5'	1.63	0.63
30:0:2659:U:H5''	38:0:4112:HOH:O	1.98	0.63
1:A:211:LYS:HB3	1:A:212:PRO:HD2	1.79	0.63
26:Z:38:PHE:HB3	26:Z:42:TYR:CD1	2.33	0.63
29:3:65:THR:O	29:3:82:GLY:HA3	1.99	0.63
30:0:90:A:H2'	30:0:91:G:O4'	1.98	0.63
30:0:1985:U:H1'	38:0:4497:HOH:O	1.98	0.63
31:9:91:C:H2'	31:9:92:G:O4'	1.99	0.63
14:N:37:ARG:HH12	31:9:6:C:C5'	1.95	0.63
14:N:164:ASP:OD1	14:N:167:ASP:HA	1.98	0.63
30:0:1149:U:H5''	30:0:1151:G:O4'	1.98	0.63
30:0:1644:C:H2'	30:0:1645:U:C6	2.31	0.63
30:0:2291:A:H8	38:0:6453:HOH:O	1.81	0.63
30:0:2675:A:H1'	30:0:2813:A:C2	2.34	0.63
30:0:2824:C:H5''	30:0:2825:C:H5'	1.80	0.63
2:B:280:VAL:HG13	2:B:333:GLU:O	1.99	0.63
4:D:131:THR:HG21	30:0:2348:C:H1'	1.79	0.63
22:V:42:ASN:HB3	38:V:7247:HOH:O	1.98	0.63
29:3:59:ASP:HB3	29:3:63:LYS:NZ	2.13	0.63
30:0:2250:G:H2'	30:0:2251:G:O4'	1.99	0.63
30:0:2766:A:O2'	30:0:2767:C:H5'	1.99	0.63
5:E:60:SER:OG	30:0:2784:A:H1'	1.98	0.63
11:K:74:VAL:CG1	11:K:113:ILE:HG12	2.29	0.63
28:2:41:HIS:HB3	28:2:44:ARG:HB2	1.80	0.63
30:0:279:C:C2'	30:0:280:C:H5'	2.29	0.63
30:0:630:A:H5''	38:0:4722:HOH:O	1.99	0.63
30:0:956:G:C8	38:0:9387:HOH:O	2.50	0.63
30:0:2782:G:H3'	38:0:5004:HOH:O	1.98	0.63
10:J:19:MET:HE3	10:J:132:LEU:HD11	1.81	0.62
12:L:57:VAL:HG21	30:0:2443:C:H5'	1.80	0.62
20:T:72:ILE:HD13	20:T:93:THR:HG22	1.81	0.62
26:Z:34:SER:HB2	38:0:7481:HOH:O	1.99	0.62
26:Z:41:ARG:HD2	30:0:1830:C:O2	1.98	0.62
27:1:2:GLY:O	27:1:6:PRO:HG2	1.99	0.62
30:0:1165:G:H21	30:0:1173:A:C5'	2.12	0.62
30:0:2349:G:H2'	30:0:2350:G:H8	1.62	0.62
29:3:54:LYS:HE2	30:0:2468:A:N7	2.14	0.62
30:0:1921:A:O2'	30:0:1922:A:H5'	1.98	0.62
30:0:1527:A:H1'	30:0:1528:A:C8	2.34	0.62
4:D:54:ALA:HB2	4:D:69:ILE:HD12	1.80	0.62
14:N:160:SER:HB3	31:9:51:A:H5'	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:49:LEU:HD12	38:U:3805:HOH:O	1.99	0.62
30:0:1351:G:H5'	38:0:3619:HOH:O	1.99	0.62
30:0:1878:G:H1'	38:0:6097:HOH:O	2.00	0.62
30:0:1889:C:H2'	30:0:1890:U:O4'	2.00	0.62
30:0:1477:C:H5'	30:0:1868:G:C5'	2.29	0.62
5:E:153:ARG:HH12	30:0:2778:A:H1'	1.65	0.62
8:H:15:PRO:HG3	30:0:1053:G:OP1	2.00	0.62
20:T:61:GLU:HG2	38:T:3851:HOH:O	1.99	0.62
30:0:229:G:O2'	30:0:230:C:H5'	2.00	0.62
30:0:790:A:H1'	30:0:1710:A:O2'	1.99	0.62
3:C:246:ARG:NH2	30:0:677:C:H4'	2.14	0.62
29:3:68:LYS:NZ	30:0:2436:U:H5'	2.14	0.62
30:0:1226:G:H5'	38:0:4509:HOH:O	1.98	0.62
15:O:51:TYR:CE2	30:0:721:A:H5''	2.35	0.62
22:V:39:ALA:H	22:V:40:PRO:HD2	1.65	0.62
26:Z:53:ILE:O	26:Z:57:MET:HB2	2.00	0.62
28:2:22:PRO:HG2	28:2:25:VAL:HG23	1.82	0.62
30:0:920:C:H4'	30:0:921:G:N2	2.14	0.62
30:0:2510:C:H5'	30:0:2511:A:OP2	1.99	0.62
17:Q:14:LEU:HD21	17:Q:43:ILE:HD12	1.82	0.62
30:0:303:C:O2'	30:0:304:G:H5'	2.00	0.62
30:0:630:A:H5'	38:0:9372:HOH:O	1.98	0.62
30:0:1752:G:H2'	38:0:7531:HOH:O	2.00	0.62
3:C:129:HIS:CE1	3:C:231:ARG:HA	2.35	0.61
23:W:64:THR:O	23:W:68:THR:HG22	2.00	0.61
30:0:236:A:H4'	30:0:237:G:C5'	2.17	0.61
30:0:1131:G:H1'	38:0:3907:HOH:O	1.99	0.61
30:0:1279:U:O2	30:0:1279:U:C2'	2.48	0.61
30:0:2251:G:H2'	30:0:2252:A:C8	2.35	0.61
30:0:2300:A:H4'	30:0:2301:A:O5'	2.00	0.61
30:0:2439:C:H5'	38:0:5449:HOH:O	1.99	0.61
30:0:2775:A:C6	30:0:2799:A:C8	2.88	0.61
31:9:91:C:H1'	38:9:9149:HOH:O	1.98	0.61
9:I:130:LEU:CD2	30:0:1167:G:H4'	2.29	0.61
22:V:55:ARG:O	22:V:59:ILE:HG12	2.01	0.61
30:0:825:U:H5''	30:0:826:U:OP1	2.00	0.61
30:0:1477:C:O2'	30:0:1478:U:H5'	1.99	0.61
30:0:2576:A:H2'	38:0:7732:HOH:O	2.00	0.61
25:Y:186:ARG:HG2	25:Y:186:ARG:HH11	1.65	0.61
30:0:2314:G:C2'	30:0:2315:C:H5'	2.30	0.61
2:B:262:ARG:HG3	30:0:2716:G:H5'	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:12:ILE:HG23	38:0:5418:HOH:O	1.98	0.61
13:M:75:ARG:NH2	13:M:78:LYS:HE2	2.16	0.61
23:W:52:VAL:HG22	23:W:53:ALA:H	1.63	0.61
24:X:71:ARG:HD2	38:X:7542:HOH:O	1.99	0.61
30:0:301:C:O2'	30:0:302:A:H5'	2.00	0.61
30:0:1711:A:O2'	30:0:1712:A:H5'	2.00	0.61
30:0:2912:C:O5'	30:0:2912:C:H6	1.83	0.61
1:A:20:SER:HB3	30:0:1872:C:H5	1.65	0.61
2:B:320:GLN:HE21	2:B:321:PRO:HD2	1.65	0.61
2:B:336:GLN:O	30:0:2862:G:H4'	2.00	0.61
9:I:91:PHE:HD2	9:I:131:GLY:HA2	1.66	0.61
12:L:67:ARG:HB2	12:L:112:GLY:HA3	1.83	0.61
30:0:39:G:N2	30:0:444:C:C2	2.68	0.61
30:0:1118:A:H8	30:0:1119:G:H5''	1.64	0.61
9:I:130:LEU:HD21	30:0:1167:G:H4'	1.81	0.61
30:0:705:C:O2	30:0:705:C:H2'	1.99	0.61
30:0:2526:C:H3'	30:0:2526:C:H6	1.65	0.61
22:V:12:THR:HG22	22:V:15:GLU:CG	2.31	0.61
30:0:228:C:H2'	30:0:229:G:H5'	1.80	0.61
30:0:877:G:C5'	30:0:878:G:OP1	2.46	0.61
30:0:1774:G:O2'	30:0:1775:A:H5'	2.01	0.61
31:9:20:G:H3'	38:9:9057:HOH:O	2.00	0.61
23:W:145:GLY:HA3	38:W:6373:HOH:O	2.00	0.61
30:0:282:C:O2	30:0:282:C:H2'	2.00	0.61
30:0:1676:G:O2'	30:0:1677:U:H5'	2.01	0.61
30:0:1856:C:H5'	30:0:1858:A:O4'	2.01	0.61
30:0:2834:G:C2	30:0:2835:C:H1'	2.35	0.61
30:0:283:U:C5	30:0:284:C:C4	2.88	0.61
30:0:807:A:H2'	30:0:808:A:C8	2.36	0.61
30:0:1398:G:H2'	30:0:1399:A:H8	1.64	0.61
8:H:174:LEU:HD21	30:0:1220:U:H4'	1.82	0.61
11:K:10:GLN:HE21	11:K:10:GLN:N	1.96	0.61
30:0:558:C:H2'	30:0:559:U:H5'	1.81	0.61
30:0:1701:A:H4'	30:0:1702:U:C5'	2.30	0.61
1:A:140:LEU:HB3	1:A:141:PRO:HD2	1.83	0.60
10:J:47:THR:HB	38:0:4807:HOH:O	2.01	0.60
38:3:9025:HOH:O	30:0:2468:A:H5'	2.00	0.60
30:0:31:C:H4'	38:0:7408:HOH:O	2.00	0.60
30:0:1878:G:HO2'	30:0:1879:U:H6	1.42	0.60
2:B:102:THR:HG23	2:B:182:VAL:HG12	1.81	0.60
2:B:190:MET:HE2	2:B:194:PHE:CD1	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:320:GLN:HE21	2:B:321:PRO:CD	2.14	0.60
3:C:27:ARG:NH2	30:0:657:G:OP1	2.34	0.60
29:3:9:THR:HG23	29:3:20:HIS:ND1	2.15	0.60
30:0:1175:G:H1'	30:0:1193:A:C2'	2.31	0.60
30:0:1697:G:H4'	38:0:9347:HOH:O	2.02	0.60
30:0:2281:C:H2'	30:0:2282:U:H5'	1.82	0.60
11:K:74:VAL:HG12	11:K:75:ARG:HG3	1.83	0.60
23:W:118:LEU:HD12	23:W:153:MET:HE3	1.82	0.60
30:0:282:C:O2'	30:0:283:U:C5'	2.49	0.60
30:0:2071:C:H5'	38:0:9540:HOH:O	2.00	0.60
30:0:2312:G:C2'	30:0:2313:C:H5'	2.30	0.60
30:0:2872:U:H2'	30:0:2873:C:O4'	2.02	0.60
25:Y:126:PRO:HG2	25:Y:128:PHE:CE1	2.36	0.60
26:Z:84:CYS:HB3	30:0:1604:G:N2	2.15	0.60
30:0:38:G:O2'	30:0:39:G:H5'	2.02	0.60
30:0:407:A:H3'	38:0:4438:HOH:O	2.01	0.60
30:0:1201:C:H5''	38:0:6211:HOH:O	2.00	0.60
30:0:1495:C:H1'	30:0:1573:A:H1'	1.83	0.60
2:B:72:THR:HB	38:B:9076:HOH:O	2.02	0.60
11:K:74:VAL:HG13	11:K:113:ILE:HG12	1.82	0.60
20:T:48:VAL:HG22	20:T:97:ARG:O	2.01	0.60
30:0:51:G:H1'	38:0:9033:HOH:O	2.01	0.60
30:0:947:U:H2'	30:0:948:G:C8	2.36	0.60
30:0:1205:U:O2'	30:0:1206:U:H5''	2.01	0.60
30:0:1398:G:O2'	30:0:1399:A:H5'	2.02	0.60
30:0:1407:A:O2'	30:0:1408:U:H3'	2.01	0.60
30:0:1972:U:C2'	30:0:1973:A:C5'	2.80	0.60
30:0:2420:G:C2'	30:0:2421:G:H5'	2.30	0.60
7:G:16:LYS:HE2	7:G:63:ARG:HH12	1.67	0.60
13:M:102:GLU:OE1	13:M:164:THR:HG21	2.01	0.60
16:P:41:ARG:HH22	30:0:1500:U:P	2.24	0.60
30:0:146:U:C2'	30:0:147:G:H5'	2.31	0.60
30:0:2893:C:O2'	30:0:2894:C:H5'	2.01	0.60
31:9:18:U:H2'	31:9:19:G:C8	2.37	0.60
31:9:23:U:O2'	31:9:24:U:H4'	2.01	0.60
8:H:72:ALA:HB2	8:H:156:ALA:HB2	1.81	0.60
15:O:14:LEU:CD2	15:O:102:ILE:HD11	2.32	0.60
18:R:135:ALA:HB1	18:R:137:ASN:HD21	1.67	0.60
29:3:31:THR:OG1	29:3:34:LYS:HD3	2.01	0.60
30:0:2353:A:H4'	30:0:2354:A:O5'	2.01	0.60
33:B:8819:CL:CL	38:B:8997:HOH:O	2.54	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:188:ARG:HD3	30:0:155:C:OP2	2.02	0.60
30:0:1844:C:O5'	30:0:1844:C:H6	1.84	0.60
30:0:2608:C:H3'	38:0:7790:HOH:O	2.02	0.60
31:9:3:A:C6	31:9:22:G:H1'	2.36	0.60
31:9:26:C:H2'	31:9:27:C:C6	2.36	0.60
31:9:29:C:H2'	31:9:30:C:C5'	2.28	0.60
2:B:79:MET:HB2	2:B:188:HIS:CE1	2.36	0.60
10:J:82:THR:CG2	30:0:1242:A:H5'	2.20	0.60
18:R:46:TYR:O	18:R:50:VAL:HG23	2.00	0.60
30:0:307:G:H3'	38:0:6667:HOH:O	2.01	0.60
30:0:567:U:H5''	38:0:5254:HOH:O	2.02	0.60
29:3:43:ASN:HB2	29:3:52:PHE:CE1	2.36	0.60
30:0:74:G:H2'	30:0:75:U:C6	2.37	0.60
30:0:947:U:H2'	30:0:948:G:H8	1.65	0.60
2:B:235:ARG:HD3	30:0:2091:G:H5''	1.83	0.59
16:P:91:LYS:O	16:P:95:GLU:HG3	2.02	0.59
30:0:319:A:H4'	30:0:338:C:C4	2.37	0.59
30:0:324:G:O2'	30:0:325:U:H5'	2.02	0.59
30:0:1878:G:O2'	30:0:1879:U:C6	2.50	0.59
31:9:63:C:O2'	31:9:64:C:H5'	2.01	0.59
11:K:130:MET:SD	21:U:25:ASP:O	2.60	0.59
13:M:82:ARG:HH22	13:M:85:ARG:HH21	1.49	0.59
22:V:8:ILE:HA	22:V:11:MET:HE3	1.84	0.59
27:1:20:ARG:HG2	30:0:111:C:O2'	2.01	0.59
30:0:1590:A:H1'	30:0:1606:A:C2	2.36	0.59
30:0:2686:C:C2	30:0:2709:G:N2	2.70	0.59
31:9:65:A:N6	31:9:112:U:C6	2.71	0.59
1:A:94:LEU:HG	1:A:99:ILE:HD11	1.84	0.59
3:C:236:THR:HA	38:C:8648:HOH:O	2.01	0.59
5:E:145:ALA:HB1	5:E:168:ILE:HD11	1.85	0.59
30:0:2403:C:H5'	38:0:6001:HOH:O	2.01	0.59
30:0:2718:C:H6	30:0:2718:C:H5'	1.67	0.59
30:0:2820:A:H2'	30:0:2821:C:C6	2.36	0.59
2:B:101:TRP:HB2	2:B:119:HIS:CD2	2.38	0.59
2:B:156:LYS:HB3	30:0:2846:C:H4'	1.84	0.59
12:L:79:ASP:HB3	38:L:8859:HOH:O	2.03	0.59
14:N:86:LEU:O	14:N:90:LEU:HG	2.02	0.59
30:0:653:U:H2'	30:0:654:A:C8	2.37	0.59
30:0:834:G:H4'	30:0:835:U:OP2	2.02	0.59
30:0:2867:G:H2'	30:0:2868:C:H6	1.67	0.59
1:A:179:MET:HG2	1:A:186:TRP:CB	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:13:GLU:OE2	6:F:78:GLU:HG2	2.01	0.59
30:0:652:G:C2	30:0:653:U:H1'	2.37	0.59
30:0:1585:C:H2'	30:0:1586:G:C8	2.37	0.59
30:0:2809:G:H2'	30:0:2810:G:C8	2.37	0.59
30:0:2831:C:H2'	30:0:2832:C:H5'	1.82	0.59
30:0:2874:G:H3'	38:0:9586:HOH:O	2.02	0.59
38:B:8993:HOH:O	30:0:2549:C:H1'	2.03	0.59
4:D:58:VAL:HG12	4:D:60:GLU:HG2	1.83	0.59
8:H:37:GLY:HA3	8:H:87:LYS:HA	1.85	0.59
30:0:812:A:H2'	30:0:813:C:H6	1.68	0.59
30:0:1702:U:H5''	38:0:7201:HOH:O	2.01	0.59
30:0:2846:C:H4'	38:0:5047:HOH:O	2.03	0.59
2:B:215:VAL:HB	38:B:9089:HOH:O	2.02	0.59
8:H:155:ARG:NH1	30:0:2503:A:H5''	2.18	0.59
30:0:542:A:H5'	30:0:542:A:C8	2.29	0.59
30:0:590:A:H2'	30:0:591:A:H5'	1.83	0.59
30:0:1380:U:C4	30:0:2748:G:C4	2.91	0.59
30:0:2065:C:O2'	30:0:2066:C:H5'	2.02	0.59
2:B:145:HIS:HD2	2:B:146:THR:O	1.85	0.59
4:D:159:PRO:O	4:D:163:VAL:HG23	2.02	0.59
11:K:41:LYS:HA	30:0:2582:G:O3'	2.03	0.59
16:P:7:LYS:HD3	16:P:21:VAL:HG22	1.85	0.59
18:R:39:THR:HG23	18:R:107:GLU:O	2.03	0.59
24:X:37:LEU:HD13	24:X:85:VAL:HG21	1.84	0.59
30:0:499:G:O2'	30:0:500:G:H5'	2.02	0.59
30:0:702:G:O2'	30:0:703:G:H5'	2.02	0.59
30:0:921:G:H4'	30:0:924:G:C6	2.37	0.59
30:0:1563:G:H4'	38:0:4215:HOH:O	2.01	0.59
30:0:1566:C:O2'	30:0:1567:G:H5'	2.03	0.59
30:0:1972:U:H2'	30:0:1973:A:H5''	1.83	0.59
31:9:54:A:C2	31:9:55:U:C2	2.91	0.59
6:F:30:LYS:HB2	6:F:97:ALA:HB3	1.84	0.59
10:J:69:TYR:CE1	30:0:2081:A:H4'	2.38	0.59
10:J:88:PRO:HD3	30:0:1104:C:H4'	1.85	0.59
13:M:137:ASN:ND2	30:0:145:A:H4'	2.18	0.59
30:0:255:A:H2'	30:0:256:C:H6	1.67	0.59
30:0:281:U:C2'	30:0:282:C:H5'	2.33	0.59
26:Z:40:ALA:HA	30:0:1773:G:C8	2.38	0.58
30:0:925:C:H3'	38:0:3826:HOH:O	2.02	0.58
30:0:1568:G:O2'	30:0:1569:U:H5'	2.03	0.58
30:0:2563:U:H2'	30:0:2565:C:O5'	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2724:U:H2'	30:0:2725:G:O4'	2.03	0.58
30:0:2826:G:C6	30:0:2913:A:C6	2.90	0.58
2:B:243:ASN:HB3	38:0:6624:HOH:O	2.02	0.58
2:B:297:VAL:HB	38:B:9076:HOH:O	2.03	0.58
8:H:98:LEU:HD11	8:H:127:ALA:HB2	1.85	0.58
25:Y:169:ARG:HD3	30:0:1328:A:C8	2.38	0.58
29:3:47:GLY:HA2	30:0:2121:G:C4'	2.25	0.58
30:0:28:G:H1'	38:0:4650:HOH:O	2.03	0.58
30:0:1245:C:O5'	30:0:1245:C:H6	1.85	0.58
30:0:2825:C:H4'	30:0:2826:G:O5'	2.03	0.58
3:C:79:ARG:O	3:C:87:ARG:HG2	2.04	0.58
4:D:28:GLY:HA2	4:D:69:ILE:HG23	1.85	0.58
9:I:83:GLY:H	30:0:1168:C:H5''	1.68	0.58
12:L:145:LEU:HB2	38:L:8836:HOH:O	2.03	0.58
13:M:28:GLN:HA	13:M:31:TRP:HB2	1.85	0.58
26:Z:34:SER:HA	30:0:797:A:H4'	1.83	0.58
30:0:951:A:C2'	30:0:952:G:H5'	2.33	0.58
30:0:1158:G:O2'	30:0:1159:G:H5'	2.03	0.58
30:0:1187:U:H2'	38:0:6880:HOH:O	2.01	0.58
30:0:1290:G:H4'	38:0:7465:HOH:O	2.02	0.58
30:0:2467:A:H5''	38:0:4285:HOH:O	2.03	0.58
20:T:52:ARG:HD2	30:0:317:A:H5''	1.85	0.58
30:0:293:A:C4	30:0:360:A:C2	2.91	0.58
30:0:1186:C:H42	30:0:1190:G:H22	1.48	0.58
30:0:2590:U:H2'	30:0:2591:C:H5'	1.85	0.58
3:C:182:ARG:HH12	30:0:450:C:H3'	1.67	0.58
12:L:18:HIS:HD2	30:0:902:G:N7	2.01	0.58
25:Y:234:VAL:HG12	25:Y:235:GLU:H	1.66	0.58
30:0:204:A:H2'	30:0:205:U:H5'	1.85	0.58
30:0:1711:A:C2'	30:0:1712:A:H5'	2.33	0.58
30:0:2784:A:O5'	30:0:2784:A:H8	1.87	0.58
10:J:127:ILE:HG22	33:J:8801:CL:CL	2.40	0.58
26:Z:70:ARG:HB2	26:Z:81:CYS:SG	2.44	0.58
30:0:1520:G:C6	30:0:1521:C:C4	2.92	0.58
2:B:162:MET:HG3	2:B:310:ARG:HD3	1.84	0.58
5:E:100:ASP:HB3	38:E:2789:HOH:O	2.02	0.58
30:0:164:G:H3'	38:0:3636:HOH:O	2.03	0.58
30:0:271:C:N4	30:0:378:A:C2	2.66	0.58
30:0:368:C:C2'	30:0:369:G:H5'	2.34	0.58
30:0:1503:U:C2'	30:0:1504:A:H5'	2.34	0.58
31:9:39:U:H1'	31:9:44:A:N6	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:267:LYS:HA	38:B:8996:HOH:O	2.04	0.58
17:Q:11:ARG:NH2	30:0:2363:G:H5''	2.19	0.58
26:Z:42:TYR:HA	30:0:1829:A:N6	2.16	0.58
30:0:482:G:H4'	30:0:508:A:N1	2.19	0.58
30:0:951:A:O2'	30:0:952:G:H5'	2.03	0.58
30:0:1662:C:H2'	30:0:1663:G:O4'	2.03	0.58
30:0:2073:G:OP2	30:0:2490:A:H5'	2.03	0.58
30:0:2493:C:O2	30:0:2493:C:H2'	2.02	0.58
30:0:2505:G:H2'	30:0:2506:A:H5'	1.86	0.58
30:0:2624:A:H1'	38:0:9769:HOH:O	2.04	0.58
31:9:54:A:C2	31:9:55:U:N3	2.72	0.58
8:H:172:GLU:HB2	38:H:248:HOH:O	2.04	0.58
22:V:1:THR:HG23	22:V:2:VAL:H	1.69	0.58
30:0:412:C:O2'	30:0:413:G:H5'	2.02	0.58
30:0:544:G:H2'	30:0:545:G:H5''	1.85	0.58
30:0:625:U:H3'	38:0:3244:HOH:O	2.03	0.58
30:0:1585:C:H2'	30:0:1586:G:H8	1.68	0.58
30:0:1634:G:H2'	30:0:1635:U:C6	2.38	0.58
30:0:1973:A:H5'	30:0:1973:A:H8	1.69	0.58
30:0:2511:A:H2'	30:0:2512:U:O4'	2.03	0.58
30:0:2581:U:H1'	38:0:4452:HOH:O	2.03	0.58
30:0:51:G:O2'	30:0:52:A:H5'	2.03	0.58
30:0:1041:U:C2'	30:0:1042:U:H5'	2.34	0.58
30:0:1160:G:H5'	30:0:1161:A:H5'	0.78	0.58
30:0:1300:G:H1'	38:0:4652:HOH:O	2.03	0.58
30:0:2812:A:N7	38:0:7497:HOH:O	2.32	0.58
1:A:75:GLY:HA2	26:Z:88:PHE:HA	1.86	0.57
2:B:125:GLU:O	2:B:129:ARG:HG3	2.03	0.57
3:C:236:THR:CG2	3:C:239:ALA:H	2.16	0.57
4:D:76:ARG:CZ	31:9:44:A:H1'	2.34	0.57
11:K:20:CYS:SG	11:K:22:ASP:OD1	2.62	0.57
15:O:10:LEU:HD13	15:O:99:GLU:HG3	1.84	0.57
30:0:12:U:C2'	30:0:13:G:H5'	2.32	0.57
30:0:1057:A:H1'	30:0:2492:U:O2'	2.03	0.57
10:J:70:PHE:HE1	30:0:2676:C:H4'	1.68	0.57
20:T:111:ARG:HB3	20:T:119:ALA:HB2	1.85	0.57
30:0:820:G:H5'	30:0:821:U:H5'	1.86	0.57
30:0:2705:U:H2'	30:0:2706:A:H8	1.68	0.57
30:0:2748:G:H5'	38:0:7523:HOH:O	2.04	0.57
30:0:1166:A:H61	30:0:1180:U:H3	1.51	0.57
1:A:53:ALA:HB2	1:A:122:SER:OG	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:48:VAL:HG13	14:N:55:ASP:HB3	1.86	0.57
26:Z:90:GLY:HA3	26:Z:95:PRO:O	2.04	0.57
30:0:590:A:C2'	30:0:591:A:H5'	2.33	0.57
30:0:821:U:H3'	38:0:3764:HOH:O	2.03	0.57
30:0:1216:G:H2'	30:0:1217:G:O4'	2.03	0.57
30:0:1256:C:H6	38:0:7140:HOH:O	1.87	0.57
30:0:1342:C:C2'	30:0:1343:C:H5'	2.34	0.57
3:C:236:THR:HG22	3:C:239:ALA:N	2.15	0.57
20:T:18:GLU:O	20:T:21:LYS:HG2	2.03	0.57
30:0:283:U:H5	30:0:284:C:C4	2.22	0.57
30:0:916:A:C2	30:0:928:G:C4	2.93	0.57
30:0:1503:U:O2'	30:0:1504:A:H5'	2.04	0.57
30:0:2712:G:H5'	38:0:5187:HOH:O	2.02	0.57
11:K:14:LYS:CB	11:K:45:PRO:HG2	2.35	0.57
14:N:154:LEU:C	14:N:156:GLU:H	2.11	0.57
29:3:51:LYS:HG3	29:3:52:PHE:CD2	2.40	0.57
30:0:694:A:H2'	30:0:695:C:C5'	2.27	0.57
30:0:727:G:H3'	30:0:728:C:H6	1.68	0.57
30:0:1552:G:H2'	30:0:1553:C:C6	2.40	0.57
30:0:1555:G:H4'	30:0:1630:A:H2	1.69	0.57
30:0:1883:U:C2'	30:0:1884:G:H5'	2.34	0.57
3:C:8:LEU:HD11	3:C:143:ASP:O	2.04	0.57
5:E:125:GLU:HB2	5:E:132:THR:HG23	1.86	0.57
30:0:544:G:C2'	30:0:545:G:H5''	2.35	0.57
30:0:1754:A:H5''	38:0:9757:HOH:O	2.04	0.57
30:0:1819:G:H2'	30:0:1820:G:H4'	1.85	0.57
30:0:2078:U:O2'	30:0:2079:G:H5'	2.05	0.57
30:0:2240:U:O2'	30:0:2241:C:H5'	2.04	0.57
30:0:2335:C:H2'	30:0:2336:G:H8	1.67	0.57
30:0:2828:G:O5'	30:0:2828:G:H8	1.87	0.57
3:C:127:ARG:HD3	3:C:129:HIS:HE1	1.70	0.57
21:U:56:ARG:HG3	21:U:56:ARG:NH1	2.19	0.57
24:X:43:VAL:HG22	24:X:76:ARG:NH1	2.20	0.57
30:0:1189:A:H1'	30:0:1209:C:C1'	2.35	0.57
30:0:1577:U:O2'	30:0:1578:C:H5'	2.05	0.57
30:0:2001:G:O2'	30:0:2002:C:H5'	2.04	0.57
1:A:153:ARG:HD3	38:A:9011:HOH:O	2.04	0.57
2:B:214:PRO:HD2	38:B:8989:HOH:O	2.05	0.57
5:E:153:ARG:NH1	30:0:2778:A:H1'	2.19	0.57
14:N:160:SER:CB	31:9:51:A:H5'	2.34	0.57
15:O:19:ARG:NH1	30:0:1276:U:H3'	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:68:HIS:O	30:0:2842:G:H5'	2.05	0.57
21:U:13:ILE:HG12	21:U:32:CYS:HB3	1.86	0.57
21:U:33:SER:O	21:U:37:GLU:HG3	2.04	0.57
25:Y:216:ARG:HD2	38:Y:8871:HOH:O	2.03	0.57
26:Z:45:VAL:HG13	26:Z:49:ARG:HE	1.70	0.57
30:0:138:U:OP2	30:0:139:C:C5	2.58	0.57
30:0:371:U:O2'	30:0:372:A:H5'	2.05	0.57
30:0:403:C:H3'	38:0:6286:HOH:O	2.05	0.57
30:0:1718:G:O2'	30:0:1719:G:H5'	2.04	0.57
30:0:2010:A:H2'	38:0:5933:HOH:O	2.03	0.57
1:A:190:ARG:HD2	30:0:1884:G:O6	2.03	0.57
2:B:41:PHE:CZ	2:B:79:MET:HG3	2.40	0.57
13:M:68:ARG:O	13:M:68:ARG:HD3	2.05	0.57
20:T:24:ARG:HH21	20:T:39:ASN:HD22	1.53	0.57
30:0:1182:C:H1'	30:0:1192:A:H8	1.69	0.57
30:0:1971:G:H5'	38:0:7053:HOH:O	2.05	0.57
30:0:2407:G:O2'	30:0:2408:A:H5'	2.05	0.57
31:9:23:U:H2'	31:9:24:U:H4'	1.87	0.57
31:9:64:C:C2'	31:9:65:A:H5'	2.35	0.57
10:J:116:LEU:HB2	10:J:119:THR:HG21	1.87	0.56
30:0:10:U:C4	30:0:532:A:C8	2.94	0.56
30:0:312:U:O2'	30:0:313:U:H5'	2.05	0.56
30:0:407:A:H2'	30:0:408:A:C8	2.40	0.56
30:0:1079:A:OP2	30:0:1080:C:N4	2.36	0.56
30:0:2251:G:H2'	30:0:2252:A:H8	1.70	0.56
30:0:2769:C:C2'	30:0:2770:G:C5'	2.78	0.56
11:K:32:ILE:HD11	11:K:56:SER:HB2	1.86	0.56
13:M:82:ARG:HD2	30:0:170:U:OP2	2.05	0.56
30:0:1020:A:H2'	30:0:1021:G:C8	2.40	0.56
30:0:1173:A:H4'	30:0:1174:A:C8	2.40	0.56
30:0:2110:G:O2'	30:0:2111:G:H5'	2.05	0.56
30:0:2265:U:H2'	30:0:2266:A:C8	2.40	0.56
30:0:2698:G:H2'	30:0:2699:A:O4'	2.05	0.56
30:0:2700:G:H3'	38:0:3575:HOH:O	2.05	0.56
11:K:98:VAL:HG13	11:K:102:GLU:HA	1.85	0.56
14:N:48:VAL:CG1	14:N:55:ASP:HB3	2.35	0.56
14:N:141:ARG:NH2	31:9:48:C:H4'	2.21	0.56
23:W:38:THR:O	23:W:42:ARG:HB2	2.04	0.56
28:2:40:ARG:HG3	28:2:45:ASN:HB2	1.85	0.56
29:3:34:LYS:HB3	38:3:9001:HOH:O	2.05	0.56
30:0:280:C:H2'	30:0:281:U:O4'	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:695:C:O2'	30:0:696:C:H5'	2.04	0.56
30:0:947:U:O2'	30:0:948:G:H5'	2.05	0.56
30:0:1183:C:N4	30:0:1184:C:H41	2.03	0.56
30:0:1616:A:H5''	30:0:1617:C:OP1	2.05	0.56
30:0:1928:C:H2'	30:0:1929:G:O4'	2.05	0.56
30:0:1948:G:O2'	30:0:1949:G:H5'	2.05	0.56
30:0:2011:A:H5'	30:0:2013:G:H1'	1.87	0.56
2:B:17:LYS:O	2:B:260:HIS:HD2	1.88	0.56
8:H:49:GLN:NE2	8:H:140:TYR:HE2	1.95	0.56
13:M:171:ARG:NH2	30:0:189:A:OP1	2.38	0.56
15:O:24:ALA:HB3	30:0:710:G:OP1	2.05	0.56
17:Q:45:PRO:O	30:0:2365:G:H4'	2.06	0.56
30:0:162:C:H2'	30:0:163:U:H5'	1.87	0.56
30:0:1735:C:H2'	30:0:1736:A:C8	2.40	0.56
30:0:2659:U:H3'	38:0:4379:HOH:O	2.05	0.56
31:9:33:U:H2'	38:9:9068:HOH:O	2.04	0.56
13:M:68:ARG:HG3	30:0:1469:C:OP1	2.05	0.56
30:0:26:U:H5	38:0:3099:HOH:O	1.89	0.56
30:0:696:C:HO2'	30:0:697:G:H5'	1.70	0.56
30:0:1904:A:H2'	30:0:1905:U:O4'	2.05	0.56
30:0:2064:U:H4'	30:0:2653:A:OP1	2.05	0.56
30:0:2289:G:O2'	30:0:2290:U:H5'	2.06	0.56
30:0:2349:G:H2'	30:0:2350:G:C8	2.38	0.56
2:B:223:ARG:HD3	33:B:8819:CL:CL	2.43	0.56
29:3:65:THR:HG23	33:3:8804:CL:CL	2.43	0.56
30:0:113:A:OP2	30:0:114:A:H2'	2.06	0.56
30:0:473:A:O2'	30:0:474:C:H5'	2.06	0.56
30:0:799:C:O2'	30:0:800:G:H5'	2.05	0.56
30:0:1042:U:O2'	30:0:1043:C:H5'	2.05	0.56
30:0:1434:A:O2'	30:0:1435:U:H2'	2.05	0.56
30:0:2502:C:H2'	30:0:2503:A:C5'	2.34	0.56
2:B:199:TYR:HE2	2:B:268:ARG:HB2	1.71	0.56
12:L:27:ARG:NH2	12:L:30:ARG:HD3	2.21	0.56
16:P:127:GLY:HA3	38:P:152:HOH:O	2.05	0.56
25:Y:165:GLU:HB3	38:0:6689:HOH:O	2.05	0.56
26:Z:34:SER:HA	30:0:797:A:C4'	2.36	0.56
29:3:18:GLN:HB3	38:3:9013:HOH:O	2.06	0.56
30:0:138:U:OP2	30:0:139:C:H5	1.88	0.56
30:0:1127:C:C5	30:0:1128:U:C4	2.94	0.56
30:0:2595:U:O2'	30:0:2596:A:H5'	2.05	0.56
31:9:54:A:H2'	31:9:55:U:H5'	1.82	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:LEU:HD21	1:A:55:VAL:HG21	1.88	0.56
3:C:4:THR:HA	3:C:15:GLU:HB3	1.88	0.56
13:M:24:GLN:HE22	13:M:27:ARG:HH11	1.53	0.56
13:M:94:ARG:HD2	30:0:158:A:OP2	2.06	0.56
21:U:44:ARG:HD3	21:U:49:LEU:CD1	2.35	0.56
21:U:56:ARG:HD2	30:0:2890:A:H1'	1.87	0.56
27:1:28:HIS:HE1	30:0:776:A:OP1	1.88	0.56
30:0:473:A:O2'	30:0:890:C:H5'	2.05	0.56
30:0:2241:C:O2'	30:0:2242:U:H5'	2.05	0.56
30:0:2514:U:OP1	30:0:2572:G:H1'	2.04	0.56
5:E:69:ILE:HA	5:E:72:MET:HE3	1.87	0.56
15:O:47:ARG:HH11	15:O:47:ARG:HG3	1.71	0.56
30:0:1679:C:H5'	38:0:9332:HOH:O	2.06	0.56
30:0:1788:U:C2	30:0:1805:G:N2	2.73	0.56
30:0:2673:U:C4	30:0:2674:G:C6	2.94	0.56
31:9:18:U:H2'	31:9:19:G:H8	1.71	0.56
2:B:68:THR:HG21	21:U:16:GLY:HA3	1.87	0.56
3:C:174:ILE:HD11	30:0:338:C:H4'	1.89	0.56
12:L:41:HIS:HD2	30:0:926:A:O2'	1.89	0.56
21:U:23:HIS:CD2	21:U:27:ALA:HB3	2.40	0.56
25:Y:142:SER:HB2	38:Y:8902:HOH:O	2.05	0.56
29:3:68:LYS:HZ1	30:0:2436:U:H5'	1.70	0.56
30:0:660:A:H4'	30:0:661:G:O5'	2.06	0.56
30:0:1020:A:H2'	30:0:1021:G:H8	1.71	0.56
30:0:1181:A:H2'	30:0:1182:C:O4'	2.06	0.56
30:0:2314:G:H2'	30:0:2315:C:H5'	1.87	0.56
30:0:2578:G:H5'	30:0:2578:G:C8	2.36	0.56
30:0:2911:C:H2'	30:0:2912:C:C6	2.42	0.56
31:9:49:G:H2'	31:9:50:G:O4'	2.06	0.56
1:A:47:HIS:HD2	30:0:1654:U:C2'	2.18	0.55
30:0:558:C:C2'	30:0:559:U:C5'	2.68	0.55
30:0:1116:U:H3	30:0:1246:A:N6	1.96	0.55
30:0:1878:G:C1'	38:0:6097:HOH:O	2.53	0.55
5:E:49:ILE:HD11	5:E:69:ILE:HD12	1.88	0.55
25:Y:99:ALA:HB2	25:Y:233:TYR:CZ	2.42	0.55
29:3:33:MET:HG2	30:0:1922:A:H2'	1.88	0.55
30:0:339:A:H2'	38:0:4203:HOH:O	2.06	0.55
30:0:628:1MA:HM11	30:0:2535:U:OP1	2.06	0.55
30:0:684:G:H5''	38:0:4053:HOH:O	2.06	0.55
30:0:858:U:H2'	30:0:859:C:H6	1.71	0.55
30:0:1613:C:H2'	30:0:1614:G:O4'	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2271:G:N3	30:0:2271:G:H2'	2.20	0.55
30:0:2325:U:O2'	30:0:2411:C:H1'	2.06	0.55
30:0:2852:A:H5''	38:0:5199:HOH:O	2.05	0.55
3:C:115:LEU:HD21	3:C:243:VAL:HG13	1.86	0.55
23:W:52:VAL:HG22	23:W:53:ALA:N	2.20	0.55
30:0:735:C:C6	30:0:736:A:C8	2.94	0.55
30:0:1165:G:H21	30:0:1173:A:H5''	1.72	0.55
30:0:1172:G:H1'	38:0:4940:HOH:O	2.05	0.55
30:0:1183:C:H41	30:0:1192:A:H5'	1.72	0.55
30:0:1512:G:O2'	30:0:1513:C:H5'	2.05	0.55
30:0:2113:G:C6	30:0:2114:C:C4	2.94	0.55
3:C:1:MET:HG2	3:C:2:GLN:H	1.72	0.55
25:Y:210:GLY:HA2	38:0:5285:HOH:O	2.06	0.55
26:Z:44:ARG:HB2	30:0:1886:A:O2'	2.05	0.55
30:0:913:A:H8	30:0:913:A:O5'	1.90	0.55
30:0:920:C:H5'	30:0:921:G:C4	2.41	0.55
30:0:2668:G:H2'	30:0:2669:U:C6	2.42	0.55
2:B:229:ARG:NH2	30:0:1753:C:O2	2.39	0.55
3:C:21:VAL:HG13	38:C:8594:HOH:O	2.05	0.55
7:G:16:LYS:HE2	7:G:63:ARG:NH1	2.21	0.55
24:X:76:ARG:HH11	24:X:76:ARG:HG3	1.72	0.55
29:3:59:ASP:HB3	29:3:63:LYS:HZ3	1.72	0.55
30:0:310:U:H2'	30:0:311:C:C6	2.41	0.55
30:0:1625:U:C6	30:0:1625:U:C3'	2.85	0.55
30:0:2250:G:N2	30:0:2251:G:H1'	2.21	0.55
3:C:149:LYS:HB2	3:C:152:GLU:HG3	1.89	0.55
3:C:162:VAL:HG22	3:C:232:LEU:HD21	1.87	0.55
38:Y:8879:HOH:O	30:0:1355:A:H5''	2.06	0.55
26:Z:63:CYS:SG	26:Z:81:CYS:CB	2.94	0.55
29:3:47:GLY:CA	30:0:2121:G:H4'	2.29	0.55
30:0:956:G:H3'	38:0:9387:HOH:O	2.06	0.55
30:0:1562:C:N4	38:0:5836:HOH:O	2.38	0.55
30:0:1909:A:H2'	30:0:1910:A:C8	2.42	0.55
2:B:36:PRO:HA	2:B:168:GLY:CA	2.36	0.55
10:J:107:ASN:C	10:J:107:ASN:HD22	2.15	0.55
23:W:119:HIS:HD2	23:W:120:PRO:O	1.89	0.55
30:0:212:A:O4'	30:0:214:U:C6	2.59	0.55
30:0:545:G:C8	30:0:545:G:C5'	2.81	0.55
30:0:571:C:O5'	30:0:571:C:H6	1.90	0.55
30:0:822:C:C2	30:0:823:U:C5	2.94	0.55
30:0:835:U:H3'	38:0:9381:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1691:A:H5''	38:0:3140:HOH:O	2.06	0.55
30:0:1736:A:H1'	38:0:7566:HOH:O	2.07	0.55
30:0:1741:U:HO2'	30:0:2723:G:H4'	1.72	0.55
2:B:102:THR:HG21	2:B:182:VAL:O	2.07	0.55
4:D:140:ARG:HH11	4:D:140:ARG:HG3	1.72	0.55
13:M:111:ASN:HB2	38:M:8852:HOH:O	2.07	0.55
29:3:90:PHE:N	29:3:90:PHE:CD1	2.75	0.55
30:0:401:C:H2'	30:0:402:U:H6	1.72	0.55
30:0:2274:A:H2'	30:0:2275:G:C8	2.42	0.55
30:0:2868:C:H1'	38:0:7107:HOH:O	2.07	0.55
31:9:59:C:C2	31:9:60:C:C5	2.94	0.55
5:E:132:THR:HB	38:E:2227:HOH:O	2.06	0.55
13:M:70:GLY:CA	30:0:2263:G:H4'	2.37	0.55
19:S:37:VAL:O	19:S:41:VAL:HG23	2.05	0.55
28:2:43:ARG:HH22	30:0:1684:A:C1'	2.16	0.55
30:0:130:C:O2'	30:0:131:A:N7	2.39	0.55
30:0:291:C:H2'	30:0:292:G:O4'	2.07	0.55
30:0:1156:C:O2'	30:0:1157:C:H5'	2.07	0.55
30:0:1166:A:C6	30:0:1181:A:C2	2.95	0.55
30:0:1175:G:H2'	30:0:1176:C:C6	2.42	0.55
30:0:1200:A:N1	30:0:1201:C:C2	2.75	0.55
1:A:132:ASP:CG	1:A:133:ARG:H	2.15	0.55
5:E:53:GLU:HB3	5:E:55:ASN:ND2	2.21	0.55
5:E:118:ILE:HG23	5:E:144:THR:HG21	1.89	0.55
21:U:51:TRP:HD1	30:0:2865:G:O2'	1.89	0.55
30:0:777:U:OP2	30:0:777:U:H4'	2.07	0.55
30:0:1849:G:H1'	30:0:2011:A:N1	2.22	0.55
30:0:1905:U:H2'	30:0:1906:C:H6	1.72	0.55
30:0:2584:G:H4'	38:0:7102:HOH:O	2.07	0.55
30:0:2689:A:C2'	30:0:2690:U:H5'	2.37	0.55
1:A:76:VAL:HG23	26:Z:87:LYS:HB3	1.88	0.54
3:C:2:GLN:HB3	38:C:8581:HOH:O	2.07	0.54
3:C:132:ASP:HB2	3:C:161:ASP:HB3	1.89	0.54
14:N:110:THR:HB	14:N:113:SER:OG	2.07	0.54
30:0:690:G:H4'	30:0:741:C:O2	2.06	0.54
30:0:820:G:H5'	30:0:821:U:C5'	2.37	0.54
30:0:941:G:C5	30:0:942:U:C4	2.95	0.54
30:0:1377:C:H6	30:0:1377:C:C5'	2.20	0.54
30:0:1903:U:O2'	30:0:1904:A:N7	2.40	0.54
30:0:1909:A:N1	30:0:2128:G:H1'	2.22	0.54
30:0:2782:G:N2	30:0:2783:A:N6	2.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:232:TRP:CZ3	30:0:2614:C:H5''	2.41	0.54
4:D:146:LYS:NZ	14:N:107:ASN:HD21	2.05	0.54
5:E:108:LEU:HD11	5:E:164:ASP:HB2	1.88	0.54
29:3:12:PRO:HG2	29:3:13:HIS:HD2	1.71	0.54
30:0:363:C:O2'	30:0:364:U:H5'	2.07	0.54
30:0:814:G:H2'	30:0:815:U:O4'	2.07	0.54
30:0:960:G:H8	38:0:5945:HOH:O	1.89	0.54
30:0:1593:C:H1'	38:0:6083:HOH:O	2.06	0.54
31:9:58:G:N7	31:9:59:C:C4	2.75	0.54
2:B:41:PHE:CE1	2:B:79:MET:HG3	2.43	0.54
2:B:140:LEU:HA	38:B:9051:HOH:O	2.05	0.54
9:I:78:ALA:HB2	9:I:95:LEU:HD21	1.89	0.54
14:N:114:LYS:O	14:N:118:ILE:HG13	2.07	0.54
14:N:130:PRO:HA	38:N:8837:HOH:O	2.06	0.54
27:1:28:HIS:HD2	27:1:30:LYS:H	1.53	0.54
30:0:1015:C:H4'	38:0:6566:HOH:O	2.06	0.54
30:0:1175:G:H4'	38:0:6842:HOH:O	2.07	0.54
30:0:2032:U:C2'	30:0:2033:G:C5'	2.86	0.54
30:0:2032:U:C2'	30:0:2033:G:H5''	2.38	0.54
30:0:2524:G:H21	30:0:2526:C:H41	1.55	0.54
30:0:2869:G:H5'	38:0:5457:HOH:O	2.07	0.54
5:E:85:GLU:HG2	5:E:130:GLU:HG2	1.89	0.54
6:F:2:VAL:HG22	6:F:57:GLU:OE1	2.08	0.54
13:M:59:GLY:HA3	13:M:141:ILE:HD12	1.90	0.54
29:3:60:LYS:C	29:3:62:THR:H	2.15	0.54
30:0:1447:U:OP1	30:0:1506:U:N3	2.39	0.54
30:0:1876:C:H4'	30:0:1877:G:OP2	2.08	0.54
30:0:2281:C:C2'	30:0:2282:U:H5'	2.38	0.54
31:9:27:C:H2'	31:9:28:U:O4'	2.08	0.54
1:A:192:VAL:CG1	1:A:207:GLN:HB3	2.38	0.54
1:A:223:ARG:NH1	30:0:2270:G:H4'	2.22	0.54
9:I:87:PRO:HD2	30:0:1180:U:H1'	1.89	0.54
9:I:91:PHE:CD2	9:I:131:GLY:HA2	2.42	0.54
12:L:143:THR:HG22	12:L:144:ASP:N	2.22	0.54
13:M:99:ARG:HE	13:M:170:ASN:ND2	1.96	0.54
15:O:19:ARG:HH22	30:0:1278:A:P	2.31	0.54
30:0:1139:U:H2'	30:0:1140:C:H6	1.72	0.54
30:0:2477:C:O2'	30:0:2478:U:H5'	2.07	0.54
31:9:36:C:C5	31:9:37:C:C5	2.96	0.54
1:A:195:ASN:ND2	30:0:877:G:C8	2.76	0.54
12:L:67:ARG:O	12:L:71:GLU:HG3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:60:LYS:HB3	29:3:62:THR:O	2.07	0.54
30:0:236:A:H4'	30:0:237:G:OP1	2.08	0.54
30:0:312:U:C2	30:0:320:G:N2	2.76	0.54
30:0:710:G:O2'	30:0:711:G:H5'	2.08	0.54
30:0:963:C:O2	30:0:1005:A:N1	2.40	0.54
30:0:1697:G:H5'	38:0:5475:HOH:O	2.08	0.54
30:0:2081:A:H2'	30:0:2082:G:O4'	2.08	0.54
30:0:2107:U:O2'	30:0:2108:A:H5'	2.07	0.54
30:0:2321:A:C4	30:0:2323:G:C8	2.95	0.54
30:0:2831:C:H3'	38:0:7197:HOH:O	2.07	0.54
16:P:35:ILE:HD13	38:P:171:HOH:O	2.08	0.54
17:Q:19:ARG:HH21	31:9:11:A:P	2.30	0.54
30:0:461:C:N3	30:0:479:G:H5'	2.22	0.54
30:0:623:U:O2'	30:0:624:U:H5'	2.08	0.54
30:0:661:G:C5	30:0:686:A:C2	2.96	0.54
30:0:960:G:N3	30:0:960:G:C3'	2.71	0.54
30:0:1617:C:C5	30:0:1643:C:H4'	2.42	0.54
30:0:2078:U:H2'	30:0:2079:G:C8	2.42	0.54
30:0:2892:G:C5	30:0:2893:C:C5	2.95	0.54
4:D:135:VAL:HG21	4:D:139:TYR:CD1	2.43	0.54
5:E:116:THR:HG22	5:E:151:LEU:HD22	1.90	0.54
18:R:99:ALA:HB1	18:R:109:MET:CE	2.37	0.54
27:1:16:HIS:HD2	30:0:470:U:O2'	1.91	0.54
30:0:1175:G:H1'	30:0:1193:A:H2'	1.89	0.54
30:0:1676:G:H1'	38:0:9441:HOH:O	2.08	0.54
30:0:1850:U:H2'	30:0:1851:G:H8	1.73	0.54
30:0:2045:G:H5''	38:0:7204:HOH:O	2.06	0.54
30:0:2256:G:O2'	30:0:2257:G:H5'	2.08	0.54
30:0:2670:G:O2'	30:0:2671:U:H5'	2.08	0.54
31:9:30:C:O2	31:9:30:C:H2'	2.08	0.54
13:M:164:THR:CG2	13:M:165:GLY:N	2.70	0.54
15:O:19:ARG:HH11	30:0:1276:U:H3'	1.73	0.54
24:X:30:MET:HE1	24:X:58:ALA:HB3	1.90	0.54
30:0:334:G:C4	30:0:335:U:C6	2.96	0.54
30:0:1625:U:H5''	38:0:5995:HOH:O	2.07	0.54
30:0:2487:C:H5	38:0:4858:HOH:O	1.91	0.54
30:0:2787:C:H5	38:0:4605:HOH:O	1.90	0.54
30:0:2908:A:O5'	30:0:2908:A:H8	1.91	0.54
25:Y:235:GLU:H	25:Y:235:GLU:CD	2.16	0.54
28:2:13:LYS:O	28:2:17:GLN:HG3	2.07	0.54
30:0:541:C:C2'	30:0:542:A:C5'	2.78	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:853:C:H2'	30:0:854:G:O4'	2.08	0.54
30:0:2831:C:H2'	30:0:2832:C:C5'	2.38	0.54
31:9:23:U:C2'	31:9:24:U:H4'	2.38	0.54
1:A:179:MET:HG2	1:A:186:TRP:HB2	1.91	0.53
2:B:238:ASN:ND2	2:B:240:GLY:H	1.92	0.53
8:H:99:ARG:NH1	30:0:1055:G:OP2	2.41	0.53
14:N:132:ASN:HD22	30:0:2413:A:H4'	1.72	0.53
25:Y:97:LEU:HA	25:Y:234:VAL:O	2.08	0.53
30:0:30:U:H5''	38:0:5777:HOH:O	2.08	0.53
30:0:338:C:H5''	38:0:3793:HOH:O	2.07	0.53
30:0:354:A:H2'	30:0:355:C:H6	1.73	0.53
30:0:1453:G:H2'	30:0:1454:U:O4'	2.07	0.53
30:0:1525:G:H5'	30:0:1526:A:OP2	2.08	0.53
30:0:2106:C:H2'	30:0:2107:U:C6	2.43	0.53
30:0:2599:A:H5''	38:0:3367:HOH:O	2.08	0.53
9:I:111:LEU:HD23	30:0:1163:G:H4'	1.90	0.53
15:O:105:ASN:HD21	15:O:109:SER:H	1.56	0.53
16:P:7:LYS:HD3	16:P:21:VAL:CG2	2.38	0.53
30:0:1268:C:H2'	30:0:1269:G:H8	1.73	0.53
30:0:2321:A:C5	30:0:2323:G:C8	2.96	0.53
30:0:2379:G:N3	30:0:2418:G:H2'	2.22	0.53
30:0:2553:A:H2'	30:0:2553:A:N3	2.23	0.53
30:0:2563:U:O2'	30:0:2564:G:H3'	2.08	0.53
30:0:2769:C:H2'	30:0:2770:G:C4'	2.37	0.53
1:A:33:GLU:O	1:A:34:ASP:HB2	2.08	0.53
2:B:212:GLN:HA	30:0:1733:A:H4'	1.89	0.53
18:R:25:PHE:HB3	38:R:8914:HOH:O	2.07	0.53
23:W:13:MET:HE2	23:W:18:GLN:CA	2.38	0.53
23:W:35:VAL:HG23	23:W:41:TYR:CD2	2.43	0.53
30:0:421:C:H2'	30:0:422:G:H8	1.74	0.53
30:0:1226:G:C4	30:0:1227:C:C5	2.96	0.53
30:0:1311:G:C2	30:0:1312:G:C8	2.97	0.53
30:0:2465:A:H5'	38:0:6910:HOH:O	2.07	0.53
31:9:73:A:H61	31:9:108:C:H42	1.57	0.53
1:A:20:SER:HB3	30:0:1872:C:C5	2.44	0.53
12:L:11:ARG:O	30:0:903:U:C2	2.61	0.53
23:W:5:VAL:HG22	23:W:32:CYS:HB2	1.91	0.53
30:0:491:C:O2'	30:0:492:C:H5'	2.09	0.53
30:0:869:G:C8	30:0:869:G:OP2	2.62	0.53
30:0:1754:A:H2'	30:0:1755:A:O4'	2.09	0.53
30:0:2703:A:H2'	30:0:2704:C:C6	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:114:G:H2'	31:9:115:C:C6	2.43	0.53
8:H:49:GLN:HG3	8:H:140:TYR:CE2	2.43	0.53
16:P:71:TYR:CE2	30:0:1790:C:H5	2.26	0.53
30:0:213:G:H22	30:0:225:G:H2'	1.72	0.53
30:0:549:A:C2	30:0:550:C:C2	2.97	0.53
30:0:597:A:O2'	30:0:598:C:H5'	2.08	0.53
30:0:718:C:O2	30:0:718:C:C2'	2.55	0.53
30:0:1271:A:H2'	30:0:1272:C:C6	2.43	0.53
30:0:1741:U:C4	30:0:2033:G:C8	2.96	0.53
30:0:1762:C:O2'	30:0:1763:C:H5'	2.08	0.53
30:0:2119:C:C2'	30:0:2120:U:H5'	2.38	0.53
30:0:2831:C:C2	30:0:2910:A:C2	2.96	0.53
30:0:2895:C:H2'	38:0:9579:HOH:O	2.08	0.53
8:H:69:ARG:HD3	38:H:239:HOH:O	2.08	0.53
11:K:89:LYS:HA	38:K:7064:HOH:O	2.08	0.53
21:U:56:ARG:CD	30:0:2890:A:H1'	2.38	0.53
30:0:466:A:H2'	30:0:467:G:O4'	2.08	0.53
30:0:535:G:C5	30:0:2063:U:C4	2.96	0.53
30:0:1278:A:C4'	30:0:1279:U:C4	2.74	0.53
30:0:2078:U:H2'	30:0:2079:G:H8	1.74	0.53
30:0:2321:A:H2'	30:0:2321:A:N3	2.24	0.53
30:0:2501:G:H1	30:0:2519:C:H42	1.56	0.53
31:9:58:G:C8	31:9:59:C:C5	2.97	0.53
2:B:305:ASP:O	2:B:306:LYS:HB2	2.09	0.53
14:N:11:ARG:HG3	14:N:14:ARG:NH1	2.23	0.53
29:3:31:THR:O	30:0:1923:G:H4'	2.09	0.53
30:0:195:C:H2'	30:0:196:G:H5'	1.91	0.53
30:0:398:U:H2'	30:0:399:C:C6	2.44	0.53
30:0:561:G:N3	30:0:562:A:C8	2.77	0.53
30:0:1706:G:C6	30:0:1707:G:C6	2.97	0.53
30:0:1806:G:C5	30:0:1807:U:C5	2.97	0.53
30:0:1819:G:H5'	38:0:5785:HOH:O	2.07	0.53
30:0:1972:U:O2'	30:0:1973:A:H5''	2.09	0.53
30:0:2321:A:H4'	30:0:2322:U:OP1	2.08	0.53
1:A:164:ARG:HB3	1:A:164:ARG:HH11	1.73	0.53
1:A:199:HIS:HD2	1:A:201:PHE:N	2.00	0.53
2:B:141:ARG:HD2	2:B:163:GLU:OE2	2.08	0.53
5:E:84:MET:HE1	5:E:148:ILE:HD12	1.91	0.53
10:J:39:VAL:HG22	10:J:107:ASN:HA	1.91	0.53
13:M:179:GLY:O	30:0:399:C:H5'	2.08	0.53
13:M:187:LEU:CD2	13:M:194:GLY:HA3	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:44:GLY:O	22:V:48:GLU:HG2	2.08	0.53
23:W:154:ARG:NH1	30:0:588:G:O6	2.40	0.53
25:Y:154:ARG:NH2	30:0:1071:G:H4'	2.23	0.53
30:0:69:A:H2'	30:0:70:A:OP2	2.09	0.53
30:0:191:A:H61	30:0:435:A:N6	2.06	0.53
30:0:424:C:H2'	30:0:425:U:C6	2.44	0.53
30:0:735:C:C5	30:0:736:A:C5	2.97	0.53
30:0:1167:G:H2'	30:0:1168:C:H6	1.71	0.53
30:0:1769:C:O2'	30:0:1770:U:H5'	2.09	0.53
30:0:2250:G:C2	30:0:2251:G:H1'	2.44	0.53
30:0:2613:G:O2'	30:0:2614:C:H5'	2.09	0.53
30:0:2864:U:C2'	30:0:2865:G:H5'	2.38	0.53
8:H:6:ALA:HA	8:H:61:ARG:HH12	1.74	0.53
10:J:41:ALA:HB3	38:J:8863:HOH:O	2.09	0.53
16:P:115:SER:OG	16:P:118:GLN:HG3	2.08	0.53
30:0:334:G:H2'	30:0:335:U:O4'	2.08	0.53
30:0:1158:G:C2'	30:0:1159:G:H5'	2.39	0.53
30:0:1913:C:H2'	30:0:1914:C:H6	1.73	0.53
30:0:1922:A:N1	30:0:2449:G:O2'	2.38	0.53
30:0:1968:A:H2'	30:0:1969:A:C8	2.44	0.53
30:0:2336:G:H2'	38:0:6275:HOH:O	2.09	0.53
9:I:108:HIS:H	9:I:109:PRO:HD2	1.74	0.53
14:N:38:LYS:HE2	14:N:107:ASN:ND2	2.24	0.53
30:0:74:G:H1	30:0:103:C:H42	1.55	0.53
30:0:1844:C:O2'	30:0:1845:A:H5'	2.08	0.53
30:0:2642:G:H2'	30:0:2643:G:O4'	2.09	0.53
1:A:45:ILE:HG22	26:Z:78:ILE:HG12	1.89	0.52
1:A:105:VAL:HG13	1:A:155:THR:O	2.09	0.52
8:H:26:ILE:HA	8:H:123:ILE:HG21	1.91	0.52
8:H:157:TYR:HD1	8:H:157:TYR:C	2.18	0.52
8:H:159:LYS:HG2	30:0:2519:C:O2	2.09	0.52
30:0:216:A:O2'	30:0:217:C:H5'	2.09	0.52
30:0:488:U:H2'	38:0:3993:HOH:O	2.08	0.52
30:0:1014:A:H2'	30:0:1015:C:H5'	1.90	0.52
30:0:1188:A:C6	30:0:1189:A:C6	2.97	0.52
30:0:1244:U:H4'	30:0:1246:A:O4'	2.09	0.52
30:0:1451:C:H5'	30:0:1505:U:C5	2.44	0.52
30:0:2037:C:H3'	38:0:6684:HOH:O	2.09	0.52
30:0:2719:A:H2'	30:0:2720:C:H5'	1.90	0.52
31:9:20:G:O2'	31:9:21:G:H5'	2.09	0.52
31:9:37:C:O2	31:9:47:A:H1'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:58:G:C6	31:9:59:C:C2	2.97	0.52
15:O:25:VAL:HG13	30:0:709:G:O3'	2.10	0.52
23:W:4:LEU:HD22	23:W:54:PHE:HB3	1.90	0.52
29:3:40:ARG:C	29:3:42:ARG:H	2.16	0.52
30:0:675:U:H2'	30:0:676:C:H5'	1.90	0.52
30:0:1164:U:H5	38:0:6024:HOH:O	1.91	0.52
3:C:43:LYS:HG2	30:0:449:A:N7	2.24	0.52
5:E:126:ILE:HA	5:E:131:LEU:HD23	1.91	0.52
13:M:24:GLN:NE2	13:M:27:ARG:HH11	2.07	0.52
13:M:73:ARG:HH21	30:0:2263:G:H5''	1.70	0.52
18:R:4:TYR:CZ	18:R:17:MET:HE2	2.44	0.52
19:S:33:SER:O	19:S:37:VAL:HG23	2.10	0.52
30:0:125:U:H2'	38:0:3760:HOH:O	2.10	0.52
30:0:271:C:C2	30:0:273:G:O4'	2.61	0.52
30:0:622:G:O2'	30:0:623:U:H5'	2.10	0.52
30:0:1515:A:H2'	30:0:1516:U:C6	2.44	0.52
30:0:1557:G:O2'	30:0:1558:C:H5'	2.09	0.52
30:0:1684:A:O2'	30:0:1685:A:H5''	2.10	0.52
30:0:2901:C:H6	30:0:2901:C:O5'	1.93	0.52
31:9:1:U:C4'	31:9:3:A:OP1	2.58	0.52
2:B:62:ARG:HA	2:B:65:MET:CE	2.38	0.52
11:K:66:ARG:HH12	30:0:1992:U:H3'	1.75	0.52
20:T:26:THR:HG23	20:T:97:ARG:HG3	1.90	0.52
23:W:130:HIS:NE2	31:9:88:G:OP1	2.42	0.52
28:2:49:GLU:HB2	38:2:131:HOH:O	2.08	0.52
30:0:24:G:N2	30:0:518:G:H1'	2.24	0.52
30:0:40:C:O5'	30:0:40:C:H6	1.93	0.52
30:0:249:G:N2	30:0:250:C:C2	2.77	0.52
30:0:1359:U:O5'	30:0:1360:C:H5''	2.10	0.52
30:0:1664:A:H8	30:0:1664:A:OP1	1.92	0.52
30:0:1865:A:H2'	30:0:1866:A:C8	2.44	0.52
30:0:2320:U:H4'	30:0:2321:A:O4'	2.09	0.52
30:0:2407:G:H2'	30:0:2408:A:O4'	2.09	0.52
30:0:2783:A:O2'	30:0:2784:A:H5'	2.09	0.52
31:9:38:A:C2	31:9:39:U:C4	2.97	0.52
2:B:226:LYS:HG2	2:B:230:GLN:NE2	2.25	0.52
3:C:96:LYS:NZ	30:0:1351:G:OP1	2.42	0.52
6:F:53:ASP:OD1	6:F:80:GLN:HB2	2.10	0.52
13:M:81:ARG:HB3	13:M:86:GLN:HG2	1.91	0.52
14:N:55:ASP:OD2	31:9:7:G:H4'	2.09	0.52
29:3:68:LYS:HG2	29:3:77:ALA:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:204:A:C2'	30:0:205:U:H5'	2.39	0.52
30:0:916:A:C2	30:0:928:G:N3	2.78	0.52
30:0:1590:A:C2	30:0:1606:A:H1'	2.44	0.52
1:A:66:ARG:HH11	1:A:66:ARG:HB2	1.74	0.52
4:D:18:ILE:HD13	4:D:84:LEU:HD12	1.91	0.52
5:E:153:ARG:HH12	30:0:2778:A:C1'	2.22	0.52
18:R:111:ILE:HG23	18:R:145:LEU:HD11	1.90	0.52
18:R:132:ARG:HH22	30:0:2055:A:H4'	1.74	0.52
20:T:106:GLU:HG3	38:T:4913:HOH:O	2.09	0.52
30:0:1087:G:O2'	33:0:8822:CL:CL	2.55	0.52
30:0:1139:U:H2'	30:0:1140:C:C6	2.45	0.52
30:0:1180:U:O2'	30:0:1181:A:H5'	2.10	0.52
30:0:1641:A:C2'	30:0:1642:A:H5'	2.40	0.52
30:0:1649:G:H1'	38:0:5498:HOH:O	2.09	0.52
31:9:49:G:O2'	31:9:50:G:H5'	2.08	0.52
2:B:223:ARG:HG3	2:B:232:TRP:O	2.10	0.52
25:Y:132:ASP:OD2	30:0:621:C:H5'	2.10	0.52
28:2:18:ASN:HD21	28:2:40:ARG:HB3	1.74	0.52
30:0:228:C:C2'	30:0:229:G:H5'	2.40	0.52
30:0:1052:G:H2'	30:0:1052:G:N3	2.24	0.52
30:0:1886:A:H4'	38:0:9333:HOH:O	2.09	0.52
30:0:1890:U:H4'	30:0:2010:A:C6	2.44	0.52
30:0:1930:A:H2'	30:0:1931:A:C8	2.44	0.52
30:0:2041:G:O2'	30:0:2042:U:H5'	2.10	0.52
30:0:2526:C:C3'	30:0:2526:C:C6	2.93	0.52
31:9:58:G:C5	31:9:59:C:C2	2.98	0.52
38:I:1549:HOH:O	30:0:1180:U:H1'	2.10	0.52
18:R:18:LEU:HB2	18:R:143:VAL:HG13	1.91	0.52
27:1:11:LYS:HG2	30:0:777:U:O2'	2.10	0.52
30:0:506:G:N2	30:0:509:A:H5''	2.18	0.52
30:0:595:U:H3'	38:0:6474:HOH:O	2.09	0.52
30:0:734:U:O2'	30:0:736:A:N7	2.33	0.52
30:0:800:G:H2'	30:0:801:U:C6	2.45	0.52
30:0:2637:A:C5'	38:0:4897:HOH:O	2.55	0.52
30:0:2651:C:H2'	30:0:2652:U:O4'	2.10	0.52
31:9:34:A:H2'	31:9:35:C:O4'	2.10	0.52
2:B:243:ASN:HB2	30:0:2607:U:OP2	2.10	0.52
6:F:91:VAL:HG12	6:F:92:GLY:N	2.20	0.52
7:G:63:ARG:O	7:G:67:LEU:HG	2.10	0.52
12:L:73:VAL:HG23	12:L:74:THR:H	1.75	0.52
30:0:599:G:H2'	30:0:600:G:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:615:G:H2'	30:0:616:U:C6	2.44	0.52
30:0:793:A:C5	30:0:794:U:C5	2.98	0.52
30:0:1183:C:C4	30:0:1184:C:N4	2.78	0.52
30:0:1522:A:C2'	30:0:1523:G:H5'	2.40	0.52
30:0:2672:C:H2'	30:0:2673:U:H6	1.74	0.52
13:M:73:ARG:HD2	13:M:73:ARG:N	2.25	0.52
29:3:4:PRO:HA	29:3:91:GLN:O	2.09	0.52
30:0:308:U:C4	30:0:342:C:H1'	2.45	0.52
30:0:818:A:C6	30:0:819:A:N1	2.78	0.52
30:0:1154:A:H2'	30:0:1155:G:C8	2.44	0.52
30:0:1422:U:H2'	30:0:1423:C:H6	1.72	0.52
30:0:1504:A:H5'	38:0:4396:HOH:O	2.10	0.52
30:0:2088:C:H2'	30:0:2089:A:C8	2.44	0.52
12:L:78:ALA:HB3	38:L:8860:HOH:O	2.11	0.51
13:M:43:PRO:HG3	13:M:62:VAL:HG21	1.91	0.51
24:X:49:ARG:HD3	24:X:84:ILE:HG12	1.92	0.51
30:0:818:A:C6	30:0:819:A:C2	2.98	0.51
30:0:1175:G:N7	30:0:1176:C:C4	2.78	0.51
30:0:1191:A:C2'	30:0:1193:A:H5'	2.38	0.51
30:0:1309:U:O2'	30:0:1310:U:H5'	2.10	0.51
30:0:1743:G:H2'	30:0:1744:G:O4'	2.10	0.51
30:0:2872:U:H2'	30:0:2873:C:H6	1.76	0.51
2:B:144:THR:HB	38:B:9096:HOH:O	2.10	0.51
14:N:7:LYS:HE3	17:Q:21:ARG:O	2.09	0.51
17:Q:87:THR:HB	38:Q:1295:HOH:O	2.10	0.51
20:T:52:ARG:HH12	30:0:308:U:H2'	1.75	0.51
26:Z:38:PHE:HB3	26:Z:42:TYR:CE1	2.46	0.51
30:0:395:A:H2'	30:0:397:A:H62	1.74	0.51
30:0:1395:C:H2'	30:0:1396:C:C6	2.46	0.51
30:0:2498:C:O2'	30:0:2499:U:H5'	2.10	0.51
30:0:2900:G:H2'	30:0:2901:C:O4'	2.10	0.51
25:Y:205:ILE:HB	25:Y:230:ASN:HD21	1.75	0.51
30:0:20:G:H5''	30:0:510:U:O4	2.09	0.51
30:0:1667:A:H5'	30:0:1667:A:H8	1.75	0.51
30:0:1992:U:H2'	30:0:1994:A:OP2	2.10	0.51
30:0:2544:G:H5'	38:0:3418:HOH:O	2.10	0.51
9:I:120:ALA:O	9:I:124:VAL:HG23	2.09	0.51
29:3:54:LYS:HE2	30:0:2468:A:C8	2.45	0.51
30:0:1641:A:H2'	30:0:1642:A:C5'	2.40	0.51
30:0:2032:U:H2'	30:0:2033:G:H5''	1.92	0.51
30:0:2614:C:O2'	30:0:2615:U:H5'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:LYS:HE2	33:A:8809:CL:CL	2.48	0.51
11:K:41:LYS:O	11:K:42:ASN:HB2	2.09	0.51
15:O:65:LEU:HD13	30:0:746:A:C6	2.45	0.51
30:0:1160:G:H2'	38:0:5597:HOH:O	2.11	0.51
30:0:1167:G:H2'	30:0:1168:C:O4'	2.11	0.51
30:0:1395:C:H2'	30:0:1396:C:H6	1.76	0.51
31:9:56:A:H3'	31:9:57:A:H5''	1.89	0.51
3:C:127:ARG:HD3	3:C:129:HIS:CE1	2.45	0.51
10:J:21:ARG:HH21	30:0:1244:U:H5''	1.76	0.51
11:K:91:GLU:HG3	38:U:151:HOH:O	2.11	0.51
17:Q:7:LEU:HD12	30:0:2424:U:H1'	1.93	0.51
30:0:254:C:O2	30:0:254:C:C2'	2.57	0.51
30:0:660:A:N6	30:0:746:A:O4'	2.43	0.51
30:0:702:G:C2	30:0:703:G:C8	2.98	0.51
30:0:2700:G:O2'	30:0:2701:G:H5'	2.09	0.51
30:0:2846:C:H3'	38:0:7070:HOH:O	2.11	0.51
30:0:2851:G:H2'	30:0:2902:A:N6	2.26	0.51
31:9:58:G:H3'	31:9:59:C:C5	2.45	0.51
2:B:234:ARG:HG3	30:0:1735:C:OP2	2.11	0.51
5:E:137:ASP:OD1	5:E:139:GLU:HB2	2.11	0.51
8:H:114:ASP:HA	38:H:204:HOH:O	2.11	0.51
17:Q:94:GLN:O	17:Q:95:GLU:HB2	2.11	0.51
24:X:56:GLU:HG2	30:0:1400:C:H4'	1.92	0.51
29:3:40:ARG:HA	29:3:52:PHE:HE1	1.73	0.51
29:3:83:TRP:NE1	30:0:2380:A:H2	2.09	0.51
30:0:37:A:H2'	30:0:38:G:C8	2.46	0.51
30:0:128:A:O2'	30:0:129:A:H5'	2.10	0.51
30:0:633:C:O2'	30:0:634:G:H5'	2.10	0.51
30:0:1019:C:O2'	30:0:1020:A:H5'	2.11	0.51
30:0:1947:G:N2	30:0:1966:U:C2	2.79	0.51
30:0:2032:U:H2'	30:0:2033:G:H5'	1.93	0.51
30:0:2719:A:C2'	30:0:2720:C:H5'	2.41	0.51
3:C:149:LYS:HE3	38:0:4023:HOH:O	2.10	0.51
3:C:219:ASN:O	3:C:222:ASP:HB2	2.11	0.51
6:F:36:THR:HG23	6:F:97:ALA:HB2	1.93	0.51
6:F:91:VAL:HG11	30:0:262:A:OP2	2.10	0.51
7:G:64:ASN:HD22	7:G:64:ASN:H	1.58	0.51
13:M:28:GLN:O	13:M:32:ARG:HG3	2.10	0.51
15:O:37:ARG:HD2	30:0:656:G:OP2	2.11	0.51
20:T:32:ARG:NH1	20:T:38:ARG:NH1	2.58	0.51
26:Z:53:ILE:HG23	38:Z:8719:HOH:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:78:ILE:HD12	38:Z:8715:HOH:O	2.11	0.51
30:0:210:U:O2'	30:0:211:U:H5'	2.11	0.51
30:0:727:G:H3'	30:0:728:C:C6	2.45	0.51
30:0:822:C:N3	30:0:823:U:C5	2.79	0.51
30:0:1236:A:O2'	30:0:1237:U:H5'	2.11	0.51
30:0:2047:C:H5'	38:0:9814:HOH:O	2.10	0.51
30:0:2456:A:O2'	30:0:2457:U:H5'	2.10	0.51
30:0:2689:A:H2'	30:0:2690:U:H5'	1.92	0.51
8:H:61:ARG:HH11	8:H:61:ARG:HG3	1.75	0.51
11:K:66:ARG:NH2	30:0:1994:A:OP1	2.44	0.51
16:P:128:GLY:HA3	30:0:801:U:O4'	2.11	0.51
24:X:61:ARG:O	30:0:2744:G:H5''	2.11	0.51
25:Y:127:GLN:HA	38:Y:8909:HOH:O	2.11	0.51
30:0:523:C:H2'	30:0:524:A:C8	2.46	0.51
30:0:1890:U:H1'	30:0:2013:G:N2	2.26	0.51
30:0:2589:U:H2'	30:0:2590:U:C6	2.46	0.51
30:0:2712:G:C5'	38:0:5187:HOH:O	2.58	0.51
2:B:80:ARG:HB2	2:B:145:HIS:CE1	2.45	0.51
8:H:31:ILE:HD11	8:H:65:LEU:HB3	1.93	0.51
16:P:118:GLN:O	16:P:122:LEU:HG	2.11	0.51
29:3:22:VAL:HG12	29:3:90:PHE:CE2	2.46	0.51
30:0:39:G:C2	30:0:444:C:C2	2.99	0.51
30:0:255:A:H2'	30:0:256:C:C6	2.46	0.51
30:0:617:C:H2'	30:0:618:G:O4'	2.11	0.51
30:0:1079:A:N1	30:0:2068:G:O2'	2.43	0.51
30:0:1186:C:N4	30:0:1187:U:C4	2.79	0.51
30:0:1568:G:H2'	30:0:1569:U:O4'	2.10	0.51
30:0:1819:G:H2'	30:0:1820:G:C5'	2.41	0.51
30:0:2526:C:O2'	30:0:2527:U:H5'	2.10	0.51
2:B:71:VAL:HG21	2:B:296:LEU:HB3	1.92	0.50
7:G:20:VAL:O	7:G:24:VAL:HG23	2.11	0.50
9:I:83:GLY:HA3	30:0:1168:C:H5'	1.93	0.50
11:K:97:ILE:HG22	11:K:98:VAL:N	2.25	0.50
22:V:12:THR:HG23	22:V:14:ALA:H	1.76	0.50
23:W:118:LEU:CD1	23:W:153:MET:HE3	2.40	0.50
26:Z:102:THR:HG23	26:Z:105:ARG:HD2	1.93	0.50
30:0:553:G:O4'	30:0:1325:G:H5'	2.10	0.50
30:0:560:U:H2'	30:0:561:G:H8	1.75	0.50
30:0:1226:G:C5	30:0:1227:C:C5	2.99	0.50
30:0:1441:G:O2'	30:0:1442:A:H5'	2.11	0.50
30:0:1511:U:O2'	30:0:1512:G:H5'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1642:A:C8	30:0:1643:C:C5	2.99	0.50
30:0:1796:A:H8	30:0:1796:A:O5'	1.94	0.50
30:0:1805:G:O2'	30:0:1806:G:H5'	2.11	0.50
30:0:2587:OMU:H2'	30:0:2589:U:H5''	1.93	0.50
3:C:127:ARG:HH21	3:C:225:PRO:HG2	1.71	0.50
25:Y:210:GLY:N	30:0:1313:A:H5''	2.27	0.50
30:0:134:U:O2	30:0:145:A:C2	2.63	0.50
30:0:1167:G:N2	30:0:1180:U:C2	2.79	0.50
30:0:2087:C:O2'	30:0:2088:C:H5'	2.11	0.50
30:0:2672:C:C2	30:0:2673:U:C6	3.00	0.50
30:0:2847:G:O2'	30:0:2848:G:H5'	2.11	0.50
2:B:248:ARG:O	2:B:251:VAL:HG22	2.11	0.50
3:C:193:LEU:HA	3:C:211:ASP:O	2.10	0.50
3:C:236:THR:HG22	3:C:239:ALA:CB	2.41	0.50
5:E:7:ILE:HG13	5:E:11:VAL:HB	1.93	0.50
9:I:124:VAL:C	9:I:126:THR:H	2.18	0.50
21:U:35:LYS:HA	30:0:2755:G:OP1	2.11	0.50
27:1:16:HIS:CD2	30:0:470:U:O2'	2.64	0.50
29:3:29:ARG:HA	38:3:9012:HOH:O	2.11	0.50
30:0:523:C:H2'	30:0:524:A:H8	1.76	0.50
30:0:876:A:H2'	30:0:876:A:N3	2.26	0.50
30:0:1087:G:H4'	30:0:1088:A:OP1	2.12	0.50
30:0:1216:G:N2	30:0:1217:G:H1'	2.26	0.50
30:0:1461:U:H2'	30:0:1462:C:C6	2.46	0.50
30:0:1735:C:H2'	30:0:1736:A:H8	1.75	0.50
30:0:2899:A:O2'	30:0:2900:G:H5'	2.12	0.50
12:L:65:ASP:HA	12:L:109:LEU:O	2.11	0.50
17:Q:64:GLU:HG3	17:Q:74:ASP:CG	2.36	0.50
29:3:10:TYR:CE1	30:0:2408:A:H1'	2.46	0.50
29:3:10:TYR:HB2	29:3:17:HIS:HE1	1.76	0.50
30:0:40:C:H2'	30:0:41:G:C8	2.46	0.50
30:0:1181:A:H2'	30:0:1182:C:C5'	2.41	0.50
30:0:1463:U:H2'	30:0:1464:C:C6	2.47	0.50
30:0:1474:C:H6	30:0:1474:C:C5'	2.17	0.50
30:0:1522:A:H2'	30:0:1523:G:H5'	1.92	0.50
30:0:1811:A:C2	30:0:2752:C:H1'	2.46	0.50
30:0:2564:G:OP2	30:0:2565:C:H5''	2.11	0.50
2:B:235:ARG:HH11	30:0:2092:G:P	2.33	0.50
7:G:16:LYS:O	7:G:20:VAL:HG23	2.11	0.50
13:M:71:SER:HB2	13:M:92:THR:CG2	2.35	0.50
17:Q:95:GLU:HA	30:0:949:U:H4'	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:73:U:H2'	30:0:74:G:C8	2.46	0.50
30:0:105:G:O2'	30:0:106:A:H5'	2.11	0.50
30:0:1015:C:O5'	30:0:1015:C:H6	1.94	0.50
30:0:1149:U:C5	30:0:1215:A:C5	3.00	0.50
30:0:1187:U:O2'	30:0:1189:A:H2	1.94	0.50
38:B:8995:HOH:O	30:0:2093:G:H5''	2.11	0.50
8:H:59:GLN:NE2	8:H:129:ARG:HE	2.10	0.50
8:H:157:TYR:C	8:H:157:TYR:CD1	2.89	0.50
14:N:37:ARG:NH1	31:9:6:C:OP1	2.44	0.50
16:P:114:LEU:HD22	16:P:118:GLN:HB3	1.93	0.50
16:P:135:ALA:O	16:P:139:ARG:HG3	2.11	0.50
30:0:119:A:H2'	30:0:120:A:C5'	2.42	0.50
30:0:372:A:C2	30:0:373:G:C4	2.99	0.50
30:0:451:C:O2'	30:0:452:G:H5'	2.12	0.50
30:0:556:C:O2'	30:0:557:C:H5'	2.11	0.50
30:0:738:G:O5'	30:0:738:G:H8	1.95	0.50
30:0:819:A:C4	30:0:821:U:C5	3.00	0.50
30:0:929:A:H5''	38:0:7060:HOH:O	2.11	0.50
30:0:2295:G:N3	30:0:2361:A:C2	2.80	0.50
30:0:2344:G:H2'	30:0:2344:G:N3	2.26	0.50
30:0:2506:A:C1'	38:0:6031:HOH:O	2.58	0.50
1:A:178:LYS:HA	30:0:1653:A:H5'	1.94	0.50
23:W:13:MET:HE2	23:W:18:GLN:HA	1.94	0.50
26:Z:42:TYR:N	30:0:1829:A:H61	2.10	0.50
29:3:3:MET:O	29:3:90:PHE:HA	2.11	0.50
30:0:10:U:O4	30:0:532:A:H8	1.95	0.50
30:0:69:A:H8	30:0:69:A:C5'	2.24	0.50
30:0:79:G:N2	30:0:97:G:H1'	2.26	0.50
30:0:716:G:C6	30:0:717:C:N4	2.80	0.50
30:0:1666:C:H42	30:0:1667:A:N6	2.10	0.50
30:0:1705:C:O2	30:0:2735:U:H5''	2.11	0.50
30:0:2415:A:C2'	30:0:2416:G:H5'	2.40	0.50
30:0:2803:C:H2'	30:0:2804:C:H6	1.77	0.50
30:0:2823:G:O2'	30:0:2824:C:H5'	2.12	0.50
31:9:75:G:N2	31:9:106:U:O2	2.36	0.50
31:9:92:G:H2'	31:9:93:A:H8	1.73	0.50
1:A:100:PRO:HG2	1:A:103:VAL:HG21	1.94	0.50
3:C:22:PHE:HA	3:C:116:ALA:HA	1.94	0.50
13:M:77:HIS:CE1	13:M:86:GLN:HG2	2.47	0.50
13:M:82:ARG:HH22	13:M:85:ARG:NH2	2.08	0.50
14:N:38:LYS:HE2	14:N:107:ASN:HD21	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:56:ILE:O	22:V:60:GLN:HG3	2.12	0.50
29:3:10:TYR:HB2	29:3:17:HIS:CE1	2.47	0.50
29:3:31:THR:HB	29:3:33:MET:HE3	1.93	0.50
30:0:59:A:C5'	38:0:4313:HOH:O	2.60	0.50
30:0:74:G:H1	30:0:103:C:N4	2.10	0.50
30:0:282:C:O2'	30:0:283:U:C4'	2.60	0.50
30:0:764:C:H2'	30:0:765:G:O4'	2.12	0.50
30:0:1878:G:C4'	38:0:6097:HOH:O	2.60	0.50
31:9:23:U:H2'	31:9:23:U:O2	2.12	0.50
1:A:141:PRO:HG2	30:0:1855:G:O6	2.12	0.50
2:B:18:ARG:HG3	2:B:256:GLN:HG3	1.93	0.50
3:C:101:ASP:HB2	30:0:750:A:O3'	2.12	0.50
12:L:24:ALA:HB2	12:L:30:ARG:HE	1.76	0.50
13:M:145:ASP:HB2	38:M:8865:HOH:O	2.11	0.50
18:R:4:TYR:CE1	18:R:17:MET:HE2	2.47	0.50
20:T:71:VAL:HG11	20:T:90:PRO:CB	2.38	0.50
23:W:6:GLN:CB	23:W:26:ILE:HD11	2.40	0.50
23:W:130:HIS:O	23:W:136:GLY:HA3	2.12	0.50
24:X:26:ALA:HB2	24:X:63:ARG:HA	1.93	0.50
29:3:3:MET:SD	29:3:88:LEU:HD23	2.52	0.50
30:0:561:G:C2	30:0:562:A:C8	3.00	0.50
30:0:814:G:H2'	30:0:815:U:H6	1.77	0.50
30:0:2253:G:O2'	30:0:2254:G:H5'	2.11	0.50
30:0:2465:A:H3'	38:0:3637:HOH:O	2.12	0.50
31:9:42:C:H5'	31:9:43:G:OP2	2.12	0.50
1:A:179:MET:HA	1:A:179:MET:HE3	1.95	0.49
2:B:66:GLU:OE1	2:B:328:ARG:HD2	2.12	0.49
4:D:58:VAL:CG1	4:D:60:GLU:HG2	2.41	0.49
13:M:159:VAL:CG1	33:M:8818:CL:CL	2.95	0.49
16:P:87:ARG:HG2	38:0:5919:HOH:O	2.10	0.49
30:0:47:G:N3	30:0:114:A:C2	2.80	0.49
30:0:952:G:N3	30:0:2302:A:H2'	2.26	0.49
30:0:1165:G:H21	30:0:1173:A:H5'	1.74	0.49
30:0:1268:C:H2'	30:0:1269:G:C8	2.46	0.49
30:0:1393:A:H2'	30:0:1394:C:C6	2.47	0.49
30:0:1601:G:H1'	38:0:9891:HOH:O	2.11	0.49
30:0:1933:G:O2'	30:0:1934:A:H5'	2.12	0.49
30:0:2854:A:C6	30:0:2905:A:C6	3.00	0.49
31:9:28:U:O2	31:9:57:A:N6	2.44	0.49
31:9:39:U:H1'	31:9:44:A:H61	1.77	0.49
4:D:35:ALA:HB2	38:D:5576:HOH:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:32:ALA:HB3	8:H:69:ARG:HH12	1.77	0.49
16:P:98:ILE:HD12	16:P:102:ARG:NE	2.27	0.49
18:R:18:LEU:O	18:R:142:ASP:HA	2.12	0.49
30:0:134:U:C2	30:0:145:A:C2	2.99	0.49
30:0:589:U:H2'	30:0:590:A:H8	1.76	0.49
30:0:873:G:N2	38:0:9173:HOH:O	2.43	0.49
30:0:1226:G:H2'	30:0:1227:C:C6	2.44	0.49
30:0:1662:C:O5'	30:0:1662:C:H6	1.94	0.49
30:0:1902:G:N2	30:0:1936:C:C2	2.80	0.49
31:9:55:U:H4'	31:9:56:A:H8	1.71	0.49
10:J:131:THR:HG22	10:J:134:GLU:H	1.77	0.49
11:K:34:VAL:HB	38:K:7169:HOH:O	2.12	0.49
25:Y:212:ARG:HB2	30:0:1315:G:C4	2.47	0.49
30:0:316:A:N3	30:0:336:G:O2'	2.41	0.49
30:0:400:C:H2'	30:0:401:C:C6	2.47	0.49
30:0:1194:A:C2	30:0:1206:U:H1'	2.47	0.49
30:0:1787:C:C4'	30:0:2883:A:O4'	2.59	0.49
30:0:1800:G:H2'	30:0:1801:A:H8	1.77	0.49
30:0:2291:A:H2'	30:0:2291:A:N3	2.28	0.49
30:0:2617:G:C2	30:0:2618:G:C8	3.00	0.49
30:0:2846:C:H2'	30:0:2847:G:H8	1.77	0.49
1:A:47:HIS:CD2	30:0:1654:U:C2'	2.92	0.49
2:B:44:TYR:OH	2:B:148:PRO:HG3	2.11	0.49
2:B:215:VAL:O	2:B:219:GLY:HA2	2.13	0.49
6:F:110:ASP:O	6:F:114:LYS:HG3	2.12	0.49
9:I:93:ALA:HB3	9:I:132:VAL:HG22	1.95	0.49
17:Q:66:LYS:HB2	17:Q:70:ALA:O	2.13	0.49
25:Y:115:ARG:NH2	30:0:1266:U:H4'	2.27	0.49
26:Z:60:ASP:HB3	26:Z:69:ASP:HB3	1.92	0.49
29:3:79:LEU:CD1	30:0:2456:A:H2	2.25	0.49
29:3:79:LEU:HD22	38:0:7515:HOH:O	2.13	0.49
30:0:36:C:C2	30:0:447:A:C2	3.00	0.49
30:0:814:G:H2'	30:0:815:U:C6	2.47	0.49
30:0:816:G:H5'	30:0:1598:A:H4'	1.94	0.49
30:0:1206:U:C5'	30:0:1206:U:H6	2.21	0.49
30:0:1255:A:H1'	38:0:7741:HOH:O	2.11	0.49
30:0:1339:G:C6	30:0:1340:G:N1	2.81	0.49
30:0:1381:A:N3	30:0:1382:G:H1'	2.28	0.49
30:0:1947:G:N2	30:0:1966:U:N3	2.60	0.49
30:0:2133:U:H4'	30:0:2134:G:H5'	1.93	0.49
30:0:2632:G:C6	30:0:2633:A:N6	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2632:G:H2'	30:0:2633:A:C8	2.46	0.49
2:B:304:PRO:HD2	2:B:307:ARG:HE	1.78	0.49
14:N:58:LEU:N	14:N:58:LEU:HD12	2.27	0.49
30:0:494:C:H1'	30:0:498:A:N6	2.27	0.49
30:0:1370:G:H5''	38:0:5497:HOH:O	2.12	0.49
30:0:1555:G:H4'	30:0:1630:A:C2	2.47	0.49
30:0:1559:A:HO2'	30:0:1561:U:H5	1.60	0.49
30:0:1733:A:C5	30:0:1734:C:C2	3.00	0.49
30:0:1787:C:O4'	30:0:2883:A:H1'	2.11	0.49
30:0:1878:G:O2'	30:0:1879:U:H6	1.90	0.49
30:0:2118:A:H5'	38:0:3996:HOH:O	2.13	0.49
30:0:2366:C:O5'	30:0:2366:C:H6	1.95	0.49
8:H:27:PRO:HD3	8:H:123:ILE:CG2	2.43	0.49
10:J:130:VAL:HG12	10:J:131:THR:H	1.78	0.49
14:N:37:ARG:HG3	14:N:37:ARG:HH11	1.77	0.49
20:T:107:LYS:HD2	30:0:97:G:C2	2.47	0.49
30:0:29:C:O2'	30:0:30:U:H5'	2.12	0.49
30:0:1174:A:C5	30:0:1201:C:H4'	2.47	0.49
30:0:1189:A:O2'	30:0:1208:C:H2'	2.12	0.49
30:0:1517:C:O2	30:0:1670:A:C2	2.66	0.49
30:0:1626:A:O2'	30:0:1627:G:H5'	2.13	0.49
30:0:1682:A:O2'	30:0:1683:G:H5''	2.12	0.49
30:0:1871:U:O4'	30:0:1873:G:C8	2.66	0.49
30:0:2335:C:C2	30:0:2350:G:C2	3.01	0.49
2:B:307:ARG:HD2	38:B:9123:HOH:O	2.12	0.49
6:F:110:ASP:O	6:F:114:LYS:N	2.44	0.49
18:R:71:LYS:HE2	30:0:2831:C:O3'	2.13	0.49
21:U:9:CYS:HB2	38:U:6796:HOH:O	2.11	0.49
29:3:12:PRO:HB3	30:0:2382:A:O2'	2.12	0.49
29:3:33:MET:HG2	30:0:1922:A:C2'	2.42	0.49
30:0:285:A:H2'	30:0:286:U:O4'	2.13	0.49
30:0:316:A:H1'	30:0:336:G:N3	2.27	0.49
30:0:549:A:C6	30:0:550:C:C4	3.00	0.49
30:0:862:U:H2'	30:0:863:G:H8	1.77	0.49
30:0:889:C:H4'	38:0:6368:HOH:O	2.13	0.49
30:0:1226:G:N3	30:0:1227:C:C6	2.81	0.49
30:0:2478:U:H2'	30:0:2479:A:C8	2.48	0.49
1:A:109:GLU:HG2	1:A:116:GLY:N	2.25	0.49
2:B:98:THR:HG22	2:B:99:GLU:N	2.28	0.49
2:B:162:MET:CE	2:B:308:LEU:HD21	2.42	0.49
3:C:233:THR:HG22	3:C:234:VAL:N	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:29:SER:HA	8:H:62:HIS:HD2	1.77	0.49
25:Y:189:ASN:C	25:Y:189:ASN:HD22	2.21	0.49
26:Z:47:ARG:HH22	30:0:1771:U:H1'	1.77	0.49
30:0:447:A:O2'	30:0:448:G:H5'	2.13	0.49
30:0:1183:C:N4	30:0:1184:C:N4	2.60	0.49
30:0:1583:U:O2'	30:0:1584:C:H5'	2.13	0.49
30:0:1706:G:C5	30:0:1707:G:C6	3.00	0.49
30:0:1760:G:H5'	30:0:1818:C:O2'	2.12	0.49
30:0:1921:A:C6	30:0:1922:A:C2	3.00	0.49
30:0:2326:C:H4'	30:0:2412:G:H4'	1.94	0.49
30:0:2826:G:H1'	30:0:2914:A:N6	2.28	0.49
31:9:110:G:N2	31:9:111:U:H1'	2.28	0.49
1:A:36:ASP:HB2	1:A:85:SER:H	1.77	0.49
14:N:25:ARG:HB3	30:0:2415:A:C2	2.47	0.49
21:U:20:MET:HE2	21:U:30:HIS:NE2	2.27	0.49
29:3:1:MET:HG2	29:3:87:ARG:O	2.11	0.49
30:0:717:C:H2'	30:0:718:C:H6	1.78	0.49
30:0:731:U:O2'	30:0:732:C:H5'	2.13	0.49
30:0:1116:U:C2	30:0:1246:A:N6	2.81	0.49
30:0:1343:C:H2'	30:0:1344:G:O5'	2.12	0.49
30:0:1453:G:C2	30:0:1675:C:C2	3.00	0.49
30:0:2103:A:N3	30:0:2103:A:H2'	2.28	0.49
30:0:2269:C:H2'	30:0:2270:G:O4'	2.12	0.49
31:9:105:A:H2'	31:9:106:U:O4'	2.12	0.49
14:N:178:THR:O	14:N:181:ASP:HB3	2.13	0.49
20:T:69:LYS:O	20:T:71:VAL:HG23	2.13	0.49
27:1:21:ARG:HD2	27:1:39:PHE:HB2	1.95	0.49
30:0:271:C:N4	30:0:378:A:H2	2.01	0.49
30:0:1119:G:H22	30:0:1246:A:H2	1.46	0.49
30:0:1351:G:H1'	38:0:4648:HOH:O	2.13	0.49
30:0:1607:A:C4	30:0:1608:G:C8	3.01	0.49
30:0:1615:A:H5'	38:0:4169:HOH:O	2.12	0.49
30:0:2497:A:C2	30:0:2524:G:C2	3.01	0.49
30:0:2536:C:H6	38:0:4998:HOH:O	1.95	0.49
31:9:8:G:C6	31:9:9:C:C4	3.00	0.49
31:9:60:C:O2'	31:9:61:C:H5'	2.13	0.49
3:C:173:LYS:HE3	30:0:1311:G:O6	2.12	0.48
4:D:25:MET:HE1	4:D:37:ALA:O	2.12	0.48
4:D:92:GLU:HB2	38:D:3862:HOH:O	2.13	0.48
6:F:63:ILE:HB	6:F:64:PRO:CD	2.37	0.48
13:M:52:GLN:OE1	13:M:116:ASN:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:55:GLN:CD	30:0:1446:U:H2'	2.37	0.48
25:Y:137:LYS:HD2	38:0:7590:HOH:O	2.11	0.48
29:3:88:LEU:HB3	29:3:90:PHE:CE1	2.48	0.48
30:0:191:A:H2'	30:0:237:G:O6	2.12	0.48
30:0:419:A:H1'	30:0:1921:A:C2	2.48	0.48
30:0:788:A:H4'	38:0:7005:HOH:O	2.12	0.48
30:0:1063:G:H4'	30:0:2307:A:H1'	1.95	0.48
30:0:1240:G:H1'	38:0:9360:HOH:O	2.12	0.48
30:0:1586:G:C2'	30:0:1587:U:H5'	2.43	0.48
30:0:1644:C:C2	30:0:1645:U:C5	3.01	0.48
30:0:2297:U:H2'	30:0:2298:C:H6	1.78	0.48
30:0:2639:G:C5	30:0:2640:U:C5	3.01	0.48
4:D:22:VAL:HG22	4:D:74:THR:HG22	1.95	0.48
11:K:98:VAL:HG11	11:K:102:GLU:HA	1.94	0.48
13:M:134:ILE:CG2	13:M:141:ILE:HD13	2.36	0.48
20:T:28:SER:O	20:T:32:ARG:HG3	2.14	0.48
21:U:19:THR:HG22	21:U:20:MET:N	2.28	0.48
30:0:106:A:C6	30:0:107:U:C4	3.00	0.48
30:0:1066:U:H2'	30:0:1067:A:C8	2.48	0.48
30:0:1765:G:O2'	30:0:1766:U:H5'	2.12	0.48
30:0:1916:C:O2'	30:0:1917:G:H5'	2.14	0.48
30:0:2646:G:C4	30:0:2647:C:C5	3.02	0.48
30:0:2713:G:O2'	30:0:2714:U:H5'	2.12	0.48
30:0:2864:U:O2'	30:0:2865:G:H5'	2.14	0.48
31:9:2:U:H4'	38:9:9107:HOH:O	2.13	0.48
31:9:19:G:C2	31:9:20:G:C8	3.00	0.48
8:H:52:LEU:HD13	8:H:153:PHE:HB3	1.95	0.48
16:P:124:ASP:O	30:0:801:U:H4'	2.13	0.48
30:0:334:G:C5	30:0:335:U:C5	3.00	0.48
30:0:595:U:O4'	33:0:8817:CL:CL	2.69	0.48
30:0:681:G:N3	30:0:681:G:H5'	2.28	0.48
30:0:1832:G:C2	30:0:1833:U:C6	3.00	0.48
30:0:1883:U:H2'	30:0:1884:G:H5'	1.94	0.48
30:0:2480:G:O2'	30:0:2481:G:H5'	2.13	0.48
30:0:2526:C:H3'	30:0:2526:C:C6	2.47	0.48
30:0:2827:A:C2	30:0:2914:A:C2	3.01	0.48
30:0:2898:G:H1'	38:0:7555:HOH:O	2.13	0.48
31:9:3:A:H2	31:9:21:G:N3	2.12	0.48
2:B:152:PRO:HD2	38:B:9102:HOH:O	2.12	0.48
8:H:35:LYS:HE3	30:0:968:G:H1'	1.95	0.48
13:M:84:LYS:HA	29:3:46:ILE:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:31:ILE:HG12	16:P:43:LEU:HD13	1.96	0.48
26:Z:42:TYR:H	30:0:1829:A:H61	1.61	0.48
30:0:120:A:H2'	30:0:120:A:N3	2.29	0.48
30:0:1015:C:H2'	30:0:1016:U:C6	2.48	0.48
30:0:1557:G:H2'	30:0:1558:C:H6	1.78	0.48
30:0:1632:A:C3'	30:0:1633:C:H5'	2.43	0.48
30:0:2700:G:H2'	30:0:2701:G:C5'	2.43	0.48
4:D:37:ALA:O	4:D:40:ILE:HG12	2.13	0.48
11:K:43:ARG:NH1	30:0:2712:G:OP1	2.46	0.48
12:L:117:GLU:HG3	12:L:117:GLU:O	2.13	0.48
14:N:78:MET:HB2	14:N:79:PRO:HD3	1.95	0.48
18:R:132:ARG:HG2	18:R:133:ALA:N	2.27	0.48
19:S:6:LYS:HB2	19:S:27:ALA:O	2.13	0.48
20:T:27:LEU:HB2	20:T:32:ARG:HG2	1.95	0.48
29:3:64:LYS:HE2	38:0:7638:HOH:O	2.12	0.48
30:0:100:C:C4	30:0:101:C:C5	3.01	0.48
30:0:222:A:H2'	30:0:223:G:O4'	2.13	0.48
30:0:677:C:H2'	30:0:678:G:H8	1.77	0.48
30:0:707:C:C2	30:0:708:A:C8	3.02	0.48
30:0:1434:A:O2'	30:0:1435:U:H6	1.92	0.48
30:0:1496:A:H5'	30:0:1572:A:H1'	1.94	0.48
30:0:1634:G:H2'	30:0:1635:U:H6	1.76	0.48
30:0:2255:A:C2	30:0:2256:G:C4	3.02	0.48
30:0:2505:G:C2'	30:0:2506:A:C5'	2.91	0.48
30:0:2672:C:H2'	30:0:2673:U:O4'	2.14	0.48
30:0:2755:G:H1'	38:0:4651:HOH:O	2.13	0.48
30:0:2772:G:O2'	30:0:2773:G:H5'	2.13	0.48
30:0:2854:A:H2'	30:0:2855:G:H8	1.78	0.48
30:0:2860:G:H2'	30:0:2861:G:C8	2.48	0.48
2:B:36:PRO:HG3	2:B:169:GLY:H	1.77	0.48
4:D:51:ARG:HH11	4:D:68:PRO:HB3	1.78	0.48
5:E:139:GLU:OE2	30:0:2781:U:H1'	2.13	0.48
10:J:60:ARG:HD3	10:J:71:TYR:CE1	2.47	0.48
15:O:88:LYS:HB3	38:O:7061:HOH:O	2.13	0.48
29:3:43:ASN:HB2	29:3:52:PHE:CD1	2.48	0.48
30:0:200:C:H6	38:0:3433:HOH:O	1.96	0.48
30:0:611:U:H2'	30:0:612:U:C6	2.48	0.48
30:0:1182:C:C1'	30:0:1192:A:H8	2.26	0.48
30:0:1207:A:OP2	30:0:1208:C:H5	1.96	0.48
30:0:1970:G:H1'	38:0:3662:HOH:O	2.13	0.48
30:0:1970:G:H4'	30:0:1971:G:C5'	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2133:U:H4'	30:0:2134:G:C5'	2.44	0.48
30:0:2598:U:O2	30:0:2600:A:C8	2.66	0.48
30:0:2617:G:H4'	38:0:4487:HOH:O	2.13	0.48
5:E:11:VAL:HG12	5:E:12:ASP:N	2.28	0.48
5:E:80:TRP:O	5:E:134:SER:HA	2.12	0.48
6:F:107:ASP:O	6:F:111:ILE:HG13	2.13	0.48
13:M:139:PRO:HA	13:M:142:GLN:HB2	1.95	0.48
16:P:94:TRP:CZ2	16:P:98:ILE:HG13	2.49	0.48
17:Q:28:ARG:HG2	38:9:9083:HOH:O	2.12	0.48
18:R:138:SER:HB2	38:0:5570:HOH:O	2.14	0.48
23:W:26:ILE:HB	38:W:5420:HOH:O	2.14	0.48
27:1:25:LYS:CD	28:2:49:GLU:H	2.25	0.48
30:0:31:C:H2'	38:0:7668:HOH:O	2.13	0.48
30:0:627:G:H2'	30:0:2071:C:C4	2.49	0.48
30:0:705:C:O2	30:0:705:C:C2'	2.62	0.48
30:0:1224:G:H2'	30:0:1225:C:C6	2.48	0.48
30:0:1278:A:O2'	30:0:1279:U:C2	2.65	0.48
30:0:1520:G:H2'	30:0:1521:C:C6	2.49	0.48
30:0:1878:G:C2	30:0:1879:U:C2	3.02	0.48
30:0:1908:G:N1	30:0:1930:A:OP2	2.46	0.48
30:0:2569:A:H8	30:0:2569:A:O5'	1.96	0.48
30:0:2707:C:O2	30:0:2707:C:C2'	2.59	0.48
1:A:162:GLY:N	26:Z:91:GLY:HA2	2.29	0.48
9:I:133:THR:HG22	9:I:134:ILE:N	2.28	0.48
16:P:11:ALA:HB1	16:P:16:VAL:O	2.14	0.48
23:W:117:ARG:HH22	30:0:1264:U:P	2.36	0.48
27:1:1:THR:HB	38:1:2852:HOH:O	2.12	0.48
28:2:10:ARG:NH2	30:0:121:U:OP2	2.44	0.48
29:3:25:VAL:HA	38:3:9036:HOH:O	2.12	0.48
30:0:99:A:C8	30:0:100:C:C6	3.02	0.48
30:0:808:A:C5	30:0:809:G:H1'	2.48	0.48
30:0:858:U:H2'	30:0:859:C:C6	2.47	0.48
30:0:1023:C:O2'	30:0:1024:G:H5'	2.14	0.48
30:0:1029:U:O2'	30:0:1273:C:OP1	2.27	0.48
30:0:1063:G:H8	38:0:9856:HOH:O	1.96	0.48
30:0:2354:A:C2	30:0:2367:A:C8	3.02	0.48
30:0:2717:C:H2'	30:0:2718:C:H5'	1.93	0.48
1:A:71:PRO:HG2	1:A:91:GLY:HA2	1.95	0.48
4:D:51:ARG:NH1	4:D:68:PRO:HB3	2.28	0.48
25:Y:235:GLU:CD	25:Y:235:GLU:N	2.72	0.48
30:0:69:A:C2'	30:0:70:A:OP2	2.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:432:G:H5''	38:0:6860:HOH:O	2.12	0.48
30:0:763:C:O2'	30:0:764:C:H5'	2.14	0.48
30:0:842:C:H4'	38:0:3427:HOH:O	2.13	0.48
30:0:920:C:C4'	30:0:921:G:C2	2.95	0.48
30:0:1177:A:H2'	30:0:1177:A:N3	2.28	0.48
30:0:1204:C:H2'	30:0:1205:U:O4'	2.14	0.48
30:0:2254:G:C2	30:0:2255:A:C8	3.01	0.48
30:0:2281:C:H5	38:0:3756:HOH:O	1.97	0.48
30:0:2505:G:H2'	30:0:2506:A:C5'	2.43	0.48
30:0:2587:OMU:H5	38:0:7464:HOH:O	2.13	0.48
30:0:2777:G:O2'	30:0:2778:A:H5'	2.13	0.48
31:9:39:U:C2'	31:9:40:C:OP1	2.62	0.48
1:A:161:GLY:HA3	38:Z:8705:HOH:O	2.13	0.48
1:A:217:ARG:HG2	1:A:229:ALA:HB2	1.95	0.48
2:B:226:LYS:HG2	2:B:230:GLN:HE21	1.78	0.48
6:F:58:GLU:HA	6:F:61:MET:SD	2.54	0.48
11:K:1:MET:N	30:0:2686:C:O2'	2.38	0.48
13:M:9:ARG:HD2	30:0:380:A:OP2	2.14	0.48
14:N:4:PRO:HG3	31:9:69:U:OP1	2.13	0.48
29:3:51:LYS:HG3	29:3:52:PHE:HD2	1.76	0.48
29:3:83:TRP:HB2	38:0:5759:HOH:O	2.14	0.48
30:0:202:U:C4	30:0:203:G:C6	3.01	0.48
30:0:1186:C:C4	30:0:1187:U:C4	3.02	0.48
30:0:1626:A:H2'	30:0:1627:G:O4'	2.14	0.48
2:B:162:MET:HE3	2:B:308:LEU:HD21	1.95	0.47
9:I:69:PRO:HA	30:0:1164:U:OP1	2.14	0.47
18:R:15:LYS:HE3	38:R:8976:HOH:O	2.14	0.47
29:3:50:GLY:CA	30:0:170:U:H1'	2.43	0.47
30:0:151:A:H2'	30:0:152:A:O4'	2.14	0.47
30:0:625:U:H5''	30:0:1044:C:H42	1.71	0.47
30:0:870:G:H2'	30:0:871:G:C5'	2.34	0.47
30:0:1188:A:C5	30:0:1189:A:C2	3.02	0.47
30:0:1337:G:C6	30:0:1338:U:C4	3.01	0.47
30:0:1337:G:C5	30:0:1338:U:C5	3.02	0.47
30:0:1471:A:H2'	30:0:1472:C:C6	2.48	0.47
30:0:1745:G:H5'	38:0:4312:HOH:O	2.14	0.47
30:0:2458:U:H3'	38:0:3241:HOH:O	2.13	0.47
30:0:2474:A:H5'	30:0:2476:C:O5'	2.14	0.47
30:0:2474:A:N7	30:0:2621:PSU:H4'	2.29	0.47
30:0:2598:U:O2	30:0:2600:A:H8	1.96	0.47
30:0:2830:U:H2'	30:0:2831:C:H6	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2848:G:O4'	30:0:2906:A:C2	2.66	0.47
1:A:27:LEU:HD21	1:A:55:VAL:CG2	2.44	0.47
2:B:84:LEU:O	2:B:99:GLU:HA	2.14	0.47
18:R:39:THR:HB	18:R:42:GLU:CD	2.39	0.47
21:U:50:GLU:OE1	30:0:2866:U:H2'	2.13	0.47
23:W:13:MET:HE2	23:W:18:GLN:N	2.29	0.47
30:0:373:G:O2'	30:0:374:U:H5'	2.14	0.47
30:0:968:G:O2'	30:0:969:G:H5'	2.14	0.47
30:0:2385:G:H2'	30:0:2386:U:C6	2.49	0.47
30:0:2855:G:C2	30:0:2904:U:N3	2.82	0.47
3:C:162:VAL:O	3:C:162:VAL:HG13	2.13	0.47
11:K:132:VAL:HG11	21:U:22:VAL:HG22	1.96	0.47
25:Y:234:VAL:HG12	25:Y:235:GLU:N	2.28	0.47
26:Z:40:ALA:HA	30:0:1773:G:H8	1.79	0.47
30:0:361:C:H2'	30:0:362:G:O4'	2.13	0.47
30:0:834:G:H3'	30:0:835:U:H4'	1.97	0.47
30:0:1947:G:OP1	30:0:1971:G:N7	2.47	0.47
30:0:2087:C:H2'	30:0:2088:C:H6	1.80	0.47
1:A:70:ALA:HB1	26:Z:89:THR:HG21	1.97	0.47
2:B:74:ILE:HD13	2:B:309:VAL:HG21	1.95	0.47
2:B:201:ASP:CB	2:B:312:ARG:HD2	2.42	0.47
8:H:88:MET:HA	8:H:139:ALA:HA	1.96	0.47
21:U:56:ARG:HB2	30:0:2890:A:N7	2.29	0.47
22:V:12:THR:CG2	22:V:15:GLU:HG3	2.40	0.47
24:X:85:VAL:HG12	24:X:86:GLU:N	2.29	0.47
30:0:407:A:H5'	38:0:6000:HOH:O	2.14	0.47
30:0:681:G:N3	30:0:681:G:H2'	2.30	0.47
30:0:699:C:C2	30:0:744:G:C2	3.03	0.47
30:0:965:A:H5'	30:0:966:U:OP2	2.14	0.47
30:0:1275:C:H2'	30:0:1276:U:H5'	1.96	0.47
30:0:1389:G:N2	30:0:1391:G:H3'	2.29	0.47
30:0:1619:G:H2'	30:0:1620:C:C6	2.49	0.47
30:0:2379:G:H4'	30:0:2380:A:O5'	2.13	0.47
30:0:2719:A:H2'	30:0:2720:C:C5'	2.44	0.47
30:0:2724:U:O5'	30:0:2724:U:H6	1.96	0.47
30:0:2857:C:H1'	38:0:5328:HOH:O	2.15	0.47
8:H:59:GLN:HE22	8:H:96:GLN:HG2	1.79	0.47
11:K:118:ALA:HA	11:K:125:ALA:HB2	1.96	0.47
17:Q:11:ARG:HD3	38:0:6238:HOH:O	2.13	0.47
28:2:15:ASP:O	28:2:18:ASN:HB2	2.15	0.47
29:3:68:LYS:HG2	29:3:77:ALA:CB	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:88:LEU:CD2	33:3:8804:CL:CL	2.86	0.47
30:0:287:C:H6	30:0:287:C:O5'	1.97	0.47
30:0:371:U:C4	30:0:372:A:N7	2.83	0.47
30:0:699:C:C6	30:0:744:G:N3	2.82	0.47
30:0:820:G:O2'	30:0:856:G:H4'	2.14	0.47
30:0:1210:G:N2	30:0:1211:G:H1'	2.29	0.47
30:0:1226:G:C4	30:0:1227:C:C6	3.02	0.47
30:0:1477:C:H4'	30:0:1868:G:OP1	2.15	0.47
30:0:1503:U:H2'	30:0:1504:A:C5'	2.45	0.47
30:0:1733:A:N7	30:0:1734:C:C4	2.82	0.47
30:0:2265:U:H2'	30:0:2266:A:H8	1.80	0.47
30:0:2781:U:C2'	30:0:2782:G:H5'	2.45	0.47
31:9:39:U:H3	31:9:42:C:H5''	1.79	0.47
31:9:73:A:H61	31:9:108:C:N4	2.13	0.47
1:A:135:VAL:HA	1:A:150:PRO:HD3	1.96	0.47
2:B:234:ARG:NH2	30:0:2039:A:OP2	2.47	0.47
7:G:64:ASN:N	7:G:64:ASN:ND2	2.62	0.47
11:K:97:ILE:HG22	11:K:98:VAL:H	1.79	0.47
13:M:68:ARG:HD2	30:0:1469:C:OP2	2.15	0.47
20:T:71:VAL:CG1	20:T:90:PRO:HB3	2.40	0.47
26:Z:34:SER:CA	30:0:797:A:H4'	2.44	0.47
29:3:9:THR:HG23	29:3:20:HIS:CE1	2.49	0.47
30:0:625:U:C5'	30:0:1044:C:N4	2.71	0.47
30:0:724:G:O2'	30:0:725:C:H5'	2.15	0.47
30:0:731:U:H2'	30:0:732:C:C6	2.50	0.47
30:0:1667:A:H5'	30:0:1667:A:C8	2.50	0.47
30:0:1760:G:C5	30:0:1761:U:C4	3.03	0.47
30:0:2375:A:H2'	30:0:2376:C:C6	2.50	0.47
30:0:2597:U:C2'	30:0:2598:U:H5'	2.45	0.47
31:9:5:G:C2'	31:9:6:C:H5'	2.45	0.47
1:A:94:LEU:HG	1:A:99:ILE:CD1	2.44	0.47
2:B:171:VAL:O	2:B:175:LEU:HB2	2.15	0.47
3:C:180:SER:HB2	38:C:8643:HOH:O	2.14	0.47
4:D:59:GLY:HA3	38:D:4886:HOH:O	2.14	0.47
8:H:6:ALA:HB3	30:0:2521:A:OP2	2.14	0.47
8:H:123:ILE:HD12	8:H:123:ILE:N	2.30	0.47
10:J:39:VAL:CG2	10:J:107:ASN:HA	2.44	0.47
13:M:15:PRO:HA	13:M:20:LEU:HD23	1.95	0.47
14:N:71:TRP:HZ2	38:N:8833:HOH:O	1.97	0.47
15:O:42:GLU:HB2	38:0:3736:HOH:O	2.15	0.47
16:P:13:VAL:HG13	16:P:14:LEU:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:41:ARG:NH1	20:T:42:VAL:O	2.47	0.47
20:T:51:LEU:HD11	20:T:97:ARG:HB2	1.97	0.47
23:W:21:LEU:HD21	23:W:48:VAL:HG11	1.96	0.47
23:W:77:ALA:HB3	38:W:5763:HOH:O	2.14	0.47
23:W:129:LYS:HE3	31:9:87:U:H2'	1.97	0.47
25:Y:151:SER:HB3	25:Y:154:ARG:HB3	1.97	0.47
30:0:432:G:H2'	30:0:433:C:H6	1.80	0.47
30:0:711:G:O2'	30:0:712:C:H5'	2.15	0.47
30:0:790:A:H1'	30:0:1710:A:H2'	1.97	0.47
30:0:1181:A:N1	30:0:1192:A:O2'	2.45	0.47
30:0:1210:G:O2'	30:0:1211:G:H5'	2.14	0.47
30:0:1333:U:H2'	30:0:1334:C:H6	1.80	0.47
30:0:1858:A:H2'	30:0:1859:A:C8	2.50	0.47
30:0:1988:C:H2'	30:0:1989:G:O4'	2.15	0.47
30:0:2509:A:H2'	30:0:2510:C:O4'	2.14	0.47
30:0:2727:A:C2'	30:0:2728:C:H5'	2.45	0.47
30:0:2781:U:H2'	30:0:2782:G:H5'	1.95	0.47
30:0:2837:U:H2'	38:0:6824:HOH:O	2.15	0.47
30:0:2858:U:H2'	30:0:2859:C:C6	2.49	0.47
30:0:2860:G:H2'	30:0:2861:G:H8	1.80	0.47
1:A:105:VAL:CG1	1:A:154:ALA:HB1	2.44	0.47
3:C:28:SER:HB2	38:C:8659:HOH:O	2.14	0.47
14:N:27:LEU:HD22	14:N:50:LEU:HD13	1.97	0.47
16:P:3:LEU:HA	16:P:6:GLN:OE1	2.14	0.47
19:S:57:THR:C	19:S:59:ASP:H	2.21	0.47
22:V:64:GLY:O	22:V:65:ASP:HB2	2.15	0.47
23:W:128:VAL:HG22	30:0:1098:A:OP1	2.15	0.47
30:0:800:G:H8	30:0:800:G:O5'	1.98	0.47
30:0:835:U:H5''	38:0:9381:HOH:O	2.14	0.47
30:0:1168:C:H2'	30:0:1169:U:H5'	1.96	0.47
30:0:1446:U:H4'	30:0:1447:U:OP2	2.14	0.47
30:0:1857:A:N6	30:0:2247:C:H1'	2.30	0.47
30:0:2059:U:H1'	38:0:4439:HOH:O	2.14	0.47
30:0:2460:A:C2	30:0:2461:U:C2	3.02	0.47
31:9:22:G:N7	31:9:55:U:C6	2.82	0.47
1:A:171:LYS:HB2	30:0:820:G:C5	2.50	0.47
2:B:212:GLN:HB2	2:B:257:THR:OG1	2.15	0.47
6:F:21:GLU:O	6:F:24:ARG:HG2	2.15	0.47
16:P:1:THR:O	30:0:1396:C:H1'	2.15	0.47
18:R:69:LYS:HB2	18:R:72:VAL:HG23	1.97	0.47
22:V:1:THR:HG23	22:V:2:VAL:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:72:PRO:HG2	38:W:5763:HOH:O	2.15	0.47
30:0:292:G:H2'	30:0:358:G:N2	2.30	0.47
30:0:561:G:H2'	30:0:562:A:H8	1.79	0.47
30:0:1889:C:O2'	30:0:1890:U:H5'	2.15	0.47
30:0:2490:A:H5''	38:0:7023:HOH:O	2.15	0.47
30:0:2858:U:H2'	30:0:2859:C:H6	1.80	0.47
30:0:2878:U:H2'	30:0:2879:A:O4'	2.14	0.47
13:M:193:LYS:HB3	30:0:392:U:C5'	2.45	0.47
14:N:170:GLU:O	14:N:174:GLU:HG3	2.14	0.47
16:P:41:ARG:NH2	30:0:1500:U:OP2	2.47	0.47
17:Q:34:ASP:O	17:Q:37:GLU:HB2	2.15	0.47
23:W:125:HIS:CE1	30:0:1097:A:C5'	2.95	0.47
30:0:249:G:O2'	30:0:250:C:H5'	2.15	0.47
30:0:1056:U:H2'	30:0:1057:A:O4'	2.14	0.47
30:0:1806:G:C4	30:0:1807:U:C6	3.03	0.47
30:0:1928:C:O2'	30:0:1929:G:H5'	2.15	0.47
30:0:2301:A:H5''	30:0:2302:A:H5'	1.96	0.47
4:D:22:VAL:HG21	30:0:2348:C:C5'	2.45	0.46
13:M:184:ARG:HG3	13:M:185:PRO:HA	1.97	0.46
16:P:13:VAL:HG13	16:P:14:LEU:H	1.80	0.46
19:S:6:LYS:HE3	19:S:29:ASP:HA	1.97	0.46
24:X:30:MET:HG2	30:0:1384:C:H5'	1.96	0.46
30:0:40:C:H5'	38:0:3836:HOH:O	2.14	0.46
30:0:137:U:OP1	30:0:259:G:O2'	2.33	0.46
30:0:589:U:H2'	30:0:590:A:C8	2.50	0.46
30:0:737:A:H2'	30:0:738:G:C8	2.49	0.46
30:0:806:A:H2'	30:0:807:A:O4'	2.15	0.46
30:0:1159:G:H1	30:0:1208:C:H42	1.63	0.46
30:0:1177:A:N1	30:0:1178:G:C4	2.82	0.46
30:0:1760:G:C6	30:0:1761:U:C4	3.03	0.46
30:0:1854:C:H2'	30:0:1875:A:H61	1.80	0.46
30:0:1942:A:O2'	30:0:1943:C:H5'	2.15	0.46
30:0:2019:A:H2'	30:0:2020:C:C6	2.49	0.46
30:0:2379:G:H4'	30:0:2380:A:C5'	2.45	0.46
30:0:2388:C:O2'	30:0:2389:U:H5'	2.14	0.46
31:9:54:A:C2'	31:9:55:U:C5'	2.85	0.46
2:B:162:MET:CE	2:B:310:ARG:HD3	2.45	0.46
2:B:223:ARG:HG3	2:B:232:TRP:C	2.40	0.46
10:J:42:GLU:HG2	10:J:43:ARG:N	2.30	0.46
21:U:47:ARG:HG3	38:U:4381:HOH:O	2.15	0.46
26:Z:70:ARG:NH1	26:Z:83:TYR:HD1	2.11	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1:10:LYS:HG3	38:1:2979:HOH:O	2.14	0.46
29:3:79:LEU:HD12	30:0:2456:A:C2	2.50	0.46
30:0:11:A:H2'	30:0:11:A:N3	2.30	0.46
30:0:61:G:C6	30:0:86:A:N6	2.83	0.46
30:0:154:C:O2'	30:0:155:C:H5'	2.14	0.46
30:0:703:G:C6	30:0:704:C:N4	2.83	0.46
30:0:1409:G:C2	30:0:1410:G:C8	3.03	0.46
30:0:1925:G:O2'	30:0:1926:G:H5'	2.15	0.46
30:0:2461:U:O2	30:0:2466:G:H1'	2.14	0.46
1:A:88:ILE:HD13	1:A:100:PRO:HD3	1.97	0.46
2:B:5:ARG:HD2	2:B:8:LYS:NZ	2.31	0.46
12:L:38:HIS:O	30:0:926:A:H1'	2.15	0.46
13:M:92:THR:HB	30:0:401:C:O2'	2.15	0.46
20:T:17:HIS:ND1	30:0:100:C:O2'	2.44	0.46
22:V:39:ALA:C	22:V:41:GLU:H	2.23	0.46
38:W:7804:HOH:O	30:0:1286:A:H5''	2.15	0.46
29:3:67:LEU:HD13	29:3:69:TYR:HE1	1.81	0.46
30:0:168:C:O5'	30:0:168:C:H6	1.98	0.46
30:0:214:U:H5'	38:0:6117:HOH:O	2.15	0.46
30:0:400:C:H2'	30:0:401:C:H6	1.80	0.46
30:0:432:G:C2	30:0:433:C:C5	3.02	0.46
30:0:604:G:H4'	30:0:605:C:O5'	2.15	0.46
30:0:1016:U:H1'	38:0:3652:HOH:O	2.15	0.46
30:0:1398:G:H4'	38:0:6650:HOH:O	2.15	0.46
30:0:1415:G:O2'	30:0:1416:G:H5'	2.15	0.46
30:0:1790:C:H2'	30:0:1791:U:H6	1.80	0.46
30:0:1825:U:O2'	30:0:1826:C:H5'	2.15	0.46
30:0:2259:C:C2	30:0:2260:A:C8	3.04	0.46
30:0:2658:G:C2	30:0:2659:U:C6	3.03	0.46
30:0:2871:G:C6	30:0:2887:G:N1	2.83	0.46
1:A:36:ASP:CB	1:A:85:SER:HB2	2.45	0.46
3:C:72:LYS:HG2	3:C:77:ALA:HA	1.96	0.46
4:D:138:GLY:HA2	31:9:29:C:O3'	2.15	0.46
9:I:96:SER:H	9:I:99:GLN:CD	2.22	0.46
10:J:90:LYS:HB2	33:J:8802:CL:CL	2.53	0.46
23:W:81:ASP:OD1	23:W:92:ASP:HB2	2.16	0.46
27:1:42:SER:HB3	30:0:1473:U:C1'	2.45	0.46
29:3:64:LYS:HD3	29:3:82:GLY:O	2.14	0.46
30:0:10:U:C4	30:0:532:A:N7	2.84	0.46
30:0:100:C:H2'	30:0:101:C:H6	1.81	0.46
30:0:128:A:O2'	30:0:129:A:C5'	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:247:A:C2	30:0:265:U:C2	3.03	0.46
30:0:440:C:C4	30:0:441:A:C6	3.04	0.46
30:0:732:C:O2'	30:0:733:U:H5'	2.14	0.46
30:0:959:C:H1'	30:0:961:A:C6	2.50	0.46
30:0:1484:G:H2'	38:0:9110:HOH:O	2.16	0.46
30:0:1603:A:C5'	30:0:1605:G:C5'	2.91	0.46
30:0:1806:G:H2'	30:0:1807:U:H6	1.78	0.46
30:0:2520:G:O2'	30:0:2521:A:H5'	2.16	0.46
31:9:3:A:H2'	38:9:9044:HOH:O	2.14	0.46
1:A:212:PRO:HB2	38:0:4344:HOH:O	2.16	0.46
2:B:199:TYR:CE2	2:B:268:ARG:HB2	2.49	0.46
30:0:364:U:H2'	30:0:365:G:O4'	2.15	0.46
30:0:780:A:H2'	30:0:781:C:C6	2.50	0.46
30:0:815:U:H5	38:0:7423:HOH:O	1.98	0.46
30:0:1477:C:C5'	30:0:1868:G:C5'	2.94	0.46
30:0:1590:A:C2	30:0:1606:A:C1'	2.99	0.46
30:0:1626:A:H2'	30:0:1627:G:C5'	2.45	0.46
30:0:2004:U:H4'	38:0:5274:HOH:O	2.14	0.46
30:0:2355:G:H2'	30:0:2355:G:N3	2.31	0.46
30:0:2356:A:H2'	30:0:2357:G:O4'	2.16	0.46
30:0:2911:C:O2'	30:0:2912:C:H5'	2.15	0.46
1:A:94:LEU:HD12	1:A:98:GLU:HB2	1.96	0.46
2:B:304:PRO:HD2	2:B:307:ARG:NE	2.31	0.46
4:D:64:ARG:HB3	4:D:67:ASP:OD2	2.15	0.46
8:H:6:ALA:HA	8:H:61:ARG:NH1	2.30	0.46
9:I:87:PRO:HD3	38:0:7103:HOH:O	2.14	0.46
10:J:130:VAL:HG12	10:J:131:THR:N	2.31	0.46
14:N:147:ILE:HD12	38:9:9091:HOH:O	2.15	0.46
18:R:48:GLU:HA	18:R:51:ILE:HD12	1.98	0.46
23:W:68:THR:HG23	23:W:69:ARG:H	1.81	0.46
30:0:39:G:O6	30:0:441:A:C2	2.68	0.46
30:0:307:G:N2	30:0:309:C:C2	2.84	0.46
30:0:396:U:O2'	30:0:397:A:P	2.73	0.46
30:0:1100:G:O2'	30:0:1107:A:N1	2.46	0.46
30:0:1215:A:O3'	30:0:1216:G:H4'	2.16	0.46
30:0:1524:U:H6	30:0:1524:U:H5''	1.81	0.46
30:0:2626:C:H2'	30:0:2627:G:C8	2.51	0.46
6:F:89:LEU:HD21	30:0:262:A:C6	2.51	0.46
9:I:112:LEU:CD1	30:0:1162:G:H1'	2.45	0.46
14:N:42:HIS:HB3	14:N:62:HIS:HE1	1.80	0.46
15:O:51:TYR:CD2	30:0:721:A:H5''	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:43:VAL:HG12	24:X:47:ALA:HB3	1.98	0.46
30:0:421:C:H2'	30:0:422:G:C8	2.50	0.46
30:0:497:A:H5''	38:0:3588:HOH:O	2.16	0.46
30:0:662:U:H1'	30:0:748:C:H1'	1.98	0.46
30:0:1187:U:C2	30:0:1189:A:OP2	2.68	0.46
30:0:1200:A:H3'	38:0:5722:HOH:O	2.15	0.46
30:0:1427:A:O2'	30:0:1428:C:H5'	2.16	0.46
30:0:1773:G:H2'	30:0:1774:G:H5'	1.98	0.46
30:0:1829:A:H2'	30:0:1830:C:C5'	2.41	0.46
30:0:2017:U:O2'	30:0:2018:A:C8	2.53	0.46
30:0:2100:A:C5'	38:0:7373:HOH:O	2.57	0.46
30:0:2314:G:O2'	30:0:2315:C:H5'	2.15	0.46
30:0:2397:G:N2	38:0:6910:HOH:O	2.49	0.46
30:0:2471:G:C5	30:0:2472:C:C5	3.03	0.46
30:0:2828:G:O5'	30:0:2828:G:C8	2.68	0.46
18:R:135:ALA:HB1	18:R:137:ASN:ND2	2.29	0.46
30:0:277:U:O2'	30:0:278:A:H5'	2.16	0.46
30:0:282:C:HO2'	30:0:368:C:N4	2.13	0.46
30:0:334:G:H2'	30:0:335:U:H6	1.81	0.46
30:0:567:U:C5'	38:0:5254:HOH:O	2.62	0.46
30:0:920:C:H5''	30:0:921:G:O5'	2.16	0.46
30:0:969:G:N1	30:0:999:C:N4	2.53	0.46
30:0:1187:U:O2'	30:0:1188:A:C8	2.69	0.46
30:0:1209:C:C2	30:0:1210:G:C8	3.03	0.46
30:0:1497:G:H4'	30:0:1627:G:O2'	2.16	0.46
30:0:2326:C:H4'	30:0:2412:G:C4'	2.46	0.46
30:0:2401:A:H2'	30:0:2402:A:C8	2.51	0.46
30:0:2612:A:H4'	38:0:3676:HOH:O	2.15	0.46
30:0:2912:C:O5'	30:0:2912:C:C6	2.66	0.46
2:B:75:GLU:C	2:B:77:PRO:HD3	2.40	0.46
10:J:131:THR:HG22	10:J:134:GLU:HG3	1.97	0.46
14:N:34:LEU:HD22	14:N:129:ILE:HD13	1.98	0.46
15:O:38:ARG:HD3	30:0:654:A:OP2	2.16	0.46
19:S:12:GLU:OE1	30:0:1444:G:H4'	2.15	0.46
20:T:48:VAL:HG23	20:T:98:VAL:HA	1.97	0.46
26:Z:34:SER:CB	30:0:797:A:H4'	2.46	0.46
30:0:488:U:C2'	38:0:3993:HOH:O	2.64	0.46
30:0:562:A:H2'	30:0:563:C:O4'	2.15	0.46
30:0:735:C:C5	30:0:736:A:C4	3.03	0.46
30:0:897:A:H2'	30:0:899:C:C5	2.50	0.46
30:0:1058:A:H2'	30:0:1060:C:H5''	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1157:C:H2'	30:0:1158:G:H8	1.80	0.46
30:0:1790:C:H2'	30:0:1791:U:C6	2.51	0.46
30:0:1812:G:H4'	30:0:1814:G:O4'	2.15	0.46
30:0:2038:A:C2	30:0:2039:A:C5	3.04	0.46
30:0:2241:C:H2'	30:0:2242:U:C6	2.50	0.46
30:0:2456:A:H1'	38:0:6579:HOH:O	2.16	0.46
31:9:15:C:N4	31:9:16:G:C6	2.84	0.46
31:9:47:A:C2	31:9:48:C:C2	3.03	0.46
13:M:94:ARG:NH2	30:0:175:G:O6	2.49	0.46
13:M:164:THR:HG22	13:M:165:GLY:N	2.30	0.46
20:T:79:LEU:HG	20:T:89:ARG:HB2	1.98	0.46
24:X:21:PRO:HD3	38:X:6179:HOH:O	2.16	0.46
25:Y:214:ARG:HH12	25:Y:230:ASN:ND2	2.13	0.46
29:3:20:HIS:CE1	29:3:71:CYS:SG	3.09	0.46
30:0:212:A:H5'	30:0:214:U:H1'	1.98	0.46
30:0:938:G:C4	30:0:1031:G:N2	2.84	0.46
30:0:1119:G:N2	30:0:1246:A:H2	2.04	0.46
30:0:1236:A:C2'	30:0:1237:U:H5'	2.46	0.46
30:0:1504:A:C5'	38:0:4396:HOH:O	2.63	0.46
30:0:1512:G:H4'	38:0:4618:HOH:O	2.15	0.46
30:0:1707:G:H1'	30:0:1711:A:N6	2.31	0.46
30:0:1809:G:H2'	30:0:1811:A:OP2	2.16	0.46
30:0:1902:G:H2'	30:0:1903:U:O4'	2.16	0.46
30:0:2011:A:H5'	30:0:2013:G:C1'	2.46	0.46
30:0:2694:A:H3'	30:0:2695:C:H6	1.81	0.46
30:0:2831:C:C2	30:0:2910:A:N1	2.84	0.46
30:0:2860:G:H1'	38:0:6785:HOH:O	2.15	0.46
3:C:35:VAL:HG21	3:C:227:GLY:HA2	1.98	0.45
4:D:63:ILE:HG13	4:D:64:ARG:N	2.32	0.45
5:E:103:VAL:HG22	5:E:115:ARG:HB3	1.96	0.45
13:M:133:LEU:O	13:M:134:ILE:HD13	2.16	0.45
30:0:56:G:H1'	38:0:5300:HOH:O	2.16	0.45
30:0:1217:G:C2	30:0:1218:U:C2	3.04	0.45
30:0:1490:G:H4'	30:0:1533:A:OP1	2.16	0.45
30:0:1516:U:H2'	30:0:1517:C:O4'	2.17	0.45
30:0:1864:C:H2'	30:0:1865:A:O4'	2.16	0.45
1:A:35:GLY:O	1:A:37:VAL:HG22	2.17	0.45
1:A:94:LEU:HD23	1:A:94:LEU:N	2.31	0.45
1:A:186:TRP:CG	1:A:187:PRO:HA	2.50	0.45
2:B:285:VAL:HA	30:0:2897:C:HO2'	1.81	0.45
2:B:320:GLN:HA	2:B:321:PRO:HD3	1.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:76:ARG:HD2	31:9:42:C:O2	2.16	0.45
9:I:83:GLY:H	30:0:1168:C:C5'	2.28	0.45
11:K:132:VAL:HG21	21:U:22:VAL:HG13	1.97	0.45
15:O:32:ARG:HH21	15:O:35:LYS:NZ	2.14	0.45
30:0:369:G:O2'	30:0:370:G:H5'	2.16	0.45
30:0:743:G:O2'	30:0:744:G:H5'	2.16	0.45
30:0:940:G:C5	30:0:1027:G:C2	3.04	0.45
30:0:1018:A:O5'	30:0:1018:A:H8	1.99	0.45
30:0:1074:G:H4'	30:0:1260:G:C6	2.52	0.45
30:0:1362:U:O2'	30:0:1363:G:H5'	2.17	0.45
30:0:1400:C:C2'	30:0:1401:G:H5'	2.46	0.45
30:0:1444:G:C6	30:0:1445:G:C5	3.05	0.45
30:0:1503:U:H2'	30:0:1504:A:H5'	1.98	0.45
30:0:1831:U:H2'	30:0:1832:G:H5'	1.98	0.45
30:0:1908:G:H1'	30:0:1931:A:N6	2.31	0.45
30:0:1987:C:O2'	30:0:1988:C:H5'	2.16	0.45
30:0:2134:G:N2	30:0:2242:U:C2	2.85	0.45
30:0:2577:A:H8	38:0:9606:HOH:O	1.99	0.45
30:0:2812:A:C2	30:0:2814:A:N7	2.85	0.45
31:9:39:U:N3	31:9:42:C:H5''	2.31	0.45
8:H:46:TYR:HA	8:H:47:PRO:HD3	1.81	0.45
9:I:113:SER:HA	30:0:1186:C:H5'	1.98	0.45
20:T:114:SER:OG	20:T:117:ASP:HB2	2.16	0.45
29:3:12:PRO:HG2	29:3:13:HIS:CD2	2.49	0.45
30:0:99:A:C8	30:0:100:C:C5	3.05	0.45
30:0:154:C:H2'	30:0:155:C:H6	1.82	0.45
30:0:191:A:N6	30:0:435:A:H62	2.14	0.45
30:0:360:A:H2'	30:0:361:C:O4'	2.16	0.45
30:0:400:C:O2'	30:0:401:C:H5'	2.17	0.45
30:0:595:U:H2'	30:0:596:C:C6	2.52	0.45
30:0:793:A:H2'	30:0:794:U:H6	1.81	0.45
30:0:1116:U:N3	30:0:1246:A:N6	2.60	0.45
30:0:1213:C:O2'	30:0:1214:G:H5'	2.17	0.45
30:0:1603:A:H5'	30:0:1605:G:C5'	2.46	0.45
30:0:1670:A:H2'	30:0:1671:U:O4'	2.16	0.45
30:0:1759:A:N3	30:0:1818:C:H2'	2.31	0.45
30:0:1948:G:H2'	30:0:1949:G:O4'	2.16	0.45
30:0:2293:G:C6	30:0:2294:C:C5	3.04	0.45
30:0:2757:A:H2'	30:0:2758:G:O4'	2.16	0.45
31:9:59:C:O5'	31:9:59:C:C6	2.63	0.45
2:B:254:GLN:HG2	2:B:255:GLY:N	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:30:GLU:HG2	38:M:8864:HOH:O	2.17	0.45
13:M:122:GLN:HB2	13:M:127:LYS:HG2	1.98	0.45
14:N:144:GLY:O	14:N:147:ILE:HG23	2.15	0.45
17:Q:15:LYS:HG3	30:0:2364:A:O3'	2.16	0.45
18:R:96:VAL:HG13	18:R:106:GLY:HA3	1.98	0.45
25:Y:144:ARG:CZ	38:Y:8916:HOH:O	2.65	0.45
26:Z:70:ARG:O	26:Z:81:CYS:SG	2.74	0.45
30:0:304:G:H8	30:0:304:G:O5'	2.00	0.45
30:0:734:U:H2'	30:0:736:A:OP2	2.16	0.45
30:0:790:A:H1'	30:0:1710:A:C2'	2.46	0.45
30:0:876:A:N3	30:0:876:A:C2'	2.79	0.45
30:0:912:A:C4	30:0:1294:A:C2	3.04	0.45
30:0:1178:G:C6	30:0:1179:C:N4	2.84	0.45
30:0:1819:G:H2'	30:0:1820:G:C4'	2.46	0.45
30:0:1964:U:H2'	30:0:1964:U:O2	2.15	0.45
30:0:1970:G:H2'	30:0:1970:G:N3	2.31	0.45
30:0:2005:G:H3'	30:0:2005:G:P	2.55	0.45
30:0:2092:G:H2'	30:0:2613:G:OP1	2.17	0.45
30:0:2438:G:H2'	30:0:2439:C:C6	2.51	0.45
31:9:29:C:C5	31:9:30:C:C5	3.04	0.45
2:B:62:ARG:HG2	2:B:65:MET:HE3	1.99	0.45
38:C:8558:HOH:O	30:0:751:U:H5'	2.16	0.45
5:E:152:THR:HG21	5:E:165:GLY:HA2	1.99	0.45
12:L:72:ASN:O	12:L:76:LEU:HG	2.17	0.45
18:R:18:LEU:HB2	18:R:143:VAL:CG1	2.46	0.45
28:2:40:ARG:HG3	28:2:45:ASN:CB	2.45	0.45
29:3:59:ASP:OD1	30:0:2460:A:H5''	2.16	0.45
30:0:420:U:O4'	30:0:1920:C:C4	2.70	0.45
30:0:659:A:H5''	38:0:7082:HOH:O	2.17	0.45
30:0:940:G:N3	30:0:1032:A:C2	2.84	0.45
30:0:1524:U:H5''	30:0:1524:U:C6	2.51	0.45
30:0:1547:A:H2'	30:0:1548:U:C6	2.52	0.45
30:0:1940:C:H1'	38:0:9382:HOH:O	2.17	0.45
30:0:2697:A:N3	30:0:2697:A:H2'	2.32	0.45
30:0:2718:C:H5'	30:0:2718:C:C6	2.50	0.45
30:0:2728:C:O5'	30:0:2728:C:H6	1.99	0.45
1:A:11:ARG:HD3	38:0:9222:HOH:O	2.16	0.45
1:A:204:GLY:N	30:0:2634:G:OP2	2.49	0.45
6:F:34:ASN:HA	13:M:4:ALA:HB2	1.98	0.45
9:I:82:THR:HG22	30:0:1168:C:H5''	1.97	0.45
12:L:57:VAL:O	12:L:57:VAL:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:34:GLU:HB3	13:M:38:GLU:HG3	1.99	0.45
14:N:33:ARG:HG3	38:N:8841:HOH:O	2.17	0.45
15:O:27:GLY:O	15:O:31:GLU:HG3	2.17	0.45
30:0:418:C:H2'	30:0:419:A:C8	2.52	0.45
30:0:634:G:O2'	30:0:1358:A:OP1	2.31	0.45
30:0:790:A:H8	38:0:6078:HOH:O	1.98	0.45
30:0:960:G:N3	30:0:960:G:C2'	2.79	0.45
30:0:1149:U:C5	30:0:1215:A:N7	2.84	0.45
30:0:1151:G:N2	30:0:1214:G:C4	2.85	0.45
30:0:1406:A:H4'	30:0:1407:A:H5''	1.98	0.45
30:0:1434:A:H4'	30:0:1435:U:H5	1.82	0.45
30:0:1523:G:C6	30:0:1524:U:C4	3.05	0.45
30:0:1883:U:H5''	30:0:2013:G:OP2	2.17	0.45
30:0:2475:C:H5'	38:0:3664:HOH:O	2.16	0.45
31:9:61:C:H2'	31:9:62:A:C8	2.46	0.45
1:A:189:VAL:HA	30:0:1845:A:OP1	2.16	0.45
2:B:119:HIS:O	2:B:121:PRO:HD3	2.16	0.45
27:1:16:HIS:HE1	30:0:775:G:OP1	1.99	0.45
29:3:35:TRP:HZ3	30:0:2432:C:OP1	2.00	0.45
30:0:92:G:H2'	30:0:93:C:H6	1.82	0.45
30:0:2385:G:H2'	30:0:2386:U:H6	1.81	0.45
30:0:2515:C:H2'	30:0:2516:G:O4'	2.16	0.45
2:B:43:GLY:O	2:B:308:LEU:HD12	2.16	0.45
4:D:50:VAL:O	4:D:71:ALA:HA	2.17	0.45
6:F:96:ALA:HA	38:F:3111:HOH:O	2.15	0.45
10:J:43:ARG:HD3	38:J:8858:HOH:O	2.17	0.45
30:0:342:C:N4	30:0:343:C:H41	2.15	0.45
30:0:343:C:O2'	30:0:344:C:H5'	2.17	0.45
30:0:387:G:C2'	30:0:388:G:H5'	2.46	0.45
30:0:916:A:C6	30:0:917:U:C4	3.05	0.45
30:0:1405:U:H4'	30:0:1406:A:H5''	1.98	0.45
30:0:1902:G:O2'	30:0:1903:U:H5'	2.16	0.45
30:0:2361:A:H2'	30:0:2362:A:C8	2.51	0.45
30:0:2887:G:H2'	30:0:2888:U:O4'	2.17	0.45
31:9:30:C:O2	31:9:30:C:C2'	2.65	0.45
31:9:72:C:O2'	31:9:73:A:H5'	2.15	0.45
1:A:20:SER:C	1:A:22:ARG:H	2.25	0.45
1:A:51:ARG:O	1:A:52:SER:HB2	2.16	0.45
2:B:86:ALA:HA	38:B:9051:HOH:O	2.16	0.45
2:B:307:ARG:HH11	2:B:307:ARG:HG3	1.82	0.45
3:C:95:GLU:HG3	38:C:8669:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:102:VAL:HG11	5:E:148:ILE:HG12	1.98	0.45
5:E:121:ASP:HB2	38:E:5899:HOH:O	2.16	0.45
21:U:6:CYS:SG	21:U:31:PHE:HA	2.56	0.45
26:Z:35:SER:HB3	26:Z:47:ARG:HB2	1.98	0.45
30:0:228:C:H2'	30:0:229:G:C5'	2.46	0.45
30:0:281:U:H5	38:0:7575:HOH:O	1.99	0.45
30:0:862:U:H2'	30:0:863:G:C8	2.52	0.45
30:0:957:A:H8	30:0:957:A:O5'	2.00	0.45
30:0:1576:G:C2	30:0:1577:U:C2	3.05	0.45
30:0:1626:A:C2'	30:0:1627:G:H5'	2.46	0.45
30:0:1850:U:H2'	30:0:1851:G:C8	2.52	0.45
30:0:2842:G:H2'	30:0:2843:A:H5'	1.98	0.45
3:C:88:SER:O	3:C:91:PRO:HD3	2.17	0.45
13:M:86:GLN:NE2	38:M:8882:HOH:O	2.50	0.45
30:0:958:G:H2'	30:0:959:C:H6	1.75	0.45
30:0:969:G:N2	30:0:1000:C:C2	2.85	0.45
30:0:1041:U:H2'	30:0:1042:U:C5'	2.46	0.45
30:0:1477:C:C5'	30:0:1868:G:H5''	2.47	0.45
30:0:1543:G:N1	30:0:1641:A:OP2	2.36	0.45
30:0:1801:A:C2	30:0:1802:G:C4	3.04	0.45
30:0:2311:A:O2'	30:0:2312:G:H5'	2.17	0.45
30:0:2511:A:H2'	30:0:2512:U:H6	1.82	0.45
31:9:33:U:C6	31:9:43:G:C8	3.05	0.45
1:A:164:ARG:NH1	1:A:164:ARG:HB3	2.31	0.44
4:D:128:LEU:HD23	4:D:129:ASP:N	2.32	0.44
5:E:153:ARG:NH1	30:0:2778:A:C1'	2.81	0.44
8:H:83:GLU:HA	38:H:243:HOH:O	2.18	0.44
10:J:107:ASN:HD21	10:J:109:TYR:HB2	1.82	0.44
16:P:81:LYS:HE3	30:0:1813:U:O2'	2.18	0.44
18:R:34:GLU:HG2	18:R:46:TYR:OH	2.17	0.44
23:W:48:VAL:HG12	23:W:52:VAL:HB	1.98	0.44
26:Z:47:ARG:O	26:Z:51:ALA:HB2	2.16	0.44
30:0:163:U:O3'	30:0:896:C:H4'	2.16	0.44
30:0:198:A:C2	30:0:2444:U:H1'	2.53	0.44
30:0:283:U:H5''	30:0:284:C:OP2	2.17	0.44
30:0:339:A:C6	30:0:342:C:N3	2.85	0.44
30:0:581:G:H5'	38:0:7663:HOH:O	2.17	0.44
30:0:1181:A:O2'	30:0:1182:C:H5'	2.17	0.44
30:0:1392:A:C6	30:0:1395:C:C2	3.05	0.44
30:0:1524:U:H6	30:0:1524:U:C5'	2.29	0.44
30:0:1584:C:O2'	30:0:1585:C:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1748:U:C5	30:0:1749:U:C4	3.06	0.44
30:0:2293:G:C6	30:0:2294:C:C4	3.05	0.44
30:0:2826:G:O6	30:0:2913:A:N6	2.50	0.44
31:9:3:A:OP2	31:9:25:G:N2	2.50	0.44
31:9:107:C:O2'	31:9:108:C:H5'	2.17	0.44
2:B:51:VAL:HG13	2:B:53:LEU:HD13	1.98	0.44
3:C:60:SER:HA	38:C:8575:HOH:O	2.17	0.44
3:C:129:HIS:HD2	3:C:165:ASP:OD2	2.01	0.44
10:J:15:ARG:HG2	10:J:16:ASP:OD1	2.17	0.44
12:L:41:HIS:CD2	30:0:926:A:O2'	2.69	0.44
13:M:49:ALA:C	13:M:54:TYR:HB3	2.42	0.44
13:M:76:ARG:HG3	38:M:8827:HOH:O	2.17	0.44
14:N:1:ALA:HB2	31:9:14:G:O2'	2.18	0.44
18:R:98:ASN:ND2	30:0:500:G:H21	2.12	0.44
20:T:81:LYS:HD2	20:T:87:VAL:HG11	1.98	0.44
23:W:10:GLU:O	23:W:13:MET:HB3	2.18	0.44
30:0:440:C:O5'	30:0:440:C:H6	2.00	0.44
30:0:711:G:C2'	30:0:712:C:H5'	2.47	0.44
30:0:1246:A:O2'	30:0:1247:A:H3'	2.17	0.44
30:0:1362:U:H2'	30:0:1363:G:C8	2.52	0.44
30:0:1434:A:H2'	30:0:1436:C:C5	2.52	0.44
9:I:130:LEU:HD21	30:0:1167:G:C4'	2.46	0.44
11:K:86:THR:HG22	11:K:87:ARG:N	2.32	0.44
13:M:71:SER:OG	13:M:72:ALA:N	2.51	0.44
18:R:59:PHE:O	18:R:63:ASN:HB3	2.18	0.44
22:V:12:THR:CG2	22:V:15:GLU:H	2.30	0.44
28:2:8:LYS:NZ	30:0:1677:U:OP2	2.43	0.44
29:3:10:TYR:CD1	30:0:2408:A:H1'	2.52	0.44
30:0:57:C:H42	30:0:89:G:H1	1.64	0.44
30:0:372:A:O2'	30:0:373:G:H5'	2.17	0.44
30:0:729:C:C2	30:0:743:G:C2	3.05	0.44
30:0:877:G:N7	30:0:885:G:C5	2.85	0.44
30:0:1016:U:O2'	30:0:2303:A:N7	2.40	0.44
30:0:1069:C:H2'	30:0:1070:A:O4'	2.18	0.44
30:0:1132:A:H2'	30:0:1133:A:C8	2.52	0.44
30:0:1202:A:C2'	30:0:1203:G:H5'	2.48	0.44
30:0:1391:G:N2	30:0:1434:A:H5''	2.32	0.44
30:0:1649:G:H1'	38:0:5049:HOH:O	2.17	0.44
30:0:1680:C:H2'	30:0:1681:G:O4'	2.17	0.44
30:0:1701:A:H5''	30:0:1702:U:H3'	1.99	0.44
30:0:2276:U:H2'	30:0:2277:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:243:ASN:HA	2:B:244:PRO:C	2.42	0.44
2:B:244:PRO:HB3	30:0:1234:U:N3	2.32	0.44
4:D:153:THR:O	4:D:156:ARG:HB2	2.16	0.44
5:E:20:ILE:O	5:E:30:THR:HA	2.17	0.44
8:H:14:LYS:HG3	38:H:183:HOH:O	2.17	0.44
12:L:22:ARG:HG2	38:0:3223:HOH:O	2.15	0.44
19:S:11:THR:H	19:S:14:ALA:HB3	1.81	0.44
20:T:48:VAL:HG22	20:T:97:ARG:C	2.42	0.44
25:Y:182:PHE:HD2	25:Y:200:THR:O	2.00	0.44
26:Z:69:ASP:O	26:Z:71:VAL:N	2.45	0.44
29:3:5:ARG:HD2	29:3:21:GLU:HG2	1.98	0.44
30:0:625:U:H5'	38:0:3177:HOH:O	2.16	0.44
30:0:1415:G:C2'	30:0:1416:G:H5'	2.47	0.44
30:0:1556:G:O2'	30:0:1557:G:H5'	2.17	0.44
30:0:2507:G:H2'	30:0:2510:C:H42	1.81	0.44
30:0:2509:A:OP2	30:0:2510:C:H5	2.00	0.44
30:0:2775:A:N6	30:0:2799:A:C8	2.86	0.44
30:0:2911:C:H2'	30:0:2912:C:H6	1.82	0.44
13:M:47:ASP:CG	13:M:48:LYS:N	2.76	0.44
18:R:80:TYR:O	30:0:2050:G:H5''	2.16	0.44
30:0:48:A:N1	30:0:148:A:O2'	2.48	0.44
30:0:1043:C:H2'	38:0:3185:HOH:O	2.18	0.44
30:0:2345:A:C3'	30:0:2346:C:H6	2.23	0.44
1:A:233:THR:HB	30:0:1942:A:H5''	1.99	0.44
3:C:6:TYR:N	3:C:6:TYR:CD1	2.86	0.44
5:E:69:ILE:HA	5:E:72:MET:CE	2.48	0.44
9:I:87:PRO:HG2	30:0:1181:A:O4'	2.18	0.44
13:M:66:SER:HB3	13:M:128:TRP:NE1	2.32	0.44
17:Q:40:HIS:HE1	30:0:949:U:O2'	2.01	0.44
20:T:97:ARG:NH2	30:0:309:C:OP1	2.51	0.44
23:W:129:LYS:CD	31:9:87:U:H2'	2.47	0.44
25:Y:99:ALA:HB2	25:Y:233:TYR:CE2	2.52	0.44
27:1:20:ARG:HB2	38:1:513:HOH:O	2.18	0.44
30:0:569:A:H5''	30:0:587:A:N1	2.32	0.44
30:0:821:U:H2'	30:0:822:C:H6	1.81	0.44
30:0:1112:G:H1	30:0:1251:C:H42	1.65	0.44
30:0:1330:A:H2	38:0:4652:HOH:O	2.00	0.44
30:0:1519:U:O2'	30:0:1520:G:H5'	2.16	0.44
30:0:1706:G:C6	30:0:1707:G:N1	2.86	0.44
30:0:1711:A:H2'	30:0:1712:A:H5'	1.99	0.44
30:0:1762:C:H2'	30:0:1763:C:H6	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2005:G:OP2	30:0:2006:C:C5'	2.66	0.44
30:0:2377:U:O2'	30:0:2378:U:H5'	2.17	0.44
30:0:2457:U:H1'	38:0:7515:HOH:O	2.17	0.44
30:0:2552:C:C6	30:0:2577:A:N7	2.85	0.44
30:0:2781:U:H2'	30:0:2782:G:C5'	2.48	0.44
30:0:2834:G:H2'	30:0:2835:C:O5'	2.17	0.44
30:0:2854:A:C6	30:0:2905:A:N1	2.86	0.44
30:0:2872:U:C2	30:0:2873:C:C6	3.05	0.44
1:A:192:VAL:HG23	30:0:1882:C:OP1	2.17	0.44
2:B:5:ARG:NH1	30:0:2547:C:OP2	2.51	0.44
2:B:241:PRO:HB3	30:0:2609:G:N3	2.33	0.44
4:D:62:ASP:HA	38:D:4233:HOH:O	2.18	0.44
4:D:86:THR:O	4:D:89:PRO:HD2	2.18	0.44
38:T:2151:HOH:O	30:0:317:A:H5'	2.17	0.44
21:U:45:GLU:HB2	21:U:48:ASN:ND2	2.32	0.44
25:Y:204:ARG:NH2	30:0:1324:G:N2	2.65	0.44
30:0:929:A:O5'	30:0:929:A:H8	2.01	0.44
30:0:1309:U:C2'	30:0:1310:U:H5'	2.48	0.44
30:0:1427:A:C2'	30:0:1428:C:H5'	2.47	0.44
30:0:2250:G:N1	30:0:2251:G:N3	2.66	0.44
30:0:2541:U:H5'	30:0:2611:G:O6	2.18	0.44
30:0:2566:A:C2	30:0:2696:G:O4'	2.71	0.44
1:A:51:ARG:C	1:A:53:ALA:H	2.26	0.44
1:A:103:VAL:HA	1:A:104:PRO:HD3	1.89	0.44
1:A:194:MET:SD	30:0:875:A:C2	3.11	0.44
2:B:195:ARG:HE	2:B:323:LEU:HD13	1.83	0.44
8:H:59:GLN:HE21	8:H:129:ARG:HE	1.65	0.44
8:H:66:GLU:HA	38:H:239:HOH:O	2.17	0.44
8:H:87:LYS:HG3	8:H:140:TYR:HD1	1.83	0.44
13:M:80:GLY:O	13:M:81:ARG:HB2	2.18	0.44
14:N:47:LEU:HD13	14:N:47:LEU:HA	1.86	0.44
16:P:13:VAL:HG11	16:P:40:VAL:CG1	2.48	0.44
20:T:19:ARG:HD3	20:T:67:LEU:O	2.18	0.44
30:0:157:G:H3'	38:0:3945:HOH:O	2.18	0.44
30:0:304:G:H1'	30:0:347:A:N6	2.32	0.44
30:0:582:U:H2'	30:0:583:C:C6	2.53	0.44
30:0:703:G:C6	30:0:704:C:C4	3.06	0.44
30:0:821:U:O2'	30:0:822:C:H5'	2.18	0.44
30:0:868:G:C4	30:0:887:G:C8	3.06	0.44
30:0:1202:A:H2'	30:0:1203:G:H5'	2.00	0.44
30:0:1679:C:O2'	30:0:1685:A:N1	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1789:G:H2'	30:0:1790:C:O5'	2.17	0.44
30:0:1950:G:H2'	30:0:1951:G:C8	2.53	0.44
30:0:1986:G:C6	30:0:1987:C:N4	2.86	0.44
30:0:2061:C:H2'	30:0:2062:A:H5'	1.99	0.44
30:0:2104:C:O2	30:0:2485:A:N1	2.50	0.44
31:9:26:C:H2'	31:9:27:C:H6	1.79	0.44
31:9:31:C:C2	31:9:50:G:C2	3.05	0.44
31:9:81:C:C2'	31:9:82:U:H5'	2.48	0.44
1:A:182:ARG:HB3	38:0:5133:HOH:O	2.18	0.44
2:B:54:VAL:HB	38:B:9083:HOH:O	2.17	0.44
2:B:279:THR:HG22	2:B:280:VAL:N	2.33	0.44
5:E:90:HIS:CE1	30:0:2694:A:H5''	2.53	0.44
8:H:39:LYS:O	30:0:969:G:H4'	2.18	0.44
10:J:75:PRO:HD3	10:J:136:SER:OG	2.18	0.44
16:P:54:LYS:HB2	30:0:1717:A:H5''	1.98	0.44
16:P:88:GLN:HB3	38:P:185:HOH:O	2.16	0.44
17:Q:25:PRO:HA	17:Q:26:PRO:HD3	1.78	0.44
29:3:10:TYR:CE2	30:0:2382:A:H1'	2.53	0.44
30:0:483:C:H2'	30:0:484:A:O4'	2.18	0.44
30:0:727:G:C2	30:0:728:C:C2	3.06	0.44
30:0:1522:A:H2'	30:0:1523:G:C5'	2.48	0.44
30:0:1937:U:O2'	30:0:1938:G:H5'	2.18	0.44
30:0:2250:G:C2	30:0:2251:G:C4	3.06	0.44
30:0:2431:C:H2'	30:0:2432:C:C6	2.53	0.44
30:0:2729:C:O2'	30:0:2730:G:H5'	2.18	0.44
3:C:174:ILE:CD1	30:0:338:C:H4'	2.48	0.43
4:D:103:ASN:ND2	4:D:133:ASN:HA	2.33	0.43
13:M:104:ARG:HG3	38:M:8866:HOH:O	2.18	0.43
14:N:12:ARG:HD3	14:N:18:THR:OG1	2.18	0.43
23:W:29:VAL:O	23:W:30:ASN:HB2	2.16	0.43
23:W:119:HIS:HE1	38:0:9568:HOH:O	2.00	0.43
25:Y:182:PHE:CG	25:Y:202:ALA:HB2	2.53	0.43
26:Z:45:VAL:O	26:Z:49:ARG:HG3	2.18	0.43
30:0:39:G:O2'	30:0:40:C:H5'	2.18	0.43
30:0:175:G:O2'	30:0:176:U:OP2	2.36	0.43
30:0:293:A:C5	30:0:360:A:C2	3.06	0.43
30:0:324:G:C6	30:0:325:U:C5	3.06	0.43
30:0:533:U:H3'	38:0:3742:HOH:O	2.18	0.43
30:0:838:C:H4'	38:0:9187:HOH:O	2.18	0.43
30:0:1166:A:C6	30:0:1167:G:C5	3.06	0.43
30:0:1167:G:O2'	30:0:1168:C:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1185:U:C5'	38:0:7447:HOH:O	2.59	0.43
30:0:1421:C:O2'	30:0:1422:U:H5'	2.18	0.43
30:0:1544:U:H2'	30:0:1545:C:H6	1.82	0.43
30:0:1592:G:O2'	30:0:1593:C:O4'	2.36	0.43
30:0:1642:A:N7	30:0:1643:C:C4	2.86	0.43
30:0:2090:G:H2'	30:0:2091:G:C8	2.53	0.43
30:0:2435:U:H4'	38:0:9269:HOH:O	2.17	0.43
30:0:2851:G:O2'	30:0:2852:A:H5'	2.17	0.43
31:9:74:G:O2'	31:9:75:G:H5'	2.18	0.43
1:A:94:LEU:HD12	1:A:98:GLU:CB	2.48	0.43
1:A:215:ILE:HG22	1:A:227:ASP:O	2.18	0.43
2:B:84:LEU:HD23	2:B:142:LEU:HD23	2.00	0.43
2:B:202:VAL:HA	2:B:310:ARG:O	2.18	0.43
3:C:193:LEU:HD12	3:C:211:ASP:O	2.18	0.43
4:D:10:PHE:CG	4:D:11:HIS:N	2.86	0.43
13:M:65:VAL:HG21	13:M:105:ALA:HB2	2.00	0.43
23:W:115:THR:HG23	38:W:5420:HOH:O	2.18	0.43
23:W:142:ASP:HB3	23:W:145:GLY:H	1.83	0.43
24:X:39:LYS:HE2	30:0:2834:G:OP1	2.17	0.43
26:Z:61:HIS:O	26:Z:69:ASP:HA	2.17	0.43
30:0:117:A:H2'	30:0:118:G:C8	2.53	0.43
30:0:532:A:N1	30:0:2660:G:O2'	2.49	0.43
30:0:692:A:N6	30:0:693:A:C2	2.86	0.43
30:0:827:A:H2'	30:0:828:G:O4'	2.18	0.43
30:0:1130:U:C2'	30:0:1131:G:H5'	2.48	0.43
30:0:1706:G:H1'	30:0:1712:A:N6	2.30	0.43
30:0:1916:C:C2	30:0:1924:A:C2	3.06	0.43
30:0:2135:A:O4'	30:0:2243:C:N4	2.51	0.43
30:0:2871:G:C4	30:0:2887:G:N2	2.86	0.43
31:9:2:U:OP2	31:9:3:A:H5'	2.18	0.43
1:A:38:ILE:HB	1:A:82:VAL:O	2.18	0.43
3:C:44:GLN:HA	38:C:8605:HOH:O	2.18	0.43
3:C:47:GLY:HA2	3:C:92:PRO:HB2	2.00	0.43
4:D:75:LEU:HD22	4:D:79:MET:HB3	2.00	0.43
20:T:14:ALA:HA	20:T:15:PRO:HD3	1.90	0.43
25:Y:154:ARG:HH21	30:0:1293:U:H5'	1.83	0.43
30:0:219:G:O5'	30:0:220:C:H5'	2.18	0.43
30:0:385:C:O5'	30:0:385:C:H6	2.02	0.43
30:0:665:A:C6	30:0:666:A:C6	3.06	0.43
30:0:820:G:H3'	30:0:820:G:N3	2.33	0.43
30:0:1062:U:O2'	30:0:2307:A:N3	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1210:G:C2	30:0:1211:G:C8	3.06	0.43
30:0:1298:U:H2'	30:0:1299:G:C8	2.53	0.43
30:0:1363:G:H2'	30:0:1364:G:C8	2.54	0.43
30:0:1815:A:H4'	30:0:2751:C:O4'	2.19	0.43
30:0:1816:C:H2'	30:0:1817:U:O4'	2.17	0.43
30:0:1949:G:N2	30:0:1964:U:C2	2.87	0.43
30:0:2112:A:H2'	30:0:2113:G:C8	2.53	0.43
30:0:2277:U:H1'	30:0:2469:A:N3	2.33	0.43
30:0:2429:A:C4'	38:0:7716:HOH:O	2.66	0.43
30:0:2594:C:O2'	30:0:2595:U:H5'	2.19	0.43
30:0:2793:A:N6	38:0:5853:HOH:O	2.50	0.43
30:0:2847:G:C2'	30:0:2848:G:H5'	2.48	0.43
3:C:6:TYR:N	3:C:6:TYR:HD1	2.17	0.43
5:E:84:MET:SD	38:E:3134:HOH:O	2.61	0.43
5:E:91:PHE:HA	5:E:92:PRO:HD3	1.89	0.43
5:E:126:ILE:HA	5:E:131:LEU:CD2	2.47	0.43
11:K:4:LEU:HD22	11:K:116:GLU:HB3	2.00	0.43
14:N:139:TRP:HA	14:N:139:TRP:CE3	2.53	0.43
30:0:36:C:H1'	38:0:3051:HOH:O	2.17	0.43
30:0:41:G:H8	30:0:41:G:O5'	2.00	0.43
30:0:152:A:O2'	30:0:153:C:H5'	2.18	0.43
30:0:234:A:H4'	30:0:437:A:O4'	2.18	0.43
30:0:1537:C:H2'	30:0:1538:C:H6	1.83	0.43
30:0:1878:G:O2'	30:0:1879:U:OP2	2.36	0.43
30:0:1980:U:O2	30:0:2008:U:H4'	2.18	0.43
31:9:39:U:O2'	31:9:42:C:H5	2.01	0.43
31:9:115:C:C4	31:9:116:C:C5	3.06	0.43
2:B:154:VAL:HA	2:B:155:PRO:HD3	1.88	0.43
3:C:39:GLN:O	3:C:43:LYS:HD3	2.18	0.43
9:I:73:LEU:HD12	9:I:107:LYS:NZ	2.33	0.43
16:P:8:ARG:HG3	38:P:188:HOH:O	2.17	0.43
23:W:6:GLN:HB2	23:W:26:ILE:CD1	2.48	0.43
30:0:148:A:O2'	30:0:149:G:H5'	2.19	0.43
30:0:772:G:H2'	30:0:773:A:O4'	2.18	0.43
30:0:1024:G:C6	30:0:1025:C:C4	3.07	0.43
30:0:1503:U:H2'	30:0:1504:A:O4'	2.19	0.43
30:0:1520:G:C2	30:0:1521:C:C2	3.07	0.43
30:0:2070:G:H2'	30:0:2072:G:OP1	2.18	0.43
30:0:2354:A:H5'	30:0:2355:G:N7	2.33	0.43
30:0:2361:A:H5'	38:0:9191:HOH:O	2.19	0.43
30:0:2429:A:H4'	38:0:7716:HOH:O	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2445:U:H2'	30:0:2446:G:C8	2.54	0.43
30:0:2451:G:H2'	30:0:2451:G:N3	2.32	0.43
30:0:2531:U:H2'	30:0:2532:A:O4'	2.19	0.43
30:0:2748:G:H1'	38:0:7881:HOH:O	2.18	0.43
30:0:2768:A:H3'	30:0:2768:A:N3	2.33	0.43
1:A:71:PRO:O	1:A:160:ALA:HB2	2.18	0.43
4:D:104:PHE:CE2	4:D:132:VAL:HB	2.54	0.43
4:D:128:LEU:HB2	38:D:6007:HOH:O	2.18	0.43
5:E:107:PHE:CE2	5:E:108:LEU:HD13	2.54	0.43
6:F:60:VAL:O	6:F:62:HIS:N	2.52	0.43
10:J:70:PHE:HE1	30:0:2676:C:C4'	2.32	0.43
13:M:164:THR:HB	38:M:8820:HOH:O	2.17	0.43
14:N:32:PRO:HD2	14:N:99:GLU:O	2.18	0.43
14:N:77:ASN:OD1	14:N:79:PRO:HD2	2.18	0.43
17:Q:11:ARG:NH2	30:0:2363:G:C5'	2.81	0.43
26:Z:55:SER:HA	38:0:7562:HOH:O	2.19	0.43
29:3:59:ASP:HB3	29:3:63:LYS:HZ1	1.83	0.43
29:3:67:LEU:CD1	29:3:69:TYR:HE1	2.31	0.43
30:0:392:U:O2'	30:0:394:G:N7	2.43	0.43
30:0:629:A:C2	30:0:2074:A:C2	3.07	0.43
30:0:1167:G:C2	30:0:1168:C:C2	3.06	0.43
30:0:1175:G:N3	30:0:1193:A:C6	2.86	0.43
30:0:1275:C:C2'	30:0:1276:U:H5'	2.49	0.43
30:0:1284:G:O2'	30:0:1285:U:H5'	2.18	0.43
30:0:1421:C:C2	30:0:1444:G:N2	2.87	0.43
30:0:1985:U:C2	30:0:1996:U:O4'	2.72	0.43
30:0:2429:A:N6	38:0:3326:HOH:O	2.51	0.43
30:0:2569:A:H2'	30:0:2570:G:O5'	2.19	0.43
30:0:2668:G:H2'	30:0:2669:U:H6	1.81	0.43
30:0:2692:G:N2	30:0:2701:G:C8	2.87	0.43
30:0:2886:C:O2'	30:0:2887:G:H5'	2.18	0.43
31:9:5:G:O2'	31:9:6:C:H5'	2.18	0.43
31:9:65:A:C4	31:9:113:C:C4	3.07	0.43
31:9:108:C:H2'	31:9:109:G:H8	1.82	0.43
2:B:27:ASN:HD21	30:0:2807:U:P	2.41	0.43
13:M:29:GLN:OE1	30:0:2244:A:H5''	2.18	0.43
13:M:70:GLY:HA3	13:M:73:ARG:HH21	1.77	0.43
14:N:91:ARG:O	14:N:94:GLU:HB2	2.19	0.43
26:Z:41:ARG:HD2	30:0:820:G:H22	1.83	0.43
30:0:85:C:H3'	30:0:86:A:H2'	2.01	0.43
30:0:102:A:C6	30:0:103:C:C4	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:273:G:H2'	30:0:274:G:O4'	2.18	0.43
30:0:284:C:OP2	30:0:284:C:H6	2.01	0.43
30:0:624:U:O4	30:0:628:1MA:H8	2.01	0.43
30:0:877:G:H3'	38:0:3106:HOH:O	2.19	0.43
30:0:1178:G:C5	30:0:1179:C:C4	3.07	0.43
30:0:1333:U:H2'	30:0:1334:C:C6	2.53	0.43
30:0:1519:U:H1'	38:0:3898:HOH:O	2.18	0.43
30:0:1552:G:C6	30:0:1634:G:C6	3.07	0.43
30:0:1602:C:H5'	38:0:6467:HOH:O	2.18	0.43
30:0:1665:G:C2	30:0:1666:C:C6	3.07	0.43
30:0:1705:C:O2	30:0:2735:U:C5'	2.65	0.43
30:0:2473:U:H2'	30:0:2476:C:H5	1.84	0.43
30:0:2507:G:H22	30:0:2512:U:H5''	1.84	0.43
30:0:2803:C:H2'	30:0:2804:C:C6	2.54	0.43
30:0:2855:G:C2	30:0:2904:U:C2	3.06	0.43
31:9:111:U:O2'	31:9:112:U:H5'	2.19	0.43
1:A:167:LYS:CE	26:Z:50:VAL:HG13	2.42	0.43
14:N:65:ASP:HB3	38:N:8820:HOH:O	2.19	0.43
14:N:168:LEU:C	14:N:170:GLU:H	2.25	0.43
16:P:58:SER:HB3	38:0:5593:HOH:O	2.18	0.43
21:U:6:CYS:HB2	21:U:13:ILE:CG1	2.49	0.43
25:Y:144:ARG:HB3	38:0:4369:HOH:O	2.18	0.43
29:3:22:VAL:HG12	29:3:90:PHE:HE2	1.83	0.43
30:0:79:G:H22	30:0:97:G:H1'	1.82	0.43
30:0:432:G:C2	30:0:433:C:C6	3.07	0.43
30:0:816:G:C6	30:0:817:G:N1	2.87	0.43
30:0:1159:G:C6	30:0:1160:G:C4	3.07	0.43
30:0:1202:A:H2'	30:0:1203:G:O4'	2.19	0.43
30:0:1255:A:H2'	30:0:1256:C:O5'	2.18	0.43
30:0:1703:G:C2	30:0:1716:A:C4	3.06	0.43
30:0:1788:U:C2	30:0:1805:G:C2	3.07	0.43
30:0:2094:G:C2	30:0:2652:U:O2	2.71	0.43
30:0:2510:C:H42	30:0:2564:G:H22	1.66	0.43
30:0:2727:A:C6	30:0:2756:U:N3	2.87	0.43
30:0:2780:C:C4	30:0:2781:U:C4	3.06	0.43
30:0:2812:A:H2	30:0:2814:A:H62	1.63	0.43
1:A:105:VAL:HG11	1:A:154:ALA:HB1	2.00	0.43
2:B:305:ASP:O	2:B:306:LYS:CB	2.66	0.43
5:E:7:ILE:HG23	5:E:45:ASP:O	2.19	0.43
5:E:95:VAL:O	5:E:126:ILE:HD12	2.18	0.43
10:J:99:GLU:HA	38:J:8871:HOH:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:134:VAL:O	16:P:137:LEU:HB3	2.19	0.43
18:R:18:LEU:HD12	18:R:143:VAL:CG1	2.49	0.43
29:3:17:HIS:ND1	30:0:2408:A:O2'	2.48	0.43
29:3:54:LYS:HE3	38:0:3005:HOH:O	2.18	0.43
30:0:191:A:H61	30:0:435:A:H62	1.67	0.43
30:0:1399:A:H2'	30:0:1400:C:C6	2.54	0.43
30:0:1667:A:H2'	30:0:1668:U:O4'	2.19	0.43
30:0:1697:G:H1'	38:0:7261:HOH:O	2.19	0.43
30:0:1712:A:H2'	30:0:1713:G:O4'	2.19	0.43
30:0:1882:C:H2'	30:0:1883:U:C6	2.53	0.43
30:0:2080:G:H2'	30:0:2081:A:C8	2.54	0.43
30:0:2328:U:C4	30:0:2329:C:C5	3.07	0.43
30:0:2332:A:H3'	30:0:2333:G:H8	1.84	0.43
31:9:11:A:H2	31:9:68:G:N3	2.17	0.43
31:9:39:U:H2'	31:9:40:C:OP1	2.18	0.43
1:A:72:GLU:HG2	26:Z:100:GLY:HA3	2.01	0.43
4:D:12:GLU:O	4:D:15:GLU:HG2	2.18	0.43
6:F:58:GLU:HB3	13:M:8:ILE:HG23	2.01	0.43
12:L:6:ARG:HD3	30:0:1299:G:O6	2.18	0.43
13:M:48:LYS:HE3	13:M:52:GLN:NE2	2.28	0.43
20:T:28:SER:HA	20:T:97:ARG:HD3	1.99	0.43
29:3:59:ASP:CG	30:0:2460:A:H5''	2.44	0.43
30:0:67:A:H5''	30:0:69:A:C8	2.54	0.43
30:0:135:G:C2	30:0:144:A:N3	2.86	0.43
30:0:393:G:C2	30:0:394:G:C4	3.06	0.43
30:0:435:A:O2'	30:0:436:A:H5'	2.19	0.43
30:0:699:C:C2	30:0:744:G:N2	2.87	0.43
30:0:793:A:C2	30:0:822:C:C2	3.06	0.43
30:0:816:G:O5'	30:0:816:G:H8	2.02	0.43
30:0:1192:A:H4'	38:0:4383:HOH:O	2.18	0.43
30:0:1342:C:H2'	30:0:1343:C:H5'	1.99	0.43
30:0:1383:U:H2'	30:0:1384:C:C6	2.54	0.43
30:0:1504:A:H4'	30:0:1506:U:C5	2.53	0.43
30:0:1600:G:OP2	30:0:1600:G:H8	2.02	0.43
30:0:1933:G:C2'	30:0:1934:A:H5'	2.48	0.43
30:0:2095:A:OP1	30:0:2096:A:H4'	2.19	0.43
30:0:2293:G:C5	30:0:2294:C:C5	3.07	0.43
30:0:2476:C:H2'	30:0:2476:C:O2	2.19	0.43
30:0:2779:G:N7	30:0:2790:C:C2	2.86	0.43
30:0:2896:A:N3	30:0:2896:A:H2'	2.34	0.43
31:9:11:A:H4'	31:9:13:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:TYR:HB2	30:0:1872:C:C5	2.54	0.42
1:A:81:GLN:H	1:A:92:ASN:ND2	2.17	0.42
3:C:142:ASP:C	3:C:144:PHE:H	2.27	0.42
3:C:156:LEU:O	3:C:160:LEU:HG	2.19	0.42
4:D:67:ASP:HA	4:D:68:PRO:HD3	1.92	0.42
5:E:81:GLU:O	5:E:172:PRO:HD3	2.19	0.42
13:M:42:ARG:HA	13:M:43:PRO:HD3	1.86	0.42
15:O:57:THR:O	15:O:111:VAL:HG23	2.19	0.42
19:S:42:GLU:O	19:S:46:ASP:HA	2.19	0.42
21:U:34:SER:HB3	38:0:3126:HOH:O	2.17	0.42
30:0:248:A:H5'	30:0:249:G:OP2	2.19	0.42
30:0:349:U:O5'	30:0:349:U:H6	2.02	0.42
30:0:577:G:C2	30:0:581:G:C6	3.07	0.42
30:0:729:C:C2	30:0:743:G:N2	2.87	0.42
30:0:877:G:N7	30:0:885:G:C6	2.87	0.42
30:0:970:U:H2'	38:0:6308:HOH:O	2.18	0.42
30:0:1287:A:H8	38:0:7887:HOH:O	2.02	0.42
31:9:16:G:C2	31:9:66:G:O6	2.72	0.42
31:9:110:G:C6	31:9:111:U:C5	3.07	0.42
3:C:24:THR:HG23	3:C:25:PRO:HD2	2.02	0.42
4:D:137:PRO:O	31:9:30:C:OP1	2.37	0.42
13:M:112:LEU:HB3	13:M:133:LEU:HB3	2.02	0.42
14:N:168:LEU:C	14:N:170:GLU:N	2.78	0.42
23:W:11:VAL:O	23:W:12:ASN:HB2	2.19	0.42
24:X:43:VAL:HG12	24:X:44:ASP:N	2.34	0.42
24:X:49:ARG:NH1	30:0:1385:G:O3'	2.51	0.42
27:1:44:LYS:HG2	30:0:148:A:H5''	2.01	0.42
30:0:95:A:H5''	30:0:97:G:O4'	2.19	0.42
30:0:188:C:H6	30:0:188:C:O5'	2.02	0.42
30:0:621:C:O2'	30:0:1357:A:N1	2.48	0.42
30:0:726:C:C2	30:0:727:G:C8	3.07	0.42
30:0:1183:C:N3	30:0:1184:C:N4	2.67	0.42
30:0:1184:C:O2'	30:0:1185:U:OP2	2.32	0.42
30:0:1568:G:C2'	30:0:1569:U:H5'	2.49	0.42
30:0:1970:G:H4'	30:0:1971:G:O5'	2.19	0.42
30:0:1981:A:C6	30:0:2005:G:H4'	2.54	0.42
30:0:2005:G:OP2	30:0:2006:C:H5''	2.19	0.42
30:0:2512:U:H4'	30:0:2514:U:O4	2.19	0.42
30:0:2531:U:H4'	38:0:9596:HOH:O	2.17	0.42
30:0:2600:A:H2'	30:0:2601:A:O4'	2.19	0.42
30:0:2853:U:C4	30:0:2906:A:N6	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:46:TYR:CE1	30:0:450:C:H4'	2.54	0.42
3:C:151:GLN:HA	3:C:151:GLN:HE21	1.84	0.42
3:C:194:PHE:HB2	3:C:212:VAL:HG12	2.00	0.42
4:D:76:ARG:NE	31:9:44:A:O4'	2.52	0.42
5:E:21:THR:HG23	5:E:30:THR:OG1	2.19	0.42
8:H:65:LEU:HA	8:H:65:LEU:HD12	1.80	0.42
26:Z:34:SER:HB3	30:0:797:A:H4'	2.00	0.42
30:0:107:U:H2'	30:0:108:U:H5'	2.01	0.42
30:0:111:C:H2'	30:0:112:G:O4'	2.19	0.42
30:0:314:G:N2	30:0:317:A:C8	2.87	0.42
30:0:354:A:H2'	30:0:355:C:C6	2.52	0.42
30:0:752:G:H2'	30:0:753:U:O4'	2.19	0.42
30:0:830:G:O2'	30:0:831:U:H5'	2.19	0.42
30:0:1115:U:H5''	30:0:1140:C:O2'	2.20	0.42
30:0:1474:C:O2'	30:0:1475:G:H5'	2.18	0.42
30:0:2248:C:O2'	30:0:2249:G:H5'	2.19	0.42
30:0:2374:G:H2'	30:0:2375:A:C8	2.53	0.42
2:B:57:GLU:HA	2:B:58:PRO:HD2	1.85	0.42
2:B:60:SER:HA	2:B:61:PRO:HD3	1.90	0.42
5:E:35:TYR:CD2	5:E:36:PRO:HD2	2.55	0.42
5:E:72:MET:O	5:E:76:VAL:HG22	2.19	0.42
5:E:106:ASN:ND2	5:E:109:GLY:HA2	2.34	0.42
12:L:38:HIS:CD2	12:L:39:GLU:HG3	2.54	0.42
19:S:57:THR:HG22	19:S:58:MET:N	2.34	0.42
20:T:24:ARG:HH21	20:T:39:ASN:ND2	2.17	0.42
26:Z:66:CYS:SG	26:Z:67:GLY:N	2.93	0.42
28:2:22:PRO:HG2	28:2:25:VAL:CG2	2.49	0.42
29:3:80:ARG:HH22	30:0:2381:C:H4'	1.84	0.42
30:0:282:C:O2'	30:0:368:C:N4	2.52	0.42
30:0:652:G:H2'	30:0:653:U:O4'	2.20	0.42
30:0:877:G:C6	30:0:885:G:C4	3.08	0.42
30:0:1195:G:N2	30:0:1205:U:C2	2.87	0.42
30:0:1350:U:H5''	38:0:5090:HOH:O	2.20	0.42
30:0:1789:G:C2'	30:0:1790:C:O5'	2.67	0.42
30:0:2362:A:H2'	30:0:2363:G:C8	2.54	0.42
30:0:2502:C:O2'	30:0:2503:A:H5'	2.19	0.42
30:0:2655:U:C4	30:0:2656:G:N7	2.87	0.42
30:0:2893:C:C2'	30:0:2894:C:H5'	2.49	0.42
31:9:36:C:C5	31:9:37:C:C4	3.08	0.42
31:9:57:A:N3	31:9:57:A:H5'	2.34	0.42
31:9:65:A:C2'	31:9:66:G:OP2	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:GLN:HB2	1:A:92:ASN:ND2	2.35	0.42
1:A:223:ARG:HH12	30:0:2270:G:C4'	2.27	0.42
2:B:162:MET:HG3	2:B:310:ARG:NH1	2.35	0.42
2:B:177:HIS:O	2:B:181:ILE:HG13	2.19	0.42
2:B:307:ARG:HG2	2:B:308:LEU:N	2.34	0.42
3:C:211:ASP:HB2	3:C:231:ARG:HH12	1.85	0.42
4:D:88:LEU:HB2	4:D:89:PRO:HD3	2.00	0.42
8:H:91:ARG:NH2	8:H:135:GLN:NE2	2.68	0.42
12:L:10:SER:O	12:L:11:ARG:HB3	2.19	0.42
15:O:105:ASN:HD21	15:O:109:SER:N	2.18	0.42
16:P:10:ALA:HA	16:P:13:VAL:HG12	2.02	0.42
24:X:12:ILE:HB	24:X:70:ILE:CG2	2.49	0.42
26:Z:38:PHE:HB3	26:Z:42:TYR:HD1	1.82	0.42
29:3:10:TYR:CD2	30:0:2382:A:H1'	2.55	0.42
30:0:138:U:P	30:0:139:C:H5	2.42	0.42
30:0:161:A:H2'	30:0:162:C:C6	2.53	0.42
30:0:165:A:H2'	30:0:166:A:OP1	2.19	0.42
30:0:265:U:C2	30:0:266:G:C8	3.07	0.42
30:0:690:G:H1'	30:0:731:U:O2'	2.20	0.42
30:0:776:A:C2	30:0:780:A:C6	3.08	0.42
30:0:1342:C:O2'	30:0:1343:C:H5'	2.18	0.42
30:0:1754:A:H8	30:0:1754:A:O5'	2.02	0.42
30:0:1757:U:H5	38:0:3214:HOH:O	2.02	0.42
30:0:1848:G:O2'	30:0:1849:G:H5'	2.19	0.42
30:0:1998:G:O2'	30:0:2026:C:H1'	2.20	0.42
30:0:2346:C:O2	30:0:2346:C:H2'	2.18	0.42
30:0:2470:A:H2'	30:0:2471:G:O5'	2.19	0.42
31:9:22:G:C6	31:9:55:U:C2	3.07	0.42
1:A:10:GLY:HA2	30:0:1861:C:O2	2.20	0.42
2:B:48:MET:O	30:0:2719:A:H5'	2.20	0.42
8:H:48:VAL:HG13	38:H:218:HOH:O	2.18	0.42
9:I:133:THR:HG22	9:I:134:ILE:H	1.83	0.42
13:M:102:GLU:CD	13:M:164:THR:HG21	2.43	0.42
13:M:185:PRO:HD3	38:0:9800:HOH:O	2.19	0.42
13:M:191:GLY:O	30:0:175:G:H3'	2.19	0.42
15:O:63:LYS:NZ	30:0:659:A:N7	2.58	0.42
24:X:71:ARG:HD3	38:X:2171:HOH:O	2.20	0.42
27:1:37:CYS:SG	27:1:39:PHE:HB2	2.59	0.42
29:3:33:MET:CG	30:0:1922:A:H2'	2.50	0.42
30:0:221:G:H2'	30:0:222:A:C8	2.55	0.42
30:0:453:A:C4	30:0:479:G:N7	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:685:C:O2'	30:0:748:C:H5''	2.19	0.42
30:0:1047:U:O5'	30:0:1047:U:H6	2.03	0.42
30:0:1097:A:H2'	30:0:1098:A:C8	2.54	0.42
30:0:1367:A:H2'	30:0:1368:U:O4'	2.20	0.42
30:0:1391:G:H2'	30:0:1392:A:H5'	2.01	0.42
30:0:1573:A:C8	30:0:1574:C:C6	3.08	0.42
30:0:1603:A:H5'	30:0:1605:G:H5'	1.99	0.42
30:0:1643:C:O2'	30:0:1644:C:H5'	2.19	0.42
30:0:1680:C:H5'	30:0:1685:A:N6	2.34	0.42
30:0:1709:G:C6	30:0:1711:A:C5	3.07	0.42
30:0:2499:U:H2'	30:0:2500:C:O4'	2.20	0.42
30:0:2805:A:C8	30:0:2806:C:C5	3.07	0.42
30:0:2842:G:C2'	30:0:2843:A:H5'	2.50	0.42
31:9:108:C:H2'	31:9:109:G:C8	2.55	0.42
1:A:26:ASP:HB2	38:0:7291:HOH:O	2.18	0.42
8:H:59:GLN:HE21	8:H:129:ARG:HG2	1.85	0.42
10:J:116:LEU:HB2	10:J:119:THR:CG2	2.49	0.42
10:J:131:THR:O	10:J:134:GLU:HB2	2.19	0.42
13:M:70:GLY:HA3	13:M:73:ARG:CZ	2.50	0.42
13:M:159:VAL:HG13	13:M:160:PHE:N	2.35	0.42
14:N:169:PRO:O	14:N:172:PHE:HB3	2.20	0.42
20:T:75:GLU:O	20:T:76:ASP:HB2	2.19	0.42
30:0:462:A:N6	30:0:477:A:C2	2.88	0.42
30:0:583:C:H2'	30:0:584:U:H6	1.85	0.42
30:0:590:A:H2'	30:0:591:A:C5'	2.48	0.42
30:0:669:G:C4	30:0:670:G:C8	3.07	0.42
30:0:795:G:H2'	38:0:9823:HOH:O	2.20	0.42
30:0:1060:C:H6	30:0:1060:C:H5'	1.85	0.42
30:0:1255:A:C2'	30:0:1256:C:O5'	2.68	0.42
30:0:1523:G:C6	30:0:1524:U:O4	2.73	0.42
30:0:1965:C:O5'	30:0:1965:C:H6	2.02	0.42
30:0:2492:U:C4	30:0:2493:C:C4	3.07	0.42
30:0:2812:A:H2	30:0:2814:A:N7	2.17	0.42
30:0:2864:U:H2'	30:0:2865:G:H5'	2.02	0.42
1:A:160:ALA:CB	26:Z:89:THR:HB	2.49	0.42
38:C:8619:HOH:O	30:0:338:C:H5'	2.19	0.42
4:D:104:PHE:CD2	4:D:104:PHE:N	2.88	0.42
13:M:30:GLU:O	13:M:34:GLU:HG3	2.19	0.42
23:W:92:ASP:OD2	23:W:94:SER:HB2	2.20	0.42
24:X:25:ARG:HD2	38:X:5356:HOH:O	2.19	0.42
26:Z:37:ARG:HG3	26:Z:38:PHE:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:451:C:C2'	30:0:452:G:H5'	2.50	0.42
30:0:711:G:N2	30:0:718:C:N1	2.67	0.42
30:0:802:G:N2	30:0:812:A:C4	2.88	0.42
30:0:877:G:C2	30:0:885:G:O4'	2.73	0.42
30:0:1241:G:H2'	30:0:1242:A:O4'	2.19	0.42
30:0:1537:C:O2'	30:0:1538:C:H5'	2.18	0.42
30:0:1541:G:O2'	30:0:1542:G:H5'	2.18	0.42
30:0:2256:G:H2'	30:0:2257:G:C5'	2.50	0.42
1:A:169:PHE:O	1:A:170:VAL:HB	2.20	0.42
2:B:8:LYS:HB3	2:B:218:TRP:O	2.19	0.42
2:B:316:ARG:HB2	30:0:2768:A:C8	2.55	0.42
3:C:87:ARG:NH2	30:0:894:A:C2	2.88	0.42
30:0:325:U:H3'	38:0:5512:HOH:O	2.19	0.42
30:0:387:G:O2'	30:0:388:G:H5'	2.20	0.42
30:0:473:A:C2'	30:0:474:C:H5'	2.49	0.42
30:0:485:A:N3	30:0:487:G:H5''	2.34	0.42
30:0:1183:C:H1'	30:0:1192:A:N6	2.35	0.42
30:0:1187:U:O2	30:0:1189:A:H5''	2.20	0.42
30:0:1413:A:H2'	30:0:1414:A:O4'	2.20	0.42
30:0:1819:G:H2'	30:0:1820:G:H5'	2.01	0.42
30:0:1840:A:H4'	30:0:1841:C:O5'	2.20	0.42
30:0:2355:G:N3	30:0:2355:G:C2'	2.83	0.42
30:0:2523:U:O2'	30:0:2524:G:H5'	2.19	0.42
31:9:74:G:C2	31:9:75:G:C8	3.08	0.42
31:9:92:G:C6	31:9:93:A:N6	2.88	0.42
5:E:77:THR:OG1	5:E:78:GLU:N	2.50	0.42
8:H:149:VAL:HG13	8:H:150:LYS:N	2.35	0.42
11:K:105:ARG:HD2	38:K:3385:HOH:O	2.19	0.42
13:M:181:GLU:CD	30:0:394:G:H1	2.27	0.42
16:P:40:VAL:O	16:P:44:VAL:HG23	2.20	0.42
17:Q:27:GLN:HB3	38:9:9083:HOH:O	2.20	0.42
23:W:10:GLU:HB3	38:W:1223:HOH:O	2.20	0.42
24:X:70:ILE:HG23	24:X:70:ILE:O	2.18	0.42
26:Z:61:HIS:CG	26:Z:95:PRO:HG3	2.55	0.42
28:2:41:HIS:CE1	30:0:1439:C:H5''	2.54	0.42
29:3:14:CYS:SG	38:3:9063:HOH:O	2.62	0.42
29:3:83:TRP:O	29:3:85:ALA:N	2.53	0.42
30:0:59:A:H5''	38:0:4313:HOH:O	2.18	0.42
30:0:67:A:H3'	30:0:67:A:OP2	2.20	0.42
30:0:293:A:C2	30:0:294:C:C6	3.08	0.42
30:0:868:G:H2'	38:0:3039:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1015:C:H2'	30:0:1016:U:H6	1.82	0.42
30:0:2700:G:C2'	30:0:2701:G:H5'	2.49	0.42
30:0:2909:G:N2	30:0:2910:A:C5	2.88	0.42
31:9:114:G:C6	31:9:115:C:N4	2.88	0.42
2:B:41:PHE:CD1	2:B:79:MET:HE2	2.54	0.41
2:B:203:ALA:HA	2:B:263:THR:HA	2.02	0.41
2:B:224:LYS:HD3	2:B:224:LYS:HA	1.83	0.41
38:I:3512:HOH:O	30:0:1163:G:N2	2.53	0.41
12:L:35:ARG:HB2	12:L:43:HIS:CD2	2.55	0.41
12:L:53:ARG:N	33:L:8810:CL:CL	2.66	0.41
12:L:73:VAL:HG21	12:L:116:HIS:CE1	2.54	0.41
13:M:89:THR:HA	38:M:8950:HOH:O	2.19	0.41
15:O:39:THR:HB	38:0:4589:HOH:O	2.19	0.41
15:O:68:GLY:HA3	30:0:745:G:O6	2.20	0.41
21:U:56:ARG:NH1	30:0:2890:A:C2	2.88	0.41
28:2:48:ASP:O	28:2:49:GLU:HB2	2.20	0.41
29:3:62:THR:CG2	29:3:63:LYS:N	2.83	0.41
30:0:314:G:C2	30:0:317:A:C8	3.08	0.41
30:0:335:U:C2'	30:0:336:G:OP1	2.68	0.41
30:0:371:U:H2'	30:0:372:A:H8	1.85	0.41
30:0:396:U:HO2'	30:0:397:A:P	2.40	0.41
30:0:628:1MA:H4'	38:0:3136:HOH:O	2.19	0.41
30:0:887:G:H2'	30:0:888:U:C6	2.54	0.41
30:0:1006:A:N3	30:0:2298:C:O2'	2.45	0.41
30:0:1182:C:H4'	30:0:1192:A:N7	2.35	0.41
30:0:1210:G:C2	30:0:1211:G:N9	2.88	0.41
30:0:1588:G:C6	30:0:1589:G:C6	3.08	0.41
30:0:1624:A:O4'	30:0:1626:A:C8	2.73	0.41
30:0:1789:G:N2	30:0:1790:C:H1'	2.35	0.41
30:0:1919:A:H4'	38:0:4820:HOH:O	2.19	0.41
30:0:2433:A:H2'	30:0:2434:A:C8	2.54	0.41
30:0:2478:U:H2'	30:0:2479:A:H8	1.85	0.41
30:0:2799:A:H5'	30:0:2800:A:P	2.59	0.41
1:A:51:ARG:NH2	1:A:53:ALA:HB3	2.35	0.41
1:A:199:HIS:CD2	1:A:200:PRO:HD2	2.55	0.41
2:B:58:PRO:HA	2:B:63:GLU:CD	2.44	0.41
4:D:76:ARG:CZ	31:9:44:A:C1'	2.98	0.41
11:K:4:LEU:HD23	11:K:4:LEU:HA	1.84	0.41
16:P:94:TRP:CH2	16:P:98:ILE:HG13	2.55	0.41
22:V:23:LEU:HD22	22:V:49:LEU:HD23	2.01	0.41
26:Z:78:ILE:HB	38:Z:8715:HOH:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1:31:LYS:O	27:1:33:VAL:HG23	2.20	0.41
29:3:5:ARG:HA	29:3:22:VAL:HG23	2.02	0.41
30:0:102:A:C6	30:0:103:C:N4	2.88	0.41
30:0:201:G:H1'	38:0:4539:HOH:O	2.19	0.41
30:0:272:A:N1	30:0:369:G:H5''	2.34	0.41
30:0:412:C:C2'	30:0:413:G:H5'	2.50	0.41
30:0:446:G:H3'	38:0:9539:HOH:O	2.20	0.41
30:0:495:A:O4'	30:0:1390:A:H1'	2.20	0.41
30:0:1163:G:C2	30:0:1184:C:N3	2.87	0.41
30:0:1178:G:H2'	30:0:1179:C:H6	1.79	0.41
30:0:1449:G:H4'	38:0:9213:HOH:O	2.20	0.41
30:0:1507:C:H4'	38:0:3595:HOH:O	2.20	0.41
30:0:1519:U:O5'	30:0:1519:U:H6	2.04	0.41
30:0:1915:U:O2	30:0:1925:G:C2	2.73	0.41
30:0:2004:U:O2	30:0:2004:U:H2'	2.20	0.41
30:0:2020:C:O2'	30:0:2021:C:H5'	2.20	0.41
30:0:2061:C:C2'	30:0:2062:A:H5'	2.51	0.41
30:0:2749:U:O2'	30:0:2751:C:OP2	2.33	0.41
30:0:2912:C:C2'	30:0:2913:A:H5'	2.50	0.41
31:9:50:G:C6	31:9:51:A:C6	3.08	0.41
31:9:56:A:C3'	31:9:57:A:C5'	2.93	0.41
2:B:211:THR:HG21	38:0:7438:HOH:O	2.20	0.41
4:D:84:LEU:HD23	4:D:84:LEU:HA	1.92	0.41
8:H:59:GLN:NE2	8:H:96:GLN:HG2	2.35	0.41
38:H:216:HOH:O	30:0:2517:A:H2	1.99	0.41
12:L:150:GLN:HB3	38:L:8869:HOH:O	2.19	0.41
21:U:31:PHE:CG	21:U:37:GLU:HG2	2.55	0.41
24:X:54:ILE:HD11	24:X:85:VAL:HG12	2.03	0.41
25:Y:157:ILE:HD13	38:0:4836:HOH:O	2.20	0.41
26:Z:34:SER:HA	30:0:797:A:C5'	2.50	0.41
30:0:38:G:C2'	30:0:39:G:H5'	2.50	0.41
30:0:236:A:H8	30:0:236:A:OP1	2.03	0.41
30:0:1212:C:C5	30:0:1213:C:C5	3.09	0.41
30:0:1303:C:O2	30:0:1353:C:H1'	2.20	0.41
30:0:1419:U:H5'	30:0:1420:C:OP2	2.21	0.41
30:0:1554:C:O2'	30:0:1631:A:H1'	2.19	0.41
30:0:1804:A:H2'	30:0:1805:G:C8	2.55	0.41
30:0:1826:C:O2'	30:0:1827:G:H5'	2.21	0.41
30:0:1878:G:O2'	30:0:1879:U:P	2.78	0.41
30:0:2256:G:C2'	30:0:2257:G:H5'	2.51	0.41
30:0:2474:A:C8	30:0:2621:PSU:H4'	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2782:G:O6	30:0:2790:C:H5''	2.19	0.41
30:0:2795:C:O2'	30:0:2796:U:C5'	2.65	0.41
30:0:2799:A:N6	30:0:2801:A:C2	2.89	0.41
2:B:69:VAL:HA	2:B:70:PRO:HD3	1.77	0.41
5:E:107:PHE:O	5:E:110:GLU:HG3	2.20	0.41
15:O:26:TRP:HA	15:O:26:TRP:CE3	2.55	0.41
19:S:17:ASP:HB3	19:S:23:LYS:HB2	2.01	0.41
24:X:23:HIS:HE1	30:0:2044:G:OP1	2.03	0.41
26:Z:34:SER:HA	30:0:797:A:H5'	2.02	0.41
30:0:107:U:C2'	30:0:108:U:H5'	2.50	0.41
30:0:281:U:C2'	30:0:282:C:C5'	2.98	0.41
30:0:517:U:H2'	30:0:518:G:H5'	2.02	0.41
30:0:552:A:H5'	38:0:5878:HOH:O	2.19	0.41
30:0:1607:A:C5	30:0:1608:G:C8	3.09	0.41
30:0:1757:U:H6	30:0:1757:U:O5'	2.04	0.41
30:0:1769:C:C2'	30:0:1770:U:H5'	2.51	0.41
30:0:1819:G:C2'	30:0:1820:G:H5'	2.50	0.41
30:0:1894:C:N4	30:0:1939:U:H2'	2.34	0.41
30:0:1928:C:C2'	30:0:1929:G:H5'	2.50	0.41
30:0:1942:A:C1'	38:0:9045:HOH:O	2.69	0.41
30:0:1997:A:H2	30:0:2026:C:O2'	2.04	0.41
30:0:2710:U:H2'	30:0:2711:U:C6	2.55	0.41
30:0:2723:G:H1'	38:0:4812:HOH:O	2.19	0.41
30:0:2815:G:H4'	30:0:2816:A:OP2	2.20	0.41
31:9:58:G:C8	31:9:59:C:C4	3.08	0.41
31:9:110:G:C6	31:9:111:U:C4	3.08	0.41
1:A:212:PRO:HA	30:0:1943:C:O4'	2.20	0.41
2:B:222:LYS:HG3	30:0:2038:A:H5''	2.01	0.41
2:B:320:GLN:HE21	2:B:321:PRO:HD3	1.84	0.41
3:C:5:ILE:HG12	3:C:139:VAL:CG1	2.50	0.41
6:F:26:THR:HB	6:F:102:GLY:HA3	2.02	0.41
7:G:23:ILE:O	7:G:27:ILE:HG13	2.20	0.41
8:H:165:ARG:HD2	38:H:241:HOH:O	2.21	0.41
10:J:54:VAL:HG11	10:J:138:THR:HG21	2.02	0.41
10:J:76:ASP:HA	38:J:8863:HOH:O	2.20	0.41
11:K:66:ARG:NH1	30:0:1992:U:H3'	2.35	0.41
14:N:132:ASN:O	14:N:135:VAL:HG12	2.21	0.41
19:S:51:GLN:HE21	19:S:53:ASN:HD21	1.67	0.41
21:U:5:GLU:HG2	21:U:6:CYS:N	2.36	0.41
25:Y:130:ARG:HB2	25:Y:142:SER:O	2.20	0.41
25:Y:152:LYS:CB	25:Y:160:LYS:HG3	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:189:ASN:HD22	25:Y:191:ASP:N	2.19	0.41
30:0:10:U:O4	30:0:532:A:OP2	2.38	0.41
30:0:343:C:H1'	38:0:5552:HOH:O	2.19	0.41
30:0:594:C:C4	30:0:595:U:C4	3.08	0.41
30:0:910:C:H2'	30:0:911:G:O4'	2.21	0.41
30:0:1063:G:O5'	30:0:2307:A:H1'	2.21	0.41
30:0:1271:A:H2'	30:0:1272:C:H6	1.84	0.41
30:0:1423:C:O2'	30:0:1424:A:H5'	2.20	0.41
30:0:1882:C:H2'	30:0:1883:U:H6	1.86	0.41
30:0:1898:G:H2'	30:0:1899:C:C6	2.55	0.41
30:0:2470:A:C2'	30:0:2471:G:O5'	2.68	0.41
30:0:2511:A:H2'	30:0:2512:U:C6	2.56	0.41
30:0:2854:A:N6	30:0:2905:A:N6	2.69	0.41
1:A:70:ALA:HA	1:A:71:PRO:HD3	1.82	0.41
2:B:241:PRO:HD2	38:B:9125:HOH:O	2.20	0.41
18:R:9:ASP:HA	18:R:10:PRO:HD2	1.90	0.41
19:S:52:VAL:HG22	19:S:66:VAL:HG13	2.03	0.41
23:W:122:ARG:NH2	38:0:5254:HOH:O	2.52	0.41
30:0:165:A:C2'	30:0:166:A:OP1	2.67	0.41
30:0:307:G:C2	30:0:309:C:C4	3.08	0.41
30:0:1540:G:C4	30:0:1541:G:C8	3.09	0.41
30:0:1666:C:C2'	30:0:1667:A:H5'	2.32	0.41
30:0:1679:C:O2	30:0:1685:A:C2	2.73	0.41
30:0:2057:U:O5'	30:0:2057:U:H6	2.03	0.41
30:0:2255:A:H2'	30:0:2256:G:O4'	2.20	0.41
30:0:2692:G:N2	30:0:2701:G:C5	2.88	0.41
31:9:60:C:O2	31:9:60:C:H2'	2.19	0.41
8:H:89:THR:O	8:H:137:PHE:HD2	2.04	0.41
21:U:17:THR:HG21	38:U:2221:HOH:O	2.21	0.41
21:U:42:LEU:HB3	30:0:1810:C:O4'	2.21	0.41
29:3:91:GLN:O	29:3:92:GLU:HB2	2.21	0.41
30:0:69:A:C8	30:0:69:A:C3'	3.04	0.41
30:0:213:G:O2'	30:0:214:U:OP2	2.39	0.41
30:0:268:U:O4	30:0:269:G:N1	2.54	0.41
30:0:393:G:C6	30:0:394:G:C6	3.09	0.41
30:0:631:A:C6	30:0:2074:A:H5'	2.56	0.41
30:0:677:C:O5'	30:0:677:C:H6	2.03	0.41
30:0:812:A:H1'	38:0:3946:HOH:O	2.20	0.41
30:0:862:U:O2'	30:0:863:G:H5'	2.20	0.41
30:0:870:G:C3'	30:0:871:G:H5''	2.51	0.41
30:0:1012:A:H8	30:0:1012:A:O5'	2.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1191:A:O5'	30:0:1191:A:C8	2.74	0.41
30:0:1196:C:H2'	30:0:1197:G:H5'	2.02	0.41
30:0:1438:G:N3	30:0:1438:G:H2'	2.35	0.41
30:0:1544:U:O2'	30:0:1545:C:H5'	2.20	0.41
30:0:1798:C:OP2	30:0:1799:G:H5''	2.20	0.41
30:0:2325:U:C2	30:0:2326:C:C6	3.09	0.41
30:0:2383:G:C6	30:0:2384:U:C4	3.08	0.41
30:0:2506:A:O2'	30:0:2507:G:C8	2.51	0.41
30:0:2668:G:N2	30:0:2669:U:C2	2.88	0.41
30:0:2668:G:O4'	30:0:2827:A:C2	2.73	0.41
1:A:47:HIS:HD2	30:0:1654:U:O2'	2.03	0.41
1:A:199:HIS:HE1	30:0:1881:A:OP1	2.04	0.41
1:A:232:ARG:CZ	30:0:1939:U:H4'	2.50	0.41
2:B:195:ARG:HG2	2:B:323:LEU:HD22	2.03	0.41
4:D:20:LYS:HG2	4:D:133:ASN:HB3	2.02	0.41
8:H:91:ARG:NH1	8:H:138:THR:OG1	2.53	0.41
10:J:107:ASN:HA	10:J:108:PRO:HD2	1.98	0.41
14:N:83:LEU:HD13	14:N:175:LEU:HD23	2.03	0.41
16:P:89:ASN:HA	38:P:165:HOH:O	2.20	0.41
18:R:114:VAL:HG13	18:R:114:VAL:O	2.20	0.41
23:W:43:GLY:HA3	30:0:945:U:O2'	2.20	0.41
26:Z:70:ARG:HB2	26:Z:81:CYS:HG	1.86	0.41
30:0:189:A:H2	30:0:205:U:O2	2.04	0.41
30:0:241:A:C2	30:0:378:A:H4'	2.55	0.41
30:0:383:A:H2'	30:0:384:G:O4'	2.21	0.41
30:0:1173:A:H2'	30:0:1177:A:H62	1.85	0.41
30:0:1209:C:O2'	30:0:1210:G:H5'	2.20	0.41
30:0:1621:G:H2'	30:0:1622:G:H8	1.86	0.41
30:0:1774:G:C2'	30:0:1775:A:H5'	2.51	0.41
30:0:1803:C:H2'	30:0:1804:A:C8	2.56	0.41
30:0:1913:C:H2'	30:0:1914:C:C6	2.54	0.41
30:0:1977:U:OP1	30:0:1977:U:H3'	2.20	0.41
30:0:2039:A:H2'	30:0:2040:C:C6	2.56	0.41
30:0:2324:G:H2'	30:0:2325:U:C6	2.56	0.41
30:0:2700:G:H2'	30:0:2701:G:O5'	2.21	0.41
31:9:82:U:H2'	31:9:83:G:C8	2.56	0.41
1:A:171:LYS:HB2	30:0:820:G:C6	2.55	0.41
2:B:74:ILE:HG13	38:B:9076:HOH:O	2.20	0.41
4:D:36:ASN:HA	38:D:7500:HOH:O	2.20	0.41
5:E:15:GLN:HG2	5:E:16:ASP:N	2.36	0.41
5:E:20:ILE:HD12	5:E:33:LEU:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:119:HIS:O	5:E:140:ALA:HB1	2.21	0.41
5:E:145:ALA:HB1	5:E:168:ILE:CD1	2.49	0.41
6:F:61:MET:O	6:F:64:PRO:HD2	2.21	0.41
12:L:113:GLN:C	30:0:700:A:H62	2.29	0.41
14:N:73:ALA:HB1	14:N:74:PRO:CD	2.51	0.41
16:P:61:ARG:NH2	30:0:2737:C:OP2	2.40	0.41
17:Q:41:LEU:HB3	17:Q:52:PHE:CZ	2.56	0.41
19:S:73:ASP:OD1	19:S:76:GLU:HG3	2.21	0.41
21:U:56:ARG:NH1	30:0:2890:A:C4	2.89	0.41
23:W:120:PRO:HG2	30:0:1095:U:O2	2.20	0.41
25:Y:152:LYS:HB3	25:Y:160:LYS:HG3	2.02	0.41
26:Z:37:ARG:C	26:Z:39:GLY:H	2.28	0.41
26:Z:47:ARG:HD2	38:Z:8718:HOH:O	2.20	0.41
30:0:20:G:H2'	30:0:21:G:O5'	2.21	0.41
30:0:51:G:C2	30:0:111:C:C2	3.08	0.41
30:0:61:G:C2	30:0:62:C:C2	3.09	0.41
30:0:265:U:C4	30:0:266:G:N7	2.89	0.41
30:0:279:C:H2'	30:0:280:C:H5'	2.01	0.41
30:0:844:A:C6	30:0:882:A:C6	3.09	0.41
30:0:1024:G:C5	30:0:1025:C:C4	3.09	0.41
30:0:1089:G:H1'	30:0:1290:G:N2	2.36	0.41
30:0:1168:C:C2'	30:0:1169:U:H5'	2.51	0.41
30:0:1193:A:C2	30:0:1194:A:N6	2.89	0.41
30:0:1207:A:H5'	30:0:1208:C:OP2	2.21	0.41
30:0:1226:G:C2	30:0:1227:C:C6	3.08	0.41
30:0:1339:G:C5	30:0:1340:G:C6	3.09	0.41
30:0:1362:U:H2'	30:0:1363:G:H8	1.86	0.41
30:0:1416:G:C2'	30:0:1417:G:H5'	2.51	0.41
30:0:1476:A:H1'	30:0:1867:G:O2'	2.21	0.41
30:0:1543:G:H2'	30:0:1544:U:C5	2.56	0.41
30:0:1553:C:O5'	30:0:1553:C:H6	2.04	0.41
30:0:1619:G:H2'	30:0:1620:C:O4'	2.21	0.41
30:0:1748:U:C6	30:0:1749:U:C5	3.09	0.41
30:0:1973:A:H5'	30:0:1973:A:C8	2.53	0.41
30:0:2366:C:P	38:0:6939:HOH:O	2.79	0.41
30:0:2453:G:H2'	30:0:2454:C:C6	2.55	0.41
30:0:2599:A:C6	30:0:2600:A:N1	2.89	0.41
30:0:2695:C:N4	30:0:2701:G:N2	2.69	0.41
30:0:2801:A:C4	30:0:2802:C:C5	3.08	0.41
31:9:29:C:C6	31:9:30:C:C6	3.08	0.41
1:A:37:VAL:HG13	38:A:9088:HOH:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:288:GLY:HA2	30:0:2898:G:H4'	2.02	0.41
38:B:9106:HOH:O	30:0:2818:A:H2	2.04	0.41
5:E:23:GLU:HG2	5:E:28:SER:CB	2.51	0.41
5:E:81:GLU:HA	5:E:133:VAL:O	2.21	0.41
13:M:68:ARG:HB2	38:M:8932:HOH:O	2.19	0.41
18:R:130:MET:HG3	38:0:7551:HOH:O	2.21	0.41
23:W:132:VAL:HG21	23:W:140:LYS:O	2.21	0.41
30:0:23:G:H1'	30:0:520:A:N6	2.35	0.41
30:0:123:U:O2'	30:0:124:C:H5'	2.21	0.41
30:0:282:C:O2	30:0:282:C:C2'	2.62	0.41
30:0:714:U:O4'	30:0:716:G:C2	2.74	0.41
30:0:736:A:H5''	38:0:4253:HOH:O	2.21	0.41
30:0:965:A:N3	30:0:965:A:H2'	2.36	0.41
30:0:1103:C:C2	30:0:1241:G:N2	2.89	0.41
30:0:1195:G:N1	30:0:1205:U:N3	2.69	0.41
30:0:1208:C:H2'	30:0:1208:C:O2	2.19	0.41
30:0:1591:A:H5'	30:0:1603:A:H61	1.86	0.41
30:0:1634:G:C4	30:0:1635:U:C5	3.08	0.41
30:0:2016:U:H2'	30:0:2017:U:O4'	2.21	0.41
30:0:2098:C:O5'	30:0:2098:C:H6	2.04	0.41
30:0:2269:C:C4	30:0:2270:G:C5	3.08	0.41
30:0:2526:C:C6	30:0:2526:C:H5'	2.56	0.41
30:0:2617:G:H5''	38:0:3896:HOH:O	2.20	0.41
31:9:14:G:H8	31:9:14:G:C5'	2.13	0.41
31:9:110:G:N3	31:9:110:G:H2'	2.35	0.41
3:C:118:THR:HG21	3:C:233:THR:HB	2.03	0.40
4:D:28:GLY:CA	4:D:69:ILE:HG23	2.51	0.40
6:F:38:LYS:HE3	30:0:244:C:OP2	2.21	0.40
6:F:70:LYS:C	6:F:72:VAL:H	2.29	0.40
13:M:72:ALA:HB3	38:M:8950:HOH:O	2.21	0.40
13:M:75:ARG:HG3	38:M:8868:HOH:O	2.20	0.40
14:N:110:THR:HA	14:N:111:PRO:HD3	1.98	0.40
19:S:11:THR:CG2	30:0:1444:G:H5''	2.50	0.40
23:W:4:LEU:CD2	23:W:54:PHE:HB3	2.51	0.40
23:W:48:VAL:HG12	23:W:48:VAL:O	2.21	0.40
25:Y:125:LYS:HB2	25:Y:126:PRO:HD2	2.03	0.40
28:2:42:TRP:HZ2	30:0:1438:G:H1'	1.87	0.40
29:3:86:GLY:HA2	38:3:9032:HOH:O	2.21	0.40
30:0:257:G:N2	30:0:258:G:C4	2.89	0.40
30:0:797:A:H2'	30:0:798:G:O4'	2.21	0.40
30:0:1170:U:O2	30:0:1172:G:H8	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1175:G:C5	30:0:1193:A:C2	3.10	0.40
30:0:1177:A:C6	30:0:1178:G:C5	3.09	0.40
30:0:1832:G:N3	30:0:1833:U:C6	2.89	0.40
30:0:2330:U:H4'	30:0:2331:C:OP1	2.20	0.40
30:0:2414:A:N1	30:0:2415:A:C6	2.90	0.40
30:0:2635:A:H2'	30:0:2636:C:H5'	1.98	0.40
30:0:2692:G:N2	30:0:2701:G:C4	2.88	0.40
3:C:206:ASN:HB2	30:0:329:A:OP2	2.20	0.40
6:F:48:VAL:CG2	6:F:74:PHE:HB3	2.51	0.40
11:K:24:THR:HB	11:K:64:MET:HE2	2.03	0.40
13:M:113:ARG:NH1	13:M:155:GLN:HB2	2.36	0.40
15:O:32:ARG:HD3	15:O:32:ARG:O	2.22	0.40
24:X:26:ALA:HB3	24:X:63:ARG:HG3	2.03	0.40
29:3:51:LYS:C	29:3:53:SER:H	2.30	0.40
30:0:69:A:C8	30:0:69:A:C5'	2.98	0.40
30:0:312:U:O2	30:0:320:G:C2	2.75	0.40
30:0:366:U:H2'	30:0:367:G:O4'	2.20	0.40
30:0:534:C:H2'	30:0:2083:A:C2	2.57	0.40
30:0:594:C:H2'	30:0:595:U:C6	2.56	0.40
30:0:596:C:H6	30:0:596:C:O5'	2.03	0.40
30:0:962:C:H2'	30:0:963:C:H5'	2.03	0.40
30:0:1634:G:C6	30:0:1635:U:C4	3.10	0.40
30:0:1681:G:H5''	30:0:1682:A:H5'	2.03	0.40
30:0:1774:G:H2'	30:0:1775:A:C5'	2.51	0.40
30:0:2121:G:C2'	30:0:2122:C:H5'	2.51	0.40
30:0:2245:C:H6	30:0:2245:C:O5'	2.04	0.40
30:0:2300:A:H4'	30:0:2301:A:N3	2.37	0.40
30:0:2335:C:N3	30:0:2350:G:C2	2.89	0.40
30:0:2501:G:H1	30:0:2519:C:N4	2.18	0.40
30:0:2831:C:C2'	30:0:2832:C:C5'	2.93	0.40
30:0:2834:G:C2'	30:0:2835:C:O5'	2.69	0.40
2:B:5:ARG:NH2	30:0:2548:C:OP2	2.55	0.40
2:B:14:GLY:HA2	2:B:15:PRO:C	2.45	0.40
2:B:188:HIS:ND1	2:B:188:HIS:N	2.69	0.40
2:B:277:GLU:N	2:B:278:PRO:CD	2.84	0.40
6:F:50:VAL:HG11	6:F:60:VAL:HG11	2.03	0.40
13:M:46:LEU:O	13:M:50:ARG:HG3	2.21	0.40
22:V:12:THR:HG23	22:V:15:GLU:H	1.86	0.40
24:X:43:VAL:HG11	24:X:82:GLU:HA	2.04	0.40
29:3:39:GLN:O	29:3:52:PHE:HE1	2.04	0.40
30:0:238:C:H4'	30:0:287:C:OP1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:249:G:O2'	30:0:266:G:H5'	2.21	0.40
30:0:462:A:H2'	38:0:4853:HOH:O	2.21	0.40
30:0:568:G:H21	30:0:590:A:H62	1.69	0.40
30:0:603:A:H4'	30:0:604:G:O5'	2.22	0.40
30:0:822:C:H2'	30:0:823:U:H6	1.86	0.40
30:0:1133:A:H2'	30:0:1134:G:H5'	2.03	0.40
30:0:1233:A:N1	30:0:2604:A:O2'	2.51	0.40
30:0:1325:G:O2'	30:0:1326:C:H5'	2.21	0.40
30:0:1474:C:C6	30:0:1474:C:C5'	2.94	0.40
30:0:1521:C:O2'	30:0:1522:A:H5'	2.22	0.40
30:0:1613:C:C6	30:0:1613:C:H3'	2.57	0.40
30:0:2311:A:H3'	38:0:7660:HOH:O	2.20	0.40
30:0:2325:U:H5''	30:0:2417:C:O2'	2.22	0.40
30:0:2493:C:O2	30:0:2493:C:C2'	2.67	0.40
30:0:2510:C:H42	30:0:2564:G:N2	2.19	0.40
1:A:20:SER:C	1:A:22:ARG:N	2.80	0.40
2:B:73:VAL:HG21	2:B:284:PHE:HZ	1.86	0.40
3:C:7:ASP:C	3:C:9:ASP:H	2.29	0.40
3:C:59:GLU:C	3:C:71:PRO:HA	2.46	0.40
3:C:100:LEU:HD22	30:0:751:U:H5''	2.03	0.40
4:D:14:ARG:HD3	31:9:56:A:O2'	2.22	0.40
5:E:23:GLU:HG2	5:E:28:SER:HB3	2.03	0.40
7:G:19:GLU:HG2	7:G:66:LEU:HD13	2.03	0.40
8:H:91:ARG:H	8:H:91:ARG:HG2	1.43	0.40
15:O:47:ARG:HG3	15:O:47:ARG:NH1	2.36	0.40
15:O:49:GLU:OE1	15:O:72:LYS:HG3	2.22	0.40
15:O:96:VAL:HG13	15:O:100:GLN:OE1	2.21	0.40
16:P:13:VAL:C	16:P:15:ASP:N	2.79	0.40
25:Y:132:ASP:OD1	25:Y:135:LYS:HD2	2.20	0.40
30:0:192:A:N6	30:0:194:A:C2	2.89	0.40
30:0:1102:C:H5	38:0:3479:HOH:O	2.04	0.40
30:0:1159:G:C2	30:0:1209:C:N3	2.89	0.40
30:0:1520:G:C6	30:0:1521:C:N4	2.89	0.40
30:0:1979:G:H1'	38:0:3061:HOH:O	2.21	0.40
30:0:2102:G:N2	30:0:2103:A:N1	2.69	0.40
30:0:2532:A:H8	30:0:2532:A:OP2	2.05	0.40
30:0:2672:C:H2'	30:0:2673:U:C6	2.53	0.40
31:9:81:C:O2'	31:9:82:U:H5'	2.21	0.40
31:9:89:C:O2'	31:9:90:G:H5'	2.22	0.40
2:B:201:ASP:N	2:B:312:ARG:O	2.53	0.40
3:C:1:MET:HG2	3:C:2:GLN:N	2.34	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:104:ASP:O	3:C:108:GLN:HG3	2.22	0.40
4:D:135:VAL:HG22	4:D:136:ARG:N	2.36	0.40
5:E:84:MET:HA	5:E:167:TYR:O	2.22	0.40
6:F:59:ILE:CD1	30:0:263:U:C2	3.04	0.40
14:N:127:LEU:HD12	14:N:127:LEU:HA	1.93	0.40
15:O:32:ARG:HA	15:O:32:ARG:NE	2.35	0.40
16:P:13:VAL:HG21	16:P:41:ARG:HG2	2.03	0.40
16:P:78:GLY:O	30:0:1813:U:H4'	2.22	0.40
18:R:99:ALA:HB1	18:R:109:MET:HE2	2.04	0.40
20:T:26:THR:HA	20:T:39:ASN:HB3	2.03	0.40
25:Y:229:LEU:O	30:0:552:A:H5''	2.22	0.40
28:2:41:HIS:HE1	30:0:1439:C:OP1	2.05	0.40
29:3:17:HIS:CG	30:0:2409:C:H4'	2.57	0.40
29:3:18:GLN:HE22	29:3:73:GLU:CD	2.30	0.40
30:0:37:A:H2'	30:0:38:G:H8	1.84	0.40
30:0:146:U:C4	30:0:147:G:C6	3.09	0.40
30:0:295:C:H2'	30:0:296:G:O4'	2.22	0.40
30:0:920:C:H5'	30:0:921:G:N3	2.37	0.40
30:0:1016:U:H2'	30:0:1017:U:O4'	2.21	0.40
30:0:1525:G:H4'	30:0:1525:G:OP1	2.21	0.40
30:0:1557:G:H2'	30:0:1558:C:C6	2.57	0.40
30:0:2004:U:H5''	30:0:2005:G:C8	2.57	0.40
30:0:2273:C:O2'	30:0:2274:A:H5'	2.22	0.40
31:9:2:U:H4'	31:9:2:U:OP2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	235/240 (98%)	200 (85%)	30 (13%)	5 (2%)	5 27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	335/338 (99%)	305 (91%)	23 (7%)	7 (2%)	5	27
3	C	244/246 (99%)	216 (88%)	26 (11%)	2 (1%)	16	50
4	D	134/177 (76%)	105 (78%)	23 (17%)	6 (4%)	2	12
5	E	170/178 (96%)	158 (93%)	11 (6%)	1 (1%)	21	56
6	F	117/120 (98%)	97 (83%)	16 (14%)	4 (3%)	3	17
7	G	25/348 (7%)	22 (88%)	3 (12%)	0	100	100
8	H	156/177 (88%)	139 (89%)	16 (10%)	1 (1%)	21	56
9	I	68/162 (42%)	49 (72%)	16 (24%)	3 (4%)	2	12
10	J	140/145 (97%)	128 (91%)	10 (7%)	2 (1%)	9	36
11	K	130/132 (98%)	120 (92%)	9 (7%)	1 (1%)	16	50
12	L	141/165 (86%)	116 (82%)	22 (16%)	3 (2%)	5	27
13	M	192/196 (98%)	171 (89%)	17 (9%)	4 (2%)	5	27
14	N	184/187 (98%)	163 (89%)	17 (9%)	4 (2%)	5	26
15	O	113/116 (97%)	106 (94%)	7 (6%)	0	100	100
16	P	141/149 (95%)	133 (94%)	8 (6%)	0	100	100
17	Q	93/96 (97%)	86 (92%)	5 (5%)	2 (2%)	5	26
18	R	148/155 (96%)	138 (93%)	9 (6%)	1 (1%)	18	53
19	S	79/85 (93%)	75 (95%)	4 (5%)	0	100	100
20	T	117/120 (98%)	108 (92%)	9 (8%)	0	100	100
21	U	51/67 (76%)	44 (86%)	6 (12%)	1 (2%)	6	28
22	V	63/71 (89%)	58 (92%)	4 (6%)	1 (2%)	7	34
23	W	152/154 (99%)	142 (93%)	9 (6%)	1 (1%)	18	53
24	X	80/92 (87%)	72 (90%)	6 (8%)	2 (2%)	4	23
25	Y	140/241 (58%)	132 (94%)	7 (5%)	1 (1%)	18	53
26	Z	71/116 (61%)	55 (78%)	12 (17%)	4 (6%)	1	8
27	1	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
28	2	42/50 (84%)	41 (98%)	1 (2%)	0	100	100
29	3	90/92 (98%)	64 (71%)	17 (19%)	9 (10%)	0	2
All	All	3705/4472 (83%)	3292 (89%)	348 (9%)	65 (2%)	6	31

All (65) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	206	THR
2	B	306	LYS
4	D	137	PRO
6	F	61	MET
6	F	101	ALA
10	J	5	GLU
12	L	80	ASP
13	M	75	ARG
14	N	154	LEU
14	N	183	ASP
14	N	184	ILE
21	U	44	ARG
26	Z	70	ARG
29	3	56	PRO
29	3	64	LYS
29	3	84	ARG
1	A	34	ASP
3	C	8	LEU
3	C	201	SER
5	E	128	GLY
12	L	21	ARG
12	L	82	ALA
13	M	81	ARG
17	Q	21	ARG
23	W	139	GLY
24	X	70	ILE
26	Z	39	GLY
29	3	4	PRO
29	3	68	LYS
29	3	72	GLY
29	3	73	GLU
2	B	169	GLY
4	D	56	ARG
9	I	83	GLY
9	I	107	LYS
11	K	10	GLN
14	N	165	ALA
26	Z	83	TYR
29	3	90	PHE
1	A	119	ALA
2	B	107	SER
2	B	184	ASP
4	D	65	GLU

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Mol	Chain	Res	Type
10	J	7	ASP
13	M	86	GLN
17	Q	18	PRO
18	R	20	GLU
1	A	24	LYS
1	A	122	SER
1	A	132	ASP
2	B	2	GLN
2	B	185	GLY
4	D	172	VAL
6	F	100	ASP
9	I	76	ASP
13	M	80	GLY
24	X	52	PRO
26	Z	105	ARG
29	3	62	THR
4	D	16	PRO
4	D	53	LYS
6	F	64	PRO
8	H	19	ARG
22	V	39	ALA
25	Y	111	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	179/182 (98%)	169 (94%)	10 (6%)	19	52
2	B	282/283 (100%)	265 (94%)	17 (6%)	17	50
3	C	193/193 (100%)	178 (92%)	15 (8%)	11	39
4	D	117/148 (79%)	110 (94%)	7 (6%)	17	50
5	E	152/156 (97%)	147 (97%)	5 (3%)	33	67
6	F	93/94 (99%)	92 (99%)	1 (1%)	65	83
7	G	27/282 (10%)	25 (93%)	2 (7%)	13	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	134/145 (92%)	124 (92%)	10 (8%)	12	41
9	I	58/130 (45%)	58 (100%)	0	100	100
10	J	118/121 (98%)	108 (92%)	10 (8%)	10	36
11	K	106/106 (100%)	102 (96%)	4 (4%)	29	63
12	L	113/127 (89%)	107 (95%)	6 (5%)	20	54
13	M	158/160 (99%)	148 (94%)	10 (6%)	16	48
14	N	149/150 (99%)	145 (97%)	4 (3%)	39	71
15	O	93/94 (99%)	93 (100%)	0	100	100
16	P	113/117 (97%)	110 (97%)	3 (3%)	39	71
17	Q	79/80 (99%)	73 (92%)	6 (8%)	12	41
18	R	117/122 (96%)	113 (97%)	4 (3%)	32	66
19	S	71/74 (96%)	70 (99%)	1 (1%)	59	80
20	T	105/106 (99%)	100 (95%)	5 (5%)	23	57
21	U	44/53 (83%)	43 (98%)	1 (2%)	44	74
22	V	51/57 (90%)	51 (100%)	0	100	100
23	W	130/130 (100%)	125 (96%)	5 (4%)	29	63
24	X	66/74 (89%)	62 (94%)	4 (6%)	17	49
25	Y	120/196 (61%)	115 (96%)	5 (4%)	26	61
26	Z	60/94 (64%)	58 (97%)	2 (3%)	33	67
27	1	46/47 (98%)	46 (100%)	0	100	100
28	2	42/46 (91%)	41 (98%)	1 (2%)	43	73
29	3	79/79 (100%)	71 (90%)	8 (10%)	7	29
All	All	3095/3646 (85%)	2949 (95%)	146 (5%)	23	58

All (146) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ARG
1	A	37	VAL
1	A	66	ARG
1	A	94	LEU
1	A	131	HIS
1	A	153	ARG
1	A	175	LYS

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Mol	Chain	Res	Type
1	A	179	MET
1	A	190	ARG
1	A	217	ARG
2	B	11	LEU
2	B	27	ASN
2	B	49	THR
2	B	56	ASP
2	B	71	VAL
2	B	84	LEU
2	B	144	THR
2	B	171	VAL
2	B	180	ASP
2	B	188	HIS
2	B	190	MET
2	B	195	ARG
2	B	254	GLN
2	B	264	GLU
2	B	277	GLU
2	B	290	VAL
2	B	312	ARG
3	C	2	GLN
3	C	16	VAL
3	C	76	ARG
3	C	78	ARG
3	C	94	THR
3	C	101	ASP
3	C	104	ASP
3	C	151	GLN
3	C	162	VAL
3	C	180	SER
3	C	187	ARG
3	C	234	VAL
3	C	236	THR
3	C	240	LEU
3	C	243	VAL
4	D	19	GLU
4	D	24	HIS
4	D	29	HIS
4	D	50	VAL
4	D	137	PRO
4	D	149	ARG
4	D	172	VAL

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Mol	Chain	Res	Type
5	E	7	ILE
5	E	100	ASP
5	E	116	THR
5	E	126	ILE
5	E	156	ASP
6	F	12	LEU
7	G	64	ASN
7	G	72	ASP
8	H	33	GLN
8	H	62	HIS
8	H	65	LEU
8	H	87	LYS
8	H	89	THR
8	H	91	ARG
8	H	99	ARG
8	H	122	LYS
8	H	157	TYR
8	H	172	GLU
10	J	39	VAL
10	J	45	VAL
10	J	46	ILE
10	J	52	GLN
10	J	74	ARG
10	J	107	ASN
10	J	120	SER
10	J	127	ILE
10	J	130	VAL
10	J	131	THR
11	K	10	GLN
11	K	24	THR
11	K	55	VAL
11	K	98	VAL
12	L	18	HIS
12	L	73	VAL
12	L	83	GLU
12	L	102	ASP
12	L	104	ASP
12	L	114	VAL
13	M	10	ASP
13	M	46	LEU
13	M	81	ARG
13	M	83	SER

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Mol	Chain	Res	Type
13	M	84	LYS
13	M	88	VAL
13	M	89	THR
13	M	91	ILE
13	M	99	ARG
13	M	164	THR
14	N	21	HIS
14	N	127	LEU
14	N	138	ASP
14	N	147	ILE
16	P	21	VAL
16	P	91	LYS
16	P	98	ILE
17	Q	16	ASN
17	Q	18	PRO
17	Q	30	VAL
17	Q	54	PRO
17	Q	75	ILE
17	Q	95	GLU
18	R	13	THR
18	R	39	THR
18	R	82	GLU
18	R	143	VAL
19	S	30	ASP
20	T	39	ASN
20	T	48	VAL
20	T	96	VAL
20	T	115	GLU
20	T	117	ASP
21	U	25	ASP
23	W	4	LEU
23	W	35	VAL
23	W	38	THR
23	W	50	ASP
23	W	146	ILE
24	X	52	PRO
24	X	72	VAL
24	X	79	GLU
24	X	82	GLU
25	Y	118	THR
25	Y	172	THR
25	Y	189	ASN

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Mol	Chain	Res	Type
25	Y	203	VAL
25	Y	235	GLU
26	Z	45	VAL
26	Z	56	GLU
28	2	18	ASN
29	3	7	PHE
29	3	15	ASN
29	3	17	HIS
29	3	36	ILE
29	3	56	PRO
29	3	62	THR
29	3	71	CYS
29	3	90	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (105) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	47	HIS
1	A	92	ASN
1	A	176	HIS
1	A	199	HIS
2	B	27	ASN
2	B	106	HIS
2	B	145	HIS
2	B	221	GLN
2	B	238	ASN
2	B	243	ASN
2	B	256	GLN
2	B	260	HIS
2	B	320	GLN
2	B	332	ASN
3	C	67	GLN
3	C	73	GLN
3	C	129	HIS
3	C	151	GLN
3	C	206	ASN
3	C	219	ASN
4	D	24	HIS
4	D	103	ASN
5	E	55	ASN
5	E	68	HIS

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Mol	Chain	Res	Type
5	E	74	HIS
5	E	90	HIS
5	E	96	ASN
5	E	106	ASN
5	E	143	GLN
5	E	150	GLN
6	F	80	GLN
7	G	64	ASN
8	H	40	GLN
8	H	59	GLN
8	H	135	GLN
9	I	106	GLN
10	J	25	GLN
10	J	52	GLN
10	J	107	ASN
11	K	10	GLN
11	K	119	GLN
12	L	18	HIS
12	L	38	HIS
12	L	41	HIS
12	L	42	ASN
12	L	43	HIS
12	L	55	GLN
13	M	24	GLN
13	M	58	GLN
13	M	77	HIS
13	M	86	GLN
13	M	126	GLN
13	M	137	ASN
13	M	142	GLN
13	M	170	ASN
14	N	107	ASN
14	N	132	ASN
15	O	110	HIS
16	P	50	GLN
16	P	66	GLN
16	P	118	GLN
17	Q	27	GLN
17	Q	40	HIS
18	R	22	GLN
18	R	94	ASN
18	R	98	ASN

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Mol	Chain	Res	Type
18	R	117	HIS
18	R	123	GLN
19	S	9	HIS
19	S	44	GLN
19	S	53	ASN
19	S	55	GLN
20	T	37	GLN
20	T	39	ASN
20	T	43	ASN
20	T	73	HIS
21	U	48	ASN
22	V	60	GLN
23	W	6	GLN
23	W	110	GLN
23	W	119	HIS
23	W	141	HIS
24	X	23	HIS
25	Y	98	GLN
25	Y	129	ASN
25	Y	133	HIS
25	Y	134	HIS
25	Y	189	ASN
26	Z	74	GLN
26	Z	80	GLN
27	1	16	HIS
27	1	28	HIS
28	2	16	ASN
28	2	17	GLN
28	2	18	ASN
28	2	41	HIS
28	2	45	ASN
29	3	2	GLN
29	3	13	HIS
29	3	15	ASN
29	3	18	GLN
29	3	20	HIS
29	3	30	GLN
29	3	78	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	0	2745/2923 (93%)	245 (8%)	22 (0%)
31	9	121/122 (99%)	19 (15%)	2 (1%)
All	All	2866/3045 (94%)	264 (9%)	24 (0%)

All (264) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	0	31	C
30	0	67	A
30	0	69	A
30	0	70	A
30	0	71	G
30	0	86	A
30	0	87	C
30	0	88	G
30	0	114	A
30	0	115	U
30	0	120	A
30	0	130	C
30	0	138	U
30	0	141	C
30	0	151	A
30	0	166	A
30	0	185	G
30	0	186	A
30	0	191	A
30	0	192	A
30	0	198	A
30	0	200	C
30	0	219	G
30	0	237	G
30	0	271	C
30	0	272	A
30	0	273	G
30	0	283	U
30	0	284	C
30	0	285	A
30	0	308	U
30	0	309	C
30	0	318	U
30	0	336	G
30	0	337	A
30	0	342	C

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Mol	Chain	Res	Type
30	0	358	G
30	0	368	C
30	0	381	G
30	0	397	A
30	0	417	G
30	0	457	U
30	0	461	C
30	0	487	G
30	0	498	A
30	0	510	U
30	0	511	A
30	0	514	G
30	0	537	G
30	0	538	C
30	0	539	G
30	0	542	A
30	0	545	G
30	0	553	G
30	0	559	U
30	0	588	G
30	0	604	G
30	0	605	C
30	0	620	A
30	0	632	A
30	0	644	G
30	0	645	U
30	0	660	A
30	0	688	A
30	0	698	A
30	0	701	U
30	0	702	G
30	0	746	A
30	0	759	C
30	0	777	U
30	0	809	G
30	0	821	U
30	0	835	U
30	0	840	U
30	0	857	A
30	0	858	U
30	0	868	G
30	0	869	G

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Mol	Chain	Res	Type
30	0	871	G
30	0	872	U
30	0	875	A
30	0	877	G
30	0	878	G
30	0	884	C
30	0	885	G
30	0	898	G
30	0	905	C
30	0	920	C
30	0	921	G
30	0	923	A
30	0	953	G
30	0	960	G
30	0	961	A
30	0	1006	A
30	0	1008	C
30	0	1011	C
30	0	1029	U
30	0	1045	G
30	0	1059	G
30	0	1060	C
30	0	1072	G
30	0	1080	C
30	0	1081	A
30	0	1088	A
30	0	1109	U
30	0	1110	G
30	0	1119	G
30	0	1130	U
30	0	1137	G
30	0	1151	G
30	0	1161	A
30	0	1166	A
30	0	1174	A
30	0	1175	G
30	0	1185	U
30	0	1192	A
30	0	1193	A
30	0	1205	U
30	0	1206	U
30	0	1208	C

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Mol	Chain	Res	Type
30	0	1216	G
30	0	1238	C
30	0	1239	G
30	0	1279	U
30	0	1289	C
30	0	1342	C
30	0	1353	C
30	0	1354	G
30	0	1360	C
30	0	1377	C
30	0	1378	G
30	0	1407	A
30	0	1460	G
30	0	1474	C
30	0	1485	A
30	0	1505	U
30	0	1506	U
30	0	1524	U
30	0	1525	G
30	0	1526	A
30	0	1528	A
30	0	1562	C
30	0	1592	G
30	0	1605	G
30	0	1617	C
30	0	1625	U
30	0	1626	A
30	0	1634	G
30	0	1656	A
30	0	1667	A
30	0	1682	A
30	0	1684	A
30	0	1685	A
30	0	1692	C
30	0	1701	A
30	0	1710	A
30	0	1722	U
30	0	1723	G
30	0	1725	C
30	0	1730	G
30	0	1731	C
30	0	1752	G

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Mol	Chain	Res	Type
30	0	1778	A
30	0	1798	C
30	0	1820	G
30	0	1829	A
30	0	1856	C
30	0	1879	U
30	0	1919	A
30	0	1942	A
30	0	1967	U
30	0	1968	A
30	0	1971	G
30	0	1973	A
30	0	1978	A
30	0	1979	G
30	0	1996	U
30	0	2006	C
30	0	2008	U
30	0	2011	A
30	0	2012	U
30	0	2013	G
30	0	2033	G
30	0	2034	U
30	0	2064	U
30	0	2072	G
30	0	2073	G
30	0	2074	A
30	0	2096	A
30	0	2101	A
30	0	2102	G
30	0	2110	G
30	0	2238	A
30	0	2243	C
30	0	2258	A
30	0	2271	G
30	0	2272	G
30	0	2317	C
30	0	2321	A
30	0	2354	A
30	0	2361	A
30	0	2369	A
30	0	2422	U
30	0	2462	G

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Mol	Chain	Res	Type
30	0	2465	A
30	0	2469	A
30	0	2476	C
30	0	2480	G
30	0	2483	A
30	0	2507	G
30	0	2509	A
30	0	2511	A
30	0	2533	C
30	0	2537	G
30	0	2541	U
30	0	2553	A
30	0	2564	G
30	0	2589	U
30	0	2601	A
30	0	2602	G
30	0	2608	C
30	0	2613	G
30	0	2638	G
30	0	2664	A
30	0	2681	A
30	0	2682	C
30	0	2718	C
30	0	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	2876	G
30	0	2890	A
30	0	2896	A
30	0	2903	C
30	0	2914	A
31	9	2	U

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Mol	Chain	Res	Type
31	9	7	G
31	9	14	G
31	9	22	G
31	9	23	U
31	9	24	U
31	9	25	G
31	9	39	U
31	9	40	C
31	9	41	C
31	9	43	G
31	9	44	A
31	9	52	A
31	9	57	A
31	9	65	A
31	9	66	G
31	9	77	A
31	9	114	G
31	9	122	C

All (24) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
30	0	129	A
30	0	341	C
30	0	396	U
30	0	545	G
30	0	603	A
30	0	604	G
30	0	644	G
30	0	699	C
30	0	834	G
30	0	857	A
30	0	871	G
30	0	877	G
30	0	1080	C
30	0	1237	U
30	0	1352	A
30	0	1685	A
30	0	1970	G
30	0	2011	A
30	0	2536	C
30	0	2718	C

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Mol	Chain	Res	Type
30	0	2761	A
30	0	2791	U
31	9	43	G
31	9	65	A

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

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	OMG	0	2588	30	23,26,27	0.34	0	32,38,41	0.35	0
30	UR3	0	2619	30	19,22,23	0.42	0	26,32,35	0.66	1 (3%)
30	OMU	0	2587	35,30	19,22,23	0.32	0	25,31,34	0.40	0
30	1MA	0	628	35,30	21,25,26	0.75	1 (4%)	30,37,40	0.68	1 (3%)
30	PSU	0	2621	30	18,21,22	1.56	2 (11%)	21,30,33	1.38	3 (14%)

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	OMG	0	2588	30	-	0/9/27/28	0/3/3/3
30	UR3	0	2619	30	-	0/7/25/26	0/2/2/2
30	OMU	0	2587	35,30	-	0/9/27/28	0/2/2/2
30	1MA	0	628	35,30	-	0/7/25/26	0/3/3/3
30	PSU	0	2621	30	-	0/7/25/26	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	0	2621	PSU	C2-N1	5.10	1.43	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	0	2621	PSU	C6-C5	2.99	1.38	1.35
30	0	628	1MA	C6-N6	2.51	1.34	1.28

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	0	2621	PSU	C6-C5-C4	3.53	120.55	118.17
30	0	2621	PSU	C6-N1-C2	-3.12	119.80	122.69
30	0	2621	PSU	O2-C2-N1	3.01	125.89	122.79
30	0	628	1MA	N1-C2-N3	2.84	129.36	126.00
30	0	2619	UR3	C4-N3-C2	2.73	126.78	124.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	0	2587	OMU	2	0
30	0	628	1MA	3	0
30	0	2621	PSU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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%)	-0.04	4 (1%) 69 45	29, 65, 98, 115	0
2	B	337/338 (99%)	-0.06	2 (0%) 85 69	31, 59, 87, 97	0
3	C	246/246 (100%)	-0.33	1 (0%) 88 76	23, 47, 69, 80	0
4	D	140/177 (79%)	0.71	9 (6%) 25 13	74, 109, 132, 140	0
5	E	172/178 (96%)	-0.01	2 (1%) 76 55	50, 74, 97, 103	0
6	F	119/120 (99%)	0.04	0 100 100	50, 73, 106, 113	0
7	G	29/348 (8%)	0.44	1 (3%) 48 27	75, 96, 105, 109	0
8	H	160/177 (90%)	0.00	5 (3%) 51 30	48, 67, 99, 109	0
9	I	70/162 (43%)	1.26	17 (24%) 2 1	134, 152, 167, 169	0
10	J	142/145 (97%)	-0.18	2 (1%) 73 51	40, 58, 75, 97	0
11	K	132/132 (100%)	-0.33	0 100 100	39, 55, 81, 86	0
12	L	145/165 (87%)	0.31	4 (2%) 55 32	35, 72, 113, 129	0
13	M	194/196 (98%)	0.10	20 (10%) 12 6	31, 46, 99, 106	0
14	N	186/187 (99%)	0.26	4 (2%) 62 39	60, 80, 126, 132	0
15	O	115/116 (99%)	-0.16	0 100 100	43, 56, 74, 80	0
16	P	143/149 (95%)	-0.13	0 100 100	40, 59, 79, 85	0
17	Q	95/96 (98%)	-0.15	0 100 100	44, 56, 72, 88	0
18	R	150/155 (96%)	-0.39	1 (0%) 84 66	33, 49, 70, 83	0
19	S	81/85 (95%)	-0.17	0 100 100	40, 62, 82, 92	0
20	T	119/120 (99%)	-0.17	1 (0%) 82 64	40, 59, 87, 116	0
21	U	53/67 (79%)	1.66	18 (33%) 1 1	107, 117, 125, 126	0
22	V	65/71 (91%)	0.18	5 (7%) 19 10	46, 74, 118, 123	0
23	W	154/154 (100%)	-0.15	1 (0%) 85 69	39, 54, 73, 87	0
24	X	82/92 (89%)	0.05	1 (1%) 76 55	46, 65, 94, 108	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	Y	142/241 (58%)	-0.34	0 100 100	30, 49, 71, 92	0
26	Z	73/116 (62%)	1.69	22 (30%) 1 1	98, 116, 126, 130	0
27	1	56/57 (98%)	-0.65	0 100 100	28, 36, 43, 48	0
28	2	46/50 (92%)	0.21	2 (4%) 40 21	31, 66, 97, 104	0
29	3	92/92 (100%)	2.17	45 (48%) 0 0	104, 119, 130, 134	0
30	0	2749/2923 (94%)	-0.76	4 (0%) 92 86	23, 51, 96, 175	0
31	9	122/122 (100%)	-0.45	2 (1%) 70 47	45, 75, 103, 154	0
All	All	6646/7517 (88%)	-0.27	173 (2%) 57 34	23, 57, 116, 175	0

All (173) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
26	Z	46	SER	8.4
29	3	39	GLN	7.4
13	M	80	GLY	6.8
29	3	46	ILE	6.5
29	3	83	TRP	6.2
29	3	36	ILE	5.8
29	3	7	PHE	5.6
13	M	79	ALA	5.5
21	U	49	LEU	5.4
29	3	38	ARG	5.3
26	Z	45	VAL	5.2
29	3	35	TRP	5.2
29	3	43	ASN	5.1
13	M	78	LYS	5.1
21	U	39	ASN	5.0
21	U	51	TRP	4.9
4	D	18	ILE	4.8
13	M	89	THR	4.8
29	3	67	LEU	4.7
9	I	128	THR	4.7
13	M	71	SER	4.6
26	Z	50	VAL	4.6
26	Z	40	ALA	4.5
13	M	70	GLY	4.5
13	M	91	ILE	4.4
29	3	34	LYS	4.2
26	Z	35	SER	4.2
13	M	75	ARG	4.2

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Mol	Chain	Res	Type	RSRZ
26	Z	58	ASN	4.1
21	U	35	LYS	4.1
13	M	76	ARG	4.1
22	V	1	THR	4.1
29	3	33	MET	4.0
29	3	37	ASP	4.0
21	U	42	LEU	4.0
29	3	9	THR	3.9
29	3	55	VAL	3.8
12	L	60	GLU	3.8
26	Z	36	GLY	3.8
2	B	204	GLY	3.7
21	U	50	GLU	3.6
29	3	41	GLU	3.6
26	Z	43	GLY	3.6
8	H	114	ASP	3.6
13	M	74	LYS	3.5
9	I	71	ALA	3.5
26	Z	42	TYR	3.5
29	3	42	ARG	3.4
26	Z	38	PHE	3.4
12	L	124	ASP	3.4
21	U	16	GLY	3.4
9	I	124	VAL	3.3
9	I	74	ILE	3.3
21	U	40	ALA	3.2
29	3	1	MET	3.2
13	M	87	GLY	3.2
29	3	3	MET	3.2
5	E	53	GLU	3.1
3	C	61	PHE	3.1
12	L	48	LYS	3.1
26	Z	64	PRO	3.1
29	3	79	LEU	3.1
1	A	237	GLY	3.0
29	3	48	ASN	3.0
26	Z	53	ILE	3.0
14	N	154	LEU	2.9
29	3	4	PRO	2.9
26	Z	103	VAL	2.9
26	Z	54	GLU	2.9
29	3	54	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
22	V	39	ALA	2.9
29	3	81	GLU	2.9
13	M	82	ARG	2.9
29	3	84	ARG	2.9
10	J	92	GLN	2.8
24	X	88	GLU	2.8
29	3	15	ASN	2.8
9	I	100	VAL	2.8
29	3	22	VAL	2.8
13	M	88	VAL	2.8
13	M	72	ALA	2.8
13	M	83	SER	2.8
13	M	86	GLN	2.7
21	U	34	SER	2.7
29	3	47	GLY	2.7
9	I	113	SER	2.7
26	Z	106	SER	2.7
31	9	1	U	2.7
29	3	69	TYR	2.7
13	M	194	GLY	2.7
26	Z	55	SER	2.7
26	Z	76	THR	2.6
4	D	174	VAL	2.6
8	H	115	GLY	2.6
4	D	55	LYS	2.6
21	U	38	ASN	2.6
28	2	35	ARG	2.6
21	U	46	ALA	2.6
4	D	63	ILE	2.5
2	B	337	GLY	2.5
29	3	53	SER	2.5
29	3	56	PRO	2.5
29	3	52	PHE	2.5
13	M	73	ARG	2.5
4	D	57	THR	2.4
31	9	2	U	2.4
13	M	77	HIS	2.4
30	0	10	U	2.4
21	U	31	PHE	2.4
21	U	52	THR	2.4
26	Z	57	MET	2.4
26	Z	44	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
22	V	2	VAL	2.4
29	3	60	LYS	2.4
22	V	43	PRO	2.4
1	A	236	GLY	2.3
9	I	70	THR	2.3
29	3	11	CYS	2.4
29	3	51	LYS	2.3
21	U	41	ASP	2.3
12	L	148	GLU	2.3
30	0	1198	U	2.3
29	3	20	HIS	2.3
21	U	22	VAL	2.3
29	3	32	GLY	2.3
21	U	54	THR	2.3
29	3	31	THR	2.3
9	I	73	LEU	2.3
8	H	132	ALA	2.3
29	3	13	HIS	2.3
29	3	40	ARG	2.2
28	2	27	LEU	2.2
29	3	85	ALA	2.2
4	D	10	PHE	2.2
10	J	70	PHE	2.2
4	D	135	VAL	2.2
9	I	103	ILE	2.2
8	H	133	GLY	2.2
9	I	85	GLY	2.2
29	3	82	GLY	2.2
9	I	97	VAL	2.2
18	R	150	PRO	2.2
22	V	36	ALA	2.2
14	N	21	HIS	2.2
29	3	44	SER	2.2
4	D	53	LYS	2.2
9	I	120	ALA	2.2
4	D	134	LEU	2.1
7	G	71	LEU	2.1
26	Z	82	SER	2.1
29	3	14	CYS	2.1
1	A	110	SER	2.1
14	N	168	LEU	2.1
8	H	171	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	52	SER	2.1
29	3	8	ASN	2.1
30	0	735	C	2.1
23	W	118	LEU	2.1
29	3	17	HIS	2.1
26	Z	39	GLY	2.1
14	N	169	PRO	2.1
9	I	67	VAL	2.1
5	E	160	ARG	2.1
21	U	9	CYS	2.1
13	M	90	ARG	2.0
9	I	104	ALA	2.0
9	I	110	ASP	2.0
26	Z	97	THR	2.0
30	0	1199	A	2.0
9	I	106	GLN	2.0
20	T	114	SER	2.0
21	U	48	ASN	2.0
9	I	68	PRO	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
30	OMU	0	2587	21/22	0.97	0.07	41,44,50,50	0
30	OMG	0	2588	24/25	0.97	0.07	39,41,42,45	0
30	UR3	0	2619	21/22	0.97	0.07	39,43,45,48	0
30	PSU	0	2621	20/21	0.97	0.07	40,43,44,44	0
30	1MA	0	628	23/24	0.98	0.07	31,36,38,38	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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
37	CD	U	8701	1/1	0.61	0.33	200,200,200,200	0
34	SR	0	8959	1/1	0.63	0.11	200,200,200,200	0
35	NA	0	8559	1/1	0.66	0.51	122,122,122,122	0
35	NA	0	8556	1/1	0.67	0.22	63,63,63,63	0
37	CD	3	8704	1/1	0.69	0.37	200,200,200,200	0
34	SR	3	8999	1/1	0.72	0.22	172,172,172,172	0
32	MG	0	8083	1/1	0.74	0.15	71,71,71,71	0
32	MG	B	8042	1/1	0.76	0.23	56,56,56,56	0
34	SR	9	8980	1/1	0.77	0.10	182,182,182,182	0
35	NA	0	8528	1/1	0.77	0.52	83,83,83,83	0
34	SR	0	8938	1/1	0.77	0.10	164,164,164,164	0
35	NA	0	8548	1/1	0.78	0.21	68,68,68,68	0
34	SR	0	8997	1/1	0.79	0.28	194,194,194,194	0
34	SR	0	8919	1/1	0.79	0.15	200,200,200,200	0
34	SR	0	8985	1/1	0.80	0.14	182,182,182,182	0
35	NA	0	8562	1/1	0.80	0.39	89,89,89,89	0
34	SR	0	9000	1/1	0.81	0.37	200,200,200,200	0
34	SR	0	8971	1/1	0.81	0.10	170,170,170,170	0
34	SR	0	8983	1/1	0.81	0.20	191,191,191,191	0
34	SR	0	9001	1/1	0.82	0.11	166,166,166,166	0
33	CL	3	8804	1/1	0.82	0.17	120,120,120,120	0
34	SR	0	8988	1/1	0.82	0.11	170,170,170,170	0
34	SR	A	8993	1/1	0.83	0.10	159,159,159,159	0
35	NA	0	8525	1/1	0.83	0.24	85,85,85,85	0
32	MG	0	8049	1/1	0.83	0.27	74,74,74,74	0
32	MG	T	8057	1/1	0.84	0.19	63,63,63,63	0
32	MG	0	8063	1/1	0.84	0.23	86,86,86,86	0
37	CD	Z	8703	1/1	0.84	0.25	200,200,200,200	0
34	SR	0	9006	1/1	0.84	0.31	180,180,180,180	0
35	NA	0	8573	1/1	0.85	0.10	55,55,55,55	0
34	SR	0	8989	1/1	0.85	0.22	200,200,200,200	0
34	SR	0	8977	1/1	0.85	0.12	181,181,181,181	0
33	CL	0	8816	1/1	0.85	0.21	94,94,94,94	0
35	NA	0	8553	1/1	0.86	0.21	70,70,70,70	0
34	SR	3	8932	1/1	0.86	0.14	158,158,158,158	0
35	NA	0	8557	1/1	0.86	0.12	59,59,59,59	0
34	SR	0	8991	1/1	0.87	0.13	193,193,193,193	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
34	SR	0	8953	1/1	0.87	0.17	200,200,200,200	0
34	SR	0	8998	1/1	0.87	0.20	184,184,184,184	0
35	NA	0	8565	1/1	0.87	0.15	70,70,70,70	0
32	MG	9	8074	1/1	0.87	0.09	63,63,63,63	0
35	NA	0	8574	1/1	0.87	0.29	54,54,54,54	0
33	CL	A	8809	1/1	0.87	0.30	100,100,100,100	0
35	NA	0	8554	1/1	0.87	0.46	65,65,65,65	0
32	MG	0	8080	1/1	0.87	0.11	68,68,68,68	0
35	NA	0	8555	1/1	0.88	0.23	50,50,50,50	0
34	SR	0	8969	1/1	0.88	0.24	192,192,192,192	0
34	SR	9	9003	1/1	0.88	0.10	177,177,177,177	0
35	NA	0	8518	1/1	0.88	0.31	75,75,75,75	0
34	SR	0	8957	1/1	0.88	0.16	200,200,200,200	0
35	NA	0	8564	1/1	0.88	0.10	57,57,57,57	0
34	SR	0	8975	1/1	0.88	0.11	171,171,171,171	0
35	NA	0	8535	1/1	0.88	0.18	64,64,64,64	0
35	NA	0	8546	1/1	0.88	0.19	80,80,80,80	0
32	MG	0	8075	1/1	0.88	0.17	83,83,83,83	0
34	SR	0	9002	1/1	0.88	0.12	157,157,157,157	0
34	SR	0	8979	1/1	0.88	0.15	198,198,198,198	0
34	SR	0	8947	1/1	0.89	0.14	194,194,194,194	0
34	SR	0	8974	1/1	0.89	0.19	164,164,164,164	0
35	NA	0	8547	1/1	0.89	0.14	47,47,47,47	0
32	MG	3	8090	1/1	0.89	0.25	80,80,80,80	0
33	CL	O	8808	1/1	0.89	0.10	87,87,87,87	0
32	MG	0	8081	1/1	0.89	0.15	80,80,80,80	0
35	NA	0	8523	1/1	0.89	0.10	51,51,51,51	0
34	SR	0	8968	1/1	0.89	0.17	177,177,177,177	0
34	SR	0	8944	1/1	0.89	0.13	165,165,165,165	0
34	SR	0	8976	1/1	0.90	0.14	197,197,197,197	0
35	NA	0	8570	1/1	0.90	0.05	25,25,25,25	0
35	NA	R	8575	1/1	0.90	0.08	89,89,89,89	0
33	CL	N	8807	1/1	0.90	0.14	99,99,99,99	0
32	MG	A	8051	1/1	0.90	0.10	101,101,101,101	0
34	SR	0	8964	1/1	0.90	0.09	129,129,129,129	0
32	MG	0	8030	1/1	0.90	0.33	86,86,86,86	0
32	MG	0	8038	1/1	0.91	0.06	61,61,61,61	0
34	SR	0	8915	1/1	0.91	0.10	118,118,118,118	0
35	NA	0	8541	1/1	0.91	0.11	54,54,54,54	0
35	NA	0	8544	1/1	0.91	0.11	41,41,41,41	0
35	NA	0	8563	1/1	0.91	0.23	65,65,65,65	0
35	NA	S	8510	1/1	0.91	0.07	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	8508	1/1	0.91	0.19	61,61,61,61	0
35	NA	0	8566	1/1	0.91	0.13	62,62,62,62	0
32	MG	0	8029	1/1	0.91	0.18	68,68,68,68	0
35	NA	0	8571	1/1	0.91	0.06	46,46,46,46	0
35	NA	0	8551	1/1	0.91	0.14	55,55,55,55	0
35	NA	0	8552	1/1	0.91	0.15	58,58,58,58	0
35	NA	0	8519	1/1	0.91	0.13	51,51,51,51	0
34	SR	B	8987	1/1	0.91	0.25	200,200,200,200	0
32	MG	0	8036	1/1	0.91	0.08	37,37,37,37	0
34	SR	S	8961	1/1	0.92	0.08	126,126,126,126	0
34	SR	0	9004	1/1	0.92	0.23	200,200,200,200	0
34	SR	0	8995	1/1	0.92	0.15	140,140,140,140	0
32	MG	0	8033	1/1	0.92	0.10	40,40,40,40	0
34	SR	0	8951	1/1	0.92	0.07	139,139,139,139	0
35	NA	R	8532	1/1	0.92	0.05	37,37,37,37	0
34	SR	0	8939	1/1	0.92	0.18	152,152,152,152	0
34	SR	0	8955	1/1	0.92	0.19	200,200,200,200	0
32	MG	0	8037	1/1	0.93	0.30	76,76,76,76	0
33	CL	B	8819	1/1	0.93	0.15	59,59,59,59	0
35	NA	0	8522	1/1	0.93	0.09	45,45,45,45	0
34	SR	0	8973	1/1	0.93	0.07	112,112,112,112	0
34	SR	F	9005	1/1	0.93	0.08	131,131,131,131	0
32	MG	0	8018	1/1	0.93	0.12	34,34,34,34	0
32	MG	0	8066	1/1	0.93	0.20	75,75,75,75	0
32	MG	0	8092	1/1	0.93	0.10	44,44,44,44	0
33	CL	0	8811	1/1	0.93	0.21	79,79,79,79	0
34	SR	0	8982	1/1	0.93	0.26	200,200,200,200	0
34	SR	0	8958	1/1	0.93	0.06	114,114,114,114	0
32	MG	0	8039	1/1	0.93	0.08	71,71,71,71	0
34	SR	0	8963	1/1	0.93	0.05	123,123,123,123	0
36	K	0	8401	1/1	0.93	0.34	156,156,156,156	0
34	SR	0	8931	1/1	0.93	0.07	110,110,110,110	0
35	NA	0	8506	1/1	0.93	0.07	58,58,58,58	0
33	CL	0	8822	1/1	0.93	0.29	97,97,97,97	0
33	CL	L	8810	1/1	0.94	0.08	64,64,64,64	0
34	SR	0	8970	1/1	0.94	0.06	131,131,131,131	0
34	SR	B	8950	1/1	0.94	0.08	113,113,113,113	0
32	MG	0	8082	1/1	0.94	0.12	66,66,66,66	0
34	SR	0	8946	1/1	0.94	0.08	123,123,123,123	0
34	SR	0	9007	1/1	0.94	0.40	179,179,179,179	0
32	MG	0	8071	1/1	0.94	0.09	31,31,31,31	0
32	MG	0	8068	1/1	0.94	0.13	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
33	CL	J	8801	1/1	0.94	0.10	71,71,71,71	0
33	CL	0	8813	1/1	0.94	0.08	46,46,46,46	0
34	SR	0	8981	1/1	0.94	0.12	157,157,157,157	0
34	SR	0	8956	1/1	0.94	0.07	151,151,151,151	0
33	CL	0	8815	1/1	0.94	0.11	87,87,87,87	0
35	NA	0	8513	1/1	0.94	0.15	66,66,66,66	0
33	CL	J	8802	1/1	0.94	0.07	76,76,76,76	0
34	SR	0	8926	1/1	0.94	0.07	109,109,109,109	0
35	NA	0	8520	1/1	0.94	0.15	39,39,39,39	0
35	NA	0	8567	1/1	0.94	0.23	68,68,68,68	0
34	SR	0	8960	1/1	0.94	0.08	152,152,152,152	0
34	SR	0	8962	1/1	0.94	0.08	179,179,179,179	0
34	SR	0	8927	1/1	0.94	0.15	196,196,196,196	0
34	SR	0	8996	1/1	0.94	0.12	199,199,199,199	0
35	NA	0	8529	1/1	0.94	0.05	41,41,41,41	0
34	SR	0	8928	1/1	0.94	0.08	146,146,146,146	0
35	NA	0	8536	1/1	0.94	0.10	40,40,40,40	0
33	CL	K	8812	1/1	0.94	0.11	48,48,48,48	0
34	SR	0	8922	1/1	0.95	0.13	169,169,169,169	0
33	CL	0	8814	1/1	0.95	0.17	72,72,72,72	0
34	SR	0	8965	1/1	0.95	0.07	127,127,127,127	0
34	SR	0	8967	1/1	0.95	0.07	133,133,133,133	0
32	MG	2	8060	1/1	0.95	0.06	35,35,35,35	0
32	MG	0	8035	1/1	0.95	0.14	61,61,61,61	0
35	NA	0	8524	1/1	0.95	0.09	54,54,54,54	0
33	CL	0	8805	1/1	0.95	0.09	70,70,70,70	0
34	SR	A	8930	1/1	0.95	0.11	125,125,125,125	0
35	NA	C	8503	1/1	0.95	0.09	45,45,45,45	0
35	NA	M	8539	1/1	0.95	0.09	32,32,32,32	0
35	NA	Q	8540	1/1	0.95	0.33	67,67,67,67	0
34	SR	0	8972	1/1	0.95	0.13	150,150,150,150	0
34	SR	0	8914	1/1	0.95	0.07	105,105,105,105	0
35	NA	0	8545	1/1	0.95	0.10	33,33,33,33	0
34	SR	0	8941	1/1	0.95	0.07	122,122,122,122	0
35	NA	9	8543	1/1	0.95	0.20	38,38,38,38	0
35	NA	9	8572	1/1	0.95	0.05	71,71,71,71	0
35	NA	0	8501	1/1	0.95	0.12	43,43,43,43	0
35	NA	0	8505	1/1	0.95	0.17	53,53,53,53	0
32	MG	0	8065	1/1	0.95	0.06	50,50,50,50	0
32	MG	0	8032	1/1	0.95	0.05	27,27,27,27	0
33	CL	Y	8820	1/1	0.96	0.07	47,47,47,47	0
32	MG	0	8040	1/1	0.96	0.17	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
34	SR	0	8992	1/1	0.96	0.14	130,130,130,130	0
34	SR	0	8994	1/1	0.96	0.16	200,200,200,200	0
33	CL	0	8803	1/1	0.96	0.16	69,69,69,69	0
34	SR	0	8942	1/1	0.96	0.07	130,130,130,130	0
35	NA	0	8533	1/1	0.96	0.10	53,53,53,53	0
34	SR	0	8924	1/1	0.96	0.15	133,133,133,133	0
34	SR	0	8925	1/1	0.96	0.09	94,94,94,94	0
35	NA	0	8502	1/1	0.96	0.06	56,56,56,56	0
32	MG	0	8091	1/1	0.96	0.09	58,58,58,58	0
34	SR	A	8929	1/1	0.96	0.11	117,117,117,117	0
32	MG	0	8017	1/1	0.96	0.05	20,20,20,20	0
35	NA	0	8511	1/1	0.96	0.06	48,48,48,48	0
32	MG	0	8079	1/1	0.96	0.06	36,36,36,36	0
35	NA	0	8550	1/1	0.96	0.11	47,47,47,47	0
35	NA	0	8515	1/1	0.96	0.07	44,44,44,44	0
34	SR	0	8933	1/1	0.96	0.13	126,126,126,126	0
34	SR	0	8986	1/1	0.96	0.08	200,200,200,200	0
34	SR	0	8935	1/1	0.96	0.05	87,87,87,87	0
34	SR	0	8916	1/1	0.97	0.05	114,114,114,114	0
32	MG	0	8016	1/1	0.97	0.05	48,48,48,48	0
35	NA	0	8537	1/1	0.97	0.13	29,29,29,29	0
35	NA	J	8538	1/1	0.97	0.08	49,49,49,49	0
34	SR	0	8954	1/1	0.97	0.05	103,103,103,103	0
34	SR	0	8920	1/1	0.97	0.10	106,106,106,106	0
34	SR	0	8921	1/1	0.97	0.04	75,75,75,75	0
34	SR	0	8984	1/1	0.97	0.05	105,105,105,105	0
32	MG	B	8043	1/1	0.97	0.20	53,53,53,53	0
32	MG	0	8041	1/1	0.97	0.17	36,36,36,36	0
33	CL	0	8817	1/1	0.97	0.08	69,69,69,69	0
32	MG	0	8077	1/1	0.97	0.08	43,43,43,43	0
33	CL	J	8821	1/1	0.97	0.07	66,66,66,66	0
35	NA	0	8507	1/1	0.97	0.06	32,32,32,32	0
32	MG	0	8047	1/1	0.97	0.17	67,67,67,67	0
35	NA	0	8509	1/1	0.97	0.08	54,54,54,54	0
32	MG	0	8004	1/1	0.97	0.07	21,21,21,21	0
32	MG	0	8050	1/1	0.97	0.10	52,52,52,52	0
35	NA	0	8560	1/1	0.97	0.11	74,74,74,74	0
35	NA	0	8561	1/1	0.97	0.22	57,57,57,57	0
35	NA	0	8514	1/1	0.97	0.07	17,17,17,17	0
32	MG	0	8055	1/1	0.97	0.04	45,45,45,45	0
34	SR	0	8937	1/1	0.97	0.05	100,100,100,100	0
32	MG	0	8020	1/1	0.97	0.12	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	MG	0	8089	1/1	0.97	0.09	59,59,59,59	0
32	MG	0	8005	1/1	0.97	0.10	34,34,34,34	0
35	NA	0	8568	1/1	0.97	0.05	38,38,38,38	0
32	MG	0	8015	1/1	0.97	0.05	25,25,25,25	0
34	SR	0	8911	1/1	0.97	0.03	79,79,79,79	0
32	MG	0	8093	1/1	0.97	0.03	28,28,28,28	0
35	NA	0	8526	1/1	0.97	0.04	33,33,33,33	0
35	NA	0	8527	1/1	0.97	0.25	54,54,54,54	0
32	MG	0	8067	1/1	0.97	0.04	32,32,32,32	0
34	SR	9	8978	1/1	0.97	0.05	125,125,125,125	0
37	CD	O	8705	1/1	0.97	0.06	93,93,93,93	0
35	NA	0	8530	1/1	0.97	0.10	49,49,49,49	0
34	SR	0	8948	1/1	0.97	0.07	103,103,103,103	0
35	NA	0	8534	1/1	0.97	0.05	37,37,37,37	0
32	MG	0	8023	1/1	0.98	0.10	24,24,24,24	0
32	MG	0	8024	1/1	0.98	0.10	96,96,96,96	0
32	MG	0	8014	1/1	0.98	0.11	21,21,21,21	0
35	NA	0	8542	1/1	0.98	0.11	51,51,51,51	0
34	SR	0	8936	1/1	0.98	0.04	87,87,87,87	0
32	MG	0	8001	1/1	0.98	0.04	26,26,26,26	0
32	MG	0	8069	1/1	0.98	0.08	55,55,55,55	0
32	MG	0	8031	1/1	0.98	0.08	52,52,52,52	0
34	SR	R	8912	1/1	0.98	0.04	86,86,86,86	0
35	NA	0	8549	1/1	0.98	0.13	77,77,77,77	0
32	MG	0	8072	1/1	0.98	0.06	47,47,47,47	0
34	SR	0	8943	1/1	0.98	0.04	72,72,72,72	0
34	SR	1	8913	1/1	0.98	0.03	100,100,100,100	0
34	SR	0	8945	1/1	0.98	0.04	107,107,107,107	0
32	MG	K	8054	1/1	0.98	0.08	40,40,40,40	0
32	MG	0	8076	1/1	0.98	0.06	27,27,27,27	0
34	SR	0	8901	1/1	0.98	0.03	63,63,63,63	0
34	SR	0	8908	1/1	0.98	0.03	77,77,77,77	0
35	NA	0	8558	1/1	0.98	0.18	44,44,44,44	0
35	NA	0	8512	1/1	0.98	0.04	36,36,36,36	0
34	SR	0	8910	1/1	0.98	0.04	99,99,99,99	0
34	SR	0	8990	1/1	0.98	0.05	125,125,125,125	0
32	MG	Y	8086	1/1	0.98	0.02	37,37,37,37	0
35	NA	0	8516	1/1	0.98	0.07	20,20,20,20	0
33	CL	R	8806	1/1	0.98	0.04	47,47,47,47	0
32	MG	0	8078	1/1	0.98	0.10	51,51,51,51	0
32	MG	0	8034	1/1	0.98	0.05	53,53,53,53	0
35	NA	0	8521	1/1	0.98	0.09	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
34	SR	0	8917	1/1	0.98	0.05	109,109,109,109	0
35	NA	0	8569	1/1	0.98	0.11	67,67,67,67	0
32	MG	0	8052	1/1	0.98	0.03	51,51,51,51	0
32	MG	0	8009	1/1	0.98	0.08	24,24,24,24	0
32	MG	0	8056	1/1	0.98	0.07	75,75,75,75	0
32	MG	0	8059	1/1	0.98	0.07	53,53,53,53	0
32	MG	0	8085	1/1	0.98	0.10	67,67,67,67	0
32	MG	0	8061	1/1	0.98	0.06	19,19,19,19	0
36	K	M	8402	1/1	0.98	0.05	60,60,60,60	0
34	SR	0	8966	1/1	0.98	0.04	97,97,97,97	0
32	MG	0	8062	1/1	0.98	0.09	57,57,57,57	0
34	SR	0	9008	1/1	0.98	0.04	97,97,97,97	0
32	MG	0	8010	1/1	0.98	0.05	24,24,24,24	0
32	MG	0	8064	1/1	0.98	0.04	33,33,33,33	0
34	SR	0	8909	1/1	0.99	0.05	89,89,89,89	0
32	MG	0	8084	1/1	0.99	0.07	24,24,24,24	0
32	MG	0	8044	1/1	0.99	0.04	52,52,52,52	0
34	SR	0	8949	1/1	0.99	0.02	102,102,102,102	0
32	MG	0	8087	1/1	0.99	0.02	26,26,26,26	0
32	MG	0	8088	1/1	0.99	0.05	35,35,35,35	0
32	MG	0	8046	1/1	0.99	0.04	26,26,26,26	0
32	MG	0	8011	1/1	0.99	0.07	24,24,24,24	0
34	SR	0	8918	1/1	0.99	0.03	71,71,71,71	0
32	MG	0	8048	1/1	0.99	0.06	20,20,20,20	0
35	NA	0	8517	1/1	0.99	0.06	21,21,21,21	0
32	MG	0	8013	1/1	0.99	0.03	24,24,24,24	0
32	MG	0	8070	1/1	0.99	0.03	40,40,40,40	0
32	MG	0	8021	1/1	0.99	0.06	25,25,25,25	0
34	SR	0	8923	1/1	0.99	0.04	85,85,85,85	0
32	MG	0	8022	1/1	0.99	0.06	17,17,17,17	0
32	MG	0	8073	1/1	0.99	0.11	51,51,51,51	0
32	MG	0	8053	1/1	0.99	0.04	45,45,45,45	0
32	MG	0	8007	1/1	0.99	0.03	18,18,18,18	0
32	MG	0	8008	1/1	0.99	0.07	26,26,26,26	0
32	MG	0	8058	1/1	0.99	0.04	22,22,22,22	0
33	CL	M	8818	1/1	0.99	0.04	39,39,39,39	0
34	SR	0	8934	1/1	0.99	0.06	99,99,99,99	0
32	MG	0	8025	1/1	0.99	0.02	30,30,30,30	0
35	NA	0	8531	1/1	0.99	0.04	15,15,15,15	0
34	SR	1	8952	1/1	0.99	0.03	72,72,72,72	0
32	MG	0	8026	1/1	0.99	0.03	27,27,27,27	0
32	MG	0	8027	1/1	0.99	0.05	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	MG	0	8002	1/1	0.99	0.03	29,29,29,29	0
34	SR	0	8940	1/1	0.99	0.02	77,77,77,77	0
34	SR	0	8903	1/1	0.99	0.04	46,46,46,46	0
34	SR	0	8904	1/1	0.99	0.07	58,58,58,58	0
34	SR	0	8906	1/1	0.99	0.07	64,64,64,64	0
34	SR	0	8907	1/1	0.99	0.02	40,40,40,40	0
32	MG	0	8003	1/1	0.99	0.08	22,22,22,22	0
35	NA	0	8504	1/1	1.00	0.03	27,27,27,27	0
32	MG	0	8028	1/1	1.00	0.02	19,19,19,19	0
34	SR	0	8902	1/1	1.00	0.04	67,67,67,67	0
32	MG	0	8019	1/1	1.00	0.04	23,23,23,23	0
32	MG	0	8006	1/1	1.00	0.03	20,20,20,20	0
34	SR	0	8905	1/1	1.00	0.09	62,62,62,62	0
32	MG	0	8045	1/1	1.00	0.03	24,24,24,24	0
37	CD	1	8702	1/1	1.00	0.04	61,61,61,61	0
32	MG	0	8012	1/1	1.00	0.02	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.