



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:19 AM UTC

PDB ID : 3CCS / pdb_00003ccs
Title : Structure of Anisomycin resistant 50S Ribosomal Subunit: 23S rRNA mutation G2482A
Authors : Blaha, G.; Gurel, G.
Deposited on : 2008-02-26
Resolution : 2.95 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

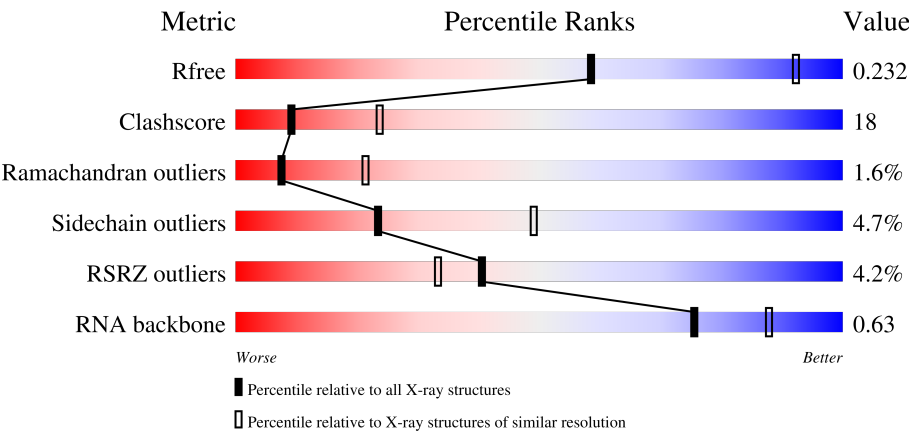
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)
RNA backbone	3983	1046 (3.16-2.76)

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	3% 64%29%6%.
2	B	338	% 59%35%5%
3	C	246	% 71%25%.
4	D	177	14% 47%28%. 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	0	8812	-	-	X	-
33	CL	Y	8820	-	-	X	-
35	NA	0	8574	-	-	-	X
37	CD	3	8704	-	-	-	X

2 Entry composition

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	0	2754	Total	C	N	O	P	0	0	0
			59019	26349	10873	19052	2745			

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

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	A	2	Total	Mg	0	0
			2	2		
32	B	1	Total	Mg	0	0
			1	1		
32	K	1	Total	Mg	0	0
			1	1		
32	T	1	Total	Mg	0	0
			1	1		
32	Y	1	Total	Mg	0	0
			1	1		
32	0	86	Total	Mg	0	0
			86	86		
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 Cl 1 1	0	0
33	B	1	Total Cl 1 1	0	0
33	J	3	Total Cl 3 3	0	0
33	L	1	Total Cl 1 1	0	0
33	M	1	Total Cl 1 1	0	0
33	N	1	Total Cl 1 1	0	0
33	O	1	Total Cl 1 1	0	0
33	R	1	Total Cl 1 1	0	0
33	Y	1	Total Cl 1 1	0	0
33	3	1	Total Cl 1 1	0	0
33	0	10	Total Cl 10 10	0	0

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

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

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	92	Total 92	Sr 92	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	B	1	Total 1	Na 1	0	0
35	C	1	Total 1	Na 1	0	0
35	H	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	1	Total 1	Na 1	0	0
35	S	1	Total 1	Na 1	0	0
35	0	65	Total 65	Na 65	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

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

- Molecule 38 is water.

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

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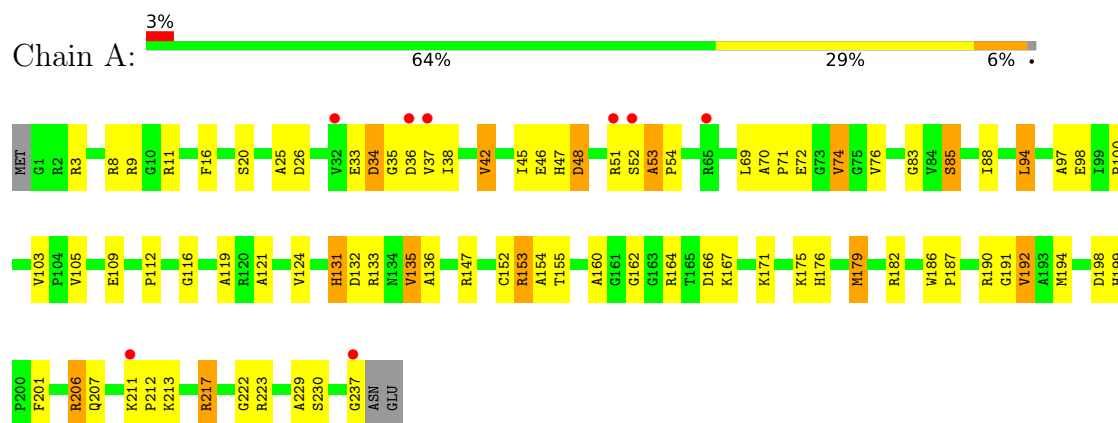
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	P	67	Total 67	O 67	0	0
38	Q	48	Total 48	O 48	0	0
38	R	77	Total 77	O 77	0	0
38	S	30	Total 30	O 30	0	0
38	T	36	Total 36	O 36	0	0
38	U	28	Total 28	O 28	0	0
38	V	13	Total 13	O 13	0	0
38	W	67	Total 67	O 67	0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

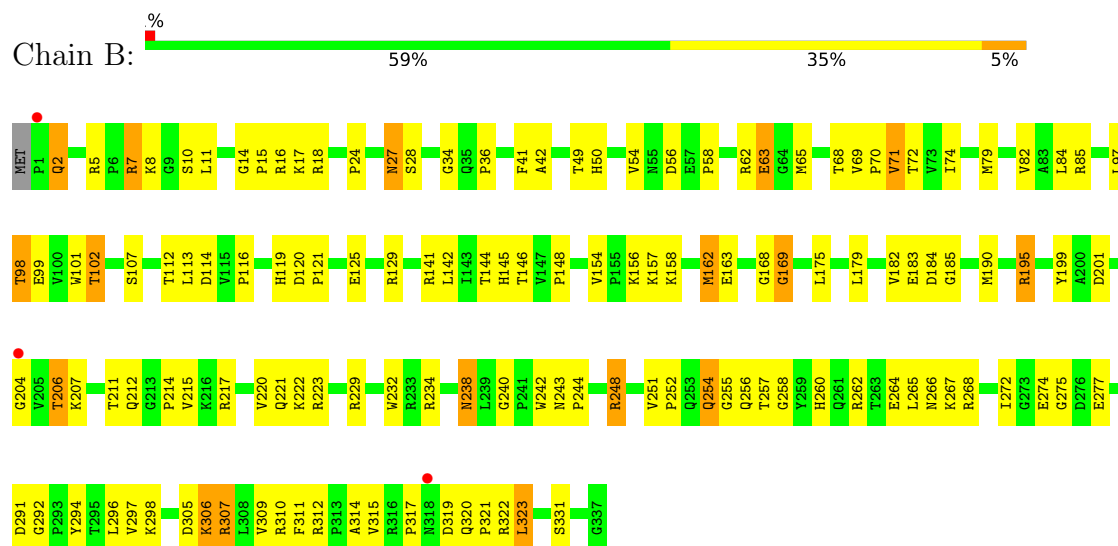
3 Residue-property plots

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

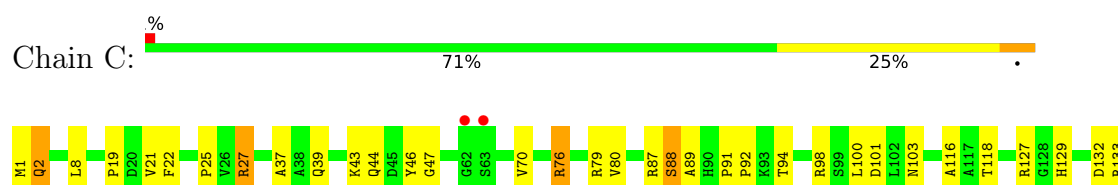
- Molecule 1: 50S ribosomal protein L2P

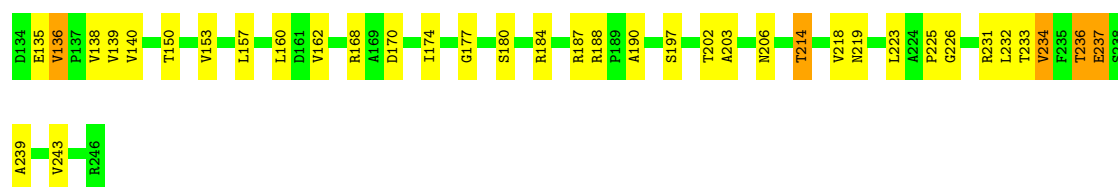


- Molecule 2: 50S ribosomal protein L3P

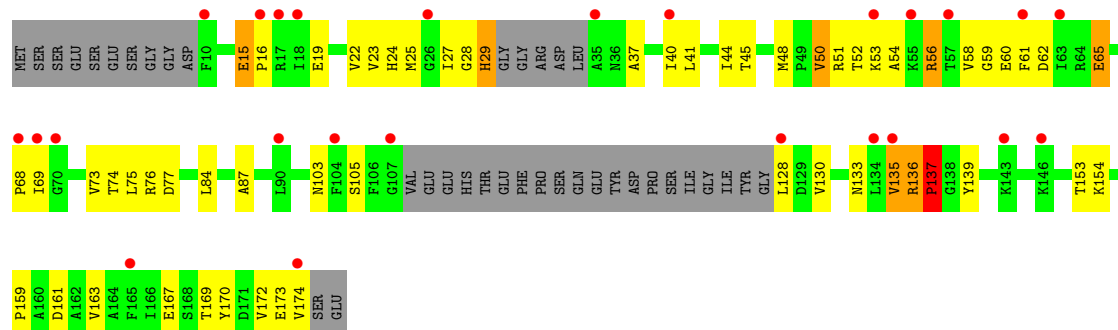


- Molecule 3: 50S ribosomal protein L4P

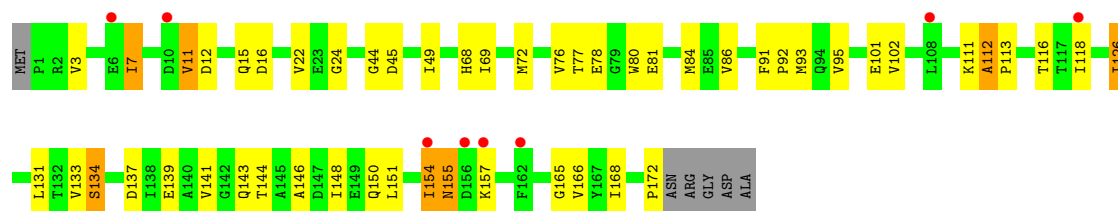




• Molecule 4: 50S ribosomal protein L5P



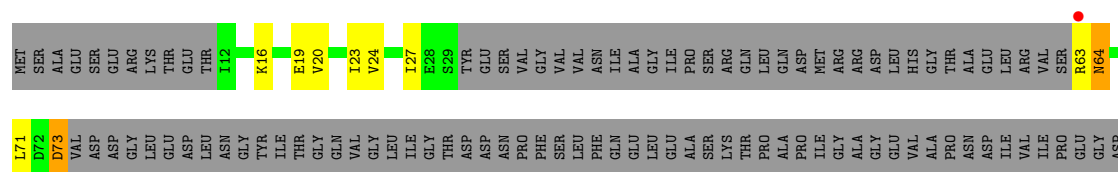
• Molecule 5: 50S ribosomal protein L6P

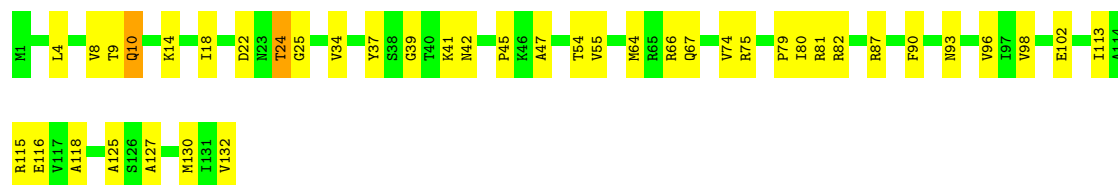


• Molecule 6: 50S ribosomal protein L7Ae

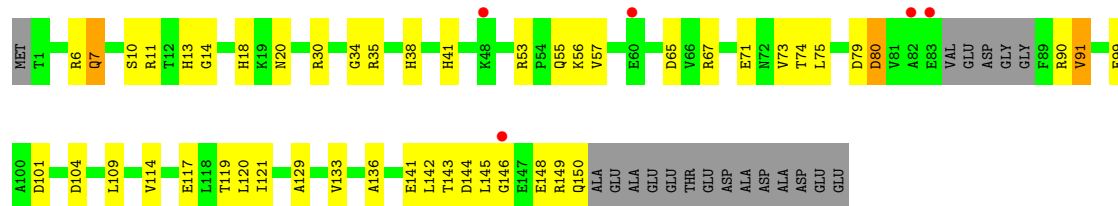


• Molecule 7: 50S ribosomal protein L10E

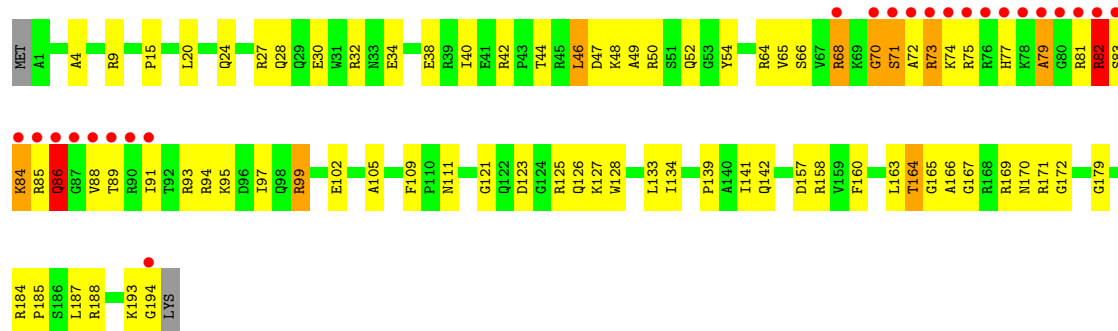




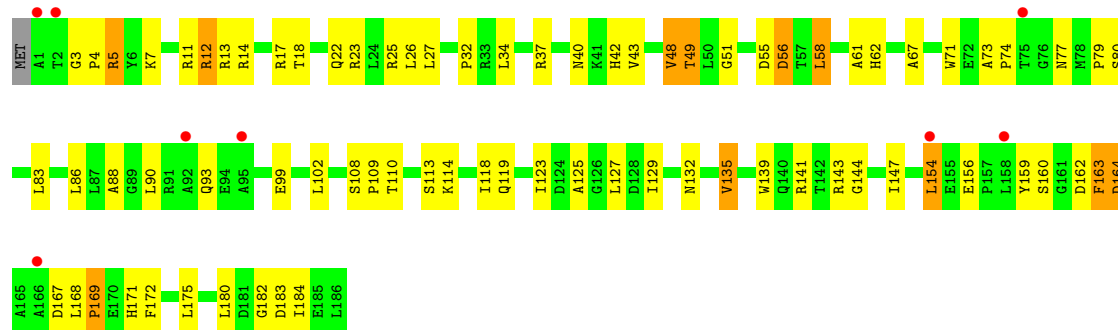
• Molecule 12: 50S ribosomal protein L15P



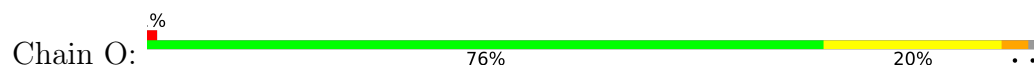
• Molecule 13: 50S ribosomal protein L15e

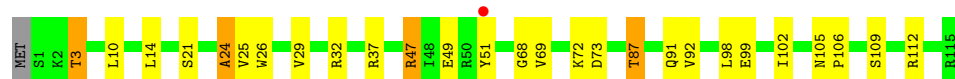


• Molecule 14: 50S ribosomal protein L18P

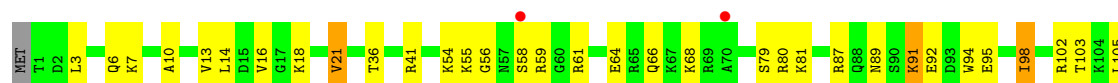


• Molecule 15: 50S ribosomal protein L18e





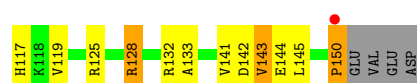
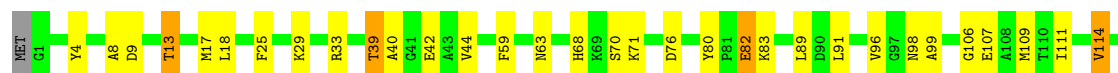
- Molecule 16: 50S ribosomal protein L19e



- Molecule 17: 50S ribosomal protein L21e



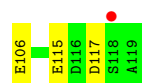
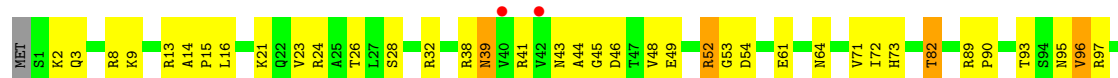
- Molecule 18: 50S ribosomal protein L22P



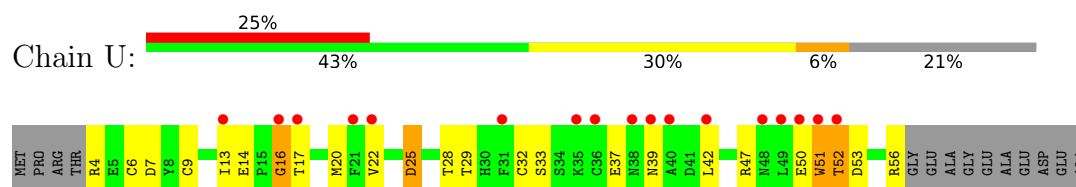
- Molecule 19: 50S ribosomal protein L23P



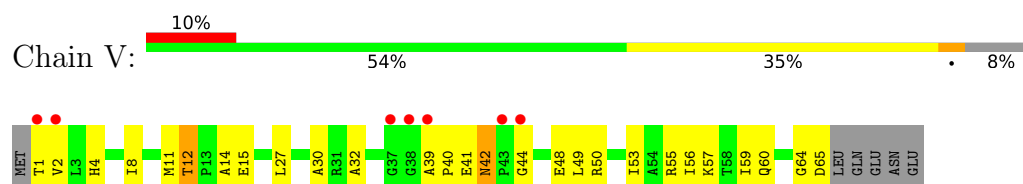
- Molecule 20: 50S ribosomal protein L24P



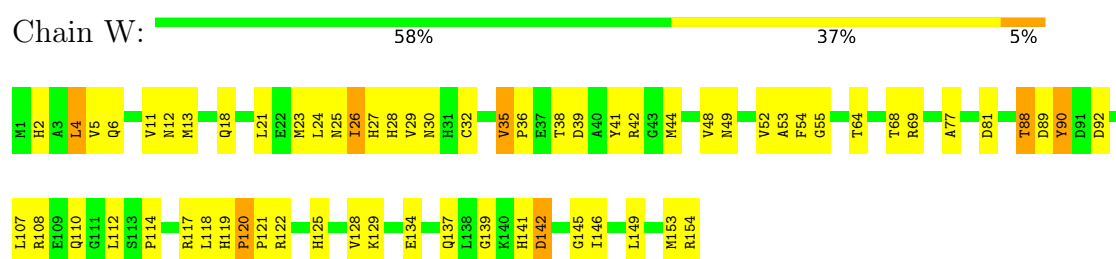
- Molecule 21: 50S ribosomal protein L24e



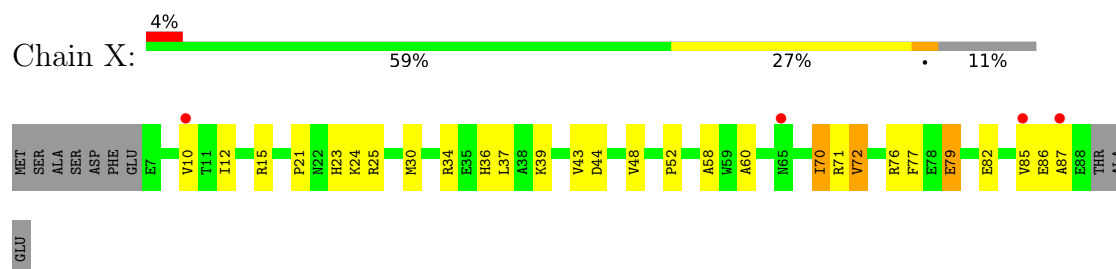
- Molecule 22: 50S ribosomal protein L29P



- Molecule 23: 50S ribosomal protein L30P



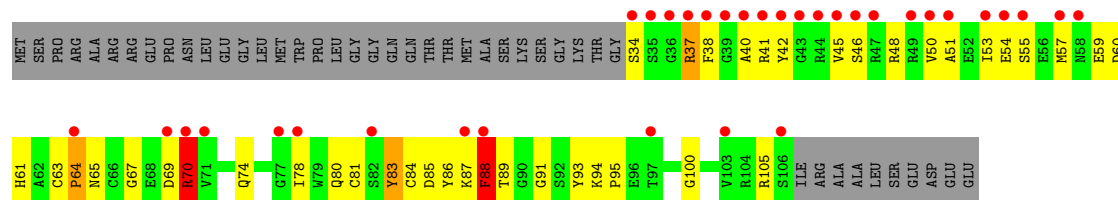
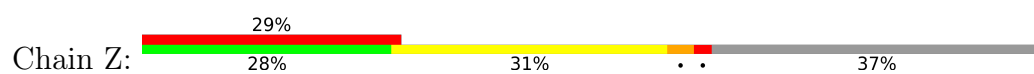
- Molecule 24: 50S ribosomal protein L31e



- Molecule 25: 50S ribosomal protein L32e



- Molecule 26: 50S ribosomal protein L37Ae



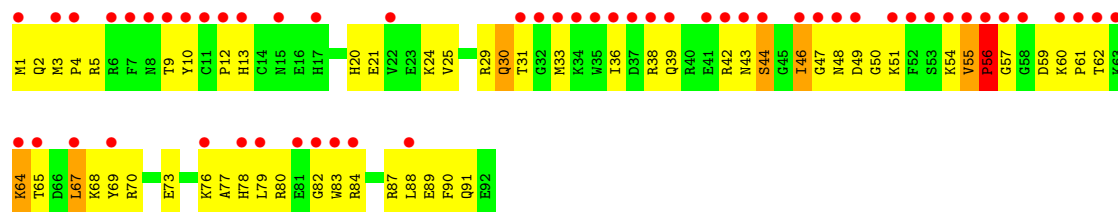
- Molecule 27: 50S ribosomal protein L37e



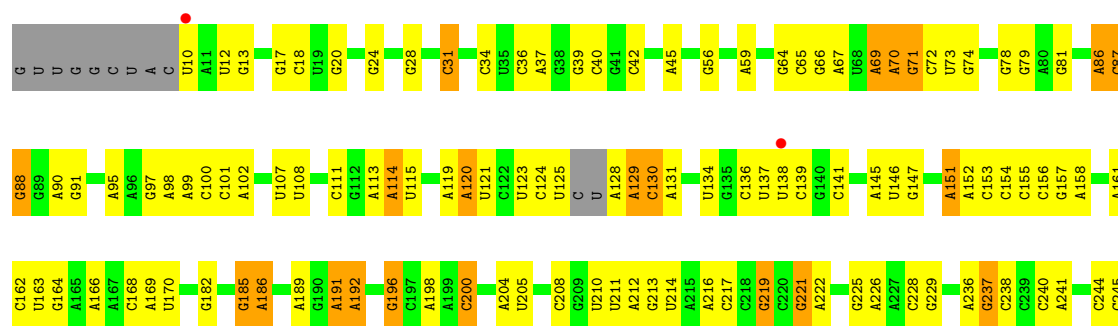
- Molecule 28: 50S ribosomal protein L39e



- Molecule 29: 50S ribosomal protein L44E

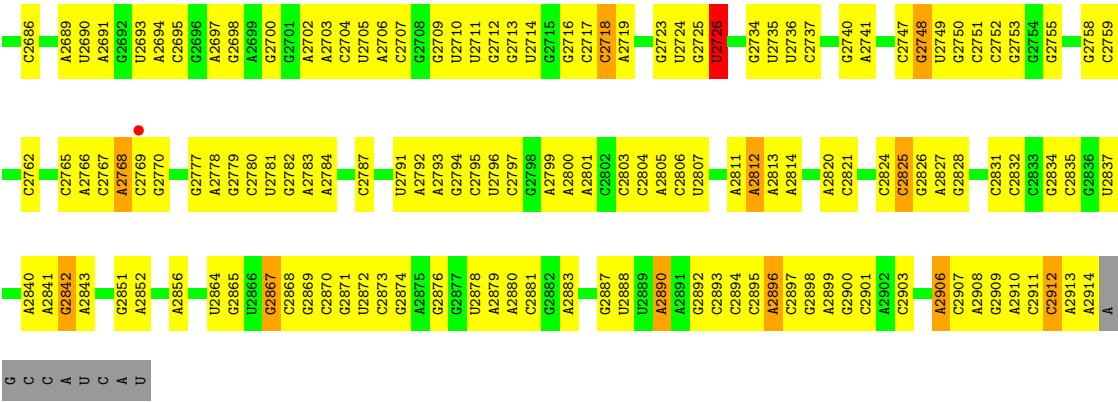


- Molecule 30: 23S RIBOSOMAL RNA

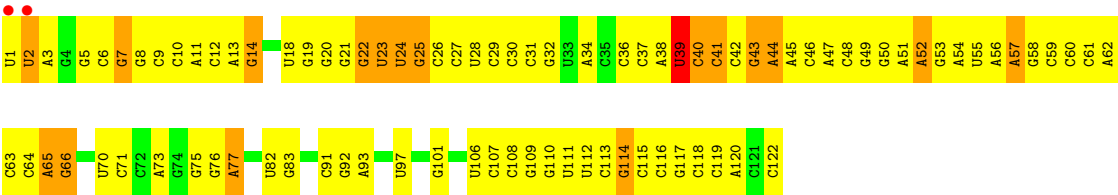








● Molecule 31: 5S RIBOSOMAL RNA



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	212.24Å 299.19Å 575.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.95 50.00 – 2.95	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.95) 91.8 (50.00-2.95)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 2.40Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.179 , 0.238 0.178 , 0.232	Depositor DCC
R_{free} test set	6547 reflections (0.98%)	wwPDB-VP
Wilson B-factor (Å ²)	62.1	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 79.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	99121	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

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

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, CL, NA, OMU, CD, MG, PSU, K, SR, 1MA, UR3

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	1.02	10/2408 (0.4%)
2	B	0.43	0/2690	1.00	10/3652 (0.3%)
3	C	0.50	0/1885	0.98	5/2552 (0.2%)
4	D	0.41	0/1111	1.03	9/1498 (0.6%)
5	E	0.42	0/1382	0.87	3/1880 (0.2%)
6	F	0.42	0/901	0.99	5/1224 (0.4%)
7	G	0.36	0/241	0.82	0/324
8	H	0.39	0/1302	0.95	4/1743 (0.2%)
9	I	0.43	0/526	0.95	1/716 (0.1%)
10	J	0.45	0/1136	0.97	1/1530 (0.1%)
11	K	0.43	0/1004	1.00	3/1351 (0.2%)
12	L	0.38	0/1130	0.95	5/1509 (0.3%)
13	M	0.51	0/1582	0.92	6/2116 (0.3%)
14	N	0.39	0/1474	1.08	15/1999 (0.8%)
15	O	0.47	0/874	0.94	3/1181 (0.3%)
16	P	0.42	0/1147	0.87	2/1528 (0.1%)
17	Q	0.42	0/749	1.05	8/1005 (0.8%)
18	R	1.30	7/1172 (0.6%)	1.39	9/1578 (0.6%)
19	S	0.43	0/648	0.95	3/875 (0.3%)
20	T	0.41	0/958	1.02	7/1289 (0.5%)
21	U	0.53	0/417	0.92	1/562 (0.2%)
22	V	0.43	0/502	1.01	3/675 (0.4%)
23	W	0.50	0/1219	0.98	3/1655 (0.2%)
24	X	0.47	0/664	1.02	5/895 (0.6%)
25	Y	0.47	0/1146	0.95	2/1536 (0.1%)
26	Z	0.51	0/584	1.06	4/781 (0.5%)
27	1	0.50	0/438	0.91	1/578 (0.2%)
28	2	0.45	0/401	0.84	0/529
29	3	0.60	0/771	1.01	5/1024 (0.5%)
30	0	0.40	0/65956	0.61	11/102865 (0.0%)
31	9	0.38	0/2904	0.56	1/4526 (0.0%)
All	All	0.44	7/98700 (0.0%)	0.73	145/147584 (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
18	R	1	0
23	W	0	1
30	0	0	34
All	All	1	35

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	R	150	PRO	CB-CG	27.21	2.85	1.49
18	R	150	PRO	CA-C	-17.67	1.15	1.52
18	R	150	PRO	CG-CD	13.41	1.96	1.50
18	R	150	PRO	N-CA	13.25	1.67	1.47
18	R	150	PRO	C-O	11.72	1.47	1.23
18	R	150	PRO	N-CD	10.80	1.62	1.47
18	R	150	PRO	CA-CB	7.89	1.69	1.53

All (145) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	R	150	PRO	CB-CA-C	-28.52	55.92	110.10
18	R	150	PRO	N-CA-C	-20.23	61.53	112.10
18	R	150	PRO	N-CA-CB	12.25	116.47	103.00
18	R	150	PRO	CA-N-CD	12.06	128.88	112.00
14	N	163	PHE	N-CA-C	-10.26	100.63	113.55
4	D	136	ARG	CA-C-N	9.71	131.98	119.84
4	D	136	ARG	C-N-CA	9.71	131.98	119.84
17	Q	25	PRO	CA-C-N	8.25	127.89	119.56
17	Q	25	PRO	C-N-CA	8.25	127.89	119.56
20	T	52	ARG	N-CA-C	7.85	123.62	113.18
5	E	11	VAL	N-CA-C	7.38	120.41	108.97
4	D	15	GLU	CA-C-N	7.22	128.87	119.84
4	D	15	GLU	C-N-CA	7.22	128.87	119.84
29	3	67	LEU	N-CA-C	6.92	120.31	110.14
6	F	62	HIS	N-CA-C	6.88	118.43	111.07
1	A	166	ASP	N-CA-C	6.87	118.76	111.28
14	N	169	PRO	N-CA-C	-6.85	105.02	114.27
24	X	77	PHE	N-CA-C	6.81	116.86	107.73
14	N	108	SER	CA-C-N	6.75	128.28	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	108	SER	C-N-CA	6.75	128.28	119.84
2	B	222	LYS	N-CA-C	-6.75	100.53	110.52
4	D	170	TYR	N-CA-C	6.72	120.35	111.28
5	E	112	ALA	CA-C-N	6.57	126.48	119.85
5	E	112	ALA	C-N-CA	6.57	126.48	119.85
18	R	150	PRO	CA-CB-CG	-6.34	92.45	104.50
12	L	91	VAL	N-CA-C	6.32	117.13	107.77
18	R	141	VAL	N-CA-C	6.30	117.55	108.48
18	R	150	PRO	CA-C-O	-6.22	100.34	119.00
22	V	42	ASN	CA-C-N	6.21	127.61	119.84
22	V	42	ASN	C-N-CA	6.21	127.61	119.84
13	M	70	GLY	N-CA-C	6.16	119.25	111.85
2	B	157	LYS	N-CA-C	-6.15	106.37	114.31
29	3	44	SER	N-CA-C	6.13	119.15	109.96
14	N	51	GLY	CA-C-N	6.11	125.84	119.05
14	N	51	GLY	C-N-CA	6.11	125.84	119.05
30	0	877	G	C2'-C3'-O3'	-6.05	104.62	113.70
20	T	89	ARG	CA-C-N	6.02	126.04	119.90
20	T	89	ARG	C-N-CA	6.02	126.04	119.90
9	I	126	THR	N-CA-C	-5.98	107.80	114.62
12	L	7	GLN	N-CA-C	5.96	118.74	111.82
30	0	1942	A	C5'-C4'-C3'	5.96	124.94	116.00
17	Q	47	VAL	CA-C-N	5.94	127.27	119.84
17	Q	47	VAL	C-N-CA	5.94	127.27	119.84
30	0	920	C	C2'-C3'-O3'	-5.93	104.81	113.70
22	V	30	ALA	N-CA-C	-5.90	105.74	113.12
8	H	143	VAL	N-CA-C	5.89	116.63	110.62
13	M	121	GLY	N-CA-C	5.85	119.19	111.70
30	0	2726	U	N1-C1'-C2'	5.84	120.75	112.00
2	B	323	LEU	N-CA-C	5.83	117.81	110.24
2	B	102	THR	N-CA-C	5.82	115.70	108.19
11	K	25	GLY	N-CA-C	-5.81	107.36	114.92
14	N	171	HIS	N-CA-C	-5.81	105.02	111.36
15	O	69	VAL	N-CA-C	5.81	117.72	108.89
23	W	77	ALA	N-CA-C	5.80	118.23	110.35
1	A	222	GLY	N-CA-C	-5.76	107.11	114.37
13	M	42	ARG	CA-C-N	5.75	125.69	119.76
13	M	42	ARG	C-N-CA	5.75	125.69	119.76
1	A	213	LYS	N-CA-C	5.75	118.49	111.82
31	9	39	U	N1-C1'-C2'	5.75	120.62	112.00
25	Y	143	TRP	N-CA-C	5.73	118.63	110.10
23	W	142	ASP	N-CA-C	-5.71	102.84	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	Q	53	HIS	CA-C-N	5.71	126.98	119.84
17	Q	53	HIS	C-N-CA	5.71	126.98	119.84
26	Z	63	CYS	CA-C-N	5.70	126.96	119.84
26	Z	63	CYS	C-N-CA	5.70	126.96	119.84
3	C	80	VAL	CA-C-N	5.69	126.95	119.84
3	C	80	VAL	C-N-CA	5.69	126.95	119.84
20	T	54	ASP	N-CA-C	-5.65	105.88	112.89
30	0	1819	G	C5'-C4'-C3'	5.64	124.46	116.00
27	1	11	LYS	N-CA-C	5.63	118.32	108.52
30	0	1504	A	N9-C1'-C2'	5.63	120.45	112.00
3	C	177	GLY	N-CA-C	5.61	117.76	112.04
12	L	80	ASP	N-CA-C	5.59	118.46	110.24
26	Z	88	PHE	N-CA-C	5.58	116.73	108.86
21	U	16	GLY	N-CA-C	-5.56	107.32	115.72
30	0	2301	A	N9-C1'-C2'	5.56	120.35	112.00
30	0	834	G	C2'-C3'-O3'	-5.54	105.39	113.70
3	C	219	ASN	N-CA-C	5.54	117.67	109.69
8	H	161	THR	N-CA-C	5.53	121.01	113.16
12	L	20	ASN	N-CA-C	5.50	119.57	111.04
20	T	95	ASN	N-CA-C	-5.50	105.00	112.26
1	A	198	ASP	N-CA-C	5.50	120.05	113.23
1	A	48	ASP	CA-C-N	5.48	125.15	119.56
1	A	48	ASP	C-N-CA	5.48	125.15	119.56
26	Z	59	GLU	N-CA-C	5.48	117.61	110.43
19	S	27	ALA	N-CA-C	-5.47	99.81	108.73
17	Q	84	ILE	N-CA-C	5.46	115.72	107.80
4	D	137	PRO	N-CA-C	5.46	123.71	112.47
4	D	44	ILE	N-CA-C	5.46	116.19	110.62
14	N	48	VAL	N-CA-C	5.45	116.15	108.36
6	F	8	VAL	CA-C-N	5.44	125.45	119.90
6	F	8	VAL	C-N-CA	5.44	125.45	119.90
14	N	135	VAL	N-CA-C	-5.41	106.56	113.22
2	B	175	LEU	N-CA-C	-5.38	105.31	111.07
24	X	12	ILE	CB-CA-C	-5.38	104.96	110.71
6	F	79	GLN	N-CA-C	5.37	118.24	109.59
24	X	79	GLU	N-CA-C	5.37	117.55	111.11
2	B	266	ASN	N-CA-C	5.35	118.58	111.30
17	Q	47	VAL	N-CA-C	5.33	113.14	107.76
25	Y	194	GLU	N-CA-C	5.28	116.86	108.67
23	W	25	ASN	N-CA-C	5.27	119.00	112.47
24	X	60	ALA	N-CA-C	5.26	116.70	111.07
2	B	120	ASP	CA-C-N	5.26	124.89	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	120	ASP	C-N-CA	5.26	124.89	119.05
15	O	24	ALA	N-CA-C	-5.25	107.55	114.31
19	S	4	VAL	N-CA-C	5.24	115.45	110.53
14	N	162	ASP	N-CA-C	5.23	116.68	109.15
1	A	135	VAL	N-CA-C	5.21	116.87	108.85
13	M	109	PHE	CA-C-N	5.21	126.35	119.84
13	M	109	PHE	C-N-CA	5.21	126.35	119.84
12	L	55	GLN	N-CA-C	5.21	118.42	111.75
11	K	54	THR	N-CA-C	-5.19	102.79	110.48
30	0	1504	A	C4'-C3'-O3'	-5.19	105.22	113.00
3	C	89	ALA	N-CA-C	5.17	117.33	111.02
14	N	13	ARG	N-CA-C	-5.17	106.13	112.90
2	B	113	LEU	N-CA-C	5.15	117.70	110.14
8	H	136	LEU	N-CA-C	-5.15	105.12	111.40
2	B	114	ASP	N-CA-C	-5.14	98.47	107.73
20	T	3	GLN	CA-C-N	5.14	124.75	119.05
20	T	3	GLN	C-N-CA	5.14	124.75	119.05
11	K	81	ARG	N-CA-C	5.13	117.08	108.73
16	P	36	THR	N-CA-C	5.12	118.04	110.46
8	H	119	ALA	N-CA-C	5.12	119.38	113.18
30	0	2313	C	O4'-C4'-C3'	-5.12	98.88	104.00
4	D	135	VAL	N-CA-C	5.12	113.94	107.70
19	S	10	VAL	N-CA-C	5.11	114.65	106.88
1	A	25	ALA	N-CA-C	5.11	116.83	109.07
15	O	51	TYR	N-CA-C	5.11	119.66	113.38
6	F	59	ILE	N-CA-C	5.11	116.44	110.62
24	X	12	ILE	N-CA-C	5.10	112.91	107.76
18	R	82	GLU	N-CA-C	5.09	116.83	111.28
10	J	88	PRO	N-CA-C	-5.07	105.63	112.48
14	N	3	GLY	CA-C-N	5.06	126.17	119.84
14	N	3	GLY	C-N-CA	5.06	126.17	119.84
14	N	182	GLY	N-CA-C	5.05	118.79	112.73
4	D	77	ASP	CB-CA-C	-5.03	110.39	117.23
18	R	70	SER	N-CA-C	5.03	116.76	111.28
29	3	55	VAL	CA-C-N	5.03	126.12	119.84
29	3	55	VAL	C-N-CA	5.03	126.12	119.84
29	3	57	GLY	N-CA-C	5.03	119.79	112.55
30	0	871	G	C5'-C4'-O4'	-5.02	102.26	109.80
1	A	53	ALA	CA-C-N	5.02	124.95	119.78
1	A	53	ALA	C-N-CA	5.02	124.95	119.78
16	P	137	LEU	N-CA-C	-5.01	105.29	111.40
14	N	168	LEU	N-CA-C	5.00	119.85	108.74

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
18	R	150	PRO	CA

All (35) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
30	0	1039	G	Sidechain
30	0	1236	A	Sidechain
30	0	1260	G	Sidechain
30	0	1430	G	Sidechain
30	0	1524	U	Sidechain
30	0	1599	U	Sidechain
30	0	1736	A	Sidechain
30	0	1741	U	Sidechain
30	0	1777	G	Sidechain
30	0	1819	G	Sidechain
30	0	1829	A	Sidechain
30	0	1878	G	Sidechain
30	0	196	G	Sidechain
30	0	1993	C	Sidechain
30	0	221	G	Sidechain
30	0	2316	G	Sidechain
30	0	2473	U	Sidechain
30	0	2493	C	Sidechain
30	0	2503	A	Sidechain
30	0	2552	C	Sidechain
30	0	2599	A	Sidechain
30	0	2630	G	Sidechain
30	0	2673	U	Sidechain
30	0	2726	U	Sidechain
30	0	2842	G	Sidechain
30	0	324	G	Sidechain
30	0	333	G	Sidechain
30	0	470	U	Sidechain
30	0	471	G	Sidechain
30	0	482	G	Sidechain
30	0	506	G	Sidechain
30	0	518	G	Sidechain
30	0	619	U	Sidechain
30	0	888	U	Sidechain
23	W	90	TYR	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1753	0	1766	86	0
2	B	2625	0	2533	112	0
3	C	1860	0	1813	63	0
4	D	1094	0	1085	40	0
5	E	1357	0	1266	42	0
6	F	890	0	843	22	0
7	G	240	0	231	9	0
8	H	1282	0	1292	33	0
9	I	519	0	500	14	0
10	J	1120	0	1098	45	0
11	K	994	0	1027	36	0
12	L	1118	0	1076	38	0
13	M	1558	0	1573	97	0
14	N	1445	0	1401	73	0
15	O	865	0	873	22	0
16	P	1136	0	1123	35	0
17	Q	735	0	729	28	0
18	R	1149	0	1122	39	0
19	S	641	0	605	16	0
20	T	950	0	924	36	0
21	U	410	0	368	26	0
22	V	499	0	511	22	0
23	W	1196	0	1137	65	0
24	X	654	0	653	20	0
25	Y	1130	0	1133	39	0
26	Z	573	0	535	52	0
27	1	431	0	426	21	0
28	2	396	0	413	21	0
29	3	755	0	732	62	0
30	0	59019	0	29809	1671	0
31	9	2599	0	1325	128	0
32	0	86	0	0	0	0
32	9	1	0	0	0	0
32	A	2	0	0	0	0
32	B	1	0	0	0	0
32	K	1	0	0	0	0
32	T	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	Y	1	0	0	0	0
33	0	10	0	0	3	0
33	3	1	0	0	1	0
33	A	1	0	0	0	0
33	B	1	0	0	0	0
33	J	3	0	0	2	0
33	L	1	0	0	0	0
33	M	1	0	0	0	0
33	N	1	0	0	0	0
33	O	1	0	0	0	0
33	R	1	0	0	0	0
33	Y	1	0	0	2	0
34	0	92	0	0	0	0
34	1	2	0	0	0	0
34	3	2	0	0	0	0
34	9	3	0	0	0	0
34	A	2	0	0	0	0
34	B	2	0	0	0	0
34	F	1	0	0	0	0
34	H	1	0	0	0	0
34	L	1	0	0	0	0
34	R	1	0	0	0	0
34	S	1	0	0	0	0
35	0	65	0	0	0	0
35	9	2	0	0	0	0
35	B	1	0	0	0	0
35	C	1	0	0	0	0
35	H	1	0	0	0	0
35	J	1	0	0	0	0
35	M	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	1	0	0	0	0
35	S	1	0	0	0	0
36	0	1	0	0	0	0
36	M	1	0	0	0	0
37	1	1	0	0	0	0
37	3	1	0	0	0	0
37	O	1	0	0	0	0
37	U	1	0	0	0	0
37	Z	1	0	0	0	0
38	0	5904	0	0	252	0
38	1	59	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	2	43	0	0	2	0
38	3	70	0	0	3	0
38	9	149	0	0	10	0
38	A	119	0	0	7	0
38	B	152	0	0	15	0
38	C	185	0	0	18	0
38	D	42	0	0	4	0
38	E	43	0	0	1	0
38	F	26	0	0	1	0
38	G	19	0	0	1	0
38	H	65	0	0	4	0
38	I	8	0	0	1	0
38	J	53	0	0	1	0
38	K	58	0	0	4	0
38	L	85	0	0	9	0
38	M	127	0	0	13	0
38	N	59	0	0	2	0
38	O	39	0	0	2	0
38	P	67	0	0	3	0
38	Q	48	0	0	1	0
38	R	77	0	0	2	0
38	S	30	0	0	2	0
38	T	36	0	0	3	0
38	U	28	0	0	4	0
38	V	13	0	0	2	0
38	W	67	0	0	3	0
38	X	21	0	0	2	0
38	Y	100	0	0	5	0
38	Z	31	0	0	7	0
All	All	99121	0	59922	2718	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

All (2718) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:150:PRO:CG	18:R:150:PRO:CD	1.96	1.41
30:0:871:G:C8	30:0:871:G:H5'	1.77	1.19
10:J:82:THR:HG23	30:0:1242:A:H5'	1.23	1.16
30:0:1165:G:H1'	30:0:1174:A:H1'	1.17	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:56:A:H2'	31:9:57:A:H5''	1.19	1.13
30:0:1559:A:H1'	38:0:5849:HOH:O	1.45	1.13
30:0:1160:G:C5'	30:0:1161:A:H5'	1.78	1.13
18:R:150:PRO:CG	18:R:150:PRO:C	2.22	1.11
31:9:29:C:H2'	31:9:30:C:H5'	1.32	1.10
15:O:3:THR:HG22	30:0:656:G:H5'	1.19	1.10
13:M:171:ARG:HD3	30:0:156:C:H5''	1.28	1.09
30:0:1160:G:H5'	30:0:1161:A:C5'	1.80	1.09
10:J:52:GLN:HE22	30:0:1119:G:H2'	1.17	1.08
30:0:871:G:H5'	30:0:871:G:H8	0.99	1.08
10:J:52:GLN:NE2	30:0:1119:G:H2'	1.69	1.07
31:9:76:G:H3'	31:9:77:A:H5''	1.33	1.05
30:0:545:G:H5'	30:0:545:G:H8	1.22	1.05
14:N:37:ARG:NH1	31:9:6:C:H5''	1.71	1.03
30:0:1603:A:H5'	30:0:1605:G:O4'	1.60	1.02
30:0:1641:A:H2'	30:0:1642:A:H5'	1.44	0.99
18:R:99:ALA:HB1	18:R:109:MET:HE1	1.43	0.99
21:U:56:ARG:HD2	30:0:2890:A:C8	1.98	0.98
30:0:1666:C:O2'	30:0:1667:A:H5''	1.63	0.98
26:Z:60:ASP:HB3	26:Z:69:ASP:HB3	1.43	0.98
11:K:10:GLN:HE21	11:K:10:GLN:H	0.99	0.97
2:B:62:ARG:HA	2:B:65:MET:HE3	1.43	0.97
30:0:1979:G:H2'	38:0:9283:HOH:O	1.65	0.97
30:0:381:G:H5''	38:0:4317:HOH:O	1.64	0.96
30:0:871:G:H8	30:0:871:G:C5'	1.78	0.96
30:0:1165:G:H21	30:0:1173:A:H5''	1.30	0.96
13:M:70:GLY:HA3	13:M:73:ARG:NH2	1.80	0.96
17:Q:15:LYS:HD3	30:0:2364:A:H5''	1.47	0.96
16:P:59:ARG:HH22	16:P:66:GLN:HE22	1.05	0.95
31:9:56:A:C2'	31:9:57:A:H5''	1.95	0.95
30:0:1474:C:H6	30:0:1474:C:H5'	1.30	0.95
18:R:8:ALA:HB1	18:R:13:THR:HG21	1.50	0.94
31:9:14:G:H5'	31:9:14:G:H8	1.32	0.94
23:W:44:MET:HE2	30:0:944:G:H21	1.32	0.94
30:0:236:A:H4'	30:0:237:G:H5'	1.49	0.94
2:B:264:GLU:HG2	2:B:267:LYS:HE3	1.50	0.94
30:0:1165:G:H21	30:0:1173:A:C5'	1.81	0.93
16:P:115:SER:H	16:P:118:GLN:HE21	1.11	0.93
30:0:2505:G:H2'	30:0:2506:A:H5'	1.50	0.93
30:0:2717:C:C2'	30:0:2718:C:H5''	1.99	0.93
30:0:2502:C:H2'	30:0:2503:A:H5'	1.52	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:108:ARG:HH21	23:W:114:PRO:HG2	1.35	0.92
1:A:211:LYS:HB3	1:A:212:PRO:HD2	1.52	0.91
3:C:27:ARG:HG2	3:C:27:ARG:HH11	1.36	0.91
30:0:2321:A:H2	30:0:2378:U:H3	1.14	0.91
15:O:3:THR:CG2	30:0:656:G:H5'	2.00	0.91
30:0:282:C:O2'	30:0:283:U:H5'	1.71	0.90
30:0:2710:U:H1'	38:0:7613:HOH:O	1.71	0.90
30:0:1118:A:H62	30:0:1244:U:H3	1.14	0.90
3:C:236:THR:HG22	3:C:239:ALA:H	1.35	0.90
29:3:60:LYS:HG3	29:3:61:PRO:HD2	1.53	0.90
30:0:2506:A:HO2'	30:0:2507:G:H8	0.90	0.90
30:0:2812:A:H2	30:0:2814:A:H62	1.19	0.90
30:0:1116:U:O2'	30:0:1118:A:H2	1.54	0.90
30:0:545:G:H5'	30:0:545:G:C8	2.06	0.89
30:0:2502:C:C2'	30:0:2503:A:H5'	2.03	0.89
33:Y:8820:CL:CL	38:0:4953:HOH:O	2.27	0.88
30:0:870:G:H2'	30:0:871:G:H5''	1.53	0.88
23:W:137:GLN:HE21	23:W:141:HIS:HE1	1.20	0.88
30:0:1119:G:H22	30:0:1246:A:H2	1.16	0.88
30:0:2700:G:H3'	38:0:3569:HOH:O	1.73	0.88
13:M:79:ALA:HB3	13:M:81:ARG:HH12	1.38	0.88
31:9:92:G:H2'	31:9:93:A:C8	2.07	0.88
30:0:1118:A:C8	30:0:1118:A:H3'	2.08	0.88
30:0:1206:U:H5'	30:0:1206:U:H6	1.39	0.88
15:O:47:ARG:HH11	15:O:47:ARG:HG3	1.35	0.88
30:0:506:G:H22	30:0:509:A:C5'	1.85	0.87
30:0:1474:C:H5'	30:0:1474:C:C6	2.10	0.87
30:0:542:A:H5'	30:0:542:A:H8	1.39	0.87
30:0:1835:U:H5	30:0:1840:A:N7	1.73	0.87
30:0:1118:A:H3'	30:0:1118:A:H8	1.39	0.87
30:0:2321:A:H4'	30:0:2322:U:OP1	1.73	0.87
30:0:363:C:H1'	38:0:5273:HOH:O	1.75	0.86
30:0:1278:A:H4'	30:0:1279:U:C4	2.10	0.86
30:0:2505:G:C2'	30:0:2506:A:H5'	2.04	0.86
1:A:70:ALA:HB1	26:Z:89:THR:HG21	1.57	0.86
30:0:1701:A:H4'	30:0:1702:U:H5''	1.55	0.86
13:M:70:GLY:HA2	30:0:2263:G:H4'	1.59	0.85
23:W:6:GLN:HB2	23:W:26:ILE:HD11	1.58	0.85
30:0:506:G:H22	30:0:509:A:H5''	1.42	0.85
26:Z:70:ARG:NH1	26:Z:83:TYR:HB2	1.91	0.85
30:0:1205:U:H2'	30:0:1206:U:H5'	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1641:A:C2'	30:0:1642:A:H5'	2.06	0.85
30:0:2717:C:H2'	30:0:2718:C:H5''	1.59	0.85
30:0:1666:C:H2'	30:0:1667:A:H5'	1.58	0.84
30:0:2321:A:H8	30:0:2322:U:HO2'	1.25	0.84
30:0:2717:C:O2'	30:0:2718:C:H5''	1.76	0.84
29:3:68:LYS:HE2	30:0:2436:U:H5'	1.60	0.84
23:W:5:VAL:HG11	23:W:153:MET:HE1	1.57	0.83
30:0:2637:A:H4'	38:0:4923:HOH:O	1.78	0.83
2:B:217:ARG:HG3	2:B:257:THR:HG22	1.58	0.83
30:0:2043:U:H3'	38:0:6696:HOH:O	1.76	0.83
23:W:125:HIS:NE2	30:0:1097:A:H5''	1.93	0.83
30:0:2010:A:H2'	38:0:5942:HOH:O	1.77	0.83
1:A:167:LYS:HE2	26:Z:50:VAL:HG13	1.61	0.83
13:M:68:ARG:NH2	13:M:73:ARG:HD3	1.94	0.83
29:3:64:LYS:HA	29:3:84:ARG:HA	1.57	0.83
30:0:380:A:H2'	38:0:7216:HOH:O	1.77	0.83
11:K:10:GLN:H	11:K:10:GLN:NE2	1.77	0.83
11:K:39:GLY:HA2	38:0:5215:HOH:O	1.76	0.83
2:B:36:PRO:HA	2:B:168:GLY:HA3	1.61	0.82
30:0:2454:C:H5''	38:0:7719:HOH:O	1.79	0.82
30:0:1189:A:H1'	30:0:1209:C:O4'	1.79	0.82
13:M:27:ARG:HH22	13:M:44:THR:HG23	1.44	0.82
30:0:1667:A:H5'	30:0:1667:A:H8	1.44	0.82
30:0:541:C:C2'	30:0:542:A:H5''	2.09	0.82
30:0:541:C:H2'	30:0:542:A:C5'	2.08	0.82
29:3:31:THR:O	30:0:1923:G:H4'	1.79	0.81
30:0:1300:G:H1'	38:0:4678:HOH:O	1.80	0.81
30:0:1184:C:H1'	38:0:7461:HOH:O	1.80	0.81
11:K:10:GLN:HE21	11:K:10:GLN:N	1.79	0.81
20:T:71:VAL:HG11	20:T:90:PRO:HB3	1.62	0.81
30:0:2769:C:O2'	30:0:2770:G:H5'	1.81	0.81
3:C:139:VAL:HG13	38:C:8658:HOH:O	1.79	0.81
30:0:559:U:H6	30:0:559:U:H5'	1.45	0.81
30:0:2005:G:H3'	30:0:2005:G:OP2	1.80	0.81
31:9:29:C:C2'	31:9:30:C:H5'	2.08	0.81
8:H:59:GLN:HE21	8:H:129:ARG:HE	1.25	0.81
18:R:39:THR:HG22	18:R:42:GLU:H	1.46	0.81
30:0:1174:A:C6	30:0:1201:C:H4'	2.14	0.81
30:0:681:G:N3	30:0:681:G:H5'	1.96	0.81
30:0:1119:G:N2	30:0:1246:A:C2	2.47	0.81
30:0:1205:U:H2'	30:0:1206:U:C5'	2.10	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1641:A:H2'	30:0:1642:A:C5'	2.09	0.81
30:0:1801:A:H3'	38:0:7607:HOH:O	1.81	0.80
28:2:43:ARG:HH22	30:0:1684:A:H1'	1.47	0.80
30:0:2748:G:H2'	38:0:7534:HOH:O	1.81	0.80
20:T:9:LYS:HE3	20:T:13:ARG:NH1	1.96	0.80
28:2:41:HIS:H	28:2:45:ASN:HD22	1.27	0.80
30:0:1593:C:H1'	38:0:6089:HOH:O	1.80	0.80
15:O:3:THR:HG22	30:0:656:G:C5'	2.09	0.80
25:Y:115:ARG:NH2	30:0:1266:U:H4'	1.97	0.80
30:0:2783:A:H3'	38:0:5225:HOH:O	1.81	0.80
31:9:39:U:H1'	31:9:44:A:H61	1.45	0.80
30:0:1603:A:H5''	30:0:1605:G:H5'	1.63	0.80
31:9:14:G:H5'	31:9:14:G:C8	2.16	0.80
9:I:112:LEU:HD11	30:0:1162:G:H1'	1.63	0.80
30:0:586:C:H5''	38:0:7275:HOH:O	1.81	0.80
22:V:12:THR:HG22	22:V:15:GLU:HG3	1.63	0.79
13:M:27:ARG:NH2	13:M:44:THR:HG23	1.96	0.79
6:F:91:VAL:HG12	6:F:92:GLY:H	1.46	0.79
38:N:8842:HOH:O	31:9:49:G:H5''	1.83	0.79
10:J:82:THR:CG2	30:0:1242:A:H5'	2.09	0.79
30:0:2419:U:H5''	30:0:2420:G:H5'	1.65	0.79
30:0:2586:U:H3	30:0:2592:G:H22	1.28	0.79
30:0:255:A:H2'	30:0:256:C:H6	1.48	0.79
30:0:1183:C:H2'	38:0:6224:HOH:O	1.82	0.79
3:C:1:MET:HG2	3:C:2:GLN:H	1.47	0.78
30:0:2635:A:O2'	30:0:2636:C:H5'	1.82	0.78
2:B:320:GLN:HE21	2:B:321:PRO:HD2	1.48	0.78
30:0:308:U:H5'	30:0:309:C:OP1	1.82	0.78
30:0:659:A:H5''	38:0:7089:HOH:O	1.83	0.78
4:D:154:LYS:H	4:D:154:LYS:HD2	1.48	0.78
30:0:123:U:H5'	38:0:6637:HOH:O	1.82	0.78
30:0:1372:A:H3'	38:0:7180:HOH:O	1.81	0.78
30:0:2485:A:H3'	38:0:5838:HOH:O	1.82	0.78
13:M:99:ARG:HE	13:M:170:ASN:HD22	1.31	0.78
25:Y:235:GLU:CD	25:Y:235:GLU:H	1.92	0.78
13:M:134:ILE:HG23	13:M:141:ILE:HD13	1.66	0.78
16:P:59:ARG:NH2	16:P:66:GLN:HE22	1.80	0.78
30:0:960:G:H4'	38:0:7423:HOH:O	1.83	0.78
30:0:1595:G:O2'	30:0:1596:U:H5'	1.84	0.78
30:0:2291:A:C8	30:0:2309:C:H5'	2.19	0.78
8:H:59:GLN:NE2	8:H:129:ARG:HE	1.82	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:541:C:H2'	30:0:542:A:H5''	1.65	0.77
30:0:2469:A:H1'	38:0:3229:HOH:O	1.83	0.77
30:0:871:G:C8	30:0:871:G:C5'	2.58	0.77
30:0:1189:A:H3'	38:0:7669:HOH:O	1.83	0.77
30:0:2420:G:O2'	30:0:2421:G:H5'	1.85	0.77
30:0:558:C:C2'	30:0:559:U:H5''	2.14	0.77
30:0:1116:U:H3	30:0:1246:A:H62	1.33	0.77
30:0:564:G:H1'	38:0:6295:HOH:O	1.84	0.77
30:0:558:C:O2'	30:0:559:U:H5''	1.85	0.77
30:0:2769:C:C2'	30:0:2770:G:H5'	2.15	0.77
30:0:1632:A:H2'	30:0:1633:C:H5'	1.67	0.76
30:0:1973:A:H5'	30:0:1973:A:H8	1.48	0.76
30:0:2703:A:H2'	30:0:2704:C:H6	1.50	0.76
30:0:283:U:H5	30:0:284:C:C4	2.02	0.76
30:0:1175:G:H1'	30:0:1193:A:H2'	1.65	0.76
31:9:1:U:H4'	31:9:3:A:OP1	1.84	0.76
30:0:2468:A:H3'	38:0:5449:HOH:O	1.84	0.76
2:B:221:GLN:HE22	11:K:42:ASN:HD22	1.33	0.76
24:X:37:LEU:HD13	24:X:85:VAL:HG21	1.68	0.76
30:0:2506:A:O2'	30:0:2507:G:H8	1.68	0.76
1:A:194:MET:HE3	1:A:199:HIS:HB2	1.67	0.76
38:C:8633:HOH:O	30:0:338:C:H5''	1.86	0.76
30:0:969:G:H1	30:0:999:C:H42	1.34	0.76
13:M:71:SER:HB3	30:0:2264:A:OP1	1.85	0.75
30:0:899:C:H5'	38:0:3190:HOH:O	1.85	0.75
4:D:105:SER:OG	30:0:2338:G:H1'	1.85	0.75
10:J:75:PRO:HG2	10:J:105:LEU:HD21	1.66	0.75
14:N:132:ASN:HD22	30:0:2413:A:H4'	1.52	0.75
30:0:282:C:H1'	30:0:368:C:N4	2.01	0.75
30:0:2505:G:H2'	30:0:2506:A:C5'	2.17	0.75
30:0:1170:U:H2'	30:0:1172:G:OP2	1.87	0.75
26:Z:70:ARG:HB2	26:Z:70:ARG:HH11	1.51	0.74
30:0:2908:A:H2'	30:0:2909:G:O4'	1.87	0.74
30:0:544:G:H2'	30:0:545:G:H5''	1.68	0.74
30:0:1741:U:O2'	30:0:2723:G:H4'	1.87	0.74
24:X:76:ARG:HH11	24:X:76:ARG:HG3	1.52	0.74
1:A:191:GLY:HA2	1:A:194:MET:HE2	1.69	0.74
3:C:218:VAL:HG12	38:C:8637:HOH:O	1.87	0.74
22:V:57:LYS:HA	22:V:60:GLN:HE21	1.52	0.74
30:0:1834:C:H2'	30:0:1840:A:N6	2.02	0.74
33:0:8813:CL:CL	38:0:4678:HOH:O	2.43	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:4:LEU:HD23	23:W:54:PHE:HB3	1.69	0.74
30:0:2781:U:C2'	30:0:2782:G:H5'	2.18	0.74
30:0:2793:A:H1'	38:0:6312:HOH:O	1.88	0.74
5:E:69:ILE:HA	5:E:72:MET:HE3	1.68	0.74
14:N:11:ARG:HD3	31:9:114:G:O6	1.88	0.74
3:C:140:VAL:HB	38:C:8660:HOH:O	1.86	0.73
4:D:22:VAL:HG22	4:D:74:THR:HG22	1.70	0.73
18:R:98:ASN:HD21	30:0:500:G:H21	1.36	0.73
30:0:1525:G:H5'	30:0:1526:A:OP2	1.89	0.73
30:0:2578:G:H5'	30:0:2578:G:H8	1.52	0.73
31:9:92:G:H2'	31:9:93:A:H8	1.50	0.73
2:B:56:ASP:HB2	2:B:322:ARG:HE	1.52	0.73
21:U:56:ARG:HH11	21:U:56:ARG:HG3	1.54	0.73
11:K:14:LYS:HB2	11:K:45:PRO:HG2	1.70	0.73
30:0:2748:G:H1'	38:0:7889:HOH:O	1.88	0.73
30:0:1279:U:O2	30:0:1279:U:H2'	1.89	0.72
30:0:619:U:H3'	38:0:3270:HOH:O	1.88	0.72
30:0:2768:A:O2'	30:0:2769:C:H5'	1.89	0.72
14:N:37:ARG:HH12	31:9:6:C:H5''	1.55	0.72
30:0:2524:G:H21	30:0:2526:C:N4	1.85	0.72
30:0:2871:G:H2'	30:0:2872:U:H6	1.54	0.72
30:0:271:C:H41	30:0:378:A:H2	1.33	0.72
30:0:558:C:H2'	30:0:559:U:C5'	2.20	0.72
2:B:179:LEU:O	2:B:183:GLU:HG2	1.89	0.72
30:0:1921:A:O2'	30:0:1922:A:H5'	1.89	0.72
30:0:2766:A:H5'	38:0:9565:HOH:O	1.88	0.72
30:0:1166:A:P	30:0:1174:A:H4'	2.29	0.72
31:9:29:C:H2'	31:9:30:C:C5'	2.17	0.72
30:0:877:G:H5'	30:0:878:G:OP1	1.89	0.72
30:0:2533:C:H5'	30:0:2533:C:H6	1.53	0.72
13:M:15:PRO:HA	13:M:20:LEU:HD23	1.70	0.72
13:M:79:ALA:H	13:M:81:ARG:HH22	1.37	0.72
30:0:544:G:C2'	30:0:545:G:H5''	2.20	0.72
30:0:836:G:H5''	38:0:9285:HOH:O	1.89	0.72
30:0:2712:G:H5'	38:0:5215:HOH:O	1.90	0.72
2:B:145:HIS:HD2	2:B:146:THR:O	1.73	0.71
13:M:66:SER:HB3	13:M:128:TRP:CD1	2.24	0.71
29:3:2:GLN:O	30:0:2320:U:H2'	1.90	0.71
31:9:54:A:O2'	31:9:55:U:H5'	1.89	0.71
14:N:159:TYR:HE1	31:9:50:G:H5''	1.55	0.71
14:N:67:ALA:HA	14:N:71:TRP:HB3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:281:U:H2'	30:0:282:C:O4'	1.90	0.71
30:0:702:G:O2'	30:0:703:G:H5'	1.90	0.71
30:0:821:U:H3'	38:0:3759:HOH:O	1.90	0.71
30:0:2534:C:H1'	38:0:3477:HOH:O	1.91	0.71
30:0:2426:G:H1'	38:0:6075:HOH:O	1.90	0.71
30:0:221:G:H5''	38:0:5725:HOH:O	1.90	0.71
30:0:1165:G:N2	30:0:1173:A:C5'	2.53	0.71
2:B:307:ARG:HH11	2:B:307:ARG:HG3	1.55	0.71
38:I:6825:HOH:O	30:0:1166:A:H2	1.73	0.71
30:0:1835:U:C5	30:0:1840:A:N7	2.57	0.71
30:0:1132:A:N6	30:0:1229:C:H2'	2.06	0.71
14:N:5:ARG:HB2	14:N:5:ARG:HH11	1.56	0.71
30:0:1589:G:N2	30:0:1605:G:H1'	2.05	0.71
30:0:1979:G:H3'	38:0:3282:HOH:O	1.88	0.71
30:0:2487:C:H5	38:0:4880:HOH:O	1.73	0.70
14:N:143:ARG:HH21	14:N:169:PRO:HB2	1.56	0.70
30:0:2514:U:OP1	30:0:2572:G:H1'	1.90	0.70
14:N:17:ARG:HB3	14:N:17:ARG:HH11	1.55	0.70
30:0:2505:G:O2'	30:0:2506:A:H5'	1.90	0.70
11:K:98:VAL:CG1	11:K:102:GLU:HA	2.20	0.70
26:Z:70:ARG:HH12	26:Z:83:TYR:HB2	1.55	0.70
30:0:1666:C:H2'	30:0:1667:A:C5'	2.21	0.70
17:Q:11:ARG:NH2	30:0:2297:U:H4'	2.07	0.70
30:0:1189:A:H1'	30:0:1209:C:C1'	2.21	0.70
18:R:132:ARG:NH2	30:0:2055:A:H4'	2.06	0.70
30:0:1209:C:H2'	30:0:1210:G:H8	1.57	0.70
30:0:2237:G:H1'	30:0:2238:A:C8	2.27	0.70
13:M:188:ARG:HD3	30:0:155:C:OP2	1.92	0.70
26:Z:80:GLN:HG3	26:Z:81:CYS:H	1.56	0.70
30:0:31:C:H2'	38:0:7677:HOH:O	1.90	0.70
38:Q:6286:HOH:O	30:0:1019:C:H5'	1.91	0.69
3:C:127:ARG:NH2	3:C:225:PRO:HG2	2.07	0.69
30:0:2251:G:H2'	30:0:2252:A:C8	2.27	0.69
2:B:36:PRO:HG3	2:B:169:GLY:H	1.57	0.69
30:0:42:C:H3'	38:0:4166:HOH:O	1.92	0.69
30:0:138:U:H5''	30:0:139:C:OP2	1.93	0.69
30:0:1451:C:H5'	30:0:1505:U:C5	2.27	0.69
30:0:1562:C:O2	30:0:1562:C:H2'	1.91	0.69
1:A:94:LEU:HD12	1:A:98:GLU:HB2	1.74	0.69
5:E:143:GLN:HE21	30:0:2780:C:H1'	1.57	0.69
9:I:91:PHE:HD2	9:I:131:GLY:HA2	1.55	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:49:THR:HB	14:N:58:LEU:HD11	1.74	0.69
4:D:28:GLY:HA2	4:D:69:ILE:HG23	1.72	0.69
13:M:79:ALA:HB3	13:M:81:ARG:NH1	2.06	0.69
30:0:287:C:H42	30:0:365:G:H1	1.41	0.69
30:0:407:A:H2'	30:0:408:A:C8	2.28	0.69
30:0:961:A:H4'	38:0:6759:HOH:O	1.91	0.69
30:0:1666:C:C2'	30:0:1667:A:C5'	2.70	0.69
30:0:2102:G:H4'	38:0:5631:HOH:O	1.92	0.69
30:0:2102:G:N2	30:0:2103:A:N1	2.40	0.69
30:0:2871:G:H2'	30:0:2872:U:C6	2.28	0.69
10:J:26:VAL:HG13	10:J:36:VAL:HG11	1.75	0.69
14:N:141:ARG:HH21	31:9:48:C:H4'	1.57	0.69
2:B:206:THR:HG21	30:0:2716:G:H5''	1.73	0.69
12:L:91:VAL:HG13	12:L:120:LEU:HD23	1.75	0.69
31:9:39:U:H3'	31:9:40:C:H5''	1.75	0.69
2:B:18:ARG:HE	2:B:256:GLN:HE21	1.41	0.69
30:0:2511:A:H2'	30:0:2512:U:O4'	1.93	0.69
30:0:2781:U:H2'	30:0:2782:G:H5'	1.73	0.69
13:M:68:ARG:O	13:M:68:ARG:HD3	1.93	0.69
30:0:969:G:H1	30:0:999:C:N4	1.91	0.69
30:0:1589:G:H22	30:0:1605:G:H1'	1.55	0.69
4:D:51:ARG:HH11	4:D:68:PRO:HB3	1.59	0.68
10:J:18:ILE:HD13	30:0:1244:U:OP1	1.92	0.68
22:V:50:ARG:HH12	30:0:56:G:H5''	1.58	0.68
30:0:317:A:H5'	38:0:3761:HOH:O	1.91	0.68
30:0:1474:C:H6	30:0:1474:C:C5'	2.06	0.68
30:0:2781:U:O2'	30:0:2782:G:H5'	1.93	0.68
2:B:41:PHE:CD1	2:B:79:MET:HE2	2.29	0.68
14:N:40:ASN:ND2	31:9:28:U:H5''	2.08	0.68
16:P:59:ARG:HH22	16:P:66:GLN:NE2	1.87	0.68
30:0:870:G:C2'	30:0:871:G:H5''	2.22	0.68
2:B:254:GLN:HG3	38:0:9697:HOH:O	1.92	0.68
13:M:99:ARG:HD2	13:M:167:GLY:HA2	1.75	0.68
29:3:59:ASP:HA	30:0:2460:A:H5''	1.74	0.68
30:0:962:C:H2'	30:0:963:C:H5'	1.74	0.68
10:J:131:THR:HB	10:J:134:GLU:HG3	1.75	0.68
28:2:35:ARG:HB2	38:2:2691:HOH:O	1.92	0.68
30:0:255:A:H2'	30:0:256:C:C6	2.29	0.68
30:0:390:G:H5'	38:0:7539:HOH:O	1.94	0.68
30:0:283:U:H5	30:0:284:C:N3	1.91	0.68
30:0:1527:A:H1'	30:0:1528:A:C8	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1634:G:H2'	30:0:1635:U:H6	1.57	0.68
30:0:1702:U:H1'	38:0:5758:HOH:O	1.93	0.68
12:L:6:ARG:HD3	30:0:1299:G:O6	1.94	0.68
13:M:171:ARG:CD	30:0:156:C:H5''	2.15	0.68
30:0:440:C:H2'	30:0:441:A:C8	2.29	0.68
30:0:2374:G:H2'	30:0:2375:A:C8	2.29	0.68
13:M:83:SER:HA	38:M:8877:HOH:O	1.94	0.68
24:X:25:ARG:HD2	38:X:5356:HOH:O	1.91	0.68
26:Z:70:ARG:HB3	38:Z:8728:HOH:O	1.93	0.68
2:B:264:GLU:CG	2:B:267:LYS:HE3	2.24	0.67
27:1:8:GLN:HE22	27:1:11:LYS:NZ	1.93	0.67
30:0:1666:C:C2'	30:0:1667:A:H5''	2.23	0.67
8:H:72:ALA:HB2	8:H:156:ALA:HB2	1.75	0.67
23:W:137:GLN:HE21	23:W:141:HIS:CE1	2.08	0.67
30:0:1158:G:C2'	30:0:1159:G:H5'	2.24	0.67
10:J:19:MET:HE3	10:J:132:LEU:HD11	1.75	0.67
10:J:90:LYS:HB2	33:J:8802:CL:CL	2.31	0.67
23:W:88:THR:HG23	23:W:110:GLN:HB3	1.76	0.67
30:0:1634:G:H2'	30:0:1635:U:C6	2.29	0.67
6:F:63:ILE:HB	6:F:64:PRO:HD3	1.74	0.67
31:9:24:U:H3'	31:9:25:G:H5'	1.75	0.67
20:T:2:LYS:HG2	30:0:447:A:OP1	1.95	0.67
30:0:283:U:C5	30:0:284:C:C4	2.83	0.67
30:0:735:C:C5	30:0:736:A:C4	2.82	0.67
30:0:1632:A:C2'	30:0:1633:C:H5'	2.24	0.67
30:0:1762:C:O2'	30:0:1763:C:H5'	1.95	0.67
31:9:91:C:H1'	38:9:9143:HOH:O	1.95	0.67
30:0:541:C:H2'	30:0:542:A:H5'	1.75	0.67
30:0:1268:C:H2'	30:0:1269:G:H8	1.59	0.67
1:A:72:GLU:HG2	26:Z:100:GLY:HA3	1.76	0.67
14:N:7:LYS:HE3	17:Q:21:ARG:O	1.95	0.67
18:R:150:PRO:CG	18:R:150:PRO:O	2.42	0.67
30:0:221:G:H2'	30:0:222:A:C8	2.30	0.67
30:0:603:A:H5''	30:0:604:G:OP1	1.94	0.67
9:I:96:SER:H	9:I:99:GLN:NE2	1.93	0.66
25:Y:187:VAL:HG23	25:Y:192:ASP:HB3	1.77	0.66
30:0:2073:G:OP2	30:0:2490:A:H5'	1.95	0.66
12:L:121:ILE:HG12	12:L:141:GLU:HB2	1.78	0.66
30:0:506:G:H22	30:0:509:A:H5'	1.60	0.66
30:0:613:C:H2'	30:0:614:U:H6	1.61	0.66
30:0:2488:A:C2	38:0:7265:HOH:O	2.48	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:18:ILE:HG22	11:K:93:ASN:HB2	1.77	0.66
30:0:451:C:O2'	30:0:452:G:H5'	1.95	0.66
18:R:18:LEU:HB2	18:R:143:VAL:HG13	1.76	0.66
30:0:1158:G:O2'	30:0:1159:G:H5'	1.96	0.66
22:V:50:ARG:NH1	30:0:56:G:H5''	2.10	0.66
30:0:849:C:H1'	38:0:6602:HOH:O	1.95	0.66
31:9:55:U:H4'	31:9:56:A:C8	2.31	0.66
25:Y:169:ARG:HD2	30:0:1328:A:OP1	1.96	0.66
30:0:2461:U:O2	30:0:2466:G:H1'	1.96	0.66
30:0:735:C:H2'	30:0:736:A:O4'	1.96	0.66
30:0:2321:A:C2	30:0:2378:U:N3	2.57	0.66
8:H:32:ALA:HB3	8:H:69:ARG:HH12	1.61	0.66
9:I:87:PRO:HD2	30:0:1180:U:H1'	1.77	0.66
30:0:558:C:H2'	30:0:559:U:H5'	1.78	0.66
2:B:162:MET:HG3	2:B:310:ARG:NH1	2.10	0.65
9:I:110:ASP:O	30:0:1163:G:H5'	1.96	0.65
3:C:233:THR:HG22	3:C:234:VAL:H	1.61	0.65
4:D:103:ASN:ND2	4:D:133:ASN:HA	2.11	0.65
4:D:103:ASN:HD22	4:D:133:ASN:HA	1.60	0.65
21:U:56:ARG:NE	30:0:2890:A:H1'	2.11	0.65
30:0:567:U:H5''	38:0:5280:HOH:O	1.97	0.65
30:0:635:A:H2'	30:0:636:G:H5''	1.77	0.65
30:0:1477:C:H5'	30:0:1868:G:C5'	2.26	0.65
30:0:1940:C:H1'	38:0:9376:HOH:O	1.96	0.65
30:0:1950:G:H2'	30:0:1951:G:C8	2.32	0.65
25:Y:187:VAL:HG23	25:Y:192:ASP:CB	2.27	0.65
29:3:1:MET:HE1	29:3:83:TRP:HE1	1.59	0.65
30:0:625:U:H5''	30:0:1044:C:N4	2.11	0.65
30:0:1925:G:O2'	30:0:1926:G:H5'	1.96	0.65
5:E:139:GLU:OE2	30:0:2781:U:H1'	1.97	0.65
30:0:2869:G:H2'	30:0:2870:C:C6	2.31	0.65
14:N:144:GLY:O	14:N:147:ILE:HG22	1.97	0.65
22:V:39:ALA:N	22:V:40:PRO:HD2	2.12	0.65
30:0:1165:G:H1'	30:0:1174:A:C1'	2.11	0.65
29:3:31:THR:HB	29:3:33:MET:HE3	1.77	0.65
30:0:1972:U:H2'	30:0:1973:A:C5'	2.27	0.65
17:Q:19:ARG:HH21	31:9:11:A:P	2.19	0.64
23:W:21:LEU:HD21	23:W:48:VAL:HG11	1.78	0.64
30:0:2458:U:H3'	38:0:3239:HOH:O	1.96	0.64
30:0:128:A:O2'	30:0:129:A:H5'	1.97	0.64
30:0:583:C:H2'	30:0:584:U:H6	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1165:G:H21	30:0:1173:A:H5'	1.63	0.64
30:0:2672:C:O2'	30:0:2673:U:H5'	1.97	0.64
30:0:2896:A:H5''	38:0:6082:HOH:O	1.96	0.64
11:K:74:VAL:HG11	11:K:113:ILE:HG12	1.79	0.64
30:0:69:A:H5'	30:0:69:A:C8	2.32	0.64
30:0:125:U:H2'	38:0:3755:HOH:O	1.97	0.64
30:0:369:G:O2'	30:0:370:G:H5'	1.98	0.64
30:0:660:A:H4'	30:0:661:G:O5'	1.98	0.64
2:B:312:ARG:HD3	2:B:315:VAL:HG13	1.79	0.64
30:0:200:C:H2'	38:0:3428:HOH:O	1.96	0.64
30:0:2488:A:H2	38:0:7265:HOH:O	1.81	0.64
4:D:25:MET:HE2	4:D:41:LEU:HG	1.79	0.64
19:S:17:ASP:HB3	19:S:23:LYS:HB2	1.79	0.64
30:0:1167:G:H2'	30:0:1168:C:O4'	1.98	0.64
13:M:70:GLY:CA	30:0:2263:G:H4'	2.28	0.64
31:9:36:C:H5'	38:9:9047:HOH:O	1.98	0.64
2:B:41:PHE:CD2	2:B:190:MET:HE3	2.32	0.64
30:0:285:A:H2'	30:0:286:U:O4'	1.97	0.64
30:0:1119:G:N2	30:0:1246:A:H2	1.89	0.64
30:0:2321:A:H8	30:0:2322:U:O2'	1.80	0.64
30:0:2781:U:H2'	30:0:2782:G:C5'	2.27	0.64
15:O:47:ARG:HG3	15:O:47:ARG:NH1	2.12	0.64
30:0:441:A:H1'	30:0:442:A:N7	2.13	0.64
30:0:1181:A:H2'	30:0:1182:C:H5'	1.78	0.64
31:9:5:G:O2'	31:9:6:C:H5'	1.97	0.64
18:R:132:ARG:HH21	30:0:2055:A:H4'	1.61	0.64
30:0:1213:C:O2'	30:0:1214:G:H5'	1.98	0.64
30:0:2436:U:H2'	30:0:2437:A:C8	2.33	0.64
30:0:2878:U:H5''	38:0:4165:HOH:O	1.98	0.64
30:0:2887:G:H2'	30:0:2888:U:C6	2.32	0.64
12:L:143:THR:HG22	12:L:144:ASP:H	1.62	0.63
30:0:2377:U:O2'	30:0:2378:U:H5'	1.98	0.63
30:0:2613:G:O2'	30:0:2614:C:H5'	1.99	0.63
31:9:24:U:H3'	31:9:25:G:C5'	2.28	0.63
30:0:2281:C:C2'	30:0:2282:U:H5'	2.28	0.63
3:C:162:VAL:HG22	3:C:232:LEU:HD21	1.81	0.63
14:N:141:ARG:NH2	31:9:48:C:H4'	2.13	0.63
21:U:4:ARG:O	21:U:13:ILE:HG22	1.98	0.63
30:0:585:C:H5''	38:0:4864:HOH:O	1.98	0.63
30:0:2831:C:C2'	30:0:2832:C:H5'	2.28	0.63
13:M:99:ARG:HE	13:M:170:ASN:ND2	1.96	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:281:U:O2'	30:0:282:C:H5'	1.97	0.63
30:0:1170:U:H1'	30:0:1172:G:N7	2.13	0.63
30:0:2869:G:H5'	38:0:5487:HOH:O	1.97	0.63
13:M:81:ARG:HB3	13:M:85:ARG:HB2	1.80	0.63
30:0:1204:C:H1'	38:0:4741:HOH:O	1.98	0.63
30:0:1268:C:H2'	30:0:1269:G:C8	2.34	0.63
30:0:1904:A:C2	30:0:1905:U:H1'	2.34	0.63
30:0:2336:G:H2'	38:0:6280:HOH:O	1.98	0.63
30:0:2868:C:H1'	38:0:7114:HOH:O	1.97	0.63
2:B:262:ARG:HG3	30:0:2716:G:H5'	1.79	0.63
3:C:174:ILE:CD1	30:0:338:C:H4'	2.29	0.63
29:3:55:VAL:HB	29:3:56:PRO:HD2	1.81	0.63
30:0:820:G:H5'	30:0:821:U:H5'	1.80	0.63
18:R:4:TYR:CE1	18:R:17:MET:HE2	2.34	0.63
30:0:424:C:H2'	30:0:425:U:H6	1.64	0.63
30:0:1528:A:H2'	30:0:1529:G:O4'	1.98	0.63
30:0:2831:C:H2'	30:0:2832:C:H5'	1.79	0.63
4:D:25:MET:SD	4:D:40:ILE:HD11	2.39	0.63
30:0:280:C:H2'	30:0:281:U:O4'	1.99	0.63
30:0:1950:G:H2'	30:0:1951:G:H8	1.64	0.63
30:0:2401:A:H2'	30:0:2402:A:C8	2.34	0.63
31:9:2:U:OP2	31:9:3:A:H5'	1.99	0.63
31:9:36:C:C5	31:9:37:C:C5	2.87	0.63
18:R:9:ASP:O	18:R:13:THR:HB	1.99	0.62
30:0:558:C:C2'	30:0:559:U:C5'	2.77	0.62
2:B:238:ASN:HD22	2:B:240:GLY:H	1.45	0.62
2:B:272:ILE:HG22	38:B:9132:HOH:O	2.00	0.62
12:L:79:ASP:HB3	38:L:9022:HOH:O	1.98	0.62
13:M:179:GLY:O	30:0:399:C:H5'	1.98	0.62
18:R:39:THR:HG23	18:R:107:GLU:O	1.99	0.62
30:0:834:G:H4'	30:0:835:U:OP2	1.99	0.62
30:0:2594:C:O2'	30:0:2595:U:H5'	1.99	0.62
30:0:2827:A:H2'	30:0:2828:G:O4'	1.99	0.62
30:0:2894:C:O2'	30:0:2895:C:H5'	1.99	0.62
11:K:66:ARG:HH22	30:0:1994:A:P	2.21	0.62
30:0:308:U:C4	30:0:342:C:H1'	2.34	0.62
30:0:1829:A:H2'	30:0:1830:C:H5'	1.81	0.62
30:0:2505:G:C2'	30:0:2506:A:C5'	2.76	0.62
15:O:10:LEU:HD13	15:O:99:GLU:HG3	1.82	0.62
30:0:249:G:O2'	30:0:250:C:H5'	1.99	0.62
30:0:256:C:H2'	30:0:257:G:O4'	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1797:A:H4'	30:0:1798:C:C5	2.33	0.62
25:Y:204:ARG:HH22	30:0:553:G:P	2.22	0.62
30:0:506:G:N2	30:0:509:A:H5''	2.14	0.62
17:Q:11:ARG:HH21	30:0:2297:U:H4'	1.62	0.62
23:W:48:VAL:HG12	23:W:52:VAL:HB	1.81	0.62
30:0:1087:G:H4'	30:0:1088:A:OP1	2.00	0.62
30:0:1230:A:H8	30:0:1230:A:OP1	1.83	0.62
30:0:2705:U:H2'	30:0:2706:A:C8	2.35	0.62
30:0:418:C:H5	38:0:5765:HOH:O	1.82	0.62
1:A:47:HIS:CD2	30:0:1654:U:H2'	2.35	0.62
13:M:24:GLN:HE21	13:M:27:ARG:HH11	1.48	0.62
17:Q:27:GLN:HE21	31:9:8:G:C5'	2.11	0.62
30:0:1625:U:H5''	38:0:6005:HOH:O	2.00	0.62
30:0:2248:C:H3'	38:0:5435:HOH:O	1.98	0.62
15:O:37:ARG:HD2	30:0:656:G:OP2	2.00	0.62
30:0:303:C:O2'	30:0:304:G:H5'	2.00	0.62
30:0:1165:G:N2	30:0:1173:A:H5''	2.09	0.62
8:H:168:VAL:HG13	38:H:9006:HOH:O	2.00	0.62
13:M:79:ALA:H	13:M:81:ARG:NH2	1.96	0.62
30:0:289:G:O2'	30:0:290:C:H5'	1.98	0.62
30:0:1477:C:H5'	30:0:1868:G:H5'	1.81	0.62
31:9:110:G:C6	31:9:111:U:C5	2.88	0.61
19:S:52:VAL:HG22	19:S:66:VAL:HG22	1.82	0.61
23:W:44:MET:CE	30:0:944:G:H21	2.09	0.61
25:Y:126:PRO:HG2	25:Y:128:PHE:CE1	2.34	0.61
30:0:545:G:H8	30:0:545:G:C5'	2.08	0.61
30:0:807:A:O2'	30:0:808:A:H5'	1.99	0.61
3:C:27:ARG:HG2	3:C:27:ARG:NH1	2.12	0.61
10:J:75:PRO:HG2	10:J:105:LEU:CD2	2.31	0.61
12:L:90:ARG:HA	12:L:119:THR:HB	1.82	0.61
14:N:83:LEU:HD13	14:N:175:LEU:HD23	1.82	0.61
20:T:9:LYS:HD2	38:0:3744:HOH:O	2.00	0.61
28:2:41:HIS:HE1	30:0:1439:C:H5''	1.65	0.61
30:0:39:G:N2	30:0:444:C:C2	2.68	0.61
30:0:1596:U:H2'	30:0:1598:A:OP2	2.00	0.61
30:0:2102:G:N2	30:0:2104:C:C2	2.69	0.61
31:9:107:C:O2'	31:9:108:C:H5'	2.00	0.61
3:C:129:HIS:CE1	3:C:231:ARG:HA	2.35	0.61
30:0:1245:C:O5'	30:0:1245:C:H6	1.84	0.61
13:M:102:GLU:OE1	13:M:164:THR:HG21	2.00	0.61
30:0:1015:C:H2'	30:0:1016:U:H6	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1:MET:HG2	3:C:2:GLN:N	2.15	0.61
3:C:236:THR:HG22	3:C:239:ALA:N	2.12	0.61
26:Z:40:ALA:HA	30:0:1773:G:C8	2.35	0.61
30:0:138:U:OP2	30:0:139:C:H5	1.84	0.61
30:0:2502:C:H2'	30:0:2503:A:C5'	2.29	0.61
30:0:2717:C:H2'	30:0:2718:C:C5'	2.30	0.61
4:D:173:GLU:HG3	4:D:174:VAL:HG23	1.83	0.61
29:3:60:LYS:CG	29:3:61:PRO:HD2	2.29	0.61
30:0:24:G:N2	30:0:518:G:H1'	2.16	0.61
30:0:559:U:H5'	30:0:559:U:C6	2.32	0.61
16:P:98:ILE:HD12	16:P:102:ARG:NE	2.16	0.61
26:Z:78:ILE:HD12	38:Z:8714:HOH:O	2.01	0.61
30:0:272:A:H5'	30:0:273:G:OP2	2.01	0.61
30:0:424:C:H2'	30:0:425:U:C6	2.35	0.61
30:0:735:C:H5	30:0:736:A:C4	2.18	0.61
30:0:2766:A:O2'	30:0:2767:C:H5'	2.00	0.61
29:3:4:PRO:HA	29:3:91:GLN:HB2	1.82	0.61
30:0:657:G:H2'	30:0:658:C:H6	1.64	0.61
30:0:946:C:H2'	30:0:947:U:H6	1.65	0.61
30:0:1015:C:H2'	30:0:1016:U:C6	2.36	0.61
27:1:8:GLN:HE22	27:1:11:LYS:HZ2	1.49	0.60
30:0:1741:U:H5'	30:0:1742:A:OP1	2.01	0.60
15:O:32:ARG:O	15:O:32:ARG:HD3	2.01	0.60
30:0:1165:G:N2	30:0:1173:A:H5'	2.15	0.60
30:0:1972:U:H2'	30:0:1973:A:H5'	1.83	0.60
30:0:2769:C:H2'	30:0:2770:G:H5'	1.82	0.60
2:B:207:LYS:HG3	30:0:2717:C:OP1	2.01	0.60
5:E:154:ILE:HD11	5:E:157:LYS:HE2	1.83	0.60
28:2:10:ARG:NH2	30:0:121:U:OP2	2.34	0.60
30:0:1181:A:C2'	30:0:1182:C:H5'	2.30	0.60
30:0:1603:A:C5'	30:0:1605:G:H5'	2.29	0.60
8:H:29:SER:HA	8:H:62:HIS:HD2	1.66	0.60
30:0:192:A:H5'	38:0:7634:HOH:O	1.99	0.60
30:0:272:A:H3'	38:0:7522:HOH:O	2.00	0.60
30:0:1183:C:N4	30:0:1184:C:H41	1.98	0.60
30:0:1603:A:C5'	30:0:1605:G:O4'	2.45	0.60
30:0:1622:G:H2'	30:0:1623:C:H5'	1.83	0.60
30:0:2102:G:C8	30:0:2538:A:O4'	2.54	0.60
30:0:2281:C:H2'	30:0:2282:U:H5'	1.83	0.60
31:9:20:G:O2'	31:9:21:G:H5'	2.02	0.60
31:9:76:G:C3'	31:9:77:A:H5''	2.21	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:107:ASN:HD22	10:J:109:TYR:H	1.48	0.60
13:M:84:LYS:HA	29:3:46:ILE:O	2.01	0.60
18:R:96:VAL:HG13	18:R:106:GLY:HA3	1.84	0.60
29:3:25:VAL:HG22	29:3:68:LYS:HG3	1.84	0.60
30:0:396:U:H3'	38:0:3920:HOH:O	2.00	0.60
30:0:851:C:O2	30:0:2022:A:H2	1.85	0.60
13:M:77:HIS:HB2	13:M:81:ARG:HH21	1.66	0.60
29:3:3:MET:SD	29:3:88:LEU:HD11	2.41	0.60
30:0:182:G:H5'	38:0:5152:HOH:O	2.01	0.60
30:0:282:C:O2'	30:0:283:U:C5'	2.48	0.60
30:0:333:G:O2'	30:0:334:G:H5'	2.01	0.60
30:0:946:C:H2'	30:0:947:U:C6	2.35	0.60
30:0:2659:U:H5''	38:0:4122:HOH:O	2.02	0.60
5:E:24:GLY:HA3	5:E:76:VAL:HB	1.82	0.60
16:P:115:SER:N	16:P:118:GLN:HE21	1.92	0.60
30:0:228:C:H2'	30:0:229:G:H5'	1.82	0.60
30:0:90:A:H2'	30:0:91:G:O4'	2.01	0.60
30:0:671:A:O2'	30:0:672:G:H2'	2.02	0.60
1:A:217:ARG:HG2	1:A:229:ALA:HB2	1.84	0.60
19:S:33:SER:O	19:S:37:VAL:HG23	2.02	0.60
23:W:6:GLN:CB	23:W:26:ILE:HD11	2.30	0.60
30:0:293:A:O2'	30:0:294:C:H5'	2.02	0.60
30:0:2793:A:H2'	38:0:4488:HOH:O	2.02	0.60
3:C:184:ARG:NH2	30:0:450:C:OP1	2.29	0.60
26:Z:37:ARG:HB2	30:0:819:A:C4'	2.32	0.60
26:Z:53:ILE:O	26:Z:57:MET:HB2	2.02	0.60
30:0:453:A:H5''	38:0:3254:HOH:O	2.02	0.60
30:0:734:U:O2'	30:0:736:A:N7	2.35	0.60
30:0:1183:C:H42	30:0:1184:C:H41	1.50	0.60
30:0:2769:C:H2'	30:0:2770:G:C5'	2.31	0.60
1:A:35:GLY:O	1:A:36:ASP:HB3	2.02	0.59
11:K:4:LEU:HD22	11:K:116:GLU:HB3	1.83	0.59
21:U:39:ASN:HB3	38:U:3805:HOH:O	2.02	0.59
27:1:9:GLY:HA2	30:0:1687:C:O2	2.02	0.59
2:B:154:VAL:CG1	2:B:156:LYS:HG2	2.31	0.59
2:B:258:GLY:H	2:B:260:HIS:CE1	2.20	0.59
30:0:2812:A:H1'	38:0:5773:HOH:O	2.01	0.59
31:9:63:C:O2'	31:9:64:C:H5'	2.02	0.59
14:N:159:TYR:CE1	31:9:50:G:H5''	2.37	0.59
27:1:1:THR:HB	38:0:7134:HOH:O	2.02	0.59
27:1:10:LYS:HG3	38:1:2979:HOH:O	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1058:A:H2'	30:0:1060:C:H5''	1.83	0.59
30:0:1819:G:H2'	30:0:1820:G:H4'	1.82	0.59
30:0:1973:A:H5'	30:0:1973:A:C8	2.35	0.59
30:0:747:G:H5'	38:0:4947:HOH:O	2.02	0.59
30:0:2321:A:H2	30:0:2378:U:N3	1.92	0.59
30:0:2472:C:O2'	30:0:2634:G:H4'	2.02	0.59
31:9:39:U:H1'	31:9:44:A:N6	2.15	0.59
9:I:112:LEU:CD1	30:0:1162:G:H1'	2.32	0.59
30:0:247:A:H2'	38:0:3921:HOH:O	2.02	0.59
30:0:2498:C:O2'	30:0:2499:U:H5'	2.03	0.59
30:0:2670:G:O2'	30:0:2671:U:H5'	2.02	0.59
30:0:2689:A:H2'	30:0:2690:U:H5'	1.85	0.59
3:C:174:ILE:HD11	30:0:338:C:H4'	1.85	0.59
13:M:9:ARG:HD2	30:0:380:A:OP2	2.02	0.59
17:Q:11:ARG:NH2	30:0:2363:G:H4'	2.18	0.59
21:U:6:CYS:SG	21:U:32:CYS:HB3	2.43	0.59
22:V:8:ILE:HA	22:V:11:MET:HE3	1.83	0.59
26:Z:64:PRO:HB2	26:Z:86:TYR:CE2	2.38	0.59
29:3:51:LYS:HB3	30:0:219:G:O2'	2.03	0.59
30:0:468:U:H3'	38:0:7561:HOH:O	2.03	0.59
30:0:1201:C:H5''	38:0:6132:HOH:O	2.02	0.59
30:0:1904:A:H2'	30:0:1905:U:O4'	2.02	0.59
17:Q:26:PRO:O	17:Q:30:VAL:HG22	2.02	0.59
30:0:214:U:H5'	38:0:6123:HOH:O	2.01	0.59
30:0:1116:U:HO2'	30:0:1118:A:H2	0.72	0.59
30:0:1377:C:H5'	30:0:1377:C:H6	1.67	0.59
4:D:62:ASP:HA	38:D:4233:HOH:O	2.03	0.59
30:0:319:A:H4'	30:0:338:C:C4	2.38	0.59
30:0:1187:U:H2'	38:0:6882:HOH:O	2.02	0.59
30:0:1634:G:H3'	38:0:3889:HOH:O	2.02	0.59
30:0:2250:G:H2'	30:0:2251:G:O4'	2.03	0.59
15:O:25:VAL:HG12	30:0:709:G:O2'	2.03	0.59
30:0:827:A:H1'	38:0:6196:HOH:O	2.02	0.59
2:B:68:THR:HG21	21:U:16:GLY:HA3	1.85	0.58
18:R:40:ALA:O	18:R:44:VAL:HG23	2.03	0.58
20:T:48:VAL:HG11	20:T:96:VAL:HG13	1.85	0.58
29:3:3:MET:O	29:3:90:PHE:HA	2.03	0.58
30:0:1118:A:C8	30:0:1118:A:C3'	2.74	0.58
30:0:1175:G:H1'	30:0:1193:A:C2'	2.31	0.58
2:B:195:ARG:HE	2:B:323:LEU:HD13	1.68	0.58
30:0:542:A:H5'	30:0:542:A:C8	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1603:A:H5'	30:0:1605:G:C4'	2.33	0.58
30:0:2353:A:H4'	30:0:2354:A:O5'	2.02	0.58
2:B:256:GLN:HG2	38:B:9129:HOH:O	2.03	0.58
30:0:482:G:H4'	30:0:508:A:N1	2.18	0.58
30:0:669:G:O2'	30:0:670:G:H5'	2.03	0.58
30:0:918:G:H5''	38:0:9099:HOH:O	2.01	0.58
30:0:1393:A:H2'	30:0:1394:C:C6	2.38	0.58
30:0:1929:G:H1'	38:0:5153:HOH:O	2.03	0.58
31:9:54:A:C2'	31:9:55:U:H5'	2.33	0.58
1:A:199:HIS:CD2	1:A:201:PHE:H	2.21	0.58
30:0:657:G:H2'	30:0:658:C:C6	2.38	0.58
30:0:1127:C:C5	30:0:1128:U:C4	2.91	0.58
30:0:1161:A:O5'	30:0:1161:A:H8	1.85	0.58
2:B:307:ARG:HG3	2:B:307:ARG:NH1	2.19	0.58
3:C:2:GLN:HB3	38:C:8594:HOH:O	2.04	0.58
12:L:30:ARG:HD2	30:0:164:G:H5''	1.85	0.58
12:L:133:VAL:HA	38:L:9035:HOH:O	2.04	0.58
13:M:68:ARG:HH21	13:M:73:ARG:HD3	1.65	0.58
30:0:812:A:H2'	30:0:813:C:C6	2.38	0.58
30:0:962:C:H2'	30:0:963:C:C5'	2.33	0.58
2:B:41:PHE:CZ	2:B:79:MET:HG3	2.39	0.58
7:G:64:ASN:HD22	7:G:64:ASN:N	1.99	0.58
12:L:80:ASP:HB2	12:L:90:ARG:O	2.03	0.58
13:M:157:ASP:HB3	13:M:160:PHE:HD1	1.68	0.58
30:0:69:A:H5'	30:0:69:A:H8	1.69	0.58
30:0:416:G:H3'	38:0:9910:HOH:O	2.02	0.58
30:0:696:C:O2'	30:0:697:G:H5'	2.03	0.58
30:0:814:G:H4'	38:0:3124:HOH:O	2.03	0.58
30:0:858:U:H5	38:0:5421:HOH:O	1.86	0.58
30:0:2256:G:O2'	30:0:2257:G:H5'	2.04	0.58
30:0:2878:U:H2'	30:0:2879:A:O4'	2.02	0.58
30:0:2900:G:H2'	30:0:2901:C:O4'	2.03	0.58
2:B:42:ALA:HB3	2:B:162:MET:HE1	1.83	0.58
2:B:125:GLU:O	2:B:129:ARG:HG3	2.03	0.58
3:C:236:THR:HA	38:C:8660:HOH:O	2.04	0.58
25:Y:133:HIS:HD2	38:Y:8886:HOH:O	1.85	0.58
28:2:41:HIS:CD2	28:2:43:ARG:H	2.22	0.58
30:0:244:C:H6	30:0:244:C:O5'	1.87	0.58
30:0:541:C:O2'	30:0:542:A:H5''	2.03	0.58
30:0:2276:U:H1'	38:0:9608:HOH:O	2.04	0.58
1:A:109:GLU:HG2	1:A:116:GLY:H	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:30:GLU:O	13:M:34:GLU:HG3	2.04	0.58
13:M:81:ARG:HG3	30:0:161:A:OP1	2.04	0.58
30:0:1221:G:H8	38:0:5971:HOH:O	1.87	0.58
30:0:1819:G:H2'	30:0:1820:G:C5'	2.34	0.58
30:0:2064:U:H5'	30:0:2652:U:H4'	1.86	0.58
31:9:1:U:C4'	31:9:3:A:OP1	2.52	0.58
29:3:60:LYS:HB2	30:0:2460:A:OP1	2.04	0.58
31:9:64:C:C2'	31:9:65:A:H5'	2.33	0.58
13:M:28:GLN:O	13:M:32:ARG:HG3	2.02	0.58
22:V:1:THR:HG23	22:V:2:VAL:H	1.69	0.58
23:W:64:THR:O	23:W:68:THR:HG22	2.04	0.58
30:0:316:A:N3	30:0:336:G:O2'	2.35	0.58
30:0:1205:U:C2'	30:0:1206:U:C5'	2.81	0.58
30:0:2867:G:H2'	30:0:2868:C:C6	2.39	0.58
3:C:25:PRO:HG2	38:C:8522:HOH:O	2.03	0.57
5:E:143:GLN:NE2	30:0:2779:G:H21	2.01	0.57
18:R:71:LYS:HE2	30:0:2831:C:O3'	2.04	0.57
26:Z:80:GLN:HG3	26:Z:81:CYS:N	2.20	0.57
30:0:1829:A:C2'	30:0:1830:C:H5'	2.34	0.57
31:9:12:C:H5'	31:9:70:U:O4'	2.04	0.57
23:W:149:LEU:HG	23:W:153:MET:HE2	1.86	0.57
24:X:30:MET:HE1	24:X:58:ALA:HB3	1.85	0.57
30:0:553:G:H5'	38:0:3481:HOH:O	2.04	0.57
30:0:695:C:O2'	30:0:696:C:H5'	2.04	0.57
30:0:1626:A:H2'	30:0:1627:G:C5'	2.35	0.57
30:0:1664:A:H8	30:0:1664:A:OP1	1.87	0.57
30:0:2499:U:H2'	30:0:2500:C:H6	1.69	0.57
31:9:108:C:H2'	31:9:109:G:C8	2.38	0.57
4:D:58:VAL:HB	4:D:62:ASP:HB2	1.86	0.57
12:L:14:GLY:O	30:0:1295:G:H5''	2.04	0.57
30:0:1197:G:H1'	30:0:1203:G:N2	2.19	0.57
30:0:1494:A:C4	30:0:1495:C:C5	2.93	0.57
16:P:81:LYS:O	30:0:1761:U:H5'	2.04	0.57
19:S:55:GLN:NE2	30:0:1446:U:H2'	2.19	0.57
20:T:26:THR:HA	20:T:39:ASN:HB3	1.86	0.57
29:3:69:TYR:HD1	29:3:78:HIS:O	1.87	0.57
30:0:544:G:C3'	30:0:545:G:H5''	2.35	0.57
30:0:558:C:H2'	30:0:559:U:H5''	1.81	0.57
30:0:1395:C:H2'	30:0:1396:C:C6	2.39	0.57
30:0:2269:C:C2'	30:0:2270:G:H5'	2.34	0.57
31:9:49:G:O2'	31:9:50:G:H5'	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:VAL:CG1	1:A:207:GLN:HB3	2.34	0.57
30:0:318:U:H5'	30:0:339:A:C2	2.39	0.57
30:0:2563:U:H2'	30:0:2565:C:O5'	2.04	0.57
30:0:2840:A:H3'	38:0:7638:HOH:O	2.04	0.57
19:S:51:GLN:HE21	19:S:53:ASN:HD21	1.52	0.57
30:0:1919:A:H4'	38:0:4844:HOH:O	2.04	0.57
30:0:2300:A:H4'	30:0:2301:A:O5'	2.05	0.57
5:E:81:GLU:HG2	5:E:134:SER:HB3	1.85	0.57
9:I:126:THR:O	9:I:130:LEU:HG	2.03	0.57
25:Y:130:ARG:HD2	38:Y:8857:HOH:O	2.04	0.57
30:0:957:A:H8	30:0:957:A:O5'	1.88	0.57
30:0:1165:G:O3'	30:0:1174:A:H4'	2.04	0.57
30:0:1201:C:H2'	30:0:1202:A:H5'	1.85	0.57
3:C:101:ASP:HB2	30:0:750:A:O3'	2.05	0.57
8:H:146:ALA:O	8:H:149:VAL:HG12	2.04	0.57
14:N:4:PRO:HD2	38:0:6759:HOH:O	2.04	0.57
30:0:2531:U:O2'	30:0:2532:A:H5'	2.05	0.57
31:9:114:G:H2'	31:9:115:C:C6	2.39	0.57
4:D:65:GLU:HA	38:D:6752:HOH:O	2.05	0.57
15:O:73:ASP:HA	15:O:92:VAL:O	2.05	0.57
20:T:53:GLY:HA3	38:T:6384:HOH:O	2.04	0.57
23:W:81:ASP:OD1	23:W:92:ASP:HB2	2.05	0.57
30:0:1200:A:H3'	38:0:5738:HOH:O	2.05	0.57
30:0:1482:A:H1'	38:0:9425:HOH:O	2.04	0.57
30:0:2032:U:H2'	30:0:2033:G:C5'	2.35	0.57
2:B:102:THR:HG23	2:B:182:VAL:HG12	1.85	0.57
23:W:137:GLN:NE2	23:W:141:HIS:HE1	1.99	0.57
29:3:25:VAL:HG12	38:0:9267:HOH:O	2.04	0.57
30:0:1697:G:H4'	38:0:9342:HOH:O	2.05	0.57
30:0:2437:A:H2'	30:0:2438:G:C8	2.40	0.57
30:0:2768:A:H2'	30:0:2769:C:O4'	2.05	0.57
30:0:2831:C:H2'	30:0:2832:C:C5'	2.35	0.57
2:B:307:ARG:HB3	38:B:9126:HOH:O	2.04	0.56
30:0:589:U:H2'	30:0:590:A:H8	1.69	0.56
30:0:1202:A:H2'	30:0:1203:G:C5'	2.34	0.56
30:0:1748:U:C5	30:0:1749:U:C5	2.92	0.56
30:0:2324:G:H1'	38:0:6095:HOH:O	2.04	0.56
2:B:229:ARG:HD2	38:0:9111:HOH:O	2.04	0.56
2:B:297:VAL:HB	38:B:9075:HOH:O	2.03	0.56
3:C:214:THR:HG23	38:C:8649:HOH:O	2.04	0.56
4:D:135:VAL:HG21	4:D:139:TYR:CD1	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:39:ALA:H	22:V:40:PRO:HD2	1.69	0.56
26:Z:45:VAL:HA	26:Z:48:ARG:HB3	1.87	0.56
30:0:1511:U:O2'	30:0:1512:G:H5'	2.05	0.56
30:0:2032:U:O2'	30:0:2033:G:H5''	2.04	0.56
30:0:2758:G:H2'	30:0:2759:C:C6	2.40	0.56
30:0:2824:C:O3'	30:0:2825:C:H6	1.88	0.56
2:B:212:GLN:HB2	2:B:257:THR:HG21	1.87	0.56
2:B:244:PRO:HB3	30:0:1234:U:N3	2.20	0.56
3:C:88:SER:HB3	3:C:91:PRO:HB3	1.87	0.56
3:C:138:VAL:HG11	3:C:160:LEU:HD13	1.87	0.56
8:H:31:ILE:HD11	8:H:65:LEU:HD23	1.87	0.56
8:H:49:GLN:HG3	8:H:140:TYR:CE2	2.40	0.56
14:N:61:ALA:HB3	14:N:88:ALA:HB2	1.88	0.56
18:R:119:VAL:HG21	18:R:142:ASP:CG	2.31	0.56
21:U:56:ARG:HD2	30:0:2890:A:N9	2.20	0.56
24:X:71:ARG:HD3	38:X:2171:HOH:O	2.04	0.56
30:0:594:C:O2'	30:0:595:U:H5'	2.05	0.56
30:0:708:A:H2'	30:0:709:G:O4'	2.05	0.56
30:0:962:C:C2'	30:0:963:C:H5'	2.35	0.56
30:0:1206:U:H6	30:0:1206:U:C5'	2.14	0.56
30:0:1426:C:H2'	38:0:9592:HOH:O	2.04	0.56
31:9:18:U:H2'	31:9:19:G:C8	2.40	0.56
31:9:38:A:H2'	31:9:39:U:C6	2.41	0.56
30:0:28:G:H1'	38:0:4676:HOH:O	2.04	0.56
30:0:31:C:H4'	38:0:7417:HOH:O	2.04	0.56
30:0:1202:A:C2'	30:0:1203:G:H5'	2.35	0.56
30:0:1236:A:C2'	30:0:1237:U:H5'	2.36	0.56
29:3:67:LEU:HD21	29:3:88:LEU:HD21	1.86	0.56
30:0:941:G:C5	30:0:942:U:C4	2.94	0.56
30:0:1523:G:H2'	30:0:1524:U:C6	2.41	0.56
30:0:2248:C:H2'	30:0:2249:G:H8	1.70	0.56
30:0:2703:A:H2'	30:0:2704:C:C6	2.37	0.56
38:B:9106:HOH:O	30:0:2672:C:H1'	2.05	0.56
14:N:58:LEU:N	14:N:58:LEU:HD12	2.20	0.56
20:T:61:GLU:HG2	38:T:3851:HOH:O	2.06	0.56
22:V:55:ARG:O	22:V:59:ILE:HG12	2.06	0.56
26:Z:37:ARG:H	26:Z:37:ARG:HD3	1.71	0.56
30:0:1559:A:OP2	30:0:1559:A:H8	1.87	0.56
13:M:24:GLN:HE21	13:M:27:ARG:NH1	2.03	0.56
30:0:711:G:C2	30:0:718:C:C2	2.93	0.56
30:0:1342:C:C2'	30:0:1343:C:H5'	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1504:A:H5'	38:0:4410:HOH:O	2.06	0.56
31:9:52:A:O2'	31:9:53:G:H5'	2.06	0.56
19:S:37:VAL:O	19:S:41:VAL:HG23	2.04	0.56
21:U:56:ARG:HG3	21:U:56:ARG:NH1	2.18	0.56
26:Z:51:ALA:O	26:Z:55:SER:HB2	2.05	0.56
30:0:119:A:H2'	30:0:120:A:H5''	1.87	0.56
30:0:1537:C:H1'	38:0:6573:HOH:O	2.05	0.56
30:0:1574:C:H2'	30:0:1575:C:H6	1.70	0.56
30:0:2559:C:H4'	38:0:7245:HOH:O	2.06	0.56
10:J:70:PHE:CE1	30:0:2676:C:H4'	2.40	0.56
19:S:51:GLN:NE2	19:S:53:ASN:HD21	2.04	0.56
28:2:41:HIS:CE1	30:0:1439:C:H5''	2.41	0.56
30:0:1202:A:H2'	30:0:1203:G:O4'	2.06	0.56
30:0:1574:C:H2'	30:0:1575:C:C6	2.41	0.56
30:0:1622:G:C2'	30:0:1623:C:H5'	2.36	0.56
30:0:1850:U:O4'	30:0:1941:A:C2	2.59	0.56
30:0:2795:C:O2'	30:0:2796:U:H5'	2.05	0.56
30:0:2897:C:O2'	30:0:2898:G:H5'	2.06	0.56
30:0:290:C:O2'	30:0:291:C:H5'	2.05	0.56
30:0:1060:C:H6	30:0:1060:C:H5'	1.71	0.56
30:0:1159:G:H21	30:0:1189:A:H8	1.53	0.56
30:0:1778:A:H2'	30:0:1779:A:H5'	1.87	0.56
30:0:2004:U:H2'	30:0:2004:U:O2	2.05	0.56
30:0:2291:A:N9	30:0:2309:C:H5'	2.21	0.56
1:A:112:PRO:HD3	1:A:152:CYS:SG	2.46	0.55
8:H:59:GLN:HE21	8:H:129:ARG:NE	2.01	0.55
26:Z:34:SER:HA	30:0:797:A:H4'	1.88	0.55
29:3:12:PRO:HD3	38:3:9032:HOH:O	2.05	0.55
30:0:2316:G:H4'	38:0:6075:HOH:O	2.06	0.55
30:0:2906:A:H5'	30:0:2907:C:O4'	2.07	0.55
3:C:46:TYR:CE2	3:C:98:ARG:NH1	2.75	0.55
13:M:77:HIS:HB2	13:M:81:ARG:HE	1.72	0.55
14:N:49:THR:HG22	14:N:56:ASP:HB3	1.88	0.55
22:V:42:ASN:HB3	38:V:7247:HOH:O	2.06	0.55
24:X:23:HIS:HE1	30:0:2044:G:OP1	1.89	0.55
30:0:299:U:C2	30:0:300:U:C6	2.95	0.55
30:0:304:G:H1'	30:0:347:A:N6	2.21	0.55
30:0:485:A:N3	30:0:487:G:H5''	2.20	0.55
30:0:595:U:O2'	30:0:596:C:H5'	2.05	0.55
30:0:1594:C:O2'	30:0:1607:A:H4'	2.07	0.55
12:L:30:ARG:HD3	30:0:164:G:H4'	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:125:HIS:HE2	30:0:1097:A:H5''	1.70	0.55
30:0:1972:U:C2'	30:0:1973:A:H5''	2.36	0.55
30:0:2718:C:H6	30:0:2718:C:H5'	1.71	0.55
30:0:2887:G:H2'	30:0:2888:U:O4'	2.07	0.55
22:V:4:HIS:HB3	38:V:6622:HOH:O	2.06	0.55
26:Z:81:CYS:O	26:Z:85:ASP:HA	2.05	0.55
30:0:12:U:H2'	30:0:13:G:H5'	1.88	0.55
30:0:1361:C:H2'	30:0:1362:U:H6	1.72	0.55
1:A:211:LYS:HB3	1:A:212:PRO:CD	2.32	0.55
13:M:82:ARG:H	13:M:82:ARG:HD3	1.72	0.55
23:W:38:THR:HG22	23:W:39:ASP:H	1.72	0.55
29:3:2:GLN:HA	29:3:89:GLU:O	2.07	0.55
30:0:136:C:H2'	30:0:137:U:O4'	2.07	0.55
30:0:536:A:H3'	38:0:5040:HOH:O	2.06	0.55
30:0:699:C:C2	30:0:744:G:C2	2.95	0.55
30:0:1809:G:H1'	38:0:7682:HOH:O	2.06	0.55
30:0:1913:C:H2'	30:0:1914:C:C6	2.41	0.55
1:A:54:PRO:HG2	1:A:160:ALA:HB3	1.89	0.55
1:A:88:ILE:HD13	1:A:100:PRO:HD3	1.88	0.55
13:M:164:THR:HG22	13:M:166:ALA:H	1.71	0.55
14:N:17:ARG:HB3	14:N:17:ARG:NH1	2.21	0.55
29:3:48:ASN:O	30:0:170:U:H4'	2.07	0.55
30:0:1342:C:O2'	30:0:1343:C:H5'	2.06	0.55
30:0:1762:C:H2'	30:0:1763:C:H6	1.71	0.55
30:0:2451:G:H8	38:0:5174:HOH:O	1.90	0.55
30:0:2812:A:C2	30:0:2814:A:N6	2.71	0.55
1:A:132:ASP:CG	1:A:133:ARG:H	2.14	0.55
2:B:74:ILE:HD13	2:B:309:VAL:HG21	1.89	0.55
8:H:29:SER:HA	8:H:62:HIS:CD2	2.41	0.55
12:L:56:LYS:HE3	30:0:2443:C:H1'	1.89	0.55
30:0:876:A:H2'	30:0:876:A:N3	2.22	0.55
30:0:2480:G:H3'	38:0:4182:HOH:O	2.07	0.55
6:F:59:ILE:CD1	30:0:263:U:C2	2.90	0.55
10:J:19:MET:HE2	10:J:79:PHE:HA	1.87	0.55
18:R:114:VAL:HA	18:R:144:GLU:O	2.06	0.55
30:0:945:U:H2'	30:0:946:C:C6	2.42	0.55
30:0:1174:A:C5	30:0:1201:C:H4'	2.41	0.55
30:0:1202:A:C8	30:0:1203:G:C8	2.95	0.55
30:0:1204:C:H2'	30:0:1205:U:O4'	2.06	0.55
30:0:1236:A:O2'	30:0:1237:U:H5'	2.07	0.55
30:0:1667:A:H5'	30:0:1667:A:C8	2.34	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2240:U:O2'	30:0:2241:C:H5'	2.06	0.55
19:S:57:THR:HG22	19:S:58:MET:N	2.21	0.55
25:Y:182:PHE:HD2	25:Y:200:THR:O	1.89	0.55
30:0:154:C:H2'	30:0:155:C:H6	1.72	0.55
30:0:2416:G:H2'	30:0:2417:C:C6	2.42	0.55
31:9:59:C:H4'	38:9:9127:HOH:O	2.06	0.55
1:A:192:VAL:HG12	38:A:9012:HOH:O	2.06	0.55
22:V:64:GLY:O	22:V:65:ASP:HB2	2.07	0.55
30:0:807:A:H2'	30:0:808:A:C8	2.41	0.55
30:0:2102:G:N3	30:0:2103:A:C6	2.75	0.55
1:A:237:GLY:O	30:0:1939:U:H5''	2.06	0.54
3:C:188:ARG:HD3	38:C:8571:HOH:O	2.07	0.54
5:E:84:MET:HE1	5:E:148:ILE:HD12	1.89	0.54
11:K:74:VAL:CG1	11:K:113:ILE:HG12	2.37	0.54
30:0:204:A:H2'	30:0:205:U:H5'	1.89	0.54
30:0:368:C:H2'	30:0:369:G:H5'	1.88	0.54
30:0:1377:C:H5'	30:0:1377:C:C6	2.42	0.54
30:0:2869:G:H2'	30:0:2870:C:H6	1.73	0.54
2:B:41:PHE:HD2	2:B:190:MET:HE3	1.70	0.54
3:C:233:THR:HG22	3:C:234:VAL:N	2.21	0.54
16:P:54:LYS:HB2	30:0:1717:A:H5''	1.90	0.54
26:Z:46:SER:O	26:Z:50:VAL:HB	2.07	0.54
30:0:1878:G:C4'	38:0:6104:HOH:O	2.55	0.54
30:0:963:C:O2	30:0:1005:A:N1	2.39	0.54
30:0:1183:C:N3	30:0:1184:C:N4	2.55	0.54
30:0:1334:C:O2'	30:0:1335:C:H5'	2.07	0.54
30:0:2372:A:H2'	30:0:2373:U:C6	2.43	0.54
30:0:2872:U:H2'	30:0:2873:C:H6	1.73	0.54
2:B:201:ASP:HB2	2:B:312:ARG:HD2	1.88	0.54
11:K:24:THR:HB	11:K:64:MET:HE2	1.89	0.54
25:Y:169:ARG:NE	33:Y:8820:CL:CL	2.73	0.54
30:0:561:G:H2'	30:0:562:A:H8	1.73	0.54
30:0:1188:A:C5	30:0:1189:A:C2	2.95	0.54
30:0:1902:G:N2	30:0:1936:C:C2	2.75	0.54
20:T:52:ARG:HD2	30:0:317:A:H5''	1.90	0.54
25:Y:216:ARG:HD2	38:Y:8874:HOH:O	2.06	0.54
30:0:951:A:C2'	30:0:952:G:H5'	2.37	0.54
30:0:1969:A:O2'	30:0:1970:G:H5'	2.08	0.54
1:A:199:HIS:HD2	1:A:201:PHE:H	1.55	0.54
4:D:76:ARG:NE	31:9:44:A:O4'	2.41	0.54
14:N:5:ARG:HB2	14:N:5:ARG:NH1	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:43:VAL:CG1	14:N:118:ILE:HD11	2.38	0.54
18:R:80:TYR:O	30:0:2050:G:H5''	2.08	0.54
30:0:314:G:N2	30:0:317:A:C8	2.75	0.54
30:0:703:G:O2'	30:0:704:C:H5'	2.07	0.54
30:0:2102:G:C2	30:0:2103:A:C6	2.95	0.54
1:A:211:LYS:HG2	38:0:7019:HOH:O	2.08	0.54
6:F:2:VAL:HG22	6:F:57:GLU:OE1	2.06	0.54
7:G:20:VAL:O	7:G:24:VAL:HG23	2.07	0.54
15:O:14:LEU:HG	15:O:102:ILE:HD11	1.89	0.54
16:P:115:SER:H	16:P:118:GLN:NE2	1.92	0.54
18:R:18:LEU:HB2	18:R:143:VAL:CG1	2.36	0.54
27:1:42:SER:HB2	38:1:354:HOH:O	2.08	0.54
29:3:79:LEU:HD13	30:0:2457:U:H1'	1.88	0.54
30:0:255:A:C5	30:0:256:C:C5	2.96	0.54
30:0:2321:A:H2'	30:0:2321:A:N3	2.22	0.54
31:9:55:U:H4'	31:9:56:A:H8	1.73	0.54
12:L:18:HIS:HD2	30:0:902:G:N7	2.05	0.54
12:L:41:HIS:H	12:L:41:HIS:CD2	2.25	0.54
27:1:1:THR:HA	38:0:9360:HOH:O	2.07	0.54
30:0:120:A:H2'	30:0:120:A:N3	2.22	0.54
30:0:535:G:C5	30:0:2063:U:C4	2.95	0.54
1:A:176:HIS:CD2	30:0:857:A:H4'	2.43	0.54
1:A:190:ARG:HD2	30:0:1884:G:O6	2.08	0.54
10:J:39:VAL:HG13	10:J:106:GLY:O	2.08	0.54
23:W:26:ILE:HB	38:W:5420:HOH:O	2.06	0.54
30:0:1130:U:H2'	30:0:1131:G:O4'	2.08	0.54
30:0:1202:A:O2'	30:0:1203:G:H5'	2.08	0.54
30:0:2326:C:H4'	30:0:2412:G:C4'	2.38	0.54
30:0:2589:U:H2'	30:0:2590:U:C6	2.42	0.54
30:0:2638:G:H5'	38:0:4923:HOH:O	2.07	0.54
1:A:179:MET:HG2	1:A:186:TRP:HB2	1.89	0.54
2:B:98:THR:HG22	2:B:99:GLU:H	1.73	0.54
3:C:237:GLU:HA	38:C:8643:HOH:O	2.08	0.54
11:K:82:ARG:NH2	11:K:115:ARG:HG2	2.22	0.54
14:N:4:PRO:HB2	30:0:1010:C:H4'	1.89	0.54
14:N:147:ILE:HD11	31:9:49:G:O3'	2.07	0.54
30:0:1163:G:H1	30:0:1184:C:N4	2.06	0.54
30:0:1176:C:H5	38:0:5727:HOH:O	1.91	0.54
30:0:1714:C:O2'	30:0:1715:C:H5'	2.08	0.54
30:0:2344:G:H8	38:0:6641:HOH:O	1.91	0.54
3:C:135:GLU:HB3	38:C:8586:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:53:ASP:OD1	6:F:80:GLN:HB2	2.08	0.53
6:F:96:ALA:HA	38:F:3111:HOH:O	2.08	0.53
8:H:15:PRO:HG3	30:0:1053:G:OP1	2.08	0.53
14:N:37:ARG:NH1	31:9:6:C:C5'	2.60	0.53
14:N:67:ALA:HA	14:N:71:TRP:CB	2.37	0.53
21:U:33:SER:O	21:U:37:GLU:HG3	2.08	0.53
29:3:33:MET:SD	30:0:2450:C:H4'	2.48	0.53
30:0:1706:G:C6	30:0:1707:G:C6	2.96	0.53
30:0:2335:C:H2'	30:0:2336:G:C8	2.43	0.53
21:U:51:TRP:HA	21:U:56:ARG:HE	1.72	0.53
29:3:48:ASN:HB3	30:0:170:U:H5'	1.91	0.53
30:0:480:C:H4'	38:0:7715:HOH:O	2.08	0.53
30:0:962:C:H5''	38:0:4907:HOH:O	2.06	0.53
30:0:1379:A:H1'	38:0:9690:HOH:O	2.08	0.53
30:0:1506:U:H6	30:0:1506:U:H5'	1.73	0.53
30:0:2347:C:H2'	30:0:2348:C:H6	1.73	0.53
30:0:2712:G:H1'	38:0:5829:HOH:O	2.08	0.53
1:A:36:ASP:HB2	1:A:85:SER:H	1.73	0.53
3:C:180:SER:HB2	38:C:8656:HOH:O	2.06	0.53
10:J:107:ASN:HD21	10:J:109:TYR:HB2	1.74	0.53
11:K:98:VAL:HG13	11:K:102:GLU:HA	1.90	0.53
23:W:88:THR:HG22	23:W:89:ASP:H	1.74	0.53
30:0:311:C:H2'	30:0:312:U:C6	2.43	0.53
30:0:2546:U:H4'	38:0:6160:HOH:O	2.09	0.53
1:A:47:HIS:HD2	30:0:1654:U:H2'	1.72	0.53
1:A:109:GLU:HG2	1:A:116:GLY:N	2.23	0.53
14:N:55:ASP:OD2	31:9:7:G:H4'	2.08	0.53
17:Q:40:HIS:HE1	30:0:949:U:O2'	1.91	0.53
24:X:43:VAL:HG11	24:X:82:GLU:HA	1.89	0.53
30:0:185:G:H4'	30:0:186:A:OP1	2.08	0.53
31:9:13:A:O2'	31:9:14:G:H5''	2.09	0.53
31:9:39:U:H3'	31:9:40:C:C5'	2.39	0.53
31:9:60:C:O2'	31:9:61:C:H5'	2.08	0.53
31:9:117:G:H2'	31:9:118:C:C6	2.44	0.53
13:M:164:THR:HG22	13:M:166:ALA:N	2.23	0.53
30:0:1205:U:H2'	30:0:1206:U:H5''	1.88	0.53
30:0:2265:U:H2'	30:0:2266:A:C8	2.43	0.53
31:9:64:C:H2'	31:9:65:A:H5'	1.90	0.53
6:F:13:GLU:OE2	6:F:78:GLU:HG2	2.09	0.53
30:0:363:C:O2'	30:0:364:U:H5'	2.09	0.53
30:0:517:U:H2'	30:0:518:G:H5'	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1014:A:H5''	31:9:101:G:O2'	2.09	0.53
30:0:1269:G:H2'	30:0:1270:U:C6	2.44	0.53
30:0:1523:G:C6	30:0:1524:U:O4	2.62	0.53
30:0:1553:C:H2'	30:0:1554:C:H6	1.74	0.53
30:0:2112:A:C8	38:0:6930:HOH:O	2.54	0.53
13:M:68:ARG:HG3	30:0:1469:C:OP1	2.09	0.53
18:R:39:THR:HB	18:R:42:GLU:HG3	1.91	0.53
30:0:10:U:O4	30:0:532:A:OP2	2.27	0.53
30:0:2371:G:H5'	38:0:5000:HOH:O	2.07	0.53
2:B:102:THR:HG21	2:B:182:VAL:O	2.09	0.53
16:P:134:VAL:O	16:P:137:LEU:HB3	2.09	0.53
30:0:2578:G:H5'	30:0:2578:G:C8	2.40	0.53
31:9:39:U:H3	31:9:42:C:H5''	1.72	0.53
31:9:76:G:H3'	31:9:77:A:C5'	2.23	0.53
14:N:132:ASN:O	14:N:135:VAL:HG12	2.09	0.53
30:0:312:U:C2	30:0:320:G:N2	2.77	0.53
30:0:454:U:C2	38:0:9033:HOH:O	2.53	0.53
30:0:1224:G:H2'	30:0:1225:C:C6	2.43	0.53
30:0:1940:C:H4'	38:0:7336:HOH:O	2.08	0.53
2:B:199:TYR:HE2	2:B:268:ARG:HB2	1.74	0.53
14:N:42:HIS:HB3	14:N:62:HIS:HE1	1.73	0.53
14:N:160:SER:CB	31:9:51:A:H5'	2.39	0.53
23:W:13:MET:HE2	23:W:18:GLN:CA	2.39	0.53
25:Y:152:LYS:HB3	25:Y:160:LYS:HG3	1.91	0.53
29:3:70:ARG:HA	29:3:77:ALA:HB2	1.91	0.53
30:0:10:U:C4	30:0:532:A:C8	2.97	0.53
30:0:279:C:O2'	30:0:280:C:H5'	2.09	0.53
30:0:821:U:H2'	30:0:822:C:H6	1.73	0.53
30:0:1515:A:H2'	30:0:1516:U:C6	2.43	0.53
1:A:51:ARG:NH2	1:A:53:ALA:HB3	2.25	0.52
2:B:211:THR:HG23	30:0:2840:A:OP1	2.08	0.52
26:Z:61:HIS:HB3	38:Z:8710:HOH:O	2.07	0.52
30:0:72:C:H5'	38:0:5876:HOH:O	2.10	0.52
30:0:853:C:H3'	38:0:4548:HOH:O	2.08	0.52
30:0:2438:G:H2'	30:0:2439:C:O4'	2.09	0.52
1:A:33:GLU:O	1:A:34:ASP:HB2	2.09	0.52
3:C:94:THR:HG22	38:C:8687:HOH:O	2.09	0.52
9:I:108:HIS:H	9:I:109:PRO:HD2	1.74	0.52
25:Y:154:ARG:HH22	30:0:1071:G:H4'	1.74	0.52
27:1:2:GLY:O	27:1:6:PRO:HG2	2.09	0.52
30:0:1180:U:H2'	30:0:1181:A:O4'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1201:C:H6	38:0:5738:HOH:O	1.93	0.52
30:0:2506:A:N6	30:0:2511:A:O2'	2.42	0.52
30:0:2748:G:H5'	38:0:7534:HOH:O	2.08	0.52
2:B:298:LYS:HD3	38:B:9095:HOH:O	2.08	0.52
12:L:145:LEU:O	12:L:148:GLU:HG3	2.09	0.52
14:N:32:PRO:HD2	14:N:99:GLU:O	2.10	0.52
17:Q:21:ARG:HH12	30:0:2353:A:H1'	1.74	0.52
23:W:68:THR:HG23	23:W:69:ARG:HG2	1.91	0.52
30:0:705:C:O2	30:0:705:C:H2'	2.08	0.52
30:0:960:G:N3	30:0:960:G:H2'	2.23	0.52
30:0:1311:G:C2	30:0:1312:G:C8	2.96	0.52
30:0:1441:G:O2'	30:0:1442:A:H5'	2.09	0.52
30:0:2499:U:H2'	30:0:2500:C:C6	2.44	0.52
2:B:18:ARG:HE	2:B:256:GLN:NE2	2.06	0.52
13:M:73:ARG:HD2	13:M:73:ARG:N	2.24	0.52
14:N:12:ARG:HD3	14:N:18:THR:OG1	2.10	0.52
30:0:324:G:O2'	30:0:325:U:H5'	2.09	0.52
30:0:506:G:N2	30:0:509:A:C5'	2.66	0.52
30:0:1928:C:H2'	30:0:1929:G:O4'	2.09	0.52
30:0:2295:G:N3	30:0:2361:A:C2	2.77	0.52
30:0:2864:U:O2'	30:0:2865:G:H5'	2.09	0.52
1:A:94:LEU:HD23	1:A:94:LEU:N	2.24	0.52
4:D:58:VAL:CG1	4:D:60:GLU:HG2	2.40	0.52
5:E:80:TRP:O	5:E:134:SER:HA	2.10	0.52
20:T:28:SER:O	20:T:32:ARG:HG3	2.10	0.52
23:W:38:THR:O	23:W:42:ARG:HB2	2.09	0.52
30:0:107:U:H2'	30:0:108:U:H5'	1.92	0.52
30:0:1375:A:C2'	30:0:1376:G:H5'	2.39	0.52
30:0:2032:U:H2'	30:0:2033:G:H5'	1.91	0.52
30:0:2831:C:O2'	30:0:2832:C:H5'	2.10	0.52
31:9:56:A:C3'	31:9:57:A:H5''	2.39	0.52
5:E:84:MET:HE2	5:E:133:VAL:CG2	2.40	0.52
5:E:118:ILE:HG23	5:E:144:THR:HG21	1.92	0.52
21:U:6:CYS:SG	21:U:13:ILE:HD12	2.49	0.52
23:W:52:VAL:HG22	23:W:53:ALA:H	1.75	0.52
25:Y:235:GLU:CD	25:Y:235:GLU:N	2.65	0.52
30:0:297:U:H2'	30:0:298:C:C6	2.43	0.52
2:B:49:THR:HG21	2:B:331:SER:O	2.10	0.52
3:C:70:VAL:HG21	30:0:1361:C:H5'	1.91	0.52
4:D:128:LEU:HB2	38:D:6007:HOH:O	2.10	0.52
13:M:77:HIS:CE1	13:M:86:GLN:HG3	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:91:ILE:HG12	38:0:7539:HOH:O	2.10	0.52
20:T:9:LYS:HE3	20:T:13:ARG:CZ	2.40	0.52
30:0:64:G:H2'	30:0:65:C:O4'	2.10	0.52
30:0:694:A:H2'	30:0:695:C:H5'	1.90	0.52
30:0:1182:C:H1'	30:0:1192:A:H8	1.74	0.52
30:0:1183:C:H2'	30:0:1183:C:O2	2.08	0.52
30:0:1269:G:H2'	30:0:1270:U:H6	1.75	0.52
30:0:1667:A:H2'	30:0:1668:U:C6	2.44	0.52
30:0:2326:C:H4'	30:0:2412:G:H4'	1.91	0.52
13:M:46:LEU:HG	38:M:8918:HOH:O	2.08	0.52
13:M:89:THR:HA	38:M:8851:HOH:O	2.10	0.52
30:0:101:C:H2'	30:0:102:A:C8	2.45	0.52
30:0:506:G:N2	30:0:508:A:H3'	2.25	0.52
30:0:952:G:N3	30:0:2302:A:H2'	2.25	0.52
30:0:1845:A:O2'	30:0:1846:U:H5'	2.10	0.52
30:0:1972:U:H2'	30:0:1973:A:H5''	1.90	0.52
30:0:1992:U:H2'	30:0:1994:A:OP2	2.10	0.52
30:0:2111:G:H1'	38:0:9051:HOH:O	2.09	0.52
30:0:2420:G:C2'	30:0:2421:G:H5'	2.39	0.52
30:0:2584:G:H4'	38:0:7109:HOH:O	2.08	0.52
30:0:2689:A:C2'	30:0:2690:U:H5'	2.40	0.52
1:A:100:PRO:HG2	1:A:103:VAL:HG21	1.91	0.52
29:3:51:LYS:HA	29:3:54:LYS:HD2	1.92	0.52
30:0:208:C:H3'	38:0:6388:HOH:O	2.10	0.52
30:0:553:G:O4'	30:0:1325:G:H5'	2.10	0.52
30:0:2549:C:O2'	30:0:2550:U:H5'	2.09	0.52
7:G:27:ILE:HD13	7:G:71:LEU:HD23	1.92	0.52
11:K:8:VAL:HG13	11:K:80:ILE:HG22	1.91	0.52
11:K:118:ALA:HA	11:K:125:ALA:HB2	1.91	0.52
14:N:11:ARG:HG3	14:N:14:ARG:NH1	2.24	0.52
14:N:119:GLN:O	14:N:123:ILE:HG13	2.10	0.52
23:W:4:LEU:O	23:W:32:CYS:HA	2.10	0.52
23:W:4:LEU:HD22	23:W:52:VAL:HG21	1.91	0.52
30:0:293:A:C4	30:0:360:A:C2	2.98	0.52
30:0:365:G:C6	30:0:366:U:C4	2.98	0.52
30:0:541:C:C2'	30:0:542:A:C5'	2.75	0.52
31:9:18:U:H2'	31:9:19:G:H8	1.74	0.52
2:B:214:PRO:HD2	38:0:9078:HOH:O	2.10	0.51
26:Z:42:TYR:HA	30:0:1829:A:H61	1.74	0.51
29:3:64:LYS:HD2	30:0:2459:G:OP2	2.11	0.51
30:0:523:C:H2'	30:0:524:A:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:960:G:N3	30:0:960:G:C2'	2.73	0.51
30:0:1189:A:H1'	30:0:1209:C:H1'	1.92	0.51
30:0:1495:C:H1'	30:0:1573:A:H1'	1.93	0.51
30:0:2526:C:O2'	30:0:2527:U:H5'	2.10	0.51
3:C:226:GLY:HA3	30:0:1308:A:O4'	2.10	0.51
14:N:4:PRO:CB	30:0:1010:C:H4'	2.40	0.51
17:Q:45:PRO:O	30:0:2365:G:H4'	2.10	0.51
29:3:42:ARG:NH1	30:0:396:U:H5'	2.25	0.51
30:0:1682:A:O2'	30:0:1683:G:H5''	2.10	0.51
31:9:22:G:H5'	31:9:23:U:OP1	2.10	0.51
5:E:22:VAL:O	5:E:76:VAL:HG11	2.10	0.51
11:K:41:LYS:HA	30:0:2582:G:O3'	2.11	0.51
14:N:102:LEU:HD13	14:N:119:GLN:HB2	1.92	0.51
22:V:44:GLY:O	22:V:48:GLU:HG2	2.10	0.51
30:0:78:G:C6	30:0:79:G:C6	2.99	0.51
30:0:1185:U:H5'	38:0:7461:HOH:O	2.10	0.51
30:0:1805:G:O2'	30:0:1806:G:H5'	2.10	0.51
30:0:2004:U:H4'	38:0:5299:HOH:O	2.09	0.51
30:0:2344:G:H2'	30:0:2344:G:N3	2.24	0.51
5:E:93:MET:HE1	5:E:165:GLY:N	2.25	0.51
5:E:143:GLN:NE2	30:0:2780:C:H1'	2.26	0.51
13:M:81:ARG:HG2	38:M:8926:HOH:O	2.11	0.51
15:O:105:ASN:HD21	15:O:109:SER:H	1.58	0.51
30:0:255:A:C4	30:0:256:C:C6	2.98	0.51
30:0:282:C:C2'	30:0:283:U:H5'	2.40	0.51
30:0:2088:C:H1'	30:0:2841:A:N1	2.25	0.51
30:0:2239:C:H2'	30:0:2240:U:C6	2.46	0.51
30:0:2269:C:O2'	30:0:2270:G:H5'	2.10	0.51
30:0:2769:C:C2'	30:0:2770:G:C5'	2.88	0.51
3:C:150:THR:HA	3:C:203:ALA:O	2.11	0.51
8:H:141:CYS:HB2	38:H:8991:HOH:O	2.10	0.51
28:2:2:LYS:HG3	30:0:1486:A:C5	2.45	0.51
30:0:1361:C:H2'	30:0:1362:U:C6	2.45	0.51
30:0:1563:G:H4'	38:0:4227:HOH:O	2.10	0.51
30:0:1788:U:C2	30:0:1805:G:N2	2.79	0.51
30:0:2269:C:H2'	30:0:2270:G:O4'	2.09	0.51
1:A:97:ALA:HA	1:A:131:HIS:NE2	2.26	0.51
5:E:93:MET:HE1	5:E:165:GLY:H	1.76	0.51
22:V:12:THR:HG23	22:V:14:ALA:H	1.75	0.51
26:Z:37:ARG:HB2	30:0:819:A:H4'	1.92	0.51
30:0:343:C:O2'	30:0:344:C:H5'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:466:A:H2'	30:0:467:G:O4'	2.10	0.51
30:0:646:G:H2'	30:0:647:U:C6	2.46	0.51
30:0:1061:C:H1'	30:0:2283:G:O6	2.10	0.51
30:0:1304:U:H2'	30:0:1305:C:C6	2.46	0.51
30:0:2851:G:O2'	30:0:2852:A:H5'	2.11	0.51
3:C:21:VAL:HG13	38:C:8606:HOH:O	2.09	0.51
13:M:24:GLN:NE2	13:M:27:ARG:NH1	2.58	0.51
13:M:86:GLN:HE22	30:0:2274:A:H1'	1.74	0.51
14:N:163:PHE:HB3	38:N:8829:HOH:O	2.11	0.51
21:U:47:ARG:HG3	38:U:4381:HOH:O	2.10	0.51
22:V:56:ILE:O	22:V:60:GLN:HG3	2.10	0.51
24:X:76:ARG:HG3	24:X:76:ARG:NH1	2.24	0.51
30:0:42:C:H1'	38:0:4670:HOH:O	2.09	0.51
30:0:1855:G:H4'	30:0:1856:C:O5'	2.10	0.51
30:0:1878:G:H1'	38:0:6104:HOH:O	2.11	0.51
30:0:2099:A:H2	38:0:3918:HOH:O	1.93	0.51
30:0:2507:G:H2'	30:0:2510:C:H42	1.75	0.51
30:0:2899:A:O2'	30:0:2900:G:H5'	2.10	0.51
31:9:3:A:OP2	31:9:25:G:N2	2.43	0.51
31:9:45:A:C5	31:9:46:C:C5	2.98	0.51
31:9:117:G:H2'	31:9:118:C:H6	1.75	0.51
2:B:162:MET:HG3	2:B:310:ARG:HH11	1.75	0.51
5:E:133:VAL:HG12	5:E:141:VAL:HG13	1.93	0.51
5:E:137:ASP:O	5:E:141:VAL:HG23	2.10	0.51
6:F:39:SER:OG	6:F:45:ALA:HB2	2.11	0.51
10:J:70:PHE:CD1	30:0:2676:C:H4'	2.46	0.51
13:M:102:GLU:CD	13:M:164:THR:HG21	2.36	0.51
14:N:114:LYS:O	14:N:118:ILE:HG13	2.10	0.51
30:0:124:C:H3'	38:0:7649:HOH:O	2.10	0.51
30:0:703:G:H2'	30:0:704:C:H6	1.76	0.51
30:0:1020:A:H1'	38:0:7218:HOH:O	2.11	0.51
30:0:1056:U:H2'	30:0:1057:A:O4'	2.10	0.51
30:0:1079:A:N1	30:0:2068:G:O2'	2.42	0.51
30:0:1581:A:C5	30:0:1582:C:C5	2.99	0.51
30:0:1626:A:O2'	30:0:1627:G:H5'	2.10	0.51
30:0:2354:A:H5'	30:0:2355:G:N7	2.26	0.51
30:0:2842:G:H2'	30:0:2843:A:H5'	1.92	0.51
1:A:223:ARG:HG3	38:A:9021:HOH:O	2.11	0.51
3:C:76:ARG:NH2	30:0:1363:G:OP1	2.44	0.51
17:Q:25:PRO:HB2	38:9:9082:HOH:O	2.11	0.51
30:0:615:G:H2'	30:0:616:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:920:C:H5'	30:0:921:G:C4	2.46	0.51
30:0:1279:U:O2	30:0:1279:U:C2'	2.58	0.51
30:0:1562:C:O2	30:0:1562:C:C2'	2.59	0.51
30:0:1701:A:H5''	30:0:1702:U:H3'	1.93	0.51
1:A:207:GLN:HA	38:A:8981:HOH:O	2.10	0.51
5:E:116:THR:HG22	5:E:151:LEU:HD22	1.92	0.51
17:Q:28:ARG:HG2	38:9:9082:HOH:O	2.11	0.51
20:T:71:VAL:HG11	20:T:90:PRO:CB	2.38	0.51
30:0:168:C:O5'	30:0:168:C:H6	1.92	0.51
30:0:255:A:C5	30:0:256:C:C4	2.99	0.51
30:0:1202:A:H2'	30:0:1203:G:H5'	1.92	0.51
30:0:1218:U:H2'	30:0:1219:U:C6	2.46	0.51
30:0:1972:U:C2'	30:0:1973:A:C5'	2.89	0.51
30:0:2345:A:H3'	30:0:2346:C:C6	2.45	0.51
6:F:34:ASN:HA	13:M:4:ALA:HB2	1.93	0.50
13:M:47:ASP:CG	13:M:48:LYS:N	2.70	0.50
14:N:164:ASP:OD1	14:N:167:ASP:HA	2.11	0.50
17:Q:11:ARG:HH22	30:0:2363:G:C5'	2.24	0.50
20:T:72:ILE:HD13	20:T:93:THR:HG22	1.92	0.50
23:W:44:MET:HE2	30:0:944:G:N2	2.14	0.50
26:Z:80:GLN:CG	26:Z:81:CYS:H	2.22	0.50
30:0:291:C:H2'	30:0:292:G:O4'	2.11	0.50
30:0:407:A:H5'	38:0:6009:HOH:O	2.11	0.50
30:0:1626:A:C2'	30:0:1627:G:H5'	2.41	0.50
1:A:179:MET:HG2	1:A:186:TRP:CB	2.41	0.50
2:B:72:THR:HB	38:B:9075:HOH:O	2.10	0.50
2:B:320:GLN:HE21	2:B:321:PRO:CD	2.20	0.50
3:C:46:TYR:CE1	30:0:450:C:H4'	2.45	0.50
30:0:151:A:H2'	30:0:152:A:O4'	2.11	0.50
30:0:1213:C:C2'	30:0:1214:G:H5'	2.42	0.50
30:0:2506:A:O2'	30:0:2507:G:C8	2.49	0.50
33:0:8812:CL:CL	38:0:5117:HOH:O	2.57	0.50
2:B:238:ASN:HD22	2:B:240:GLY:N	2.10	0.50
30:0:396:U:O2'	30:0:397:A:P	2.70	0.50
30:0:1589:G:H4'	38:0:6843:HOH:O	2.10	0.50
30:0:1934:A:C8	30:0:1935:C:C5	3.00	0.50
30:0:2758:G:H2'	30:0:2759:C:H6	1.76	0.50
1:A:162:GLY:N	26:Z:91:GLY:HA2	2.26	0.50
3:C:47:GLY:HA2	3:C:92:PRO:HB2	1.93	0.50
38:C:8676:HOH:O	30:0:2100:A:H5'	2.12	0.50
5:E:81:GLU:O	5:E:172:PRO:HD3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:139:PRO:HA	13:M:142:GLN:HB2	1.93	0.50
21:U:9:CYS:HB2	38:U:6796:HOH:O	2.12	0.50
23:W:5:VAL:HG22	23:W:32:CYS:HB2	1.94	0.50
25:Y:115:ARG:HH22	30:0:1266:U:H4'	1.72	0.50
30:0:99:A:C8	30:0:100:C:C5	2.99	0.50
30:0:549:A:O2'	30:0:550:C:H5'	2.11	0.50
30:0:1189:A:O2'	30:0:1208:C:H2'	2.12	0.50
30:0:2533:C:H5'	30:0:2533:C:C6	2.42	0.50
30:0:2724:U:H2'	30:0:2725:G:O4'	2.12	0.50
30:0:2896:A:N3	30:0:2896:A:H2'	2.26	0.50
1:A:135:VAL:HG21	1:A:147:ARG:HB3	1.94	0.50
5:E:84:MET:HE1	5:E:148:ILE:CD1	2.41	0.50
18:R:150:PRO:CG	18:R:150:PRO:CB	2.85	0.50
28:2:8:LYS:NZ	30:0:1677:U:OP2	2.44	0.50
30:0:693:A:H2'	30:0:694:A:C8	2.46	0.50
30:0:920:C:H4'	30:0:921:G:C2	2.46	0.50
30:0:1118:A:H8	30:0:1119:G:H5''	1.75	0.50
3:C:197:SER:HB3	38:C:8583:HOH:O	2.12	0.50
13:M:72:ALA:HB3	38:M:8944:HOH:O	2.12	0.50
13:M:184:ARG:HG3	13:M:185:PRO:HA	1.93	0.50
16:P:41:ARG:HH22	30:0:1500:U:P	2.34	0.50
17:Q:11:ARG:NH1	30:0:2363:G:O3'	2.45	0.50
28:2:22:PRO:HG2	28:2:25:VAL:HG23	1.94	0.50
30:0:216:A:O2'	30:0:217:C:H5'	2.12	0.50
30:0:1180:U:O2'	30:0:1181:A:H5'	2.11	0.50
30:0:1183:C:N3	30:0:1184:C:C5	2.79	0.50
30:0:1759:A:N3	30:0:1818:C:H2'	2.27	0.50
30:0:2072:G:C6	30:0:2533:C:H1'	2.47	0.50
2:B:158:LYS:HB2	38:0:4101:HOH:O	2.11	0.50
6:F:36:THR:HG23	6:F:97:ALA:HB2	1.94	0.50
10:J:75:PRO:HD3	10:J:136:SER:OG	2.12	0.50
23:W:4:LEU:CD2	23:W:54:PHE:HB3	2.39	0.50
30:0:39:G:C2	30:0:444:C:C2	3.00	0.50
30:0:559:U:H6	30:0:559:U:C5'	2.20	0.50
30:0:820:G:H5'	30:0:821:U:C5'	2.41	0.50
30:0:1158:G:H2'	30:0:1159:G:H5'	1.93	0.50
30:0:1395:C:H2'	30:0:1396:C:H6	1.77	0.50
30:0:1494:A:H1'	30:0:1495:C:C6	2.47	0.50
30:0:1819:G:H2'	30:0:1820:G:C4'	2.42	0.50
30:0:2416:G:H2'	30:0:2417:C:H6	1.76	0.50
30:0:2781:U:C2'	30:0:2782:G:C5'	2.89	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:82:THR:HG23	30:0:1242:A:C5'	2.17	0.50
10:J:88:PRO:HD3	30:0:1104:C:H4'	1.94	0.50
11:K:34:VAL:HG22	11:K:47:ALA:HB2	1.94	0.50
14:N:160:SER:HB3	31:9:51:A:H5'	1.93	0.50
23:W:121:PRO:CA	23:W:153:MET:HG2	2.42	0.50
30:0:204:A:C2'	30:0:205:U:H5'	2.41	0.50
30:0:441:A:C2	30:0:442:A:N6	2.80	0.50
30:0:523:C:H2'	30:0:524:A:H8	1.77	0.50
30:0:1610:G:H2'	30:0:1611:G:O4'	2.12	0.50
30:0:1765:G:H1'	30:0:1780:G:N2	2.26	0.50
30:0:2354:A:H5'	30:0:2355:G:C5	2.46	0.50
30:0:2598:U:O2	30:0:2600:A:H8	1.95	0.50
31:9:61:C:H2'	31:9:62:A:H8	1.76	0.50
10:J:22:VAL:O	10:J:26:VAL:HG23	2.12	0.50
10:J:76:ASP:HA	38:J:8863:HOH:O	2.11	0.50
14:N:169:PRO:O	14:N:172:PHE:HB3	2.12	0.50
27:1:28:HIS:HE1	30:0:776:A:OP1	1.95	0.50
30:0:932:U:H2'	30:0:933:C:C6	2.47	0.50
30:0:1160:G:H5'	30:0:1161:A:H5'	0.83	0.50
30:0:1226:G:H5'	38:0:4526:HOH:O	2.11	0.50
30:0:1398:G:H2'	30:0:1399:A:C8	2.47	0.50
30:0:1947:G:H2'	30:0:1948:G:H8	1.77	0.50
30:0:2269:C:H2'	30:0:2270:G:C5'	2.42	0.50
30:0:2330:U:H4'	30:0:2331:C:OP1	2.11	0.50
31:9:58:G:C8	31:9:59:C:C5	3.00	0.50
6:F:58:GLU:HA	6:F:61:MET:HE2	1.92	0.49
27:1:28:HIS:HD2	27:1:30:LYS:H	1.58	0.49
30:0:88:G:H8	30:0:88:G:H5'	1.76	0.49
30:0:299:U:N3	30:0:300:U:C5	2.80	0.49
30:0:1100:G:O2'	30:0:1107:A:N1	2.43	0.49
30:0:1365:C:H4'	38:0:4606:HOH:O	2.12	0.49
30:0:1541:G:O2'	30:0:1542:G:H5'	2.11	0.49
30:0:1791:U:O2'	30:0:1792:C:H5'	2.12	0.49
30:0:2502:C:O2'	30:0:2503:A:H5'	2.12	0.49
1:A:153:ARG:HB2	1:A:153:ARG:HH11	1.77	0.49
6:F:48:VAL:HG23	6:F:74:PHE:CB	2.41	0.49
13:M:94:ARG:HD2	30:0:158:A:OP2	2.11	0.49
15:O:24:ALA:HB3	30:0:710:G:OP1	2.12	0.49
18:R:117:HIS:HD2	30:0:20:G:H21	1.61	0.49
30:0:249:G:N2	30:0:250:C:C2	2.80	0.49
30:0:951:A:O2'	30:0:952:G:H5'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1188:A:C6	30:0:1189:A:C6	3.00	0.49
30:0:1964:U:H2'	30:0:1964:U:O2	2.10	0.49
30:0:2705:U:H2'	30:0:2706:A:H8	1.73	0.49
31:9:114:G:H2'	31:9:115:C:H6	1.76	0.49
2:B:24:PRO:HG3	2:B:204:GLY:HA2	1.94	0.49
4:D:76:ARG:NH1	31:9:42:C:O2	2.45	0.49
5:E:15:GLN:HG2	5:E:16:ASP:N	2.28	0.49
11:K:8:VAL:HG12	11:K:9:THR:N	2.26	0.49
13:M:68:ARG:HD3	13:M:68:ARG:C	2.37	0.49
18:R:111:ILE:HG23	18:R:145:LEU:HD11	1.94	0.49
30:0:699:C:O2'	30:0:744:G:H1'	2.12	0.49
30:0:876:A:N3	30:0:876:A:C2'	2.75	0.49
30:0:2002:C:H2'	30:0:2003:U:H5'	1.94	0.49
31:9:20:G:H3'	38:9:9055:HOH:O	2.12	0.49
31:9:49:G:H2'	31:9:50:G:O4'	2.12	0.49
23:W:11:VAL:HG11	30:0:1086:A:C6	2.48	0.49
23:W:90:TYR:N	23:W:90:TYR:CD1	2.80	0.49
24:X:21:PRO:HG2	24:X:24:LYS:HD3	1.94	0.49
26:Z:38:PHE:HB3	26:Z:42:TYR:HD1	1.78	0.49
30:0:696:C:HO2'	30:0:697:G:H5'	1.77	0.49
30:0:816:G:H5'	30:0:1598:A:H4'	1.94	0.49
30:0:1191:A:H2'	30:0:1193:A:H5'	1.95	0.49
30:0:1453:G:H2'	30:0:1454:U:O4'	2.13	0.49
30:0:2316:G:H8	38:0:5642:HOH:O	1.95	0.49
2:B:212:GLN:HA	30:0:1733:A:H4'	1.94	0.49
6:F:50:VAL:HG13	6:F:60:VAL:HG11	1.95	0.49
11:K:22:ASP:HB2	38:K:5264:HOH:O	2.13	0.49
14:N:18:THR:HG21	38:9:9099:HOH:O	2.12	0.49
15:O:25:VAL:HG23	15:O:26:TRP:N	2.27	0.49
23:W:119:HIS:HE1	38:0:9557:HOH:O	1.96	0.49
29:3:38:ARG:CB	29:3:42:ARG:HH12	2.25	0.49
30:0:445:U:O2'	30:0:446:G:H5'	2.12	0.49
30:0:514:G:OP1	30:0:514:G:H2'	2.12	0.49
30:0:1206:U:H5'	30:0:1206:U:C6	2.31	0.49
30:0:1526:A:H4'	30:0:1527:A:H5'	1.95	0.49
30:0:1942:A:O2'	30:0:1943:C:H5'	2.11	0.49
30:0:2612:A:H4'	38:0:3666:HOH:O	2.13	0.49
1:A:51:ARG:C	1:A:53:ALA:H	2.20	0.49
2:B:28:SER:HB2	30:0:2807:U:OP2	2.13	0.49
2:B:199:TYR:CE2	2:B:268:ARG:HB2	2.48	0.49
11:K:98:VAL:HG11	11:K:102:GLU:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:43:VAL:HG12	24:X:44:ASP:N	2.27	0.49
30:0:314:G:C2	30:0:317:A:C8	3.01	0.49
30:0:352:A:H2'	30:0:353:G:C8	2.48	0.49
30:0:1159:G:H2'	30:0:1160:G:O4'	2.11	0.49
30:0:1375:A:H2'	30:0:1376:G:H5'	1.95	0.49
31:9:7:G:H5'	38:9:9099:HOH:O	2.11	0.49
8:H:19:ARG:HH12	30:0:1008:C:H5''	1.78	0.49
14:N:77:ASN:OD1	14:N:79:PRO:HD2	2.13	0.49
27:1:16:HIS:HD2	30:0:470:U:O2'	1.95	0.49
29:3:48:ASN:ND2	30:0:169:A:H1'	2.27	0.49
30:0:128:A:C8	30:0:128:A:H3'	2.47	0.49
30:0:2135:A:O4'	30:0:2243:C:N4	2.45	0.49
30:0:2265:U:H2'	30:0:2266:A:H8	1.77	0.49
30:0:2820:A:H2'	30:0:2821:C:C6	2.46	0.49
7:G:16:LYS:O	7:G:20:VAL:HG23	2.13	0.49
21:U:9:CYS:HA	21:U:52:THR:HG22	1.94	0.49
30:0:661:G:C5	30:0:686:A:C2	3.01	0.49
30:0:1181:A:C2	30:0:1192:A:C8	3.00	0.49
30:0:1209:C:H2'	30:0:1210:G:C8	2.42	0.49
30:0:1572:A:H3'	38:0:4098:HOH:O	2.13	0.49
30:0:1765:G:O2'	30:0:1766:U:H5'	2.12	0.49
30:0:1976:G:H1'	30:0:2005:G:N2	2.28	0.49
30:0:2237:G:H1'	30:0:2238:A:H8	1.77	0.49
30:0:2707:C:O2	30:0:2707:C:H2'	2.13	0.49
30:0:2805:A:C8	30:0:2806:C:C5	3.01	0.49
31:9:52:A:H2'	31:9:53:G:H8	1.76	0.49
38:L:9036:HOH:O	30:0:196:G:H2'	2.12	0.49
13:M:133:LEU:O	13:M:134:ILE:HD13	2.13	0.49
30:0:264:G:H1'	30:0:265:U:H5	1.78	0.49
30:0:1521:C:H2'	30:0:1522:A:H8	1.78	0.49
30:0:2254:G:H1'	38:0:5527:HOH:O	2.12	0.49
30:0:2359:G:H3'	38:0:5674:HOH:O	2.13	0.49
30:0:2635:A:C2'	30:0:2636:C:H5'	2.41	0.49
1:A:46:GLU:C	26:Z:78:ILE:HD11	2.38	0.49
14:N:132:ASN:HD22	30:0:2413:A:C4'	2.25	0.49
19:S:49:VAL:HG13	19:S:66:VAL:HG13	1.95	0.49
26:Z:64:PRO:HB2	26:Z:86:TYR:HE2	1.78	0.49
29:3:68:LYS:HE3	30:0:2435:U:O2'	2.12	0.49
30:0:526:U:H2'	30:0:527:U:C6	2.48	0.49
30:0:727:G:H3'	30:0:728:C:H6	1.78	0.49
30:0:1118:A:C8	30:0:1119:G:H5''	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1118:A:N6	30:0:1244:U:H3	1.95	0.49
30:0:1566:C:O2'	30:0:1567:G:H5'	2.12	0.49
30:0:1586:G:O2'	30:0:1587:U:H5'	2.13	0.49
30:0:1913:C:H2'	30:0:1914:C:H6	1.76	0.49
30:0:2289:G:O2'	30:0:2291:A:N6	2.45	0.49
30:0:2911:C:H2'	30:0:2912:C:C6	2.48	0.49
2:B:7:ARG:HG2	2:B:7:ARG:HH11	1.77	0.48
4:D:23:VAL:HG12	4:D:130:VAL:HG22	1.95	0.48
5:E:11:VAL:HG12	5:E:12:ASP:N	2.27	0.48
6:F:91:VAL:HG12	6:F:92:GLY:N	2.22	0.48
17:Q:11:ARG:HH22	30:0:2363:G:H5''	1.78	0.48
25:Y:174:VAL:HG23	25:Y:177:LYS:HD2	1.94	0.48
30:0:10:U:O4	30:0:532:A:H8	1.96	0.48
30:0:59:A:H5'	38:0:4330:HOH:O	2.13	0.48
30:0:146:U:O2'	30:0:147:G:H5'	2.12	0.48
30:0:691:G:O2'	30:0:693:A:N7	2.46	0.48
30:0:2269:C:H2'	30:0:2270:G:H5'	1.95	0.48
2:B:71:VAL:HG21	2:B:296:LEU:HB3	1.95	0.48
3:C:236:THR:H	3:C:239:ALA:HB3	1.78	0.48
16:P:64:GLU:HG2	38:P:169:HOH:O	2.13	0.48
21:U:50:GLU:O	21:U:56:ARG:HG2	2.13	0.48
29:3:5:ARG:O	29:3:21:GLU:HA	2.12	0.48
30:0:1447:U:H3'	30:0:1506:U:O2	2.12	0.48
30:0:1641:A:O2'	30:0:1642:A:H5'	2.13	0.48
30:0:2061:C:C2'	30:0:2062:A:H5'	2.43	0.48
30:0:2073:G:C6	30:0:2489:G:H4'	2.48	0.48
30:0:2710:U:O2'	30:0:2711:U:H5'	2.13	0.48
1:A:212:PRO:HB2	38:A:8985:HOH:O	2.13	0.48
2:B:49:THR:HG22	2:B:50:HIS:H	1.79	0.48
11:K:74:VAL:HG21	11:K:96:VAL:HG23	1.95	0.48
13:M:70:GLY:HA3	13:M:73:ARG:CZ	2.42	0.48
13:M:164:THR:CG2	13:M:165:GLY:N	2.75	0.48
20:T:8:ARG:NH1	30:0:31:C:OP2	2.46	0.48
25:Y:145:LYS:O	25:Y:147:ARG:HG2	2.13	0.48
30:0:305:A:C5	30:0:329:A:C2	3.02	0.48
30:0:311:C:H2'	30:0:312:U:H6	1.77	0.48
30:0:344:C:H2'	30:0:345:G:O4'	2.12	0.48
30:0:598:C:H2'	30:0:599:G:H8	1.77	0.48
30:0:682:A:H2'	30:0:683:G:O4'	2.13	0.48
30:0:1461:U:H2'	30:0:1462:C:C6	2.48	0.48
30:0:1566:C:H2'	30:0:1567:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1922:A:N1	30:0:2449:G:O2'	2.46	0.48
30:0:2509:A:H2'	30:0:2510:C:O4'	2.13	0.48
30:0:2512:U:H4'	30:0:2514:U:O4	2.13	0.48
30:0:2616:G:H1'	38:0:9428:HOH:O	2.12	0.48
12:L:143:THR:HG22	12:L:144:ASP:N	2.28	0.48
13:M:72:ALA:C	13:M:74:LYS:H	2.20	0.48
30:0:370:G:O2'	30:0:371:U:H5'	2.14	0.48
30:0:1706:G:C6	30:0:1707:G:N1	2.81	0.48
30:0:2271:G:N3	30:0:2271:G:H2'	2.27	0.48
13:M:48:LYS:HE3	13:M:52:GLN:HE21	1.78	0.48
18:R:18:LEU:HG	18:R:91:LEU:HD13	1.95	0.48
26:Z:37:ARG:HB2	30:0:819:A:O4'	2.14	0.48
29:3:64:LYS:HA	29:3:84:ARG:CA	2.38	0.48
30:0:645:U:O2	30:0:761:A:H2	1.97	0.48
30:0:809:G:H2'	30:0:810:G:H8	1.78	0.48
30:0:816:G:C6	30:0:817:G:N1	2.82	0.48
30:0:1188:A:H5'	38:0:7418:HOH:O	2.12	0.48
30:0:1626:A:H2'	30:0:1627:G:H5'	1.96	0.48
30:0:1835:U:H3'	38:0:5569:HOH:O	2.12	0.48
30:0:2511:A:H2'	30:0:2512:U:C6	2.47	0.48
30:0:2626:C:H2'	30:0:2627:G:C8	2.49	0.48
30:0:2651:C:H2'	30:0:2652:U:O4'	2.13	0.48
30:0:2673:U:C4	30:0:2674:G:C6	3.01	0.48
11:K:130:MET:SD	21:U:25:ASP:O	2.71	0.48
13:M:74:LYS:O	13:M:88:VAL:HG13	2.13	0.48
14:N:48:VAL:CG1	14:N:55:ASP:HB3	2.43	0.48
20:T:48:VAL:HG12	20:T:49:GLU:N	2.29	0.48
23:W:6:GLN:HB2	23:W:26:ILE:CD1	2.36	0.48
26:Z:74:GLN:HG2	26:Z:80:GLN:HB2	1.95	0.48
29:3:64:LYS:HD3	29:3:82:GLY:O	2.13	0.48
30:0:421:C:H4'	30:0:1919:A:C6	2.49	0.48
30:0:1187:U:O2'	30:0:1188:A:C8	2.64	0.48
30:0:1684:A:O2'	30:0:1685:A:H5''	2.14	0.48
30:0:1905:U:H2'	30:0:1906:C:H6	1.79	0.48
30:0:2713:G:O2'	30:0:2714:U:H5'	2.13	0.48
1:A:72:GLU:HG2	26:Z:100:GLY:CA	2.40	0.48
1:A:171:LYS:HB2	30:0:820:G:C5	2.49	0.48
2:B:74:ILE:HG13	38:B:9075:HOH:O	2.13	0.48
4:D:48:MET:HE2	31:9:41:C:H5''	1.94	0.48
5:E:101:GLU:HB2	5:E:116:THR:O	2.13	0.48
12:L:65:ASP:HA	12:L:109:LEU:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:33:ARG:NH1	38:R:8944:HOH:O	2.47	0.48
25:Y:170:SER:OG	25:Y:175:ARG:HG3	2.14	0.48
30:0:154:C:H2'	30:0:155:C:C6	2.49	0.48
30:0:1343:C:H2'	30:0:1344:G:O5'	2.12	0.48
30:0:2608:C:H2'	38:0:3561:HOH:O	2.13	0.48
31:9:23:U:O2	31:9:23:U:H2'	2.14	0.48
2:B:84:LEU:HD23	2:B:142:LEU:HD23	1.96	0.48
8:H:157:TYR:CD1	8:H:157:TYR:C	2.90	0.48
10:J:75:PRO:HB3	10:J:132:LEU:HB3	1.96	0.48
10:J:135:ILE:O	10:J:139:LEU:HG	2.14	0.48
13:M:73:ARG:HH22	30:0:2263:G:H5''	1.77	0.48
17:Q:27:GLN:HE21	31:9:8:G:H5''	1.75	0.48
23:W:107:LEU:O	23:W:112:LEU:HB2	2.13	0.48
30:0:228:C:C2'	30:0:229:G:H5'	2.44	0.48
30:0:284:C:H4'	30:0:285:A:H8	1.79	0.48
30:0:533:U:H3'	38:0:3736:HOH:O	2.13	0.48
30:0:589:U:H2'	30:0:590:A:C8	2.47	0.48
30:0:1168:C:H5	38:0:7488:HOH:O	1.96	0.48
30:0:1422:U:H2'	30:0:1423:C:C6	2.49	0.48
30:0:1632:A:C3'	30:0:1633:C:H5'	2.44	0.48
30:0:2524:G:N2	30:0:2526:C:N4	2.57	0.48
8:H:157:TYR:C	8:H:157:TYR:HD1	2.21	0.48
13:M:49:ALA:C	13:M:54:TYR:HB3	2.38	0.48
23:W:13:MET:HE2	23:W:18:GLN:N	2.29	0.48
38:2:3526:HOH:O	30:0:1413:A:H5''	2.14	0.48
30:0:581:G:O2'	30:0:582:U:H5'	2.13	0.48
30:0:1795:G:H2'	30:0:1796:A:O4'	2.13	0.48
30:0:1965:C:H2'	30:0:1966:U:C6	2.49	0.48
30:0:2614:C:O2'	30:0:2615:U:H5'	2.13	0.48
31:9:38:A:H2	31:9:43:G:H5''	1.77	0.48
1:A:36:ASP:HA	1:A:83:GLY:HA3	1.96	0.48
2:B:24:PRO:CG	2:B:204:GLY:HA2	2.44	0.48
2:B:36:PRO:CA	2:B:168:GLY:HA3	2.40	0.48
3:C:206:ASN:HB2	30:0:329:A:OP2	2.13	0.48
4:D:52:THR:HG21	30:0:2346:C:O2'	2.13	0.48
13:M:40:ILE:HG21	13:M:64:ARG:NH2	2.29	0.48
14:N:139:TRP:HA	14:N:139:TRP:CE3	2.49	0.48
20:T:38:ARG:NH1	38:0:6667:HOH:O	2.47	0.48
23:W:134:GLU:OE2	31:9:97:U:H1'	2.14	0.48
24:X:85:VAL:HG12	24:X:86:GLU:N	2.29	0.48
30:0:113:A:C8	30:0:114:A:C8	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:138:U:OP2	30:0:139:C:C5	2.67	0.48
30:0:542:A:H2'	30:0:543:G:O4'	2.14	0.48
30:0:1592:G:C4	30:0:1593:C:C5	3.02	0.48
30:0:1706:G:C5	30:0:1707:G:C6	3.02	0.48
30:0:1790:C:H2'	30:0:1791:U:H6	1.79	0.48
30:0:2296:C:H2'	30:0:2297:U:H6	1.79	0.48
30:0:2842:G:C2'	30:0:2843:A:H5'	2.44	0.48
31:9:5:G:C2'	31:9:6:C:H5'	2.43	0.48
1:A:36:ASP:O	1:A:38:ILE:N	2.44	0.47
1:A:42:VAL:HG21	1:A:74:VAL:CG1	2.44	0.47
5:E:154:ILE:HD11	5:E:157:LYS:HB2	1.96	0.47
11:K:37:TYR:HB3	38:K:7169:HOH:O	2.14	0.47
14:N:22:GLN:O	14:N:26:LEU:HB2	2.14	0.47
18:R:39:THR:HB	18:R:42:GLU:CG	2.44	0.47
20:T:43:ASN:C	20:T:45:GLY:H	2.22	0.47
23:W:11:VAL:O	23:W:12:ASN:HB2	2.14	0.47
30:0:764:C:H2'	30:0:765:G:O4'	2.14	0.47
30:0:1735:C:H2'	30:0:1736:A:C8	2.49	0.47
30:0:1878:G:C1'	38:0:6104:HOH:O	2.62	0.47
30:0:2074:A:H2'	38:0:3520:HOH:O	2.13	0.47
10:J:107:ASN:ND2	10:J:109:TYR:H	2.11	0.47
16:P:102:ARG:NH2	30:0:1596:U:C5	2.82	0.47
29:3:38:ARG:HB3	29:3:42:ARG:HH12	1.79	0.47
30:0:24:G:H22	30:0:518:G:H1'	1.79	0.47
30:0:45:A:N6	30:0:147:G:C4	2.83	0.47
30:0:844:A:C6	30:0:882:A:C6	3.02	0.47
30:0:2864:U:C2'	30:0:2865:G:H5'	2.44	0.47
2:B:41:PHE:HB3	2:B:190:MET:CE	2.44	0.47
2:B:54:VAL:HB	38:B:9084:HOH:O	2.13	0.47
4:D:58:VAL:HG12	4:D:60:GLU:HG2	1.96	0.47
25:Y:187:VAL:HG23	25:Y:192:ASP:HB2	1.96	0.47
26:Z:65:ASN:HD22	26:Z:84:CYS:HB2	1.80	0.47
27:1:20:ARG:HG2	30:0:111:C:O2'	2.14	0.47
28:2:29:THR:HG22	30:0:86:A:O4'	2.14	0.47
30:0:301:C:H2'	30:0:302:A:H8	1.79	0.47
30:0:703:G:H2'	30:0:704:C:C6	2.49	0.47
30:0:1205:U:C2'	30:0:1206:U:H5''	2.44	0.47
30:0:1787:C:H4'	30:0:2883:A:O4'	2.14	0.47
30:0:2241:C:O2'	30:0:2242:U:H5'	2.14	0.47
30:0:2890:A:H2'	30:0:2890:A:N3	2.29	0.47
31:9:52:A:H2'	31:9:53:G:O4'	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:305:ASP:O	2:B:306:LYS:HB2	2.15	0.47
3:C:153:VAL:O	3:C:157:LEU:HG	2.15	0.47
10:J:19:MET:HE1	10:J:78:ILE:HG22	1.96	0.47
10:J:86:MET:HE2	30:0:1241:G:N3	2.28	0.47
14:N:154:LEU:C	14:N:156:GLU:H	2.20	0.47
16:P:55:LYS:HG3	16:P:56:GLY:N	2.29	0.47
20:T:48:VAL:HG13	20:T:97:ARG:O	2.14	0.47
25:Y:106:THR:HG23	25:Y:107:PRO:HD2	1.96	0.47
29:3:10:TYR:HE2	30:0:2382:A:H1'	1.80	0.47
30:0:95:A:H5''	30:0:97:G:O4'	2.14	0.47
30:0:1561:U:H5'	38:0:7421:HOH:O	2.13	0.47
30:0:1603:A:H5''	30:0:1604:G:H3'	1.96	0.47
30:0:2032:U:C2'	30:0:2033:G:C5'	2.93	0.47
30:0:2784:A:O5'	30:0:2784:A:H8	1.98	0.47
31:9:108:C:H2'	31:9:109:G:H8	1.79	0.47
1:A:45:ILE:HG22	26:Z:78:ILE:HG12	1.96	0.47
10:J:54:VAL:HG11	10:J:138:THR:HG21	1.95	0.47
10:J:107:ASN:HD22	10:J:107:ASN:C	2.22	0.47
13:M:75:ARG:HB2	38:M:8905:HOH:O	2.14	0.47
20:T:64:ASN:HB3	20:T:73:HIS:HB2	1.96	0.47
30:0:292:G:H2'	30:0:358:G:N2	2.30	0.47
30:0:599:G:H2'	30:0:600:G:H8	1.79	0.47
30:0:810:G:H2'	30:0:811:C:C6	2.49	0.47
30:0:1217:G:C2	30:0:1218:U:C2	3.03	0.47
30:0:1942:A:H3'	38:0:7336:HOH:O	2.14	0.47
30:0:2336:G:C2'	38:0:6280:HOH:O	2.60	0.47
30:0:2697:A:H2'	30:0:2698:G:O4'	2.15	0.47
30:0:2908:A:O5'	30:0:2908:A:H8	1.97	0.47
1:A:186:TRP:CG	1:A:187:PRO:HA	2.50	0.47
2:B:5:ARG:NH2	30:0:2548:C:OP2	2.47	0.47
6:F:50:VAL:HG21	6:F:63:ILE:HG21	1.97	0.47
10:J:131:THR:HG22	10:J:133:GLY:H	1.79	0.47
13:M:65:VAL:HG21	13:M:105:ALA:HB2	1.97	0.47
13:M:91:ILE:HD11	38:M:8830:HOH:O	2.15	0.47
23:W:119:HIS:HD2	23:W:120:PRO:O	1.97	0.47
23:W:120:PRO:HG2	30:0:1095:U:O2	2.14	0.47
29:3:46:ILE:HG12	38:0:3138:HOH:O	2.14	0.47
29:3:79:LEU:HB2	38:0:6581:HOH:O	2.14	0.47
30:0:371:U:H2'	30:0:372:A:C8	2.49	0.47
30:0:960:G:N3	30:0:960:G:H3'	2.30	0.47
30:0:1181:A:H2'	30:0:1182:C:C5'	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1318:A:H4'	30:0:1343:C:H4'	1.96	0.47
30:0:1359:U:C5	30:0:2101:A:C8	3.03	0.47
30:0:2510:C:H5'	30:0:2511:A:OP2	2.13	0.47
2:B:98:THR:HG23	30:0:2820:A:OP1	2.15	0.47
18:R:68:HIS:CD2	18:R:76:ASP:HB2	2.50	0.47
23:W:88:THR:HB	38:W:6679:HOH:O	2.14	0.47
23:W:121:PRO:HA	23:W:153:MET:HG2	1.96	0.47
29:3:50:GLY:HA3	38:0:9164:HOH:O	2.14	0.47
30:0:282:C:H1'	30:0:368:C:H41	1.78	0.47
30:0:484:A:N1	30:0:506:G:H4'	2.30	0.47
30:0:512:G:O3'	30:0:513:A:H8	1.97	0.47
30:0:677:C:O2'	30:0:678:G:H5'	2.14	0.47
30:0:1042:U:O2'	30:0:1043:C:H5'	2.15	0.47
30:0:1173:A:H4'	30:0:1174:A:C8	2.49	0.47
30:0:1523:G:C6	30:0:1524:U:C4	3.03	0.47
30:0:1769:C:O2'	30:0:1770:U:H5'	2.15	0.47
30:0:1790:C:H2'	30:0:1791:U:C6	2.50	0.47
30:0:1864:C:H2'	30:0:1865:A:O4'	2.14	0.47
30:0:1882:C:H2'	30:0:1883:U:H6	1.80	0.47
30:0:2598:U:O2	30:0:2600:A:C8	2.68	0.47
30:0:2686:C:C2	30:0:2709:G:N2	2.82	0.47
1:A:121:ALA:O	1:A:124:VAL:HG22	2.14	0.47
3:C:127:ARG:HD3	3:C:129:HIS:HE1	1.80	0.47
17:Q:14:LEU:HD21	17:Q:43:ILE:HD12	1.97	0.47
20:T:24:ARG:HH21	20:T:39:ASN:HD22	1.63	0.47
22:V:39:ALA:N	22:V:40:PRO:CD	2.77	0.47
23:W:29:VAL:O	23:W:30:ASN:HB2	2.13	0.47
29:3:24:LYS:HE3	29:3:90:PHE:CE1	2.50	0.47
30:0:304:G:H8	30:0:304:G:O5'	1.98	0.47
30:0:1183:C:C2	30:0:1184:C:C5	3.03	0.47
30:0:1187:U:O2'	30:0:1189:A:H2	1.98	0.47
30:0:1377:C:H6	30:0:1377:C:C5'	2.28	0.47
30:0:2134:G:N2	30:0:2242:U:C2	2.83	0.47
30:0:2253:G:H2'	30:0:2254:G:H8	1.80	0.47
30:0:2329:C:O2'	30:0:2330:U:H5'	2.14	0.47
30:0:2383:G:C6	30:0:2384:U:C4	3.03	0.47
30:0:2752:C:O2'	30:0:2753:G:H5'	2.15	0.47
8:H:91:ARG:HB2	30:0:1003:U:OP1	2.15	0.47
25:Y:99:ALA:HB2	25:Y:233:TYR:CZ	2.50	0.47
25:Y:137:LYS:HD2	30:0:521:A:H5''	1.97	0.47
30:0:36:C:C2	30:0:447:A:C2	3.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:371:U:H2'	30:0:372:A:H8	1.80	0.47
30:0:447:A:O2'	30:0:448:G:H5'	2.15	0.47
30:0:1029:U:O2'	30:0:1273:C:OP1	2.31	0.47
30:0:1966:U:O5'	30:0:1966:U:H6	1.98	0.47
30:0:2096:A:H2'	30:0:2539:U:O4'	2.14	0.47
30:0:2769:C:H2'	30:0:2770:G:O4'	2.14	0.47
3:C:103:ASN:ND2	30:0:663:C:H5''	2.29	0.47
13:M:111:ASN:HB2	38:M:8849:HOH:O	2.14	0.47
17:Q:11:ARG:CZ	30:0:2363:G:H4'	2.44	0.47
18:R:82:GLU:HG3	18:R:83:LYS:N	2.29	0.47
22:V:39:ALA:C	22:V:41:GLU:H	2.22	0.47
23:W:154:ARG:NH1	30:0:588:G:O6	2.47	0.47
25:Y:189:ASN:C	25:Y:189:ASN:HD22	2.23	0.47
30:0:613:C:H2'	30:0:614:U:C6	2.46	0.47
30:0:805:G:N2	30:0:807:A:H3'	2.30	0.47
30:0:1878:G:O2'	30:0:1879:U:C5	2.66	0.47
30:0:2604:A:H5'	38:0:5775:HOH:O	2.14	0.47
3:C:127:ARG:CZ	3:C:225:PRO:HG2	2.44	0.46
5:E:7:ILE:HG23	5:E:45:ASP:O	2.15	0.46
30:0:1350:U:H4'	38:0:5115:HOH:O	2.15	0.46
30:0:1477:C:H4'	30:0:1868:G:OP1	2.15	0.46
30:0:1477:C:C5'	30:0:1868:G:H5''	2.45	0.46
30:0:1969:A:C2'	30:0:1970:G:H5'	2.45	0.46
11:K:34:VAL:HB	38:K:7169:HOH:O	2.15	0.46
16:P:120:ARG:HD2	30:0:1594:C:OP2	2.14	0.46
29:3:69:TYR:O	29:3:77:ALA:HA	2.15	0.46
30:0:629:A:C2	30:0:2074:A:C2	3.03	0.46
30:0:735:C:H3'	30:0:736:A:C8	2.50	0.46
30:0:877:G:C5'	30:0:878:G:OP1	2.62	0.46
30:0:921:G:H4'	30:0:924:G:N1	2.30	0.46
30:0:1116:U:C2	30:0:1246:A:N6	2.83	0.46
30:0:1163:G:N1	30:0:1184:C:N4	2.64	0.46
30:0:1634:G:H2'	38:0:3889:HOH:O	2.15	0.46
30:0:1701:A:H4'	30:0:1702:U:C5'	2.37	0.46
30:0:1838:U:O2'	30:0:2644:C:H5'	2.15	0.46
30:0:1949:G:H22	30:0:1964:U:H1'	1.79	0.46
3:C:129:HIS:HE1	3:C:231:ARG:HA	1.77	0.46
7:G:63:ARG:N	38:G:2569:HOH:O	2.48	0.46
16:P:87:ARG:HG2	38:P:186:HOH:O	2.15	0.46
20:T:32:ARG:NH1	20:T:38:ARG:HH12	2.13	0.46
22:V:27:LEU:HA	22:V:49:LEU:HD13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:130:C:O2'	30:0:131:A:N7	2.46	0.46
30:0:530:C:H4'	30:0:612:U:H4'	1.97	0.46
30:0:790:A:H2'	30:0:791:A:O4'	2.16	0.46
30:0:1197:G:H1'	30:0:1203:G:C2	2.51	0.46
30:0:1545:C:H1'	30:0:1641:A:N6	2.29	0.46
30:0:1617:C:C5	30:0:1643:C:H4'	2.50	0.46
30:0:1797:A:O3'	30:0:1798:C:C6	2.69	0.46
30:0:1928:C:C2'	30:0:1929:G:H5'	2.45	0.46
30:0:2102:G:C2	30:0:2103:A:N6	2.83	0.46
30:0:2256:G:H2'	30:0:2257:G:C5'	2.46	0.46
30:0:2347:C:H2'	30:0:2348:C:C6	2.50	0.46
30:0:2526:C:C6	30:0:2526:C:H5'	2.50	0.46
4:D:29:HIS:ND1	4:D:29:HIS:N	2.61	0.46
5:E:84:MET:HG2	5:E:168:ILE:HA	1.98	0.46
21:U:13:ILE:HG13	38:U:3194:HOH:O	2.15	0.46
27:1:25:LYS:O	27:1:25:LYS:HG2	2.16	0.46
29:3:47:GLY:HA2	30:0:2121:G:H4'	1.97	0.46
30:0:238:C:H4'	30:0:287:C:OP1	2.16	0.46
30:0:254:C:O2	30:0:254:C:H2'	2.14	0.46
30:0:834:G:C4'	30:0:835:U:OP2	2.61	0.46
30:0:2297:U:H1'	38:0:5172:HOH:O	2.16	0.46
30:0:2438:G:H2'	30:0:2439:C:C6	2.50	0.46
30:0:2445:U:H2'	30:0:2446:G:C8	2.51	0.46
1:A:171:LYS:HB2	30:0:820:G:C6	2.50	0.46
6:F:111:ILE:O	6:F:115:VAL:HG23	2.15	0.46
10:J:80:LYS:HE3	10:J:101:VAL:O	2.14	0.46
12:L:10:SER:O	12:L:11:ARG:HB3	2.16	0.46
21:U:56:ARG:HD2	30:0:2890:A:C1'	2.46	0.46
30:0:2434:A:H2'	30:0:2435:U:O4'	2.15	0.46
29:3:1:MET:HG2	29:3:87:ARG:O	2.16	0.46
30:0:100:C:H2'	30:0:101:C:H6	1.80	0.46
30:0:101:C:H2'	30:0:102:A:H8	1.80	0.46
30:0:461:C:N3	30:0:479:G:H5'	2.31	0.46
30:0:660:A:N6	30:0:746:A:O4'	2.49	0.46
30:0:1154:A:H2'	30:0:1155:G:C8	2.50	0.46
30:0:1434:A:H2'	30:0:1436:C:C5	2.51	0.46
31:9:14:G:H8	31:9:14:G:C5'	2.16	0.46
2:B:144:THR:HG22	2:B:145:HIS:N	2.31	0.46
8:H:48:VAL:HA	8:H:170:ARG:O	2.15	0.46
10:J:69:TYR:CE1	30:0:2081:A:H4'	2.50	0.46
14:N:11:ARG:NH1	31:9:8:G:O6	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:115:SER:OG	16:P:118:GLN:HG3	2.16	0.46
27:1:16:HIS:HE1	30:0:775:G:OP1	1.97	0.46
28:2:43:ARG:NH2	30:0:1684:A:H1'	2.25	0.46
30:0:17:G:H2'	30:0:18:C:C6	2.51	0.46
30:0:134:U:C2	30:0:145:A:C2	3.04	0.46
30:0:365:G:C5	30:0:366:U:C5	3.04	0.46
30:0:517:U:C2'	30:0:518:G:H5'	2.46	0.46
30:0:561:G:O2'	30:0:562:A:H5'	2.15	0.46
30:0:1503:U:H2'	30:0:1504:A:O4'	2.16	0.46
30:0:1878:G:O2'	30:0:1879:U:OP2	2.33	0.46
2:B:85:ARG:NH1	38:B:9106:HOH:O	2.47	0.46
2:B:232:TRP:CZ3	30:0:2614:C:H5''	2.51	0.46
12:L:34:GLY:HA2	38:L:9017:HOH:O	2.16	0.46
19:S:43:GLU:HB3	38:S:7106:HOH:O	2.16	0.46
26:Z:41:ARG:HH12	30:0:821:U:H4'	1.81	0.46
29:3:30:GLN:HB3	38:3:9051:HOH:O	2.16	0.46
30:0:241:A:C2	30:0:378:A:H4'	2.51	0.46
30:0:1526:A:H4'	30:0:1527:A:C5'	2.45	0.46
30:0:1764:C:O2'	30:0:1765:G:H5'	2.15	0.46
30:0:1845:A:C2'	30:0:1846:U:H5'	2.45	0.46
30:0:1871:U:O4'	30:0:1873:G:C8	2.69	0.46
30:0:1894:C:N4	30:0:1939:U:H2'	2.30	0.46
30:0:2537:G:H5''	30:0:2538:A:H5''	1.98	0.46
30:0:2812:A:N7	38:0:7508:HOH:O	2.36	0.46
31:9:3:A:H2	31:9:21:G:N3	2.14	0.46
31:9:47:A:C2	31:9:48:C:C2	3.04	0.46
1:A:230:SER:HB2	30:0:1852:A:H4'	1.97	0.46
3:C:43:LYS:HG2	30:0:449:A:N7	2.31	0.46
14:N:22:GLN:HG3	30:0:2415:A:C2	2.51	0.46
20:T:16:LEU:HB2	30:0:100:C:H4'	1.98	0.46
25:Y:189:ASN:HA	25:Y:217:ILE:HD11	1.97	0.46
30:0:545:G:C8	30:0:545:G:C5'	2.88	0.46
30:0:594:C:C2'	30:0:595:U:H5'	2.46	0.46
30:0:1021:G:O2'	30:0:1022:A:H5'	2.16	0.46
30:0:1132:A:H61	30:0:1229:C:H2'	1.80	0.46
30:0:1294:A:H2'	30:0:1295:G:O4'	2.16	0.46
30:0:1346:U:H2'	30:0:1347:U:C6	2.50	0.46
30:0:1634:G:C4	30:0:1635:U:C5	3.03	0.46
30:0:2624:A:H1'	38:0:9764:HOH:O	2.14	0.46
38:C:8575:HOH:O	20:T:2:LYS:HE2	2.15	0.46
13:M:169:ARG:HD2	38:M:8885:HOH:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:372:A:H2'	30:0:373:G:C8	2.51	0.46
30:0:483:C:C4	30:0:484:A:C6	3.04	0.46
30:0:603:A:H4'	30:0:604:G:O5'	2.15	0.46
30:0:1012:A:H8	30:0:1012:A:O5'	1.99	0.46
30:0:1166:A:C6	30:0:1181:A:C2	3.04	0.46
30:0:1588:G:C6	30:0:1589:G:N1	2.84	0.46
30:0:1615:A:H4'	38:0:5868:HOH:O	2.16	0.46
30:0:1615:A:H5'	38:0:4181:HOH:O	2.15	0.46
30:0:2017:U:O2'	30:0:2018:A:C8	2.66	0.46
30:0:2276:U:H2'	30:0:2277:U:C6	2.51	0.46
30:0:2488:A:H1'	38:0:9096:HOH:O	2.16	0.46
31:9:65:A:C2'	31:9:66:G:OP2	2.64	0.46
11:K:14:LYS:NZ	38:K:1163:HOH:O	2.48	0.45
23:W:118:LEU:HD12	23:W:153:MET:HE3	1.97	0.45
25:Y:151:SER:HB3	25:Y:154:ARG:HB3	1.98	0.45
30:0:71:G:H8	38:0:3908:HOH:O	1.98	0.45
30:0:255:A:C4	30:0:256:C:C5	3.05	0.45
30:0:1052:G:H2'	30:0:1052:G:N3	2.31	0.45
30:0:1119:G:C5	30:0:1243:C:C4	3.04	0.45
30:0:1409:G:C2	30:0:1410:G:C8	3.04	0.45
30:0:1520:G:C6	30:0:1521:C:C4	3.05	0.45
30:0:1756:G:H1'	38:0:6244:HOH:O	2.15	0.45
30:0:1890:U:H4'	30:0:2010:A:C6	2.51	0.45
30:0:2740:G:H2'	30:0:2741:A:O4'	2.15	0.45
1:A:33:GLU:H	1:A:33:GLU:CD	2.24	0.45
2:B:58:PRO:HA	2:B:63:GLU:CD	2.40	0.45
14:N:37:ARG:NH1	31:9:6:C:OP1	2.48	0.45
28:2:28:LYS:O	30:0:87:C:H2'	2.17	0.45
30:0:293:A:C5	30:0:360:A:C2	3.04	0.45
30:0:633:C:O2'	30:0:634:G:H5'	2.15	0.45
30:0:810:G:H2'	30:0:811:C:H6	1.81	0.45
30:0:1625:U:H4'	38:0:4661:HOH:O	2.15	0.45
30:0:1768:C:H2'	30:0:1769:C:O4'	2.16	0.45
30:0:2057:U:O5'	30:0:2057:U:H6	1.98	0.45
30:0:2717:C:C2'	30:0:2718:C:C5'	2.84	0.45
17:Q:25:PRO:HA	17:Q:26:PRO:HD3	1.65	0.45
23:W:13:MET:HE2	23:W:18:GLN:HA	1.98	0.45
27:1:11:LYS:HG2	30:0:777:U:O2'	2.17	0.45
29:3:70:ARG:NH2	29:3:77:ALA:HB3	2.31	0.45
30:0:612:U:H2'	30:0:613:C:C6	2.52	0.45
30:0:1131:G:C6	30:0:1230:A:C4	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1310:U:C2'	30:0:1311:G:O5'	2.64	0.45
30:0:1588:G:C6	30:0:1589:G:C6	3.04	0.45
30:0:1730:G:H4'	30:0:1731:C:H6	1.82	0.45
30:0:1856:C:H1'	38:0:5858:HOH:O	2.17	0.45
30:0:1882:C:H2'	30:0:1883:U:C6	2.51	0.45
30:0:1902:G:O2'	30:0:1903:U:H5'	2.16	0.45
30:0:2298:C:O2'	30:0:2299:G:H5'	2.17	0.45
31:9:28:U:O2	31:9:57:A:N6	2.50	0.45
1:A:192:VAL:HG13	1:A:207:GLN:HB3	1.99	0.45
2:B:275:GLY:O	2:B:291:ASP:HA	2.16	0.45
12:L:142:LEU:HG	12:L:146:GLY:HA3	1.99	0.45
13:M:88:VAL:HG13	38:M:8902:HOH:O	2.16	0.45
14:N:34:LEU:HD22	14:N:129:ILE:HD13	1.98	0.45
18:R:128:ARG:NH2	30:0:2054:A:C2	2.84	0.45
26:Z:34:SER:HA	30:0:797:A:C4'	2.46	0.45
30:0:670:G:H2'	30:0:671:A:C8	2.51	0.45
30:0:1342:C:H2'	30:0:1343:C:H5'	1.99	0.45
30:0:2438:G:H2'	30:0:2439:C:H6	1.81	0.45
2:B:243:ASN:HA	2:B:244:PRO:C	2.41	0.45
3:C:236:THR:CG2	3:C:239:ALA:H	2.17	0.45
11:K:115:ARG:HG3	11:K:116:GLU:N	2.32	0.45
14:N:40:ASN:HD22	31:9:28:U:H5''	1.82	0.45
29:3:9:THR:HG23	29:3:20:HIS:ND1	2.32	0.45
30:0:169:A:HO2'	30:0:170:U:H6	1.63	0.45
30:0:1187:U:C2	30:0:1189:A:OP2	2.70	0.45
30:0:1540:G:C4	30:0:1541:G:C8	3.05	0.45
30:0:1613:C:H2'	30:0:1614:G:O4'	2.15	0.45
30:0:1758:U:O2'	30:0:1759:A:H5'	2.15	0.45
30:0:2032:U:C2'	30:0:2033:G:H5''	2.46	0.45
30:0:2315:C:H4'	30:0:2425:A:C6	2.51	0.45
1:A:9:ARG:HG2	1:A:16:PHE:CD2	2.52	0.45
8:H:123:ILE:HD12	8:H:123:ILE:N	2.32	0.45
8:H:165:ARG:HD2	38:H:9029:HOH:O	2.16	0.45
8:H:170:ARG:HD2	38:H:8987:HOH:O	2.15	0.45
10:J:42:GLU:HG2	10:J:43:ARG:HG3	1.98	0.45
12:L:75:LEU:HD21	38:O:7543:HOH:O	2.17	0.45
15:O:87:THR:O	15:O:91:GLN:HG3	2.17	0.45
21:U:14:GLU:O	21:U:17:THR:HB	2.16	0.45
25:Y:142:SER:HB2	38:Y:8903:HOH:O	2.16	0.45
30:0:1016:U:H2'	30:0:1017:U:O4'	2.17	0.45
30:0:1132:A:N3	30:0:2521:A:O2'	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1278:A:H4'	30:0:1279:U:C5	2.49	0.45
30:0:1535:G:H2'	30:0:1536:C:C6	2.52	0.45
30:0:1603:A:H5''	30:0:1605:G:C5'	2.39	0.45
30:0:2104:C:O2	30:0:2485:A:N1	2.49	0.45
30:0:2505:G:H3'	38:0:5626:HOH:O	2.17	0.45
30:0:2591:C:H2'	30:0:2592:G:O4'	2.16	0.45
2:B:254:GLN:HG2	2:B:255:GLY:N	2.31	0.45
7:G:71:LEU:C	7:G:73:ASP:H	2.23	0.45
8:H:12:ILE:HG23	8:H:129:ARG:CZ	2.47	0.45
8:H:99:ARG:NH1	30:0:1055:G:OP2	2.50	0.45
21:U:6:CYS:SG	21:U:13:ILE:HB	2.57	0.45
24:X:30:MET:HG2	30:0:1384:C:H5'	1.98	0.45
30:0:212:A:O4'	30:0:214:U:C6	2.70	0.45
30:0:352:A:H2'	30:0:353:G:H8	1.79	0.45
30:0:2321:A:C4	30:0:2323:G:C8	3.05	0.45
30:0:2778:A:C2	30:0:2797:C:O2	2.70	0.45
1:A:47:HIS:HD2	30:0:1654:U:C2'	2.30	0.45
1:A:105:VAL:CG1	1:A:154:ALA:HB1	2.47	0.45
3:C:170:ASP:OD2	30:0:330:C:H5	2.00	0.45
14:N:86:LEU:HD12	14:N:125:ALA:HB2	1.99	0.45
14:N:110:THR:HB	14:N:113:SER:OG	2.17	0.45
18:R:132:ARG:HG2	18:R:133:ALA:N	2.31	0.45
23:W:129:LYS:HE2	30:0:1098:A:O3'	2.17	0.45
30:0:213:G:N2	30:0:225:G:H2'	2.31	0.45
30:0:226:A:H1'	30:0:393:G:C5	2.51	0.45
30:0:644:G:H1'	38:0:6390:HOH:O	2.16	0.45
30:0:727:G:C2	30:0:728:C:C2	3.05	0.45
30:0:867:A:H2	30:0:880:C:O2	2.00	0.45
30:0:921:G:H4'	30:0:924:G:C6	2.52	0.45
30:0:1151:G:H2'	38:0:5008:HOH:O	2.17	0.45
30:0:1346:U:H2'	30:0:1347:U:H6	1.82	0.45
30:0:2071:C:H5'	38:0:9532:HOH:O	2.17	0.45
30:0:2679:G:H2'	30:0:2681:A:OP2	2.17	0.45
31:9:26:C:H5''	38:9:9049:HOH:O	2.17	0.45
2:B:252:PRO:HD2	30:0:2548:C:H5'	1.99	0.45
3:C:27:ARG:HH11	3:C:27:ARG:CG	2.15	0.45
4:D:154:LYS:HD2	4:D:154:LYS:N	2.22	0.45
12:L:136:ALA:HB3	38:L:9035:HOH:O	2.17	0.45
16:P:91:LYS:O	16:P:95:GLU:HG3	2.17	0.45
25:Y:132:ASP:OD2	30:0:621:C:H5'	2.17	0.45
30:0:113:A:H3'	30:0:114:A:H5''	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:282:C:H2'	30:0:283:U:O4'	2.16	0.45
30:0:482:G:O4'	30:0:511:A:C2	2.70	0.45
30:0:559:U:H2'	30:0:560:U:O4'	2.17	0.45
30:0:941:G:C6	30:0:942:U:C4	3.05	0.45
30:0:1755:A:H2'	30:0:1756:G:O4'	2.16	0.45
30:0:2596:A:H2	33:0:8812:CL:CL	2.37	0.45
30:0:2650:U:O2'	30:0:2651:C:H5'	2.16	0.45
30:0:2691:A:H5'	30:0:2693:U:H1'	1.99	0.45
30:0:2735:U:H2'	30:0:2736:U:C6	2.52	0.45
31:9:82:U:H2'	31:9:83:G:C8	2.52	0.45
1:A:76:VAL:HG23	26:Z:87:LYS:O	2.17	0.45
2:B:5:ARG:HD2	2:B:8:LYS:HE2	1.99	0.45
3:C:39:GLN:O	3:C:43:LYS:HD3	2.17	0.45
18:R:25:PHE:CE2	18:R:29:LYS:HE2	2.51	0.45
25:Y:142:SER:OG	30:0:1331:G:OP2	2.32	0.45
30:0:792:G:O2'	30:0:793:A:H5'	2.16	0.45
30:0:1249:U:H2'	30:0:1250:C:H6	1.82	0.45
30:0:1878:G:O2'	30:0:1879:U:P	2.74	0.45
30:0:2010:A:C2'	38:0:5942:HOH:O	2.51	0.45
30:0:2252:A:C5	30:0:2253:G:H1'	2.51	0.45
14:N:25:ARG:HG2	30:0:2416:G:O2'	2.17	0.44
15:O:98:LEU:O	15:O:102:ILE:HG13	2.17	0.44
16:P:68:LYS:HE2	30:0:1787:C:OP1	2.16	0.44
18:R:114:VAL:HG13	18:R:114:VAL:O	2.18	0.44
28:2:41:HIS:H	28:2:45:ASN:ND2	2.04	0.44
30:0:65:C:O2'	30:0:66:G:H5'	2.16	0.44
30:0:152:A:H2'	30:0:153:C:C6	2.52	0.44
30:0:699:C:C2	30:0:744:G:N2	2.85	0.44
30:0:797:A:N6	30:0:816:G:H1'	2.32	0.44
30:0:1209:C:C2	30:0:1210:G:C8	3.04	0.44
30:0:1268:C:O2'	30:0:1269:G:H5'	2.16	0.44
30:0:2301:A:H5''	30:0:2302:A:H5'	1.99	0.44
30:0:2335:C:H2'	30:0:2336:G:H8	1.80	0.44
30:0:2837:U:H2'	38:0:6825:HOH:O	2.15	0.44
31:9:1:U:O3'	31:9:3:A:C5'	2.65	0.44
1:A:206:ARG:HH21	30:0:2629:C:N4	2.16	0.44
4:D:25:MET:HE1	4:D:37:ALA:O	2.17	0.44
8:H:46:TYR:HA	8:H:47:PRO:HD3	1.81	0.44
21:U:42:LEU:O	30:0:1810:C:H5'	2.17	0.44
23:W:35:VAL:HG23	23:W:41:TYR:CD2	2.52	0.44
30:0:365:G:C5	30:0:366:U:C4	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:598:C:H2'	30:0:599:G:C8	2.51	0.44
30:0:1310:U:H2'	30:0:1311:G:O5'	2.17	0.44
30:0:1949:G:N2	30:0:1964:U:H1'	2.32	0.44
30:0:2074:A:H1'	38:0:9875:HOH:O	2.16	0.44
30:0:2250:G:C2	30:0:2251:G:H1'	2.52	0.44
30:0:2493:C:O2	30:0:2493:C:H2'	2.17	0.44
30:0:2734:G:O2'	30:0:2735:U:H5'	2.17	0.44
31:9:1:U:O3'	31:9:3:A:H5''	2.16	0.44
38:B:9136:HOH:O	21:U:17:THR:HG21	2.16	0.44
5:E:3:VAL:HG22	5:E:49:ILE:HB	2.00	0.44
7:G:64:ASN:N	7:G:64:ASN:ND2	2.65	0.44
14:N:11:ARG:HG3	14:N:14:ARG:HH12	1.82	0.44
23:W:24:LEU:O	23:W:26:ILE:HG22	2.18	0.44
26:Z:65:ASN:HB2	26:Z:84:CYS:SG	2.58	0.44
28:2:22:PRO:HG2	28:2:25:VAL:CG2	2.48	0.44
30:0:40:C:O5'	30:0:40:C:H6	2.01	0.44
30:0:307:G:C2	30:0:309:C:C4	3.05	0.44
30:0:734:U:H2'	30:0:736:A:OP2	2.17	0.44
30:0:970:U:H2'	38:0:6313:HOH:O	2.16	0.44
30:0:1206:U:C6	30:0:1206:U:C3'	3.01	0.44
30:0:1279:U:C5'	30:0:1280:A:OP2	2.65	0.44
30:0:1461:U:H2'	30:0:1462:C:H6	1.83	0.44
30:0:1735:C:O2'	30:0:1736:A:H5'	2.17	0.44
30:0:2004:U:H2'	30:0:2005:G:OP1	2.17	0.44
30:0:2410:G:O2'	30:0:2411:C:H5'	2.18	0.44
30:0:2642:G:H2'	30:0:2643:G:O4'	2.16	0.44
30:0:2777:G:O2'	30:0:2778:A:H5'	2.17	0.44
3:C:226:GLY:HA3	30:0:1308:A:C4'	2.48	0.44
4:D:22:VAL:HA	4:D:73:VAL:O	2.17	0.44
4:D:154:LYS:H	4:D:154:LYS:CD	2.24	0.44
5:E:84:MET:HG2	5:E:168:ILE:HD13	1.98	0.44
13:M:47:ASP:CG	13:M:48:LYS:H	2.25	0.44
13:M:73:ARG:NH2	30:0:2263:G:H5''	2.32	0.44
20:T:71:VAL:HG12	20:T:72:ILE:N	2.32	0.44
30:0:161:A:H2'	30:0:162:C:C6	2.52	0.44
30:0:664:U:O4	30:0:681:G:H5''	2.16	0.44
30:0:711:G:C2	30:0:718:C:O2	2.70	0.44
30:0:1928:C:O2'	30:0:1929:G:H5'	2.17	0.44
30:0:2663:U:N3	30:0:2664:A:N6	2.65	0.44
30:0:2755:G:H1'	38:0:4677:HOH:O	2.17	0.44
1:A:11:ARG:HD3	38:0:9221:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:162:VAL:CG2	3:C:232:LEU:HD21	2.47	0.44
4:D:159:PRO:O	4:D:163:VAL:HG23	2.17	0.44
5:E:95:VAL:HG11	5:E:131:LEU:HD11	1.99	0.44
6:F:48:VAL:HG23	6:F:74:PHE:HB3	1.99	0.44
18:R:125:ARG:HG2	38:R:8942:HOH:O	2.17	0.44
20:T:23:VAL:HG23	20:T:41:ARG:HG3	2.00	0.44
30:0:1076:G:C2	30:0:1084:C:C2	3.06	0.44
30:0:1477:C:H5'	30:0:1868:G:H5''	1.98	0.44
30:0:2245:C:H6	30:0:2245:C:O5'	2.00	0.44
31:9:82:U:H2'	31:9:83:G:H8	1.82	0.44
3:C:37:ALA:HA	3:C:100:LEU:HD12	2.00	0.44
9:I:114:TYR:CD1	9:I:114:TYR:N	2.86	0.44
10:J:63:ILE:CD1	30:0:1236:A:C8	3.01	0.44
12:L:129:ALA:O	12:L:133:VAL:HG23	2.17	0.44
13:M:97:ILE:HD13	13:M:127:LYS:HD2	2.00	0.44
13:M:123:ASP:OD1	13:M:126:GLN:HG2	2.18	0.44
14:N:93:GLN:HA	14:N:93:GLN:HE21	1.82	0.44
15:O:49:GLU:OE1	15:O:72:LYS:HG3	2.17	0.44
16:P:18:LYS:O	16:P:21:VAL:HG13	2.18	0.44
19:S:57:THR:CG2	19:S:58:MET:N	2.79	0.44
21:U:7:ASP:HB2	21:U:29:THR:HG23	2.00	0.44
30:0:81:G:N3	30:0:98:A:C2	2.85	0.44
30:0:549:A:C2	30:0:550:C:C2	3.06	0.44
30:0:737:A:H2'	30:0:738:G:O4'	2.18	0.44
30:0:1028:U:H1'	38:0:3631:HOH:O	2.18	0.44
30:0:1067:A:H5'	38:0:4344:HOH:O	2.18	0.44
30:0:1116:U:C2'	30:0:1118:A:H2	2.28	0.44
30:0:2119:C:O2'	30:0:2120:U:H5'	2.18	0.44
30:0:2313:C:H4'	38:0:6558:HOH:O	2.18	0.44
30:0:2325:U:O2'	30:0:2411:C:H1'	2.18	0.44
30:0:2887:G:H2'	30:0:2888:U:H6	1.79	0.44
4:D:56:ARG:NH2	30:0:2332:A:H5'	2.32	0.44
12:L:149:ARG:O	12:L:150:GLN:HB2	2.17	0.44
13:M:171:ARG:NH2	30:0:189:A:OP1	2.50	0.44
16:P:41:ARG:NH2	30:0:1500:U:OP2	2.49	0.44
17:Q:3:SER:O	17:Q:8:GLU:HG3	2.18	0.44
25:Y:116:LEU:HD23	25:Y:116:LEU:HA	1.80	0.44
27:1:1:THR:O	30:0:1836:A:H1'	2.17	0.44
29:3:62:THR:HG21	30:0:2317:C:H5'	1.98	0.44
30:0:295:C:H2'	30:0:296:G:O4'	2.18	0.44
30:0:462:A:H2'	38:0:4875:HOH:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:615:G:H2'	30:0:616:U:H6	1.83	0.44
30:0:725:C:H2'	30:0:726:C:O5'	2.18	0.44
30:0:912:A:C4	30:0:1294:A:C2	3.05	0.44
30:0:1014:A:H2'	30:0:1015:C:H5'	1.99	0.44
30:0:1249:U:H2'	30:0:1250:C:C6	2.53	0.44
30:0:1597:A:C4	30:0:1598:A:C8	3.05	0.44
30:0:1883:U:C2'	30:0:1884:G:H5'	2.48	0.44
2:B:119:HIS:O	2:B:121:PRO:HD3	2.18	0.44
14:N:73:ALA:HB1	14:N:74:PRO:CD	2.48	0.44
15:O:21:SER:OG	15:O:106:PRO:HB2	2.18	0.44
23:W:122:ARG:NH2	23:W:154:ARG:HG2	2.33	0.44
25:Y:234:VAL:HG12	25:Y:235:GLU:N	2.33	0.44
29:3:2:GLN:HB3	29:3:91:GLN:CD	2.43	0.44
30:0:368:C:C2'	30:0:369:G:H5'	2.48	0.44
30:0:1246:A:C4	30:0:1248:A:C8	3.06	0.44
30:0:1307:A:H2'	30:0:1308:A:C8	2.53	0.44
30:0:1603:A:C5'	30:0:1605:G:C5'	2.96	0.44
30:0:1730:G:H4'	30:0:1731:C:C6	2.52	0.44
30:0:1771:U:O2'	30:0:1773:G:N7	2.50	0.44
30:0:1773:G:C2'	30:0:1774:G:H5'	2.48	0.44
30:0:2105:C:H2'	30:0:2106:C:C6	2.53	0.44
30:0:2128:G:C5	30:0:2129:U:C5	3.06	0.44
30:0:2276:U:O2'	30:0:2277:U:H5'	2.18	0.44
30:0:2457:U:O2'	30:0:2458:U:H5'	2.17	0.44
30:0:2588:OMG:HM23	30:0:2617:G:C2	2.53	0.44
30:0:2793:A:H2'	30:0:2794:G:H5'	2.00	0.44
1:A:26:ASP:OD2	30:0:1872:C:H4'	2.18	0.44
2:B:242:TRP:CZ2	30:0:2607:U:C4	3.06	0.44
3:C:27:ARG:HD2	38:O:327:HOH:O	2.17	0.44
13:M:95:LYS:HE2	30:0:157:G:H4'	1.99	0.44
14:N:147:ILE:HD11	31:9:50:G:OP1	2.18	0.44
17:Q:62:THR:O	17:Q:64:GLU:HG2	2.18	0.44
27:1:21:ARG:HD2	27:1:37:CYS:SG	2.57	0.44
30:0:416:G:H2'	38:0:9910:HOH:O	2.16	0.44
30:0:559:U:C6	30:0:559:U:C3'	3.01	0.44
30:0:1066:U:H2'	30:0:1067:A:C8	2.53	0.44
30:0:1254:C:O2'	30:0:1255:A:H5'	2.18	0.44
30:0:1657:A:H2'	30:0:1658:A:C8	2.53	0.44
30:0:2072:G:H3'	30:0:2073:G:C5'	2.48	0.44
30:0:2473:U:O2'	30:0:2474:A:H5''	2.18	0.44
4:D:59:GLY:HA3	38:D:4886:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:117:GLU:HB3	38:L:9018:HOH:O	2.18	0.43
13:M:102:GLU:OE2	13:M:164:THR:HG21	2.17	0.43
13:M:134:ILE:CG2	13:M:141:ILE:HD13	2.42	0.43
20:T:48:VAL:CG1	20:T:49:GLU:N	2.81	0.43
23:W:27:HIS:C	23:W:28:HIS:HD2	2.26	0.43
24:X:72:VAL:HG22	24:X:85:VAL:HG12	2.00	0.43
30:0:297:U:H2'	30:0:298:C:H6	1.83	0.43
30:0:590:A:H2'	30:0:591:A:O4'	2.18	0.43
30:0:653:U:H2'	30:0:654:A:C8	2.52	0.43
30:0:1198:U:C6	30:0:1200:A:OP2	2.71	0.43
30:0:1592:G:H1'	30:0:1593:C:C6	2.53	0.43
30:0:2256:G:C2'	30:0:2257:G:H5'	2.48	0.43
1:A:182:ARG:HG2	1:A:182:ARG:HH11	1.83	0.43
2:B:223:ARG:HG3	2:B:232:TRP:O	2.17	0.43
3:C:118:THR:O	3:C:136:VAL:HG13	2.18	0.43
4:D:45:THR:HB	4:D:75:LEU:HD21	1.99	0.43
5:E:111:LYS:HE3	30:0:2690:U:H4'	1.99	0.43
12:L:41:HIS:CD2	30:0:926:A:O2'	2.71	0.43
16:P:10:ALA:HA	16:P:13:VAL:HG12	2.01	0.43
17:Q:1:PRO:HA	30:0:2299:G:O6	2.18	0.43
19:S:50:GLU:HB3	19:S:67:ARG:NH2	2.33	0.43
20:T:38:ARG:HG3	20:T:38:ARG:HH11	1.83	0.43
30:0:549:A:C6	30:0:550:C:C4	3.07	0.43
30:0:596:C:H2'	30:0:597:A:C8	2.53	0.43
30:0:1477:C:O2'	30:0:1478:U:H5'	2.17	0.43
30:0:1973:A:H2'	30:0:1974:G:O4'	2.17	0.43
30:0:2387:U:H2'	30:0:2388:C:C6	2.52	0.43
30:0:2543:G:H2'	30:0:2544:G:O4'	2.18	0.43
31:9:64:C:O2'	31:9:65:A:H5'	2.18	0.43
1:A:211:LYS:HB2	38:A:9038:HOH:O	2.18	0.43
2:B:18:ARG:HG3	2:B:256:GLN:HG3	2.00	0.43
14:N:67:ALA:CA	14:N:71:TRP:HB3	2.44	0.43
20:T:48:VAL:HG11	20:T:96:VAL:CG1	2.46	0.43
25:Y:144:ARG:NH1	38:Y:8882:HOH:O	2.51	0.43
25:Y:148:GLY:HA3	30:0:622:G:P	2.59	0.43
30:0:107:U:C2'	30:0:108:U:H5'	2.48	0.43
30:0:1362:U:H5'	38:0:3253:HOH:O	2.18	0.43
30:0:1702:U:H5''	38:0:7207:HOH:O	2.19	0.43
30:0:2321:A:N1	30:0:2378:U:O2	2.52	0.43
2:B:199:TYR:HE1	2:B:319:ASP:HB2	1.83	0.43
2:B:234:ARG:HG3	30:0:1735:C:OP2	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:305:ASP:O	2:B:306:LYS:CB	2.66	0.43
16:P:138:GLU:C	16:P:140:TYR:H	2.25	0.43
22:V:50:ARG:HH12	30:0:56:G:C5'	2.30	0.43
26:Z:94:LYS:HA	38:Z:8719:HOH:O	2.18	0.43
30:0:275:G:N2	30:0:376:C:C2	2.87	0.43
30:0:496:G:H3'	38:0:7658:HOH:O	2.18	0.43
30:0:853:C:H2'	30:0:854:G:O4'	2.17	0.43
30:0:920:C:H5''	30:0:921:G:O5'	2.18	0.43
30:0:1183:C:H41	30:0:1192:A:P	2.42	0.43
30:0:1878:G:O2'	30:0:1879:U:C6	2.60	0.43
30:0:2474:A:H4'	30:0:2475:C:O5'	2.18	0.43
30:0:2834:G:H2'	30:0:2835:C:O5'	2.18	0.43
12:L:34:GLY:HA3	12:L:38:HIS:CE1	2.52	0.43
29:3:39:GLN:HG2	29:3:43:ASN:OD1	2.19	0.43
30:0:40:C:H4'	38:0:6993:HOH:O	2.18	0.43
30:0:1809:G:H2'	30:0:1811:A:OP2	2.19	0.43
30:0:2355:G:H5''	30:0:2356:A:OP2	2.19	0.43
5:E:69:ILE:HA	5:E:72:MET:CE	2.44	0.43
6:F:14:ASP:O	6:F:18:GLU:HG3	2.18	0.43
14:N:86:LEU:O	14:N:90:LEU:HG	2.19	0.43
22:V:49:LEU:O	22:V:53:ILE:HG13	2.18	0.43
29:3:3:MET:HE1	29:3:83:TRP:CH2	2.52	0.43
30:0:557:C:O2'	30:0:558:C:H5'	2.19	0.43
30:0:1185:U:H2'	30:0:1186:C:C6	2.54	0.43
30:0:1471:A:H2'	30:0:1472:C:C6	2.54	0.43
30:0:2039:A:H2'	30:0:2040:C:C6	2.53	0.43
30:0:2102:G:N2	30:0:2104:C:N3	2.67	0.43
30:0:2346:C:C6	30:0:2346:C:O5'	2.72	0.43
30:0:2718:C:H5'	30:0:2718:C:C6	2.52	0.43
1:A:51:ARG:HH21	1:A:53:ALA:HB3	1.82	0.43
1:A:190:ARG:NH2	1:A:207:GLN:OE1	2.52	0.43
1:A:217:ARG:HG2	1:A:229:ALA:CB	2.48	0.43
11:K:66:ARG:NH2	30:0:1994:A:OP1	2.52	0.43
20:T:82:THR:HG21	30:0:488:U:O2'	2.19	0.43
24:X:15:ARG:NH1	30:0:2896:A:OP1	2.51	0.43
25:Y:117:LEU:HB2	25:Y:174:VAL:HG21	1.99	0.43
28:2:20:ARG:NH1	28:2:39:ARG:HH21	2.17	0.43
28:2:40:ARG:HG3	28:2:45:ASN:CB	2.48	0.43
30:0:328:U:C2	30:0:348:C:H4'	2.53	0.43
30:0:459:A:H4'	38:0:9455:HOH:O	2.17	0.43
30:0:750:A:H2'	30:0:751:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:878:G:H4'	30:0:1835:U:H4'	2.00	0.43
30:0:1173:A:H4'	30:0:1174:A:H8	1.83	0.43
30:0:1427:A:C2'	30:0:1428:C:H5'	2.49	0.43
30:0:1566:C:H2'	30:0:1567:G:C8	2.54	0.43
30:0:1773:G:H4'	38:0:3505:HOH:O	2.19	0.43
30:0:2103:A:N3	30:0:2103:A:H2'	2.33	0.43
30:0:2379:G:N3	30:0:2418:G:H2'	2.34	0.43
30:0:2564:G:OP2	30:0:2565:C:H5''	2.18	0.43
31:9:45:A:N7	31:9:46:C:C5	2.87	0.43
1:A:192:VAL:O	1:A:207:GLN:HG2	2.18	0.43
3:C:132:ASP:O	3:C:133:ARG:HG3	2.19	0.43
4:D:103:ASN:ND2	4:D:133:ASN:HD22	2.17	0.43
5:E:91:PHE:HE1	30:0:2694:A:H4'	1.83	0.43
38:M:8865:HOH:O	30:0:2244:A:H1'	2.18	0.43
14:N:49:THR:HG22	14:N:56:ASP:CB	2.49	0.43
14:N:109:PRO:HB3	30:0:2413:A:N7	2.34	0.43
18:R:59:PHE:O	18:R:63:ASN:HB3	2.18	0.43
23:W:122:ARG:HG3	23:W:122:ARG:HH11	1.84	0.43
26:Z:95:PRO:HD2	38:Z:8719:HOH:O	2.18	0.43
30:0:119:A:H2'	30:0:120:A:C5'	2.49	0.43
30:0:361:C:H2'	30:0:362:G:O4'	2.19	0.43
30:0:2681:A:H4'	30:0:2682:C:OP1	2.19	0.43
30:0:2694:A:H3'	30:0:2695:C:H6	1.84	0.43
31:9:110:G:C2	31:9:111:U:C6	3.07	0.43
31:9:110:G:C5	31:9:111:U:C5	3.07	0.43
2:B:42:ALA:CB	2:B:162:MET:HE1	2.49	0.43
2:B:116:PRO:HG3	30:0:2821:C:H4'	2.01	0.43
2:B:215:VAL:HB	38:B:9090:HOH:O	2.19	0.43
8:H:6:ALA:HB3	30:0:2521:A:OP2	2.19	0.43
8:H:6:ALA:HA	8:H:61:ARG:NH1	2.34	0.43
9:I:69:PRO:HA	30:0:1164:U:OP1	2.19	0.43
26:Z:40:ALA:O	30:0:2018:A:H2	2.02	0.43
26:Z:88:PHE:CD2	26:Z:88:PHE:N	2.86	0.43
30:0:636:G:H5'	30:0:2059:U:OP2	2.19	0.43
30:0:802:G:H2'	30:0:803:C:C6	2.54	0.43
30:0:920:C:C5	30:0:2467:A:OP1	2.72	0.43
30:0:1099:G:H2'	30:0:1100:G:O4'	2.19	0.43
30:0:1156:C:O2'	30:0:1157:C:H5'	2.19	0.43
30:0:1592:G:HO2'	30:0:1593:C:H6	1.67	0.43
30:0:1937:U:O2'	30:0:1938:G:H5'	2.18	0.43
30:0:2487:C:C5	38:0:4880:HOH:O	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2523:U:H2'	30:0:2524:G:O4'	2.18	0.43
30:0:2581:U:H1'	38:0:4466:HOH:O	2.17	0.43
1:A:48:ASP:HB3	1:A:51:ARG:HG3	2.00	0.43
1:A:230:SER:CB	30:0:1852:A:H4'	2.49	0.43
4:D:136:ARG:HA	4:D:137:PRO:HD3	1.84	0.43
5:E:91:PHE:HA	5:E:92:PRO:HD3	1.86	0.43
10:J:93:ARG:HB3	10:J:93:ARG:HH11	1.84	0.43
16:P:58:SER:HB3	38:0:5616:HOH:O	2.18	0.43
16:P:129:GLY:HA2	38:P:153:HOH:O	2.18	0.43
23:W:122:ARG:NH2	38:0:5280:HOH:O	2.51	0.43
24:X:15:ARG:NH2	30:0:2856:A:OP1	2.52	0.43
24:X:34:ARG:NH1	24:X:48:VAL:O	2.51	0.43
29:3:13:HIS:HD2	29:3:76:LYS:HB3	1.83	0.43
30:0:236:A:H8	30:0:236:A:OP1	2.02	0.43
30:0:301:C:H2'	30:0:302:A:C8	2.54	0.43
30:0:308:U:C4	30:0:342:C:C1'	3.01	0.43
30:0:1456:C:H2'	30:0:1457:U:C6	2.53	0.43
30:0:1561:U:C5'	38:0:7421:HOH:O	2.67	0.43
30:0:1758:U:H2'	30:0:1759:A:O4'	2.19	0.43
30:0:1923:G:H2'	30:0:1924:A:H8	1.83	0.43
30:0:2252:A:H2'	30:0:2253:G:O4'	2.19	0.43
31:9:3:A:N6	31:9:22:G:H1'	2.34	0.43
2:B:141:ARG:HD2	2:B:163:GLU:OE2	2.19	0.42
10:J:131:THR:HG22	10:J:133:GLY:N	2.34	0.42
12:L:117:GLU:HG3	12:L:117:GLU:O	2.19	0.42
12:L:150:GLN:HB3	38:L:9032:HOH:O	2.18	0.42
30:0:290:C:C2'	30:0:291:C:H5'	2.49	0.42
30:0:412:C:O2'	30:0:413:G:H5'	2.18	0.42
30:0:612:U:H2'	30:0:613:C:H6	1.84	0.42
30:0:1016:U:O2'	30:0:2303:A:N7	2.40	0.42
30:0:1095:U:H2'	30:0:1096:U:O4'	2.18	0.42
30:0:1552:G:C6	30:0:1634:G:C6	3.07	0.42
30:0:1748:U:C5	30:0:1749:U:C4	3.07	0.42
30:0:1882:C:O2'	30:0:2012:U:OP2	2.32	0.42
30:0:2070:G:H2'	30:0:2072:G:OP1	2.19	0.42
30:0:2499:U:H1'	38:0:9433:HOH:O	2.19	0.42
30:0:2553:A:H2'	30:0:2553:A:N3	2.34	0.42
30:0:2587:OMU:H2'	30:0:2589:U:H5''	2.01	0.42
31:9:65:A:N6	31:9:112:U:C6	2.86	0.42
1:A:135:VAL:HG22	1:A:136:ALA:N	2.35	0.42
5:E:146:ALA:O	5:E:150:GLN:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:105:ASN:HD21	15:O:109:SER:N	2.17	0.42
15:O:112:ARG:NH2	30:0:719:C:O2'	2.52	0.42
17:Q:64:GLU:HG3	17:Q:74:ASP:OD2	2.18	0.42
19:S:57:THR:C	19:S:59:ASP:H	2.27	0.42
30:0:271:C:C2	30:0:273:G:O4'	2.73	0.42
30:0:696:C:H4'	38:0:7268:HOH:O	2.19	0.42
30:0:706:G:N2	30:0:707:C:H41	2.17	0.42
30:0:1562:C:N4	38:0:5849:HOH:O	2.49	0.42
30:0:1878:G:H4'	38:0:6104:HOH:O	2.19	0.42
30:0:1878:G:H5''	38:0:5160:HOH:O	2.18	0.42
30:0:2061:C:H2'	30:0:2062:A:H5'	1.99	0.42
30:0:2415:A:H2'	30:0:2416:G:H5'	2.01	0.42
30:0:2842:G:H2'	30:0:2843:A:C5'	2.48	0.42
1:A:8:ARG:HG2	38:A:8978:HOH:O	2.20	0.42
2:B:8:LYS:HG3	2:B:220:VAL:HG12	2.01	0.42
2:B:17:LYS:O	2:B:260:HIS:HD2	2.02	0.42
2:B:217:ARG:HG3	2:B:257:THR:CG2	2.41	0.42
12:L:11:ARG:O	30:0:903:U:C2	2.72	0.42
13:M:84:LYS:HB2	30:0:170:U:OP1	2.18	0.42
16:P:105:LEU:HD21	16:P:137:LEU:HD11	2.01	0.42
17:Q:2:SER:HA	38:0:6711:HOH:O	2.19	0.42
23:W:2:HIS:HD2	23:W:55:GLY:C	2.27	0.42
23:W:142:ASP:HB3	23:W:145:GLY:H	1.83	0.42
27:1:25:LYS:HD2	28:2:48:ASP:HA	2.02	0.42
30:0:113:A:H3'	30:0:114:A:C5'	2.48	0.42
30:0:128:A:C8	30:0:128:A:C3'	2.99	0.42
30:0:276:C:H6	30:0:276:C:O5'	2.02	0.42
30:0:1206:U:C6	30:0:1206:U:H3'	2.55	0.42
30:0:1345:A:H2'	30:0:1346:U:C6	2.54	0.42
30:0:1407:A:O2'	30:0:1408:U:H3'	2.20	0.42
30:0:1544:U:O2'	30:0:1545:C:H5'	2.19	0.42
30:0:1757:U:H6	30:0:1757:U:O5'	2.03	0.42
30:0:2035:C:O5'	30:0:2035:C:H6	2.02	0.42
30:0:2787:C:H5	38:0:4627:HOH:O	2.02	0.42
1:A:70:ALA:HA	1:A:71:PRO:HD3	1.73	0.42
1:A:135:VAL:HG11	1:A:147:ARG:NH2	2.34	0.42
4:D:50:VAL:HG13	31:9:41:C:O4'	2.19	0.42
4:D:54:ALA:HB2	30:0:2346:C:H5'	2.01	0.42
5:E:126:ILE:HA	5:E:131:LEU:HD23	2.00	0.42
11:K:79:PRO:HB3	11:K:87:ARG:HB3	2.02	0.42
12:L:7:GLN:HB3	12:L:13:HIS:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:97:ILE:HG21	13:M:127:LYS:HD2	2.01	0.42
18:R:68:HIS:O	30:0:2842:G:H5'	2.19	0.42
29:3:3:MET:HA	29:3:4:PRO:HD2	1.86	0.42
30:0:707:C:C2	30:0:708:A:C8	3.07	0.42
30:0:1173:A:C2	30:0:1177:A:C8	3.07	0.42
30:0:1393:A:N1	30:0:1725:C:O2'	2.44	0.42
30:0:1585:C:H2'	30:0:1586:G:H8	1.84	0.42
30:0:1804:A:H2'	30:0:1805:G:C8	2.53	0.42
30:0:1902:G:C2	30:0:1936:C:C2	3.07	0.42
30:0:2709:G:N2	38:0:7613:HOH:O	2.53	0.42
30:0:2828:G:O5'	30:0:2828:G:H8	2.03	0.42
2:B:310:ARG:HB3	38:B:9121:HOH:O	2.19	0.42
10:J:45:VAL:CG2	10:J:129:PHE:HD1	2.32	0.42
11:K:64:MET:HA	11:K:67:GLN:HE21	1.84	0.42
12:L:53:ARG:NH2	12:L:57:VAL:HG12	2.34	0.42
16:P:103:THR:O	16:P:107:GLU:HG3	2.19	0.42
19:S:6:LYS:HD3	38:S:2519:HOH:O	2.20	0.42
23:W:128:VAL:HG22	30:0:1098:A:OP1	2.19	0.42
30:0:407:A:H3'	38:0:4452:HOH:O	2.19	0.42
30:0:420:U:O4'	30:0:1920:C:C4	2.73	0.42
30:0:727:G:H3'	30:0:728:C:C6	2.54	0.42
30:0:849:C:H2'	30:0:850:U:O4'	2.20	0.42
30:0:939:A:N1	30:0:1027:G:O2'	2.45	0.42
30:0:1321:A:H2'	30:0:1322:G:C8	2.55	0.42
30:0:1420:C:O2	30:0:1420:C:H2'	2.19	0.42
30:0:1933:G:O2'	30:0:1934:A:H5'	2.19	0.42
30:0:2480:G:O2'	30:0:2481:G:H5'	2.19	0.42
31:9:58:G:H3'	31:9:59:C:C6	2.54	0.42
2:B:101:TRP:HB2	2:B:119:HIS:CD2	2.54	0.42
2:B:145:HIS:CD2	2:B:146:THR:O	2.63	0.42
2:B:215:VAL:HA	2:B:220:VAL:HG22	2.00	0.42
2:B:234:ARG:NH2	30:0:2039:A:OP2	2.53	0.42
5:E:112:ALA:HA	5:E:113:PRO:HD3	1.77	0.42
5:E:137:ASP:OD1	5:E:139:GLU:HB2	2.19	0.42
8:H:61:ARG:HH11	8:H:61:ARG:HG3	1.85	0.42
13:M:188:ARG:NH1	30:0:154:C:H3'	2.35	0.42
30:0:154:C:O2'	30:0:155:C:H5'	2.18	0.42
30:0:273:G:H2'	30:0:274:G:O4'	2.20	0.42
30:0:299:U:C2	30:0:300:U:C5	3.08	0.42
30:0:571:C:O5'	30:0:571:C:H6	2.02	0.42
30:0:1006:A:H2'	30:0:1007:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1559:A:OP2	30:0:1559:A:C8	2.70	0.42
1:A:217:ARG:NH2	30:0:1853:C:O2'	2.53	0.42
2:B:14:GLY:HA2	2:B:15:PRO:C	2.44	0.42
2:B:314:ALA:HB3	2:B:317:PRO:HG3	2.02	0.42
8:H:117:ARG:HH12	30:0:2287:C:N4	2.17	0.42
13:M:46:LEU:HD22	13:M:50:ARG:CD	2.50	0.42
13:M:172:GLY:HA2	38:0:9086:HOH:O	2.19	0.42
14:N:143:ARG:HG2	14:N:172:PHE:CD2	2.54	0.42
30:0:17:G:H2'	30:0:18:C:H6	1.84	0.42
30:0:137:U:OP1	30:0:259:G:O2'	2.36	0.42
30:0:947:U:O2'	30:0:948:G:H5'	2.20	0.42
30:0:1168:C:C5	30:0:1169:U:C4	3.08	0.42
30:0:1454:U:H5''	30:0:1455:C:OP2	2.19	0.42
30:0:1883:U:O2'	30:0:1884:G:H5'	2.19	0.42
30:0:1924:A:H1'	38:0:5731:HOH:O	2.19	0.42
30:0:2274:A:H2'	30:0:2275:G:C8	2.54	0.42
30:0:2321:A:C5	30:0:2323:G:C8	3.07	0.42
1:A:190:ARG:NH1	30:0:1845:A:OP2	2.53	0.42
2:B:190:MET:HE1	2:B:311:PHE:CD1	2.55	0.42
2:B:252:PRO:HD3	38:0:9818:HOH:O	2.18	0.42
11:K:132:VAL:HG11	21:U:22:VAL:HG22	2.02	0.42
13:M:74:LYS:HB3	38:M:8944:HOH:O	2.20	0.42
19:S:8:PRO:HD2	22:V:32:ALA:HA	2.02	0.42
20:T:106:GLU:HG3	38:T:4913:HOH:O	2.20	0.42
24:X:70:ILE:O	24:X:70:ILE:HG23	2.20	0.42
26:Z:42:TYR:HA	30:0:1829:A:N6	2.35	0.42
29:3:64:LYS:HB3	29:3:82:GLY:O	2.20	0.42
30:0:162:C:H2'	30:0:163:U:H5'	2.02	0.42
30:0:396:U:HO2'	30:0:397:A:P	2.43	0.42
30:0:644:G:H5'	30:0:644:G:N3	2.35	0.42
30:0:918:G:C2	30:0:926:A:C2	3.08	0.42
30:0:1188:A:C5	30:0:1189:A:N1	2.88	0.42
30:0:1539:U:O2'	30:0:1540:G:H5'	2.20	0.42
30:0:1576:G:H2'	30:0:1577:U:C6	2.54	0.42
30:0:1815:A:H2'	30:0:1816:C:O4'	2.20	0.42
30:0:2354:A:C2	30:0:2367:A:C8	3.08	0.42
30:0:2671:U:C2'	30:0:2672:C:O5'	2.68	0.42
30:0:2673:U:O2'	30:0:2674:G:H5'	2.20	0.42
30:0:2690:U:C4	30:0:2691:A:C5	3.07	0.42
31:9:91:C:H2'	31:9:92:G:O4'	2.18	0.42
31:9:116:C:O2'	31:9:117:G:H5'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:10:ARG:HD2	8:H:161:THR:HG21	2.01	0.42
10:J:74:ARG:O	10:J:78:ILE:HG12	2.20	0.42
13:M:48:LYS:HE3	13:M:52:GLN:NE2	2.34	0.42
13:M:187:LEU:HD22	13:M:194:GLY:HA3	2.01	0.42
25:Y:160:LYS:HD3	25:Y:160:LYS:HA	1.87	0.42
28:2:43:ARG:HH22	30:0:1684:A:C1'	2.26	0.42
30:0:151:A:H2'	30:0:152:A:C8	2.55	0.42
30:0:710:G:O2'	30:0:711:G:H5'	2.20	0.42
30:0:820:G:O2'	30:0:856:G:H4'	2.20	0.42
30:0:1198:U:H2'	30:0:1200:A:OP2	2.20	0.42
30:0:1200:A:H4'	38:0:7330:HOH:O	2.19	0.42
30:0:1474:C:C6	30:0:1474:C:C5'	2.89	0.42
30:0:1573:A:H2'	30:0:1574:C:O4'	2.20	0.42
30:0:2332:A:H2'	38:0:5623:HOH:O	2.19	0.42
30:0:2458:U:O2'	30:0:2459:G:H5'	2.20	0.42
30:0:2474:A:N7	30:0:2621:PSU:H4'	2.34	0.42
30:0:2893:C:O2'	30:0:2894:C:H5'	2.19	0.42
1:A:94:LEU:HD12	1:A:98:GLU:CB	2.47	0.42
4:D:167:GLU:C	4:D:169:THR:H	2.28	0.42
10:J:52:GLN:HE21	30:0:1119:G:H5'	1.84	0.42
18:R:89:LEU:HD23	18:R:89:LEU:HA	1.82	0.42
18:R:98:ASN:ND2	30:0:500:G:H21	2.11	0.42
20:T:48:VAL:CG1	20:T:96:VAL:HG13	2.50	0.42
23:W:139:GLY:O	23:W:141:HIS:CD2	2.73	0.42
24:X:10:VAL:HG11	24:X:36:HIS:HE1	1.85	0.42
30:0:191:A:H2'	30:0:237:G:O6	2.20	0.42
30:0:364:U:H2'	30:0:365:G:O4'	2.20	0.42
30:0:1158:G:H2'	30:0:1159:G:C5'	2.50	0.42
30:0:1181:A:N1	30:0:1192:A:O2'	2.45	0.42
30:0:1314:U:H5''	30:0:1316:G:O4'	2.19	0.42
30:0:1538:C:O2'	30:0:1539:U:H5'	2.19	0.42
30:0:1585:C:H2'	30:0:1586:G:C8	2.54	0.42
30:0:1794:G:N2	30:0:1796:A:H3'	2.35	0.42
31:9:29:C:C5	31:9:30:C:C6	3.08	0.42
1:A:20:SER:HB3	30:0:1872:C:H5	1.85	0.41
2:B:49:THR:HG22	2:B:331:SER:HB3	2.02	0.41
6:F:54:VAL:HG13	30:0:263:U:C4	2.55	0.41
8:H:151:GLU:OE1	8:H:151:GLU:HA	2.19	0.41
9:I:91:PHE:CD2	9:I:131:GLY:HA2	2.44	0.41
10:J:42:GLU:HG2	10:J:43:ARG:N	2.34	0.41
23:W:21:LEU:HD21	23:W:48:VAL:CG1	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:41:ARG:HD3	38:Z:8717:HOH:O	2.19	0.41
29:3:44:SER:HA	29:3:49:ASP:CG	2.45	0.41
30:0:299:U:H2'	30:0:300:U:H6	1.85	0.41
30:0:1135:G:H5'	38:0:5913:HOH:O	2.19	0.41
30:0:1316:G:H5''	38:0:5311:HOH:O	2.20	0.41
30:0:1345:A:H2'	30:0:1346:U:H6	1.85	0.41
30:0:1359:U:C5	30:0:2101:A:H8	2.38	0.41
30:0:1531:U:O2	30:0:1661:A:C2	2.73	0.41
30:0:1734:C:O5'	30:0:1734:C:H6	2.03	0.41
31:9:73:A:N1	31:9:108:C:O2	2.53	0.41
1:A:135:VAL:HG11	1:A:147:ARG:HH21	1.85	0.41
11:K:41:LYS:O	11:K:42:ASN:HB2	2.21	0.41
16:P:61:ARG:NH2	30:0:2737:C:OP2	2.45	0.41
20:T:14:ALA:HA	20:T:15:PRO:HD3	1.89	0.41
20:T:52:ARG:O	30:0:317:A:OP1	2.37	0.41
25:Y:154:ARG:NH2	30:0:1071:G:H4'	2.36	0.41
26:Z:65:ASN:ND2	26:Z:84:CYS:SG	2.91	0.41
30:0:34:C:H1'	38:0:9175:HOH:O	2.18	0.41
30:0:257:G:N2	30:0:258:G:C4	2.88	0.41
30:0:559:U:C4	30:0:560:U:C4	3.08	0.41
30:0:567:U:H5''	38:0:6387:HOH:O	2.19	0.41
30:0:820:G:N3	30:0:1831:U:H1'	2.35	0.41
30:0:1333:U:H2'	30:0:1334:C:C6	2.54	0.41
30:0:1405:U:H2'	38:0:6827:HOH:O	2.20	0.41
30:0:1441:G:H1'	38:0:7755:HOH:O	2.19	0.41
30:0:1572:A:C2	30:0:1573:A:C4	3.08	0.41
30:0:1832:G:H5''	38:0:9044:HOH:O	2.19	0.41
30:0:1926:G:C4	30:0:1927:A:C8	3.08	0.41
30:0:1980:U:O2'	30:0:1981:A:H5'	2.20	0.41
30:0:1997:A:C6	30:0:1998:G:C5	3.09	0.41
31:9:3:A:C8	31:9:26:C:O2	2.72	0.41
1:A:51:ARG:NH2	1:A:69:LEU:HD11	2.36	0.41
3:C:19:PRO:HG2	3:C:22:PHE:CE1	2.56	0.41
5:E:101:GLU:HA	5:E:118:ILE:HG13	2.01	0.41
13:M:72:ALA:C	13:M:74:LYS:N	2.77	0.41
15:O:29:VAL:HG11	15:O:98:LEU:HD21	2.02	0.41
18:R:99:ALA:CB	18:R:109:MET:HE1	2.32	0.41
20:T:71:VAL:CG1	20:T:90:PRO:HB3	2.40	0.41
28:2:40:ARG:HD2	28:2:47:THR:HG22	2.01	0.41
30:0:282:C:O2'	30:0:283:U:C4'	2.69	0.41
30:0:778:C:C4	30:0:779:U:C4	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:818:A:C6	30:0:819:A:C2	3.07	0.41
30:0:1116:U:C2'	30:0:1118:A:C2	3.04	0.41
30:0:1168:C:C5	30:0:1169:U:C5	3.09	0.41
30:0:1168:C:C4	30:0:1169:U:C4	3.08	0.41
30:0:2675:A:H1'	30:0:2813:A:C2	2.56	0.41
30:0:2909:G:H2'	30:0:2910:A:H8	1.85	0.41
31:9:39:U:C2'	31:9:40:C:OP1	2.68	0.41
31:9:119:C:H2'	31:9:120:A:C8	2.55	0.41
14:N:40:ASN:HD21	31:9:28:U:H5''	1.83	0.41
14:N:42:HIS:CB	14:N:62:HIS:HE1	2.33	0.41
29:3:69:TYR:CE1	29:3:80:ARG:HB2	2.55	0.41
30:0:271:C:N4	30:0:378:A:C2	2.76	0.41
30:0:546:C:O5'	30:0:546:C:H6	2.03	0.41
30:0:820:G:C5'	30:0:821:U:H5'	2.46	0.41
30:0:1015:C:C2	30:0:1016:U:C5	3.09	0.41
30:0:1246:A:C5	30:0:1248:A:C5	3.09	0.41
30:0:1607:A:C4	30:0:1608:G:C8	3.08	0.41
30:0:2011:A:H5'	30:0:2013:G:H1'	2.01	0.41
30:0:2092:G:H5''	30:0:2613:G:OP1	2.21	0.41
30:0:2874:G:H3'	38:0:9578:HOH:O	2.21	0.41
31:9:7:G:C5'	38:9:9099:HOH:O	2.68	0.41
31:9:31:C:O2'	31:9:32:G:H5'	2.20	0.41
9:I:123:VAL:O	9:I:127:CYS:SG	2.78	0.41
10:J:116:LEU:HB2	10:J:119:THR:HG21	2.02	0.41
13:M:68:ARG:CZ	13:M:73:ARG:HD3	2.51	0.41
16:P:3:LEU:HA	16:P:6:GLN:OE1	2.21	0.41
17:Q:21:ARG:HG2	17:Q:22:GLY:H	1.86	0.41
22:V:12:THR:H	22:V:15:GLU:HB2	1.85	0.41
23:W:117:ARG:HD3	30:0:1287:A:O4'	2.20	0.41
25:Y:187:VAL:HG13	25:Y:205:ILE:HA	2.02	0.41
29:3:46:ILE:HA	38:0:7897:HOH:O	2.20	0.41
30:0:293:A:P	30:0:358:G:H22	2.43	0.41
30:0:488:U:H2'	38:0:4003:HOH:O	2.20	0.41
30:0:652:G:H8	38:0:3003:HOH:O	2.03	0.41
30:0:932:U:H1'	30:0:1296:A:H1'	2.02	0.41
30:0:1183:C:O2	30:0:1183:C:C2'	2.68	0.41
30:0:1191:A:H8	30:0:1191:A:H3'	1.84	0.41
30:0:1335:C:H2'	30:0:1336:U:C6	2.56	0.41
30:0:1545:C:H2'	30:0:1546:G:O4'	2.20	0.41
30:0:2799:A:N6	30:0:2801:A:C2	2.89	0.41
31:9:1:U:O3'	31:9:3:A:OP1	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:9:C:H2'	31:9:10:C:H5'	2.03	0.41
31:9:112:U:H2'	31:9:113:C:H5'	2.02	0.41
3:C:27:ARG:NH1	3:C:27:ARG:CG	2.79	0.41
11:K:34:VAL:CG2	11:K:47:ALA:HB2	2.51	0.41
12:L:6:ARG:NH1	30:0:1299:G:N7	2.68	0.41
13:M:77:HIS:CG	13:M:81:ARG:HB2	2.56	0.41
14:N:23:ARG:O	14:N:27:LEU:HG	2.21	0.41
16:P:80:ARG:HG2	16:P:87:ARG:CZ	2.50	0.41
17:Q:16:ASN:HD22	17:Q:16:ASN:HA	1.67	0.41
23:W:24:LEU:HD21	23:W:44:MET:SD	2.61	0.41
27:1:16:HIS:CD2	30:0:470:U:O2'	2.72	0.41
28:2:2:LYS:HG3	30:0:1486:A:C4	2.55	0.41
29:3:73:GLU:HB3	38:3:9056:HOH:O	2.21	0.41
30:0:69:A:H2'	30:0:70:A:OP2	2.20	0.41
30:0:69:A:C2'	30:0:70:A:OP2	2.69	0.41
30:0:822:C:C2	30:0:823:U:C5	3.08	0.41
30:0:1362:U:H2'	30:0:1363:G:C8	2.55	0.41
30:0:1427:A:O2'	30:0:1428:C:H5'	2.21	0.41
30:0:1563:G:H4'	30:0:1564:C:H5'	2.01	0.41
30:0:1757:U:H5	38:0:3211:HOH:O	2.03	0.41
30:0:1903:U:O2'	30:0:1904:A:C8	2.73	0.41
30:0:1915:U:H2'	30:0:1916:C:O4'	2.21	0.41
30:0:2092:G:H2'	30:0:2613:G:OP1	2.21	0.41
30:0:2409:C:H5''	38:0:4005:HOH:O	2.20	0.41
4:D:84:LEU:HA	4:D:87:ALA:HB3	2.02	0.41
5:E:77:THR:OG1	5:E:78:GLU:N	2.52	0.41
5:E:155:ASN:ND2	5:E:155:ASN:H	2.17	0.41
6:F:60:VAL:O	6:F:61:MET:C	2.64	0.41
7:G:71:LEU:C	7:G:73:ASP:N	2.78	0.41
16:P:13:VAL:HG13	16:P:14:LEU:N	2.36	0.41
23:W:23:MET:O	30:0:1025:C:H5'	2.21	0.41
23:W:38:THR:HG22	38:W:3580:HOH:O	2.21	0.41
30:0:130:C:H2'	38:0:3150:HOH:O	2.21	0.41
30:0:186:A:OP1	30:0:186:A:H4'	2.21	0.41
30:0:396:U:H1'	30:0:397:A:OP1	2.20	0.41
30:0:536:A:N1	30:0:2075:G:O2'	2.50	0.41
30:0:964:G:C4	30:0:965:A:C8	3.08	0.41
30:0:1051:C:H2'	30:0:1052:G:O4'	2.20	0.41
30:0:1339:G:C6	30:0:1340:G:N1	2.89	0.41
30:0:1741:U:HO2'	30:0:2723:G:H4'	1.82	0.41
30:0:1947:G:H2'	30:0:1948:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2872:U:C2	30:0:2873:C:C6	3.08	0.41
30:0:2880:A:H2'	30:0:2881:C:H5'	2.02	0.41
31:9:70:U:H2'	31:9:71:C:O4'	2.20	0.41
3:C:22:PHE:HA	3:C:116:ALA:HA	2.02	0.41
30:0:73:U:O2'	30:0:74:G:H5'	2.21	0.41
30:0:240:C:O2	30:0:240:C:H2'	2.20	0.41
30:0:397:A:H1'	30:0:417:G:H1'	2.03	0.41
30:0:706:G:O2'	30:0:707:C:H6	2.03	0.41
30:0:800:G:H2'	30:0:801:U:C6	2.56	0.41
30:0:1215:A:O3'	30:0:1216:G:C4'	2.69	0.41
30:0:1337:G:C6	30:0:1338:U:C4	3.09	0.41
30:0:1682:A:H5''	38:0:9458:HOH:O	2.20	0.41
30:0:2780:C:C4	30:0:2781:U:C4	3.09	0.41
30:0:2892:G:C6	30:0:2893:C:C4	3.09	0.41
1:A:45:ILE:HD12	26:Z:89:THR:HG23	2.02	0.41
1:A:132:ASP:CG	1:A:133:ARG:N	2.78	0.41
2:B:27:ASN:HD21	30:0:2807:U:P	2.43	0.41
2:B:69:VAL:HA	2:B:70:PRO:HD3	1.82	0.41
2:B:162:MET:HE3	2:B:310:ARG:HD2	2.03	0.41
2:B:274:GLU:HA	2:B:292:GLY:O	2.21	0.41
3:C:44:GLN:HA	38:C:8614:HOH:O	2.21	0.41
3:C:87:ARG:NH2	30:0:894:A:C2	2.89	0.41
4:D:15:GLU:HA	4:D:16:PRO:HD3	1.73	0.41
6:F:57:GLU:O	6:F:61:MET:HG3	2.21	0.41
10:J:45:VAL:HG21	10:J:129:PHE:CD1	2.56	0.41
11:K:75:ARG:HD2	11:K:90:PHE:CD2	2.55	0.41
12:L:53:ARG:HD2	30:0:2441:U:H4'	2.02	0.41
14:N:48:VAL:HG11	14:N:55:ASP:HB3	2.02	0.41
20:T:32:ARG:NH1	20:T:38:ARG:NH1	2.68	0.41
26:Z:54:GLU:HB3	38:Z:8731:HOH:O	2.21	0.41
29:3:29:ARG:HG2	29:3:30:GLN:N	2.35	0.41
29:3:88:LEU:HD22	33:3:8804:CL:CL	2.58	0.41
30:0:37:A:C2	30:0:446:G:C2	3.09	0.41
30:0:99:A:C8	30:0:100:C:C6	3.09	0.41
30:0:210:U:O2'	30:0:211:U:H5'	2.21	0.41
30:0:565:A:N6	30:0:593:A:C8	2.88	0.41
30:0:1244:U:H4'	30:0:1246:A:O4'	2.21	0.41
30:0:1351:G:H1'	38:0:4673:HOH:O	2.21	0.41
30:0:1423:C:O2'	30:0:1424:A:H5'	2.20	0.41
30:0:1523:G:C5	30:0:1524:U:C4	3.08	0.41
30:0:1819:G:C2'	30:0:1820:G:H5'	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1834:C:H2'	30:0:1840:A:H62	1.82	0.41
30:0:2296:C:H2'	30:0:2297:U:C6	2.56	0.41
30:0:2345:A:H3'	30:0:2346:C:C5	2.56	0.41
30:0:2438:G:C6	30:0:2439:C:C4	3.08	0.41
31:9:75:G:H1	31:9:106:U:H3	1.69	0.41
1:A:47:HIS:CD2	30:0:1654:U:C2'	3.02	0.41
2:B:244:PRO:HG3	2:B:248:ARG:NH2	2.35	0.41
3:C:127:ARG:HD3	3:C:129:HIS:CE1	2.56	0.41
4:D:53:LYS:HE3	31:9:40:C:H42	1.85	0.41
13:M:158:ARG:HB2	13:M:163:LEU:HB2	2.02	0.41
13:M:193:LYS:HB3	30:0:392:U:C5'	2.51	0.41
14:N:22:GLN:HG3	30:0:2415:A:H2	1.85	0.41
15:O:68:GLY:HA3	30:0:745:G:O6	2.20	0.41
16:P:81:LYS:HG2	38:0:9540:HOH:O	2.20	0.41
21:U:20:MET:HG3	21:U:28:THR:HG23	2.03	0.41
24:X:43:VAL:HG12	24:X:44:ASP:H	1.84	0.41
25:Y:126:PRO:HG2	25:Y:128:PHE:CZ	2.56	0.41
27:1:38:GLY:HA3	38:1:6935:HOH:O	2.20	0.41
30:0:39:G:C2	30:0:444:C:N3	2.89	0.41
30:0:375:G:C4	30:0:411:A:C6	3.09	0.41
30:0:407:A:H8	38:0:4452:HOH:O	2.04	0.41
30:0:622:G:O2'	30:0:623:U:H5'	2.21	0.41
30:0:685:C:O2	30:0:748:C:H4'	2.21	0.41
30:0:1193:A:C2	30:0:1194:A:N6	2.89	0.41
30:0:1419:U:H2'	30:0:1685:A:C2	2.56	0.41
30:0:1769:C:C2'	30:0:1770:U:H5'	2.51	0.41
30:0:2002:C:C2'	30:0:2003:U:H5'	2.50	0.41
30:0:2064:U:H5'	30:0:2652:U:O3'	2.21	0.41
4:D:172:VAL:HG12	4:D:173:GLU:N	2.36	0.40
8:H:12:ILE:HG12	8:H:59:GLN:HG3	2.02	0.40
10:J:47:THR:O	10:J:53:ILE:HD11	2.21	0.40
13:M:46:LEU:HD22	13:M:50:ARG:HD2	2.03	0.40
13:M:95:LYS:HA	13:M:170:ASN:HD21	1.86	0.40
19:S:42:GLU:HG2	19:S:49:VAL:HG23	2.03	0.40
26:Z:53:ILE:HG23	26:Z:93:TYR:HB3	2.02	0.40
26:Z:54:GLU:HG2	26:Z:57:MET:HE2	2.03	0.40
26:Z:65:ASN:HD22	26:Z:84:CYS:CB	2.33	0.40
30:0:375:G:C2	30:0:411:A:C2	3.08	0.40
30:0:1008:C:H2'	30:0:1009:U:C6	2.56	0.40
30:0:1327:G:C6	30:0:1331:G:C6	3.09	0.40
30:0:1656:A:H2'	30:0:1657:A:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2765:C:H2'	30:0:2766:A:C8	2.56	0.40
31:9:14:G:C8	31:9:14:G:C5'	2.95	0.40
1:A:47:HIS:HA	38:A:9024:HOH:O	2.20	0.40
2:B:112:THR:HA	2:B:158:LYS:HZ2	1.87	0.40
5:E:139:GLU:OE2	30:0:2781:U:C1'	2.68	0.40
5:E:166:VAL:HB	38:E:6341:HOH:O	2.19	0.40
7:G:19:GLU:O	7:G:23:ILE:HG13	2.21	0.40
10:J:127:ILE:HG22	33:J:8801:CL:CL	2.58	0.40
11:K:74:VAL:HG12	11:K:75:ARG:HG3	2.02	0.40
12:L:73:VAL:HG23	12:L:74:THR:H	1.86	0.40
16:P:7:LYS:HD3	16:P:21:VAL:HG22	2.03	0.40
17:Q:80:LYS:HG2	17:Q:82:LYS:HE3	2.02	0.40
23:W:4:LEU:HD23	23:W:4:LEU:HA	1.88	0.40
27:1:28:HIS:CE1	27:1:31:LYS:HE2	2.56	0.40
30:0:245:C:N4	30:0:246:G:C6	2.89	0.40
30:0:559:U:C6	30:0:559:U:H3'	2.57	0.40
30:0:1398:G:H2'	30:0:1399:A:H8	1.85	0.40
30:0:1497:G:H4'	30:0:1627:G:O2'	2.21	0.40
30:0:1531:U:C2	30:0:1661:A:C2	3.10	0.40
30:0:1543:G:N1	30:0:1641:A:OP2	2.41	0.40
30:0:1576:G:H2'	30:0:1577:U:H6	1.87	0.40
30:0:1577:U:O2'	30:0:1578:C:H5'	2.21	0.40
30:0:1589:G:C2	30:0:1605:G:N3	2.89	0.40
30:0:1626:A:H2'	30:0:1627:G:O4'	2.21	0.40
30:0:1947:G:N2	30:0:1966:U:C2	2.89	0.40
30:0:1972:U:O2'	30:0:1973:A:H5''	2.22	0.40
30:0:2319:C:H2'	30:0:2320:U:H5'	2.03	0.40
30:0:2526:C:H3'	30:0:2526:C:H6	1.86	0.40
2:B:148:PRO:HD2	38:B:9047:HOH:O	2.21	0.40
3:C:168:ARG:NH2	3:C:190:ALA:O	2.55	0.40
9:I:78:ALA:HB1	9:I:93:ALA:CB	2.51	0.40
9:I:120:ALA:O	9:I:124:VAL:HG23	2.21	0.40
10:J:57:TYR:O	10:J:61:VAL:HG23	2.21	0.40
12:L:117:GLU:HG2	38:L:9025:HOH:O	2.20	0.40
13:M:64:ARG:HD2	38:M:8879:HOH:O	2.21	0.40
13:M:74:LYS:O	13:M:88:VAL:HG22	2.21	0.40
26:Z:65:ASN:CB	26:Z:84:CYS:SG	3.08	0.40
29:3:3:MET:HE1	29:3:83:TRP:HH2	1.86	0.40
30:0:372:A:H2'	30:0:373:G:H8	1.86	0.40
30:0:464:G:HO2'	30:0:465:U:P	2.44	0.40
30:0:611:U:O5'	30:0:611:U:H6	2.05	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:727:G:N2	30:0:728:C:H1'	2.36	0.40
30:0:1074:G:H4'	30:0:1260:G:C6	2.57	0.40
30:0:1333:U:H2'	30:0:1334:C:H6	1.86	0.40
30:0:1461:U:H1'	38:0:7457:HOH:O	2.21	0.40
30:0:1749:U:O2	30:0:1751:G:C8	2.75	0.40
30:0:1926:G:H2'	30:0:1927:A:H8	1.86	0.40
30:0:2867:G:H2'	30:0:2868:C:H6	1.86	0.40
31:9:2:U:OP2	31:9:2:U:H4'	2.22	0.40
1:A:105:VAL:HG13	1:A:155:THR:O	2.21	0.40
2:B:294:TYR:HE2	38:B:9123:HOH:O	2.03	0.40
6:F:58:GLU:HG3	6:F:61:MET:HE2	2.03	0.40
8:H:8:MET:SD	30:0:2494:G:H4'	2.61	0.40
8:H:91:ARG:O	30:0:1003:U:H4'	2.22	0.40
12:L:56:LYS:NZ	38:L:9036:HOH:O	2.54	0.40
12:L:67:ARG:O	12:L:71:GLU:HG3	2.22	0.40
14:N:58:LEU:HD12	14:N:58:LEU:H	1.85	0.40
16:P:89:ASN:HB3	16:P:92:GLU:HB2	2.03	0.40
24:X:39:LYS:HE2	30:0:2834:G:OP1	2.22	0.40
25:Y:210:GLY:N	30:0:1313:A:H5''	2.36	0.40
26:Z:57:MET:HE3	38:0:6264:HOH:O	2.21	0.40
30:0:113:A:OP2	30:0:114:A:H2'	2.21	0.40
30:0:1936:C:H2'	30:0:1937:U:C6	2.56	0.40
30:0:1982:C:H2'	30:0:1983:C:O4'	2.21	0.40
30:0:2248:C:H2'	30:0:2249:G:C8	2.54	0.40
30:0:2803:C:H2'	30:0:2804:C:H6	1.86	0.40
30:0:2826:G:C6	30:0:2913:A:C6	3.10	0.40
31:9:27:C:C4	31:9:28:U:C5	3.09	0.40
1:A:88:ILE:O	1:A:88:ILE:HG22	2.20	0.40
1:A:164:ARG:NH2	30:0:1877:G:OP1	2.53	0.40
2:B:10:SER:O	2:B:16:ARG:NH1	2.45	0.40
13:M:34:GLU:HB3	13:M:38:GLU:HG3	2.02	0.40
16:P:59:ARG:HD3	38:0:6252:HOH:O	2.22	0.40
20:T:21:LYS:HA	20:T:24:ARG:HD2	2.04	0.40
23:W:139:GLY:O	23:W:141:HIS:HD2	2.04	0.40
30:0:506:G:N2	30:0:509:A:H5'	2.31	0.40
30:0:724:G:O2'	30:0:725:C:H5'	2.21	0.40
30:0:763:C:O2'	30:0:764:C:H5'	2.21	0.40
30:0:1130:U:H4'	38:0:6109:HOH:O	2.21	0.40
30:0:1135:G:O2'	30:0:1136:U:H5'	2.22	0.40
30:0:1163:G:C2	30:0:1184:C:N3	2.89	0.40
30:0:1191:A:H3'	30:0:1191:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1397:C:O2'	30:0:1398:G:H5'	2.22	0.40
30:0:1589:G:H5'	38:0:6843:HOH:O	2.20	0.40
30:0:1815:A:H4'	30:0:2751:C:O4'	2.22	0.40
30:0:2295:G:N3	30:0:2361:A:H2	2.17	0.40
30:0:2321:A:H1'	30:0:2322:U:H3'	2.04	0.40
30:0:2354:A:N1	30:0:2367:A:O2'	2.53	0.40
30:0:2694:A:C6	30:0:2702:A:C8	3.09	0.40
30:0:2803:C:C4	30:0:2804:C:C5	3.10	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	235/240 (98%)	202 (86%)	27 (12%)	6 (3%)	4	12
2	B	335/338 (99%)	309 (92%)	17 (5%)	9 (3%)	4	11
3	C	244/246 (99%)	222 (91%)	20 (8%)	2 (1%)	16	37
4	D	134/177 (76%)	110 (82%)	20 (15%)	4 (3%)	3	9
5	E	170/178 (96%)	157 (92%)	12 (7%)	1 (1%)	21	45
6	F	117/120 (98%)	106 (91%)	7 (6%)	4 (3%)	3	7
7	G	25/348 (7%)	24 (96%)	1 (4%)	0	100	100
8	H	156/177 (88%)	144 (92%)	10 (6%)	2 (1%)	9	26
9	I	68/162 (42%)	52 (76%)	12 (18%)	4 (6%)	1	2
10	J	140/145 (97%)	131 (94%)	8 (6%)	1 (1%)	18	40
11	K	130/132 (98%)	121 (93%)	8 (6%)	1 (1%)	16	37
12	L	141/165 (86%)	120 (85%)	21 (15%)	0	100	100
13	M	192/196 (98%)	179 (93%)	9 (5%)	4 (2%)	5	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	N	184/187 (98%)	163 (89%)	17 (9%)	4 (2%)	5	15
15	O	113/116 (97%)	107 (95%)	6 (5%)	0	100	100
16	P	141/149 (95%)	133 (94%)	8 (6%)	0	100	100
17	Q	93/96 (97%)	85 (91%)	7 (8%)	1 (1%)	11	29
18	R	148/155 (96%)	140 (95%)	7 (5%)	1 (1%)	18	40
19	S	79/85 (93%)	74 (94%)	5 (6%)	0	100	100
20	T	117/120 (98%)	107 (92%)	8 (7%)	2 (2%)	7	20
21	U	51/67 (76%)	42 (82%)	8 (16%)	1 (2%)	6	16
22	V	63/71 (89%)	58 (92%)	5 (8%)	0	100	100
23	W	152/154 (99%)	140 (92%)	10 (7%)	2 (1%)	9	26
24	X	80/92 (87%)	74 (92%)	4 (5%)	2 (2%)	4	13
25	Y	140/241 (58%)	137 (98%)	3 (2%)	0	100	100
26	Z	71/116 (61%)	58 (82%)	8 (11%)	5 (7%)	1	1
27	1	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
28	2	42/50 (84%)	39 (93%)	2 (5%)	1 (2%)	4	13
29	3	90/92 (98%)	74 (82%)	13 (14%)	3 (3%)	3	7
All	All	3705/4472 (83%)	3359 (91%)	286 (8%)	60 (2%)	7	21

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	ASP
1	A	37	VAL
1	A	74	VAL
4	D	65	GLU
4	D	137	PRO
8	H	19	ARG
11	K	127	ALA
13	M	82	ARG
14	N	154	LEU
14	N	183	ASP
14	N	184	ILE
26	Z	105	ARG
29	3	64	LYS
2	B	306	LYS
6	F	61	MET

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Mol	Chain	Res	Type
6	F	101	ALA
13	M	71	SER
21	U	51	TRP
24	X	70	ILE
26	Z	70	ARG
2	B	184	ASP
3	C	8	LEU
5	E	44	GLY
6	F	27	GLY
9	I	83	GLY
20	T	44	ALA
23	W	36	PRO
23	W	49	ASN
24	X	87	ALA
26	Z	67	GLY
29	3	46	ILE
2	B	2	GLN
2	B	107	SER
4	D	56	ARG
9	I	106	GLN
13	M	86	GLN
20	T	46	ASP
26	Z	83	TYR
28	2	37	HIS
1	A	52	SER
1	A	119	ALA
2	B	206	THR
3	C	79	ARG
10	J	65	ASN
13	M	79	ALA
18	R	114	VAL
29	3	56	PRO
2	B	63	GLU
6	F	104	ALA
8	H	171	GLY
14	N	164	ASP
4	D	27	ILE
17	Q	48	PRO
2	B	34	GLY
2	B	169	GLY
26	Z	64	PRO
2	B	185	GLY

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Mol	Chain	Res	Type
9	I	108	HIS
9	I	131	GLY
1	A	42	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	179/182 (98%)	169 (94%)	10 (6%)	19	43
2	B	282/283 (100%)	265 (94%)	17 (6%)	17	40
3	C	193/193 (100%)	180 (93%)	13 (7%)	15	36
4	D	117/148 (79%)	109 (93%)	8 (7%)	14	35
5	E	152/156 (97%)	144 (95%)	8 (5%)	20	45
6	F	93/94 (99%)	93 (100%)	0	100	100
7	G	27/282 (10%)	25 (93%)	2 (7%)	13	32
8	H	134/145 (92%)	126 (94%)	8 (6%)	17	40
9	I	58/130 (45%)	56 (97%)	2 (3%)	32	58
10	J	118/121 (98%)	114 (97%)	4 (3%)	32	58
11	K	106/106 (100%)	103 (97%)	3 (3%)	38	62
12	L	113/127 (89%)	108 (96%)	5 (4%)	25	51
13	M	158/160 (99%)	148 (94%)	10 (6%)	16	38
14	N	149/150 (99%)	141 (95%)	8 (5%)	20	44
15	O	93/94 (99%)	90 (97%)	3 (3%)	34	59
16	P	113/117 (97%)	107 (95%)	6 (5%)	20	45
17	Q	79/80 (99%)	78 (99%)	1 (1%)	61	78
18	R	117/122 (96%)	113 (97%)	4 (3%)	32	58
19	S	71/74 (96%)	68 (96%)	3 (4%)	26	53
20	T	105/106 (99%)	100 (95%)	5 (5%)	23	48
21	U	44/53 (83%)	41 (93%)	3 (7%)	14	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	V	51/57 (90%)	50 (98%)	1 (2%)	48	71
23	W	130/130 (100%)	124 (95%)	6 (5%)	24	50
24	X	66/74 (89%)	63 (96%)	3 (4%)	24	50
25	Y	120/196 (61%)	116 (97%)	4 (3%)	33	58
26	Z	60/94 (64%)	57 (95%)	3 (5%)	22	47
27	1	46/47 (98%)	45 (98%)	1 (2%)	45	69
28	2	42/46 (91%)	41 (98%)	1 (2%)	43	67
29	3	79/79 (100%)	75 (95%)	4 (5%)	21	47
All	All	3095/3646 (85%)	2949 (95%)	146 (5%)	23	49

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

Mol	Chain	Res	Type
1	A	3	ARG
1	A	85	SER
1	A	94	LEU
1	A	131	HIS
1	A	153	ARG
1	A	175	LYS
1	A	179	MET
1	A	192	VAL
1	A	206	ARG
1	A	217	ARG
2	B	2	GLN
2	B	7	ARG
2	B	11	LEU
2	B	27	ASN
2	B	71	VAL
2	B	82	VAL
2	B	97	LEU
2	B	98	THR
2	B	162	MET
2	B	195	ARG
2	B	238	ASN
2	B	248	ARG
2	B	251	VAL
2	B	254	GLN
2	B	265	LEU
2	B	277	GLU

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Mol	Chain	Res	Type
2	B	307	ARG
3	C	2	GLN
3	C	27	ARG
3	C	76	ARG
3	C	88	SER
3	C	136	VAL
3	C	187	ARG
3	C	202	THR
3	C	214	THR
3	C	223	LEU
3	C	234	VAL
3	C	236	THR
3	C	237	GLU
3	C	243	VAL
4	D	19	GLU
4	D	24	HIS
4	D	29	HIS
4	D	50	VAL
4	D	61	PHE
4	D	137	PRO
4	D	153	THR
4	D	161	ASP
5	E	7	ILE
5	E	68	HIS
5	E	86	VAL
5	E	102	VAL
5	E	126	ILE
5	E	134	SER
5	E	154	ILE
5	E	155	ASN
7	G	64	ASN
7	G	73	ASP
8	H	21	GLU
8	H	33	GLN
8	H	61	ARG
8	H	62	HIS
8	H	65	LEU
8	H	87	LYS
8	H	91	ARG
8	H	157	TYR
9	I	114	TYR
9	I	127	CYS

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Mol	Chain	Res	Type
10	J	46	ILE
10	J	52	GLN
10	J	74	ARG
10	J	130	VAL
11	K	10	GLN
11	K	24	THR
11	K	55	VAL
12	L	35	ARG
12	L	99	GLU
12	L	101	ASP
12	L	104	ASP
12	L	114	VAL
13	M	46	LEU
13	M	68	ARG
13	M	73	ARG
13	M	82	ARG
13	M	84	LYS
13	M	86	GLN
13	M	93	ARG
13	M	99	ARG
13	M	125	ARG
13	M	164	THR
14	N	5	ARG
14	N	12	ARG
14	N	49	THR
14	N	56	ASP
14	N	58	LEU
14	N	80	SER
14	N	127	LEU
14	N	180	LEU
15	O	3	THR
15	O	47	ARG
15	O	87	THR
16	P	16	VAL
16	P	21	VAL
16	P	79	SER
16	P	91	LYS
16	P	94	TRP
16	P	98	ILE
17	Q	16	ASN
18	R	13	THR
18	R	39	THR

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Mol	Chain	Res	Type
18	R	128	ARG
18	R	143	VAL
19	S	30	ASP
19	S	44	GLN
19	S	72	ASP
20	T	39	ASN
20	T	82	THR
20	T	96	VAL
20	T	115	GLU
20	T	117	ASP
21	U	25	ASP
21	U	52	THR
21	U	53	ASP
22	V	12	THR
23	W	4	LEU
23	W	26	ILE
23	W	35	VAL
23	W	88	THR
23	W	120	PRO
23	W	146	ILE
24	X	52	PRO
24	X	72	VAL
24	X	79	GLU
25	Y	154	ARG
25	Y	189	ASN
25	Y	203	VAL
25	Y	235	GLU
26	Z	37	ARG
26	Z	70	ARG
26	Z	88	PHE
27	1	21	ARG
28	2	18	ASN
29	3	30	GLN
29	3	36	ILE
29	3	56	PRO
29	3	65	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (99) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	HIS
1	A	199	HIS

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Mol	Chain	Res	Type
2	B	2	GLN
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	286	ASN
2	B	320	GLN
3	C	2	GLN
3	C	67	GLN
3	C	73	GLN
3	C	103	ASN
3	C	129	HIS
4	D	103	ASN
4	D	133	ASN
5	E	55	ASN
5	E	68	HIS
5	E	90	HIS
5	E	106	ASN
5	E	143	GLN
7	G	64	ASN
8	H	40	GLN
8	H	59	GLN
8	H	75	HIS
8	H	131	GLN
9	I	99	GLN
9	I	106	GLN
10	J	25	GLN
10	J	52	GLN
10	J	89	HIS
10	J	107	ASN
10	J	142	ASN
11	K	10	GLN
11	K	35	HIS
11	K	44	HIS
11	K	67	GLN
12	L	18	HIS
12	L	41	HIS
12	L	43	HIS

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Mol	Chain	Res	Type
13	M	24	GLN
13	M	170	ASN
14	N	40	ASN
14	N	53	ASN
14	N	93	GLN
14	N	107	ASN
14	N	132	ASN
14	N	140	GLN
15	O	71	GLN
16	P	66	GLN
16	P	73	HIS
16	P	118	GLN
17	Q	16	ASN
17	Q	27	GLN
17	Q	40	HIS
18	R	61	GLN
18	R	94	ASN
18	R	98	ASN
18	R	117	HIS
19	S	7	HIS
19	S	44	GLN
19	S	53	ASN
19	S	55	GLN
20	T	39	ASN
20	T	73	HIS
21	U	38	ASN
21	U	39	ASN
21	U	48	ASN
22	V	4	HIS
22	V	34	GLN
22	V	60	GLN
23	W	2	HIS
23	W	27	HIS
23	W	28	HIS
23	W	110	GLN
23	W	119	HIS
23	W	141	HIS
24	X	23	HIS
24	X	36	HIS
25	Y	98	GLN
25	Y	119	GLN
25	Y	134	HIS

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Mol	Chain	Res	Type
25	Y	149	GLN
25	Y	189	ASN
26	Z	80	GLN
27	1	8	GLN
27	1	16	HIS
27	1	28	HIS
28	2	16	ASN
28	2	18	ASN
28	2	41	HIS
28	2	45	ASN
29	3	15	ASN
29	3	30	GLN
29	3	48	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	0	2745/2923 (93%)	254 (9%)	21 (0%)
31	9	121/122 (99%)	19 (15%)	2 (1%)
All	All	2866/3045 (94%)	273 (9%)	23 (0%)

All (273) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	0	31	C
30	0	67	A
30	0	69	A
30	0	70	A
30	0	71	G
30	0	86	A
30	0	87	C
30	0	88	G
30	0	114	A
30	0	115	U
30	0	120	A
30	0	130	C
30	0	141	C
30	0	151	A
30	0	166	A
30	0	185	G
30	0	186	A

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Mol	Chain	Res	Type
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	308	U
30	0	309	C
30	0	318	U
30	0	336	G
30	0	337	A
30	0	358	G
30	0	381	G
30	0	397	A
30	0	409	U
30	0	417	G
30	0	461	C
30	0	473	A
30	0	487	G
30	0	498	A
30	0	510	U
30	0	511	A
30	0	514	G
30	0	537	G
30	0	538	C
30	0	539	G
30	0	542	A
30	0	545	G
30	0	553	G
30	0	559	U
30	0	581	G
30	0	588	G
30	0	604	G
30	0	620	A
30	0	632	A
30	0	644	G
30	0	645	U

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Mol	Chain	Res	Type
30	0	660	A
30	0	688	A
30	0	699	C
30	0	701	U
30	0	759	C
30	0	777	U
30	0	809	G
30	0	821	U
30	0	835	U
30	0	840	U
30	0	846	A
30	0	857	A
30	0	858	U
30	0	868	G
30	0	869	G
30	0	871	G
30	0	872	U
30	0	875	A
30	0	877	G
30	0	878	G
30	0	882	A
30	0	884	C
30	0	885	G
30	0	898	G
30	0	905	C
30	0	920	C
30	0	921	G
30	0	923	A
30	0	953	G
30	0	960	G
30	0	961	A
30	0	1006	A
30	0	1008	C
30	0	1029	U
30	0	1045	G
30	0	1059	G
30	0	1060	C
30	0	1072	G
30	0	1081	A
30	0	1088	A
30	0	1109	U
30	0	1110	G

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Mol	Chain	Res	Type
30	0	1119	G
30	0	1130	U
30	0	1137	G
30	0	1151	G
30	0	1164	U
30	0	1165	G
30	0	1166	A
30	0	1174	A
30	0	1175	G
30	0	1185	U
30	0	1192	A
30	0	1193	A
30	0	1205	U
30	0	1206	U
30	0	1216	G
30	0	1234	U
30	0	1238	C
30	0	1239	G
30	0	1242	A
30	0	1279	U
30	0	1289	C
30	0	1331	G
30	0	1342	C
30	0	1353	C
30	0	1360	C
30	0	1377	C
30	0	1378	G
30	0	1407	A
30	0	1474	C
30	0	1485	A
30	0	1488	U
30	0	1505	U
30	0	1506	U
30	0	1524	U
30	0	1525	G
30	0	1526	A
30	0	1528	A
30	0	1559	A
30	0	1562	C
30	0	1592	G
30	0	1625	U
30	0	1626	A

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Mol	Chain	Res	Type
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	1732	A
30	0	1752	G
30	0	1778	A
30	0	1779	A
30	0	1798	C
30	0	1819	G
30	0	1820	G
30	0	1829	A
30	0	1856	C
30	0	1879	U
30	0	1919	A
30	0	1942	A
30	0	1968	A
30	0	1971	G
30	0	1973	A
30	0	1978	A
30	0	1979	G
30	0	1996	U
30	0	2006	C
30	0	2008	U
30	0	2011	A
30	0	2012	U
30	0	2013	G
30	0	2033	G
30	0	2034	U
30	0	2064	U
30	0	2072	G
30	0	2073	G

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Mol	Chain	Res	Type
30	0	2074	A
30	0	2096	A
30	0	2101	A
30	0	2102	G
30	0	2103	A
30	0	2110	G
30	0	2243	C
30	0	2258	A
30	0	2271	G
30	0	2272	G
30	0	2291	A
30	0	2317	C
30	0	2321	A
30	0	2322	U
30	0	2354	A
30	0	2361	A
30	0	2369	A
30	0	2422	U
30	0	2462	G
30	0	2469	A
30	0	2476	C
30	0	2483	A
30	0	2507	G
30	0	2509	A
30	0	2511	A
30	0	2513	A
30	0	2526	C
30	0	2527	U
30	0	2533	C
30	0	2537	G
30	0	2541	U
30	0	2553	A
30	0	2564	G
30	0	2570	G
30	0	2589	U
30	0	2601	A
30	0	2602	G
30	0	2608	C
30	0	2613	G
30	0	2634	G
30	0	2637	A
30	0	2638	G

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Mol	Chain	Res	Type
30	0	2649	A
30	0	2664	A
30	0	2676	C
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	2867	G
30	0	2876	G
30	0	2890	A
30	0	2896	A
30	0	2903	C
30	0	2906	A
30	0	2912	C
30	0	2914	A
31	9	2	U
31	9	7	G
31	9	14	G
31	9	22	G
31	9	23	U
31	9	24	U
31	9	25	G
31	9	34	A
31	9	39	U
31	9	40	C
31	9	41	C
31	9	43	G
31	9	44	A
31	9	52	A
31	9	57	A

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Mol	Chain	Res	Type
31	9	66	G
31	9	77	A
31	9	114	G
31	9	122	C

All (23) RNA pucker outliers are listed below:

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

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

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

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

RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
30	1MA	0	628	35,30	21,25,26	0.74	1 (4%)	30,37,40	0.81	1 (3%)
30	OMG	0	2588	30	23,26,27	0.31	0	32,38,41	0.37	0
30	OMU	0	2587	30	19,22,23	0.39	0	25,31,34	0.42	0
30	UR3	0	2619	30	19,22,23	0.50	0	26,32,35	0.69	1 (3%)
30	PSU	0	2621	30	18,21,22	1.47	2 (11%)	21,30,33	1.41	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	1MA	0	628	35,30	-	2/7/25/26	0/3/3/3
30	OMG	0	2588	30	-	0/9/27/28	0/3/3/3
30	OMU	0	2587	30	-	0/9/27/28	0/2/2/2
30	UR3	0	2619	30	-	0/7/25/26	0/2/2/2
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	4.72	1.42	1.36
30	0	2621	PSU	C6-C5	2.72	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	3.61	120.61	118.17
30	0	2621	PSU	C6-N1-C2	-3.20	119.72	122.69
30	0	2621	PSU	O2-C2-N1	2.98	125.86	122.79
30	0	2619	UR3	C4-N3-C2	2.88	126.90	124.58
30	0	628	1MA	N1-C2-N3	2.72	129.23	126.00

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
30	0	628	1MA	C2'-C1'-N9-C4

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Mol	Chain	Res	Type	Atoms
30	0	628	1MA	C2'-C1'-N9-C8

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	0	2588	OMG	1	0
30	0	2587	OMU	1	0
30	0	2621	PSU	1	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	237/240 (98%)	0.14	8 (3%) 48 41	36, 71, 108, 128	0
2	B	337/338 (99%)	0.06	3 (0%) 81 76	38, 67, 98, 112	0
3	C	246/246 (100%)	-0.12	2 (0%) 82 78	32, 56, 80, 91	0
4	D	140/177 (79%)	1.16	25 (17%) 3 3	89, 121, 144, 151	0
5	E	172/178 (96%)	0.25	8 (4%) 36 30	57, 83, 104, 113	0
6	F	119/120 (99%)	0.31	2 (1%) 69 62	64, 88, 121, 131	0
7	G	29/348 (8%)	0.66	1 (3%) 48 41	92, 107, 116, 118	0
8	H	160/177 (90%)	0.53	10 (6%) 26 22	65, 89, 118, 127	0
9	I	70/162 (43%)	1.96	31 (44%) 0 0	145, 162, 177, 179	0
10	J	142/145 (97%)	0.01	2 (1%) 73 67	47, 63, 86, 105	0
11	K	132/132 (100%)	-0.10	0 100 100	45, 63, 91, 100	0
12	L	145/165 (87%)	0.47	5 (3%) 48 41	41, 88, 131, 140	0
13	M	194/196 (98%)	0.42	24 (12%) 8 8	37, 53, 115, 122	0
14	N	186/187 (99%)	0.47	8 (4%) 40 32	70, 90, 134, 139	0
15	O	115/116 (99%)	0.12	1 (0%) 81 76	46, 64, 81, 87	0
16	P	143/149 (95%)	0.16	4 (2%) 55 47	48, 67, 85, 96	0
17	Q	95/96 (98%)	0.10	4 (4%) 40 33	57, 69, 89, 97	0
18	R	150/155 (96%)	-0.31	1 (0%) 84 80	39, 56, 79, 95	0
19	S	81/85 (95%)	-0.05	1 (1%) 76 71	52, 70, 89, 104	0
20	T	119/120 (99%)	0.04	3 (2%) 58 50	48, 67, 95, 125	0
21	U	53/67 (79%)	1.71	17 (32%) 1 1	112, 125, 131, 134	0
22	V	65/71 (91%)	0.47	7 (10%) 11 10	51, 83, 131, 135	0
23	W	154/154 (100%)	0.04	0 100 100	45, 62, 79, 92	0
24	X	82/92 (89%)	0.14	4 (4%) 35 29	54, 72, 95, 109	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	Y	142/241 (58%)	-0.15	0 100 100	30, 53, 78, 97	0
26	Z	73/116 (62%)	2.39	34 (46%) 0 0	111, 130, 139, 142	0
27	1	56/57 (98%)	-0.64	0 100 100	30, 39, 47, 65	0
28	2	46/50 (92%)	0.36	4 (8%) 16 14	39, 72, 104, 110	0
29	3	92/92 (100%)	2.89	55 (59%) 0 0	123, 135, 142, 148	0
30	0	2749/2923 (94%)	-0.59	14 (0%) 87 83	25, 58, 106, 183	0
31	9	122/122 (100%)	-0.30	2 (1%) 70 63	51, 90, 111, 159	0
All	All	6646/7517 (88%)	-0.06	280 (4%) 40 33	25, 66, 129, 183	0

All (280) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	M	80	GLY	11.9
29	3	84	ARG	8.3
13	M	78	LYS	7.9
9	I	70	THR	7.4
26	Z	42	TYR	7.4
26	Z	50	VAL	7.3
13	M	81	ARG	7.0
26	Z	36	GLY	7.0
9	I	128	THR	7.0
26	Z	45	VAL	6.7
13	M	89	THR	6.6
13	M	74	LYS	6.5
29	3	41	GLU	6.3
13	M	83	SER	6.2
29	3	46	ILE	6.2
13	M	91	ILE	6.2
22	V	1	THR	6.2
29	3	83	TRP	6.2
29	3	34	LYS	6.1
26	Z	38	PHE	6.0
9	I	74	ILE	5.9
29	3	7	PHE	5.9
29	3	32	GLY	5.8
29	3	38	ARG	5.7
26	Z	58	ASN	5.7
21	U	49	LEU	5.7
13	M	76	ARG	5.6
26	Z	35	SER	5.6

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Mol	Chain	Res	Type	RSRZ
13	M	82	ARG	5.5
29	3	33	MET	5.4
26	Z	46	SER	5.4
29	3	48	ASN	5.3
13	M	88	VAL	5.3
29	3	39	GLN	5.3
29	3	79	LEU	5.2
13	M	79	ALA	5.1
26	Z	40	ALA	5.1
13	M	70	GLY	5.0
4	D	10	PHE	4.9
29	3	11	CYS	4.9
13	M	85	ARG	4.9
26	Z	34	SER	4.9
9	I	104	ALA	4.9
29	3	1	MET	4.9
29	3	31	THR	4.8
29	3	3	MET	4.8
13	M	87	GLY	4.8
29	3	60	LYS	4.7
21	U	51	TRP	4.7
26	Z	37	ARG	4.6
29	3	82	GLY	4.6
9	I	71	ALA	4.6
29	3	35	TRP	4.5
29	3	10	TYR	4.5
29	3	47	GLY	4.5
13	M	90	ARG	4.5
8	H	115	GLY	4.4
8	H	171	GLY	4.4
4	D	18	ILE	4.4
8	H	174	LEU	4.4
4	D	63	ILE	4.4
29	3	22	VAL	4.3
29	3	51	LYS	4.3
21	U	39	ASN	4.2
29	3	17	HIS	4.2
9	I	113	SER	4.2
29	3	55	VAL	4.2
29	3	37	ASP	4.2
29	3	4	PRO	4.1
21	U	16	GLY	4.1

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Mol	Chain	Res	Type	RSRZ
8	H	114	ASP	4.1
13	M	73	ARG	4.1
9	I	103	ILE	4.1
29	3	36	ILE	4.1
29	3	12	PRO	4.0
21	U	22	VAL	4.0
13	M	86	GLN	3.9
22	V	2	VAL	3.9
13	M	77	HIS	3.9
26	Z	39	GLY	3.9
5	E	154	ILE	3.9
13	M	72	ALA	3.9
29	3	88	LEU	3.8
29	3	67	LEU	3.8
4	D	135	VAL	3.8
9	I	124	VAL	3.8
30	0	1199	A	3.8
29	3	13	HIS	3.7
28	2	49	GLU	3.7
13	M	71	SER	3.7
13	M	75	ARG	3.7
1	A	32	VAL	3.7
12	L	82	ALA	3.6
9	I	85	GLY	3.6
30	0	1172	G	3.6
21	U	21	PHE	3.6
29	3	81	GLU	3.6
14	N	154	LEU	3.6
26	Z	53	ILE	3.5
31	9	1	U	3.5
29	3	44	SER	3.5
5	E	108	LEU	3.5
9	I	120	ALA	3.5
26	Z	64	PRO	3.5
13	M	84	LYS	3.4
29	3	64	LYS	3.4
22	V	43	PRO	3.4
26	Z	106	SER	3.4
30	0	734	U	3.4
26	Z	82	SER	3.4
29	3	43	ASN	3.4
21	U	42	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
26	Z	78	ILE	3.4
4	D	107	GLY	3.3
30	0	735	C	3.3
13	M	194	GLY	3.3
26	Z	57	MET	3.3
29	3	63	LYS	3.2
26	Z	47	ARG	3.2
29	3	9	THR	3.2
30	0	10	U	3.2
29	3	76	LYS	3.2
28	2	48	ASP	3.2
26	Z	51	ALA	3.2
9	I	100	VAL	3.2
21	U	40	ALA	3.2
29	3	54	LYS	3.1
9	I	127	CYS	3.1
21	U	50	GLU	3.1
29	3	52	PHE	3.1
30	0	1190	G	3.1
9	I	73	LEU	3.1
21	U	52	THR	3.1
1	A	52	SER	3.0
26	Z	55	SER	3.0
21	U	13	ILE	3.0
29	3	56	PRO	3.0
30	0	1171	A	3.0
4	D	35	ALA	3.0
26	Z	43	GLY	3.0
4	D	55	LYS	3.0
20	T	42	VAL	3.0
29	3	69	TYR	3.0
4	D	90	LEU	3.0
8	H	16	ALA	3.0
29	3	62	THR	3.0
19	S	81	ILE	2.9
12	L	60	GLU	2.9
9	I	112	LEU	2.9
4	D	16	PRO	2.9
29	3	42	ARG	2.9
24	X	65	ASN	2.9
29	3	15	ASN	2.9
22	V	39	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
31	9	2	U	2.8
21	U	31	PHE	2.8
9	I	106	GLN	2.8
26	Z	54	GLU	2.8
21	U	38	ASN	2.8
2	B	204	GLY	2.8
4	D	26	GLY	2.8
22	V	44	GLY	2.8
30	0	1160	G	2.8
29	3	65	THR	2.7
7	G	63	ARG	2.7
9	I	107	LYS	2.7
26	Z	71	VAL	2.7
9	I	134	ILE	2.7
10	J	70	PHE	2.7
4	D	174	VAL	2.7
9	I	67	VAL	2.7
26	Z	41	ARG	2.6
4	D	40	ILE	2.6
12	L	48	LYS	2.6
26	Z	70	ARG	2.6
4	D	165	PHE	2.6
14	N	95	ALA	2.6
26	Z	44	ARG	2.6
12	L	83	GLU	2.6
2	B	318	ASN	2.6
18	R	150	PRO	2.5
4	D	69	ILE	2.5
20	T	118	SER	2.5
4	D	68	PRO	2.5
1	A	237	GLY	2.5
13	M	68	ARG	2.5
29	3	6	ARG	2.5
9	I	66	GLY	2.5
12	L	146	GLY	2.5
17	Q	12	GLY	2.5
24	X	85	VAL	2.5
1	A	51	ARG	2.4
16	P	70	ALA	2.4
24	X	87	ALA	2.4
16	P	114	LEU	2.4
26	Z	77	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
4	D	53	LYS	2.4
4	D	146	LYS	2.4
14	N	158	LEU	2.4
8	H	81	GLY	2.4
9	I	132	VAL	2.4
4	D	57	THR	2.4
2	B	1	PRO	2.4
24	X	10	VAL	2.4
26	Z	103	VAL	2.4
3	C	63	SER	2.4
8	H	160	ILE	2.4
1	A	211	LYS	2.3
4	D	17	ARG	2.3
29	3	8	ASN	2.3
21	U	36	CYS	2.3
30	0	1000	C	2.3
29	3	78	HIS	2.3
26	Z	49	ARG	2.3
5	E	156	ASP	2.3
17	Q	20	ASP	2.3
5	E	157	LYS	2.3
30	0	138	U	2.3
30	0	1185	U	2.3
1	A	37	VAL	2.3
20	T	40	VAL	2.3
29	3	57	GLY	2.3
14	N	92	ALA	2.3
16	P	143	ALA	2.3
5	E	118	ILE	2.3
9	I	117	THR	2.3
22	V	38	GLY	2.3
5	E	162	PHE	2.3
21	U	48	ASN	2.3
26	Z	69	ASP	2.3
21	U	35	LYS	2.3
6	F	37	THR	2.3
14	N	2	THR	2.3
29	3	53	SER	2.3
1	A	65	ARG	2.2
14	N	75	THR	2.2
14	N	1	ALA	2.2
26	Z	87	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
17	Q	23	THR	2.2
4	D	128	LEU	2.2
8	H	66	GLU	2.2
8	H	117	ARG	2.2
29	3	61	PRO	2.2
29	3	58	GLY	2.2
28	2	38	LYS	2.2
5	E	6	GLU	2.2
9	I	68	PRO	2.2
9	I	123	VAL	2.2
15	O	51	TYR	2.2
9	I	119	ALA	2.2
9	I	114	TYR	2.1
16	P	58	SER	2.1
28	2	35	ARG	2.1
26	Z	97	THR	2.1
4	D	134	LEU	2.1
9	I	118	ASN	2.1
29	3	49	ASP	2.1
30	0	2769	C	2.1
30	0	1198	U	2.1
21	U	17	THR	2.1
9	I	129	SER	2.0
17	Q	17	LYS	2.0
9	I	95	LEU	2.0
9	I	130	LEU	2.0
3	C	62	GLY	2.0
4	D	104	PHE	2.0
22	V	37	GLY	2.0
30	0	960	G	2.0
1	A	36	ASP	2.0
5	E	10	ASP	2.0
4	D	143	LYS	2.0
6	F	8	VAL	2.0
8	H	143	VAL	2.0
9	I	111	LEU	2.0
9	I	116	LEU	2.0
4	D	61	PHE	2.0
4	D	70	GLY	2.0
26	Z	88	PHE	2.0
14	N	166	ALA	2.0
10	J	45	VAL	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	OMG	0	2588	24/25	0.97	0.06	41,43,46,50	0
30	UR3	0	2619	21/22	0.97	0.06	47,49,51,54	0
30	PSU	0	2621	20/21	0.97	0.06	39,41,53,53	0
30	OMU	0	2587	21/22	0.98	0.07	43,47,50,51	0
30	1MA	0	628	23/24	0.98	0.07	38,44,47,47	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
35	NA	0	8573	1/1	0.61	0.20	73,73,73,73	0
34	SR	0	9006	1/1	0.66	0.33	200,200,200,200	0
34	SR	9	9003	1/1	0.67	0.11	187,187,187,187	0
37	CD	3	8704	1/1	0.67	0.42	200,200,200,200	0
35	NA	0	8525	1/1	0.71	0.36	75,75,75,75	0
32	MG	0	8063	1/1	0.72	0.36	116,116,116,116	0
35	NA	0	8511	1/1	0.73	0.14	81,81,81,81	0
33	CL	3	8804	1/1	0.75	0.15	128,128,128,128	0
34	SR	0	8983	1/1	0.75	0.20	197,197,197,197	0
34	SR	9	8980	1/1	0.76	0.12	183,183,183,183	0
35	NA	0	8556	1/1	0.76	0.21	71,71,71,71	0
35	NA	J	8538	1/1	0.77	0.17	78,78,78,78	0
34	SR	0	8997	1/1	0.77	0.27	189,189,189,189	0
34	SR	0	8976	1/1	0.77	0.21	193,193,193,193	0
34	SR	0	9004	1/1	0.78	0.29	200,200,200,200	0
35	NA	0	8574	1/1	0.78	0.44	60,60,60,60	0
32	MG	0	8082	1/1	0.78	0.12	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	8522	1/1	0.80	0.27	82,82,82,82	0
34	SR	0	8953	1/1	0.80	0.18	200,200,200,200	0
37	CD	Z	8703	1/1	0.81	0.24	200,200,200,200	0
34	SR	L	8969	1/1	0.81	0.32	200,200,200,200	0
35	NA	H	8518	1/1	0.82	0.51	91,91,91,91	0
35	NA	0	8559	1/1	0.83	0.47	77,77,77,77	0
34	SR	0	8959	1/1	0.83	0.08	200,200,200,200	0
32	MG	0	8092	1/1	0.83	0.25	76,76,76,76	0
34	SR	0	8977	1/1	0.83	0.07	200,200,200,200	0
35	NA	0	8557	1/1	0.83	0.16	65,65,65,65	0
34	SR	0	8994	1/1	0.84	0.41	200,200,200,200	0
37	CD	U	8701	1/1	0.84	0.29	200,200,200,200	0
35	NA	0	8528	1/1	0.84	0.21	76,76,76,76	0
33	CL	A	8809	1/1	0.84	0.23	104,104,104,104	0
35	NA	0	8571	1/1	0.85	0.12	79,79,79,79	0
32	MG	0	8090	1/1	0.85	0.20	97,97,97,97	0
35	NA	0	8548	1/1	0.85	0.17	56,56,56,56	0
34	SR	B	8987	1/1	0.85	0.21	200,200,200,200	0
34	SR	0	9001	1/1	0.85	0.09	177,177,177,177	0
34	SR	0	8991	1/1	0.85	0.21	180,180,180,180	0
35	NA	0	8520	1/1	0.86	0.19	56,56,56,56	0
35	NA	0	8563	1/1	0.86	0.63	117,117,117,117	0
34	SR	0	8996	1/1	0.86	0.17	200,200,200,200	0
32	MG	0	8081	1/1	0.86	0.27	88,88,88,88	0
32	MG	A	8051	1/1	0.86	0.10	94,94,94,94	0
34	SR	0	8971	1/1	0.86	0.13	192,192,192,192	0
35	NA	0	8508	1/1	0.86	0.18	52,52,52,52	0
34	SR	3	8999	1/1	0.86	0.12	187,187,187,187	0
34	SR	0	9002	1/1	0.87	0.12	193,193,193,193	0
34	SR	0	8988	1/1	0.87	0.08	173,173,173,173	0
32	MG	B	8042	1/1	0.87	0.18	69,69,69,69	0
34	SR	0	8939	1/1	0.87	0.12	144,144,144,144	0
34	SR	0	8955	1/1	0.88	0.20	200,200,200,200	0
32	MG	0	8089	1/1	0.88	0.09	65,65,65,65	0
34	SR	0	8947	1/1	0.88	0.14	200,200,200,200	0
32	MG	0	8085	1/1	0.88	0.18	76,76,76,76	0
34	SR	0	8992	1/1	0.89	0.27	159,159,159,159	0
34	SR	0	8993	1/1	0.89	0.07	167,167,167,167	0
34	SR	0	8956	1/1	0.89	0.08	169,169,169,169	0
35	NA	0	8562	1/1	0.89	0.39	82,82,82,82	0
32	MG	0	8080	1/1	0.89	0.07	83,83,83,83	0
33	CL	0	8805	1/1	0.89	0.18	98,98,98,98	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
34	SR	0	8922	1/1	0.89	0.15	168,168,168,168	0
33	CL	0	8815	1/1	0.89	0.17	89,89,89,89	0
33	CL	0	8822	1/1	0.89	0.25	88,88,88,88	0
34	SR	A	8930	1/1	0.89	0.11	142,142,142,142	0
32	MG	0	8075	1/1	0.89	0.07	55,55,55,55	0
34	SR	0	8986	1/1	0.90	0.31	200,200,200,200	0
32	MG	0	8040	1/1	0.90	0.22	86,86,86,86	0
34	SR	0	8938	1/1	0.90	0.08	183,183,183,183	0
34	SR	0	8968	1/1	0.90	0.11	177,177,177,177	0
32	MG	0	8032	1/1	0.90	0.07	52,52,52,52	0
34	SR	0	8973	1/1	0.90	0.10	146,146,146,146	0
35	NA	Q	8540	1/1	0.90	0.13	79,79,79,79	0
35	NA	0	8566	1/1	0.90	0.19	63,63,63,63	0
34	SR	3	8932	1/1	0.90	0.24	178,178,178,178	0
32	MG	9	8074	1/1	0.90	0.16	87,87,87,87	0
34	SR	0	9000	1/1	0.90	0.16	183,183,183,183	0
34	SR	0	8979	1/1	0.90	0.12	196,196,196,196	0
35	NA	0	8524	1/1	0.90	0.13	73,73,73,73	0
34	SR	0	8919	1/1	0.90	0.12	168,168,168,168	0
35	NA	0	8536	1/1	0.91	0.05	64,64,64,64	0
34	SR	0	8985	1/1	0.91	0.12	164,164,164,164	0
34	SR	0	8974	1/1	0.91	0.22	166,166,166,166	0
34	SR	0	8975	1/1	0.91	0.10	149,149,149,149	0
35	NA	9	8543	1/1	0.91	0.26	61,61,61,61	0
36	K	0	8401	1/1	0.91	0.30	139,139,139,139	0
34	SR	0	8982	1/1	0.91	0.23	200,200,200,200	0
35	NA	0	8506	1/1	0.91	0.12	83,83,83,83	0
32	MG	T	8057	1/1	0.91	0.18	65,65,65,65	0
33	CL	J	8802	1/1	0.92	0.07	67,67,67,67	0
32	MG	0	8031	1/1	0.92	0.09	83,83,83,83	0
35	NA	0	8529	1/1	0.92	0.08	48,48,48,48	0
35	NA	0	8535	1/1	0.92	0.17	67,67,67,67	0
34	SR	0	9007	1/1	0.92	0.52	200,200,200,200	0
35	NA	0	8544	1/1	0.92	0.34	79,79,79,79	0
34	SR	0	8944	1/1	0.92	0.13	172,172,172,172	0
35	NA	9	8572	1/1	0.92	0.08	88,88,88,88	0
35	NA	0	8550	1/1	0.92	0.13	71,71,71,71	0
34	SR	0	8915	1/1	0.92	0.08	126,126,126,126	0
32	MG	0	8038	1/1	0.92	0.07	74,74,74,74	0
33	CL	J	8801	1/1	0.92	0.10	95,95,95,95	0
35	NA	0	8551	1/1	0.93	0.32	63,63,63,63	0
35	NA	0	8554	1/1	0.93	0.27	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
34	SR	0	8957	1/1	0.93	0.21	200,200,200,200	0
35	NA	B	8552	1/1	0.93	0.23	89,89,89,89	0
35	NA	0	8558	1/1	0.93	0.19	58,58,58,58	0
33	CL	0	8816	1/1	0.93	0.18	85,85,85,85	0
35	NA	0	8560	1/1	0.93	0.20	118,118,118,118	0
35	NA	0	8527	1/1	0.93	0.22	72,72,72,72	0
34	SR	0	8989	1/1	0.93	0.15	178,178,178,178	0
35	NA	0	8564	1/1	0.93	0.09	69,69,69,69	0
34	SR	0	8927	1/1	0.93	0.10	181,181,181,181	0
35	NA	0	8502	1/1	0.93	0.12	69,69,69,69	0
34	SR	0	8970	1/1	0.93	0.08	125,125,125,125	0
35	NA	0	8537	1/1	0.93	0.08	50,50,50,50	0
35	NA	0	8541	1/1	0.93	0.07	64,64,64,64	0
34	SR	0	8933	1/1	0.93	0.10	135,135,135,135	0
35	NA	0	8545	1/1	0.93	0.28	58,58,58,58	0
35	NA	0	8547	1/1	0.93	0.44	67,67,67,67	0
32	MG	0	8030	1/1	0.93	0.25	90,90,90,90	0
32	MG	0	8037	1/1	0.93	0.26	77,77,77,77	0
35	NA	0	8555	1/1	0.94	0.13	52,52,52,52	0
32	MG	0	8071	1/1	0.94	0.18	60,60,60,60	0
32	MG	0	8073	1/1	0.94	0.22	72,72,72,72	0
32	MG	0	8047	1/1	0.94	0.19	66,66,66,66	0
32	MG	0	8077	1/1	0.94	0.07	48,48,48,48	0
34	SR	0	8958	1/1	0.94	0.06	116,116,116,116	0
32	MG	0	8053	1/1	0.94	0.08	63,63,63,63	0
32	MG	0	8055	1/1	0.94	0.10	62,62,62,62	0
34	SR	B	8950	1/1	0.94	0.10	130,130,130,130	0
32	MG	0	8035	1/1	0.94	0.12	66,66,66,66	0
35	NA	0	8570	1/1	0.94	0.12	61,61,61,61	0
34	SR	F	9005	1/1	0.94	0.07	147,147,147,147	0
34	SR	H	8972	1/1	0.94	0.18	164,164,164,164	0
35	NA	R	8532	1/1	0.94	0.11	50,50,50,50	0
35	NA	S	8510	1/1	0.94	0.06	44,44,44,44	0
34	SR	0	8946	1/1	0.94	0.07	137,137,137,137	0
32	MG	0	8083	1/1	0.94	0.15	55,55,55,55	0
34	SR	0	8998	1/1	0.94	0.19	178,178,178,178	0
34	SR	0	8951	1/1	0.94	0.07	155,155,155,155	0
35	NA	0	8514	1/1	0.94	0.15	55,55,55,55	0
32	MG	0	8069	1/1	0.95	0.24	102,102,102,102	0
33	CL	N	8807	1/1	0.95	0.17	87,87,87,87	0
35	NA	0	8561	1/1	0.95	0.34	65,65,65,65	0
35	NA	0	8509	1/1	0.95	0.11	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
34	SR	A	8929	1/1	0.95	0.23	139,139,139,139	0
32	MG	0	8078	1/1	0.95	0.11	65,65,65,65	0
35	NA	0	8565	1/1	0.95	0.15	78,78,78,78	0
32	MG	0	8064	1/1	0.95	0.06	45,45,45,45	0
35	NA	0	8546	1/1	0.95	0.12	94,94,94,94	0
35	NA	0	8521	1/1	0.95	0.11	64,64,64,64	0
34	SR	0	8962	1/1	0.95	0.12	172,172,172,172	0
34	SR	0	8967	1/1	0.95	0.10	131,131,131,131	0
33	CL	0	8814	1/1	0.95	0.15	79,79,79,79	0
35	NA	0	8526	1/1	0.95	0.05	46,46,46,46	0
36	K	M	8402	1/1	0.95	0.13	87,87,87,87	0
34	SR	0	8920	1/1	0.95	0.07	127,127,127,127	0
32	MG	0	8091	1/1	0.95	0.06	56,56,56,56	0
34	SR	0	8926	1/1	0.95	0.08	122,122,122,122	0
35	NA	0	8533	1/1	0.95	0.13	70,70,70,70	0
35	NA	0	8542	1/1	0.96	0.27	58,58,58,58	0
35	NA	C	8503	1/1	0.96	0.06	46,46,46,46	0
32	MG	0	8067	1/1	0.96	0.04	35,35,35,35	0
33	CL	O	8808	1/1	0.96	0.09	86,86,86,86	0
35	NA	M	8539	1/1	0.96	0.07	42,42,42,42	0
34	SR	0	8984	1/1	0.96	0.07	119,119,119,119	0
32	MG	0	8039	1/1	0.96	0.12	84,84,84,84	0
34	SR	S	8961	1/1	0.96	0.07	128,128,128,128	0
35	NA	0	8553	1/1	0.96	0.25	89,89,89,89	0
33	CL	0	8803	1/1	0.96	0.12	60,60,60,60	0
35	NA	0	8505	1/1	0.96	0.36	53,53,53,53	0
32	MG	0	8020	1/1	0.96	0.18	41,41,41,41	0
35	NA	0	8507	1/1	0.96	0.11	43,43,43,43	0
34	SR	0	8910	1/1	0.96	0.05	108,108,108,108	0
33	CL	0	8811	1/1	0.96	0.11	81,81,81,81	0
34	SR	0	8917	1/1	0.96	0.07	114,114,114,114	0
35	NA	0	8513	1/1	0.96	0.18	68,68,68,68	0
32	MG	0	8033	1/1	0.96	0.07	63,63,63,63	0
34	SR	0	8995	1/1	0.96	0.10	150,150,150,150	0
32	MG	0	8049	1/1	0.96	0.07	64,64,64,64	0
34	SR	0	8963	1/1	0.96	0.04	133,133,133,133	0
32	MG	0	8026	1/1	0.96	0.04	50,50,50,50	0
35	NA	0	8567	1/1	0.96	0.20	78,78,78,78	0
35	NA	0	8568	1/1	0.96	0.13	54,54,54,54	0
35	NA	0	8569	1/1	0.96	0.11	50,50,50,50	0
34	SR	0	8924	1/1	0.96	0.13	124,124,124,124	0
32	MG	0	8036	1/1	0.96	0.09	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	MG	Y	8086	1/1	0.96	0.04	50,50,50,50	0
34	SR	0	8928	1/1	0.96	0.06	137,137,137,137	0
35	NA	0	8575	1/1	0.96	0.20	103,103,103,103	0
33	CL	B	8819	1/1	0.96	0.12	69,69,69,69	0
35	NA	0	8530	1/1	0.96	0.15	74,74,74,74	0
32	MG	0	8017	1/1	0.96	0.07	40,40,40,40	0
34	SR	9	8978	1/1	0.96	0.06	157,157,157,157	0
32	MG	0	8066	1/1	0.96	0.14	69,69,69,69	0
34	SR	0	8941	1/1	0.96	0.07	114,114,114,114	0
34	SR	0	8942	1/1	0.96	0.06	124,124,124,124	0
35	NA	0	8516	1/1	0.97	0.14	39,39,39,39	0
32	MG	0	8052	1/1	0.97	0.04	44,44,44,44	0
34	SR	0	8914	1/1	0.97	0.11	133,133,133,133	0
32	MG	0	8072	1/1	0.97	0.03	59,59,59,59	0
35	NA	0	8523	1/1	0.97	0.14	54,54,54,54	0
34	SR	0	8916	1/1	0.97	0.09	105,105,105,105	0
34	SR	0	8981	1/1	0.97	0.11	161,161,161,161	0
32	MG	0	8029	1/1	0.97	0.25	59,59,59,59	0
34	SR	0	8954	1/1	0.97	0.06	108,108,108,108	0
33	CL	0	8817	1/1	0.97	0.05	72,72,72,72	0
32	MG	0	8043	1/1	0.97	0.08	52,52,52,52	0
33	CL	J	8821	1/1	0.97	0.08	77,77,77,77	0
33	CL	M	8818	1/1	0.97	0.06	49,49,49,49	0
32	MG	0	8087	1/1	0.97	0.04	38,38,38,38	0
34	SR	0	8960	1/1	0.97	0.06	151,151,151,151	0
32	MG	0	8076	1/1	0.97	0.04	40,40,40,40	0
35	NA	0	8501	1/1	0.97	0.09	39,39,39,39	0
33	CL	Y	8820	1/1	0.97	0.07	52,52,52,52	0
34	SR	0	8964	1/1	0.97	0.05	134,134,134,134	0
34	SR	0	8965	1/1	0.97	0.07	134,134,134,134	0
32	MG	0	8056	1/1	0.97	0.06	57,57,57,57	0
34	SR	0	8935	1/1	0.97	0.04	103,103,103,103	0
32	MG	0	8060	1/1	0.97	0.05	53,53,53,53	0
32	MG	0	8079	1/1	0.97	0.10	66,66,66,66	0
35	NA	0	8512	1/1	0.97	0.08	56,56,56,56	0
32	MG	0	8070	1/1	0.97	0.06	66,66,66,66	0
33	CL	0	8813	1/1	0.97	0.05	60,60,60,60	0
34	SR	0	8936	1/1	0.98	0.04	95,95,95,95	0
32	MG	0	8003	1/1	0.98	0.07	38,38,38,38	0
32	MG	0	8024	1/1	0.98	0.10	62,62,62,62	0
34	SR	0	8990	1/1	0.98	0.06	137,137,137,137	0
32	MG	0	8010	1/1	0.98	0.06	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
34	SR	0	8966	1/1	0.98	0.05	105,105,105,105	0
32	MG	0	8068	1/1	0.98	0.04	56,56,56,56	0
34	SR	0	8943	1/1	0.98	0.06	84,84,84,84	0
32	MG	0	8034	1/1	0.98	0.05	50,50,50,50	0
35	NA	0	8531	1/1	0.98	0.04	39,39,39,39	0
32	MG	0	8016	1/1	0.98	0.06	40,40,40,40	0
35	NA	0	8534	1/1	0.98	0.06	50,50,50,50	0
34	SR	0	8921	1/1	0.98	0.05	83,83,83,83	0
34	SR	0	8948	1/1	0.98	0.05	115,115,115,115	0
33	CL	L	8810	1/1	0.98	0.05	64,64,64,64	0
34	SR	R	8912	1/1	0.98	0.05	95,95,95,95	0
34	SR	0	8925	1/1	0.98	0.07	98,98,98,98	0
32	MG	0	8044	1/1	0.98	0.05	58,58,58,58	0
34	SR	1	8952	1/1	0.98	0.04	90,90,90,90	0
32	MG	A	8050	1/1	0.98	0.03	64,64,64,64	0
34	SR	0	9008	1/1	0.98	0.03	92,92,92,92	0
34	SR	0	8931	1/1	0.98	0.05	111,111,111,111	0
35	NA	0	8549	1/1	0.98	0.19	56,56,56,56	0
35	NA	0	8517	1/1	0.98	0.04	38,38,38,38	0
37	CD	O	8705	1/1	0.98	0.04	100,100,100,100	0
35	NA	0	8519	1/1	0.98	0.07	52,52,52,52	0
32	MG	0	8093	1/1	0.98	0.03	36,36,36,36	0
33	CL	R	8806	1/1	0.98	0.06	58,58,58,58	0
34	SR	0	8923	1/1	0.99	0.02	109,109,109,109	0
32	MG	0	8048	1/1	0.99	0.09	29,29,29,29	0
32	MG	0	8018	1/1	0.99	0.08	33,33,33,33	0
32	MG	0	8006	1/1	0.99	0.04	44,44,44,44	0
32	MG	0	8021	1/1	0.99	0.04	33,33,33,33	0
32	MG	0	8009	1/1	0.99	0.10	34,34,34,34	0
32	MG	0	8025	1/1	0.99	0.02	37,37,37,37	0
32	MG	0	8058	1/1	0.99	0.02	18,18,18,18	0
34	SR	0	8934	1/1	0.99	0.09	133,133,133,133	0
35	NA	0	8504	1/1	0.99	0.04	40,40,40,40	0
32	MG	0	8059	1/1	0.99	0.05	51,51,51,51	0
32	MG	0	8002	1/1	0.99	0.04	40,40,40,40	0
34	SR	0	8937	1/1	0.99	0.05	113,113,113,113	0
32	MG	0	8061	1/1	0.99	0.03	36,36,36,36	0
34	SR	1	8913	1/1	0.99	0.06	95,95,95,95	0
34	SR	0	8940	1/1	0.99	0.03	93,93,93,93	0
32	MG	0	8062	1/1	0.99	0.09	56,56,56,56	0
32	MG	0	8027	1/1	0.99	0.04	47,47,47,47	0
32	MG	0	8084	1/1	0.99	0.09	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	8515	1/1	0.99	0.04	32,32,32,32	0
34	SR	0	8901	1/1	0.99	0.05	66,66,66,66	0
34	SR	0	8945	1/1	0.99	0.04	105,105,105,105	0
34	SR	0	8902	1/1	0.99	0.02	68,68,68,68	0
34	SR	0	8904	1/1	0.99	0.08	57,57,57,57	0
34	SR	0	8905	1/1	0.99	0.13	72,72,72,72	0
34	SR	0	8949	1/1	0.99	0.04	117,117,117,117	0
34	SR	0	8907	1/1	0.99	0.02	63,63,63,63	0
34	SR	0	8908	1/1	0.99	0.04	85,85,85,85	0
34	SR	0	8909	1/1	0.99	0.07	93,93,93,93	0
32	MG	0	8014	1/1	0.99	0.09	37,37,37,37	0
34	SR	0	8911	1/1	0.99	0.03	88,88,88,88	0
32	MG	0	8065	1/1	0.99	0.03	42,42,42,42	0
32	MG	0	8088	1/1	0.99	0.02	35,35,35,35	0
33	CL	0	8812	1/1	0.99	0.06	61,61,61,61	0
32	MG	0	8041	1/1	0.99	0.05	36,36,36,36	0
34	SR	0	8918	1/1	0.99	0.02	85,85,85,85	0
32	MG	0	8015	1/1	0.99	0.04	45,45,45,45	0
32	MG	K	8054	1/1	0.99	0.07	57,57,57,57	0
32	MG	0	8046	1/1	0.99	0.04	45,45,45,45	0
32	MG	0	8005	1/1	0.99	0.08	42,42,42,42	0
32	MG	0	8022	1/1	1.00	0.08	33,33,33,33	0
32	MG	0	8023	1/1	1.00	0.05	28,28,28,28	0
32	MG	0	8007	1/1	1.00	0.03	36,36,36,36	0
32	MG	0	8008	1/1	1.00	0.06	31,31,31,31	0
32	MG	0	8001	1/1	1.00	0.03	36,36,36,36	0
32	MG	0	8004	1/1	1.00	0.01	29,29,29,29	0
32	MG	0	8028	1/1	1.00	0.04	34,34,34,34	0
32	MG	0	8011	1/1	1.00	0.04	25,25,25,25	0
34	SR	0	8903	1/1	1.00	0.08	57,57,57,57	0
32	MG	0	8019	1/1	1.00	0.05	29,29,29,29	0
32	MG	0	8012	1/1	1.00	0.02	25,25,25,25	0
34	SR	0	8906	1/1	1.00	0.04	67,67,67,67	0
32	MG	0	8013	1/1	1.00	0.02	28,28,28,28	0
37	CD	1	8702	1/1	1.00	0.05	61,61,61,61	0
32	MG	0	8045	1/1	1.00	0.02	31,31,31,31	0

6.5 Other polymers

There are no such residues in this entry.