Full wwPDB X-ray Structure Validation Report

Jan 31, 2016 – 08:55 PM GMT

PDB ID	:	1M1K
Title	:	Co-crystal structure of azithromycin bound to the 50S ribosomal subunit of Haloarcula marismortui
Authors	:	Hansen, J.L.; Ippolito, J.A.; Ban, N.; Nissen, P.; Moore, P.B.; Steitz, T.A.
Deposited on	:	2002-06-19
Resolution	:	3.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

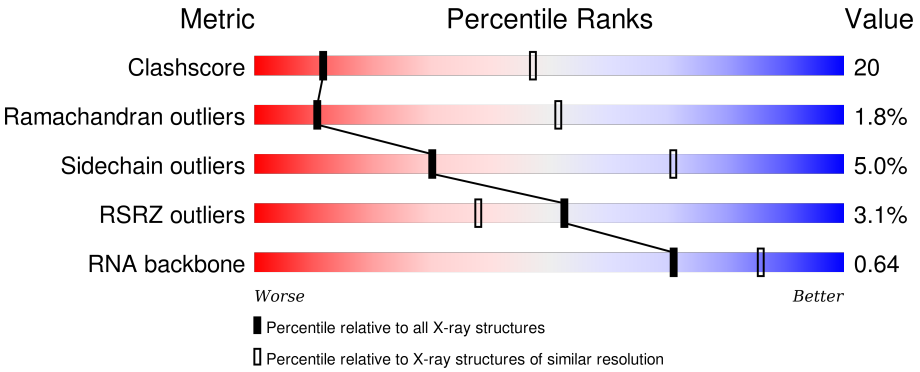
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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))
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)
RNA backbone	2183	1079 (3.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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 <=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	2922	51% 36% 7% • 6%
2	B	122	5% 43% 42% 9% 6%
3	C	239	5% 52% 42% 5% •
4	D	337	51% 43% 6%
5	E	246	61% 34% 6%

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Mol	Chain	Length	Quality of chain
6	F	176	26% 20% 49% 9% 20%
7	G	177	2% 56% 40%
8	H	119	9% 54% 45%
9	I	348	3% 5% 92%
10	J	167	1% 34% 52% 7% 7%
11	K	145	59% 34% 6%
12	L	132	61% 39%
13	M	164	9% 50% 38% 12%
14	N	194	1% 43% 51% 6%
15	O	186	8% 42% 52% 6%
16	P	115	60% 38%
17	Q	148	3% 66% 30%
18	R	95	66% 32%
19	S	154	61% 34%
20	T	84	1% 73% 24%
21	U	119	5% 54% 43%
22	V	66	41% 39% 20%
23	W	70	20% 46% 44% 7%
24	X	154	48% 47% 5%
25	Y	91	1% 44% 41% 5% 10%
26	Z	240	40% 16% 41%
27	1	73	7% 40% 55% 5%
28	2	56	61% 39%
29	3	48	2% 46% 48%
30	4	92	4% 63% 34%

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
31	ZIT	A	8600	-	-	-	X
32	MG	A	8024	-	-	-	X
32	MG	A	8044	-	-	-	X
32	MG	A	8060	-	-	-	X
32	MG	A	8064	-	-	-	X
32	MG	A	8066	-	-	-	X
34	NA	A	8303	-	-	-	X
34	NA	A	8305	-	-	-	X
34	NA	A	8321	-	-	-	X
34	NA	A	8323	-	-	-	X
34	NA	A	8325	-	-	-	X
34	NA	A	8326	-	-	-	X
34	NA	A	8331	-	-	-	X
34	NA	A	8335	-	-	-	X
34	NA	A	8350	-	-	-	X
34	NA	A	8356	-	-	-	X
34	NA	A	8359	-	-	-	X
34	NA	A	8361	-	-	-	X
34	NA	A	8362	-	-	-	X
34	NA	A	8364	-	-	-	X
34	NA	A	8365	-	-	-	X
34	NA	A	8366	-	-	-	X
34	NA	A	8368	-	-	-	X
34	NA	A	8369	-	-	-	X
34	NA	A	8371	-	-	-	X
34	NA	A	8372	-	-	-	X
34	NA	A	8373	-	-	-	X
34	NA	A	8374	-	-	-	X
34	NA	A	8376	-	-	-	X
34	NA	A	8377	-	-	-	X
34	NA	A	8378	-	-	-	X
34	NA	A	8382	-	-	-	X
34	NA	B	8383	-	-	-	X
34	NA	M	8380	-	-	-	X
34	NA	S	8386	-	-	-	X
35	CL	4	8504	-	-	-	X
35	CL	A	8505	-	-	-	X
35	CL	A	8513	-	-	X	-
35	CL	A	8515	-	-	-	X
35	CL	D	8519	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	CL	K	8502	-	-	X	-
35	CL	N	8518	-	-	X	-
35	CL	O	8507	-	-	X	-

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 98587 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 RNA chain called 23S RRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	2754	59017	26346	10878	19048	2745	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	560	C	U	CONFLICT	GB 3377779

- Molecule 2 is a RNA chain called 5S RRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	122	2600	1160	472	847	121	0	0	0

- Molecule 3 is a protein called RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	237	1754	1072	352	325	5	0	0	0

- Molecule 4 is a protein called RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	337	2624	1616	493	510	5	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	PRO	DELETION	UNP P20279
D	310	ARG	PHE	CONFLICT	UNP P20279

- Molecule 5 is a protein called RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	246	Total	C	N	O	S	0	0	0
			1858	1131	344	382	1			

- Molecule 6 is a protein called RIBOSOMAL PROTEIN L5.

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

- Molecule 7 is a protein called RIBOSOMAL PROTEIN L6.

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

- Molecule 8 is a protein called RIBOSOMAL PROTEIN L7AE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	119	Total	C	N	O	S	0	0	0
			885	552	141	191	1			

- Molecule 9 is a protein called RIBOSOMAL PROTEIN L10.

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

- Molecule 10 is a protein called RIBOSOMAL PROTEIN L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	156	Total	C	N	O	S	0	0	0
			1215	766	233	212	4			

- Molecule 11 is a protein called RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	142	Total	C	N	O	S	0	0	0
			1119	696	199	221	3			

- Molecule 12 is a protein called RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	132	Total	C	N	O	S	0	0	0
			993	609	189	191	4			

- Molecule 13 is a protein called RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	M	145	Total	C	N	O	0	0	0
			1114	668	222	224			

- Molecule 14 is a protein called RIBOSOMAL PROTEIN L15E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	194	Total	C	N	O	S	0	0	0
			1605	988	346	266	5			

- Molecule 15 is a protein called RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	186	Total	C	N	O	S	0	0	0
			1444	895	262	285	2			

- Molecule 16 is a protein called RIBOSOMAL PROTEIN L18E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
16	P	115	Total	C	N	O	0	0	0
			864	529	161	174			

- Molecule 17 is a protein called RIBOSOMAL PROTEIN L19E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	Q	143	Total	C	N	O	0	0	0
			1133	680	230	223			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	71	LYS	TYR	CONFLICT	UNP P14119

- Molecule 18 is a protein called RIBOSOMAL PROTEIN L21E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	95	Total	C	N	O	0	0	0
			734	450	141	143			

- Molecule 19 is a protein called RIBOSOMAL PROTEIN L22.

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

- Molecule 20 is a protein called RIBOSOMAL PROTEIN L23.

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

- Molecule 21 is a protein called RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	U	119	Total	C	N	O	0	0	0
			949	568	180	201			

- Molecule 22 is a protein called RIBOSOMAL PROTEIN L24E.

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

- Molecule 23 is a protein called RIBOSOMAL PROTEIN L29.

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

- Molecule 24 is a protein called RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	X	154	Total	C	N	O	S	0	0	0
			1195	737	209	243	6			

- Molecule 25 is a protein called RIBOSOMAL PROTEIN L31E.

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

- Molecule 26 is a protein called RIBOSOMAL PROTEIN L32E.

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

- Molecule 27 is a protein called RIBOSOMAL PROTEIN L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	1	73	Total	C	N	O	S	0	0	0
			563	359	111	86	7			

- Molecule 28 is a protein called RIBOSOMAL PROTEIN L37E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	2	56	Total	C	N	O	S	0	0	0
			430	258	86	82	4			

- Molecule 29 is a protein called RIBOSOMAL PROTEIN L39E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	3	46	Total	C	N	O	S	0	0	0
			393	238	86	68	1			

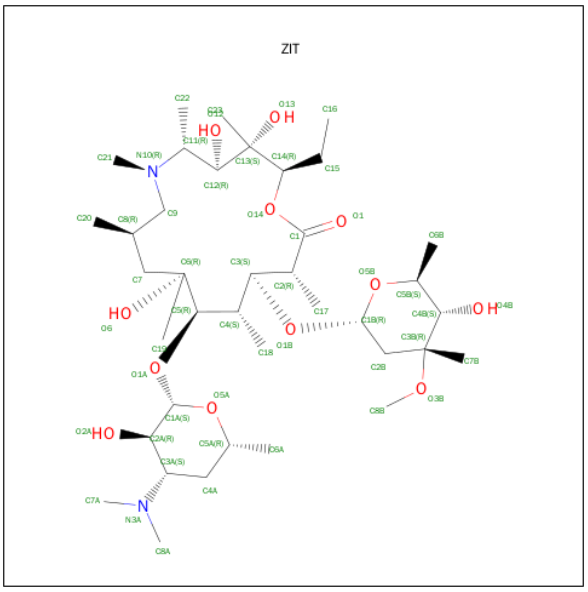
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	?	-	ARG	DELETION	UNP P22452

- Molecule 30 is a protein called RIBOSOMAL PROTEIN L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	4	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 31 is AZITHROMYCIN (three-letter code: ZIT) (formula: $C_{38}H_{72}N_2O_{12}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
31	A	1	Total C N O 52 38 2 12	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
32	1	1	Total Mg 1 1	0	0
32	D	1	Total Mg 1 1	0	0
32	B	1	Total Mg 1 1	0	0
32	C	1	Total Mg 1 1	0	0
32	Z	1	Total Mg 1 1	0	0
32	A	109	Total Mg 109 109	0	0
32	4	1	Total Mg 1 1	0	0
32	U	1	Total Mg 1 1	0	0
32	L	1	Total Mg 1 1	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
33	A	2	Total K 2 2	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
34	J	2	Total Na 2 2	0	0
34	K	1	Total Na 1 1	0	0
34	E	1	Total Na 1 1	0	0
34	B	2	Total Na 2 2	0	0
34	C	1	Total Na 1 1	0	0
34	A	71	Total Na 71 71	0	0
34	T	1	Total Na 1 1	0	0
34	N	1	Total Na 1 1	0	0
34	U	1	Total Na 1 1	0	0
34	R	1	Total Na 1 1	0	0
34	S	3	Total Na 3 3	0	0
34	M	1	Total Na 1 1	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
35	P	1	Total Cl 1 1	0	0
35	D	1	Total Cl 1 1	0	0
35	K	4	Total Cl 4 4	0	0
35	C	1	Total Cl 1 1	0	0
35	A	9	Total Cl 9 9	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
35	4	1	Total Cl 1 1	0	0
35	N	1	Total Cl 1 1	0	0
35	O	1	Total Cl 1 1	0	0
35	R	1	Total Cl 1 1	0	0
35	L	1	Total Cl 1 1	0	0
35	S	1	Total Cl 1 1	0	0

- Molecule 36 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
36	P	1	Total Cd 1 1	0	0
36	2	1	Total Cd 1 1	0	0
36	1	1	Total Cd 1 1	0	0
36	4	1	Total Cd 1 1	0	0
36	V	1	Total Cd 1 1	0	0

- Molecule 37 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
37	A	5898	Total O 5898 5898	0	0
37	B	140	Total O 140 140	0	0
37	C	129	Total O 129 129	0	0
37	D	152	Total O 152 152	0	0
37	E	169	Total O 169 169	0	0
37	F	52	Total O 52 52	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
37	G	42	Total O 42 42	0	0
37	H	28	Total O 28 28	0	0
37	I	21	Total O 21 21	0	0
37	J	81	Total O 81 81	0	0
37	K	56	Total O 56 56	0	0
37	L	61	Total O 61 61	0	0
37	M	81	Total O 81 81	0	0
37	N	129	Total O 129 129	0	0
37	O	68	Total O 68 68	0	0
37	P	45	Total O 45 45	0	0
37	Q	69	Total O 69 69	0	0
37	R	56	Total O 56 56	0	0
37	S	89	Total O 89 89	0	0
37	T	36	Total O 36 36	0	0
37	U	39	Total O 39 39	0	0
37	V	27	Total O 27 27	0	0
37	W	15	Total O 15 15	0	0
37	X	73	Total O 73 73	0	0
37	Y	30	Total O 30 30	0	0
37	Z	93	Total O 93 93	0	0
37	1	38	Total O 38 38	0	0

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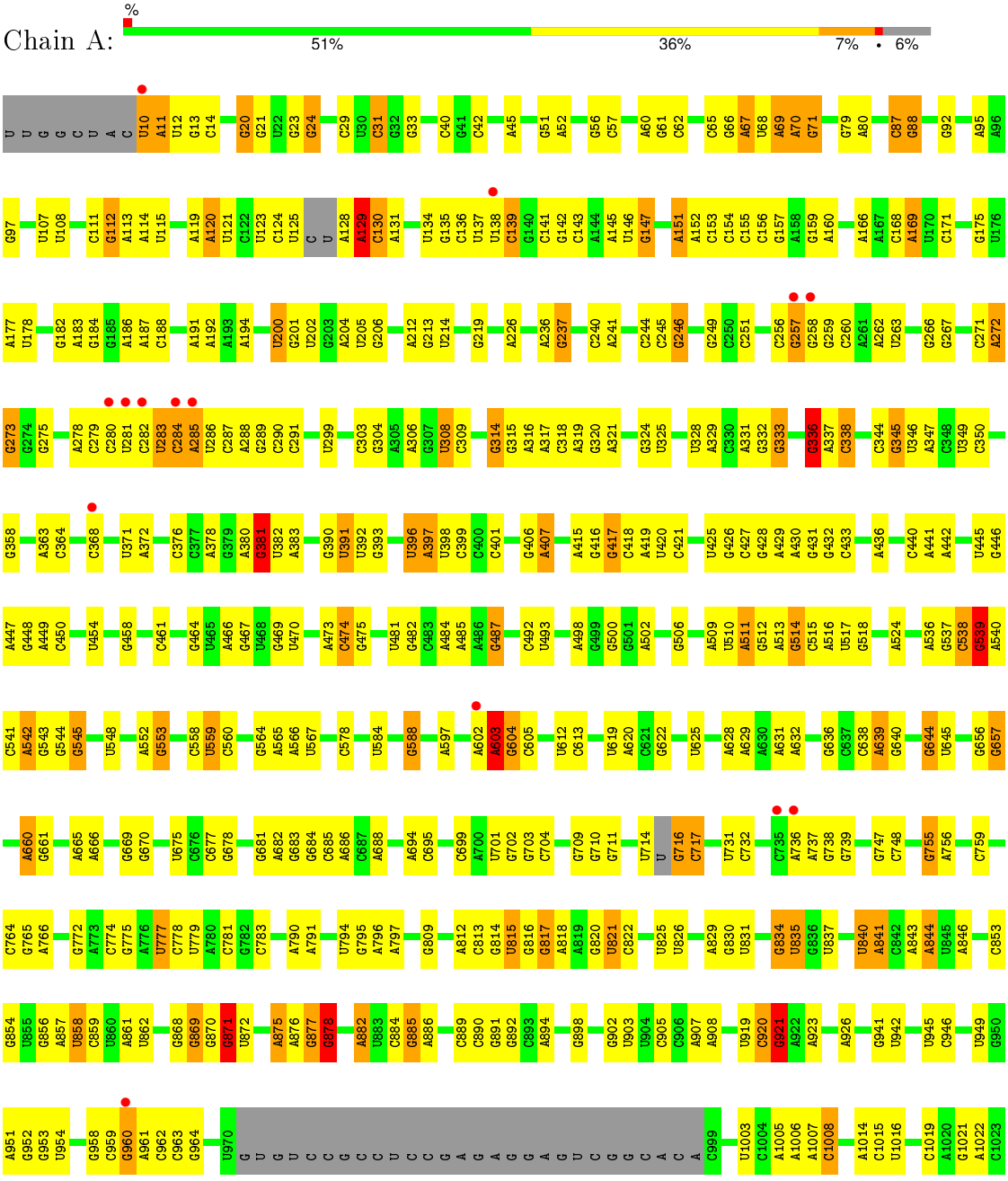
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
37	2	57	Total O 57 57	0	0
37	3	39	Total O 39 39	0	0
37	4	72	Total O 72 72	0	0

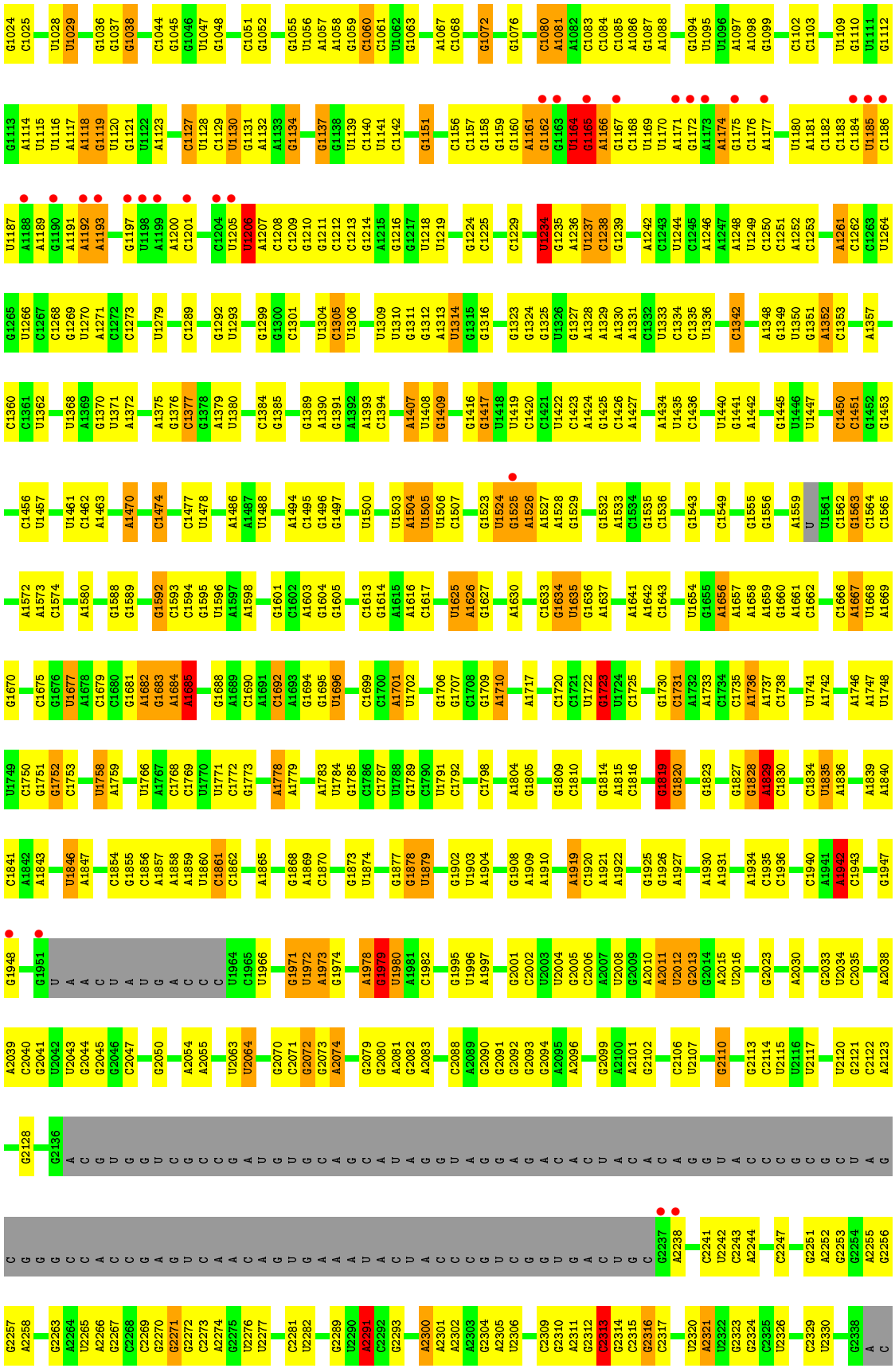
3 Residue-property plots (i)

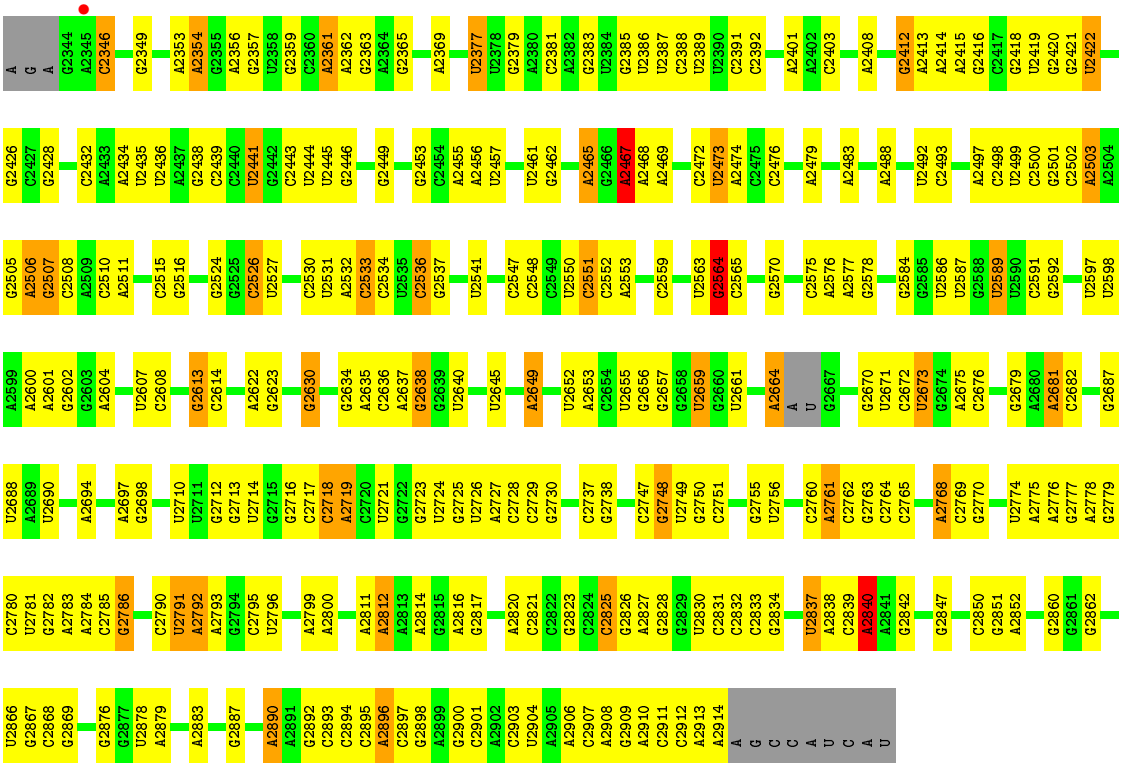
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (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: 23S RRNA

Chain A:

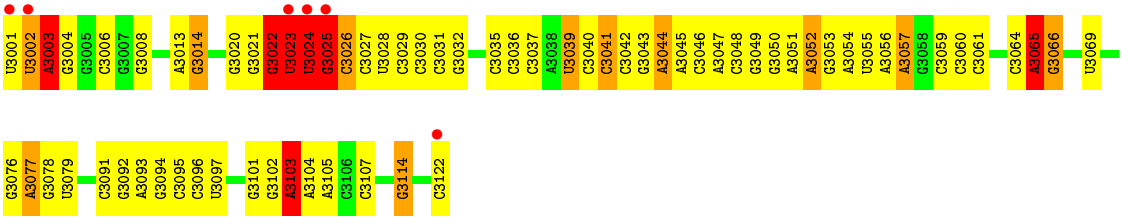






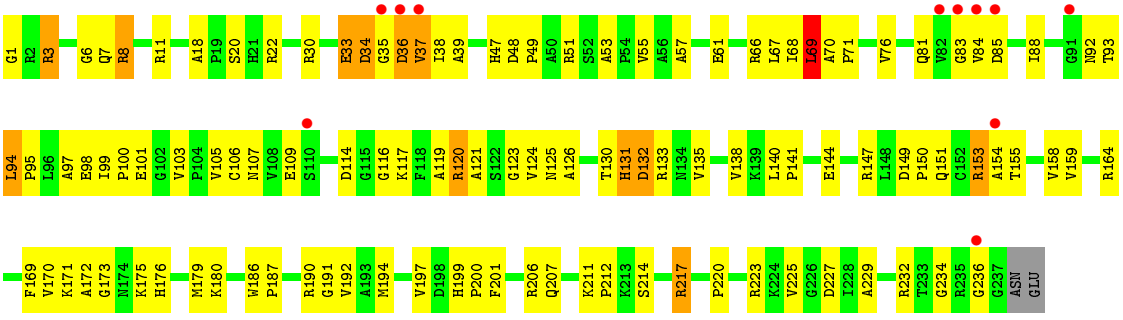
- Molecule 2: 5S RRNA

Chain B:



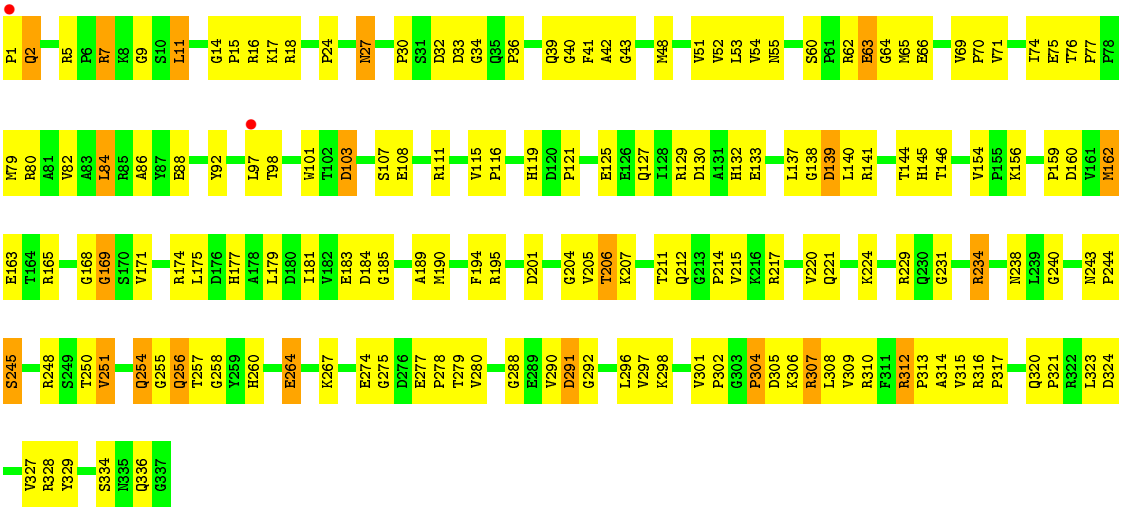
- Molecule 3: RIBOSOMAL PROTEIN L2

Chain C:



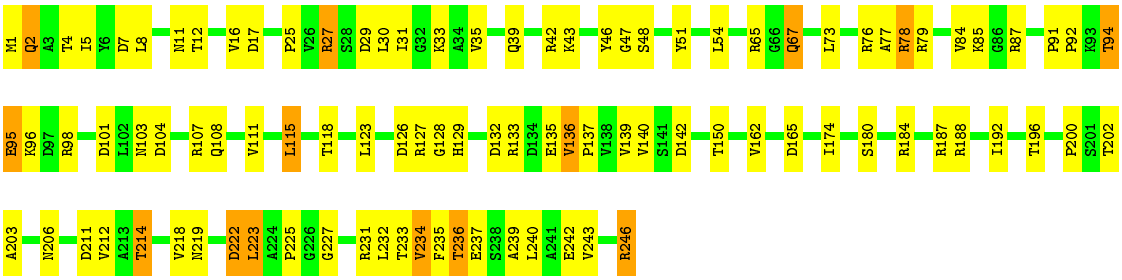
- Molecule 4: RIBOSOMAL PROTEIN L3

Chain D:



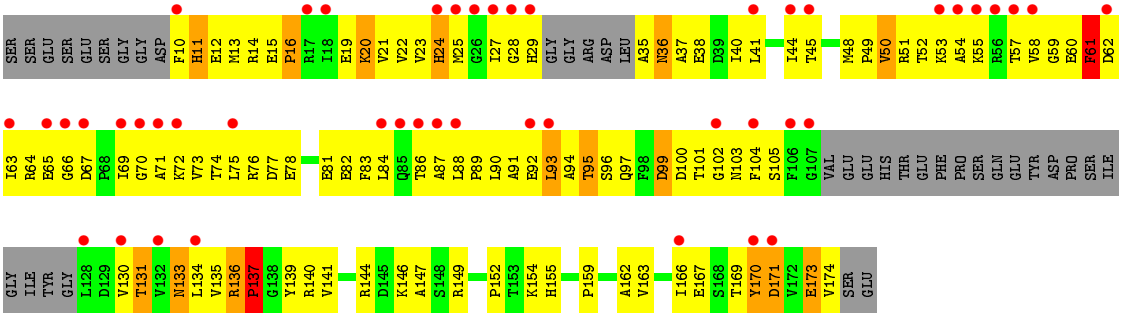
• Molecule 5: RIBOSOMAL PROTEIN L4

Chain E:



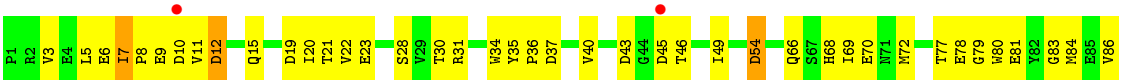
• Molecule 6: RIBOSOMAL PROTEIN L5

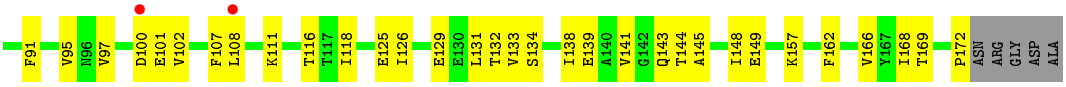
Chain F:



• Molecule 7: RIBOSOMAL PROTEIN L6

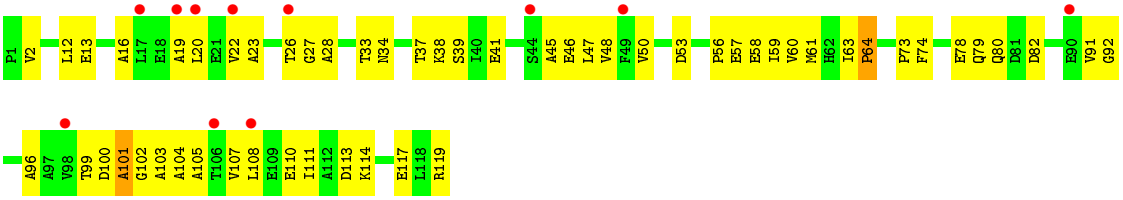
Chain G:





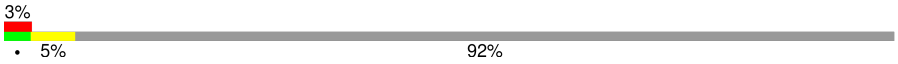
- Molecule 8: RIBOSOMAL PROTEIN L7AE

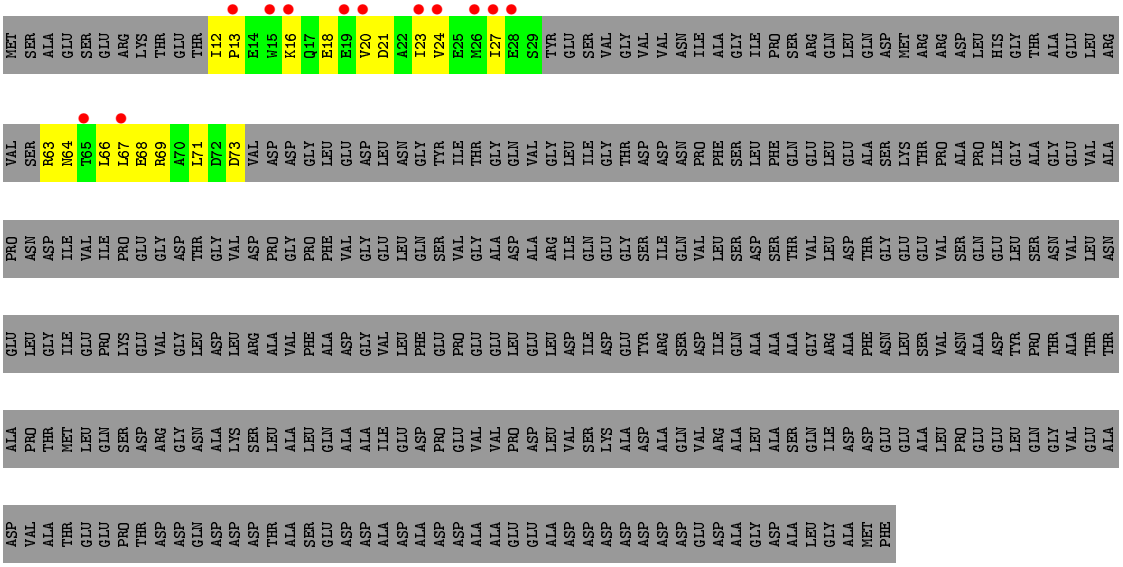
Chain H:



- Molecule 9: RIBOSOMAL PROTEIN L10

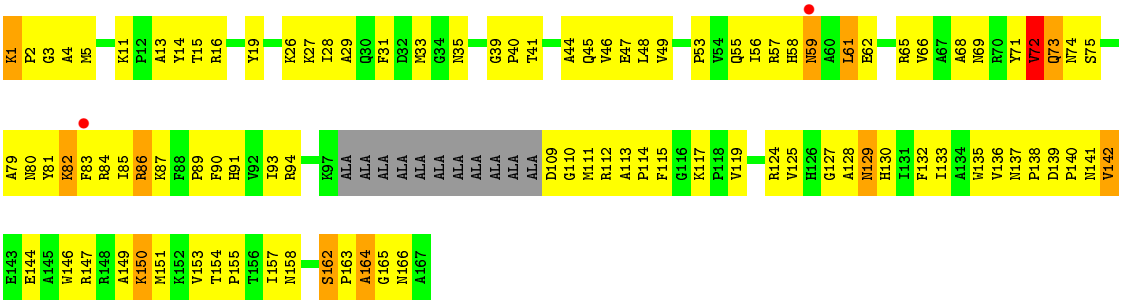
Chain I:





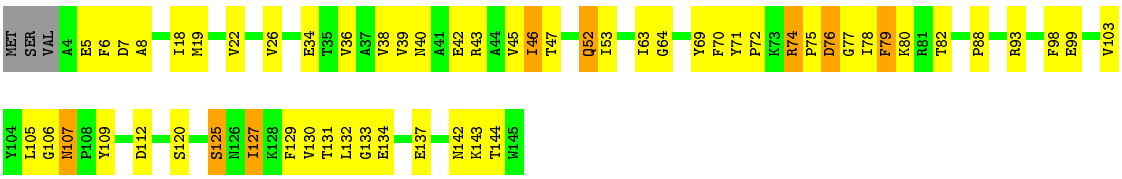
- Molecule 10: RIBOSOMAL PROTEIN L10E

Chain J:



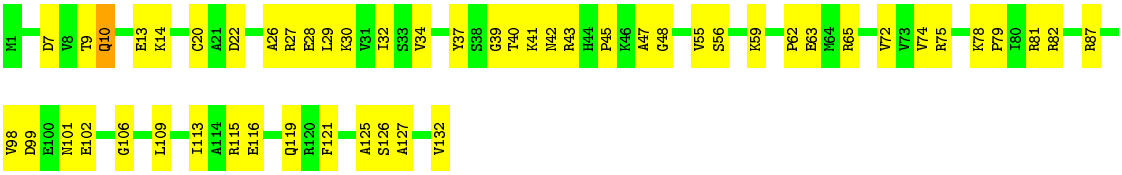
- Molecule 11: RIBOSOMAL PROTEIN L13

Chain K:



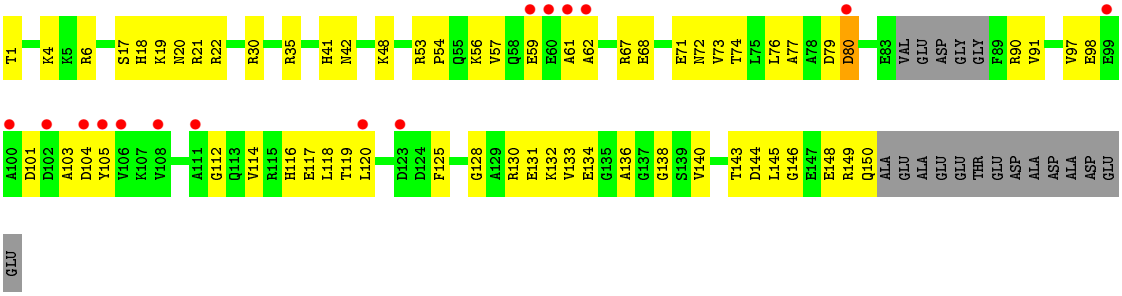
• Molecule 12: RIBOSOMAL PROTEIN L14

Chain L:



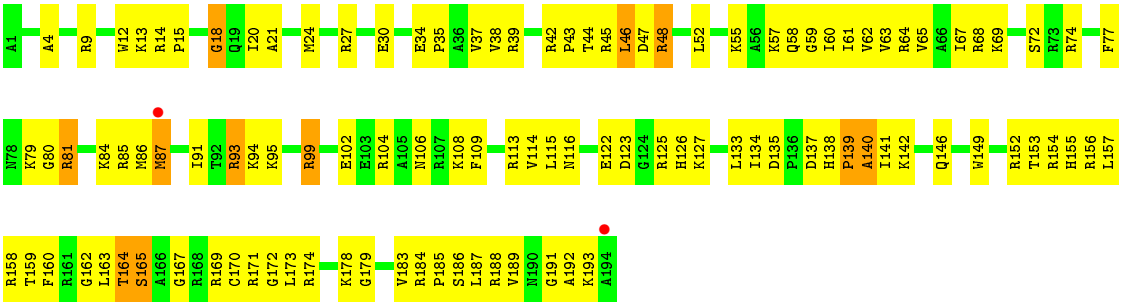
• Molecule 13: RIBOSOMAL PROTEIN L15

Chain M:



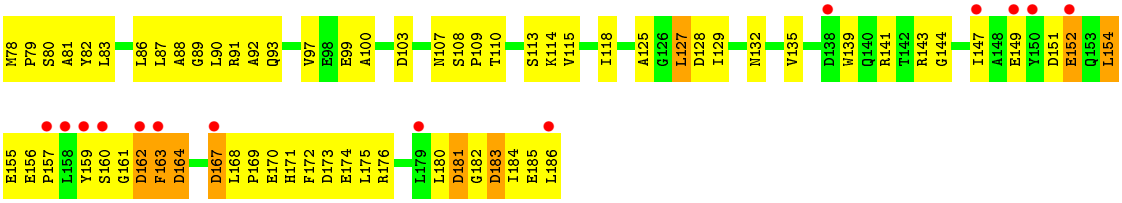
• Molecule 14: RIBOSOMAL PROTEIN L15E

Chain N:

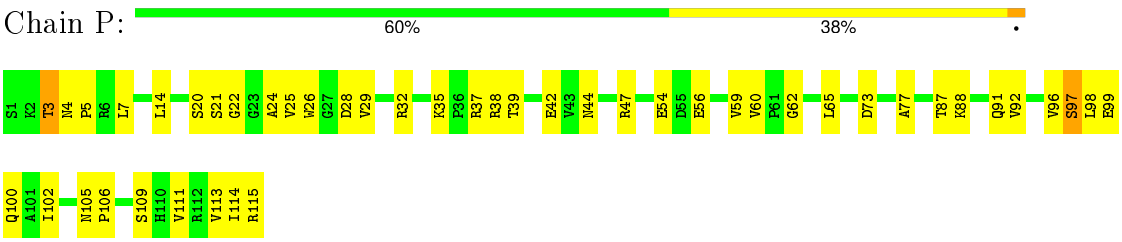


• Molecule 15: RIBOSOMAL PROTEIN L18

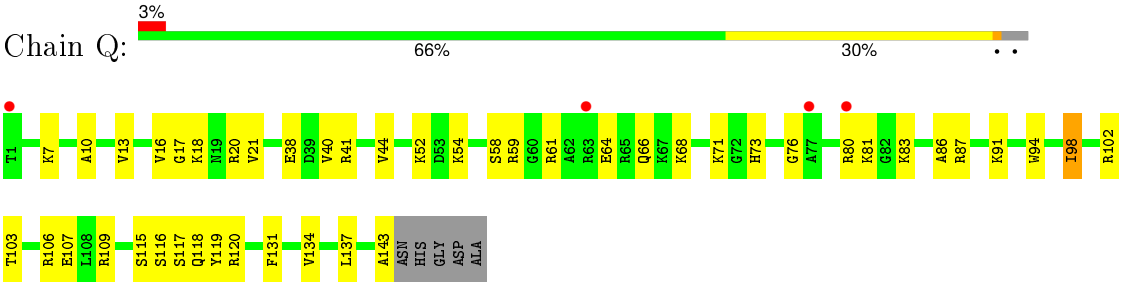
Chain O:



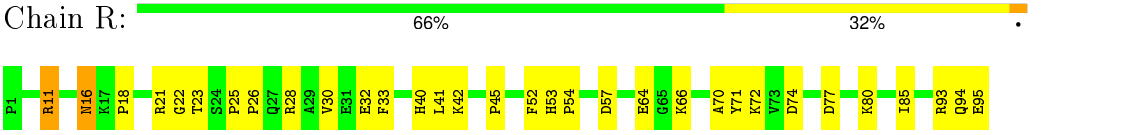
• Molecule 16: RIBOSOMAL PROTEIN L18E



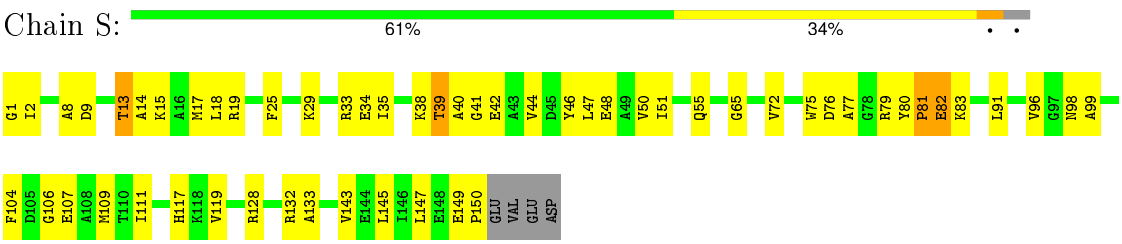
• Molecule 17: RIBOSOMAL PROTEIN L19E



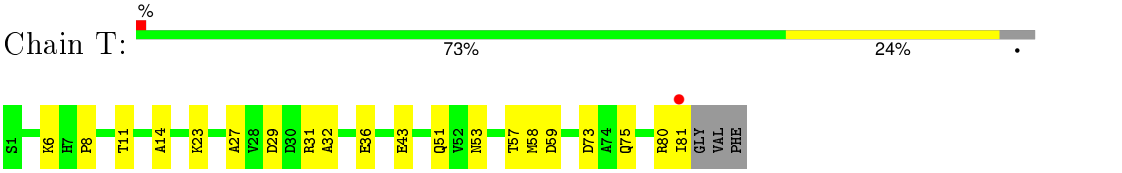
• Molecule 18: RIBOSOMAL PROTEIN L21E



• Molecule 19: RIBOSOMAL PROTEIN L22

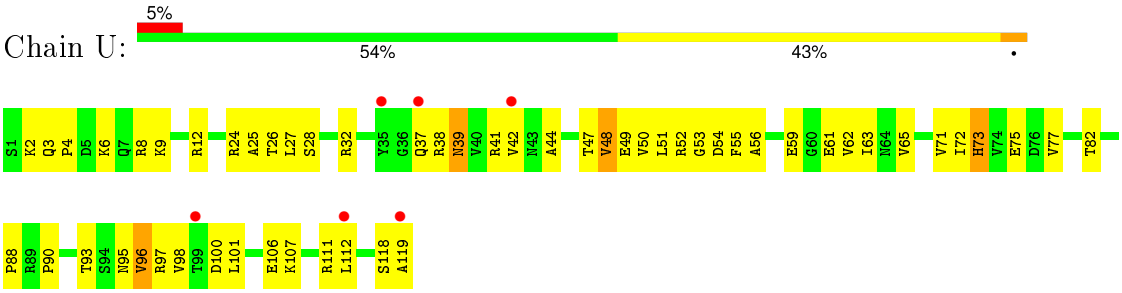


• Molecule 20: RIBOSOMAL PROTEIN L23



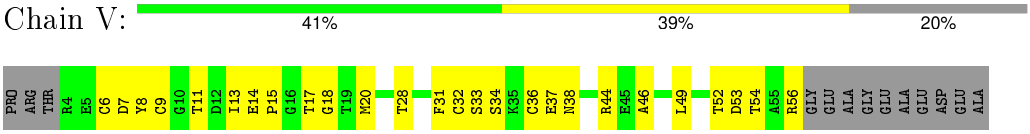
• Molecule 21: RIBOSOMAL PROTEIN L24

Chain U:



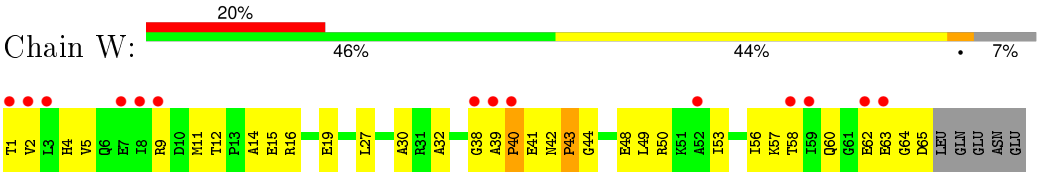
- Molecule 22: RIBOSOMAL PROTEIN L24E

Chain V:



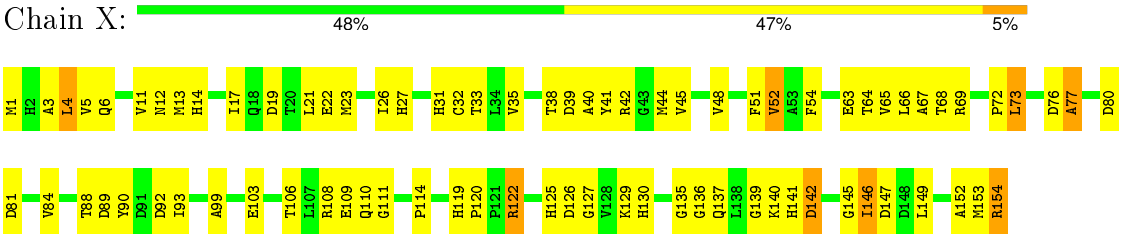
- Molecule 23: RIBOSOMAL PROTEIN L29

Chain W:



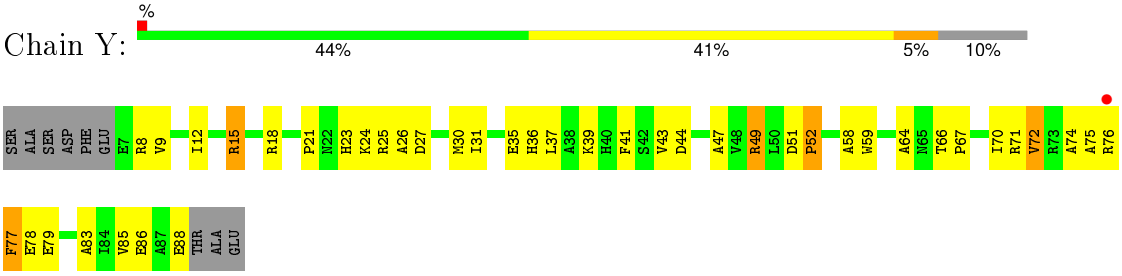
- Molecule 24: RIBOSOMAL PROTEIN L30

Chain X:



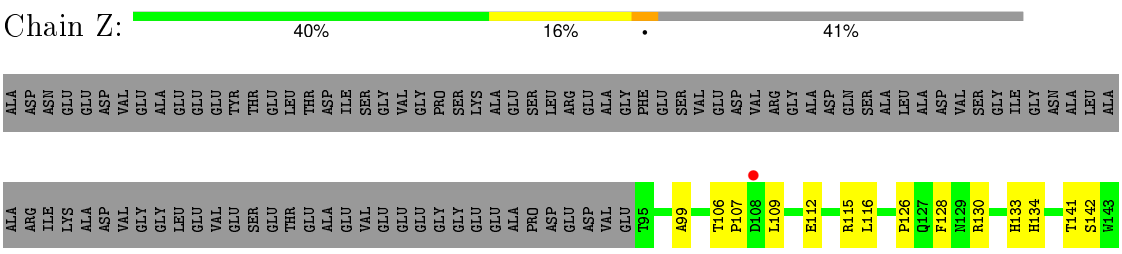
- Molecule 25: RIBOSOMAL PROTEIN L31E

Chain Y:

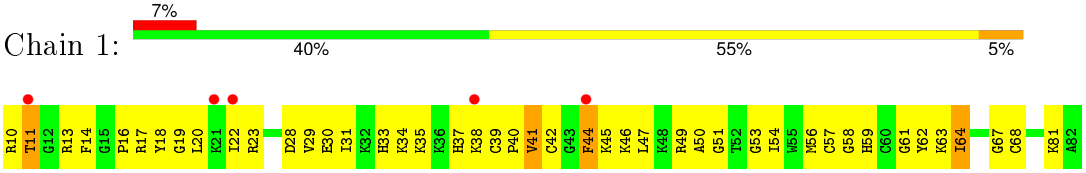


- Molecule 26: RIBOSOMAL PROTEIN L32E

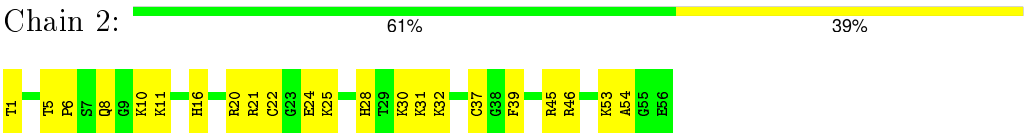
Chain Z:



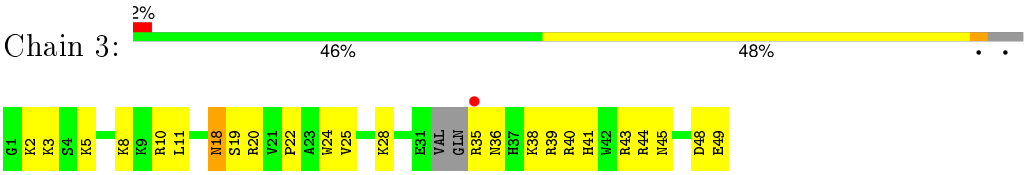
- Molecule 27: RIBOSOMAL PROTEIN L37Ae



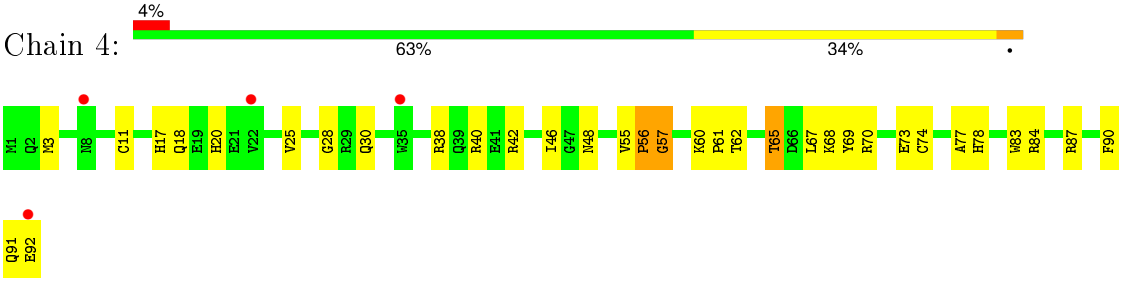
- Molecule 28: RIBOSOMAL PROTEIN L37E



- Molecule 29: RIBOSOMAL PROTEIN L39E



- Molecule 30: RIBOSOMAL PROTEIN L44E



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	213.75Å 301.57Å 574.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.20 49.69 – 3.00	Depositor EDS
% Data completeness (in resolution range)	91.9 (20.00-3.20) 87.9 (49.69-3.00)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.27 (at 3.01Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.214 , 0.250 0.198 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	60.7	Xtriage
Anisotropy	0.511	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 74.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Outliers	0 of 366469 reflections	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	98587	wwPDB-VP
Average B, all atoms (Å^2)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CL, NA, K, ZIT, CD

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	0.59	1/66076 (0.0%)	0.76	33/103052 (0.0%)
2	B	0.92	16/2905 (0.6%)	0.98	20/4528 (0.4%)
3	C	0.47	0/1787	0.75	0/2409
4	D	0.52	0/2689	0.74	0/3652
5	E	0.49	0/1883	0.73	0/2551
6	F	0.43	0/1111	0.68	0/1498
7	G	0.48	0/1382	0.67	0/1880
8	H	0.44	0/896	0.64	0/1219
9	I	0.51	0/241	0.63	0/324
10	J	0.50	0/1246	0.82	2/1686 (0.1%)
11	K	0.53	0/1135	0.69	0/1530
12	L	0.57	1/1003 (0.1%)	0.78	0/1351
13	M	0.47	0/1126	0.76	0/1504
14	N	0.56	0/1633	0.81	1/2180 (0.0%)
15	O	0.44	0/1473	0.74	0/1999
16	P	0.49	0/873	0.69	0/1181
17	Q	0.49	0/1143	0.66	0/1521
18	R	0.52	0/748	0.78	0/1005
19	S	0.52	0/1172	0.77	0/1578
20	T	0.48	0/648	0.69	0/875
21	U	0.46	0/957	0.73	0/1289
22	V	0.47	0/417	0.67	0/562
23	W	0.43	0/502	0.63	0/675
24	X	0.52	0/1218	0.72	0/1655
25	Y	0.49	0/664	0.71	0/895
26	Z	0.50	0/1146	0.73	0/1536
27	1	0.52	0/575	0.75	0/763
28	2	0.57	0/437	0.78	0/578
29	3	0.45	0/398	0.63	0/527
30	4	0.57	0/771	0.73	0/1024
All	All	0.57	18/98255 (0.0%)	0.76	56/147027 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	141
2	B	0	5
All	All	1	146

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3025	G	O3'-P	10.69	1.74	1.61
2	B	3025	G	C4'-O4'	9.77	1.58	1.45
2	B	3023	U	C2'-O2'	9.46	1.53	1.41
2	B	3026	C	P-O5'	-8.76	1.50	1.59
2	B	3003	A	C5'-C4'	8.50	1.61	1.51
2	B	3023	U	O5'-C5'	8.22	1.57	1.44
2	B	3025	G	C2'-C1'	7.80	1.61	1.53
2	B	3025	G	N9-C4	-7.75	1.31	1.38
2	B	3026	C	P-OP2	-7.49	1.36	1.49
2	B	3025	G	O4'-C1'	6.51	1.50	1.41
2	B	3025	G	C2-N3	-6.08	1.27	1.32
2	B	3024	U	O4'-C1'	5.91	1.49	1.41
2	B	3022	G	O3'-P	5.88	1.68	1.61
2	B	3022	G	O5'-C5'	-5.87	1.33	1.42
12	L	63	GLU	CB-CG	5.85	1.63	1.52
2	B	3025	G	C4'-C3'	5.64	1.59	1.53
1	A	1206	U	P-OP2	5.57	1.58	1.49
2	B	3025	G	P-OP2	-5.16	1.40	1.49

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1164	U	OP1-P-O3'	-19.12	63.13	105.20
1	A	1164	U	OP2-P-O3'	-17.65	66.37	105.20
1	A	1165	G	O5'-P-OP1	-12.66	94.31	105.70
2	B	3024	U	O5'-P-OP2	11.59	124.60	110.70
2	B	3026	C	O5'-P-OP2	-11.13	95.68	105.70
2	B	3023	U	P-O5'-C5'	10.35	137.46	120.90
1	A	1563	G	C2'-C3'-O3'	9.97	131.43	109.50
1	A	1942	A	C5'-C4'-C3'	9.05	130.49	116.00
2	B	3024	U	C5'-C4'-O4'	8.54	119.34	109.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	3025	G	O5'-P-OP2	-8.52	98.04	105.70
1	A	1979	G	C2'-C3'-O3'	7.60	126.21	109.50
2	B	3039	U	N1-C1'-C2'	7.23	123.40	114.00
2	B	3024	U	OP1-P-O3'	6.81	120.18	105.20
1	A	1592	G	N9-C1'-C2'	6.78	122.81	114.00
10	J	74	ASN	N-CA-C	-6.62	93.12	111.00
1	A	1165	G	OP1-P-OP2	6.53	129.40	119.60
1	A	1942	A	C5'-C4'-O4'	6.43	116.82	109.10
1	A	1165	G	O5'-P-OP2	-6.43	99.91	105.70
2	B	3103	A	C5'-C4'-O4'	6.42	116.80	109.10
1	A	1738	C	O4'-C4'-C3'	-6.42	97.58	104.00
2	B	3024	U	P-O5'-C5'	6.24	130.88	120.90
1	A	2467	A	C1'-O4'-C4'	-5.97	105.13	109.90
1	A	1504	A	C1'-O4'-C4'	-5.79	105.27	109.90
1	A	2313	C	C5'-C4'-O4'	5.73	115.98	109.10
2	B	3026	C	C5'-C4'-O4'	5.69	115.93	109.10
2	B	3025	G	N3-C4-N9	-5.67	122.60	126.00
1	A	2312	G	N9-C1'-C2'	-5.65	105.79	112.00
2	B	3023	U	OP2-P-O3'	-5.65	92.78	105.20
14	N	139	PRO	N-CA-C	-5.60	97.54	112.10
1	A	1971	G	O4'-C1'-N9	5.58	112.66	108.20
2	B	3024	U	C4'-C3'-O3'	5.51	124.02	113.00
2	B	3026	C	OP1-P-OP2	5.48	127.82	119.60
1	A	2664	A	N9-C1'-C2'	5.42	121.05	114.00
1	A	314	G	N9-C1'-C2'	-5.40	106.06	112.00
1	A	2291	A	N9-C1'-C2'	5.40	121.02	114.00
1	A	871	G	C5'-C4'-O4'	-5.40	102.62	109.10
2	B	3103	A	C4'-C3'-C2'	-5.36	97.24	102.60
1	A	1342	C	N1-C1'-C2'	-5.33	106.13	112.00
10	J	110	GLY	N-CA-C	-5.33	99.77	113.10
1	A	2311	A	N9-C1'-C2'	-5.33	106.14	112.00
1	A	921	G	N9-C1'-C2'	5.30	120.89	114.00
1	A	1819	G	C5'-C4'-C3'	5.29	124.47	116.00
1	A	1683	G	N9-C1'-C2'	5.26	120.84	114.00
1	A	841	A	C1'-O4'-C4'	-5.25	105.70	109.90
2	B	3022	G	N9-C1'-C2'	5.24	120.82	114.00
1	A	2313	C	C4'-C3'-C2'	-5.22	97.38	102.60
2	B	3025	G	C6-N1-C2	5.20	128.22	125.10
1	A	381	G	N9-C1'-C2'	5.18	120.73	114.00
2	B	3025	G	C2'-C3'-O3'	5.15	121.95	113.70
1	A	206	G	C5'-C4'-C3'	-5.15	107.76	116.00
1	A	129	A	C2'-C3'-O3'	5.14	121.92	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	603	A	N9-C1'-C2'	5.10	120.63	114.00
2	B	3023	U	C5'-C4'-C3'	5.08	124.12	116.00
1	A	1829	A	N9-C1'-C2'	-5.06	106.43	112.00
2	B	3003	A	C4'-C3'-C2'	-5.03	97.57	102.60
1	A	1723	G	N9-C1'-C2'	5.02	120.53	114.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	1563	G	C3'

All (146) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1005	A	Sidechain
1	A	1036	G	Sidechain
1	A	1038	G	Sidechain
1	A	1118	A	Sidechain
1	A	112	G	Sidechain
1	A	1127	C	Sidechain
1	A	1134	G	Sidechain
1	A	1156	C	Sidechain
1	A	1206	U	Sidechain
1	A	1234	U	Sidechain
1	A	1264	U	Sidechain
1	A	1305	C	Sidechain
1	A	1314	U	Sidechain
1	A	1348	A	Sidechain
1	A	1349	G	Sidechain
1	A	1350	U	Sidechain
1	A	1371	U	Sidechain
1	A	1379	A	Sidechain
1	A	1390	A	Sidechain
1	A	1417	G	Sidechain
1	A	1447	U	Sidechain
1	A	146	U	Sidechain
1	A	147	G	Sidechain
1	A	1470	A	Sidechain
1	A	1635	U	Sidechain
1	A	1677	U	Sidechain
1	A	1685	A	Sidechain
1	A	1688	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1694	G	Sidechain
1	A	1696	U	Sidechain
1	A	171	C	Sidechain
1	A	1720	C	Sidechain
1	A	1736	A	Sidechain
1	A	1737	A	Sidechain
1	A	1758	U	Sidechain
1	A	1809	G	Sidechain
1	A	1819	G	Sidechain
1	A	1823	G	Sidechain
1	A	1828	G	Sidechain
1	A	1829	A	Sidechain
1	A	1835	U	Sidechain
1	A	1839	A	Sidechain
1	A	1846	U	Sidechain
1	A	1860	U	Sidechain
1	A	1861	C	Sidechain
1	A	1865	A	Sidechain
1	A	1877	G	Sidechain
1	A	1878	G	Sidechain
1	A	1908	G	Sidechain
1	A	1922	A	Sidechain
1	A	194	A	Sidechain
1	A	1972	U	Sidechain
1	A	1978	A	Sidechain
1	A	20	G	Sidechain
1	A	2023	G	Sidechain
1	A	2035	C	Sidechain
1	A	2047	C	Sidechain
1	A	2088	C	Sidechain
1	A	2110	G	Sidechain
1	A	2115	U	Sidechain
1	A	2117	U	Sidechain
1	A	2123	A	Sidechain
1	A	2263	G	Sidechain
1	A	2293	G	Sidechain
1	A	2300	A	Sidechain
1	A	2306	U	Sidechain
1	A	2313	C	Sidechain
1	A	2316	G	Sidechain
1	A	2377	U	Sidechain
1	A	2381	C	Sidechain

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Mol	Chain	Res	Type	Group
1	A	24	G	Sidechain
1	A	2412	G	Sidechain
1	A	2439	C	Sidechain
1	A	2441	U	Sidechain
1	A	2444	U	Sidechain
1	A	246	G	Sidechain
1	A	2465	A	Sidechain
1	A	2473	U	Sidechain
1	A	2479	A	Sidechain
1	A	2492	U	Sidechain
1	A	2493	C	Sidechain
1	A	2503	A	Sidechain
1	A	2506	A	Sidechain
1	A	2530	C	Sidechain
1	A	2551	C	Sidechain
1	A	2564	G	Sidechain
1	A	257	G	Sidechain
1	A	2607	U	Sidechain
1	A	2622	A	Sidechain
1	A	2623	G	Sidechain
1	A	2630	G	Sidechain
1	A	2640	U	Sidechain
1	A	2659	U	Sidechain
1	A	2673	U	Sidechain
1	A	2675	A	Sidechain
1	A	2774	U	Sidechain
1	A	2790	C	Sidechain
1	A	2793	A	Sidechain
1	A	2837	U	Sidechain
1	A	2840	A	Sidechain
1	A	2842	G	Sidechain
1	A	2887	G	Sidechain
1	A	33	G	Sidechain
1	A	333	G	Sidechain
1	A	336	G	Sidechain
1	A	391	U	Sidechain
1	A	396	U	Sidechain
1	A	397	A	Sidechain
1	A	407	A	Sidechain
1	A	436	A	Sidechain
1	A	458	G	Sidechain
1	A	474	C	Sidechain

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Mol	Chain	Res	Type	Group
1	A	481	U	Sidechain
1	A	482	G	Sidechain
1	A	502	A	Sidechain
1	A	515	C	Sidechain
1	A	517	U	Sidechain
1	A	518	G	Sidechain
1	A	539	G	Sidechain
1	A	548	U	Sidechain
1	A	552	A	Sidechain
1	A	565	A	Sidechain
1	A	619	U	Sidechain
1	A	631	A	Sidechain
1	A	636	G	Sidechain
1	A	639	A	Sidechain
1	A	657	G	Sidechain
1	A	678	G	Sidechain
1	A	755	G	Sidechain
1	A	766	A	Sidechain
1	A	781	C	Sidechain
1	A	815	U	Sidechain
1	A	817	G	Sidechain
1	A	844	A	Sidechain
1	A	871	G	Sidechain
1	A	878	G	Sidechain
1	A	891	G	Sidechain
1	A	898	G	Sidechain
1	A	903	U	Sidechain
1	A	919	U	Sidechain
1	A	954	U	Sidechain
2	B	3022	G	Sidechain
2	B	3024	U	Sidechain
2	B	3052	A	Sidechain
2	B	3065	A	Sidechain
2	B	3094	G	Sidechain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	59017	0	29803	1165	0
2	B	2600	0	1326	84	0
3	C	1754	0	1763	129	0
4	D	2624	0	2533	180	0
5	E	1858	0	1816	125	0
6	F	1094	0	1085	143	0
7	G	1357	0	1266	84	0
8	H	885	0	854	66	0
9	I	240	0	231	25	0
10	J	1215	0	1215	152	0
11	K	1119	0	1098	68	0
12	L	993	0	1027	56	0
13	M	1114	0	1072	67	0
14	N	1605	0	1676	159	0
15	O	1444	0	1401	142	0
16	P	864	0	873	46	0
17	Q	1133	0	1127	51	0
18	R	734	0	728	28	0
19	S	1149	0	1122	64	0
20	T	641	0	605	22	0
21	U	949	0	923	55	0
22	V	410	0	364	36	0
23	W	499	0	511	33	0
24	X	1195	0	1137	99	0
25	Y	654	0	653	50	0
26	Z	1130	0	1133	59	0
27	1	563	0	597	51	0
28	2	430	0	426	28	0
29	3	393	0	406	30	0
30	4	755	0	728	41	0
31	A	52	0	72	2	0
32	1	1	0	0	0	0
32	4	1	0	0	0	0
32	A	109	0	0	1	0
32	B	1	0	0	0	0
32	C	1	0	0	0	0
32	D	1	0	0	0	0
32	L	1	0	0	0	0
32	U	1	0	0	0	0
32	Z	1	0	0	0	0
33	A	2	0	0	0	0
34	A	71	0	0	0	0
34	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	C	1	0	0	0	0
34	E	1	0	0	0	0
34	J	2	0	0	0	0
34	K	1	0	0	0	0
34	M	1	0	0	0	0
34	N	1	0	0	0	0
34	R	1	0	0	0	0
34	S	3	0	0	0	0
34	T	1	0	0	0	0
34	U	1	0	0	0	0
35	4	1	0	0	0	0
35	A	9	0	0	3	0
35	C	1	0	0	0	0
35	D	1	0	0	0	0
35	K	4	0	0	4	0
35	L	1	0	0	0	0
35	N	1	0	0	2	0
35	O	1	0	0	2	0
35	P	1	0	0	0	0
35	R	1	0	0	0	0
35	S	1	0	0	0	0
36	1	1	0	0	0	0
36	2	1	0	0	0	0
36	4	1	0	0	0	0
36	P	1	0	0	0	0
36	V	1	0	0	0	0
37	1	38	0	0	8	0
37	2	57	0	0	4	0
37	3	39	0	0	4	0
37	4	72	0	0	12	0
37	A	5898	0	0	232	0
37	B	140	0	0	15	0
37	C	129	0	0	24	0
37	D	152	0	0	27	0
37	E	169	0	0	34	0
37	F	52	0	0	18	0
37	G	42	0	0	13	0
37	H	28	0	0	10	0
37	I	21	0	0	5	0
37	J	81	0	0	17	0
37	K	56	0	0	6	0
37	L	61	0	0	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	M	81	0	0	19	0
37	N	129	0	0	22	0
37	O	68	0	0	20	0
37	P	45	0	0	13	0
37	Q	69	0	0	6	0
37	R	56	0	0	3	0
37	S	89	0	0	8	0
37	T	36	0	0	4	0
37	U	39	0	0	5	0
37	V	27	0	0	5	0
37	W	15	0	0	3	0
37	X	73	0	0	7	0
37	Y	30	0	0	8	0
37	Z	93	0	0	14	0
All	All	98587	0	59571	3047	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 20.

All (3047) 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)
1:A:1160:G:H5'	1:A:1161:A:H5'	1.22	1.15
25:Y:37:LEU:HD13	25:Y:85:VAL:HG21	1.26	1.13
21:U:71:VAL:HG11	21:U:90:PRO:HB3	1.33	1.11
10:J:86:ARG:NH1	10:J:133:ILE:HG13	1.67	1.10
1:A:871:G:H8	1:A:871:G:H5'	1.14	1.07
23:W:12:THR:HG22	23:W:15:GLU:HG3	1.34	1.07
27:1:10:ARG:HA	37:1:8415:HOH:O	1.55	1.07
5:E:236:THR:HG22	5:E:239:ALA:H	1.11	1.06
1:A:156:C:H5"	14:N:171:ARG:HD3	1.35	1.05
1:A:871:G:C8	1:A:871:G:H5'	1.89	1.05
2:B:3023:U:H5"	2:B:3024:U:OP2	1.55	1.04
2:B:3076:G:H3'	2:B:3077:A:H5"	1.38	1.04
1:A:541:C:H2'	1:A:542:A:H5"	1.38	1.03
29:3:39:ARG:HG2	37:3:3143:HOH:O	1.57	1.03
15:O:47:LEU:HD11	15:O:127:LEU:HD21	1.41	1.02
1:A:542:A:H8	1:A:542:A:H5'	1.22	1.02
10:J:162:SER:HB2	10:J:163:PRO:HD3	1.40	1.01
6:F:25:MET:HE2	6:F:41:LEU:HG	1.39	1.00
4:D:321:PRO:HA	37:D:8662:HOH:O	1.61	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:45:GLN:HB3	10:J:163:PRO:HD2	1.40	0.99
10:J:86:ARG:HH11	10:J:133:ILE:HG13	0.85	0.99
10:J:165:GLY:HA3	37:J:8401:HOH:O	1.61	0.99
10:J:26:LYS:HD2	10:J:28:ILE:HD12	1.45	0.98
2:B:3056:A:H2'	2:B:3057:A:H5"	1.44	0.98
12:L:29:LEU:HB3	12:L:55:VAL:HG11	1.44	0.98
14:N:35:PRO:HG2	14:N:38:VAL:HG23	1.43	0.98
19:S:99:ALA:HB1	19:S:109:MET:HE1	1.42	0.98
14:N:164:THR:HG22	14:N:167:GLY:H	1.24	0.98
1:A:1474:C:H5'	1:A:1474:C:H6	1.28	0.97
1:A:962:C:H1'	15:O:5:ARG:NH1	1.80	0.97
4:D:140:LEU:HA	37:D:8583:HOH:O	1.63	0.97
12:L:10:GLN:NE2	12:L:10:GLN:H	1.63	0.97
1:A:1134:G:H4'	10:J:151:MET:HE1	1.45	0.97
13:M:79:ASP:HB3	37:M:8432:HOH:O	1.65	0.96
1:A:1751:G:H2'	1:A:1752:G:H5"	1.44	0.96
14:N:87:MET:HG2	30:4:46:ILE:HG21	1.45	0.96
6:F:134:LEU:HD11	6:F:166:ILE:HD11	1.48	0.95
17:Q:115:SER:H	17:Q:118:GLN:HE21	0.95	0.95
5:E:5:ILE:HD11	5:E:16:VAL:HG23	1.48	0.94
14:N:64:ARG:HD2	37:N:8585:HOH:O	1.66	0.94
1:A:1835:U:H5	1:A:1840:A:N7	1.66	0.94
12:L:81:ARG:HB2	12:L:87:ARG:HH11	1.32	0.93
1:A:871:G:C5'	1:A:871:G:H8	1.82	0.93
14:N:102:GLU:OE1	14:N:164:THR:HG21	1.69	0.93
10:J:142:VAL:HG13	37:J:8383:HOH:O	1.69	0.92
10:J:4:ALA:HB3	37:J:8367:HOH:O	1.69	0.92
5:E:236:THR:HG21	37:E:8370:HOH:O	1.70	0.92
2:B:3006:C:H5"	15:O:37:ARG:NH1	1.83	0.92
1:A:960:G:H4'	37:A:7000:HOH:O	1.68	0.92
1:A:1667:A:H8	1:A:1667:A:H5'	1.32	0.92
10:J:2:PRO:HB2	37:J:8367:HOH:O	1.69	0.91
12:L:10:GLN:HE21	12:L:10:GLN:H	0.95	0.91
1:A:856:G:H2'	37:A:5003:HOH:O	1.71	0.91
14:N:87:MET:HB3	30:4:46:ILE:HD13	1.51	0.91
27:1:46:LYS:HD3	27:1:59:HIS:HB2	1.52	0.90
4:D:62:ARG:HA	4:D:65:MET:HE3	1.53	0.90
24:X:88:THR:HB	37:X:6679:HOH:O	1.72	0.90
3:C:211:LYS:HB3	3:C:212:PRO:HD2	1.54	0.90
24:X:137:GLN:HE21	24:X:141:HIS:HE1	1.16	0.90
11:K:76:ASP:HA	37:K:5907:HOH:O	1.69	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:187:VAL:HG23	26:Z:192:ASP:HB2	1.52	0.90
19:S:8:ALA:HB1	19:S:13:THR:HG21	1.54	0.89
10:J:29:ALA:HB3	10:J:65:ARG:HH12	1.37	0.89
1:A:1372:A:H3'	37:A:6759:HOH:O	1.71	0.89
1:A:1119:G:H22	1:A:1246:A:H2	1.20	0.89
37:A:3259:HOH:O	14:N:79:LYS:HD3	1.71	0.89
5:E:127:ARG:NH2	5:E:225:PRO:HG2	1.87	0.89
5:E:115:LEU:HD13	5:E:223:LEU:HD21	1.54	0.89
37:A:4432:HOH:O	14:N:14:ARG:HG2	1.72	0.89
14:N:94:LYS:HE3	37:N:8581:HOH:O	1.73	0.88
6:F:64:ARG:HG2	6:F:67:ASP:HB3	1.56	0.88
14:N:35:PRO:CG	14:N:38:VAL:HG23	2.02	0.88
15:O:144:GLY:O	15:O:147:ILE:HG22	1.72	0.88
12:L:10:GLN:N	12:L:10:GLN:HE21	1.72	0.88
37:A:3362:HOH:O	14:N:189:VAL:HG21	1.74	0.88
24:X:88:THR:HG22	24:X:89:ASP:H	1.37	0.88
29:3:41:HIS:H	29:3:45:ASN:HD22	1.21	0.88
22:V:14:GLU:OE1	22:V:15:PRO:HD2	1.73	0.87
10:J:86:ARG:HH11	10:J:133:ILE:CG1	1.80	0.87
17:Q:115:SER:H	17:Q:118:GLN:NE2	1.73	0.87
5:E:246:ARG:NH1	5:E:246:ARG:HB3	1.90	0.87
1:A:870:G:H2'	1:A:871:G:H5"	1.53	0.87
15:O:7:LYS:HE3	18:R:21:ARG:O	1.73	0.87
1:A:645:U:OP2	13:M:4:LYS:HE2	1.72	0.87
10:J:150:LYS:HE2	37:J:8385:HOH:O	1.76	0.86
6:F:105:SER:HB2	6:F:131:THR:HG23	1.56	0.86
1:A:2717:C:H2'	1:A:2718:C:H5"	1.56	0.86
13:M:68:GLU:HA	37:M:8417:HOH:O	1.73	0.86
3:C:7:GLN:O	37:C:8515:HOH:O	1.92	0.86
1:A:2506:A:HO2'	1:A:2507:G:H8	0.89	0.86
1:A:1209:C:H4'	37:A:4854:HOH:O	1.76	0.86
1:A:1166:A:H1'	1:A:1192:A:C2	2.10	0.86
5:E:104:ASP:HA	5:E:107:ARG:HH12	1.38	0.86
1:A:2586:U:H3	1:A:2592:G:H22	1.23	0.86
6:F:154:LYS:H	6:F:154:LYS:HD2	1.38	0.85
1:A:506:G:H22	1:A:509:A:C5'	1.89	0.85
27:1:49:ARG:HD2	37:1:8429:HOH:O	1.75	0.85
10:J:26:LYS:HG2	10:J:28:ILE:H	1.39	0.85
1:A:236:A:H4'	1:A:237:G:H5'	1.59	0.85
37:A:3303:HOH:O	14:N:157:LEU:HD11	1.75	0.85
1:A:541:C:C2'	1:A:542:A:H5"	2.07	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1116:U:H3	1:A:1246:A:H62	1.21	0.85
10:J:162:SER:HB2	10:J:163:PRO:CD	2.06	0.85
5:E:78:ARG:HG3	5:E:78:ARG:HH11	1.39	0.85
14:N:52:LEU:HD11	37:N:8615:HOH:O	1.75	0.84
2:B:3023:U:C5'	2:B:3024:U:OP2	2.24	0.84
5:E:246:ARG:HH11	5:E:246:ARG:HB3	1.41	0.84
20:T:57:THR:HG22	20:T:59:ASP:H	1.40	0.84
25:Y:15:ARG:HH11	25:Y:15:ARG:HB3	1.42	0.84
10:J:59:ASN:H	10:J:59:ASN:HD22	1.25	0.84
37:A:6348:HOH:O	15:O:4:PRO:HD2	1.77	0.84
7:G:100:ASP:HB2	37:G:2789:HOH:O	1.77	0.84
30:4:60:LYS:HG3	30:4:61:PRO:HD2	1.59	0.84
1:A:545:G:H8	1:A:545:G:H5'	1.43	0.83
4:D:264:GLU:HG2	4:D:267:LYS:HE2	1.59	0.83
14:N:164:THR:HG23	14:N:165:SER:N	1.94	0.83
4:D:86:ALA:HA	37:D:8583:HOH:O	1.78	0.83
1:A:214:U:H5'	37:A:5719:HOH:O	1.77	0.83
19:S:44:VAL:O	19:S:48:GLU:HG3	1.78	0.83
14:N:61:ILE:HG13	37:N:8622:HOH:O	1.78	0.83
25:Y:78:GLU:HG2	25:Y:79:GLU:H	1.42	0.83
24:X:122:ARG:HH21	24:X:154:ARG:HD2	1.41	0.83
10:J:59:ASN:HD22	10:J:59:ASN:N	1.77	0.82
12:L:81:ARG:HB2	12:L:87:ARG:NH1	1.94	0.82
1:A:1116:U:HO2'	1:A:1118:A:H2	0.83	0.82
7:G:20:ILE:HD11	7:G:40:VAL:HG11	1.61	0.82
7:G:97:VAL:HG12	37:G:4191:HOH:O	1.80	0.82
10:J:49:VAL:O	10:J:157:ILE:HG23	1.79	0.82
3:C:88:ILE:HD13	3:C:100:PRO:HD3	1.61	0.82
5:E:236:THR:HG22	5:E:239:ALA:N	1.95	0.82
1:A:962:C:H1'	15:O:5:ARG:HH12	1.45	0.82
13:M:133:VAL:HA	37:M:8445:HOH:O	1.76	0.82
1:A:1603:A:H5'	1:A:1605:G:O4'	1.78	0.82
23:W:1:THR:HG23	23:W:2:VAL:H	1.44	0.82
4:D:212:GLN:HB2	4:D:257:THR:HG21	1.61	0.81
16:P:47:ARG:HG3	16:P:47:ARG:HH11	1.45	0.81
6:F:20:LYS:HA	6:F:75:LEU:O	1.81	0.81
5:E:236:THR:HA	37:E:8448:HOH:O	1.78	0.81
1:A:1666:C:O2'	1:A:1667:A:H5"	1.80	0.81
14:N:80:GLY:O	14:N:81:ARG:HD3	1.81	0.81
15:O:49:THR:HG22	15:O:56:ASP:HB2	1.63	0.81
1:A:506:G:H22	1:A:509:A:H5"	1.46	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1242:A:H5'	11:K:82:THR:HG23	1.60	0.81
7:G:15:GLN:HG3	7:G:20:ILE:HG12	1.60	0.81
20:T:51:GLN:HE21	20:T:53:ASN:HD21	1.26	0.81
27:1:58:GLY:HA3	37:1:8439:HOH:O	1.81	0.81
1:A:1184:C:H1'	37:A:7039:HOH:O	1.81	0.80
8:H:46:GLU:O	8:H:73:PRO:HD2	1.81	0.80
1:A:1160:G:H5'	1:A:1161:A:C5'	2.09	0.80
1:A:2426:G:H1'	37:A:5671:HOH:O	1.79	0.80
24:X:68:THR:HG23	24:X:69:ARG:HG2	1.61	0.80
6:F:146:LYS:NZ	15:O:107:ASN:HD21	1.78	0.80
25:Y:37:LEU:CD1	25:Y:85:VAL:HG21	2.10	0.80
12:L:14:LYS:HB2	12:L:45:PRO:HG2	1.64	0.80
37:A:7026:HOH:O	4:D:211:THR:HG21	1.81	0.80
12:L:74:VAL:HG11	12:L:113:ILE:HG12	1.63	0.80
1:A:542:A:C8	1:A:542:A:H5'	2.13	0.80
1:A:1119:G:N2	1:A:1246:A:C2	2.50	0.80
1:A:1205:U:H2'	1:A:1206:U:H5'	1.62	0.80
1:A:1474:C:H5'	1:A:1474:C:C6	2.16	0.80
1:A:1160:G:C5'	1:A:1161:A:H5'	2.08	0.80
15:O:87:LEU:HD12	15:O:186:LEU:HD21	1.63	0.80
3:C:199:HIS:HD2	3:C:201:PHE:H	1.30	0.80
1:A:1625:U:H4'	37:A:4242:HOH:O	1.81	0.79
10:J:27:LYS:H	10:J:58:HIS:HD2	1.27	0.79
21:U:61:GLU:HG3	37:U:3851:HOH:O	1.80	0.79
25:Y:71:ARG:HB3	25:Y:88:GLU:OE1	1.81	0.79
23:W:4:HIS:HB3	37:W:6622:HOH:O	1.83	0.79
2:B:3056:A:C2'	2:B:3057:A:H5"	2.12	0.79
27:1:37:HIS:HB2	27:1:47:LEU:HB2	1.65	0.79
3:C:100:PRO:HG2	3:C:103:VAL:HG21	1.64	0.79
10:J:139:ASP:N	10:J:140:PRO:HD3	1.98	0.79
10:J:150:LYS:HB2	10:J:157:ILE:HD12	1.63	0.79
3:C:153:ARG:HB2	3:C:153:ARG:HH11	1.47	0.79
19:S:9:ASP:O	19:S:13:THR:HB	1.83	0.79
30:4:70:ARG:HG2	30:4:77:ALA:HB2	1.63	0.79
3:C:105:VAL:HG11	3:C:154:ALA:HB1	1.65	0.79
17:Q:115:SER:N	17:Q:118:GLN:HE21	1.79	0.78
27:1:38:LYS:HE2	27:1:45:LYS:HE2	1.64	0.78
21:U:48:VAL:HG22	21:U:97:ARG:O	1.83	0.78
24:X:6:GLN:HB2	24:X:26:ILE:HD12	1.65	0.78
1:A:282:C:H1'	1:A:368:C:N4	1.98	0.78
14:N:152:ARG:HG3	37:N:8555:HOH:O	1.84	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1450:C:H4'	1:A:1451:C:OP2	1.83	0.78
4:D:162:MET:HE3	4:D:308:LEU:HD21	1.65	0.78
37:A:6446:HOH:O	14:N:178:LYS:HB2	1.83	0.78
10:J:41:THR:HA	37:J:8398:HOH:O	1.83	0.78
26:Z:220:GLU:HG2	37:Z:8137:HOH:O	1.82	0.78
10:J:55:GLN:HE21	10:J:124:ARG:HE	1.30	0.78
2:B:3048:C:H4'	15:O:141:ARG:HH21	1.49	0.78
1:A:2676:C:H4'	11:K:70:PHE:CE1	2.18	0.78
3:C:125:ASN:HB3	3:C:158:VAL:HG12	1.65	0.77
15:O:86:LEU:HD12	15:O:125:ALA:HB2	1.65	0.77
14:N:106:ASN:HD22	14:N:114:VAL:HG23	1.47	0.77
7:G:132:THR:HB	37:G:2227:HOH:O	1.84	0.77
15:O:113:SER:HB2	37:O:8559:HOH:O	1.83	0.77
2:B:3014:G:H8	2:B:3014:G:H5'	1.49	0.77
1:A:711:G:H1'	37:A:6665:HOH:O	1.84	0.77
24:X:122:ARG:HG2	24:X:122:ARG:HH11	1.50	0.77
4:D:201:ASP:HB2	4:D:312:ARG:HD2	1.67	0.77
10:J:137:ASN:O	10:J:139:ASP:N	2.18	0.77
1:A:1947:G:OP2	37:A:3246:HOH:O	2.02	0.77
5:E:1:MET:HG2	5:E:2:GLN:H	1.48	0.77
3:C:199:HIS:CD2	3:C:201:PHE:H	2.02	0.77
9:I:23:ILE:HD13	9:I:67:LEU:HD23	1.65	0.77
15:O:48:VAL:CG1	15:O:55:ASP:HB3	2.14	0.77
1:A:31:C:H4'	37:A:6994:HOH:O	1.84	0.77
10:J:140:PRO:HB3	37:J:8383:HOH:O	1.85	0.77
14:N:87:MET:CG	30:4:46:ILE:HG21	2.14	0.77
7:G:37:ASP:OD1	11:K:125:SER:HB3	1.85	0.77
6:F:64:ARG:CG	6:F:67:ASP:HB3	2.15	0.77
27:1:38:LYS:HG2	27:1:45:LYS:HG2	1.66	0.77
1:A:1116:U:O2'	1:A:1118:A:H2	1.65	0.76
1:A:1165:G:H4'	1:A:1174:A:O2'	1.85	0.76
13:M:148:GLU:HA	37:M:8444:HOH:O	1.84	0.76
13:M:53:ARG:HH22	13:M:57:VAL:HG12	1.50	0.76
30:4:25:VAL:HG22	30:4:68:LYS:HG3	1.66	0.76
24:X:88:THR:HG22	24:X:89:ASP:N	2.00	0.76
26:Z:187:VAL:HG23	26:Z:192:ASP:CB	2.15	0.76
3:C:35:GLY:O	3:C:36:ASP:HB3	1.84	0.76
1:A:288:A:H61	1:A:364:C:H42	1.34	0.76
16:P:32:ARG:O	16:P:32:ARG:HD3	1.85	0.76
1:A:447:A:OP1	21:U:2:LYS:HG2	1.85	0.76
10:J:47:GLU:HB3	10:J:133:ILE:HD13	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:C:H4'	1:A:285:A:O5'	1.84	0.76
11:K:74:ARG:HH11	11:K:74:ARG:HB3	1.49	0.76
1:A:1187:U:H2'	37:A:6468:HOH:O	1.85	0.76
1:A:1191:A:H3'	1:A:1192:A:H5"	1.67	0.76
1:A:31:C:H2'	37:A:7262:HOH:O	1.85	0.76
1:A:2054:A:N3	19:S:128:ARG:NH2	2.33	0.76
1:A:1118:A:C8	1:A:1118:A:H3'	2.21	0.76
26:Z:200:THR:HG22	26:Z:201:GLU:HG3	1.68	0.76
1:A:2506:A:O2'	1:A:2507:G:H8	1.66	0.76
1:A:544:G:H2'	1:A:545:G:H5"	1.67	0.76
5:E:214:THR:HG21	37:E:8398:HOH:O	1.85	0.76
2:B:3049:G:H5"	37:B:8465:HOH:O	1.85	0.75
5:E:2:GLN:HB3	37:E:8336:HOH:O	1.86	0.75
1:A:657:G:OP1	5:E:27:ARG:NH2	2.16	0.75
28:2:10:LYS:HG3	37:2:8433:HOH:O	1.85	0.75
37:A:4244:HOH:O	20:T:23:LYS:HE2	1.87	0.75
7:G:81:GLU:HG2	7:G:134:SER:HB3	1.67	0.75
14:N:104:ARG:O	14:N:108:LYS:HE2	1.86	0.75
4:D:175:LEU:HD23	4:D:175:LEU:C	2.06	0.75
17:Q:115:SER:OG	17:Q:118:GLN:HG3	1.85	0.75
2:B:3006:C:H5"	15:O:37:ARG:HH12	1.49	0.75
1:A:1151:G:OP1	9:I:16:LYS:NZ	2.20	0.75
19:S:39:THR:HG23	19:S:107:GLU:O	1.85	0.75
12:L:62:PRO:HG3	12:L:65:ARG:HH21	1.52	0.75
5:E:214:THR:HG23	37:E:8433:HOH:O	1.86	0.75
28:2:25:LYS:HG2	28:2:25:LYS:O	1.86	0.75
15:O:71:TRP:CE3	15:O:175:LEU:HD22	2.22	0.75
1:A:2063:U:OP2	37:A:9303:HOH:O	2.04	0.75
1:A:2676:C:H4'	11:K:70:PHE:HE1	1.51	0.75
26:Z:133:HIS:HD2	37:Z:8169:HOH:O	1.70	0.75
5:E:5:ILE:HD11	5:E:16:VAL:CG2	2.17	0.74
4:D:238:ASN:HD22	4:D:240:GLY:H	1.34	0.74
24:X:137:GLN:HE21	24:X:141:HIS:CE1	2.05	0.74
22:V:14:GLU:O	22:V:17:THR:HB	1.86	0.74
1:A:2533:C:H6	1:A:2533:C:H5'	1.51	0.74
1:A:21:G:H5'	19:S:2:ILE:HA	1.70	0.74
1:A:188:C:H5"	14:N:163:LEU:HD21	1.70	0.74
1:A:2690:U:O2'	7:G:111:LYS:HE3	1.87	0.74
2:B:3023:U:H3'	37:B:8478:HOH:O	1.86	0.74
6:F:25:MET:HE1	6:F:37:ALA:HB1	1.70	0.74
12:L:74:VAL:CG1	12:L:113:ILE:HG12	2.18	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:55:PHE:HB2	37:U:6384:HOH:O	1.86	0.74
1:A:2717:C:C2'	1:A:2718:C:H5"	2.17	0.74
19:S:99:ALA:HB1	19:S:109:MET:CE	2.18	0.74
30:4:73:GLU:HB3	37:4:8561:HOH:O	1.87	0.74
1:A:1234:U:N3	4:D:244:PRO:HB3	2.02	0.74
17:Q:143:ALA:HA	37:Q:2178:HOH:O	1.87	0.74
4:D:307:ARG:HH11	4:D:307:ARG:HB2	1.51	0.74
1:A:560:C:H42	1:A:597:A:H61	1.36	0.74
1:A:871:G:C5'	1:A:871:G:C8	2.62	0.73
6:F:27:ILE:HG22	6:F:28:GLY:H	1.52	0.73
4:D:42:ALA:HB1	4:D:308:LEU:HD11	1.68	0.73
1:A:2637:A:H5'	37:A:8857:HOH:O	1.87	0.73
14:N:38:VAL:O	14:N:63:VAL:HG13	1.87	0.73
1:A:1751:G:C2'	1:A:1752:G:H5"	2.18	0.73
37:A:4797:HOH:O	12:L:39:GLY:HA2	1.88	0.73
6:F:25:MET:CE	6:F:41:LEU:HG	2.18	0.73
1:A:1667:A:H5'	1:A:1667:A:C8	2.21	0.73
21:U:47:THR:HB	21:U:100:ASP:HB3	1.69	0.73
3:C:121:ALA:O	3:C:124:VAL:HG22	1.86	0.73
1:A:2812:A:H2	1:A:2814:A:H62	1.33	0.73
10:J:141:ASN:HA	37:J:8369:HOH:O	1.88	0.73
24:X:88:THR:HG23	24:X:110:GLN:NE2	2.03	0.73
1:A:2851:G:O2'	1:A:2852:A:H5'	1.87	0.73
1:A:1118:A:H3'	1:A:1118:A:H8	1.53	0.73
7:G:11:VAL:HG12	7:G:12:ASP:N	2.04	0.73
1:A:1164:U:H3	1:A:1192:A:H2	1.36	0.73
1:A:2508:C:H2'	37:A:6330:HOH:O	1.89	0.73
13:M:67:ARG:O	13:M:71:GLU:HG3	1.88	0.73
17:Q:38:GLU:HA	17:Q:41:ARG:HH11	1.53	0.73
4:D:195:ARG:HG2	4:D:323:LEU:HD22	1.71	0.73
14:N:84:LYS:HE2	37:N:8575:HOH:O	1.89	0.73
1:A:289:G:H22	1:A:363:A:H2	1.37	0.73
11:K:99:GLU:HA	37:K:7377:HOH:O	1.87	0.73
27:1:40:PRO:HD3	27:1:47:LEU:HD11	1.71	0.73
8:H:63:ILE:HB	8:H:64:PRO:HD3	1.71	0.73
15:O:164:ASP:CG	15:O:167:ASP:HA	2.09	0.73
1:A:2638:G:H1'	37:A:7334:HOH:O	1.87	0.73
4:D:82:VAL:O	4:D:82:VAL:HG12	1.88	0.72
37:A:5369:HOH:O	14:N:170:CYS:SG	2.47	0.72
14:N:104:ARG:O	14:N:108:LYS:HG2	1.89	0.72
20:T:57:THR:HG22	20:T:59:ASP:N	2.02	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:143:THR:HG22	13:M:144:ASP:N	2.04	0.72
15:O:83:LEU:HD13	15:O:175:LEU:HD23	1.72	0.72
25:Y:25:ARG:HD2	37:Y:3861:HOH:O	1.87	0.72
6:F:49:PRO:HG3	37:F:5828:HOH:O	1.88	0.72
6:F:95:THR:O	6:F:97:GLN:N	2.17	0.72
1:A:346:U:H4'	37:A:6416:HOH:O	1.88	0.72
5:E:107:ARG:HB3	5:E:107:ARG:NH1	2.04	0.72
1:A:559:U:H6	1:A:559:U:H5'	1.53	0.72
1:A:450:C:OP1	5:E:184:ARG:NH2	2.18	0.72
24:X:122:ARG:NH2	24:X:154:ARG:HD2	2.03	0.72
6:F:88:LEU:HB2	6:F:89:PRO:HD3	1.71	0.72
37:A:4523:HOH:O	2:B:3103:A:H4'	1.89	0.72
14:N:87:MET:CB	30:4:46:ILE:HD13	2.18	0.72
2:B:3006:C:OP1	15:O:37:ARG:NH1	2.22	0.72
9:I:12:ILE:N	9:I:13:PRO:HD3	2.03	0.72
6:F:136:ARG:HD2	6:F:155:HIS:O	1.89	0.72
3:C:95:PRO:HG2	3:C:98:GLU:HG2	1.72	0.72
1:A:2780:C:H1'	7:G:143:GLN:HE21	1.53	0.72
7:G:84:MET:HE1	7:G:148:ILE:HD12	1.70	0.72
26:Z:141:THR:HG23	37:Z:8175:HOH:O	1.89	0.72
15:O:164:ASP:OD2	15:O:167:ASP:HA	1.90	0.72
10:J:47:GLU:HB3	10:J:133:ILE:CD1	2.18	0.71
11:K:19:MET:CE	11:K:132:LEU:HD11	2.20	0.71
13:M:114:VAL:HG11	37:M:8445:HOH:O	1.90	0.71
20:T:51:GLN:NE2	20:T:53:ASN:HD21	1.88	0.71
1:A:2716:G:H5"	4:D:206:THR:HG21	1.71	0.71
8:H:96:ALA:HA	37:H:3111:HOH:O	1.90	0.71
5:E:132:ASP:HB3	37:E:8360:HOH:O	1.90	0.71
14:N:74:ARG:HH11	14:N:74:ARG:HG3	1.55	0.71
26:Z:200:THR:HG22	26:Z:201:GLU:CG	2.21	0.71
1:A:1684:A:H1'	29:3:43:ARG:HH22	1.55	0.71
10:J:26:LYS:HD2	10:J:28:ILE:CD1	2.20	0.71
1:A:1118:A:H62	1:A:1244:U:H3	1.39	0.71
5:E:140:VAL:HB	37:E:8448:HOH:O	1.89	0.71
24:X:154:ARG:C	37:X:4276:HOH:O	2.28	0.71
1:A:281:U:H2'	1:A:282:C:O4'	1.90	0.71
20:T:51:GLN:HE21	20:T:53:ASN:ND2	1.88	0.71
25:Y:72:VAL:HG22	25:Y:85:VAL:HG12	1.73	0.71
5:E:27:ARG:HG3	5:E:29:ASP:OD1	1.89	0.71
4:D:36:PRO:HA	4:D:168:GLY:CA	2.21	0.71
19:S:18:LEU:HD12	19:S:143:VAL:HG11	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:603:A:H5"	1:A:604:G:OP1	1.90	0.71
10:J:162:SER:CB	10:J:163:PRO:HD3	2.19	0.71
14:N:164:THR:HG22	14:N:167:GLY:N	2.04	0.71
15:O:183:ASP:OD2	15:O:186:LEU:HD12	1.90	0.71
30:4:70:ARG:HD3	37:4:8539:HOH:O	1.90	0.71
13:M:53:ARG:NH2	13:M:57:VAL:HG12	2.05	0.71
1:A:2779:G:H21	7:G:143:GLN:NE2	1.89	0.71
1:A:541:C:H2'	1:A:542:A:C5'	2.18	0.70
1:A:1185:U:H2'	1:A:1186:C:C6	2.26	0.70
27:1:62:TYR:CE2	27:1:64:ILE:HG23	2.26	0.70
4:D:36:PRO:HA	4:D:168:GLY:HA3	1.73	0.70
1:A:1187:U:HO2'	1:A:1189:A:H2	1.37	0.70
6:F:55:LYS:HA	37:F:6752:HOH:O	1.91	0.70
1:A:2044:G:OP1	25:Y:23:HIS:HE1	1.73	0.70
2:B:3039:U:H1'	2:B:3044:A:H61	1.57	0.70
1:A:2890:A:H1'	22:V:56:ARG:NH2	2.07	0.70
4:D:221:GLN:HE22	12:L:42:ASN:HD22	1.39	0.70
6:F:23:VAL:HG23	6:F:23:VAL:O	1.92	0.70
1:A:1666:C:H2'	1:A:1667:A:H5'	1.73	0.70
37:A:5870:HOH:O	6:F:99:ASP:HA	1.90	0.70
2:B:3026:C:P	37:B:8441:HOH:O	2.48	0.70
24:X:4:LEU:HD23	24:X:54:PHE:HB3	1.72	0.70
2:B:3035:C:H5"	37:B:8455:HOH:O	1.91	0.69
1:A:2768:A:H2'	1:A:2769:C:O4'	1.91	0.69
3:C:105:VAL:CG1	3:C:154:ALA:HB1	2.21	0.69
1:A:2812:A:N7	37:A:7092:HOH:O	2.24	0.69
1:A:2346:C:O2'	6:F:52:THR:HG21	1.92	0.69
8:H:91:VAL:HG12	8:H:92:GLY:H	1.57	0.69
6:F:35:ALA:N	37:F:5576:HOH:O	2.24	0.69
15:O:71:TRP:HE3	15:O:175:LEU:HD22	1.56	0.69
7:G:107:PHE:CE2	7:G:108:LEU:HD13	2.28	0.69
3:C:173:GLY:O	3:C:176:HIS:HB3	1.91	0.69
1:A:21:G:C5'	19:S:2:ILE:HA	2.22	0.69
35:A:8513:CL:CL	37:A:4259:HOH:O	2.46	0.69
12:L:22:ASP:HB2	37:L:5264:HOH:O	1.92	0.69
1:A:381:G:H5"	37:A:3894:HOH:O	1.92	0.69
23:W:64:GLY:O	23:W:65:ASP:HB2	1.91	0.69
1:A:1127:C:H2'	1:A:1128:U:H5'	1.72	0.69
10:J:130:HIS:CD2	10:J:133:ILE:HD11	2.27	0.69
11:K:107:ASN:ND2	11:K:109:TYR:H	1.90	0.69
1:A:1441:G:O2'	1:A:1442:A:H5'	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1080:C:H4'	1:A:1081:A:OP1	1.92	0.69
1:A:2301:A:H5"	1:A:2302:A:H5'	1.73	0.69
14:N:30:GLU:O	14:N:34:GLU:HG3	1.92	0.69
1:A:1328:A:N7	1:A:1329:A:C5	2.61	0.69
16:P:87:THR:O	16:P:91:GLN:HG3	1.93	0.69
12:L:55:VAL:HG12	12:L:56:SER:N	2.08	0.69
14:N:164:THR:CG2	14:N:165:SER:N	2.55	0.69
1:A:282:C:H1'	1:A:368:C:H42	1.58	0.69
1:A:1170:U:O2'	1:A:1172:G:N7	2.24	0.69
5:E:129:HIS:HE1	5:E:231:ARG:HA	1.58	0.69
14:N:34:GLU:HB3	14:N:35:PRO:HD2	1.75	0.68
1:A:1835:U:C5	1:A:1840:A:N7	2.55	0.68
6:F:95:THR:C	6:F:97:GLN:H	1.96	0.68
1:A:1973:A:H5'	1:A:1973:A:H8	1.57	0.68
21:U:63:ILE:HD11	21:U:75:GLU:HB2	1.75	0.68
4:D:297:VAL:HB	37:D:8607:HOH:O	1.93	0.68
4:D:190:MET:HE2	4:D:194:PHE:CD1	2.28	0.68
1:A:1862:C:H1'	37:A:6790:HOH:O	1.92	0.68
1:A:1160:G:N3	37:A:5210:HOH:O	2.26	0.68
1:A:820:G:O2'	1:A:856:G:H4'	1.94	0.68
10:J:139:ASP:HA	37:J:8373:HOH:O	1.93	0.68
6:F:69:ILE:O	6:F:69:ILE:HG22	1.93	0.68
11:K:88:PRO:HA	35:K:8502:CL:CL	2.30	0.68
14:N:139:PRO:O	14:N:140:ALA:HB3	1.93	0.68
37:A:3935:HOH:O	16:P:37:ARG:HG3	1.94	0.68
10:J:84:ARG:NH2	10:J:135:TRP:HH2	1.91	0.68
1:A:2420:G:O2'	1:A:2421:G:H5'	1.94	0.68
23:W:58:THR:O	23:W:62:GLU:HG3	1.94	0.68
25:Y:76:ARG:HH11	25:Y:76:ARG:HG3	1.58	0.68
26:Z:189:ASN:HA	26:Z:217:ILE:HD11	1.74	0.68
22:V:9:CYS:HA	22:V:52:THR:HG23	1.74	0.68
2:B:3028:U:H2'	2:B:3029:C:C6	2.29	0.68
1:A:2414:A:H2'	1:A:2415:A:C8	2.28	0.68
1:A:1209:C:H2'	1:A:1210:G:H8	1.59	0.68
26:Z:186:ARG:HH11	26:Z:186:ARG:HG2	1.59	0.68
27:1:19:GLY:O	27:1:23:ARG:HG2	1.93	0.67
15:O:80:SER:HB2	37:O:8536:HOH:O	1.93	0.67
10:J:3:GLY:HA2	10:J:57:ARG:HH12	1.57	0.67
12:L:62:PRO:HG3	12:L:65:ARG:NH2	2.09	0.67
23:W:39:ALA:N	23:W:40:PRO:HD2	2.09	0.67
5:E:104:ASP:HA	5:E:107:ARG:NH1	2.08	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:110:GLU:HG2	37:H:6926:HOH:O	1.95	0.67
1:A:2265:U:H2'	1:A:2266:A:C8	2.30	0.67
1:A:1119:G:N2	1:A:1246:A:H2	1.91	0.67
1:A:2064:U:OP1	37:A:9929:HOH:O	2.12	0.67
1:A:1003:U:O2	10:J:90:PHE:HZ	1.78	0.67
6:F:38:GLU:OE2	6:F:51:ARG:CZ	2.43	0.67
10:J:46:VAL:HG12	10:J:146:TRP:HZ3	1.59	0.67
8:H:50:VAL:HG13	8:H:60:VAL:HG11	1.77	0.67
6:F:99:ASP:HB2	6:F:103:ASN:HB2	1.77	0.67
5:E:129:HIS:CE1	5:E:231:ARG:HA	2.30	0.67
8:H:53:ASP:OD1	8:H:80:GLN:HB2	1.94	0.67
3:C:131:HIS:O	3:C:132:ASP:HB2	1.93	0.67
1:A:1733:A:H4'	4:D:212:GLN:HA	1.75	0.67
24:X:65:VAL:HA	24:X:68:THR:HG22	1.77	0.67
25:Y:71:ARG:HD3	37:Y:2171:HOH:O	1.95	0.67
10:J:55:GLN:NE2	10:J:124:ARG:HE	1.93	0.67
19:S:39:THR:HB	19:S:42:GLU:HG3	1.76	0.67
5:E:233:THR:HG22	5:E:234:VAL:N	2.08	0.67
14:N:138:HIS:ND1	14:N:139:PRO:O	2.22	0.67
1:A:1594:C:OP2	17:Q:120:ARG:HD2	1.94	0.67
1:A:1119:G:H2'	11:K:52:GLN:NE2	2.09	0.67
1:A:506:G:H22	1:A:509:A:H5'	1.60	0.67
8:H:99:THR:HA	37:H:3461:HOH:O	1.95	0.67
8:H:39:SER:HB3	8:H:45:ALA:HB2	1.77	0.67
2:B:3023:U:C4'	2:B:3024:U:OP2	2.39	0.66
26:Z:187:VAL:CG2	26:Z:192:ASP:HB2	2.26	0.66
24:X:21:LEU:HD22	24:X:26:ILE:HD11	1.75	0.66
1:A:2578:G:H8	1:A:2578:G:H5'	1.60	0.66
20:T:80:ARG:NH1	37:T:8346:HOH:O	2.28	0.66
1:A:2004:U:H4'	37:A:4881:HOH:O	1.94	0.66
1:A:1919:A:H4'	37:A:4419:HOH:O	1.95	0.66
11:K:133:GLY:O	11:K:137:GLU:HG3	1.95	0.66
14:N:139:PRO:O	14:N:140:ALA:CB	2.43	0.66
1:A:69:A:H8	1:A:69:A:H5'	1.60	0.66
1:A:885:G:OP2	37:A:8984:HOH:O	2.14	0.66
3:C:192:VAL:HB	37:C:8596:HOH:O	1.94	0.66
4:D:71:VAL:HG11	4:D:296:LEU:HB3	1.76	0.66
37:A:7154:HOH:O	27:1:31:ILE:HG13	1.95	0.66
1:A:870:G:C2'	1:A:871:G:H5"	2.23	0.66
14:N:38:VAL:C	14:N:63:VAL:HG13	2.15	0.66
1:A:1328:A:OP1	26:Z:169:ARG:HD2	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:25:ARG:NH1	37:Y:3861:HOH:O	2.29	0.66
24:X:149:LEU:HG	24:X:153:MET:HE2	1.75	0.66
26:Z:212:ARG:HD2	37:Z:8186:HOH:O	1.95	0.66
1:A:1213:C:O2'	1:A:1214:G:H5'	1.96	0.66
1:A:2391:C:OP1	37:A:8913:HOH:O	2.14	0.66
6:F:57:THR:HG23	6:F:63:ILE:HG22	1.77	0.66
1:A:1847:A:OP1	3:C:175:LYS:HG3	1.96	0.66
23:W:12:THR:HG22	23:W:15:GLU:CG	2.18	0.66
1:A:2349:G:OP1	6:F:20:LYS:NZ	2.28	0.66
3:C:36:ASP:OD2	3:C:85:ASP:HB2	1.95	0.66
1:A:2361:A:H5"	37:A:8601:HOH:O	1.94	0.66
3:C:200:PRO:O	37:C:8589:HOH:O	2.14	0.66
10:J:14:TYR:H	10:J:91:HIS:CE1	2.13	0.66
1:A:2587:U:H2'	1:A:2589:U:H5"	1.78	0.66
14:N:87:MET:CB	30:4:46:ILE:HG21	2.25	0.66
29:3:41:HIS:H	29:3:45:ASN:ND2	1.94	0.66
11:K:93:ARG:HH11	11:K:93:ARG:HB3	1.59	0.66
37:A:7029:HOH:O	5:E:188:ARG:HD2	1.95	0.66
1:A:2630:G:O6	3:C:206:ARG:NH2	2.28	0.66
3:C:76:VAL:HG23	27:1:63:LYS:HB3	1.77	0.66
21:U:48:VAL:HG22	21:U:97:ARG:C	2.15	0.66
2:B:3029:C:H2'	2:B:3030:C:H5'	1.77	0.66
1:A:2064:U:H5'	1:A:2652:U:O3'	1.96	0.66
1:A:204:A:H2'	1:A:205:U:H5'	1.77	0.66
1:A:1330:A:H5"	1:A:1331:A:OP2	1.95	0.66
29:3:41:HIS:N	29:3:45:ASN:HD22	1.92	0.66
1:A:1159:G:P	37:A:3869:HOH:O	2.53	0.66
14:N:157:LEU:HB3	14:N:160:PHE:HD1	1.60	0.66
6:F:97:GLN:O	6:F:97:GLN:HG2	1.96	0.66
11:K:107:ASN:HD21	11:K:109:TYR:HB2	1.61	0.66
1:A:428:G:OP1	37:A:5799:HOH:O	2.13	0.66
25:Y:15:ARG:NH1	25:Y:15:ARG:HB3	2.10	0.65
25:Y:25:ARG:HG2	37:Y:5356:HOH:O	1.96	0.65
4:D:41:PHE:CD1	4:D:79:MET:HE2	2.31	0.65
27:1:28:ASP:O	27:1:31:ILE:HG22	1.96	0.65
4:D:18:ARG:HG3	4:D:256:GLN:HG3	1.77	0.65
1:A:681:G:N3	1:A:681:G:H5'	2.11	0.65
1:A:2488:A:H61	1:A:2534:C:H42	1.43	0.65
17:Q:59:ARG:NH2	17:Q:66:GLN:HE22	1.95	0.65
1:A:2719:A:C2	4:D:70:PRO:HG3	2.31	0.65
1:A:1119:G:H8	11:K:52:GLN:HE22	1.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:135:VAL:HG22	6:F:136:ARG:H	1.61	0.65
10:J:35:ASN:ND2	10:J:80:ASN:HA	2.11	0.65
1:A:629:A:N7	37:A:9440:HOH:O	2.30	0.65
4:D:175:LEU:O	4:D:175:LEU:HD23	1.96	0.65
1:A:69:A:C8	1:A:69:A:H5'	2.31	0.65
26:Z:216:ARG:HD3	37:Z:8157:HOH:O	1.95	0.65
3:C:1:GLY:N	37:C:8611:HOH:O	2.28	0.65
6:F:19:GLU:O	6:F:20:LYS:HG2	1.96	0.65
1:A:2064:U:H4'	1:A:2653:A:OP1	1.97	0.65
23:W:44:GLY:O	23:W:48:GLU:HG2	1.96	0.65
14:N:59:GLY:HA3	14:N:141:ILE:CD1	2.26	0.65
37:B:8473:HOH:O	15:O:23:ARG:HD3	1.96	0.65
8:H:91:VAL:HG12	8:H:92:GLY:N	2.11	0.65
7:G:6:GLU:HA	7:G:46:THR:HG22	1.77	0.65
1:A:299:U:H5'	37:A:6908:HOH:O	1.97	0.65
4:D:145:HIS:HD2	4:D:146:THR:O	1.78	0.65
1:A:316:A:H5'	21:U:54:ASP:OD2	1.97	0.65
19:S:106:GLY:HA2	19:S:109:MET:HE3	1.79	0.65
3:C:105:VAL:HG12	3:C:106:CYS:N	2.12	0.65
1:A:2502:C:C2'	1:A:2503:A:H5'	2.27	0.65
22:V:52:THR:HG22	22:V:54:THR:H	1.62	0.65
1:A:131:A:OP2	37:A:9746:HOH:O	2.14	0.65
1:A:2821:C:H4'	4:D:116:PRO:HB3	1.76	0.65
6:F:41:LEU:HA	6:F:44:ILE:HG22	1.79	0.65
10:J:57:ARG:O	10:J:61:LEU:HD22	1.97	0.65
1:A:2536:C:OP1	37:A:9702:HOH:O	2.12	0.65
4:D:2:GLN:HA	37:D:8622:HOH:O	1.96	0.65
14:N:60:ILE:C	14:N:61:ILE:HD12	2.17	0.65
1:A:545:G:C8	1:A:545:G:H5'	2.30	0.65
24:X:4:LEU:HD22	24:X:52:VAL:HG21	1.79	0.65
2:B:3014:G:H5'	2:B:3014:G:C8	2.30	0.65
24:X:72:PRO:HG2	24:X:77:ALA:HB3	1.78	0.65
35:K:8501:CL:CL	37:K:4038:HOH:O	2.51	0.65
6:F:37:ALA:O	6:F:40:ILE:HG12	1.97	0.64
20:T:58:MET:SD	29:3:8:LYS:HE3	2.37	0.64
6:F:174:VAL:HG13	37:F:6555:HOH:O	1.96	0.64
1:A:1130:U:H2'	1:A:1131:G:O4'	1.97	0.64
1:A:2908:A:H2'	1:A:2909:G:O4'	1.97	0.64
1:A:1377:C:H5'	1:A:1377:C:H6	1.62	0.64
24:X:88:THR:HG23	24:X:110:GLN:HE21	1.63	0.64
12:L:74:VAL:HG12	12:L:75:ARG:HG3	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:19:MET:HE2	11:K:132:LEU:HD11	1.77	0.64
30:4:69:TYR:HB2	30:4:78:HIS:CE1	2.32	0.64
1:A:272:A:H3'	37:A:7105:HOH:O	1.98	0.64
4:D:125:GLU:O	4:D:129:ARG:HG3	1.96	0.64
14:N:87:MET:HB3	30:4:46:ILE:HG21	1.79	0.64
5:E:78:ARG:NH1	5:E:78:ARG:HG3	2.08	0.64
17:Q:38:GLU:HA	17:Q:41:ARG:NH1	2.12	0.64
1:A:1329:A:N1	35:A:8513:CL:CL	2.67	0.64
27:1:61:GLY:HA3	37:1:8427:HOH:O	1.97	0.64
5:E:236:THR:CG2	5:E:239:ALA:H	2.00	0.64
3:C:125:ASN:CB	3:C:158:VAL:HG12	2.27	0.64
15:O:143:ARG:HA	15:O:172:PHE:CD2	2.33	0.64
11:K:80:LYS:HE2	11:K:98:PHE:CZ	2.32	0.64
25:Y:15:ARG:HH11	25:Y:15:ARG:CB	2.10	0.64
10:J:3:GLY:HA2	10:J:57:ARG:NH1	2.12	0.64
1:A:282:C:O2'	1:A:283:U:H5'	1.98	0.64
15:O:159:TYR:HB3	15:O:162:ASP:HB2	1.80	0.64
15:O:43:VAL:HG11	15:O:81:ALA:HA	1.79	0.64
13:M:136:ALA:HB3	37:M:8445:HOH:O	1.97	0.64
1:A:558:C:O2'	1:A:559:U:H5"	1.98	0.64
7:G:7:ILE:HD11	7:G:11:VAL:C	2.18	0.64
1:A:1874:U:H2'	3:C:120:ARG:HG3	1.79	0.64
4:D:16:ARG:NE	37:D:8556:HOH:O	2.11	0.64
21:U:52:ARG:HB2	21:U:95:ASN:HB3	1.80	0.64
4:D:258:GLY:H	4:D:260:HIS:CE1	2.14	0.64
4:D:179:LEU:O	4:D:183:GLU:HG2	1.98	0.64
17:Q:103:THR:HA	17:Q:106:ARG:NH1	2.12	0.64
1:A:182:G:H5'	37:A:4731:HOH:O	1.98	0.64
11:K:88:PRO:CA	35:K:8502:CL:CL	2.83	0.64
1:A:2783:A:H3'	37:A:4807:HOH:O	1.98	0.64
1:A:821:U:O2'	1:A:822:C:H5'	1.98	0.64
15:O:154:LEU:O	15:O:155:GLU:HB3	1.98	0.64
6:F:23:VAL:HG22	6:F:73:VAL:HB	1.80	0.64
4:D:162:MET:CE	4:D:308:LEU:HD21	2.27	0.64
5:E:129:HIS:CE1	5:E:232:LEU:H	2.16	0.64
5:E:180:SER:HB2	37:E:8442:HOH:O	1.97	0.64
14:N:172:GLY:O	14:N:183:VAL:HG11	1.98	0.64
8:H:58:GLU:HA	8:H:61:MET:HE2	1.80	0.63
19:S:18:LEU:HB2	19:S:143:VAL:HG12	1.79	0.63
2:B:3092:G:H2'	2:B:3093:A:C8	2.34	0.63
24:X:41:TYR:O	24:X:45:VAL:HG13	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1741:U:H5'	1:A:1742:A:OP1	1.97	0.63
6:F:64:ARG:CD	6:F:67:ASP:HB3	2.28	0.63
1:A:2748:G:H2'	37:A:7117:HOH:O	1.97	0.63
25:Y:71:ARG:CD	37:Y:2171:HOH:O	2.47	0.63
30:4:65:THR:HG23	30:4:67:LEU:HG	1.80	0.63
1:A:2547:C:OP2	4:D:5:ARG:NH1	2.31	0.63
5:E:219:ASN:O	5:E:222:ASP:OD1	2.16	0.63
24:X:13:MET:HE3	24:X:17:ILE:HG22	1.80	0.63
26:Z:99:ALA:HB2	26:Z:233:TYR:CZ	2.33	0.63
4:D:75:GLU:C	4:D:77:PRO:HD3	2.19	0.63
6:F:25:MET:HE1	6:F:37:ALA:O	1.99	0.63
1:A:1441:G:H1'	37:A:7340:HOH:O	1.98	0.63
1:A:2270:G:H4'	3:C:223:ARG:HH12	1.63	0.63
1:A:2502:C:H2'	1:A:2503:A:H5'	1.80	0.63
14:N:81:ARG:HG3	14:N:85:ARG:HB2	1.81	0.63
5:E:242:GLU:HG3	37:E:8378:HOH:O	1.97	0.63
4:D:48:MET:N	37:D:8560:HOH:O	2.31	0.63
1:A:1015:C:H2'	1:A:1016:U:H6	1.63	0.63
3:C:94:LEU:HD23	3:C:94:LEU:N	2.13	0.63
21:U:71:VAL:HG11	21:U:90:PRO:CB	2.20	0.63
12:L:81:ARG:HD3	12:L:87:ARG:NH1	2.14	0.63
6:F:146:LYS:HZ3	15:O:107:ASN:HD21	1.44	0.63
1:A:281:U:H3'	37:A:6777:HOH:O	1.99	0.63
1:A:2363:G:O3'	18:R:11:ARG:NH1	2.32	0.63
1:A:1878:G:H1'	37:A:5700:HOH:O	1.97	0.63
21:U:65:VAL:HG22	21:U:72:ILE:HG22	1.81	0.63
1:A:1771:U:H4'	27:1:20:LEU:HD21	1.79	0.63
1:A:1735:C:O2'	1:A:1736:A:H5'	1.99	0.63
37:A:6598:HOH:O	3:C:211:LYS:HG2	1.99	0.63
5:E:127:ARG:HH11	5:E:127:ARG:HG2	1.62	0.63
1:A:2419:U:H5"	1:A:2420:G:H5'	1.80	0.63
1:A:2468:A:H61	30:4:48:ASN:HD21	1.45	0.63
11:K:52:GLN:HG3	11:K:53:ILE:N	2.14	0.62
10:J:59:ASN:H	10:J:59:ASN:ND2	1.96	0.62
22:V:52:THR:HG22	22:V:54:THR:N	2.13	0.62
1:A:111:C:O2'	28:2:20:ARG:HG2	1.99	0.62
2:B:3001:U:O3'	2:B:3003:A:H5"	1.99	0.62
1:A:2416:G:O2'	37:A:9212:HOH:O	2.15	0.62
1:A:1679:C:H5'	37:A:8905:HOH:O	1.98	0.62
27:1:29:VAL:O	27:1:33:HIS:HB2	1.99	0.62
1:A:419:A:H1'	1:A:1921:A:C2	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:42:ASN:HB3	37:W:7247:HOH:O	1.99	0.62
5:E:12:THR:HB	37:E:8438:HOH:O	1.98	0.62
13:M:125:PHE:CZ	13:M:140:VAL:HG13	2.34	0.62
1:A:1503:U:H2'	1:A:1504:A:O4'	1.98	0.62
1:A:755:G:O2'	1:A:756:A:H5'	1.99	0.62
5:E:139:VAL:HG13	37:E:8445:HOH:O	1.98	0.62
1:A:2099:G:N2	31:A:8600:ZIT:H181	2.14	0.62
1:A:2383:G:N3	37:A:6280:HOH:O	2.31	0.62
25:Y:31:ILE:O	25:Y:35:GLU:HG3	2.00	0.62
1:A:960:G:N3	1:A:960:G:H2'	2.15	0.62
4:D:62:ARG:HA	4:D:65:MET:CE	2.28	0.62
14:N:186:SER:OG	14:N:189:VAL:HG12	1.99	0.62
19:S:18:LEU:HG	19:S:91:LEU:HD13	1.82	0.62
8:H:19:ALA:O	8:H:22:VAL:HG22	2.00	0.62
6:F:144:ARG:NH2	37:F:3839:HOH:O	2.32	0.62
1:A:542:A:H8	1:A:542:A:C5'	2.07	0.62
13:M:133:VAL:HB	37:M:8431:HOH:O	1.99	0.62
15:O:151:ASP:O	15:O:154:LEU:HB2	2.00	0.62
26:Z:107:PRO:HB3	26:Z:182:PHE:CE2	2.34	0.62
26:Z:235:GLU:CD	26:Z:235:GLU:H	2.03	0.62
15:O:33:ARG:NH1	15:O:103:ASP:OD2	2.31	0.62
3:C:53:ALA:HB3	37:C:8609:HOH:O	2.00	0.62
22:V:37:GLU:HB3	37:V:408:HOH:O	1.98	0.62
12:L:115:ARG:HG3	12:L:116:GLU:N	2.14	0.62
11:K:74:ARG:O	11:K:78:ILE:HG12	1.99	0.62
4:D:195:ARG:HD2	4:D:324:ASP:OD1	2.00	0.62
22:V:13:ILE:HG12	22:V:32:CYS:HB3	1.80	0.62
2:B:3013:A:O2'	2:B:3014:G:H5"	2.00	0.62
24:X:81:ASP:OD1	24:X:92:ASP:HB2	2.00	0.62
8:H:2:VAL:HG22	8:H:57:GLU:OE1	2.00	0.62
4:D:30:PRO:HB2	4:D:39:GLN:NE2	2.15	0.62
1:A:1789:G:O6	17:Q:73:HIS:HE1	1.83	0.62
3:C:109:GLU:HG2	3:C:116:GLY:H	1.65	0.62
1:A:1701:A:H4'	1:A:1702:U:H5"	1.80	0.62
1:A:1701:A:H5'	37:A:5859:HOH:O	1.99	0.62
7:G:166:VAL:HG12	37:G:3134:HOH:O	1.98	0.62
24:X:54:PHE:CZ	24:X:140:LYS:HB2	2.35	0.62
1:A:2526:C:O2'	1:A:2527:U:H5'	2.00	0.62
25:Y:21:PRO:HG2	25:Y:24:LYS:HD3	1.81	0.62
14:N:12:TRP:CE2	14:N:20:ILE:HD11	2.35	0.62
1:A:1116:U:O2'	1:A:1118:A:C2	2.46	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:57:VAL:HG12	13:M:57:VAL:O	2.00	0.61
37:A:3767:HOH:O	26:Z:186:ARG:HD2	1.99	0.61
15:O:61:ALA:HB3	15:O:88:ALA:HB2	1.82	0.61
1:A:396:U:H1'	37:A:7204:HOH:O	1.99	0.61
15:O:12:ARG:HD3	15:O:18:THR:OG1	2.00	0.61
27:1:13:ARG:NH1	27:1:14:PHE:CE2	2.68	0.61
5:E:236:THR:H	5:E:239:ALA:HB3	1.65	0.61
1:A:1306:U:OP1	5:E:184:ARG:HD2	2.00	0.61
1:A:1003:U:O2	10:J:90:PHE:CZ	2.53	0.61
4:D:141:ARG:HG2	4:D:165:ARG:HA	1.82	0.61
10:J:33:MET:HB2	10:J:83:PHE:HB3	1.82	0.61
5:E:118:THR:O	5:E:136:VAL:HG13	2.01	0.61
25:Y:41:PHE:O	25:Y:43:VAL:HG23	2.00	0.61
4:D:204:GLY:HA3	37:D:8658:HOH:O	1.99	0.61
6:F:44:ILE:HG23	6:F:45:THR:HG23	1.82	0.61
9:I:12:ILE:N	9:I:13:PRO:CD	2.64	0.61
1:A:1329:A:H2	37:A:4259:HOH:O	1.83	0.61
11:K:45:VAL:HG23	11:K:130:VAL:O	2.01	0.61
1:A:2694:A:H4'	7:G:91:PHE:CE1	2.35	0.61
20:T:81:ILE:HG23	37:T:8337:HOH:O	2.00	0.61
10:J:53:PRO:HG3	10:J:127:GLY:H	1.64	0.61
15:O:78:MET:HB2	15:O:79:PRO:HD3	1.82	0.61
14:N:74:ARG:HG3	14:N:74:ARG:NH1	2.15	0.61
6:F:99:ASP:CB	6:F:103:ASN:H	2.13	0.61
3:C:101:GLU:OE2	3:C:131:HIS:HB2	2.00	0.61
26:Z:107:PRO:HB3	26:Z:182:PHE:CD2	2.36	0.61
1:A:1200:A:H4'	37:A:6912:HOH:O	1.99	0.61
10:J:144:GLU:HA	10:J:144:GLU:OE1	2.00	0.61
1:A:1313:A:H5'	26:Z:208:LYS:O	2.00	0.61
9:I:63:ARG:N	37:I:2569:HOH:O	2.33	0.61
8:H:50:VAL:HG21	8:H:63:ILE:HG21	1.83	0.61
1:A:2827:A:H2'	1:A:2828:G:O4'	1.99	0.61
23:W:49:LEU:O	23:W:53:ILE:HG13	1.99	0.61
30:4:62:THR:HB	37:4:8551:HOH:O	2.00	0.61
1:A:2501:G:H1'	37:A:4118:HOH:O	2.00	0.61
1:A:1119:G:H2'	11:K:52:GLN:HE22	1.64	0.61
4:D:51:VAL:CG2	4:D:327:VAL:HG13	2.30	0.61
1:A:2710:U:H1'	37:A:7196:HOH:O	2.00	0.61
5:E:237:GLU:HB2	37:E:8426:HOH:O	2.00	0.61
10:J:27:LYS:N	10:J:58:HIS:HD2	1.96	0.61
4:D:307:ARG:HH11	4:D:307:ARG:CB	2.13	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1130:U:H5'	37:A:7245:HOH:O	2.00	0.61
1:A:2320:U:H4'	1:A:2321:A:O4'	2.01	0.61
26:Z:126:PRO:HG2	26:Z:128:PHE:CE1	2.36	0.61
37:A:4405:HOH:O	11:K:47:THR:HB	1.99	0.61
6:F:166:ILE:HD12	37:F:6326:HOH:O	2.01	0.61
1:A:182:G:H4'	14:N:157:LEU:HD13	1.82	0.61
1:A:184:G:H5"	14:N:153:THR:HG22	1.83	0.61
6:F:146:LYS:NZ	15:O:107:ASN:ND2	2.47	0.61
1:A:558:C:H2'	1:A:559:U:H5'	1.83	0.61
13:M:104:ASP:O	13:M:105:TYR:HB3	2.00	0.61
14:N:87:MET:HG2	30:4:46:ILE:CG2	2.27	0.61
14:N:185:PRO:HG2	14:N:189:VAL:HG11	1.81	0.61
1:A:2505:G:O2'	1:A:2506:A:H5'	2.01	0.61
8:H:100:ASP:HB3	37:H:5691:HOH:O	2.01	0.61
3:C:153:ARG:CB	3:C:153:ARG:HH11	2.14	0.61
2:B:3002:U:H4'	2:B:3002:U:OP2	2.00	0.61
16:P:42:GLU:HB2	37:P:2176:HOH:O	2.00	0.61
32:A:8036:MG:MG	37:A:7398:HOH:O	1.43	0.61
1:A:738:G:H3'	37:A:6619:HOH:O	2.00	0.61
1:A:240:C:H4'	14:N:146:GLN:NE2	2.16	0.60
37:A:4040:HOH:O	14:N:146:GLN:HG2	1.99	0.60
22:V:52:THR:CG2	22:V:54:THR:HB	2.31	0.60
16:P:26:TRP:N	37:P:3062:HOH:O	2.34	0.60
1:A:2081:A:H4'	11:K:69:TYR:CE1	2.35	0.60
4:D:55:ASN:HB3	4:D:63:GLU:HA	1.83	0.60
5:E:85:LYS:NZ	37:E:8326:HOH:O	2.24	0.60
1:A:2403:C:H3'	37:A:4787:HOH:O	2.01	0.60
24:X:130:HIS:O	24:X:136:GLY:HA3	2.01	0.60
30:4:17:HIS:O	30:4:18:GLN:HG3	2.01	0.60
1:A:1205:U:H2'	1:A:1206:U:C5'	2.30	0.60
7:G:31:ARG:NH1	7:G:68:HIS:CG	2.70	0.60
1:A:1120:U:H5"	1:A:1120:U:C6	2.36	0.60
4:D:305:ASP:O	4:D:306:LYS:HB2	2.02	0.60
1:A:1636:G:O2'	1:A:1637:A:H5'	2.00	0.60
1:A:1008:C:H5"	10:J:16:ARG:HH12	1.65	0.60
25:Y:66:THR:HG23	25:Y:67:PRO:HD2	1.82	0.60
10:J:139:ASP:H	10:J:140:PRO:HD3	1.66	0.60
7:G:49:ILE:HD11	7:G:69:ILE:HD12	1.83	0.60
6:F:65:GLU:HG3	37:F:6752:HOH:O	2.00	0.60
3:C:190:ARG:NH2	3:C:207:GLN:OE1	2.33	0.60
5:E:84:VAL:O	5:E:85:LYS:HB2	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:C:H2'	1:A:137:U:O4'	2.00	0.60
1:A:2392:C:N3	37:A:4421:HOH:O	2.31	0.60
10:J:136:VAL:HG22	10:J:137:ASN:O	2.01	0.60
10:J:26:LYS:HG2	10:J:28:ILE:N	2.15	0.60
7:G:20:ILE:CD1	7:G:40:VAL:HG11	2.30	0.60
7:G:23:GLU:HG2	7:G:28:SER:CB	2.32	0.60
1:A:2346:C:H6	1:A:2346:C:O5'	1.83	0.60
10:J:53:PRO:HA	10:J:125:VAL:O	2.02	0.60
1:A:1200:A:C4'	37:A:6912:HOH:O	2.49	0.60
1:A:321:A:H1'	37:A:6605:HOH:O	2.02	0.60
10:J:71:TYR:C	10:J:73:GLN:H	2.05	0.60
1:A:212:A:O4'	1:A:214:U:C6	2.55	0.60
25:Y:78:GLU:CG	25:Y:79:GLU:H	2.14	0.60
1:A:1151:G:OP1	9:I:63:ARG:NH1	2.35	0.60
6:F:93:LEU:HB3	6:F:97:GLN:OE1	2.02	0.60
1:A:2672:C:H1'	37:A:6256:HOH:O	2.01	0.60
4:D:66:GLU:OE1	4:D:328:ARG:HD2	2.02	0.60
20:T:43:GLU:HB3	37:T:8344:HOH:O	2.01	0.60
1:A:1834:C:H2'	1:A:1840:A:N6	2.17	0.60
1:A:285:A:H2'	1:A:286:U:O4'	2.02	0.60
11:K:131:THR:HG22	11:K:134:GLU:H	1.65	0.60
1:A:2756:U:H3	1:A:2896:A:H2	1.46	0.60
1:A:2121:G:OP2	37:A:3095:HOH:O	2.17	0.60
27:1:30:GLU:HA	27:1:33:HIS:HB3	1.84	0.60
6:F:101:THR:HG22	37:F:7400:HOH:O	2.01	0.60
15:O:37:ARG:NE	37:O:8534:HOH:O	2.34	0.60
10:J:58:HIS:HA	10:J:61:LEU:HD23	1.83	0.60
4:D:301:VAL:HG13	4:D:302:PRO:HD2	1.83	0.60
7:G:101:GLU:HB2	7:G:116:THR:O	2.02	0.60
14:N:52:LEU:HD21	37:N:8615:HOH:O	2.02	0.59
13:M:53:ARG:NH2	13:M:57:VAL:CG1	2.65	0.59
1:A:2768:A:O2'	1:A:2769:C:H5'	2.02	0.59
3:C:69:LEU:HD21	3:C:120:ARG:HB3	1.82	0.59
14:N:69:LYS:HG2	14:N:127:LYS:HG3	1.82	0.59
21:U:24:ARG:HH21	21:U:39:ASN:HD22	1.48	0.59
1:A:1134:G:H4'	10:J:151:MET:CE	2.27	0.59
3:C:211:LYS:NZ	37:C:8574:HOH:O	2.35	0.59
8:H:28:ALA:HB3	8:H:99:THR:O	2.02	0.59
27:1:53:GLY:HA2	27:1:67:GLY:O	2.01	0.59
7:G:157:LYS:NZ	37:G:2401:HOH:O	2.35	0.59
24:X:139:GLY:O	24:X:141:HIS:HD2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:135:VAL:HG21	6:F:139:TYR:CD1	2.38	0.59
15:O:169:PRO:O	15:O:172:PHE:HB3	2.02	0.59
1:A:1766:U:O2	1:A:1778:A:H5'	2.02	0.59
8:H:58:GLU:OE1	14:N:27:ARG:NH2	2.31	0.59
26:Z:185:VAL:HG12	37:Z:8158:HOH:O	2.00	0.59
5:E:104:ASP:O	5:E:108:GLN:HG3	2.03	0.59
3:C:191:GLY:HA2	3:C:194:MET:HE3	1.84	0.59
14:N:113:ARG:NH2	14:N:156:ARG:HG2	2.18	0.59
4:D:168:GLY:N	4:D:174:ARG:HD3	2.17	0.59
1:A:2256:G:O2'	1:A:2257:G:H5'	2.02	0.59
1:A:1159:G:H21	1:A:1189:A:H8	1.49	0.59
1:A:1165:G:OP1	1:A:1165:G:H3'	2.03	0.59
20:T:53:ASN:ND2	37:T:8323:HOH:O	2.35	0.59
4:D:314:ALA:HB3	4:D:317:PRO:HG3	1.85	0.59
4:D:207:LYS:HG2	4:D:304:PRO:HB3	1.84	0.59
1:A:2694:A:H4'	7:G:91:PHE:HE1	1.66	0.59
1:A:1058:A:H2'	1:A:1060:C:H5"	1.83	0.59
1:A:2434:A:O3'	30:4:28:GLY:HA3	2.03	0.59
2:B:3107:C:C5	37:B:8437:HOH:O	2.52	0.59
5:E:16:VAL:HG12	5:E:17:ASP:N	2.17	0.59
10:J:163:PRO:O	10:J:164:ALA:HB2	2.03	0.59
4:D:62:ARG:CA	4:D:65:MET:HE3	2.29	0.59
2:B:3039:U:H1'	2:B:3044:A:N6	2.17	0.59
1:A:2363:G:O2'	18:R:11:ARG:HG3	2.03	0.59
1:A:151:A:C2	1:A:442:A:C8	2.90	0.59
1:A:544:G:C2'	1:A:545:G:H5"	2.31	0.59
1:A:1249:U:H2'	1:A:1250:C:C6	2.37	0.59
37:A:6798:HOH:O	14:N:13:LYS:HE2	2.03	0.59
16:P:14:LEU:HD23	16:P:102:ILE:HD11	1.83	0.59
1:A:1187:U:O2'	1:A:1189:A:H2	1.85	0.59
11:K:74:ARG:CB	11:K:74:ARG:HH11	2.14	0.59
4:D:41:PHE:HB3	4:D:190:MET:HE1	1.84	0.59
37:A:8703:HOH:O	5:E:103:ASN:HB3	2.02	0.59
1:A:156:C:H5"	14:N:171:ARG:CD	2.23	0.59
14:N:61:ILE:HA	37:N:8622:HOH:O	2.03	0.59
12:L:74:VAL:HG13	12:L:113:ILE:HG23	1.84	0.59
7:G:23:GLU:HG2	7:G:28:SER:HB3	1.85	0.59
10:J:127:GLY:O	10:J:128:ALA:HB3	2.03	0.59
3:C:33:GLU:O	3:C:34:ASP:HB2	2.02	0.59
1:A:263:U:O4'	8:H:59:ILE:HD13	2.02	0.59
28:2:28:HIS:HD2	28:2:31:LYS:H	1.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1819:G:H2'	1:A:1820:G:H4'	1.85	0.59
1:A:1119:G:H8	11:K:52:GLN:NE2	2.01	0.59
2:B:3048:C:H4'	15:O:141:ARG:NH2	2.18	0.59
13:M:143:THR:HG22	13:M:145:LEU:H	1.66	0.59
1:A:558:C:H2'	1:A:559:U:C5'	2.33	0.59
1:A:396:U:H5'	30:4:42:ARG:HH12	1.67	0.59
16:P:25:VAL:HG23	16:P:26:TRP:N	2.18	0.59
5:E:235:PHE:HE2	5:E:243:VAL:HG21	1.66	0.59
1:A:449:A:N7	5:E:43:LYS:HG2	2.17	0.59
2:B:3025:G:N2	37:B:8507:HOH:O	2.36	0.59
5:E:1:MET:HG2	5:E:2:GLN:N	2.16	0.58
1:A:2769:C:C2'	1:A:2770:G:H5'	2.33	0.58
28:2:20:ARG:HB2	37:2:8413:HOH:O	2.02	0.58
14:N:146:GLN:NE2	37:N:8645:HOH:O	2.36	0.58
3:C:114:ASP:HB2	3:C:117:LYS:HE2	1.84	0.58
1:A:2878:U:H2'	1:A:2879:A:O4'	2.03	0.58
23:W:39:ALA:C	23:W:41:GLU:H	2.06	0.58
4:D:16:ARG:NH2	37:D:8556:HOH:O	2.34	0.58
3:C:37:VAL:HG22	37:C:8599:HOH:O	2.02	0.58
28:2:21:ARG:HD2	28:2:37:CYS:SG	2.42	0.58
1:A:157:G:H4'	14:N:95:LYS:HE3	1.85	0.58
3:C:81:GLN:HB2	3:C:92:ASN:ND2	2.18	0.58
24:X:4:LEU:HD22	24:X:52:VAL:CG2	2.33	0.58
1:A:1234:U:C4	4:D:244:PRO:HB3	2.39	0.58
6:F:86:THR:O	6:F:90:LEU:HG	2.03	0.58
26:Z:106:THR:HG23	26:Z:107:PRO:HD2	1.85	0.58
1:A:1423:C:O2'	1:A:1424:A:H5'	2.03	0.58
37:A:9350:HOH:O	13:M:41:HIS:HE1	1.86	0.58
14:N:12:TRP:O	14:N:15:PRO:HD3	2.02	0.58
1:A:2256:G:C2'	1:A:2257:G:H5'	2.33	0.58
1:A:566:A:H2'	1:A:567:U:O4'	2.03	0.58
15:O:34:LEU:HA	15:O:47:LEU:HD23	1.86	0.58
6:F:50:VAL:O	6:F:71:ALA:HA	2.03	0.58
10:J:48:LEU:HG	10:J:157:ILE:HG21	1.85	0.58
1:A:1192:A:O2'	1:A:1193:A:OP1	2.21	0.58
16:P:47:ARG:NH1	16:P:47:ARG:HG3	2.17	0.58
8:H:28:ALA:CB	8:H:99:THR:HG23	2.32	0.58
24:X:21:LEU:HD22	24:X:26:ILE:CD1	2.33	0.58
4:D:79:MET:HE1	37:D:8627:HOH:O	2.03	0.58
4:D:154:VAL:HG12	4:D:156:LYS:HG2	1.86	0.58
1:A:1182:C:H1'	1:A:1192:A:H8	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:6:GLN:HB2	24:X:26:ILE:CD1	2.32	0.58
4:D:162:MET:HG3	4:D:310:ARG:CZ	2.34	0.58
1:A:2834:G:OP1	25:Y:39:LYS:HE2	2.01	0.58
22:V:11:THR:HG22	22:V:53:ASP:OD2	2.03	0.58
6:F:54:ALA:HB2	6:F:69:ILE:HD12	1.86	0.58
1:A:558:C:C2'	1:A:559:U:H5"	2.33	0.58
21:U:101:LEU:HD13	21:U:112:LEU:HD11	1.86	0.58
29:3:18:ASN:HD21	29:3:40:ARG:H	1.52	0.58
9:I:12:ILE:HA	37:I:4499:HOH:O	2.03	0.58
1:A:1559:A:H1'	37:A:5443:HOH:O	2.04	0.58
12:L:106:GLY:HA3	37:L:5264:HOH:O	2.02	0.58
1:A:656:G:OP2	16:P:37:ARG:HD2	2.03	0.58
1:A:241:A:C2	1:A:378:A:H4'	2.39	0.58
1:A:2094:G:H4'	4:D:245:SER:HB3	1.85	0.58
12:L:55:VAL:HG12	12:L:56:SER:H	1.68	0.58
5:E:107:ARG:NE	37:E:8454:HOH:O	2.25	0.58
37:A:5895:HOH:O	6:F:55:LYS:HB2	2.04	0.58
4:D:7:ARG:NH1	4:D:11:LEU:HD22	2.18	0.58
1:A:396:U:H5'	30:4:42:ARG:NH1	2.18	0.58
13:M:149:ARG:O	13:M:150:GLN:HB2	2.03	0.58
1:A:2276:U:H2'	1:A:2277:U:C6	2.38	0.58
12:L:28:GLU:HB3	12:L:59:LYS:HB2	1.86	0.58
37:A:7282:HOH:O	5:E:94:THR:HG21	2.04	0.58
10:J:47:GLU:CB	10:J:133:ILE:HD13	2.34	0.57
1:A:2721:U:H4'	12:L:87:ARG:HG3	1.86	0.57
3:C:186:TRP:CG	3:C:187:PRO:HA	2.39	0.57
19:S:119:VAL:HG12	19:S:119:VAL:O	2.03	0.57
1:A:1528:A:H2'	1:A:1529:G:O4'	2.04	0.57
19:S:18:LEU:HD12	19:S:143:VAL:CG1	2.34	0.57
1:A:2265:U:H2'	1:A:2266:A:H8	1.67	0.57
1:A:2472:C:O2'	1:A:2634:G:H4'	2.04	0.57
1:A:281:U:O2'	1:A:282:C:H5'	2.04	0.57
14:N:59:GLY:HA3	14:N:141:ILE:HD11	1.86	0.57
24:X:31:HIS:ND1	37:X:2229:HOH:O	2.32	0.57
1:A:1086:A:C6	24:X:11:VAL:HG11	2.38	0.57
2:B:3107:C:H5	37:B:8437:HOH:O	1.86	0.57
25:Y:75:ALA:O	25:Y:83:ALA:HA	2.04	0.57
1:A:20:G:H21	19:S:117:HIS:HD2	1.51	0.57
1:A:280:C:H2'	1:A:281:U:O4'	2.05	0.57
13:M:145:LEU:O	13:M:148:GLU:HG3	2.03	0.57
1:A:204:A:C2'	1:A:205:U:H5'	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:G:OP1	37:A:3304:HOH:O	2.17	0.57
16:P:39:THR:O	16:P:115:ARG:NH2	2.37	0.57
1:A:1191:A:C3'	1:A:1192:A:H5"	2.35	0.57
15:O:86:LEU:O	15:O:90:LEU:HG	2.05	0.57
5:E:27:ARG:HG2	5:E:30:LEU:HG	1.86	0.57
4:D:40:GLY:O	37:D:8557:HOH:O	2.17	0.57
9:I:64:ASN:HD22	9:I:64:ASN:N	2.02	0.57
14:N:87:MET:HB2	14:N:91:ILE:HD11	1.87	0.57
37:B:8465:HOH:O	15:O:147:ILE:HD12	2.04	0.57
37:A:7029:HOH:O	5:E:188:ARG:CD	2.52	0.57
1:A:2488:A:H1'	37:A:8685:HOH:O	2.05	0.57
1:A:1028:U:H1'	37:A:3225:HOH:O	2.05	0.57
15:O:100:ALA:O	15:O:129:ILE:HG23	2.04	0.57
29:3:22:PRO:HG2	29:3:25:VAL:CG2	2.34	0.57
1:A:283:U:H5	1:A:284:C:N4	2.02	0.57
24:X:38:THR:HG22	24:X:39:ASP:H	1.69	0.57
1:A:2310:G:OP2	10:J:114:PRO:HD2	2.04	0.57
1:A:2866:U:C2	37:A:7073:HOH:O	2.53	0.57
3:C:18:ALA:O	3:C:20:SER:N	2.34	0.57
21:U:37:GLN:OE1	21:U:118:SER:HA	2.05	0.57
10:J:65:ARG:CZ	37:J:8387:HOH:O	2.53	0.57
7:G:69:ILE:HA	7:G:72:MET:CE	2.35	0.57
1:A:629:A:C2	1:A:2074:A:C2	2.93	0.57
3:C:94:LEU:HG	3:C:99:ILE:HD11	1.87	0.57
19:S:82:GLU:HG3	19:S:83:LYS:N	2.19	0.57
20:T:29:ASP:OD1	20:T:31:ARG:NH1	2.38	0.57
1:A:1730:G:H5'	1:A:1731:C:C5	2.40	0.57
6:F:23:VAL:HG21	6:F:45:THR:HG21	1.87	0.57
1:A:2502:C:H4'	10:J:151:MET:SD	2.45	0.57
4:D:168:GLY:O	4:D:169:GLY:O	2.22	0.57
1:A:2769:C:H2'	1:A:2770:G:O4'	2.05	0.57
1:A:2415:A:C2	15:O:25:ARG:HB3	2.40	0.57
1:A:2657:G:OP1	4:D:17:LYS:HB2	2.05	0.57
37:A:6281:HOH:O	26:Z:165:GLU:HB3	2.04	0.57
10:J:166:ASN:N	10:J:166:ASN:HD22	2.02	0.56
2:B:3006:C:C5'	15:O:37:ARG:NH1	2.62	0.56
1:A:1244:U:OP1	11:K:18:ILE:HD13	2.05	0.56
1:A:21:G:H4'	19:S:2:ILE:HG22	1.87	0.56
1:A:2748:G:H5'	37:A:7117:HOH:O	2.05	0.56
1:A:2256:G:H2'	1:A:2257:G:H5'	1.87	0.56
4:D:280:VAL:CG1	4:D:334:SER:HA	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:22:VAL:HG22	6:F:74:THR:HG22	1.87	0.56
1:A:1474:C:C5'	1:A:1474:C:H6	2.11	0.56
1:A:2635:A:O2'	1:A:2636:C:H5'	2.05	0.56
1:A:1266:U:H4'	26:Z:115:ARG:HH21	1.70	0.56
2:B:3020:G:O2'	2:B:3021:G:H5'	2.05	0.56
4:D:329:TYR:CE2	22:V:15:PRO:HG2	2.40	0.56
1:A:183:A:O2'	1:A:184:G:H5'	2.06	0.56
37:A:4544:HOH:O	10:J:57:ARG:HG3	2.05	0.56
13:M:143:THR:CG2	13:M:144:ASP:N	2.68	0.56
4:D:138:GLY:O	4:D:139:ASP:O	2.23	0.56
16:P:25:VAL:O	16:P:29:VAL:HG23	2.04	0.56
1:A:200:U:H2'	37:A:3028:HOH:O	2.04	0.56
37:A:5094:HOH:O	4:D:298:LYS:HD3	2.04	0.56
23:W:56:ILE:O	23:W:60:GLN:HG3	2.05	0.56
1:A:2659:U:H4'	19:S:76:ASP:HB3	1.87	0.56
1:A:371:U:H2'	1:A:372:A:H8	1.70	0.56
1:A:1753:C:O2	4:D:229:ARG:NH2	2.38	0.56
10:J:44:ALA:HA	10:J:163:PRO:O	2.06	0.56
4:D:254:GLN:HG2	4:D:255:GLY:N	2.19	0.56
13:M:143:THR:HG22	13:M:144:ASP:H	1.71	0.56
8:H:110:GLU:O	8:H:114:LYS:HG3	2.05	0.56
15:O:64:SER:C	15:O:66:LEU:H	2.09	0.56
1:A:1333:U:H2'	1:A:1334:C:C6	2.41	0.56
26:Z:144:ARG:NE	37:Z:8197:HOH:O	2.39	0.56
1:A:168:C:O2'	1:A:169:A:H5'	2.05	0.56
7:G:172:PRO:HB3	37:G:6931:HOH:O	2.06	0.56
1:A:1909:A:H2'	1:A:1910:A:C8	2.39	0.56
1:A:797:A:C4'	27:1:10:ARG:N	2.69	0.56
15:O:89:GLY:O	15:O:92:ALA:HB3	2.06	0.56
6:F:163:VAL:HA	37:F:6326:HOH:O	2.04	0.56
24:X:110:GLN:HA	24:X:110:GLN:NE2	2.20	0.56
10:J:59:ASN:ND2	10:J:59:ASN:N	2.50	0.56
12:L:34:VAL:HB	37:L:7169:HOH:O	2.06	0.56
4:D:7:ARG:HG2	4:D:7:ARG:HH11	1.69	0.56
1:A:2713:G:O2'	1:A:2714:U:H5'	2.05	0.56
5:E:79:ARG:O	5:E:87:ARG:HG2	2.06	0.56
1:A:328:U:O4'	5:E:202:THR:HG22	2.05	0.56
1:A:775:G:OP1	28:2:16:HIS:HE1	1.89	0.56
1:A:175:G:H2'	14:N:192:ALA:HB3	1.87	0.56
14:N:162:GLY:HA2	37:N:8519:HOH:O	2.04	0.56
26:Z:189:ASN:ND2	26:Z:192:ASP:H	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:107:ARG:HH11	5:E:107:ARG:HB3	1.70	0.56
1:A:450:C:H4'	5:E:46:TYR:CE1	2.41	0.56
1:A:1699:C:H4'	37:A:6017:HOH:O	2.06	0.56
1:A:2011:A:P	37:A:5537:HOH:O	2.63	0.56
5:E:236:THR:C	37:E:8445:HOH:O	2.44	0.56
8:H:99:THR:O	8:H:99:THR:HG23	2.05	0.56
1:A:2780:C:H1'	7:G:143:GLN:NE2	2.20	0.56
22:V:46:ALA:HB1	22:V:52:THR:HG21	1.88	0.56
14:N:172:GLY:C	14:N:183:VAL:HG11	2.26	0.56
1:A:154:C:C2	1:A:155:C:C5	2.93	0.56
1:A:2830:U:H3'	37:A:4804:HOH:O	2.05	0.56
1:A:1393:A:H2'	1:A:1394:C:C6	2.41	0.56
2:B:3041:C:O4'	6:F:50:VAL:HG23	2.06	0.56
1:A:1137:G:H1'	37:A:3455:HOH:O	2.05	0.56
37:A:4628:HOH:O	17:Q:68:LYS:HD3	2.06	0.56
1:A:661:G:C5	1:A:686:A:C2	2.93	0.56
15:O:47:LEU:HD13	15:O:97:VAL:HG11	1.88	0.56
1:A:1189:A:H1'	1:A:1209:C:C1'	2.36	0.56
10:J:27:LYS:H	10:J:58:HIS:CD2	2.17	0.56
14:N:191:GLY:O	14:N:192:ALA:HB3	2.06	0.56
6:F:11:HIS:O	6:F:12:GLU:HB3	2.05	0.56
16:P:7:LEU:HD22	37:P:5650:HOH:O	2.05	0.56
28:2:1:THR:HB	37:2:8457:HOH:O	2.04	0.56
4:D:215:VAL:HB	4:D:234:ARG:HH12	1.71	0.56
1:A:1181:A:H2'	1:A:1182:C:O4'	2.05	0.56
4:D:307:ARG:HH11	4:D:307:ARG:CG	2.18	0.56
25:Y:25:ARG:CZ	37:Y:3861:HOH:O	2.52	0.56
1:A:694:A:H2'	1:A:695:C:H5'	1.87	0.56
5:E:142:ASP:OD1	5:E:237:GLU:HB3	2.05	0.55
6:F:44:ILE:HG12	6:F:83:PHE:HE1	1.71	0.55
15:O:38:LYS:HD2	15:O:114:LYS:HE3	1.87	0.55
19:S:39:THR:HB	19:S:42:GLU:CG	2.35	0.55
1:A:135:G:OP1	37:A:6873:HOH:O	2.18	0.55
2:B:3078:G:H22	2:B:3102:G:H2'	1.71	0.55
1:A:2724:U:H2'	1:A:2725:G:O4'	2.05	0.55
1:A:512:G:O3'	1:A:513:A:H8	1.89	0.55
1:A:952:G:H4'	37:A:3606:HOH:O	2.06	0.55
1:A:485:A:N3	1:A:487:G:H5"	2.21	0.55
6:F:105:SER:CB	6:F:131:THR:HG23	2.33	0.55
12:L:75:ARG:CZ	37:L:4172:HOH:O	2.53	0.55
1:A:283:U:H5"	1:A:284:C:P	2.46	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:558:C:H5'	37:A:4832:HOH:O	2.06	0.55
4:D:146:THR:O	4:D:159:PRO:HB3	2.05	0.55
1:A:1015:C:H2'	1:A:1016:U:C6	2.40	0.55
4:D:24:PRO:HG2	4:D:204:GLY:HA2	1.87	0.55
29:3:22:PRO:HG2	29:3:25:VAL:HG23	1.87	0.55
2:B:3078:G:N2	2:B:3102:G:H2'	2.22	0.55
21:U:4:PRO:O	21:U:8:ARG:HG3	2.05	0.55
6:F:36:ASN:HA	37:F:7500:HOH:O	2.06	0.55
1:A:1362:U:H5'	37:A:9849:HOH:O	2.05	0.55
15:O:170:GLU:O	15:O:174:GLU:HG3	2.06	0.55
37:A:8978:HOH:O	14:N:94:LYS:HE2	2.07	0.55
2:B:3069:U:OP1	15:O:4:PRO:HG3	2.05	0.55
3:C:191:GLY:HA2	3:C:194:MET:CE	2.36	0.55
4:D:7:ARG:NH1	4:D:11:LEU:CD2	2.69	0.55
1:A:1086:A:N6	24:X:11:VAL:HG11	2.22	0.55
1:A:877:G:H3'	37:A:9699:HOH:O	2.05	0.55
18:R:32:GLU:HA	18:R:71:TYR:OH	2.06	0.55
14:N:37:VAL:HG13	14:N:63:VAL:HG11	1.87	0.55
3:C:105:VAL:HG11	3:C:154:ALA:CB	2.36	0.55
6:F:99:ASP:HB3	6:F:103:ASN:H	1.71	0.55
30:4:69:TYR:CB	30:4:78:HIS:CE1	2.89	0.55
1:A:1497:G:H4'	1:A:1627:G:O2'	2.07	0.55
1:A:1925:G:O2'	1:A:1926:G:H5'	2.06	0.55
21:U:48:VAL:HG13	21:U:49:GLU:N	2.21	0.55
1:A:567:U:H5"	37:A:5977:HOH:O	2.05	0.55
16:P:59:VAL:HG23	16:P:111:VAL:HG23	1.87	0.55
1:A:1176:C:H1'	37:A:3506:HOH:O	2.07	0.55
37:A:4444:HOH:O	14:N:174:ARG:HG2	2.07	0.55
8:H:28:ALA:HB3	8:H:99:THR:HG23	1.89	0.55
23:W:39:ALA:N	23:W:40:PRO:CD	2.69	0.55
1:A:317:A:H5"	21:U:52:ARG:HD2	1.89	0.55
15:O:154:LEU:HG	15:O:155:GLU:H	1.71	0.55
20:T:29:ASP:OD1	20:T:31:ARG:HG3	2.05	0.55
1:A:2291:A:C8	1:A:2309:C:H5'	2.42	0.55
1:A:1102:C:H2'	1:A:1103:C:H6	1.72	0.55
25:Y:9:VAL:HG13	25:Y:88:GLU:OE2	2.06	0.55
21:U:48:VAL:HG23	21:U:98:VAL:HA	1.87	0.55
24:X:26:ILE:O	24:X:26:ILE:HG13	2.05	0.55
7:G:11:VAL:CG1	7:G:12:ASP:N	2.69	0.55
6:F:135:VAL:HG22	6:F:136:ARG:N	2.21	0.55
7:G:3:VAL:HG22	7:G:49:ILE:HB	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:154:LEU:HG	15:O:155:GLU:N	2.21	0.55
1:A:470:U:O2'	28:2:16:HIS:HD2	1.89	0.55
13:M:77:ALA:HB3	37:M:8402:HOH:O	2.05	0.55
30:4:11:CYS:HB2	30:4:20:HIS:CE1	2.42	0.55
1:A:538:C:OP2	26:Z:134:HIS:HE1	1.89	0.55
1:A:814:G:H4'	37:A:9719:HOH:O	2.05	0.55
1:A:2428:G:N7	30:4:60:LYS:NZ	2.50	0.55
24:X:21:LEU:HD21	24:X:48:VAL:HG11	1.87	0.55
2:B:3047:A:C2	2:B:3048:C:C2	2.94	0.55
15:O:184:ILE:HG22	15:O:185:GLU:HG3	1.88	0.55
1:A:324:G:O2'	1:A:325:U:H5'	2.07	0.55
1:A:2816:A:H5"	1:A:2817:G:H5'	1.89	0.55
10:J:109:ASP:HB2	37:J:8347:HOH:O	2.05	0.55
1:A:344:C:H2'	1:A:345:G:O4'	2.07	0.55
4:D:214:PRO:HD2	37:D:8522:HOH:O	2.06	0.55
1:A:2777:G:O2'	1:A:2778:A:H5'	2.06	0.55
24:X:88:THR:CG2	24:X:89:ASP:H	2.15	0.55
5:E:77:ALA:O	5:E:78:ARG:HG3	2.07	0.55
26:Z:186:ARG:NH1	26:Z:186:ARG:HG2	2.21	0.55
23:W:39:ALA:O	23:W:41:GLU:N	2.40	0.55
1:A:2795:C:O2'	1:A:2796:U:H5'	2.06	0.55
3:C:217:ARG:HG2	3:C:229:ALA:HB2	1.88	0.55
1:A:2247:C:H5"	37:A:6916:HOH:O	2.07	0.55
1:A:2314:G:C2'	1:A:2315:C:H5'	2.37	0.55
10:J:62:GLU:OE2	10:J:66:VAL:CG2	2.54	0.55
1:A:1166:A:H61	1:A:1180:U:H3	1.54	0.55
4:D:175:LEU:C	4:D:175:LEU:CD2	2.75	0.55
2:B:3044:A:O4'	6:F:76:ARG:NE	2.40	0.55
1:A:1909:A:N1	1:A:2128:G:H1'	2.22	0.55
13:M:73:VAL:HG23	13:M:74:THR:H	1.70	0.55
1:A:88:G:H8	1:A:88:G:H5'	1.71	0.55
1:A:2453:G:H3'	37:A:5499:HOH:O	2.06	0.55
1:A:245:C:H2'	1:A:246:G:H5'	1.89	0.55
26:Z:154:ARG:O	26:Z:154:ARG:HG2	2.07	0.55
1:A:1391:G:C5	1:A:1435:U:C4	2.95	0.55
8:H:58:GLU:HG3	8:H:61:MET:HE1	1.89	0.54
1:A:1189:A:H1'	1:A:1209:C:O4'	2.07	0.54
15:O:48:VAL:HG12	37:O:8554:HOH:O	2.05	0.54
37:A:6994:HOH:O	21:U:9:LYS:HB2	2.06	0.54
10:J:35:ASN:HD21	10:J:80:ASN:HA	1.72	0.54
14:N:59:GLY:HA3	14:N:141:ILE:HD12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:16:VAL:HG12	17:Q:17:GLY:N	2.22	0.54
1:A:2679:G:H2'	1:A:2681:A:OP2	2.06	0.54
1:A:383:A:H4'	37:A:4903:HOH:O	2.07	0.54
1:A:56:G:H5"	23:W:50:ARG:NH1	2.22	0.54
10:J:39:GLY:O	10:J:41:THR:N	2.40	0.54
10:J:75:SER:O	10:J:79:ALA:HB2	2.07	0.54
15:O:155:GLU:O	15:O:156:GLU:HG3	2.08	0.54
1:A:2256:G:H2'	1:A:2257:G:C5'	2.37	0.54
1:A:602:A:O2'	1:A:605:C:H4'	2.07	0.54
6:F:170:TYR:O	6:F:171:ASP:HB3	2.06	0.54
1:A:777:U:O2'	28:2:11:LYS:HG2	2.07	0.54
1:A:542:A:H2'	1:A:543:G:O4'	2.06	0.54
10:J:83:PHE:HZ	10:J:146:TRP:HE1	1.54	0.54
22:V:14:GLU:OE1	22:V:15:PRO:CD	2.52	0.54
8:H:46:GLU:OE1	8:H:100:ASP:HA	2.08	0.54
3:C:36:ASP:O	3:C:38:ILE:N	2.41	0.54
4:D:238:ASN:ND2	4:D:240:GLY:H	2.05	0.54
7:G:7:ILE:HD11	7:G:11:VAL:O	2.07	0.54
4:D:82:VAL:CG1	4:D:82:VAL:O	2.53	0.54
1:A:1995:G:O2'	1:A:1997:A:N7	2.40	0.54
10:J:85:ILE:HB	10:J:132:PHE:CE2	2.42	0.54
10:J:5:MET:HG3	37:J:8367:HOH:O	2.07	0.54
27:1:58:GLY:CA	37:1:8439:HOH:O	2.50	0.54
19:S:18:LEU:HB2	19:S:143:VAL:CG1	2.37	0.54
1:A:894:A:C2	5:E:87:ARG:NH2	2.75	0.54
1:A:1787:C:OP1	17:Q:68:LYS:HE2	2.07	0.54
1:A:138:U:H5"	1:A:139:C:OP2	2.08	0.54
1:A:2241:C:O2'	1:A:2242:U:H5'	2.06	0.54
6:F:54:ALA:CB	6:F:69:ILE:HD12	2.37	0.54
15:O:37:ARG:HD3	35:O:8507:CL:CL	2.45	0.54
4:D:51:VAL:HG23	4:D:329:TYR:O	2.08	0.54
1:A:1015:C:C2	1:A:1016:U:C5	2.95	0.54
1:A:396:U:OP2	30:4:38:ARG:NH1	2.39	0.54
1:A:2070:G:H5"	37:A:3359:HOH:O	2.06	0.54
18:R:25:PRO:HB2	37:R:4350:HOH:O	2.07	0.54
10:J:69:ASN:O	10:J:72:VAL:HG12	2.07	0.54
7:G:15:GLN:NE2	7:G:40:VAL:O	2.41	0.54
15:O:49:THR:CG2	15:O:56:ASP:HB2	2.36	0.54
8:H:100:ASP:O	8:H:101:ALA:O	2.26	0.54
1:A:1299:G:H5'	37:A:3648:HOH:O	2.08	0.54
1:A:2548:C:OP2	4:D:5:ARG:NH2	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:223:ARG:HG3	37:C:8604:HOH:O	2.06	0.54
6:F:10:PHE:CE1	6:F:11:HIS:HB3	2.42	0.54
1:A:877:G:H5'	1:A:878:G:OP1	2.07	0.54
1:A:2324:G:H4'	1:A:2418:G:O2'	2.07	0.54
1:A:1505:U:H5'	1:A:1505:U:H6	1.72	0.54
37:A:8936:HOH:O	29:3:3:LYS:HE3	2.07	0.54
30:4:56:PRO:N	37:4:8550:HOH:O	2.39	0.54
27:1:11:THR:CG2	27:1:23:ARG:HB2	2.38	0.54
17:Q:143:ALA:HA	37:Q:5521:HOH:O	2.05	0.54
1:A:2781:U:C2'	1:A:2782:G:H5'	2.37	0.54
1:A:1299:G:O6	13:M:6:ARG:HD3	2.08	0.54
24:X:38:THR:O	24:X:42:ARG:HB2	2.08	0.54
28:2:28:HIS:CD2	28:2:31:LYS:H	2.26	0.54
1:A:319:A:H4'	1:A:338:C:C4	2.43	0.54
1:A:902:G:N7	13:M:18:HIS:HD2	2.06	0.54
1:A:2761:A:C4	1:A:2763:G:C8	2.95	0.54
19:S:106:GLY:HA2	19:S:109:MET:CE	2.38	0.54
37:A:6203:HOH:O	10:J:150:LYS:HE2	2.08	0.54
17:Q:13:VAL:HG21	17:Q:41:ARG:HG2	1.88	0.54
4:D:221:GLN:HE22	12:L:42:ASN:ND2	2.05	0.54
24:X:149:LEU:HG	24:X:153:MET:CE	2.38	0.54
1:A:669:G:O2'	1:A:670:G:H5'	2.07	0.54
17:Q:71:LYS:HG3	17:Q:71:LYS:O	2.08	0.54
1:A:2359:G:N7	37:A:3279:HOH:O	2.34	0.54
15:O:139:TRP:HA	15:O:139:TRP:CE3	2.43	0.54
37:A:9144:HOH:O	4:D:267:LYS:HD3	2.06	0.54
3:C:36:ASP:HA	3:C:83:GLY:HA3	1.90	0.54
1:A:2270:G:H4'	3:C:223:ARG:NH1	2.21	0.54
7:G:86:VAL:CG1	7:G:129:GLU:HA	2.37	0.54
1:A:1523:G:H2'	1:A:1524:U:C6	2.43	0.54
1:A:1641:A:H2'	1:A:1642:A:H5'	1.89	0.54
10:J:26:LYS:HD3	10:J:89:PRO:HG3	1.90	0.54
1:A:2837:U:H1'	4:D:307:ARG:HH12	1.73	0.54
11:K:88:PRO:C	35:K:8502:CL:CL	2.83	0.54
28:2:8:GLN:HE22	28:2:11:LYS:NZ	2.06	0.54
26:Z:112:GLU:OE1	26:Z:112:GLU:HA	2.08	0.54
1:A:714:U:H3'	37:A:6516:HOH:O	2.07	0.54
1:A:812:A:H1'	37:A:3533:HOH:O	2.07	0.54
11:K:75:PRO:HG2	11:K:105:LEU:HD21	1.89	0.54
5:E:200:PRO:HB3	5:E:212:VAL:HG23	1.90	0.54
10:J:86:ARG:HD3	10:J:130:HIS:HD2	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:5:VAL:HG22	24:X:32:CYS:HB2	1.90	0.53
24:X:13:MET:HE3	24:X:17:ILE:CG2	2.37	0.53
37:A:7253:HOH:O	14:N:154:ARG:HB2	2.07	0.53
29:3:48:ASP:O	29:3:49:GLU:HB2	2.08	0.53
21:U:32:ARG:NH1	21:U:38:ARG:HH12	2.06	0.53
12:L:30:LYS:O	12:L:55:VAL:HG13	2.08	0.53
27:1:57:CYS:SG	27:1:59:HIS:HB3	2.48	0.53
5:E:115:LEU:O	5:E:118:THR:HB	2.07	0.53
3:C:100:PRO:HG2	3:C:103:VAL:CG2	2.35	0.53
24:X:21:LEU:HD21	24:X:48:VAL:CG1	2.39	0.53
7:G:31:ARG:HH12	7:G:68:HIS:CE1	2.27	0.53
1:A:485:A:O2'	1:A:487:G:H5'	2.08	0.53
1:A:2326:U:H4'	1:A:2412:G:H4'	1.91	0.53
7:G:79:GLY:HA3	37:G:7046:HOH:O	2.08	0.53
22:V:6:CYS:O	22:V:8:TYR:N	2.41	0.53
16:P:21:SER:OG	16:P:106:PRO:HB2	2.08	0.53
1:A:1669:A:H2'	1:A:1670:G:C8	2.43	0.53
24:X:4:LEU:O	24:X:32:CYS:HA	2.09	0.53
7:G:22:VAL:O	7:G:28:SER:HA	2.08	0.53
1:A:2780:C:H2'	1:A:2781:U:C6	2.44	0.53
10:J:75:SER:C	10:J:79:ALA:HB2	2.29	0.53
1:A:2359:G:H3'	37:A:5266:HOH:O	2.08	0.53
22:V:8:TYR:OH	37:V:3805:HOH:O	2.18	0.53
1:A:2251:G:H2'	1:A:2252:A:C8	2.44	0.53
1:A:2001:G:O2'	1:A:2002:C:H5'	2.09	0.53
1:A:2755:G:H1'	37:A:4258:HOH:O	2.08	0.53
1:A:779:U:H5'	1:A:1836:A:C2	2.42	0.53
10:J:46:VAL:O	10:J:146:TRP:HH2	1.91	0.53
15:O:90:LEU:HB2	15:O:186:LEU:HD22	1.90	0.53
7:G:31:ARG:HH12	7:G:68:HIS:CG	2.26	0.53
5:E:162:VAL:HG12	5:E:192:ILE:HD11	1.89	0.53
5:E:162:VAL:HG13	5:E:232:LEU:HD21	1.90	0.53
1:A:316:A:N3	1:A:336:G:O2'	2.40	0.53
1:A:2656:G:O2'	1:A:2657:G:H5'	2.09	0.53
1:A:2314:G:H2'	1:A:2315:C:H5'	1.91	0.53
4:D:14:GLY:HA2	4:D:15:PRO:C	2.29	0.53
1:A:1097:A:H5"	24:X:125:HIS:CE1	2.43	0.53
5:E:133:ARG:HD2	37:E:8406:HOH:O	2.08	0.53
5:E:47:GLY:HA2	5:E:92:PRO:HB2	1.89	0.53
26:Z:189:ASN:HD22	26:Z:189:ASN:C	2.12	0.53
6:F:154:LYS:H	6:F:154:LYS:CD	2.15	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:11:VAL:HG13	7:G:23:GLU:O	2.08	0.53
3:C:109:GLU:HG2	3:C:116:GLY:N	2.23	0.53
27:1:13:ARG:NH1	27:1:14:PHE:CZ	2.77	0.53
22:V:6:CYS:C	22:V:8:TYR:H	2.12	0.53
15:O:82:TYR:C	15:O:82:TYR:CD2	2.82	0.53
1:A:257:G:O2'	1:A:258:G:H5'	2.08	0.53
1:A:1654:U:H2'	3:C:47:HIS:CD2	2.44	0.53
6:F:38:GLU:HB3	6:F:49:PRO:HG2	1.91	0.53
24:X:122:ARG:NH1	24:X:122:ARG:HG2	2.23	0.53
6:F:86:THR:C	6:F:89:PRO:HD2	2.28	0.53
9:I:12:ILE:HG22	9:I:12:ILE:O	2.08	0.53
1:A:315:G:C6	1:A:316:A:C6	2.96	0.53
1:A:272:A:H5'	1:A:273:G:OP2	2.09	0.53
1:A:1873:G:H2'	1:A:1874:U:H5'	1.90	0.53
27:1:42:CYS:SG	27:1:44:PHE:HB2	2.48	0.53
25:Y:51:ASP:OD2	25:Y:52:PRO:HD2	2.08	0.53
24:X:129:LYS:HG2	37:X:1990:HOH:O	2.09	0.53
10:J:130:HIS:CG	10:J:133:ILE:HD11	2.43	0.53
6:F:25:MET:CE	6:F:37:ALA:HB1	2.36	0.53
5:E:127:ARG:NH1	5:E:127:ARG:HG2	2.23	0.53
8:H:47:LEU:HB2	8:H:108:LEU:HD11	1.91	0.53
27:1:38:LYS:HE2	27:1:45:LYS:CE	2.34	0.53
11:K:19:MET:HE3	11:K:132:LEU:HD11	1.89	0.53
16:P:25:VAL:HG23	16:P:26:TRP:H	1.74	0.53
1:A:1778:A:H2'	1:A:1779:A:H5'	1.91	0.53
1:A:660:A:H4'	1:A:661:G:O5'	2.09	0.53
30:4:55:VAL:HB	30:4:56:PRO:HD2	1.91	0.53
1:A:1495:C:H1'	1:A:1573:A:H1'	1.91	0.53
37:E:8356:HOH:O	16:P:3:THR:HG21	2.08	0.53
1:A:474:C:O3'	5:E:73:LEU:HD21	2.09	0.53
14:N:67:ILE:CD1	14:N:104:ARG:HD2	2.39	0.53
1:A:1666:C:C2'	1:A:1667:A:C5'	2.87	0.53
1:A:1477:C:H5'	1:A:1868:G:C5'	2.39	0.53
25:Y:43:VAL:CG1	25:Y:47:ALA:HB3	2.38	0.53
3:C:1:GLY:HA2	3:C:197:VAL:HG23	1.91	0.53
4:D:2:GLN:CD	37:D:8622:HOH:O	2.46	0.53
1:A:407:A:H5'	37:A:5603:HOH:O	2.07	0.53
1:A:1097:A:H5"	24:X:125:HIS:NE2	2.24	0.53
1:A:1168:C:H2'	1:A:1169:U:O4'	2.08	0.53
4:D:320:GLN:HG3	4:D:321:PRO:HD2	1.90	0.53
1:A:1164:U:C4'	1:A:1165:G:OP1	2.52	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:182:GLY:N	37:O:8571:HOH:O	2.41	0.53
28:2:25:LYS:HE2	37:3:7213:HOH:O	2.09	0.53
1:A:289:G:N2	1:A:363:A:H2	2.04	0.53
7:G:31:ARG:HH12	7:G:68:HIS:CD2	2.27	0.53
1:A:2064:U:H5'	1:A:2652:U:H4'	1.90	0.53
8:H:22:VAL:HG21	8:H:104:ALA:HB2	1.90	0.53
23:W:57:LYS:HA	23:W:60:GLN:HE21	1.73	0.53
37:A:3421:HOH:O	10:J:11:LYS:HE2	2.08	0.53
1:A:2613:G:O2'	1:A:2614:C:H5'	2.09	0.53
5:E:51:TYR:CE2	28:2:53:LYS:HB3	2.44	0.53
1:A:628:A:C8	1:A:2071:C:N4	2.77	0.53
37:A:8903:HOH:O	27:1:16:PRO:HG3	2.07	0.53
10:J:139:ASP:N	10:J:140:PRO:CD	2.71	0.53
1:A:1589:G:N2	1:A:1605:G:H1'	2.24	0.53
4:D:119:HIS:O	4:D:121:PRO:HD3	2.08	0.53
1:A:2779:G:H1'	37:A:5684:HOH:O	2.09	0.53
10:J:81:TYR:C	10:J:81:TYR:CD1	2.81	0.53
19:S:29:LYS:NZ	37:S:8540:HOH:O	2.41	0.53
12:L:32:ILE:HD11	12:L:56:SER:HB3	1.90	0.52
14:N:35:PRO:HD2	14:N:38:VAL:HG21	1.91	0.52
25:Y:78:GLU:HG2	25:Y:79:GLU:N	2.17	0.52
24:X:26:ILE:O	24:X:26:ILE:CG1	2.56	0.52
14:N:149:TRP:O	14:N:152:ARG:HG2	2.09	0.52
1:A:1500:U:P	17:Q:41:ARG:HH22	2.31	0.52
1:A:92:G:H4'	23:W:44:GLY:HA3	1.90	0.52
37:A:4405:HOH:O	11:K:47:THR:CB	2.55	0.52
1:A:2271:G:H2'	1:A:2271:G:N3	2.24	0.52
1:A:1783:A:O2'	1:A:1784:U:H5'	2.09	0.52
1:A:830:G:O2'	1:A:831:U:H5'	2.09	0.52
10:J:150:LYS:HA	10:J:153:VAL:HG22	1.91	0.52
12:L:34:VAL:CG2	12:L:47:ALA:HB2	2.40	0.52
4:D:304:PRO:HD2	4:D:307:ARG:HD2	1.92	0.52
27:1:30:GLU:HA	27:1:33:HIS:CB	2.40	0.52
4:D:24:PRO:CG	4:D:204:GLY:HA2	2.39	0.52
1:A:2435:U:H1'	37:A:5006:HOH:O	2.09	0.52
4:D:274:GLU:HA	4:D:292:GLY:O	2.08	0.52
14:N:164:THR:HB	37:N:8519:HOH:O	2.10	0.52
5:E:234:VAL:O	5:E:234:VAL:HG22	2.08	0.52
24:X:38:THR:HG22	24:X:39:ASP:N	2.25	0.52
1:A:1527:A:H1'	1:A:1528:A:C8	2.44	0.52
4:D:74:ILE:HD13	4:D:309:VAL:HG21	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:32:ALA:HA	20:T:36:GLU:OE1	2.09	0.52
1:A:682:A:H3'	1:A:683:G:H8	1.74	0.52
5:E:16:VAL:HG12	5:E:17:ASP:H	1.73	0.52
8:H:46:GLU:N	37:H:3461:HOH:O	2.43	0.52
15:O:167:ASP:O	15:O:168:LEU:HD23	2.10	0.52
1:A:1268:C:O2'	26:Z:169:ARG:HB2	2.08	0.52
5:E:129:HIS:HD2	5:E:165:ASP:OD2	1.91	0.52
1:A:259:G:H21	14:N:58:GLN:NE2	2.06	0.52
28:2:28:HIS:CD2	28:2:30:LYS:HB2	2.44	0.52
15:O:180:LEU:O	15:O:181:ASP:HB3	2.08	0.52
24:X:141:HIS:HB2	24:X:146:ILE:HG12	1.90	0.52
1:A:1847:A:OP1	3:C:175:LYS:NZ	2.42	0.52
1:A:1855:G:H8	3:C:144:GLU:OE2	1.93	0.52
1:A:2082:G:O2'	1:A:2083:A:H5'	2.08	0.52
1:A:962:C:C1'	15:O:5:ARG:NH1	2.65	0.52
37:E:8364:HOH:O	21:U:2:LYS:HE2	2.09	0.52
1:A:2769:C:O2'	1:A:2770:G:H5'	2.09	0.52
1:A:51:G:O2'	1:A:52:A:H5'	2.10	0.52
1:A:1819:G:H5'	37:A:4285:HOH:O	2.10	0.52
6:F:10:PHE:CG	6:F:11:HIS:N	2.77	0.52
14:N:154:ARG:HD3	37:N:8640:HOH:O	2.10	0.52
24:X:125:HIS:HD2	24:X:127:GLY:H	1.57	0.52
1:A:119:A:H2'	1:A:120:A:H5"	1.91	0.52
25:Y:18:ARG:NH1	37:Y:4132:HOH:O	2.41	0.52
21:U:12:ARG:NH1	37:U:3035:HOH:O	2.42	0.52
14:N:37:VAL:CG1	14:N:63:VAL:HG11	2.40	0.52
1:A:1666:C:H2'	1:A:1667:A:C5'	2.40	0.52
1:A:2718:C:H6	1:A:2718:C:H5'	1.75	0.52
24:X:122:ARG:HG2	24:X:152:ALA:O	2.09	0.52
1:A:1947:G:N2	1:A:1966:U:C2	2.78	0.52
15:O:48:VAL:HG11	15:O:55:ASP:HB3	1.89	0.52
11:K:77:GLY:O	11:K:78:ILE:C	2.48	0.52
1:A:2781:U:H2'	1:A:2782:G:H5'	1.91	0.52
1:A:1127:C:C2'	1:A:1128:U:H5'	2.40	0.52
1:A:2604:A:H5'	37:A:5367:HOH:O	2.09	0.52
1:A:1562:C:H2'	1:A:1562:C:O2	2.10	0.52
1:A:1934:A:C8	1:A:1935:C:C5	2.97	0.52
11:K:142:ASN:O	11:K:144:THR:N	2.43	0.52
10:J:62:GLU:OE2	10:J:66:VAL:HG23	2.09	0.52
1:A:1942:A:O2'	1:A:1943:C:H5'	2.10	0.52
3:C:211:LYS:HB3	3:C:212:PRO:CD	2.33	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1118:A:H8	1:A:1119:G:H5"	1.75	0.52
5:E:214:THR:HB	37:E:8325:HOH:O	2.10	0.52
5:E:233:THR:CG2	5:E:234:VAL:N	2.73	0.52
3:C:51:ARG:NH2	37:C:8609:HOH:O	2.42	0.52
1:A:818:A:O2'	27:1:13:ARG:HD3	2.10	0.52
26:Z:126:PRO:HG2	26:Z:128:PHE:CZ	2.44	0.52
1:A:1470:A:OP1	14:N:93:ARG:HD2	2.10	0.52
17:Q:18:LYS:O	17:Q:21:VAL:HG22	2.09	0.52
37:A:3640:HOH:O	4:D:27:ASN:HB2	2.10	0.52
15:O:11:ARG:HG3	15:O:14:ARG:NH1	2.24	0.52
25:Y:72:VAL:HG22	25:Y:85:VAL:CG1	2.38	0.52
10:J:28:ILE:HA	10:J:62:GLU:OE1	2.10	0.52
8:H:58:GLU:HA	8:H:61:MET:HG3	1.92	0.52
26:Z:185:VAL:HA	37:Z:8152:HOH:O	2.08	0.52
12:L:34:VAL:HG22	12:L:47:ALA:HB2	1.91	0.52
1:A:67:A:H5"	1:A:69:A:C8	2.45	0.52
1:A:1333:U:H2'	1:A:1334:C:H6	1.75	0.52
21:U:38:ARG:HG3	21:U:38:ARG:HH11	1.74	0.52
4:D:27:ASN:HB3	37:D:8630:HOH:O	2.08	0.52
24:X:142:ASP:HB3	24:X:145:GLY:H	1.73	0.52
10:J:129:ASN:HD22	10:J:129:ASN:N	2.08	0.52
22:V:34:SER:O	22:V:38:ASN:ND2	2.42	0.52
3:C:97:ALA:HB2	3:C:150:PRO:HB2	1.91	0.52
6:F:58:VAL:HG12	6:F:59:GLY:N	2.25	0.52
1:A:2862:G:H4'	4:D:336:GLN:O	2.10	0.52
10:J:46:VAL:HG12	10:J:146:TRP:CZ3	2.43	0.52
1:A:1209:C:C2	1:A:1210:G:C8	2.97	0.52
1:A:183:A:H5'	14:N:157:LEU:HD12	1.92	0.52
1:A:290:C:O2'	1:A:291:C:H5'	2.10	0.52
15:O:159:TYR:HE2	15:O:163:PHE:HE2	1.58	0.52
1:A:2044:G:OP1	25:Y:23:HIS:CE1	2.60	0.52
1:A:2329:C:O2'	1:A:2330:U:H5'	2.10	0.52
19:S:132:ARG:CZ	37:S:8587:HOH:O	2.58	0.52
24:X:88:THR:CG2	24:X:89:ASP:N	2.72	0.51
10:J:56:ILE:HG22	10:J:61:LEU:HD22	1.91	0.51
1:A:2779:G:O2'	1:A:2780:C:H5'	2.10	0.51
6:F:99:ASP:CB	6:F:103:ASN:HB2	2.39	0.51
1:A:1973:A:H5'	1:A:1973:A:C8	2.43	0.51
1:A:1120:U:H6	1:A:1120:U:H5"	1.75	0.51
24:X:31:HIS:HB3	37:X:5420:HOH:O	2.10	0.51
1:A:245:C:C2'	1:A:246:G:H5'	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:431:G:P	14:N:48:ARG:HH12	2.34	0.51
1:A:644:G:H5'	1:A:644:G:N3	2.24	0.51
23:W:27:LEU:O	23:W:30:ALA:N	2.43	0.51
1:A:329:A:OP2	5:E:206:ASN:HB2	2.09	0.51
18:R:16:ASN:ND2	18:R:45:PRO:HG2	2.25	0.51
1:A:920:C:H5'	1:A:921:G:C4	2.45	0.51
1:A:684:G:H2'	1:A:685:C:C6	2.45	0.51
14:N:186:SER:O	14:N:189:VAL:HG12	2.10	0.51
7:G:11:VAL:HG12	7:G:12:ASP:H	1.75	0.51
22:V:52:THR:HG22	22:V:54:THR:HB	1.93	0.51
24:X:42:ARG:O	24:X:45:VAL:HG22	2.10	0.51
26:Z:144:ARG:CZ	37:Z:8197:HOH:O	2.59	0.51
1:A:1654:U:H2'	3:C:47:HIS:HD2	1.74	0.51
1:A:1123:A:C6	1:A:1238:C:H5'	2.45	0.51
1:A:1717:A:H5"	17:Q:54:LYS:HB2	1.93	0.51
1:A:2894:C:O2'	1:A:2895:C:H5'	2.09	0.51
4:D:217:ARG:HG3	4:D:257:THR:HG22	1.91	0.51
1:A:92:G:H5'	37:W:7247:HOH:O	2.10	0.51
14:N:173:LEU:HD23	14:N:183:VAL:HG12	1.92	0.51
13:M:104:ASP:HB3	37:M:8437:HOH:O	2.09	0.51
26:Z:144:ARG:HH11	26:Z:144:ARG:HG3	1.75	0.51
1:A:319:A:H4'	1:A:338:C:C5	2.46	0.51
1:A:331:A:C6	1:A:332:G:C4	2.97	0.51
4:D:231:GLY:N	37:D:8524:HOH:O	2.35	0.51
6:F:23:VAL:CG2	6:F:23:VAL:O	2.58	0.51
2:B:3049:G:H2'	2:B:3050:G:O4'	2.10	0.51
1:A:1189:A:H1'	1:A:1209:C:H1'	1.93	0.51
19:S:39:THR:HG22	19:S:42:GLU:H	1.74	0.51
21:U:55:PHE:CD2	21:U:77:VAL:HG13	2.46	0.51
14:N:77:PHE:HD2	37:N:8527:HOH:O	1.94	0.51
17:Q:94:TRP:CZ2	17:Q:98:ILE:HG13	2.46	0.51
3:C:170:VAL:HG22	27:1:22:ILE:HG23	1.92	0.51
1:A:1595:G:O2'	1:A:1596:U:H5'	2.11	0.51
21:U:49:GLU:OE2	21:U:97:ARG:HD2	2.11	0.51
10:J:14:TYR:N	10:J:91:HIS:CE1	2.79	0.51
1:A:1151:G:P	9:I:16:LYS:HZ1	2.30	0.51
15:O:73:ALA:N	37:O:8567:HOH:O	2.44	0.51
23:W:64:GLY:O	23:W:65:ASP:CB	2.56	0.51
10:J:75:SER:HB3	10:J:79:ALA:HB1	1.92	0.51
15:O:152:GLU:C	15:O:154:LEU:H	2.12	0.51
8:H:16:ALA:HA	8:H:111:ILE:HD13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:2:28:HIS:CE1	28:2:31:LYS:HE2	2.45	0.51
14:N:48:ARG:NH2	37:N:8562:HOH:O	2.42	0.51
1:A:2764:C:H2'	1:A:2765:C:H6	1.74	0.51
15:O:47:LEU:HD12	15:O:92:ALA:HB1	1.92	0.51
14:N:43:PRO:HG3	14:N:62:VAL:HG21	1.93	0.51
14:N:106:ASN:ND2	35:N:8518:CL:CL	2.81	0.51
4:D:76:THR:N	4:D:77:PRO:HD3	2.26	0.51
6:F:10:PHE:CD1	6:F:11:HIS:N	2.78	0.51
4:D:215:VAL:HA	4:D:220:VAL:HG22	1.93	0.51
1:A:907:A:H2'	1:A:908:A:H8	1.76	0.51
12:L:101:ASN:HB3	37:L:6456:HOH:O	2.11	0.51
3:C:105:VAL:CG1	3:C:106:CYS:N	2.74	0.51
1:A:2044:G:C6	1:A:2045:G:C5	2.98	0.51
8:H:107:VAL:O	8:H:111:ILE:HG13	2.10	0.51
1:A:2392:C:H4'	37:R:2875:HOH:O	2.10	0.51
14:N:122:GLU:OE2	14:N:127:LYS:HE2	2.11	0.51
19:S:33:ARG:NH1	37:S:8544:HOH:O	2.44	0.51
14:N:45:ARG:CZ	14:N:48:ARG:HG3	2.41	0.51
1:A:113:A:OP2	1:A:114:A:H2'	2.11	0.51
1:A:1132:A:N6	1:A:1229:C:H2'	2.26	0.51
26:Z:172:THR:HG22	26:Z:173:ALA:N	2.25	0.51
27:1:59:HIS:HA	37:1:8441:HOH:O	2.09	0.51
1:A:1192:A:H3'	1:A:1193:A:H5'	1.91	0.51
21:U:48:VAL:CG2	21:U:98:VAL:HA	2.40	0.51
1:A:558:C:C2'	1:A:559:U:C5'	2.89	0.51
4:D:82:VAL:HG12	4:D:101:TRP:CE3	2.46	0.51
2:B:3042:C:H2'	37:B:8500:HOH:O	2.10	0.51
22:V:31:PHE:CE2	22:V:37:GLU:HA	2.46	0.51
37:A:5104:HOH:O	14:N:58:GLN:HG3	2.10	0.51
19:S:79:ARG:C	19:S:81:PRO:HD3	2.31	0.51
37:A:3804:HOH:O	29:3:38:LYS:HE3	2.11	0.51
1:A:1804:A:H2'	1:A:1805:G:C8	2.44	0.51
18:R:66:LYS:HB2	18:R:70:ALA:O	2.11	0.51
10:J:65:ARG:HB3	37:J:8387:HOH:O	2.10	0.51
10:J:65:ARG:NH1	37:J:8387:HOH:O	2.44	0.51
37:B:8519:HOH:O	15:O:107:ASN:HB3	2.10	0.51
1:A:1477:C:O2'	1:A:1478:U:H5'	2.11	0.51
22:V:9:CYS:CA	22:V:52:THR:HG23	2.40	0.51
11:K:130:VAL:HG12	11:K:131:THR:N	2.26	0.51
4:D:7:ARG:CD	4:D:9:GLY:O	2.59	0.51
21:U:24:ARG:HH21	21:U:39:ASN:ND2	2.08	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:64:ASN:O	9:I:68:GLU:HG3	2.11	0.51
1:A:2866:U:H4'	1:A:2867:G:H5'	1.92	0.51
1:A:154:C:H2'	1:A:155:C:H6	1.76	0.51
24:X:125:HIS:CD2	24:X:127:GLY:H	2.29	0.51
1:A:1940:C:H4'	37:A:6918:HOH:O	2.10	0.51
6:F:102:GLY:O	6:F:134:LEU:HD12	2.11	0.51
27:1:46:LYS:O	27:1:57:CYS:HA	2.10	0.51
8:H:50:VAL:CG2	8:H:63:ILE:HG21	2.40	0.51
6:F:57:THR:HG23	6:F:63:ILE:CB	2.41	0.51
4:D:305:ASP:O	4:D:306:LYS:CB	2.58	0.51
1:A:2712:G:OP1	12:L:43:ARG:NH1	2.43	0.51
1:A:790:A:H1'	1:A:1710:A:H2'	1.93	0.51
1:A:2832:C:H5	37:A:6784:HOH:O	1.94	0.51
19:S:47:LEU:O	19:S:51:ILE:HG13	2.09	0.51
25:Y:26:ALA:HB1	25:Y:59:TRP:CE2	2.45	0.51
6:F:53:LYS:HA	6:F:67:ASP:O	2.11	0.50
1:A:1174:A:C5	1:A:1201:C:H4'	2.46	0.50
13:M:143:THR:CG2	13:M:144:ASP:H	2.23	0.50
4:D:238:ASN:HD22	4:D:240:GLY:N	2.06	0.50
11:K:131:THR:HG22	11:K:133:GLY:N	2.26	0.50
4:D:7:ARG:HD3	4:D:9:GLY:O	2.12	0.50
24:X:13:MET:CE	24:X:17:ILE:HG22	2.40	0.50
1:A:256:C:H2'	1:A:257:G:O4'	2.11	0.50
17:Q:98:ILE:HD12	17:Q:102:ARG:NE	2.26	0.50
2:B:3055:U:H4'	2:B:3056:A:C8	2.46	0.50
37:A:4118:HOH:O	10:J:151:MET:HE2	2.11	0.50
24:X:122:ARG:CG	24:X:152:ALA:O	2.59	0.50
3:C:88:ILE:HD13	3:C:100:PRO:CD	2.36	0.50
15:O:163:PHE:HA	37:O:8519:HOH:O	2.10	0.50
1:A:2781:U:H1'	7:G:139:GLU:OE2	2.11	0.50
1:A:1060:C:H5'	1:A:1060:C:H6	1.76	0.50
13:M:73:VAL:HG23	13:M:74:THR:N	2.25	0.50
1:A:338:C:H4'	5:E:174:ILE:CD1	2.41	0.50
37:A:5771:HOH:O	29:3:44:ARG:HG2	2.10	0.50
7:G:21:THR:HG23	7:G:30:THR:OG1	2.11	0.50
24:X:106:THR:OG1	24:X:109:GLU:HG3	2.11	0.50
1:A:1116:U:H3	1:A:1246:A:N6	2.01	0.50
5:E:107:ARG:HH11	5:E:107:ARG:CB	2.24	0.50
8:H:107:VAL:HG23	37:H:6617:HOH:O	2.11	0.50
1:A:2365:G:H4'	18:R:45:PRO:O	2.11	0.50
1:A:920:C:H4'	1:A:921:G:C2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1139:U:H2'	1:A:1140:C:C6	2.46	0.50
1:A:1162:G:H2'	37:A:6156:HOH:O	2.11	0.50
1:A:639:A:H2'	1:A:640:G:C8	2.45	0.50
6:F:27:ILE:O	6:F:69:ILE:HG22	2.11	0.50
15:O:163:PHE:HE1	15:O:171:HIS:HD1	1.59	0.50
7:G:84:MET:HE1	7:G:148:ILE:CD1	2.42	0.50
15:O:61:ALA:CB	15:O:88:ALA:HB2	2.41	0.50
4:D:54:VAL:HB	37:D:8614:HOH:O	2.11	0.50
16:P:14:LEU:CD2	16:P:102:ILE:HD11	2.40	0.50
13:M:134:GLU:HA	13:M:138:GLY:O	2.12	0.50
4:D:275:GLY:O	4:D:291:ASP:HA	2.11	0.50
1:A:710:G:OP1	16:P:24:ALA:HB3	2.12	0.50
1:A:125:U:H2'	37:A:3346:HOH:O	2.11	0.50
10:J:85:ILE:O	10:J:85:ILE:HG23	2.12	0.50
14:N:186:SER:OG	14:N:189:VAL:CG1	2.59	0.50
15:O:182:GLY:O	15:O:183:ASP:O	2.29	0.50
15:O:171:HIS:CE1	37:O:8567:HOH:O	2.64	0.50
7:G:69:ILE:HA	7:G:72:MET:HE3	1.92	0.50
6:F:140:ARG:O	6:F:144:ARG:HG2	2.11	0.50
1:A:1102:C:H2'	1:A:1103:C:C6	2.46	0.50
1:A:1351:G:OP1	5:E:96:LYS:NZ	2.41	0.50
24:X:108:ARG:HE	24:X:114:PRO:HG3	1.76	0.50
1:A:1161:A:H8	1:A:1161:A:O5'	1.95	0.50
23:W:12:THR:HG23	23:W:14:ALA:H	1.76	0.50
7:G:81:GLU:HG2	7:G:134:SER:CB	2.39	0.50
1:A:951:A:C2'	1:A:952:G:H5'	2.42	0.50
16:P:38:ARG:NH1	37:P:7674:HOH:O	2.45	0.50
5:E:33:LYS:HE2	37:E:8358:HOH:O	2.12	0.50
16:P:88:LYS:O	37:P:4826:HOH:O	2.20	0.50
1:A:2113:G:C6	1:A:2114:C:C4	3.00	0.50
19:S:104:PHE:HB2	19:S:109:MET:HE1	1.93	0.50
11:K:52:GLN:HG3	11:K:53:ILE:H	1.74	0.50
1:A:2506:A:O2'	1:A:2507:G:O5'	2.30	0.50
1:A:1594:C:C2	1:A:1601:G:C2	3.00	0.50
1:A:2004:U:O2	1:A:2004:U:H2'	2.11	0.50
2:B:3031:C:O2'	2:B:3032:G:H5'	2.11	0.50
1:A:825:U:H5"	1:A:826:U:OP1	2.12	0.50
1:A:1462:C:H2'	1:A:1463:A:C8	2.47	0.50
1:A:553:G:P	26:Z:204:ARG:HH22	2.34	0.50
6:F:27:ILE:HD11	6:F:37:ALA:CB	2.42	0.50
10:J:166:ASN:ND2	10:J:166:ASN:N	2.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:26:LYS:HD2	10:J:28:ILE:CG1	2.42	0.50
14:N:63:VAL:HG21	14:N:109:PHE:CE1	2.47	0.50
14:N:52:LEU:HD13	14:N:116:ASN:HB3	1.94	0.50
4:D:103:ASP:HB2	37:D:8595:HOH:O	2.11	0.50
19:S:15:LYS:HE3	37:S:8581:HOH:O	2.12	0.50
1:A:625:U:H5"	1:A:1044:C:N4	2.26	0.50
1:A:1846:U:O2'	3:C:172:ALA:HB2	2.11	0.50
27:1:11:THR:HG23	27:1:23:ARG:HD2	1.94	0.50
2:B:3076:G:C3'	2:B:3077:A:H5"	2.23	0.50
19:S:39:THR:HG22	19:S:41:GLY:N	2.26	0.50
6:F:94:ALA:HB3	6:F:174:VAL:HA	1.94	0.50
9:I:12:ILE:HD12	37:I:692:HOH:O	2.11	0.50
2:B:3030:C:OP1	6:F:137:PRO:O	2.29	0.50
1:A:2274:A:H1'	14:N:86:MET:SD	2.52	0.50
1:A:113:A:OP2	1:A:114:A:H5"	2.12	0.50
1:A:399:C:H5'	14:N:179:GLY:O	2.12	0.50
4:D:248:ARG:O	4:D:251:VAL:HG13	2.11	0.50
1:A:514:G:OP1	1:A:514:G:H2'	2.12	0.50
1:A:1525:G:H5'	1:A:1526:A:OP2	2.12	0.50
5:E:111:VAL:HB	37:E:8322:HOH:O	2.11	0.50
2:B:3059:C:H2'	2:B:3060:C:C6	2.47	0.50
14:N:35:PRO:HD2	14:N:38:VAL:CG2	2.42	0.49
14:N:165:SER:HB3	37:N:8533:HOH:O	2.12	0.49
1:A:1840:A:H4'	1:A:1841:C:O5'	2.12	0.49
1:A:2506:A:C1'	37:A:5633:HOH:O	2.60	0.49
14:N:114:VAL:HB	14:N:159:THR:HG23	1.94	0.49
4:D:162:MET:CE	4:D:310:ARG:HD3	2.42	0.49
1:A:306:A:P	21:U:38:ARG:HH21	2.35	0.49
1:A:638:C:H2'	1:A:639:A:C8	2.47	0.49
27:1:51:GLY:HA3	37:1:8417:HOH:O	2.11	0.49
7:G:145:ALA:HB1	7:G:168:ILE:CD1	2.42	0.49
2:B:3036:C:C5	2:B:3037:C:C5	3.00	0.49
1:A:275:G:C2	1:A:376:C:N3	2.80	0.49
1:A:820:G:C5	3:C:171:LYS:HB2	2.48	0.49
1:A:182:G:O3'	14:N:157:LEU:CD1	2.61	0.49
6:F:146:LYS:HZ1	15:O:107:ASN:HD21	1.54	0.49
17:Q:41:ARG:O	17:Q:44:VAL:HB	2.12	0.49
1:A:1003:U:HO2'	10:J:90:PHE:HE1	1.60	0.49
29:3:22:PRO:HB2	29:3:24:TRP:CD1	2.47	0.49
6:F:11:HIS:C	6:F:13:MET:H	2.15	0.49
1:A:816:G:H5'	1:A:1598:A:H4'	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:731:U:O2'	1:A:732:C:H5'	2.12	0.49
24:X:139:GLY:O	24:X:141:HIS:CD2	2.64	0.49
4:D:205:VAL:O	4:D:307:ARG:NE	2.45	0.49
6:F:95:THR:C	6:F:97:GLN:N	2.60	0.49
1:A:2300:A:H4'	1:A:2301:A:O5'	2.13	0.49
4:D:41:PHE:HA	4:D:79:MET:HE2	1.93	0.49
11:K:45:VAL:HG22	11:K:46:ILE:N	2.25	0.49
1:A:1120:U:H5'	1:A:1121:G:OP2	2.12	0.49
1:A:1422:U:H2'	1:A:1423:C:C6	2.48	0.49
1:A:275:G:N2	1:A:376:C:C2	2.80	0.49
1:A:703:G:O2'	1:A:704:C:H5'	2.12	0.49
7:G:43:ASP:HA	37:G:5864:HOH:O	2.12	0.49
8:H:105:ALA:HB2	37:H:5522:HOH:O	2.12	0.49
10:J:48:LEU:HD13	10:J:146:TRP:HB3	1.93	0.49
8:H:101:ALA:HB2	8:H:108:LEU:HD22	1.94	0.49
3:C:170:VAL:HG13	27:1:22:ILE:HG21	1.95	0.49
30:4:3:MET:O	30:4:90:PHE:HA	2.11	0.49
16:P:105:ASN:HD21	16:P:109:SER:H	1.61	0.49
1:A:152:A:O2'	1:A:153:C:H5'	2.12	0.49
6:F:27:ILE:HG22	6:F:28:GLY:N	2.22	0.49
3:C:194:MET:HE1	3:C:199:HIS:HB2	1.95	0.49
30:4:74:CYS:N	37:4:8561:HOH:O	2.46	0.49
25:Y:25:ARG:HD3	25:Y:64:ALA:O	2.13	0.49
2:B:3020:G:P	37:B:8435:HOH:O	2.71	0.49
7:G:77:THR:OG1	7:G:78:GLU:N	2.44	0.49
1:A:2729:C:H2'	1:A:2730:G:H8	1.78	0.49
16:P:113:VAL:O	16:P:114:ILE:HD13	2.13	0.49
16:P:99:GLU:HA	37:P:7481:HOH:O	2.12	0.49
10:J:154:THR:HB	10:J:155:PRO:HD3	1.95	0.49
1:A:665:A:H2'	1:A:666:A:C8	2.47	0.49
15:O:141:ARG:HB3	37:O:8570:HOH:O	2.13	0.49
4:D:314:ALA:CB	4:D:317:PRO:HG3	2.42	0.49
26:Z:200:THR:HG22	26:Z:201:GLU:HG2	1.94	0.49
17:Q:10:ALA:O	17:Q:13:VAL:HG12	2.13	0.49
1:A:1684:A:O2'	1:A:1685:A:H5"	2.13	0.49
22:V:20:MET:CG	22:V:28:THR:HG23	2.43	0.49
24:X:51:PHE:CD1	24:X:51:PHE:N	2.79	0.49
5:E:35:VAL:HG21	5:E:227:GLY:HA2	1.93	0.49
17:Q:131:PHE:CD1	17:Q:137:LEU:HD13	2.46	0.49
1:A:390:G:C5	1:A:391:U:C5	3.00	0.49
10:J:26:LYS:HD3	10:J:89:PRO:CG	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:140:LEU:HD23	37:D:8583:HOH:O	2.13	0.49
15:O:37:ARG:NH2	37:O:8534:HOH:O	2.45	0.49
1:A:1189:A:O2'	1:A:1208:C:H2'	2.12	0.49
6:F:99:ASP:O	6:F:159:PRO:HG3	2.13	0.49
6:F:57:THR:HG23	6:F:63:ILE:CG2	2.41	0.49
14:N:9:ARG:HG3	37:N:8544:HOH:O	2.12	0.49
2:B:3064:C:H2'	2:B:3065:A:H5'	1.95	0.49
1:A:716:G:O5'	37:A:5790:HOH:O	2.20	0.49
3:C:149:ASP:OD1	3:C:151:GLN:HB2	2.12	0.49
1:A:1682:A:H5"	37:A:9036:HOH:O	2.12	0.49
5:E:236:THR:O	5:E:237:GLU:C	2.50	0.49
6:F:19:GLU:O	6:F:133:ASN:HB3	2.12	0.49
14:N:113:ARG:NH1	14:N:152:ARG:O	2.42	0.49
21:U:38:ARG:NH1	21:U:38:ARG:HG3	2.27	0.49
5:E:133:ARG:NH2	37:E:8421:HOH:O	2.46	0.49
2:B:3095:C:O2'	2:B:3096:C:H5'	2.13	0.49
1:A:1370:G:C4	37:A:9727:HOH:O	2.65	0.49
1:A:797:A:H4'	27:1:10:ARG:N	2.27	0.49
6:F:23:VAL:HG21	6:F:45:THR:CG2	2.42	0.49
12:L:45:PRO:HB2	37:L:7169:HOH:O	2.13	0.49
1:A:2837:U:H2'	37:A:6412:HOH:O	2.13	0.49
1:A:2420:G:H4'	37:A:3671:HOH:O	2.13	0.49
5:E:84:VAL:O	5:E:85:LYS:CB	2.60	0.49
1:A:440:C:H2'	1:A:441:A:C8	2.48	0.49
1:A:169:A:H4'	37:N:8534:HOH:O	2.12	0.49
12:L:132:VAL:C	37:L:3160:HOH:O	2.51	0.49
1:A:1235:G:C1'	11:K:63:ILE:HG23	2.42	0.49
6:F:51:ARG:HD3	37:F:7636:HOH:O	2.13	0.49
14:N:108:LYS:N	14:N:108:LYS:HD3	2.28	0.49
19:S:96:VAL:HG13	19:S:106:GLY:HA3	1.94	0.49
1:A:1119:G:C8	11:K:52:GLN:NE2	2.81	0.49
6:F:64:ARG:HG2	6:F:66:GLY:O	2.13	0.49
1:A:1205:U:C2'	1:A:1206:U:C5'	2.90	0.49
3:C:200:PRO:HG2	3:C:225:VAL:HG21	1.95	0.49
24:X:76:ASP:O	24:X:77:ALA:C	2.51	0.49
1:A:2896:A:N3	1:A:2896:A:H2'	2.28	0.49
1:A:449:A:C8	5:E:43:LYS:HG2	2.47	0.49
1:A:812:A:H2'	1:A:813:C:C6	2.48	0.49
13:M:72:ASN:HB2	37:M:8453:HOH:O	2.12	0.49
37:A:8974:HOH:O	27:1:34:LYS:HD3	2.13	0.49
15:O:132:ASN:O	15:O:135:VAL:HG12	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:85:VAL:HG12	25:Y:86:GLU:N	2.27	0.48
10:J:31:PHE:CD2	10:J:85:ILE:HG23	2.48	0.48
2:B:3055:U:H4'	2:B:3056:A:H8	1.78	0.48
1:A:2505:G:H8	37:A:5216:HOH:O	1.96	0.48
1:A:1166:A:H1'	1:A:1192:A:N1	2.26	0.48
24:X:48:VAL:O	24:X:48:VAL:CG1	2.59	0.48
19:S:76:ASP:OD1	19:S:77:ALA:N	2.45	0.48
15:O:139:TRP:HA	15:O:139:TRP:HE3	1.78	0.48
21:U:28:SER:O	21:U:32:ARG:HG3	2.12	0.48
1:A:907:A:H2'	1:A:908:A:C8	2.47	0.48
4:D:84:LEU:HD13	4:D:84:LEU:O	2.13	0.48
1:A:1236:A:H2'	1:A:1237:U:O4'	2.13	0.48
30:4:40:ARG:HD2	37:4:8549:HOH:O	2.13	0.48
10:J:44:ALA:HB3	10:J:136:VAL:O	2.13	0.48
1:A:1118:A:C8	1:A:1118:A:C3'	2.85	0.48
1:A:2428:G:C4	1:A:2461:U:C5	3.01	0.48
8:H:101:ALA:HB2	8:H:108:LEU:CD2	2.43	0.48
19:S:39:THR:HB	19:S:42:GLU:CD	2.33	0.48
37:A:9381:HOH:O	12:L:39:GLY:HA3	2.12	0.48
1:A:289:G:O2'	1:A:290:C:H5'	2.12	0.48
25:Y:43:VAL:HG12	25:Y:44:ASP:N	2.27	0.48
2:B:3029:C:C2'	2:B:3030:C:H5'	2.43	0.48
37:A:5846:HOH:O	17:Q:59:ARG:HD3	2.13	0.48
21:U:26:THR:HA	21:U:39:ASN:HB3	1.95	0.48
1:A:1334:C:H2'	1:A:1335:C:H6	1.77	0.48
12:L:101:ASN:O	12:L:102:GLU:HB2	2.13	0.48
12:L:48:GLY:C	37:L:5632:HOH:O	2.50	0.48
1:A:2597:U:OP2	37:A:3404:HOH:O	2.20	0.48
12:L:55:VAL:CG1	12:L:56:SER:N	2.77	0.48
26:Z:187:VAL:O	26:Z:187:VAL:HG13	2.13	0.48
14:N:79:LYS:NZ	37:N:8566:HOH:O	2.46	0.48
3:C:199:HIS:HD2	3:C:201:PHE:HB2	1.78	0.48
11:K:107:ASN:HD22	11:K:109:TYR:H	1.59	0.48
1:A:1972:U:H2'	1:A:1973:A:C5'	2.43	0.48
1:A:2421:G:H3'	1:A:2422:U:H5"	1.95	0.48
25:Y:76:ARG:HG3	25:Y:76:ARG:NH1	2.26	0.48
1:A:2547:C:H2'	1:A:2548:C:H6	1.78	0.48
1:A:2727:A:H2'	1:A:2728:C:H5'	1.94	0.48
28:2:28:HIS:CD2	28:2:31:LYS:HG3	2.48	0.48
37:L:1387:HOH:O	22:V:20:MET:HE3	2.13	0.48
1:A:2791:U:H1'	1:A:2792:A:H5"	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2356:A:H2'	1:A:2357:G:O4'	2.13	0.48
5:E:107:ARG:NH2	37:E:8454:HOH:O	2.44	0.48
9:I:73:ASP:O	37:I:2218:HOH:O	2.20	0.48
7:G:31:ARG:NH1	37:G:5919:HOH:O	2.45	0.48
1:A:1299:G:N2	37:A:4259:HOH:O	2.46	0.48
1:A:1701:A:H4'	1:A:1702:U:C5'	2.42	0.48
19:S:132:ARG:HG2	19:S:133:ALA:N	2.27	0.48
1:A:1425:G:O2'	1:A:1426:C:H5'	2.13	0.48
8:H:26:THR:HB	8:H:102:GLY:HA3	1.95	0.48
15:O:157:PRO:HA	37:O:8526:HOH:O	2.12	0.48
1:A:837:U:H4'	37:A:9979:HOH:O	2.12	0.48
1:A:1930:A:H2'	1:A:1931:A:C8	2.48	0.48
6:F:35:ALA:HB1	37:F:3279:HOH:O	2.11	0.48
24:X:110:GLN:HA	24:X:110:GLN:HE21	1.78	0.48
1:A:2727:A:C5	1:A:2756:U:C4	3.01	0.48
1:A:2834:G:C4	1:A:2847:G:N2	2.81	0.48
1:A:390:G:C4	1:A:391:U:C6	3.02	0.48
1:A:2445:U:H2'	1:A:2446:G:C8	2.48	0.48
3:C:123:GLY:HA2	3:C:159:VAL:O	2.14	0.48
1:A:2904:U:H4'	25:Y:8:ARG:NH1	2.28	0.48
1:A:1486:A:C5	29:3:2:LYS:HG3	2.48	0.48
5:E:237:GLU:N	37:E:8445:HOH:O	2.46	0.48
6:F:23:VAL:HG12	6:F:130:VAL:HG22	1.96	0.48
1:A:1117:A:C2	1:A:1244:U:C2	3.01	0.48
30:4:18:GLN:OE1	30:4:73:GLU:HB3	2.13	0.48
11:K:107:ASN:HD22	11:K:107:ASN:C	2.17	0.48
1:A:2821:C:H4'	4:D:116:PRO:CB	2.41	0.48
13:M:61:ALA:HA	37:M:8437:HOH:O	2.14	0.48
1:A:1057:A:C6	1:A:1058:A:C6	3.02	0.48
11:K:75:PRO:HG2	11:K:105:LEU:CD2	2.44	0.48
1:A:1162:G:H2'	1:A:1162:G:N3	2.28	0.48
1:A:1768:C:H2'	1:A:1769:C:O4'	2.14	0.48
1:A:130:C:H5'	37:A:4789:HOH:O	2.13	0.48
19:S:34:GLU:HG2	19:S:46:TYR:OH	2.14	0.48
19:S:35:ILE:O	19:S:38:LYS:HB2	2.13	0.48
5:E:65:ARG:HG3	5:E:67:GLN:HB2	1.95	0.48
16:P:54:GLU:HG2	16:P:73:ASP:O	2.14	0.48
1:A:2401:A:H5'	37:A:9075:HOH:O	2.12	0.48
10:J:31:PHE:HA	10:J:85:ILE:CG2	2.44	0.48
27:1:11:THR:OG1	27:1:23:ARG:HB2	2.14	0.48
3:C:199:HIS:CD2	3:C:201:PHE:HB2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:C:N3	1:A:155:C:C5	2.81	0.48
1:A:1114:A:H2'	1:A:1115:U:H6	1.77	0.48
18:R:93:ARG:HH11	18:R:93:ARG:HG3	1.78	0.48
19:S:14:ALA:HB3	19:S:147:LEU:HB2	1.96	0.48
1:A:2559:C:H4'	37:A:6828:HOH:O	2.13	0.48
1:A:29:C:OP2	37:A:9723:HOH:O	2.20	0.48
20:T:6:LYS:HB2	20:T:27:ALA:O	2.13	0.48
18:R:77:ASP:N	18:R:80:LYS:O	2.44	0.48
6:F:41:LEU:HA	6:F:44:ILE:CG2	2.44	0.48
3:C:192:VAL:HG12	3:C:207:GLN:HB3	1.95	0.48
3:C:76:VAL:CG2	27:1:63:LYS:HB3	2.43	0.48
26:Z:99:ALA:HB2	26:Z:233:TYR:CE2	2.48	0.48
4:D:55:ASN:HB3	4:D:64:GLY:H	1.78	0.48
8:H:59:ILE:O	8:H:59:ILE:HG22	2.14	0.48
1:A:371:U:H2'	1:A:372:A:C8	2.47	0.48
15:O:139:TRP:HH2	15:O:176:ARG:HH11	1.62	0.48
8:H:34:ASN:HA	14:N:4:ALA:HB2	1.96	0.48
1:A:1507:C:H4'	37:A:3185:HOH:O	2.13	0.48
1:A:2385:G:H2'	1:A:2386:U:H6	1.78	0.48
1:A:23:G:C6	1:A:24:G:N1	2.81	0.48
17:Q:83:LYS:O	17:Q:86:ALA:HB3	2.14	0.48
37:A:3555:HOH:O	30:4:57:GLY:HA2	2.14	0.48
8:H:37:THR:O	8:H:41:GLU:HG3	2.13	0.48
5:E:246:ARG:CB	5:E:246:ARG:HH11	2.19	0.48
1:A:1180:U:H2'	1:A:1181:A:O4'	2.14	0.48
1:A:484:A:N1	1:A:506:G:H4'	2.29	0.48
1:A:559:U:H2'	1:A:560:C:O4'	2.14	0.48
1:A:2780:C:H2'	1:A:2781:U:H6	1.78	0.48
7:G:84:MET:HB2	7:G:131:LEU:HB2	1.94	0.48
1:A:51:G:N2	1:A:111:C:C2	2.81	0.48
1:A:920:C:H5"	1:A:921:G:O5'	2.14	0.48
1:A:40:C:H6	1:A:40:C:O5'	1.97	0.48
1:A:2906:A:H5'	1:A:2907:C:O4'	2.14	0.48
25:Y:12:ILE:HG23	25:Y:36:HIS:CG	2.48	0.48
1:A:612:U:H2'	1:A:613:C:C6	2.49	0.48
13:M:1:THR:HA	37:M:8393:HOH:O	2.13	0.48
5:E:118:THR:HG22	5:E:137:PRO:HB3	1.96	0.48
20:T:57:THR:CG2	20:T:58:MET:N	2.77	0.48
19:S:39:THR:O	19:S:40:ALA:C	2.51	0.48
30:4:65:THR:HB	30:4:83:TRP:H	1.78	0.48
10:J:71:TYR:C	10:J:73:GLN:N	2.66	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2326:U:H4'	1:A:2412:G:C4'	2.44	0.48
1:A:682:A:H2'	1:A:683:G:O4'	2.14	0.48
13:M:128:GLY:O	13:M:132:LYS:HG3	2.13	0.48
23:W:16:ARG:NH2	23:W:63:GLU:HG3	2.29	0.48
1:A:675:U:O2'	5:E:42:ARG:NH1	2.47	0.48
10:J:117:LYS:O	10:J:119:VAL:HG13	2.13	0.48
1:A:349:U:O2'	1:A:350:C:H5'	2.14	0.48
12:L:125:ALA:C	12:L:127:ALA:H	2.17	0.48
1:A:797:A:O4'	27:1:10:ARG:N	2.47	0.47
8:H:58:GLU:HG3	8:H:61:MET:CE	2.44	0.47
12:L:9:THR:O	12:L:10:GLN:C	2.50	0.47
24:X:137:GLN:HG3	24:X:137:GLN:O	2.14	0.47
1:A:2507:G:H2'	1:A:2510:C:H42	1.79	0.47
17:Q:143:ALA:CA	37:Q:5521:HOH:O	2.61	0.47
2:B:3026:C:OP2	37:B:8441:HOH:O	2.19	0.47
1:A:1593:C:OP1	17:Q:117:SER:HB3	2.14	0.47
11:K:131:THR:HB	11:K:134:GLU:HG3	1.95	0.47
4:D:1:PRO:O	4:D:2:GLN:HB2	2.14	0.47
1:A:1741:U:O2'	1:A:2723:G:H4'	2.13	0.47
4:D:141:ARG:HD2	4:D:163:GLU:OE2	2.13	0.47
1:A:1462:C:O2'	1:A:1463:A:H5'	2.14	0.47
1:A:795:G:N3	1:A:817:G:C2	2.82	0.47
24:X:22:GLU:HG2	24:X:27:HIS:CD2	2.48	0.47
16:P:77:ALA:HB1	16:P:98:LEU:HD12	1.96	0.47
19:S:111:ILE:HG23	19:S:145:LEU:HD11	1.96	0.47
2:B:3056:A:H1'	6:F:14:ARG:HG2	1.97	0.47
1:A:1947:G:P	37:A:3246:HOH:O	2.69	0.47
1:A:736:A:H2'	1:A:737:A:O4'	2.13	0.47
1:A:1634:G:H3'	37:A:3471:HOH:O	2.13	0.47
4:D:280:VAL:HG13	4:D:334:SER:HA	1.96	0.47
1:A:56:G:H5"	23:W:50:ARG:HH12	1.78	0.47
1:A:1167:G:O2'	1:A:1168:C:H5'	2.14	0.47
19:S:72:VAL:CG1	19:S:75:TRP:HB3	2.44	0.47
17:Q:61:ARG:NH1	17:Q:61:ARG:HG3	2.28	0.47
4:D:52:VAL:O	4:D:53:LEU:HD12	2.14	0.47
21:U:73:HIS:CD2	21:U:88:PRO:HG3	2.48	0.47
7:G:9:GLU:HA	37:G:5240:HOH:O	2.13	0.47
1:A:128:A:H3'	1:A:128:A:C8	2.49	0.47
14:N:57:LYS:HB3	14:N:60:ILE:HD12	1.96	0.47
3:C:171:LYS:NZ	37:C:8527:HOH:O	2.41	0.47
2:B:3049:G:O2'	2:B:3050:G:H5'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:120:LEU:HD12	13:M:133:VAL:HG21	1.95	0.47
3:C:153:ARG:NH1	3:C:153:ARG:HB2	2.23	0.47
1:A:447:A:O2'	1:A:448:G:H5'	2.15	0.47
1:A:401:C:P	37:A:5369:HOH:O	2.72	0.47
1:A:603:A:H4'	1:A:604:G:O5'	2.14	0.47
6:F:99:ASP:HB2	6:F:103:ASN:H	1.79	0.47
1:A:2361:A:H2'	1:A:2362:A:C8	2.48	0.47
1:A:1878:G:C1'	37:A:5700:HOH:O	2.60	0.47
1:A:737:A:H2'	1:A:738:G:O4'	2.14	0.47
14:N:154:ARG:HG3	37:N:8612:HOH:O	2.15	0.47
1:A:514:G:O5'	1:A:514:G:H8	1.97	0.47
1:A:2385:G:H2'	1:A:2386:U:C6	2.49	0.47
24:X:90:TYR:CD1	24:X:90:TYR:N	2.81	0.47
4:D:177:HIS:O	4:D:181:ILE:HG13	2.14	0.47
12:L:20:CYS:HB3	12:L:26:ALA:O	2.15	0.47
1:A:1019:C:O2	18:R:94:GLN:NE2	2.47	0.47
1:A:1440:U:P	37:A:4043:HOH:O	2.72	0.47
24:X:63:GLU:HG2	24:X:93:ILE:HG22	1.96	0.47
23:W:11:MET:HB3	23:W:15:GLU:HB2	1.95	0.47
14:N:27:ARG:O	14:N:30:GLU:N	2.45	0.47
24:X:122:ARG:HH22	24:X:154:ARG:C	2.18	0.47
12:L:109:LEU:HD13	12:L:113:ILE:HD11	1.95	0.47
5:E:1:MET:HG2	5:E:2:GLN:NE2	2.30	0.47
16:P:35:LYS:HD3	37:P:3360:HOH:O	2.15	0.47
25:Y:76:ARG:O	25:Y:77:PHE:HB3	2.14	0.47
22:V:52:THR:HG21	22:V:54:THR:HB	1.96	0.47
11:K:93:ARG:NH1	11:K:93:ARG:HB3	2.27	0.47
6:F:169:THR:O	6:F:170:TYR:HB2	2.15	0.47
1:A:2274:A:C4'	14:N:77:PHE:HE1	2.27	0.47
17:Q:131:PHE:CE1	17:Q:137:LEU:HD13	2.49	0.47
1:A:1114:A:H2'	1:A:1115:U:C6	2.49	0.47
1:A:2377:U:O5'	1:A:2377:U:H6	1.97	0.47
4:D:189:ALA:HB1	37:D:8567:HOH:O	2.14	0.47
17:Q:80:ARG:HG2	17:Q:87:ARG:CZ	2.44	0.47
1:A:542:A:C8	1:A:542:A:C5'	2.91	0.47
4:D:315:VAL:HG23	4:D:316:ARG:HG2	1.96	0.47
6:F:84:LEU:C	6:F:86:THR:H	2.18	0.47
1:A:2769:C:H2'	1:A:2770:G:H5'	1.97	0.47
1:A:2415:A:O2'	15:O:29:SER:HB3	2.13	0.47
20:T:29:ASP:CG	20:T:31:ARG:NH1	2.68	0.47
5:E:54:LEU:HD23	5:E:79:ARG:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:A:H5"	1:A:97:G:O4'	2.14	0.47
1:A:516:A:OP2	37:A:5223:HOH:O	2.20	0.47
1:A:2389:U:H4'	18:R:53:HIS:HD2	1.80	0.47
7:G:34:TRP:HA	37:G:4572:HOH:O	2.14	0.47
1:A:107:U:H2'	1:A:108:U:H5'	1.96	0.47
11:K:103:VAL:HG12	37:K:5907:HOH:O	2.14	0.47
30:4:60:LYS:CG	30:4:61:PRO:HD2	2.40	0.47
8:H:47:LEU:HD22	8:H:108:LEU:CD1	2.45	0.47
15:O:141:ARG:N	37:O:8570:HOH:O	2.47	0.47
4:D:36:PRO:HA	4:D:168:GLY:HA2	1.93	0.47
22:V:33:SER:O	22:V:37:GLU:HG3	2.14	0.47
1:A:2524:G:H21	1:A:2526:C:N4	2.12	0.47
21:U:24:ARG:O	21:U:93:THR:OG1	2.23	0.47
1:A:319:A:H2'	1:A:320:G:C8	2.49	0.47
19:S:29:LYS:HD3	37:S:8533:HOH:O	2.15	0.47
1:A:1370:G:N3	37:A:9727:HOH:O	2.35	0.47
1:A:536:A:H3'	37:A:4623:HOH:O	2.13	0.47
10:J:26:LYS:CG	10:J:28:ILE:H	2.17	0.47
10:J:26:LYS:HD2	10:J:28:ILE:HB	1.96	0.47
10:J:157:ILE:HG22	10:J:158:ASN:N	2.30	0.47
1:A:960:G:N3	1:A:960:G:C2'	2.77	0.47
3:C:211:LYS:NZ	37:C:8625:HOH:O	2.46	0.47
1:A:1209:C:H2'	1:A:1210:G:C8	2.46	0.47
3:C:194:MET:CE	3:C:199:HIS:HB2	2.45	0.47
1:A:2769:C:H2'	1:A:2770:G:C5'	2.44	0.47
26:Z:106:THR:CG2	26:Z:107:PRO:HD2	2.45	0.47
14:N:69:LYS:HD3	14:N:125:ARG:HA	1.96	0.47
28:2:21:ARG:HD2	28:2:39:PHE:HB2	1.96	0.47
37:A:9350:HOH:O	13:M:41:HIS:CE1	2.62	0.47
1:A:1543:G:N1	1:A:1641:A:OP2	2.34	0.47
2:B:3008:G:O6	15:O:11:ARG:NH1	2.47	0.47
19:S:132:ARG:NH1	37:S:8587:HOH:O	2.48	0.47
1:A:2389:U:H4'	18:R:53:HIS:CD2	2.50	0.47
1:A:2775:A:C6	1:A:2799:A:C8	3.02	0.47
1:A:2456:A:H2'	1:A:2457:U:C6	2.50	0.47
17:Q:58:SER:HB3	37:Q:4744:HOH:O	2.13	0.47
1:A:844:A:C6	1:A:882:A:C5	3.02	0.47
1:A:584:U:H3'	37:A:5674:HOH:O	2.13	0.47
24:X:66:LEU:HA	24:X:66:LEU:HD23	1.79	0.47
1:A:1218:U:H2'	1:A:1219:U:C6	2.50	0.47
1:A:1385:G:O3'	25:Y:49:ARG:NH1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3076:G:C8	2:B:3077:A:H2'	2.50	0.47
10:J:84:ARG:CZ	10:J:135:TRP:HH2	2.26	0.47
24:X:6:GLN:HA	24:X:52:VAL:HG23	1.96	0.47
1:A:1377:C:H1'	37:A:6844:HOH:O	2.14	0.47
1:A:1878:G:O2'	1:A:1879:U:C6	2.67	0.47
1:A:694:A:C2'	1:A:695:C:H5'	2.45	0.47
19:S:25:PHE:CE2	19:S:29:LYS:CE	2.98	0.47
19:S:33:ARG:NH2	37:S:8533:HOH:O	2.39	0.47
13:M:112:GLY:O	13:M:132:LYS:NZ	2.33	0.47
7:G:162:PHE:CD1	7:G:162:PHE:N	2.82	0.47
1:A:889:C:H2'	1:A:890:C:C6	2.50	0.47
1:A:1453:G:N2	1:A:1675:C:C2	2.83	0.47
1:A:1161:A:O5'	1:A:1161:A:C8	2.68	0.47
1:A:677:C:H4'	5:E:246:ARG:NH2	2.30	0.47
9:I:67:LEU:O	9:I:71:LEU:HG	2.15	0.47
24:X:76:ASP:O	24:X:77:ALA:O	2.33	0.47
1:A:926:A:O2'	13:M:41:HIS:CD2	2.68	0.47
18:R:40:HIS:CE1	18:R:94:GLN:HA	2.50	0.47
1:A:142:G:O2'	1:A:143:C:H5'	2.14	0.47
1:A:1304:U:H2'	1:A:1305:C:C6	2.50	0.47
13:M:17:SER:C	13:M:19:LYS:H	2.18	0.47
1:A:10:U:H5'	37:A:5616:HOH:O	2.13	0.47
1:A:2474:A:N3	37:A:4234:HOH:O	2.36	0.47
1:A:739:G:N7	37:A:7119:HOH:O	2.46	0.47
6:F:64:ARG:O	6:F:67:ASP:OD2	2.32	0.47
1:A:308:U:H5'	21:U:97:ARG:NH2	2.30	0.47
9:I:16:LYS:O	9:I:20:VAL:HG23	2.15	0.47
1:A:1477:C:H5'	1:A:1868:G:H5"	1.96	0.47
3:C:169:PHE:O	3:C:170:VAL:HB	2.15	0.47
1:A:2531:U:O2'	1:A:2532:A:H5'	2.14	0.47
5:E:196:THR:HG23	37:E:8395:HOH:O	2.14	0.47
19:S:17:MET:HE1	19:S:19:ARG:NH2	2.30	0.47
3:C:11:ARG:HD3	37:C:8519:HOH:O	2.15	0.47
1:A:2785:C:H4'	1:A:2786:G:OP2	2.15	0.47
3:C:100:PRO:O	3:C:103:VAL:HG23	2.14	0.46
24:X:65:VAL:CA	24:X:68:THR:HG22	2.45	0.46
1:A:1151:G:P	9:I:16:LYS:NZ	2.87	0.46
3:C:175:LYS:HE2	37:C:8577:HOH:O	2.15	0.46
13:M:59:GLU:HG2	13:M:104:ASP:OD2	2.14	0.46
1:A:474:C:O3'	5:E:73:LEU:CD2	2.63	0.46
1:A:329:A:H5'	1:A:347:A:C1'	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:101:ASN:O	12:L:102:GLU:CB	2.63	0.46
37:L:7438:HOH:O	22:V:20:MET:HE1	2.15	0.46
21:U:106:GLU:HG3	37:U:4913:HOH:O	2.14	0.46
1:A:1616:A:H5"	1:A:1617:C:OP1	2.14	0.46
1:A:564:G:H1'	37:A:5885:HOH:O	2.15	0.46
13:M:101:ASP:C	13:M:103:ALA:H	2.17	0.46
1:A:962:C:H5"	37:A:4487:HOH:O	2.14	0.46
5:E:246:ARG:NE	37:E:8419:HOH:O	2.48	0.46
15:O:175:LEU:HD11	37:O:8539:HOH:O	2.15	0.46
17:Q:10:ALA:HA	17:Q:13:VAL:HG12	1.96	0.46
3:C:69:LEU:C	3:C:69:LEU:HD12	2.34	0.46
1:A:2783:A:O2'	1:A:2784:A:H5'	2.15	0.46
13:M:73:VAL:HG21	13:M:116:HIS:CD2	2.50	0.46
25:Y:30:MET:HE1	25:Y:58:ALA:HB3	1.96	0.46
1:A:2445:U:H2'	1:A:2446:G:H8	1.80	0.46
21:U:41:ARG:NH1	21:U:42:VAL:O	2.49	0.46
1:A:2900:G:H2'	1:A:2901:C:O4'	2.15	0.46
1:A:2737:C:H2'	37:A:5721:HOH:O	2.14	0.46
1:A:622:G:H5'	1:A:1357:A:H61	1.79	0.46
20:T:11:THR:H	20:T:14:ALA:HB3	1.80	0.46
1:A:2897:C:H2'	1:A:2898:G:H8	1.78	0.46
24:X:80:ASP:O	24:X:84:VAL:HG23	2.15	0.46
10:J:57:ARG:HG3	10:J:57:ARG:HH11	1.81	0.46
1:A:21:G:H5"	19:S:1:GLY:O	2.16	0.46
1:A:2415:A:N3	15:O:26:LEU:HD13	2.30	0.46
16:P:26:TRP:HB2	37:P:3062:HOH:O	2.14	0.46
1:A:2656:G:C2'	1:A:2657:G:H5'	2.45	0.46
15:O:184:ILE:HG22	15:O:185:GLU:N	2.30	0.46
19:S:25:PHE:CE2	19:S:29:LYS:HE2	2.50	0.46
5:E:150:THR:HA	5:E:203:ALA:O	2.16	0.46
20:T:73:ASP:OD1	20:T:75:GLN:HB2	2.15	0.46
8:H:117:GLU:C	8:H:119:ARG:H	2.19	0.46
28:2:5:THR:N	28:2:6:PRO:HD2	2.29	0.46
24:X:1:MET:HB2	24:X:103:GLU:HG2	1.97	0.46
14:N:39:ARG:HA	14:N:63:VAL:HG22	1.98	0.46
10:J:157:ILE:CG2	10:J:158:ASN:N	2.79	0.46
14:N:87:MET:HG3	14:N:87:MET:H	1.29	0.46
1:A:506:G:N2	1:A:509:A:H5"	2.22	0.46
1:A:182:G:O3'	14:N:157:LEU:HD13	2.16	0.46
20:T:57:THR:C	20:T:59:ASP:H	2.19	0.46
24:X:122:ARG:NH1	24:X:122:ARG:CG	2.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:65:VAL:HA	24:X:68:THR:CG2	2.45	0.46
24:X:21:LEU:HB3	24:X:26:ILE:HG12	1.97	0.46
1:A:841:A:OP2	19:S:128:ARG:HD2	2.15	0.46
9:I:12:ILE:HB	37:I:4714:HOH:O	2.15	0.46
1:A:1594:C:C2	1:A:1601:G:N2	2.83	0.46
24:X:13:MET:HA	37:X:4944:HOH:O	2.16	0.46
1:A:1250:C:O2'	1:A:1251:C:H5'	2.16	0.46
22:V:44:ARG:CB	37:V:3805:HOH:O	2.63	0.46
1:A:380:A:OP2	14:N:9:ARG:HD2	2.16	0.46
12:L:99:ASP:OD1	12:L:101:ASN:N	2.47	0.46
19:S:111:ILE:HG23	19:S:145:LEU:CD1	2.45	0.46
15:O:50:LEU:HA	15:O:50:LEU:HD12	1.71	0.46
27:1:50:ALA:HB3	27:1:54:ILE:HG22	1.97	0.46
26:Z:178:HIS:CG	26:Z:179:PRO:HD2	2.51	0.46
37:B:8465:HOH:O	15:O:147:ILE:HB	2.15	0.46
1:A:283:U:H5"	1:A:284:C:OP2	2.16	0.46
4:D:243:ASN:HA	4:D:244:PRO:C	2.36	0.46
6:F:94:ALA:O	6:F:95:THR:O	2.33	0.46
1:A:1384:C:H5'	25:Y:30:MET:HG2	1.96	0.46
1:A:275:G:C2	1:A:376:C:C2	3.04	0.46
1:A:2443:C:H3'	37:A:3056:HOH:O	2.15	0.46
11:K:39:VAL:HG12	11:K:40:ASN:ND2	2.31	0.46
1:A:426:G:H2'	1:A:427:C:O4'	2.15	0.46
3:C:70:ALA:HA	3:C:71:PRO:HD3	1.74	0.46
1:A:382:U:O2'	1:A:430:A:H1'	2.15	0.46
14:N:155:HIS:CE1	14:N:158:ARG:HE	2.33	0.46
3:C:232:ARG:NH2	3:C:236:GLY:O	2.40	0.46
1:A:1902:G:N2	1:A:1936:C:C2	2.83	0.46
6:F:23:VAL:CG2	6:F:73:VAL:HB	2.45	0.46
14:N:164:THR:HG23	14:N:165:SER:OG	2.15	0.46
10:J:1:LYS:HA	10:J:2:PRO:HD3	1.67	0.46
5:E:118:THR:CG2	5:E:137:PRO:HB3	2.45	0.46
16:P:47:ARG:NH1	37:P:4564:HOH:O	2.48	0.46
15:O:71:TRP:N	37:O:8539:HOH:O	2.48	0.46
8:H:110:GLU:HA	8:H:113:ASP:OD2	2.15	0.46
1:A:2909:G:O2'	1:A:2910:A:H5'	2.16	0.46
1:A:51:G:C2	1:A:111:C:C2	3.04	0.46
1:A:1335:C:H2'	1:A:1336:U:C6	2.51	0.46
1:A:2673:U:C2	1:A:2817:G:N2	2.84	0.46
1:A:816:G:C6	1:A:817:G:N1	2.83	0.46
27:1:34:LYS:HE2	37:1:8426:HOH:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:G:P	37:A:6989:HOH:O	2.72	0.46
15:O:32:PRO:HD2	15:O:99:GLU:O	2.16	0.46
17:Q:64:GLU:HG2	37:Q:2495:HOH:O	2.14	0.46
1:A:121:U:OP2	29:3:10:ARG:NH2	2.36	0.46
7:G:5:LEU:HD21	7:G:66:GLN:HG3	1.98	0.46
14:N:164:THR:HG23	14:N:165:SER:H	1.76	0.46
1:A:2500:C:O2'	1:A:2501:G:H5'	2.16	0.46
5:E:218:VAL:HG12	37:E:8419:HOH:O	2.15	0.46
1:A:1185:U:H5'	37:A:7039:HOH:O	2.16	0.46
15:O:91:ARG:HG3	15:O:186:LEU:HD23	1.98	0.46
1:A:2533:C:C6	1:A:2533:C:H5'	2.41	0.46
1:A:2266:A:H2'	1:A:2267:G:C8	2.51	0.46
6:F:58:VAL:CG1	6:F:59:GLY:N	2.78	0.46
1:A:425:U:O2'	1:A:426:G:H5'	2.16	0.46
2:B:3041:C:H4'	6:F:48:MET:HB2	1.98	0.46
6:F:41:LEU:CA	6:F:44:ILE:HG22	2.45	0.46
19:S:8:ALA:CB	19:S:13:THR:HG21	2.37	0.46
14:N:184:ARG:HG3	14:N:185:PRO:HA	1.98	0.46
4:D:211:THR:HA	4:D:255:GLY:O	2.16	0.46
3:C:85:ASP:HA	37:C:8620:HOH:O	2.14	0.46
1:A:1377:C:C6	1:A:1377:C:H5'	2.47	0.46
12:L:82:ARG:NH2	12:L:115:ARG:HG2	2.31	0.46
18:R:28:ARG:HG2	37:R:4350:HOH:O	2.16	0.46
1:A:80:A:H5"	21:U:41:ARG:CZ	2.46	0.46
1:A:2443:C:O3'	13:M:56:LYS:HE3	2.15	0.46
6:F:91:ALA:HB1	37:F:5198:HOH:O	2.16	0.46
1:A:177:A:H2'	1:A:178:U:O4'	2.16	0.46
1:A:2502:C:C4'	10:J:151:MET:HG2	2.46	0.46
6:F:21:VAL:HG13	6:F:131:THR:O	2.16	0.46
4:D:43:GLY:O	4:D:308:LEU:HD12	2.15	0.46
5:E:27:ARG:O	5:E:31:ILE:HG13	2.16	0.46
1:A:559:U:C6	1:A:559:U:H5'	2.42	0.46
8:H:60:VAL:HG12	8:H:60:VAL:O	2.16	0.46
15:O:73:ALA:HB2	15:O:163:PHE:CZ	2.51	0.46
7:G:68:HIS:O	7:G:72:MET:HG3	2.16	0.46
1:A:1301:C:O2'	1:A:1331:A:H4'	2.16	0.46
1:A:396:U:O2'	1:A:418:C:H4'	2.16	0.46
1:A:2712:G:O2'	1:A:2713:G:H5'	2.16	0.46
1:A:1461:U:H2'	1:A:1462:C:C6	2.51	0.46
1:A:429:A:C6	1:A:430:A:C6	3.04	0.46
14:N:123:ASP:OD1	14:N:123:ASP:C	2.54	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1419:U:O2	1:A:1419:U:H3'	2.16	0.46
1:A:2432:C:OP1	13:M:48:LYS:NZ	2.38	0.46
10:J:132:PHE:O	10:J:133:ILE:HD13	2.16	0.46
14:N:35:PRO:CG	14:N:38:VAL:CG2	2.87	0.46
3:C:36:ASP:HB2	3:C:84:VAL:N	2.31	0.46
1:A:2072:G:C6	1:A:2533:C:H1'	2.51	0.46
10:J:35:ASN:ND2	10:J:79:ALA:O	2.49	0.46
1:A:2251:G:H4'	37:A:6980:HOH:O	2.16	0.46
1:A:716:G:C2'	1:A:717:C:O5'	2.64	0.46
3:C:66:ARG:HH11	3:C:66:ARG:HB2	1.80	0.46
4:D:132:HIS:HB2	4:D:137:LEU:HD22	1.97	0.46
10:J:26:LYS:CD	10:J:28:ILE:HB	2.46	0.45
1:A:2346:C:O3'	6:F:52:THR:HG23	2.16	0.45
1:A:2361:A:H5'	1:A:2361:A:H8	1.81	0.45
1:A:2645:U:H4'	31:A:8600:ZIT:H172	1.98	0.45
1:A:702:G:O2'	1:A:703:G:H5'	2.16	0.45
1:A:941:G:O2'	1:A:942:U:H5'	2.16	0.45
1:A:1368:U:O5'	1:A:1368:U:H6	1.99	0.45
1:A:861:A:H2'	1:A:862:U:C6	2.51	0.45
21:U:96:VAL:HG13	21:U:97:ARG:N	2.31	0.45
13:M:54:PRO:HG2	13:M:57:VAL:CG2	2.47	0.45
7:G:11:VAL:CG1	7:G:12:ASP:H	2.29	0.45
8:H:50:VAL:CG1	8:H:60:VAL:HG11	2.43	0.45
7:G:95:VAL:O	7:G:126:ILE:HD13	2.16	0.45
11:K:45:VAL:HG21	11:K:129:PHE:CD1	2.52	0.45
4:D:144:THR:HG22	4:D:145:HIS:N	2.31	0.45
17:Q:103:THR:O	17:Q:107:GLU:HG3	2.16	0.45
15:O:154:LEU:CG	15:O:155:GLU:H	2.27	0.45
1:A:380:A:H5"	14:N:48:ARG:NH2	2.31	0.45
1:A:790:A:H2'	1:A:791:A:O4'	2.16	0.45
21:U:6:LYS:NZ	37:U:644:HOH:O	2.42	0.45
1:A:2413:A:N7	15:O:109:PRO:HB3	2.32	0.45
1:A:1450:C:C4'	1:A:1451:C:OP2	2.59	0.45
6:F:94:ALA:HB3	6:F:174:VAL:CA	2.46	0.45
3:C:200:PRO:HD3	37:C:8523:HOH:O	2.15	0.45
1:A:314:G:N2	1:A:316:A:H3'	2.31	0.45
1:A:1129:C:H5"	1:A:1130:U:OP2	2.16	0.45
3:C:93:THR:C	3:C:94:LEU:HD23	2.36	0.45
1:A:1060:C:O2'	1:A:1061:C:H5'	2.16	0.45
1:A:1669:A:H2'	1:A:1670:G:H8	1.81	0.45
1:A:1617:C:C4	1:A:1643:C:H4'	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:492:C:C2'	1:A:493:U:H5'	2.46	0.45
4:D:88:GLU:O	4:D:88:GLU:HG3	2.15	0.45
7:G:133:VAL:HG12	7:G:141:VAL:HG13	1.98	0.45
30:4:87:ARG:HG3	37:4:8572:HOH:O	2.16	0.45
1:A:57:C:H5"	37:A:6335:HOH:O	2.16	0.45
10:J:84:ARG:CZ	10:J:135:TRP:CH2	3.00	0.45
15:O:37:ARG:HA	15:O:37:ARG:HD3	1.82	0.45
15:O:37:ARG:HA	35:O:8507:CL:CL	2.53	0.45
14:N:114:VAL:HG21	14:N:159:THR:HG21	1.99	0.45
3:C:153:ARG:HD3	37:C:8533:HOH:O	2.15	0.45
1:A:2661:U:H3	1:A:2812:A:H62	1.64	0.45
1:A:2814:A:OP2	37:A:4646:HOH:O	2.21	0.45
1:A:2852:A:H5"	37:A:4808:HOH:O	2.16	0.45
6:F:92:GLU:O	6:F:93:LEU:O	2.33	0.45
6:F:84:LEU:HA	6:F:87:ALA:HB3	1.98	0.45
5:E:211:ASP:HB2	5:E:231:ARG:HH12	1.81	0.45
1:A:1972:U:H2'	1:A:1973:A:H5'	1.99	0.45
4:D:248:ARG:HG2	37:K:3517:HOH:O	2.15	0.45
16:P:77:ALA:HA	16:P:96:VAL:O	2.16	0.45
1:A:45:A:N6	1:A:147:G:C4	2.84	0.45
13:M:20:ASN:O	13:M:22:ARG:N	2.50	0.45
1:A:278:A:H2'	1:A:279:C:O4'	2.17	0.45
4:D:320:GLN:HG3	4:D:321:PRO:CD	2.46	0.45
12:L:87:ARG:CZ	37:L:4854:HOH:O	2.63	0.45
5:E:246:ARG:NH2	37:E:8419:HOH:O	2.50	0.45
1:A:236:A:H4'	1:A:237:G:OP1	2.16	0.45
7:G:97:VAL:C	37:G:4191:HOH:O	2.54	0.45
10:J:13:ALA:HA	10:J:91:HIS:CE1	2.52	0.45
7:G:132:THR:HG23	7:G:132:THR:O	2.16	0.45
4:D:36:PRO:CA	4:D:168:GLY:HA3	2.43	0.45
3:C:192:VAL:HG12	3:C:192:VAL:O	2.16	0.45
28:2:37:CYS:SG	28:2:39:PHE:HB2	2.56	0.45
17:Q:16:VAL:CG1	17:Q:17:GLY:N	2.80	0.45
6:F:59:GLY:O	6:F:61:PHE:N	2.38	0.45
24:X:90:TYR:CE2	24:X:99:ALA:HB2	2.51	0.45
1:A:303:C:H2'	1:A:304:G:O4'	2.16	0.45
1:A:1815:A:H4'	1:A:2751:C:O4'	2.16	0.45
12:L:72:VAL:HG11	12:L:121:PHE:CD1	2.52	0.45
14:N:37:VAL:HG22	14:N:65:VAL:HG22	1.99	0.45
1:A:1750:C:N4	1:A:1751:G:C6	2.85	0.45
26:Z:187:VAL:HG12	26:Z:205:ILE:HA	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:A:C4'	1:A:237:G:H5'	2.40	0.45
1:A:2316:G:H4'	37:A:5671:HOH:O	2.16	0.45
3:C:132:ASP:OD1	3:C:133:ARG:N	2.48	0.45
1:A:240:C:O2	1:A:240:C:H2'	2.17	0.45
22:V:6:CYS:C	22:V:8:TYR:N	2.70	0.45
16:P:73:ASP:HA	16:P:92:VAL:O	2.17	0.45
24:X:67:ALA:HB2	24:X:93:ILE:HD13	1.98	0.45
8:H:48:VAL:CG2	8:H:74:PHE:HB3	2.46	0.45
3:C:39:ALA:HB3	3:C:61:GLU:OE2	2.16	0.45
37:A:3563:HOH:O	21:U:82:THR:HA	2.17	0.45
1:A:2860:G:H1'	37:A:6376:HOH:O	2.16	0.45
15:O:37:ARG:CZ	37:O:8534:HOH:O	2.64	0.45
1:A:1118:A:C8	1:A:1119:G:H5"	2.52	0.45
29:3:18:ASN:HA	29:3:18:ASN:HD22	1.58	0.45
22:V:17:THR:HG22	22:V:18:GLY:N	2.31	0.45
1:A:1209:C:O2	1:A:1210:G:C8	2.69	0.45
15:O:38:LYS:HB2	15:O:38:LYS:HE3	1.64	0.45
1:A:2781:U:H2'	1:A:2782:G:C5'	2.46	0.45
6:F:159:PRO:O	6:F:162:ALA:HB3	2.16	0.45
25:Y:43:VAL:HG22	25:Y:76:ARG:NH1	2.32	0.45
1:A:885:G:H5"	1:A:886:A:H5'	1.99	0.45
1:A:1730:G:H5'	1:A:1731:C:C6	2.52	0.45
1:A:1335:C:OP2	26:Z:207:SER:CB	2.65	0.45
1:A:625:U:H5'	37:A:9771:HOH:O	2.15	0.45
8:H:48:VAL:HG23	8:H:74:PHE:CB	2.47	0.45
1:A:2353:A:H4'	1:A:2354:A:O5'	2.17	0.45
1:A:123:U:H2'	1:A:124:C:C6	2.52	0.45
1:A:1197:G:N2	37:A:5811:HOH:O	2.49	0.45
3:C:164:ARG:HB2	27:1:68:CYS:SG	2.56	0.45
26:Z:187:VAL:HB	37:Z:8158:HOH:O	2.17	0.45
1:A:1205:U:C2'	1:A:1206:U:H5'	2.41	0.45
13:M:130:ARG:NH2	37:M:8418:HOH:O	2.50	0.45
1:A:2851:G:C2'	1:A:2852:A:H5'	2.47	0.45
2:B:3042:C:O2	6:F:76:ARG:NH1	2.50	0.45
7:G:107:PHE:CZ	7:G:108:LEU:HD13	2.52	0.45
3:C:94:LEU:HG	3:C:99:ILE:CD1	2.46	0.45
2:B:3064:C:C2'	2:B:3065:A:H5'	2.47	0.45
1:A:716:G:H2'	1:A:717:C:O5'	2.17	0.45
2:B:3096:C:H2'	2:B:3097:U:C6	2.52	0.45
30:4:91:GLN:O	30:4:92:GLU:HB2	2.17	0.45
13:M:97:VAL:HG12	13:M:98:GLU:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2106:C:H2'	1:A:2107:U:C6	2.51	0.45
1:A:2670:G:O2'	1:A:2671:U:H5'	2.16	0.45
18:R:72:LYS:HG2	18:R:85:ILE:HD13	1.99	0.45
14:N:55:LYS:HB2	14:N:60:ILE:CD1	2.46	0.45
30:4:70:ARG:HG2	30:4:70:ARG:NH1	2.32	0.45
15:O:67:ALA:HA	15:O:71:TRP:H	1.82	0.45
27:1:56:MET:HA	27:1:62:TYR:O	2.17	0.45
6:F:65:GLU:HA	37:F:6752:HOH:O	2.16	0.45
1:A:1593:C:OP1	17:Q:117:SER:CB	2.65	0.45
1:A:1635:U:O2'	1:A:1636:G:H5'	2.17	0.45
19:S:119:VAL:CG1	19:S:119:VAL:O	2.63	0.45
19:S:82:GLU:HG3	19:S:83:LYS:H	1.81	0.45
22:V:49:LEU:HD11	37:V:3805:HOH:O	2.16	0.45
1:A:2729:C:O2'	1:A:2730:G:H5'	2.17	0.45
1:A:949:U:O2'	18:R:40:HIS:HE1	2.00	0.45
1:A:2050:G:H5"	19:S:80:TYR:O	2.17	0.45
1:A:1574:C:O5'	1:A:1574:C:H6	1.99	0.45
2:B:3004:G:O2'	15:O:44:ARG:NH2	2.50	0.45
1:A:1252:A:H2'	1:A:1253:C:O4'	2.17	0.45
18:R:64:GLU:HG3	18:R:74:ASP:OD2	2.17	0.45
23:W:12:THR:HG23	23:W:14:ALA:N	2.32	0.45
27:1:10:ARG:HG3	27:1:11:THR:N	2.32	0.45
15:O:38:LYS:HE2	15:O:107:ASN:ND2	2.32	0.45
24:X:3:ALA:O	24:X:54:PHE:HA	2.17	0.45
5:E:214:THR:CG2	37:E:8433:HOH:O	2.55	0.45
15:O:163:PHE:O	15:O:164:ASP:O	2.35	0.45
14:N:20:ILE:O	14:N:24:MET:HG2	2.17	0.45
1:A:1634:G:H2'	1:A:1635:U:C6	2.51	0.45
10:J:71:TYR:O	10:J:73:GLN:N	2.50	0.45
37:A:8939:HOH:O	28:2:1:THR:HA	2.17	0.45
1:A:1810:C:OP1	22:V:44:ARG:NE	2.28	0.45
1:A:830:G:H2'	1:A:831:U:C6	2.51	0.45
14:N:47:ASP:CG	14:N:48:ARG:N	2.71	0.45
16:P:96:VAL:HG13	16:P:100:GLN:HB2	1.99	0.45
15:O:58:LEU:N	15:O:58:LEU:HD12	2.32	0.45
28:2:22:CYS:SG	28:2:24:GLU:HB2	2.57	0.45
6:F:15:GLU:HA	6:F:16:PRO:HD3	1.89	0.45
1:A:2273:C:OP1	37:A:9184:HOH:O	2.21	0.45
1:A:1535:G:H2'	1:A:1536:C:C6	2.52	0.45
1:A:2039:A:H4'	1:A:2760:C:O2'	2.17	0.45
1:A:542:A:H1'	37:A:4253:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1666:C:O2'	1:A:1667:A:C5'	2.60	0.44
1:A:869:G:OP1	14:N:79:LYS:HE2	2.16	0.44
1:A:1164:U:O4'	1:A:1165:G:OP1	2.34	0.44
4:D:307:ARG:CG	4:D:307:ARG:NH1	2.80	0.44
6:F:167:GLU:OE2	6:F:173:GLU:HG2	2.17	0.44
37:A:9534:HOH:O	25:Y:23:HIS:HD2	1.99	0.44
1:A:1549:C:N3	1:A:1637:A:C2	2.84	0.44
1:A:1008:C:OP1	10:J:16:ARG:NH2	2.49	0.44
1:A:251:C:H1'	14:N:58:GLN:HE22	1.81	0.44
2:B:3078:G:O2'	2:B:3079:U:P	2.75	0.44
17:Q:16:VAL:CG1	17:Q:20:ARG:HB2	2.48	0.44
1:A:2898:G:H4'	4:D:288:GLY:HA2	1.98	0.44
10:J:82:LYS:NZ	10:J:82:LYS:CB	2.80	0.44
1:A:2911:C:H2'	1:A:2912:C:C6	2.53	0.44
1:A:2387:U:H2'	1:A:2388:C:C6	2.51	0.44
29:3:36:ASN:HB3	29:3:39:ARG:NE	2.32	0.44
10:J:58:HIS:CE1	10:J:59:ASN:ND2	2.85	0.44
3:C:101:GLU:HG2	3:C:131:HIS:ND1	2.32	0.44
15:O:143:ARG:HH12	15:O:173:ASP:CG	2.18	0.44
1:A:88:G:N7	29:3:28:LYS:HD2	2.31	0.44
30:4:56:PRO:HA	37:4:8550:HOH:O	2.17	0.44
1:A:764:C:C2'	1:A:765:G:H5'	2.46	0.44
1:A:1532:G:C6	1:A:1533:A:C6	3.05	0.44
1:A:1095:U:O2	24:X:120:PRO:HG2	2.17	0.44
9:I:63:ARG:HB2	9:I:66:LEU:HG	1.99	0.44
15:O:48:VAL:HG13	15:O:55:ASP:HB3	1.95	0.44
17:Q:13:VAL:HG11	17:Q:40:VAL:CG1	2.48	0.44
2:B:3039:U:H3'	2:B:3040:C:H5"	1.98	0.44
3:C:220:PRO:HD2	3:C:223:ARG:HD3	1.99	0.44
3:C:51:ARG:HB2	37:C:8609:HOH:O	2.16	0.44
26:Z:144:ARG:CG	26:Z:144:ARG:HH11	2.29	0.44
1:A:120:A:H2'	1:A:120:A:N3	2.32	0.44
1:A:2274:A:H4'	14:N:77:PHE:HE1	1.82	0.44
7:G:36:PRO:HD3	11:K:127:ILE:HD12	1.98	0.44
1:A:764:C:H2'	1:A:765:G:O4'	2.17	0.44
7:G:118:ILE:HG23	7:G:144:THR:HG21	1.99	0.44
1:A:963:C:H2'	1:A:964:G:C8	2.52	0.44
18:R:41:LEU:HB3	18:R:52:PHE:CZ	2.52	0.44
1:A:1746:A:N3	1:A:1748:U:C4	2.85	0.44
14:N:74:ARG:HD3	14:N:91:ILE:HD12	2.00	0.44
30:4:70:ARG:HG2	30:4:70:ARG:HH11	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:143:THR:HG21	37:M:8412:HOH:O	2.16	0.44
11:K:19:MET:HE1	11:K:79:PHE:HA	1.99	0.44
1:A:1926:G:H2'	1:A:1927:A:C8	2.53	0.44
15:O:139:TRP:CH2	15:O:176:ARG:NH1	2.85	0.44
2:B:3031:C:H2'	2:B:3032:G:O4'	2.17	0.44
13:M:72:ASN:O	13:M:76:LEU:HG	2.18	0.44
1:A:2791:U:H4'	1:A:2792:A:OP1	2.17	0.44
1:A:492:C:O2'	1:A:493:U:H5'	2.18	0.44
1:A:201:G:N2	1:A:202:U:C2	2.86	0.44
1:A:853:C:H2'	1:A:854:G:O4'	2.17	0.44
1:A:244:C:OP2	8:H:38:LYS:HE3	2.18	0.44
1:A:1157:C:C2	1:A:1158:G:C8	3.05	0.44
1:A:2243:C:HO2'	1:A:2244:A:H8	1.66	0.44
2:B:3027:C:OP1	15:O:39:SER:OG	2.33	0.44
5:E:246:ARG:CZ	37:E:8419:HOH:O	2.65	0.44
21:U:49:GLU:OE2	21:U:97:ARG:NH1	2.43	0.44
5:E:27:ARG:HD2	16:P:5:PRO:HD2	2.00	0.44
19:S:39:THR:HG22	19:S:41:GLY:H	1.82	0.44
26:Z:133:HIS:CD2	37:Z:8169:HOH:O	2.57	0.44
37:A:4797:HOH:O	12:L:37:TYR:CE1	2.70	0.44
1:A:2781:U:O2'	1:A:2782:G:H5'	2.18	0.44
1:A:1299:G:N7	13:M:6:ARG:NH1	2.65	0.44
1:A:2719:A:N1	4:D:70:PRO:HG3	2.32	0.44
15:O:154:LEU:O	15:O:155:GLU:CB	2.63	0.44
4:D:248:ARG:O	4:D:251:VAL:CG1	2.66	0.44
1:A:61:G:C2	1:A:62:C:C2	3.05	0.44
1:A:266:G:C2	1:A:267:G:C8	3.06	0.44
2:B:3104:A:O2'	2:B:3105:A:H5'	2.18	0.44
1:A:1747:A:O3'	1:A:2584:G:H5'	2.17	0.44
1:A:2505:G:C2'	1:A:2506:A:H5'	2.47	0.44
23:W:1:THR:HG23	23:W:2:VAL:N	2.23	0.44
8:H:99:THR:O	8:H:100:ASP:HB2	2.18	0.44
37:A:9281:HOH:O	4:D:254:GLN:HG3	2.16	0.44
10:J:141:ASN:CA	37:J:8369:HOH:O	2.56	0.44
7:G:11:VAL:HG11	7:G:22:VAL:HG13	2.00	0.44
3:C:192:VAL:CG1	3:C:207:GLN:HB3	2.48	0.44
1:A:2723:G:H1'	37:A:4410:HOH:O	2.16	0.44
27:1:30:GLU:O	27:1:33:HIS:HB3	2.17	0.44
3:C:48:ASP:HB3	37:C:8609:HOH:O	2.17	0.44
22:V:36:CYS:O	22:V:37:GLU:C	2.56	0.44
13:M:41:HIS:O	13:M:42:ASN:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1730:G:H4'	1:A:1731:C:O5'	2.17	0.44
1:A:686:A:O2'	1:A:747:G:H4'	2.18	0.44
1:A:1072:G:OP2	26:Z:154:ARG:NH2	2.51	0.44
4:D:27:ASN:HD22	4:D:27:ASN:H	1.66	0.44
1:A:1854:C:O2'	1:A:1858:A:N3	2.45	0.44
37:A:5139:HOH:O	12:L:41:LYS:HE3	2.17	0.44
2:B:3054:A:O2'	2:B:3055:U:H5'	2.18	0.44
15:O:161:GLY:O	15:O:162:ASP:C	2.55	0.44
15:O:143:ARG:NH1	15:O:173:ASP:OD1	2.51	0.44
1:A:2727:A:N6	1:A:2756:U:C6	2.86	0.44
2:B:3020:G:H3'	37:B:8435:HOH:O	2.17	0.44
1:A:2659:U:C4'	19:S:76:ASP:HB3	2.48	0.44
15:O:108:SER:HA	15:O:109:PRO:HD3	1.84	0.44
28:2:45:ARG:NH1	37:2:8435:HOH:O	2.50	0.44
24:X:40:ALA:O	24:X:44:MET:HG3	2.18	0.44
1:A:1380:U:O4	1:A:2043:U:H4'	2.17	0.44
14:N:46:LEU:HB2	37:N:8606:HOH:O	2.17	0.44
11:K:6:PHE:HB3	11:K:109:TYR:OH	2.18	0.44
4:D:129:ARG:O	4:D:133:GLU:HG3	2.18	0.44
1:A:2673:U:C2	1:A:2817:G:C2	3.06	0.44
1:A:2274:A:N3	14:N:86:MET:CE	2.81	0.44
17:Q:134:VAL:O	17:Q:137:LEU:HB3	2.17	0.44
1:A:10:U:HO2'	1:A:11:A:P	2.41	0.44
1:A:382:U:C5	1:A:406:G:N2	2.86	0.44
1:A:941:G:C5	1:A:942:U:C4	3.06	0.44
1:A:134:U:C2	1:A:145:A:C2	3.06	0.44
37:A:5709:HOH:O	29:3:20:ARG:HB3	2.17	0.44
23:W:12:THR:CG2	23:W:15:GLU:HG3	2.24	0.44
10:J:140:PRO:HA	10:J:142:VAL:HG12	1.99	0.44
14:N:67:ILE:HD11	14:N:104:ARG:HD2	1.98	0.44
15:O:73:ALA:HB1	15:O:74:PRO:CD	2.47	0.44
15:O:73:ALA:HB1	15:O:74:PRO:HD2	1.99	0.44
11:K:19:MET:HE3	11:K:132:LEU:HD21	1.99	0.44
6:F:99:ASP:HB2	6:F:103:ASN:CB	2.47	0.44
1:A:316:A:H1'	1:A:336:G:N3	2.32	0.44
1:A:241:A:N1	1:A:378:A:H4'	2.33	0.44
1:A:1085:C:H2'	1:A:1086:A:O4'	2.18	0.44
1:A:2831:C:H2'	1:A:2832:C:H5'	2.00	0.44
1:A:1021:G:O2'	1:A:1022:A:H5'	2.18	0.44
1:A:945:U:H2'	1:A:946:C:C6	2.53	0.44
8:H:79:GLN:HG3	8:H:82:ASP:OD2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:57:ALA:HA	3:C:67:LEU:HD23	2.00	0.44
1:A:511:A:H1'	37:A:7229:HOH:O	2.18	0.44
1:A:2467:A:H2'	37:A:5033:HOH:O	2.18	0.44
1:A:2563:U:H2'	1:A:2565:C:O5'	2.17	0.44
14:N:18:GLY:O	14:N:21:ALA:HB3	2.18	0.44
25:Y:85:VAL:HG12	25:Y:86:GLU:H	1.83	0.43
2:B:3041:C:C6	6:F:50:VAL:HG21	2.52	0.43
2:B:3056:A:C3'	2:B:3057:A:H5"	2.48	0.43
1:A:159:G:H5"	14:N:74:ARG:HH22	1.82	0.43
1:A:213:G:O2'	1:A:214:U:OP2	2.36	0.43
11:K:6:PHE:O	11:K:8:ALA:N	2.51	0.43
1:A:2421:G:H3'	1:A:2422:U:C5'	2.48	0.43
1:A:204:A:H2'	1:A:205:U:C5'	2.46	0.43
4:D:16:ARG:NH1	37:D:8618:HOH:O	2.51	0.43
1:A:926:A:O2'	13:M:41:HIS:HD2	2.00	0.43
1:A:2251:G:H2'	1:A:2252:A:H8	1.83	0.43
28:2:5:THR:HB	28:2:6:PRO:CD	2.48	0.43
1:A:2649:A:H8	1:A:2649:A:H5'	1.82	0.43
29:3:35:ARG:HB2	37:3:2691:HOH:O	2.17	0.43
1:A:1434:A:H2'	1:A:1436:C:C5	2.53	0.43
17:Q:109:ARG:NH1	17:Q:119:TYR:CE2	2.86	0.43
1:A:1656:A:H2'	1:A:1657:A:O4'	2.18	0.43
1:A:469:G:C6	1:A:473:A:N6	2.86	0.43
24:X:126:ASP:HB3	24:X:135:GLY:O	2.18	0.43
1:A:1667:A:H2'	1:A:1668:U:C6	2.53	0.43
1:A:821:U:H2'	1:A:822:C:H6	1.82	0.43
24:X:146:ILE:HG22	24:X:147:ASP:N	2.33	0.43
14:N:157:LEU:HA	35:N:8518:CL:CL	2.55	0.43
4:D:316:ARG:N	4:D:317:PRO:HD3	2.34	0.43
7:G:80:TRP:O	7:G:134:SER:HA	2.17	0.43
1:A:259:G:O2'	1:A:260:C:H5'	2.18	0.43
4:D:279:THR:OG1	4:D:290:VAL:HB	2.18	0.43
1:A:2289:G:H21	1:A:2291:A:H2	1.60	0.43
10:J:72:VAL:HG11	10:J:81:TYR:CZ	2.53	0.43
13:M:17:SER:C	13:M:19:LYS:N	2.71	0.43
1:A:426:G:C2	1:A:427:C:C2	3.06	0.43
1:A:1902:G:H2'	1:A:1903:U:O4'	2.19	0.43
1:A:416:G:OP1	1:A:417:G:H5'	2.18	0.43
8:H:79:GLN:HB2	8:H:82:ASP:OD2	2.18	0.43
5:E:123:LEU:HD23	5:E:123:LEU:HA	1.88	0.43
1:A:1311:G:C2	1:A:1312:G:C8	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1555:G:O2'	1:A:1556:G:H5'	2.18	0.43
1:A:2697:A:H2'	1:A:2698:G:O4'	2.18	0.43
1:A:283:U:H5	1:A:284:C:H42	1.66	0.43
9:I:20:VAL:O	9:I:24:VAL:HG23	2.18	0.43
7:G:7:ILE:HG22	7:G:45:ASP:O	2.19	0.43
1:A:1313:A:H5"	26:Z:210:GLY:N	2.32	0.43
21:U:25:ALA:O	21:U:39:ASN:CB	2.67	0.43
1:A:1056:U:H2'	1:A:1057:A:O4'	2.18	0.43
1:A:135:G:H1'	14:N:135:ASP:OD2	2.18	0.43
1:A:812:A:C6	1:A:813:C:C4	3.06	0.43
7:G:9:GLU:HG3	7:G:10:ASP:N	2.33	0.43
4:D:132:HIS:CE1	4:D:171:VAL:HG21	2.53	0.43
1:A:1420:C:C2	1:A:1445:G:N2	2.86	0.43
1:A:1352:A:N1	5:E:48:SER:HB3	2.33	0.43
10:J:112:ARG:O	10:J:113:ALA:C	2.56	0.43
1:A:843:A:C2	1:A:846:A:C8	3.06	0.43
10:J:165:GLY:C	10:J:166:ASN:HD22	2.22	0.43
1:A:2840:A:OP1	4:D:211:THR:HG23	2.18	0.43
5:E:46:TYR:CE2	5:E:98:ARG:NH1	2.86	0.43
3:C:192:VAL:CG1	3:C:192:VAL:O	2.66	0.43
1:A:2909:G:H2'	1:A:2910:A:H8	1.83	0.43
1:A:470:U:O2'	28:2:16:HIS:CD2	2.69	0.43
1:A:2776:A:H2'	1:A:2777:G:O4'	2.17	0.43
27:1:41:VAL:HG12	27:1:42:CYS:N	2.32	0.43
1:A:920:C:H4'	1:A:921:G:N2	2.33	0.43
1:A:1047:U:H2'	1:A:1048:G:H8	1.84	0.43
5:E:25:PRO:HD2	37:E:8424:HOH:O	2.17	0.43
23:W:5:VAL:CG1	23:W:9:ARG:NH1	2.81	0.43
1:A:1076:G:C2	1:A:1084:C:C2	3.06	0.43
1:A:1098:A:H2'	1:A:1099:G:O4'	2.18	0.43
1:A:2497:A:H2'	1:A:2498:C:C6	2.52	0.43
1:A:2379:G:N7	1:A:2408:A:N1	2.65	0.43
15:O:86:LEU:HD12	15:O:125:ALA:CB	2.43	0.43
1:A:68:U:O2'	1:A:69:A:H5"	2.18	0.43
23:W:42:ASN:O	23:W:44:GLY:N	2.51	0.43
1:A:1878:G:O2'	1:A:1879:U:P	2.76	0.43
3:C:51:ARG:CZ	37:C:8609:HOH:O	2.66	0.43
1:A:396:U:H4'	37:4:8531:HOH:O	2.18	0.43
4:D:139:ASP:HB2	4:D:165:ARG:HE	1.84	0.43
4:D:63:GLU:HG3	4:D:63:GLU:O	2.18	0.43
1:A:814:G:H2'	1:A:815:U:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1562:C:H42	1:A:2738:G:H1	1.65	0.43
3:C:150:PRO:HG3	37:C:8598:HOH:O	2.18	0.43
8:H:26:THR:HB	8:H:102:GLY:C	2.39	0.43
1:A:1815:A:H3'	1:A:1816:C:C6	2.53	0.43
24:X:73:LEU:HA	24:X:73:LEU:HD12	1.81	0.43
1:A:1309:U:C2'	1:A:1310:U:H5'	2.49	0.43
1:A:1407:A:O2'	1:A:1408:U:H3'	2.19	0.43
1:A:1323:G:C2	1:A:1324:G:C8	3.07	0.43
1:A:794:U:H5	37:A:3763:HOH:O	2.01	0.43
14:N:137:ASP:HA	14:N:142:LYS:HE3	2.01	0.43
1:A:2868:C:H2'	1:A:2869:G:O4'	2.19	0.43
15:O:5:ARG:HG3	18:R:18:PRO:CB	2.49	0.43
1:A:2502:C:C4'	10:J:151:MET:SD	3.06	0.43
14:N:115:LEU:HD13	14:N:116:ASN:HB2	2.01	0.43
1:A:1603:A:H5"	1:A:1604:G:H3'	1.99	0.43
10:J:55:GLN:HE22	10:J:91:HIS:CD2	2.37	0.43
7:G:69:ILE:HA	7:G:72:MET:HE2	2.00	0.43
1:A:604:G:H2'	37:A:7331:HOH:O	2.18	0.43
8:H:91:VAL:CG1	8:H:92:GLY:H	2.28	0.43
4:D:11:LEU:HA	37:D:8618:HOH:O	2.19	0.43
8:H:22:VAL:CG2	8:H:104:ALA:HB2	2.49	0.43
18:R:25:PRO:HA	18:R:26:PRO:HD3	1.85	0.43
1:A:2833:C:O2	1:A:2906:A:O2'	2.36	0.43
21:U:50:VAL:HG12	21:U:56:ALA:HA	2.00	0.43
1:A:876:A:H2'	1:A:876:A:N3	2.34	0.43
7:G:54:ASP:OD1	7:G:54:ASP:N	2.52	0.43
1:A:783:C:OP1	3:C:180:LYS:HE3	2.19	0.43
10:J:45:GLN:HG3	10:J:135:TRP:NE1	2.34	0.43
14:N:39:ARG:NH2	37:N:8622:HOH:O	2.52	0.43
11:K:38:VAL:HB	11:K:103:VAL:HG13	2.00	0.43
1:A:2506:A:H1'	37:A:3327:HOH:O	2.19	0.43
1:A:1164:U:C1'	1:A:1165:G:OP1	2.66	0.43
9:I:66:LEU:O	9:I:69:ARG:HB3	2.18	0.43
7:G:11:VAL:HG11	7:G:22:VAL:CG1	2.49	0.43
7:G:23:GLU:HG2	7:G:28:SER:HB2	2.01	0.43
1:A:1301:C:O4'	1:A:1330:A:C2	2.71	0.43
1:A:1327:G:C6	1:A:1331:A:C6	3.07	0.43
1:A:2255:A:C6	1:A:2256:G:C5	3.06	0.43
4:D:156:LYS:HE3	37:D:8635:HOH:O	2.18	0.43
1:A:661:G:C4	1:A:686:A:C2	3.07	0.43
18:R:93:ARG:NH1	18:R:93:ARG:HG3	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1314:U:H5"	1:A:1316:G:O4'	2.19	0.43
11:K:22:VAL:O	11:K:26:VAL:HG23	2.19	0.43
11:K:26:VAL:HG13	11:K:36:VAL:HG11	1.99	0.43
16:P:56:GLU:HB2	37:P:6111:HOH:O	2.17	0.43
3:C:214:SER:HA	3:C:227:ASP:O	2.18	0.43
1:A:1375:A:C2'	1:A:1376:G:H5'	2.49	0.43
1:A:392:U:C5'	14:N:193:LYS:HB3	2.49	0.43
10:J:31:PHE:HD2	10:J:85:ILE:O	2.01	0.43
6:F:35:ALA:O	6:F:37:ALA:N	2.52	0.43
25:Y:78:GLU:CG	25:Y:79:GLU:N	2.80	0.43
4:D:168:GLY:H	4:D:174:ARG:HD3	1.82	0.43
1:A:1269:G:H5"	35:A:8520:CL:CL	2.55	0.43
4:D:41:PHE:HB3	4:D:190:MET:CE	2.48	0.43
1:A:2269:C:C2'	1:A:2270:G:H5'	2.48	0.43
1:A:137:U:OP1	1:A:259:G:O2'	2.36	0.43
28:2:28:HIS:O	28:2:32:LYS:N	2.43	0.43
15:O:100:ALA:O	15:O:129:ILE:HG12	2.17	0.43
1:A:1787:C:H4'	1:A:2883:A:O4'	2.18	0.43
6:F:11:HIS:O	6:F:12:GLU:CB	2.66	0.43
18:R:33:PHE:N	18:R:71:TYR:OH	2.46	0.43
1:A:1783:A:C2'	1:A:1784:U:H5'	2.49	0.43
3:C:135:VAL:N	37:C:8598:HOH:O	2.50	0.43
26:Z:109:LEU:HA	37:Z:8159:HOH:O	2.18	0.43
23:W:19:GLU:HA	23:W:19:GLU:OE1	2.19	0.43
37:A:7470:HOH:O	15:O:1:ALA:CB	2.67	0.43
1:A:13:G:H2'	1:A:14:C:C6	2.54	0.43
1:A:958:G:O2'	1:A:959:C:H5'	2.19	0.43
6:F:24:HIS:HB2	6:F:72:LYS:CB	2.49	0.43
1:A:1659:A:H2'	1:A:1660:G:O4'	2.19	0.43
14:N:42:ARG:HA	14:N:43:PRO:HD3	1.79	0.43
2:B:3050:G:C6	2:B:3051:A:C6	3.06	0.43
8:H:101:ALA:HA	37:H:5413:HOH:O	2.19	0.43
24:X:64:THR:O	24:X:68:THR:HG22	2.18	0.43
17:Q:143:ALA:HB2	37:Q:5521:HOH:O	2.18	0.43
7:G:84:MET:CE	7:G:148:ILE:CD1	2.97	0.43
5:E:233:THR:HG22	5:E:234:VAL:H	1.82	0.43
15:O:77:ASN:OD1	15:O:80:SER:HB2	2.19	0.43
14:N:59:GLY:CA	14:N:141:ILE:HD11	2.48	0.43
20:T:29:ASP:OD2	20:T:31:ARG:NH1	2.51	0.43
1:A:1861:C:H4'	3:C:6:GLY:O	2.19	0.43
1:A:892:G:H5"	28:2:54:ALA:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:77:ASP:HB3	6:F:78:GLU:H	1.56	0.43
19:S:65:GLY:C	37:S:8517:HOH:O	2.57	0.43
21:U:71:VAL:CG1	21:U:90:PRO:HB3	2.24	0.43
29:3:19:SER:O	29:3:36:ASN:ND2	2.52	0.43
6:F:49:PRO:CG	37:F:5828:HOH:O	2.57	0.43
6:F:49:PRO:HA	6:F:73:VAL:HG22	2.01	0.43
26:Z:187:VAL:HG23	26:Z:192:ASP:HB3	2.00	0.43
5:E:223:LEU:HD12	5:E:223:LEU:HA	1.78	0.43
1:A:1450:C:O2'	1:A:1494:A:H5'	2.19	0.43
9:I:71:LEU:C	9:I:73:ASP:H	2.21	0.43
8:H:104:ALA:HA	37:H:6617:HOH:O	2.19	0.43
1:A:2010:A:H2'	37:A:5537:HOH:O	2.19	0.43
1:A:829:A:C6	1:A:830:G:N7	2.87	0.43
3:C:135:VAL:HG21	3:C:147:ARG:NH1	2.33	0.43
2:B:3065:A:O2'	2:B:3066:G:P	2.76	0.43
1:A:392:U:H4'	14:N:193:LYS:HB3	2.01	0.43
24:X:19:ASP:O	24:X:23:MET:HG3	2.18	0.43
6:F:29:HIS:C	37:F:5858:HOH:O	2.57	0.43
11:K:71:TYR:CG	11:K:72:PRO:HD2	2.54	0.43
1:A:1828:G:H2'	1:A:1829:A:H5'	2.00	0.43
9:I:18:GLU:O	9:I:21:ASP:HB2	2.18	0.43
3:C:22:ARG:NH1	37:C:8567:HOH:O	2.52	0.43
14:N:38:VAL:O	14:N:63:VAL:CG1	2.62	0.42
1:A:820:G:H5'	1:A:821:U:H5'	2.00	0.42
4:D:217:ARG:HG3	4:D:257:THR:CG2	2.49	0.42
21:U:49:GLU:HB3	21:U:59:GLU:CG	2.49	0.42
1:A:1269:G:H2'	1:A:1270:U:C6	2.54	0.42
15:O:22:GLN:HG2	15:O:26:LEU:HD22	2.00	0.42
1:A:2820:A:H2'	1:A:2821:C:O4'	2.19	0.42
1:A:2269:C:H2'	1:A:2270:G:H5'	1.99	0.42
1:A:539:G:H2'	1:A:540:A:C8	2.54	0.42
4:D:248:ARG:NH2	37:D:8526:HOH:O	2.51	0.42
1:A:2281:C:C2'	1:A:2282:U:H5'	2.48	0.42
6:F:60:GLU:O	6:F:62:ASP:N	2.52	0.42
2:B:3051:A:H5'	15:O:160:SER:HB3	2.01	0.42
1:A:1166:A:N3	1:A:1166:A:H2'	2.34	0.42
13:M:130:ARG:HA	37:M:8431:HOH:O	2.19	0.42
24:X:48:VAL:O	24:X:48:VAL:HG12	2.18	0.42
1:A:1947:G:H2'	1:A:1948:G:C8	2.53	0.42
1:A:290:C:H2'	1:A:291:C:O4'	2.19	0.42
6:F:173:GLU:O	6:F:174:VAL:C	2.58	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:80:SER:CB	37:O:8536:HOH:O	2.62	0.42
24:X:38:THR:HG22	37:X:3580:HOH:O	2.18	0.42
1:A:1335:C:H2'	1:A:1336:U:H6	1.83	0.42
24:X:108:ARG:O	24:X:111:GLY:N	2.49	0.42
2:B:3060:C:O2'	2:B:3061:C:H5'	2.19	0.42
1:A:1114:A:O2'	1:A:1115:U:H5'	2.19	0.42
1:A:2760:C:H5"	37:A:4902:HOH:O	2.19	0.42
1:A:1657:A:H2'	1:A:1658:A:C8	2.54	0.42
1:A:1375:A:H2'	1:A:1376:G:H5'	2.01	0.42
25:Y:70:ILE:HG23	25:Y:70:ILE:O	2.19	0.42
1:A:420:U:H2'	1:A:421:C:C6	2.54	0.42
1:A:42:C:H1'	37:A:4252:HOH:O	2.18	0.42
6:F:48:MET:HA	6:F:49:PRO:HD3	1.84	0.42
10:J:147:ARG:HA	10:J:150:LYS:NZ	2.34	0.42
3:C:211:LYS:HB2	37:C:8624:HOH:O	2.17	0.42
3:C:211:LYS:CB	3:C:212:PRO:HD2	2.35	0.42
4:D:329:TYR:HE2	22:V:15:PRO:HG2	1.80	0.42
3:C:88:ILE:CD1	3:C:100:PRO:HD3	2.40	0.42
14:N:80:GLY:O	14:N:81:ARG:CD	2.61	0.42
13:M:148:GLU:HG2	37:M:8425:HOH:O	2.20	0.42
21:U:55:PHE:CG	21:U:77:VAL:HG13	2.54	0.42
12:L:22:ASP:OD1	12:L:22:ASP:C	2.57	0.42
1:A:1127:C:C5	1:A:1128:U:C4	3.07	0.42
1:A:1014:A:H5"	2:B:3101:G:O2'	2.19	0.42
1:A:111:C:H2'	1:A:112:G:O4'	2.19	0.42
1:A:2092:G:H2'	1:A:2613:G:OP1	2.20	0.42
1:A:1044:C:H5	37:A:6177:HOH:O	2.01	0.42
11:K:34:GLU:HA	11:K:34:GLU:OE1	2.19	0.42
5:E:76:ARG:HD2	37:E:8429:HOH:O	2.19	0.42
8:H:56:PRO:CG	14:N:44:THR:HA	2.49	0.42
21:U:96:VAL:CG1	21:U:97:ARG:N	2.83	0.42
4:D:312:ARG:HG2	4:D:313:PRO:N	2.34	0.42
6:F:52:THR:HB	6:F:70:GLY:O	2.19	0.42
1:A:1014:A:H2'	1:A:1015:C:H5'	2.01	0.42
22:V:44:ARG:HB2	37:V:3805:HOH:O	2.19	0.42
1:A:1940:C:H5"	3:C:234:GLY:HA3	2.02	0.42
1:A:128:A:O2'	1:A:129:A:H5'	2.19	0.42
1:A:1380:U:H5'	37:A:8803:HOH:O	2.19	0.42
20:T:8:PRO:HD2	23:W:32:ALA:HA	2.02	0.42
1:A:1029:U:O2'	1:A:1273:C:OP1	2.34	0.42
1:A:1869:A:H2'	1:A:1870:C:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1:11:THR:HG21	27:1:23:ARG:HB2	2.01	0.42
15:O:113:SER:CB	37:O:8559:HOH:O	2.55	0.42
1:A:2436:U:H5'	30:4:68:LYS:HE2	1.99	0.42
1:A:1920:C:O2'	1:A:1921:A:H5'	2.19	0.42
1:A:2756:U:N3	1:A:2896:A:H2	2.14	0.42
13:M:42:ASN:HB2	37:M:8421:HOH:O	2.18	0.42
4:D:154:VAL:CG1	4:D:156:LYS:HG2	2.49	0.42
1:A:1559:A:C1'	37:A:5443:HOH:O	2.66	0.42
4:D:279:THR:CG2	4:D:280:VAL:N	2.82	0.42
1:A:775:G:H3'	37:A:4010:HOH:O	2.20	0.42
1:A:1857:A:N6	1:A:2247:C:H1'	2.34	0.42
1:A:844:A:C6	1:A:882:A:C6	3.08	0.42
11:K:39:VAL:HG13	11:K:106:GLY:O	2.19	0.42
23:W:5:VAL:HG11	23:W:9:ARG:NH1	2.34	0.42
13:M:91:VAL:O	13:M:91:VAL:HG13	2.19	0.42
1:A:2079:G:H2'	1:A:2080:G:O4'	2.20	0.42
14:N:133:LEU:O	14:N:134:ILE:HD13	2.19	0.42
16:P:60:VAL:C	16:P:62:GLY:H	2.23	0.42
14:N:169:ARG:HD2	37:N:8590:HOH:O	2.20	0.42
10:J:31:PHE:HE2	10:J:87:LYS:O	2.03	0.42
21:U:51:LEU:HD11	21:U:97:ARG:HB2	2.02	0.42
10:J:15:THR:HG22	10:J:91:HIS:HA	2.01	0.42
1:A:1820:G:C6	1:A:2030:A:C2	3.08	0.42
1:A:1389:G:N2	1:A:1391:G:H3'	2.35	0.42
3:C:47:HIS:O	3:C:49:PRO:HD3	2.19	0.42
1:A:682:A:H3'	1:A:683:G:C8	2.55	0.42
11:K:63:ILE:HG22	11:K:64:GLY:N	2.33	0.42
1:A:2408:A:H2	37:4:8516:HOH:O	2.01	0.42
1:A:500:G:H21	19:S:98:ASN:HD21	1.66	0.42
1:A:1052:G:C5	1:A:1063:G:C6	3.08	0.42
15:O:93:GLN:HG2	37:O:8557:HOH:O	2.19	0.42
1:A:1785:G:OP1	17:Q:76:GLY:HA3	2.20	0.42
1:A:1183:C:N4	37:A:3977:HOH:O	2.46	0.42
1:A:2040:C:H2'	1:A:2041:G:O4'	2.20	0.42
14:N:61:ILE:N	14:N:61:ILE:HD12	2.34	0.42
1:A:1206:U:H2'	1:A:1207:A:O4'	2.19	0.42
3:C:199:HIS:HD2	3:C:201:PHE:N	2.07	0.42
6:F:93:LEU:HG	37:F:3862:HOH:O	2.19	0.42
4:D:115:VAL:HA	4:D:116:PRO:HD3	1.88	0.42
1:A:553:G:O4'	1:A:1325:G:H5'	2.19	0.42
1:A:1555:G:H4'	1:A:1630:A:H2	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1007:A:H2'	10:J:19:TYR:CZ	2.55	0.42
15:O:62:HIS:HB3	15:O:65:ASP:OD1	2.19	0.42
26:Z:155:ARG:NH1	37:Z:8147:HOH:O	2.52	0.42
1:A:2892:G:C6	1:A:2893:C:C4	3.08	0.42
1:A:1094:G:H21	24:X:119:HIS:CE1	2.38	0.42
37:A:9118:HOH:O	17:Q:81:LYS:HG2	2.20	0.42
19:S:50:VAL:HG22	19:S:55:GLN:O	2.20	0.42
6:F:104:PHE:CE2	6:F:166:ILE:CD1	3.02	0.42
1:A:1189:A:N3	37:A:7254:HOH:O	2.52	0.42
1:A:1165:G:O2'	1:A:1166:A:OP1	2.25	0.42
7:G:15:GLN:HG2	7:G:19:ASP:O	2.20	0.42
13:M:130:ARG:O	13:M:131:GLU:C	2.57	0.42
15:O:67:ALA:C	15:O:69:TYR:N	2.73	0.42
1:A:187:A:H3'	1:A:188:C:H6	1.83	0.42
7:G:7:ILE:HA	7:G:8:PRO:HD3	1.88	0.42
1:A:1270:U:H2'	1:A:1271:A:C8	2.55	0.42
1:A:1331:A:OP2	26:Z:142:SER:OG	2.37	0.42
2:B:3078:G:O2'	2:B:3079:U:OP2	2.37	0.42
16:P:59:VAL:CG2	16:P:111:VAL:HG23	2.49	0.42
5:E:200:PRO:HB3	5:E:212:VAL:CG2	2.50	0.42
1:A:524:A:H5"	19:S:29:LYS:HE2	2.01	0.42
14:N:72:SER:HB2	14:N:93:ARG:HG2	2.01	0.42
17:Q:98:ILE:O	17:Q:98:ILE:HD13	2.19	0.42
1:A:2764:C:H2'	1:A:2765:C:C6	2.54	0.42
1:A:772:G:N2	1:A:890:C:O2	2.53	0.42
18:R:41:LEU:HD12	18:R:41:LEU:N	2.34	0.42
6:F:60:GLU:C	6:F:62:ASP:N	2.73	0.42
1:A:65:C:O2'	1:A:66:G:H5'	2.19	0.42
5:E:95:GLU:CD	5:E:95:GLU:H	2.14	0.42
3:C:3:ARG:HB2	3:C:8:ARG:NE	2.35	0.42
4:D:127:GLN:HG3	37:D:8646:HOH:O	2.19	0.42
1:A:2015:A:H2'	1:A:2016:U:O4'	2.19	0.42
1:A:2575:C:H2'	1:A:2576:A:O4'	2.19	0.42
1:A:834:G:H4'	1:A:835:U:OP2	2.19	0.42
1:A:2687:G:O2'	1:A:2688:U:H5'	2.19	0.42
5:E:4:THR:HB	5:E:135:GLU:OE1	2.19	0.42
5:E:218:VAL:CG1	37:E:8419:HOH:O	2.67	0.42
27:1:39:CYS:HA	27:1:40:PRO:HD3	1.95	0.42
21:U:27:LEU:HD23	21:U:98:VAL:HB	2.02	0.42
15:O:110:THR:HB	15:O:113:SER:OG	2.19	0.42
16:P:32:ARG:HE	16:P:35:LYS:HD2	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:43:VAL:HG13	15:O:118:ILE:HD11	2.02	0.42
22:V:31:PHE:CG	22:V:37:GLU:HG2	2.55	0.42
8:H:33:THR:HG21	8:H:59:ILE:O	2.20	0.42
9:I:64:ASN:ND2	9:I:64:ASN:N	2.68	0.42
1:A:1523:G:C6	1:A:1524:U:O4	2.73	0.42
2:B:3114:G:O6	15:O:11:ARG:HD3	2.20	0.42
1:A:622:G:H5'	1:A:1357:A:N6	2.34	0.42
18:R:30:VAL:HG12	18:R:30:VAL:O	2.20	0.42
1:A:287:C:O5'	1:A:287:C:H6	2.02	0.42
4:D:277:GLU:N	4:D:278:PRO:HD2	2.35	0.42
1:A:1979:G:O2'	1:A:1980:U:OP1	2.38	0.42
5:E:7:ASP:OD1	5:E:11:ASN:O	2.37	0.42
1:A:578:C:O2	1:A:1112:G:H4'	2.20	0.42
2:B:3057:A:H5'	2:B:3057:A:N3	2.35	0.42
29:3:40:ARG:HG3	29:3:45:ASN:CB	2.50	0.42
29:3:41:HIS:O	29:3:45:ASN:HB2	2.20	0.42
1:A:2591:C:H2'	1:A:2592:G:O4'	2.20	0.42
9:I:63:ARG:O	9:I:67:LEU:HG	2.20	0.42
4:D:41:PHE:CZ	4:D:79:MET:HG3	2.55	0.42
11:K:42:GLU:O	11:K:131:THR:HG23	2.19	0.42
1:A:441:A:H1'	1:A:442:A:N7	2.35	0.42
1:A:2247:C:C5'	37:A:6916:HOH:O	2.67	0.42
1:A:1391:G:C6	1:A:1435:U:C5	3.08	0.42
1:A:332:G:O2'	1:A:333:G:H5'	2.20	0.42
7:G:149:GLU:OE1	7:G:168:ILE:HG12	2.20	0.42
1:A:731:U:H2'	1:A:732:C:C6	2.55	0.42
1:A:2791:U:C1'	1:A:2792:A:H5"	2.50	0.42
1:A:201:G:N1	1:A:202:U:C4	2.88	0.42
1:A:858:U:H2'	1:A:859:C:C6	2.54	0.42
12:L:27:ARG:HD2	37:L:4747:HOH:O	2.19	0.42
1:A:2012:U:H2'	1:A:2013:G:OP1	2.19	0.42
1:A:1772:C:H5'	1:A:1773:G:C5	2.55	0.42
1:A:2503:A:OP1	10:J:147:ARG:NH2	2.48	0.41
1:A:1191:A:N1	1:A:1206:U:O4	2.53	0.41
1:A:1862:C:N4	1:A:1868:G:C6	2.88	0.41
1:A:2362:A:H2'	1:A:2363:G:C8	2.55	0.41
14:N:95:LYS:HG2	14:N:99:ARG:HB3	2.02	0.41
1:A:154:C:C2	1:A:155:C:C6	3.08	0.41
1:A:902:G:N7	13:M:18:HIS:CD2	2.85	0.41
16:P:96:VAL:CG1	16:P:97:SER:N	2.82	0.41
1:A:2912:C:H2'	1:A:2913:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1496:G:H5'	1:A:1572:A:H1'	2.02	0.41
4:D:32:ASP:HA	37:D:8575:HOH:O	2.19	0.41
1:A:2570:G:H5"	37:A:4485:HOH:O	2.20	0.41
4:D:130:ASP:HB2	37:D:8599:HOH:O	2.19	0.41
1:A:1164:U:H6	1:A:1164:U:O5'	2.03	0.41
1:A:1182:C:H1'	1:A:1192:A:C8	2.52	0.41
3:C:105:VAL:HG13	3:C:155:THR:O	2.20	0.41
5:E:27:ARG:CG	5:E:29:ASP:OD1	2.66	0.41
6:F:174:VAL:CG1	37:F:6555:HOH:O	2.64	0.41
7:G:126:ILE:HB	7:G:131:LEU:CD2	2.50	0.41
15:O:154:LEU:CG	15:O:155:GLU:N	2.81	0.41
26:Z:106:THR:HG22	26:Z:107:PRO:O	2.20	0.41
1:A:2896:A:OP1	37:A:3447:HOH:O	2.22	0.41
1:A:2120:U:H2'	1:A:2121:G:O4'	2.19	0.41
1:A:2473:U:O3'	1:A:2474:A:H3'	2.19	0.41
13:M:62:ALA:HB2	13:M:103:ALA:CB	2.50	0.41
1:A:79:G:N2	1:A:80:A:N6	2.68	0.41
1:A:2498:C:O2'	1:A:2499:U:H5'	2.20	0.41
1:A:1829:A:H2'	1:A:1830:C:H5'	2.02	0.41
15:O:42:HIS:CG	15:O:62:HIS:HE1	2.38	0.41
1:A:834:G:H3'	1:A:835:U:H4'	2.03	0.41
1:A:2438:G:H5'	37:4:8552:HOH:O	2.21	0.41
1:A:2825:C:H4'	1:A:2826:G:O5'	2.20	0.41
4:D:80:ARG:HD3	37:D:8608:HOH:O	2.20	0.41
1:A:464:G:N2	1:A:475:G:H2'	2.34	0.41
1:A:1292:G:HO2'	1:A:1293:U:H6	1.65	0.41
29:3:19:SER:HB3	37:3:4479:HOH:O	2.19	0.41
1:A:588:G:O6	24:X:154:ARG:NH1	2.53	0.41
4:D:313:PRO:O	4:D:314:ALA:C	2.59	0.41
15:O:175:LEU:CD1	37:O:8539:HOH:O	2.68	0.41
15:O:67:ALA:HA	15:O:71:TRP:HB3	2.02	0.41
17:Q:13:VAL:HG11	17:Q:40:VAL:HG11	2.02	0.41
11:K:46:ILE:HA	37:K:1123:HOH:O	2.19	0.41
4:D:54:VAL:O	4:D:55:ASN:C	2.58	0.41
14:N:122:GLU:HB2	14:N:126:HIS:O	2.20	0.41
6:F:170:TYR:N	6:F:170:TYR:CD1	2.89	0.41
1:A:1565:C:O4'	1:A:2738:G:H1'	2.21	0.41
6:F:59:GLY:C	6:F:61:PHE:H	2.20	0.41
1:A:398:U:H2'	1:A:399:C:C6	2.55	0.41
1:A:415:A:O2'	1:A:416:G:H5'	2.20	0.41
1:A:160:A:C4	1:A:177:A:C2	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:A:H1'	1:A:393:G:C5	2.55	0.41
1:A:1707:G:N2	1:A:1709:G:H3'	2.36	0.41
10:J:47:GLU:CB	10:J:133:ILE:CD1	2.93	0.41
6:F:23:VAL:HG23	6:F:41:LEU:HD22	2.01	0.41
6:F:81:GLU:O	6:F:83:PHE:N	2.54	0.41
2:B:3053:G:O2'	2:B:3054:A:H5'	2.20	0.41
10:J:83:PHE:CE1	10:J:146:TRP:NE1	2.88	0.41
1:A:2506:A:H1'	37:A:5633:HOH:O	2.20	0.41
1:A:1603:A:H5'	1:A:1605:G:C4'	2.49	0.41
12:L:13:GLU:O	12:L:14:LYS:C	2.59	0.41
37:A:5825:HOH:O	22:V:56:ARG:HD3	2.19	0.41
1:A:1477:C:C5'	1:A:1868:G:H5"	2.50	0.41
25:Y:30:MET:CE	25:Y:58:ALA:HB3	2.50	0.41
7:G:34:TRP:O	11:K:127:ILE:HD11	2.19	0.41
8:H:13:GLU:OE2	8:H:78:GLU:HG2	2.21	0.41
1:A:2838:A:H2'	1:A:2839:C:O4'	2.20	0.41
1:A:1758:U:H2'	1:A:1759:A:O4'	2.21	0.41
37:A:4923:HOH:O	21:U:3:GLN:HG2	2.19	0.41
1:A:1677:U:OP2	29:3:8:LYS:NZ	2.48	0.41
7:G:125:GLU:O	7:G:132:THR:HG22	2.20	0.41
9:I:23:ILE:O	9:I:27:ILE:HG13	2.20	0.41
5:E:192:ILE:CG2	5:E:234:VAL:HG12	2.51	0.41
16:P:26:TRP:HA	16:P:26:TRP:CE3	2.56	0.41
1:A:2252:A:C5	1:A:2253:G:H1'	2.55	0.41
17:Q:7:LYS:CD	17:Q:21:VAL:CG2	2.99	0.41
16:P:97:SER:HB3	16:P:100:GLN:HE21	1.85	0.41
4:D:132:HIS:CE1	4:D:171:VAL:CG2	3.04	0.41
13:M:90:ARG:NH1	13:M:119:THR:HG21	2.35	0.41
30:4:30:GLN:HE21	30:4:30:GLN:HB3	1.69	0.41
1:A:1843:A:O5'	1:A:1843:A:C8	2.73	0.41
1:A:1614:G:H2'	37:A:4202:HOH:O	2.21	0.41
5:E:126:ASP:C	5:E:128:GLY:N	2.72	0.41
5:E:5:ILE:HD13	37:E:8426:HOH:O	2.20	0.41
1:A:820:G:C6	3:C:171:LYS:HB2	2.56	0.41
13:M:146:GLY:C	13:M:148:GLU:H	2.24	0.41
4:D:101:TRP:HB2	4:D:119:HIS:CD2	2.56	0.41
1:A:1327:G:N1	1:A:1331:A:C6	2.88	0.41
17:Q:103:THR:O	17:Q:106:ARG:HB3	2.21	0.41
1:A:419:A:C2	1:A:2449:G:C2	3.08	0.41
13:M:125:PHE:CE1	13:M:140:VAL:HG13	2.56	0.41
1:A:2321:A:C4	1:A:2323:G:N7	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:30:MET:HE3	25:Y:59:TRP:HE1	1.85	0.41
4:D:177:HIS:NE2	4:D:181:ILE:HD11	2.36	0.41
7:G:66:GLN:O	7:G:70:GLU:HG3	2.21	0.41
1:A:249:G:O2'	1:A:266:G:H5'	2.20	0.41
1:A:1690:C:C5	1:A:1692:C:C4	3.09	0.41
8:H:20:LEU:O	8:H:23:ALA:HB3	2.20	0.41
1:A:1683:G:H1'	1:A:1723:G:HO2'	1.86	0.41
10:J:84:ARG:NH2	10:J:135:TRP:CH2	2.81	0.41
10:J:149:ALA:C	10:J:151:MET:H	2.24	0.41
1:A:1943:C:O4'	3:C:212:PRO:HA	2.20	0.41
17:Q:38:GLU:CA	17:Q:41:ARG:NH1	2.82	0.41
1:A:2779:G:H21	7:G:143:GLN:HE22	1.64	0.41
1:A:2890:A:H1'	22:V:56:ARG:HH21	1.82	0.41
1:A:1268:C:H2'	1:A:1269:G:H8	1.86	0.41
10:J:111:MET:O	10:J:114:PRO:HD3	2.21	0.41
1:A:1626:A:H2'	1:A:1627:G:H5'	2.02	0.41
1:A:329:A:H5'	1:A:347:A:H1'	2.03	0.41
1:A:97:G:C2	21:U:107:LYS:HD2	2.55	0.41
1:A:876:A:N3	1:A:876:A:C2'	2.83	0.41
1:A:1051:C:H2'	1:A:1052:G:O4'	2.21	0.41
1:A:1706:G:C5	1:A:1707:G:C6	3.09	0.41
1:A:1409:G:H5'	37:A:3305:HOH:O	2.21	0.41
21:U:111:ARG:HB3	21:U:119:ALA:HB2	2.02	0.41
1:A:1791:U:H2'	1:A:1792:C:C6	2.56	0.41
1:A:1661:A:O2'	1:A:1662:C:H5'	2.21	0.41
1:A:1246:A:C4	1:A:1248:A:C8	3.09	0.41
15:O:87:LEU:CD1	15:O:186:LEU:HD21	2.44	0.41
24:X:14:HIS:HB2	24:X:17:ILE:HG13	2.02	0.41
1:A:2323:G:H5'	37:A:6592:HOH:O	2.20	0.41
10:J:114:PRO:O	10:J:115:PHE:C	2.58	0.41
7:G:35:TYR:HA	11:K:127:ILE:HD12	2.03	0.41
1:A:2281:C:H2'	1:A:2282:U:H5'	2.03	0.41
14:N:187:LEU:HD23	14:N:187:LEU:HA	1.91	0.41
1:A:2515:C:H2'	1:A:2516:G:O4'	2.20	0.41
1:A:2304:G:C6	1:A:2305:A:C6	3.08	0.41
2:B:3057:A:O2'	6:F:152:PRO:HD2	2.21	0.41
4:D:60:SER:C	4:D:62:ARG:H	2.23	0.41
3:C:211:LYS:HD3	37:C:8614:HOH:O	2.19	0.41
1:A:1588:G:C6	1:A:1589:G:C6	3.09	0.41
8:H:27:GLY:HA3	37:H:5413:HOH:O	2.21	0.41
1:A:875:A:C2	3:C:194:MET:SD	3.14	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:115:VAL:HG23	37:O:8559:HOH:O	2.19	0.41
1:A:1947:G:N2	1:A:1966:U:O2	2.53	0.41
37:A:6976:HOH:O	21:U:2:LYS:HE2	2.19	0.41
5:E:27:ARG:HD2	5:E:29:ASP:OD1	2.21	0.41
15:O:175:LEU:HA	15:O:175:LEU:HD12	1.89	0.41
8:H:60:VAL:CG1	8:H:60:VAL:O	2.69	0.41
15:O:159:TYR:CE2	15:O:163:PHE:HE2	2.37	0.41
8:H:91:VAL:CG1	8:H:92:GLY:N	2.80	0.41
23:W:38:GLY:C	23:W:40:PRO:HD2	2.41	0.41
11:K:42:GLU:HG2	11:K:43:ARG:HG3	2.02	0.41
26:Z:216:ARG:CD	37:Z:8157:HOH:O	2.64	0.41
1:A:2727:A:C6	1:A:2756:U:C4	3.08	0.41
4:D:156:LYS:NZ	4:D:160:ASP:OD2	2.49	0.41
1:A:87:C:H2'	29:3:28:LYS:O	2.21	0.41
1:A:383:A:C2	1:A:407:A:C4	3.08	0.41
26:Z:112:GLU:O	26:Z:116:LEU:HG	2.21	0.41
1:A:524:A:C5'	19:S:29:LYS:HE2	2.50	0.41
18:R:16:ASN:HA	18:R:16:ASN:HD22	1.55	0.41
1:A:795:G:HO2'	1:A:796:A:P	2.44	0.41
1:A:1218:U:H2'	1:A:1219:U:H6	1.86	0.41
1:A:1675:C:H5"	29:3:5:LYS:HD2	2.03	0.41
1:A:303:C:O2'	1:A:304:G:H5'	2.21	0.41
6:F:15:GLU:O	6:F:16:PRO:O	2.39	0.41
1:A:963:C:H6	1:A:963:C:O5'	2.04	0.41
1:A:2497:A:H2'	1:A:2498:C:H6	1.86	0.41
26:Z:149:GLN:HB3	26:Z:149:GLN:HE21	1.73	0.41
1:A:1067:A:O2'	24:X:12:ASN:OD1	2.36	0.41
1:A:445:U:H2'	1:A:446:G:H8	1.85	0.41
1:A:1456:C:H2'	1:A:1457:U:C6	2.56	0.41
1:A:774:C:H5'	28:2:46:ARG:HH21	1.86	0.41
29:3:11:LEU:HD23	29:3:11:LEU:HA	1.86	0.41
1:A:1695:G:C6	1:A:1696:U:C4	3.09	0.41
10:J:136:VAL:HG23	37:J:8344:HOH:O	2.20	0.41
10:J:68:ALA:HB2	10:J:149:ALA:HB2	2.03	0.41
1:A:821:U:H2'	1:A:822:C:C6	2.56	0.41
1:A:2637:A:H5'	37:A:3941:HOH:O	2.20	0.41
27:1:31:ILE:O	27:1:35:LYS:HG3	2.20	0.41
26:Z:130:ARG:HB2	26:Z:142:SER:O	2.20	0.41
4:D:69:VAL:HA	4:D:70:PRO:HD3	1.90	0.41
2:B:3003:A:N6	2:B:3022:G:H1'	2.36	0.41
1:A:2727:A:N1	1:A:2756:U:C2	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:951:A:H2'	1:A:952:G:H5'	2.03	0.41
13:M:73:VAL:HG11	13:M:118:LEU:HD21	2.03	0.41
1:A:1168:C:H5	37:A:7071:HOH:O	2.04	0.41
1:A:1804:A:H2'	1:A:1805:G:H8	1.86	0.41
1:A:1427:A:H61	1:A:1440:U:H1'	1.86	0.41
10:J:82:LYS:HB2	10:J:82:LYS:HZ2	1.86	0.41
1:A:1261:A:C8	1:A:1261:A:O5'	2.74	0.41
1:A:2090:G:N2	1:A:2655:U:C2	2.89	0.41
1:A:2093:G:H5"	37:A:9062:HOH:O	2.21	0.41
1:A:1211:G:O2'	1:A:1212:C:H5'	2.20	0.41
1:A:454:U:C2	37:A:8623:HOH:O	2.57	0.41
1:A:1055:G:OP2	10:J:94:ARG:NH1	2.54	0.41
1:A:1037:G:C2	1:A:1038:G:C8	3.09	0.41
2:B:3057:A:C8	6:F:141:VAL:HG21	2.56	0.40
14:N:37:VAL:HG21	14:N:108:LYS:CG	2.51	0.40
14:N:62:VAL:C	14:N:63:VAL:HG23	2.41	0.40
5:E:127:ARG:CZ	5:E:225:PRO:HG2	2.49	0.40
2:B:3050:G:C6	2:B:3051:A:N6	2.89	0.40
4:D:51:VAL:HG21	4:D:327:VAL:HG13	2.03	0.40
24:X:32:CYS:SG	24:X:33:THR:N	2.94	0.40
15:O:72:GLU:H	15:O:171:HIS:CE1	2.39	0.40
1:A:262:A:OP2	8:H:91:VAL:HG11	2.22	0.40
3:C:107:ASN:OD1	3:C:116:GLY:HA3	2.21	0.40
13:M:104:ASP:HB2	37:M:8448:HOH:O	2.21	0.40
1:A:1634:G:H2'	1:A:1635:U:H6	1.86	0.40
5:E:39:GLN:O	5:E:43:LYS:HD3	2.21	0.40
1:A:154:C:P	14:N:188:ARG:HH12	2.44	0.40
1:A:778:C:C4	1:A:779:U:C4	3.09	0.40
1:A:685:C:O2	1:A:748:C:H4'	2.20	0.40
12:L:99:ASP:OD1	12:L:99:ASP:C	2.58	0.40
1:A:1681:G:H4'	1:A:1682:A:N3	2.36	0.40
19:S:72:VAL:HG11	19:S:75:TRP:HB3	2.02	0.40
1:A:2455:A:H2'	1:A:2456:A:O4'	2.21	0.40
1:A:12:U:H2'	1:A:13:G:H5'	2.02	0.40
1:A:1024:G:C5	1:A:1025:C:C4	3.09	0.40
16:P:22:GLY:CA	37:P:2823:HOH:O	2.69	0.40
4:D:92:TYR:CD1	4:D:92:TYR:N	2.89	0.40
1:A:70:A:H4'	1:A:71:G:O5'	2.21	0.40
19:S:149:GLU:HA	19:S:150:PRO:HD3	1.87	0.40
3:C:140:LEU:HB3	3:C:141:PRO:HD2	2.03	0.40
6:F:35:ALA:C	6:F:37:ALA:N	2.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2502:C:H4'	10:J:151:MET:HG2	2.03	0.40
29:3:18:ASN:ND2	29:3:40:ARG:H	2.15	0.40
24:X:5:VAL:O	24:X:52:VAL:HG22	2.21	0.40
1:A:2441:U:H4'	13:M:53:ARG:HD2	2.03	0.40
7:G:139:GLU:CG	37:G:5919:HOH:O	2.69	0.40
23:W:39:ALA:C	23:W:41:GLU:N	2.74	0.40
1:A:1003:U:O2'	10:J:90:PHE:HE1	2.03	0.40
4:D:7:ARG:NH2	4:D:250:THR:O	2.54	0.40
2:B:3091:C:H2'	2:B:3092:G:O4'	2.21	0.40
30:4:84:ARG:HD3	37:4:8551:HOH:O	2.21	0.40
1:A:709:G:O2'	16:P:25:VAL:HG12	2.21	0.40
1:A:2001:G:C2'	1:A:2002:C:H5'	2.52	0.40
1:A:1309:U:O2'	1:A:1310:U:H5'	2.22	0.40
1:A:958:G:H2'	1:A:959:C:C6	2.55	0.40
1:A:2090:G:H2'	1:A:2091:G:C8	2.56	0.40
1:A:1141:U:H2'	1:A:1142:C:H6	1.86	0.40
16:P:44:ASN:OD1	16:P:65:LEU:HB2	2.21	0.40
3:C:126:ALA:HB1	3:C:138:VAL:CG1	2.51	0.40
1:A:432:G:O2'	1:A:433:C:H5'	2.21	0.40
2:B:3045:A:H2'	2:B:3046:C:H6	1.86	0.40
1:A:2038:A:OP2	4:D:224:LYS:NZ	2.43	0.40
1:A:840:U:O2	1:A:2055:A:H1'	2.22	0.40
25:Y:74:ALA:CB	25:Y:85:VAL:HG22	2.52	0.40
12:L:87:ARG:NE	37:L:4854:HOH:O	2.53	0.40
11:K:52:GLN:CG	11:K:53:ILE:N	2.85	0.40
3:C:130:THR:HG22	3:C:131:HIS:O	2.20	0.40
1:A:1593:C:O2'	1:A:1594:C:H5'	2.22	0.40
1:A:1058:A:H2'	1:A:1060:C:C5'	2.49	0.40
16:P:4:ASN:HB3	16:P:7:LEU:HB3	2.04	0.40
1:A:2453:G:H5"	37:M:8415:HOH:O	2.20	0.40
1:A:1495:C:C1'	1:A:1573:A:H1'	2.52	0.40
1:A:2456:A:H2'	1:A:2457:U:H6	1.84	0.40
12:L:40:THR:O	12:L:41:LYS:C	2.60	0.40
1:A:1827:G:H2'	1:A:1828:G:C8	2.56	0.40
1:A:1613:C:H2'	1:A:1614:G:O4'	2.21	0.40
18:R:42:LYS:HD2	18:R:42:LYS:HA	1.93	0.40
3:C:30:ARG:HB3	3:C:30:ARG:HE	1.70	0.40
18:R:22:GLY:O	18:R:23:THR:C	2.59	0.40
1:A:1068:C:OP2	37:A:3868:HOH:O	2.22	0.40
1:A:466:A:H2'	1:A:467:G:O4'	2.22	0.40
6:F:104:PHE:CE2	6:F:166:ILE:HD13	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:71:ARG:HD2	37:Y:7542:HOH:O	2.22	0.40
1:A:282:C:H2'	1:A:283:U:O4'	2.20	0.40
15:O:143:ARG:NH1	15:O:173:ASP:OD2	2.40	0.40
1:A:2121:G:O2'	1:A:2122:C:H5'	2.21	0.40
1:A:1730:G:C5'	1:A:1731:C:C6	3.04	0.40
1:A:538:C:H5"	1:A:539:G:C8	2.56	0.40
16:P:99:GLU:CG	37:P:6044:HOH:O	2.68	0.40
16:P:99:GLU:HG3	37:P:6044:HOH:O	2.21	0.40
7:G:83:GLY:O	7:G:169:THR:N	2.41	0.40
1:A:1859:A:N6	37:A:9721:HOH:O	2.42	0.40
21:U:44:ALA:HA	21:U:62:VAL:HG12	2.03	0.40
1:A:2550:U:O2'	1:A:2551:C:H5'	2.21	0.40
4:D:108:GLU:HB3	4:D:111:ARG:HD2	2.03	0.40
10:J:163:PRO:HG2	37:J:8339:HOH:O	2.21	0.40
1:A:2812:A:H1'	37:A:5365:HOH:O	2.21	0.40
4:D:195:ARG:NH1	4:D:324:ASP:OD1	2.52	0.40
6:F:173:GLU:HG3	6:F:174:VAL:N	2.37	0.40
7:G:138:ILE:HG23	7:G:139:GLU:N	2.36	0.40
11:K:19:MET:HE3	11:K:132:LEU:CD1	2.50	0.40
1:A:1594:C:C5	17:Q:120:ARG:CZ	3.04	0.40
11:K:130:VAL:CG1	11:K:131:THR:N	2.84	0.40
15:O:149:GLU:O	15:O:152:GLU:HB2	2.22	0.40
1:A:2270:G:C4'	3:C:223:ARG:HH12	2.31	0.40
1:A:2823:G:H4'	1:A:2827:A:O4'	2.21	0.40
6:F:59:GLY:C	6:F:61:PHE:N	2.75	0.40
8:H:26:THR:HG21	8:H:103:ALA:CB	2.52	0.40
1:A:1815:A:H2'	1:A:1816:C:O4'	2.21	0.40
1:A:2564:G:OP2	1:A:2565:C:H5"	2.22	0.40
1:A:1706:G:C6	1:A:1707:G:C6	3.09	0.40
1:A:2598:U:H2'	1:A:2600:A:OP2	2.22	0.40
1:A:1224:G:H2'	1:A:1225:C:C6	2.56	0.40
1:A:1416:G:H2'	1:A:1417:G:H5'	2.03	0.40
1:A:2552:C:C6	1:A:2577:A:N7	2.89	0.40
12:L:78:LYS:HA	12:L:79:PRO:HD3	1.80	0.40
27:1:17:ARG:O	27:1:18:TYR:HB2	2.21	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
3	C	235/239 (98%)	204 (87%)	26 (11%)	5 (2%)	9 46
4	D	335/337 (99%)	303 (90%)	23 (7%)	9 (3%)	6 39
5	E	244/246 (99%)	220 (90%)	23 (9%)	1 (0%)	39 80
6	F	134/176 (76%)	94 (70%)	26 (19%)	14 (10%)	1 4
7	G	170/177 (96%)	160 (94%)	10 (6%)	0	100 100
8	H	117/119 (98%)	103 (88%)	12 (10%)	2 (2%)	11 52
9	I	25/348 (7%)	24 (96%)	1 (4%)	0	100 100
10	J	152/167 (91%)	130 (86%)	17 (11%)	5 (3%)	5 32
11	K	140/145 (97%)	130 (93%)	7 (5%)	3 (2%)	9 46
12	L	130/132 (98%)	116 (89%)	12 (9%)	2 (2%)	13 55
13	M	141/164 (86%)	119 (84%)	20 (14%)	2 (1%)	14 57
14	N	192/194 (99%)	174 (91%)	15 (8%)	3 (2%)	12 54
15	O	184/186 (99%)	164 (89%)	13 (7%)	7 (4%)	4 28
16	P	113/115 (98%)	108 (96%)	4 (4%)	1 (1%)	21 67
17	Q	141/148 (95%)	135 (96%)	5 (4%)	1 (1%)	26 72
18	R	93/95 (98%)	86 (92%)	6 (6%)	1 (1%)	17 62
19	S	148/154 (96%)	139 (94%)	8 (5%)	1 (1%)	26 72
20	T	79/84 (94%)	74 (94%)	5 (6%)	0	100 100
21	U	117/119 (98%)	107 (92%)	9 (8%)	1 (1%)	21 67
22	V	51/66 (77%)	46 (90%)	4 (8%)	1 (2%)	9 48
23	W	63/70 (90%)	57 (90%)	4 (6%)	2 (3%)	5 33
24	X	152/154 (99%)	145 (95%)	6 (4%)	1 (1%)	26 72
25	Y	80/91 (88%)	71 (89%)	8 (10%)	1 (1%)	15 59
26	Z	140/240 (58%)	137 (98%)	3 (2%)	0	100 100
27	1	71/73 (97%)	61 (86%)	8 (11%)	2 (3%)	6 37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
28	2	54/56 (96%)	52 (96%)	2 (4%)	0	100 100
29	3	42/48 (88%)	42 (100%)	0	0	100 100
30	4	90/92 (98%)	84 (93%)	4 (4%)	2 (2%)	8 45
All	All	3633/4235 (86%)	3285 (90%)	281 (8%)	67 (2%)	11 51

All (67) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	139	ASP
6	F	93	LEU
6	F	95	THR
6	F	173	GLU
8	H	101	ALA
10	J	162	SER
10	J	164	ALA
11	K	143	LYS
13	M	21	ARG
13	M	80	ASP
15	O	154	LEU
15	O	164	ASP
15	O	183	ASP
23	W	43	PRO
24	X	77	ALA
3	C	34	ASP
3	C	37	VAL
3	C	132	ASP
4	D	34	GLY
4	D	169	GLY
4	D	184	ASP
6	F	16	PRO
6	F	20	LYS
6	F	61	PHE
6	F	171	ASP
10	J	40	PRO
10	J	138	PRO
11	K	5	GLU
14	N	140	ALA
14	N	165	SER
15	O	162	ASP
15	O	181	ASP
22	V	7	ASP

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Mol	Chain	Res	Type
30	4	57	GLY
4	D	107	SER
5	E	8	LEU
6	F	36	ASN
6	F	137	PRO
6	F	147	ALA
12	L	119	GLN
25	Y	77	PHE
6	F	11	HIS
6	F	82	GLU
6	F	170	TYR
11	K	7	ASP
14	N	18	GLY
15	O	65	ASP
15	O	167	ASP
17	Q	116	SER
27	1	81	LYS
30	4	56	PRO
3	C	69	LEU
3	C	119	ALA
4	D	206	THR
4	D	291	ASP
6	F	96	SER
8	H	64	PRO
12	L	126	SER
16	P	20	SER
4	D	2	GLN
4	D	185	GLY
21	U	53	GLY
10	J	72	VAL
23	W	40	PRO
27	1	41	VAL
19	S	81	PRO
18	R	54	PRO

5.3.2 Protein sidechains (i)

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	
3	C	179/181 (99%)	166 (93%)	13 (7%)	17	57
4	D	282/282 (100%)	263 (93%)	19 (7%)	20	60
5	E	193/193 (100%)	175 (91%)	18 (9%)	11	41
6	F	117/147 (80%)	107 (92%)	10 (8%)	13	47
7	G	152/155 (98%)	148 (97%)	4 (3%)	54	85
8	H	92/92 (100%)	91 (99%)	1 (1%)	80	94
9	I	27/283 (10%)	27 (100%)	0	100	100
10	J	122/122 (100%)	111 (91%)	11 (9%)	12	43
11	K	118/121 (98%)	108 (92%)	10 (8%)	13	47
12	L	106/106 (100%)	103 (97%)	3 (3%)	51	84
13	M	112/126 (89%)	108 (96%)	4 (4%)	42	79
14	N	166/166 (100%)	158 (95%)	8 (5%)	31	72
15	O	149/149 (100%)	143 (96%)	6 (4%)	38	77
16	P	93/93 (100%)	90 (97%)	3 (3%)	46	81
17	Q	113/116 (97%)	110 (97%)	3 (3%)	52	85
18	R	79/79 (100%)	75 (95%)	4 (5%)	29	70
19	S	117/121 (97%)	114 (97%)	3 (3%)	54	85
20	T	71/73 (97%)	71 (100%)	0	100	100
21	U	105/105 (100%)	101 (96%)	4 (4%)	40	78
22	V	44/52 (85%)	44 (100%)	0	100	100
23	W	51/56 (91%)	50 (98%)	1 (2%)	63	88
24	X	130/130 (100%)	122 (94%)	8 (6%)	23	64
25	Y	66/73 (90%)	61 (92%)	5 (8%)	16	55
26	Z	120/195 (62%)	112 (93%)	8 (7%)	20	60
27	1	56/56 (100%)	53 (95%)	3 (5%)	27	68
28	2	46/46 (100%)	46 (100%)	0	100	100
29	3	42/44 (96%)	41 (98%)	1 (2%)	57	86
30	4	79/79 (100%)	78 (99%)	1 (1%)	76	92
All	All	3027/3441 (88%)	2876 (95%)	151 (5%)	30	71

All (151) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	3	ARG
3	C	8	ARG
3	C	33	GLU
3	C	36	ASP
3	C	55	VAL
3	C	68	ILE
3	C	69	LEU
3	C	94	LEU
3	C	120	ARG
3	C	131	HIS
3	C	153	ARG
3	C	179	MET
3	C	217	ARG
4	D	7	ARG
4	D	11	LEU
4	D	27	ASN
4	D	33	ASP
4	D	63	GLU
4	D	84	LEU
4	D	97	LEU
4	D	98	THR
4	D	103	ASP
4	D	162	MET
4	D	234	ARG
4	D	245	SER
4	D	251	VAL
4	D	254	GLN
4	D	256	GLN
4	D	264	GLU
4	D	304	PRO
4	D	307	ARG
4	D	312	ARG
5	E	2	GLN
5	E	27	ARG
5	E	67	GLN
5	E	78	ARG
5	E	91	PRO
5	E	94	THR
5	E	95	GLU
5	E	101	ASP
5	E	115	LEU
5	E	136	VAL
5	E	187	ARG

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Mol	Chain	Res	Type
5	E	214	THR
5	E	222	ASP
5	E	223	LEU
5	E	234	VAL
5	E	236	THR
5	E	240	LEU
5	E	246	ARG
6	F	24	HIS
6	F	50	VAL
6	F	61	PHE
6	F	99	ASP
6	F	100	ASP
6	F	131	THR
6	F	133	ASN
6	F	136	ARG
6	F	137	PRO
6	F	149	ARG
7	G	7	ILE
7	G	12	ASP
7	G	54	ASP
7	G	102	VAL
8	H	12	LEU
10	J	1	LYS
10	J	59	ASN
10	J	61	LEU
10	J	72	VAL
10	J	73	GLN
10	J	82	LYS
10	J	86	ARG
10	J	93	ILE
10	J	129	ASN
10	J	142	VAL
10	J	150	LYS
11	K	46	ILE
11	K	52	GLN
11	K	74	ARG
11	K	76	ASP
11	K	79	PHE
11	K	107	ASN
11	K	112	ASP
11	K	120	SER
11	K	125	SER

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Mol	Chain	Res	Type
11	K	127	ILE
12	L	7	ASP
12	L	10	GLN
12	L	98	VAL
13	M	30	ARG
13	M	35	ARG
13	M	80	ASP
13	M	117	GLU
14	N	46	LEU
14	N	48	ARG
14	N	68	ARG
14	N	81	ARG
14	N	87	MET
14	N	93	ARG
14	N	99	ARG
14	N	164	THR
15	O	26	LEU
15	O	43	VAL
15	O	127	LEU
15	O	128	ASP
15	O	152	GLU
15	O	163	PHE
16	P	3	THR
16	P	28	ASP
16	P	97	SER
17	Q	52	LYS
17	Q	91	LYS
17	Q	98	ILE
18	R	11	ARG
18	R	16	ASN
18	R	57	ASP
18	R	95	GLU
19	S	13	THR
19	S	39	THR
19	S	82	GLU
21	U	39	ASN
21	U	48	VAL
21	U	73	HIS
21	U	96	VAL
23	W	43	PRO
24	X	4	LEU
24	X	35	VAL

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Mol	Chain	Res	Type
24	X	52	VAL
24	X	73	LEU
24	X	122	ARG
24	X	142	ASP
24	X	146	ILE
24	X	154	ARG
25	Y	15	ARG
25	Y	27	ASP
25	Y	49	ARG
25	Y	52	PRO
25	Y	72	VAL
26	Z	154	ARG
26	Z	163	THR
26	Z	172	THR
26	Z	186	ARG
26	Z	189	ASN
26	Z	200	THR
26	Z	203	VAL
26	Z	235	GLU
27	1	11	THR
27	1	44	PHE
27	1	64	ILE
29	3	18	ASN
30	4	65	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (92) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	47	HIS
3	C	92	ASN
3	C	127	GLN
3	C	199	HIS
4	D	27	ASN
4	D	145	HIS
4	D	238	ASN
4	D	260	HIS
4	D	318	ASN
4	D	332	ASN
5	E	2	GLN
5	E	39	GLN
5	E	129	HIS
5	E	163	HIS

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Mol	Chain	Res	Type
6	F	103	ASN
6	F	133	ASN
7	G	90	HIS
7	G	106	ASN
7	G	143	GLN
9	I	17	GLN
9	I	64	ASN
10	J	8	ASN
10	J	35	ASN
10	J	55	GLN
10	J	58	HIS
10	J	59	ASN
10	J	69	ASN
10	J	74	ASN
10	J	80	ASN
10	J	91	HIS
10	J	129	ASN
10	J	130	HIS
10	J	137	ASN
10	J	166	ASN
11	K	52	GLN
11	K	107	ASN
12	L	10	GLN
12	L	42	ASN
13	M	18	HIS
13	M	41	HIS
13	M	42	ASN
13	M	58	GLN
13	M	116	HIS
14	N	26	HIS
14	N	58	GLN
14	N	89	ASN
14	N	176	GLN
15	O	93	GLN
15	O	107	ASN
15	O	153	GLN
16	P	53	GLN
16	P	100	GLN
17	Q	50	GLN
17	Q	66	GLN
17	Q	73	HIS
17	Q	118	GLN

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Mol	Chain	Res	Type
18	R	16	ASN
18	R	40	HIS
19	S	61	GLN
19	S	94	ASN
19	S	98	ASN
19	S	113	HIS
19	S	117	HIS
19	S	123	GLN
20	T	53	ASN
21	U	39	ASN
21	U	73	HIS
22	V	39	ASN
23	W	60	GLN
24	X	27	HIS
24	X	28	HIS
24	X	87	HIS
24	X	110	GLN
24	X	119	HIS
24	X	125	HIS
24	X	141	HIS
25	Y	23	HIS
26	Z	134	HIS
26	Z	149	GLN
26	Z	189	ASN
27	1	33	HIS
27	1	70	GLN
28	2	8	GLN
28	2	16	HIS
28	2	28	HIS
29	3	16	ASN
29	3	18	ASN
29	3	41	HIS
29	3	45	ASN
30	4	15	ASN
30	4	30	GLN
30	4	48	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2747/2922 (94%)	245 (8%)	36 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	121/122 (99%)	14 (11%)	6 (4%)
All	All	2868/3044 (94%)	259 (9%)	42 (1%)

All (259) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	A
1	A	31	C
1	A	60	A
1	A	67	A
1	A	69	A
1	A	70	A
1	A	71	G
1	A	87	C
1	A	88	G
1	A	115	U
1	A	120	A
1	A	130	C
1	A	139	C
1	A	141	C
1	A	151	A
1	A	166	A
1	A	169	A
1	A	186	A
1	A	191	A
1	A	192	A
1	A	200	U
1	A	219	G
1	A	237	G
1	A	271	C
1	A	272	A
1	A	273	G
1	A	283	U
1	A	284	C
1	A	285	A
1	A	308	U
1	A	309	C
1	A	318	C
1	A	336	G
1	A	337	A
1	A	345	G
1	A	358	G

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Mol	Chain	Res	Type
1	A	381	G
1	A	397	A
1	A	417	G
1	A	461	C
1	A	487	G
1	A	498	A
1	A	510	U
1	A	511	A
1	A	514	G
1	A	537	G
1	A	538	C
1	A	539	G
1	A	542	A
1	A	545	G
1	A	553	G
1	A	559	U
1	A	588	G
1	A	604	G
1	A	620	A
1	A	632	A
1	A	644	G
1	A	660	A
1	A	688	A
1	A	701	U
1	A	717	C
1	A	759	C
1	A	777	U
1	A	809	G
1	A	821	U
1	A	835	U
1	A	840	U
1	A	857	A
1	A	858	U
1	A	868	G
1	A	869	G
1	A	871	G
1	A	872	U
1	A	875	A
1	A	877	G
1	A	878	G
1	A	882	A
1	A	884	C

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Mol	Chain	Res	Type
1	A	885	G
1	A	905	C
1	A	920	C
1	A	921	G
1	A	923	A
1	A	953	G
1	A	960	G
1	A	961	A
1	A	1006	A
1	A	1008	C
1	A	1029	U
1	A	1045	G
1	A	1059	G
1	A	1060	C
1	A	1072	G
1	A	1081	A
1	A	1083	C
1	A	1087	G
1	A	1088	A
1	A	1109	U
1	A	1110	G
1	A	1119	G
1	A	1130	U
1	A	1137	G
1	A	1151	G
1	A	1161	A
1	A	1162	G
1	A	1164	U
1	A	1165	G
1	A	1166	A
1	A	1171	A
1	A	1174	A
1	A	1175	G
1	A	1177	A
1	A	1185	U
1	A	1192	A
1	A	1193	A
1	A	1206	U
1	A	1216	G
1	A	1234	U
1	A	1238	C
1	A	1239	G

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Mol	Chain	Res	Type
1	A	1262	C
1	A	1279	U
1	A	1289	C
1	A	1342	C
1	A	1353	C
1	A	1360	C
1	A	1377	C
1	A	1407	A
1	A	1409	G
1	A	1451	C
1	A	1474	C
1	A	1488	U
1	A	1505	U
1	A	1506	U
1	A	1524	U
1	A	1525	G
1	A	1526	A
1	A	1564	C
1	A	1580	A
1	A	1592	G
1	A	1625	U
1	A	1626	A
1	A	1633	C
1	A	1634	G
1	A	1656	A
1	A	1667	A
1	A	1682	A
1	A	1684	A
1	A	1685	A
1	A	1692	C
1	A	1701	A
1	A	1710	A
1	A	1722	U
1	A	1723	G
1	A	1725	C
1	A	1731	C
1	A	1752	G
1	A	1778	A
1	A	1798	C
1	A	1820	G
1	A	1829	A
1	A	1856	C

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Mol	Chain	Res	Type
1	A	1879	U
1	A	1904	A
1	A	1919	A
1	A	1942	A
1	A	1971	G
1	A	1973	A
1	A	1974	G
1	A	1978	A
1	A	1980	U
1	A	1982	C
1	A	1996	U
1	A	2006	C
1	A	2008	U
1	A	2011	A
1	A	2012	U
1	A	2013	G
1	A	2033	G
1	A	2034	U
1	A	2064	U
1	A	2072	G
1	A	2073	G
1	A	2074	A
1	A	2096	A
1	A	2101	A
1	A	2102	G
1	A	2110	G
1	A	2238	A
1	A	2258	A
1	A	2271	G
1	A	2272	G
1	A	2291	A
1	A	2317	C
1	A	2321	A
1	A	2346	C
1	A	2354	A
1	A	2361	A
1	A	2369	A
1	A	2422	U
1	A	2462	G
1	A	2465	A
1	A	2467	A
1	A	2469	A

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Mol	Chain	Res	Type
1	A	2476	C
1	A	2483	A
1	A	2507	G
1	A	2511	A
1	A	2533	C
1	A	2537	G
1	A	2541	U
1	A	2553	A
1	A	2564	G
1	A	2589	U
1	A	2601	A
1	A	2602	G
1	A	2608	C
1	A	2613	G
1	A	2638	G
1	A	2649	A
1	A	2664	A
1	A	2681	A
1	A	2682	C
1	A	2718	C
1	A	2719	A
1	A	2726	U
1	A	2747	C
1	A	2748	G
1	A	2749	U
1	A	2750	G
1	A	2762	C
1	A	2768	A
1	A	2786	G
1	A	2792	A
1	A	2800	A
1	A	2811	A
1	A	2812	A
1	A	2825	C
1	A	2840	A
1	A	2850	C
1	A	2876	G
1	A	2890	A
1	A	2896	A
1	A	2903	C
1	A	2914	A
2	B	3002	U

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Mol	Chain	Res	Type
2	B	3003	A
2	B	3014	G
2	B	3022	G
2	B	3024	U
2	B	3041	C
2	B	3043	G
2	B	3044	A
2	B	3052	A
2	B	3057	A
2	B	3066	G
2	B	3077	A
2	B	3114	G
2	B	3122	C

All (42) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	10	U
1	A	69	A
1	A	129	A
1	A	284	C
1	A	338	C
1	A	603	A
1	A	644	G
1	A	699	C
1	A	716	G
1	A	834	G
1	A	857	A
1	A	871	G
1	A	877	G
1	A	1080	C
1	A	1164	U
1	A	1237	U
1	A	1261	A
1	A	1352	A
1	A	1450	C
1	A	1563	G
1	A	1667	A
1	A	1692	C
1	A	1814	G
1	A	1856	C
1	A	1942	A

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Mol	Chain	Res	Type
1	A	1979	G
1	A	2005	G
1	A	2011	A
1	A	2313	C
1	A	2467	A
1	A	2526	C
1	A	2536	C
1	A	2649	A
1	A	2718	C
1	A	2761	A
1	A	2791	U
2	B	3023	U
2	B	3024	U
2	B	3025	G
2	B	3043	G
2	B	3065	A
2	B	3103	A

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 233 ligands modelled in this entry, 232 are monoatomic - leaving 1 for Mogul analysis.

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	$\#\|Z\| > 2$
31	ZIT	A	8600	-	54,54,54	1.68	10 (18%)	76,83,83	1.27	7 (9%)

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
31	ZIT	A	8600	-	-	0/72/107/107	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	A	8600	ZIT	C9-C8	2.05	1.61	1.53
31	A	8600	ZIT	O5A-C5A	2.30	1.49	1.44
31	A	8600	ZIT	C13-C14	2.43	1.59	1.54
31	A	8600	ZIT	C4-C5	2.78	1.61	1.54
31	A	8600	ZIT	C4A-C5A	2.80	1.57	1.51
31	A	8600	ZIT	C2B-C3B	2.99	1.60	1.52
31	A	8600	ZIT	C11-N10	3.28	1.54	1.49
31	A	8600	ZIT	C7-C6	4.06	1.61	1.54
31	A	8600	ZIT	C3A-N3A	4.11	1.57	1.48
31	A	8600	ZIT	C2-C3	4.37	1.65	1.55

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
31	A	8600	ZIT	C6-C5-C4	-4.10	108.35	114.11
31	A	8600	ZIT	C14-C13-C12	-2.06	104.66	108.11
31	A	8600	ZIT	C7A-N3A-C3A	2.01	118.91	113.09
31	A	8600	ZIT	O1B-C3-C4	2.29	111.08	108.19
31	A	8600	ZIT	C2A-C3A-N3A	2.34	117.17	110.62
31	A	8600	ZIT	C17-C2-C3	2.59	118.73	112.97
31	A	8600	ZIT	O1A-C5-C6	2.92	110.17	106.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
31	A	8600	ZIT	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	2754/2922 (94%)	-0.07	42 (1%) 76 63	27, 56, 101, 149	0
2	B	122/122 (100%)	0.10	6 (4%) 33 20	43, 71, 98, 158	0
3	C	237/239 (99%)	0.08	11 (4%) 36 23	38, 62, 93, 114	0
4	D	337/337 (100%)	-0.10	2 (0%) 90 84	29, 64, 90, 99	0
5	E	246/246 (100%)	-0.12	0 100 100	30, 58, 81, 92	0
6	F	140/176 (79%)	1.40	46 (32%) 0 0	61, 108, 124, 131	0
7	G	172/177 (97%)	0.35	4 (2%) 64 49	50, 76, 97, 102	0
8	H	119/119 (100%)	0.49	11 (9%) 11 6	62, 82, 106, 110	0
9	I	29/348 (8%)	1.71	12 (41%) 0 0	80, 100, 109, 109	0
10	J	156/167 (93%)	0.06	2 (1%) 79 67	43, 65, 94, 101	0
11	K	142/145 (97%)	-0.10	0 100 100	45, 57, 80, 97	0
12	L	132/132 (100%)	-0.12	0 100 100	38, 58, 80, 87	0
13	M	145/164 (88%)	0.50	15 (10%) 9 5	33, 77, 113, 123	0
14	N	194/194 (100%)	-0.14	2 (1%) 84 75	42, 56, 73, 84	0
15	O	186/186 (100%)	0.40	15 (8%) 15 8	52, 74, 114, 124	0
16	P	115/115 (100%)	0.08	0 100 100	52, 66, 84, 88	0
17	Q	143/148 (96%)	0.25	4 (2%) 56 42	45, 65, 80, 89	0
18	R	95/95 (100%)	-0.08	0 100 100	38, 54, 70, 82	0
19	S	150/154 (97%)	-0.19	0 100 100	40, 54, 74, 82	0
20	T	81/84 (96%)	0.01	1 (1%) 81 69	55, 71, 90, 97	0
21	U	119/119 (100%)	0.46	6 (5%) 32 19	52, 69, 92, 103	0
22	V	53/66 (80%)	0.01	0 100 100	51, 64, 82, 89	0
23	W	65/70 (92%)	1.15	14 (21%) 1 1	62, 83, 118, 124	0
24	X	154/154 (100%)	-0.34	0 100 100	38, 56, 76, 85	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
25	Y	82/91 (90%)	0.15	1 (1%) 81 69	53, 67, 91, 107	0
26	Z	142/240 (59%)	-0.08	1 (0%) 89 83	33, 56, 77, 94	0
27	1	73/73 (100%)	0.06	5 (6%) 20 11	59, 71, 87, 94	0
28	2	56/56 (100%)	-0.29	0 100 100	35, 46, 51, 52	0
29	3	46/48 (95%)	0.14	1 (2%) 65 50	44, 72, 96, 106	0
30	4	92/92 (100%)	0.39	4 (4%) 39 25	44, 66, 79, 90	0
All	All	6577/7279 (90%)	0.05	205 (3%) 52 38	27, 62, 101, 158	0

All (205) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	3001	U	8.4
23	W	1	THR	7.7
9	I	27	ILE	6.0
6	F	57	THR	6.0
15	O	186	LEU	5.7
2	B	3024	U	5.4
6	F	88	LEU	5.4
21	U	119	ALA	5.3
2	B	3023	U	4.8
15	O	162	ASP	4.7
1	A	1173	A	4.7
6	F	69	ILE	4.6
6	F	62	ASP	4.6
1	A	1175	G	4.6
6	F	63	ILE	4.4
6	F	56	ARG	4.3
23	W	39	ALA	4.2
6	F	18	ILE	4.2
13	M	104	ASP	4.2
1	A	735	C	4.1
1	A	1172	G	4.0
6	F	25	MET	3.9
13	M	59	GLU	3.9
9	I	23	ILE	3.9
6	F	27	ILE	3.8
1	A	1198	U	3.8
6	F	85	GLN	3.8
15	O	160	SER	3.8
30	4	22	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
8	H	106	THR	3.7
13	M	105	TYR	3.7
13	M	60	GLU	3.7
6	F	58	VAL	3.6
1	A	282	C	3.6
6	F	10	PHE	3.6
15	O	179	LEU	3.6
1	A	1162	G	3.6
1	A	1190	G	3.6
1	A	2237	G	3.5
23	W	38	GLY	3.5
3	C	36	ASP	3.4
1	A	1171	A	3.4
23	W	3	LEU	3.4
20	T	81	ILE	3.4
6	F	70	GLY	3.3
15	O	149	GLU	3.3
6	F	87	ALA	3.3
15	O	138	ASP	3.3
3	C	85	ASP	3.2
1	A	1948	G	3.2
9	I	26	MET	3.2
3	C	82	VAL	3.2
6	F	84	LEU	3.2
9	I	24	VAL	3.2
1	A	1199	A	3.2
6	F	128	LEU	3.2
23	W	59	ILE	3.1
6	F	17	ARG	3.1
23	W	8	ILE	3.1
23	W	40	PRO	3.1
1	A	960	G	3.1
1	A	1951	G	3.1
1	A	1186	C	3.0
13	M	61	ALA	3.0
13	M	123	ASP	3.0
6	F	44	ILE	3.0
1	A	1177	A	3.0
1	A	2345	A	3.0
7	G	45	ASP	3.0
23	W	52	ALA	3.0
2	B	3025	G	2.9

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Mol	Chain	Res	Type	RSRZ
6	F	166	ILE	2.9
6	F	104	PHE	2.9
27	1	11	THR	2.9
6	F	54	ALA	2.9
1	A	1204	C	2.9
6	F	66	GLY	2.8
21	U	42	VAL	2.8
8	H	17	LEU	2.8
6	F	132	VAL	2.8
21	U	112	LEU	2.8
1	A	138	U	2.8
6	F	130	VAL	2.8
6	F	26	GLY	2.8
9	I	13	PRO	2.8
6	F	45	THR	2.7
10	J	59	ASN	2.7
7	G	10	ASP	2.7
15	O	158	LEU	2.7
1	A	284	C	2.7
17	Q	1	THR	2.7
7	G	100	ASP	2.7
1	A	285	A	2.7
1	A	1188	A	2.7
3	C	35	GLY	2.6
9	I	15	TRP	2.6
13	M	102	ASP	2.6
21	U	37	GLN	2.6
6	F	107	GLY	2.6
6	F	134	LEU	2.6
13	M	99	GLU	2.6
1	A	1525	G	2.6
13	M	106	VAL	2.6
6	F	102	GLY	2.5
9	I	28	GLU	2.5
4	D	97	LEU	2.5
6	F	75	LEU	2.5
8	H	49	PHE	2.5
1	A	2238	A	2.5
3	C	91	GLY	2.5
27	1	21	LYS	2.5
30	4	92	GLU	2.5
6	F	93	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
15	O	152	GLU	2.5
1	A	1163	G	2.5
1	A	1197	G	2.5
6	F	55	LYS	2.5
13	M	100	ALA	2.5
17	Q	77	ALA	2.5
15	O	159	TYR	2.5
9	I	16	LYS	2.5
1	A	1205	U	2.4
3	C	154	ALA	2.4
23	W	9	ARG	2.4
23	W	58	THR	2.4
1	A	1193	A	2.4
6	F	24	HIS	2.4
8	H	44	SER	2.4
23	W	62	GLU	2.4
6	F	71	ALA	2.4
1	A	736	A	2.4
29	3	35	ARG	2.4
4	D	1	PRO	2.4
15	O	147	ILE	2.4
9	I	20	VAL	2.4
15	O	150	TYR	2.4
13	M	108	VAL	2.4
6	F	65	GLU	2.3
6	F	72	LYS	2.3
8	H	26	THR	2.3
13	M	111	ALA	2.3
6	F	53	LYS	2.3
3	C	236	GLY	2.3
2	B	3002	U	2.3
14	N	87	MET	2.3
27	1	38	LYS	2.3
6	F	170	TYR	2.3
8	H	20	LEU	2.3
8	H	108	LEU	2.3
9	I	65	THR	2.3
13	M	120	LEU	2.3
15	O	167	ASP	2.3
1	A	1167	G	2.2
13	M	80	ASP	2.2
6	F	29	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
23	W	7	GLU	2.2
1	A	1201	C	2.2
2	B	3122	C	2.2
3	C	84	VAL	2.2
30	4	35	TRP	2.2
1	A	1185	U	2.2
15	O	157	PRO	2.2
17	Q	63	ARG	2.2
6	F	171	ASP	2.2
8	H	22	VAL	2.2
8	H	98	VAL	2.2
25	Y	76	ARG	2.2
15	O	163	PHE	2.2
1	A	281	U	2.1
1	A	602	A	2.1
8	H	90	GLU	2.1
13	M	62	ALA	2.1
6	F	67	ASP	2.1
8	H	19	ALA	2.1
1	A	368	C	2.1
6	F	86	THR	2.1
30	4	8	ASN	2.1
27	1	44	PHE	2.1
3	C	37	VAL	2.1
21	U	99	THR	2.1
6	F	106	PHE	2.1
10	J	83	PHE	2.1
1	A	1184	C	2.1
23	W	63	GLU	2.1
9	I	67	LEU	2.1
1	A	1192	A	2.1
3	C	83	GLY	2.1
7	G	108	LEU	2.1
26	Z	108	ASP	2.1
1	A	258	G	2.1
1	A	1165	G	2.1
6	F	41	LEU	2.1
9	I	19	GLU	2.1
27	1	22	ILE	2.1
6	F	28	GLY	2.1
23	W	2	VAL	2.1
1	A	257	G	2.1

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Mol	Chain	Res	Type	RSRZ
14	N	194	ALA	2.1
3	C	110	SER	2.0
1	A	10	U	2.0
1	A	280	C	2.0
6	F	92	GLU	2.0
15	O	68	GLU	2.0
17	Q	80	ARG	2.0
21	U	35	TYR	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
35	CL	A	8515	1/1	0.66	0.88	82.65	110,110,110,110	0
34	NA	A	8374	1/1	0.31	1.55	69.20	89,89,89,89	0
34	NA	A	8356	1/1	0.90	0.70	61.24	78,78,78,78	0
34	NA	A	8362	1/1	0.94	0.67	42.13	62,62,62,62	0
34	NA	A	8378	1/1	0.91	1.10	32.36	48,48,48,48	0
34	NA	A	8321	1/1	0.91	0.47	32.11	42,42,42,42	0
32	MG	A	8064	1/1	0.92	0.44	20.95	36,36,36,36	0
34	NA	B	8383	1/1	0.81	0.54	20.65	40,40,40,40	0
34	NA	A	8326	1/1	0.64	1.01	20.05	92,92,92,92	0
34	NA	A	8303	1/1	0.66	0.40	19.95	54,54,54,54	0
34	NA	A	8323	1/1	0.81	0.44	19.57	57,57,57,57	0
34	NA	A	8371	1/1	0.74	0.34	19.33	48,48,48,48	0
32	MG	A	8066	1/1	0.72	0.70	19.25	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
34	NA	A	8377	1/1	0.75	0.33	18.16	68,68,68,68	0
34	NA	A	8359	1/1	0.94	0.53	14.81	75,75,75,75	0
34	NA	A	8361	1/1	0.95	0.51	14.28	46,46,46,46	0
34	NA	M	8380	1/1	0.90	0.65	13.08	75,75,75,75	0
32	MG	A	8024	1/1	0.79	0.48	11.78	79,79,79,79	0
35	CL	A	8505	1/1	0.83	0.43	11.03	92,92,92,92	0
34	NA	A	8372	1/1	0.87	0.48	10.82	87,87,87,87	0
34	NA	A	8373	1/1	0.81	0.53	10.39	67,67,67,67	0
34	NA	A	8325	1/1	0.87	0.27	9.41	62,62,62,62	0
34	NA	A	8376	1/1	0.94	0.28	9.01	49,49,49,49	0
34	NA	A	8366	1/1	0.82	0.40	8.81	79,79,79,79	0
34	NA	A	8368	1/1	0.81	0.26	8.18	65,65,65,65	0
34	NA	A	8335	1/1	0.96	0.27	7.88	61,61,61,61	0
34	NA	A	8369	1/1	0.93	0.33	7.68	55,55,55,55	0
34	NA	S	8386	1/1	0.51	0.45	6.62	97,97,97,97	0
34	NA	A	8382	1/1	0.90	0.29	6.23	74,74,74,74	0
35	CL	D	8519	1/1	0.92	0.44	5.70	65,65,65,65	0
34	NA	A	8350	1/1	0.98	0.21	5.64	43,43,43,43	0
34	NA	A	8364	1/1	0.64	0.23	5.38	52,52,52,52	0
34	NA	A	8305	1/1	0.77	0.25	5.20	46,46,46,46	0
32	MG	A	8044	1/1	0.98	0.21	4.30	58,58,58,58	0
31	ZIT	A	8600	52/52	0.84	0.29	4.13	81,91,95,96	0
34	NA	A	8365	1/1	0.86	0.58	4.12	76,76,76,76	0
35	CL	4	8504	1/1	0.86	0.54	2.83	93,93,93,93	0
32	MG	A	8060	1/1	0.95	0.20	2.09	51,51,51,51	0
34	NA	A	8331	1/1	0.93	0.19	2.08	55,55,55,55	0
35	CL	P	8508	1/1	0.82	0.36	1.76	97,97,97,97	0
34	NA	U	8343	1/1	0.89	0.25	1.47	38,38,38,38	0
34	NA	S	8337	1/1	0.81	0.21	1.35	58,58,58,58	0
35	CL	A	8510	1/1	0.77	0.34	1.06	97,97,97,97	0
34	NA	A	8379	1/1	0.95	0.18	1.01	52,52,52,52	0
32	MG	A	8112	1/1	0.88	0.22	0.90	50,50,50,50	0
32	MG	A	8013	1/1	0.96	0.20	0.85	56,56,56,56	0
32	MG	A	8067	1/1	0.88	0.21	0.45	51,51,51,51	0
34	NA	A	8314	1/1	0.93	0.18	-0.10	48,48,48,48	0
32	MG	A	8049	1/1	0.89	0.19	-0.10	74,74,74,74	0
34	NA	C	8345	1/1	0.93	0.21	-0.17	57,57,57,57	0
34	NA	A	8332	1/1	0.75	0.16	-0.20	50,50,50,50	0
32	MG	A	8053	1/1	0.78	0.15	-0.33	40,40,40,40	0
33	K	A	8201	1/1	0.96	0.16	-0.61	70,70,70,70	0
34	NA	A	8381	1/1	0.81	0.15	-0.66	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
32	MG	A	8058	1/1	0.98	0.18	-0.73	62,62,62,62	0
36	CD	1	8403	1/1	0.97	0.12	-0.75	77,77,77,77	0
32	MG	Z	8109	1/1	0.94	0.17	-0.78	61,61,61,61	0
32	MG	A	8059	1/1	0.94	0.15	-0.89	56,56,56,56	0
32	MG	A	8086	1/1	0.94	0.12	-0.98	56,56,56,56	0
35	CL	N	8518	1/1	0.94	0.20	-1.31	65,65,65,65	0
32	MG	A	8057	1/1	0.91	0.18	-1.33	54,54,54,54	0
36	CD	V	8401	1/1	1.00	0.11	-1.42	75,75,75,75	0
34	NA	A	8324	1/1	0.94	0.09	-1.43	48,48,48,48	0
36	CD	4	8404	1/1	0.96	0.11	-1.44	75,75,75,75	0
32	MG	A	8032	1/1	0.97	0.15	-1.44	63,63,63,63	0
35	CL	L	8512	1/1	0.90	0.13	-1.47	55,55,55,55	0
32	MG	A	8004	1/1	0.97	0.11	-1.48	60,60,60,60	0
34	NA	A	8333	1/1	0.89	0.12	-1.59	51,51,51,51	0
34	NA	A	8353	1/1	0.95	0.12	-1.60	46,46,46,46	0
36	CD	2	8402	1/1	0.99	0.08	-1.67	70,70,70,70	0
32	MG	A	8071	1/1	0.86	0.13	-1.67	85,85,85,85	0
34	NA	J	8309	1/1	0.96	0.15	-1.71	43,43,43,43	0
34	NA	K	8346	1/1	0.95	0.15	-2.00	33,33,33,33	0
33	K	A	8202	1/1	0.98	0.14	-2.04	61,61,61,61	0
32	MG	A	8008	1/1	0.95	0.13	-2.19	61,61,61,61	0
32	MG	A	8096	1/1	0.79	0.10	-2.27	64,64,64,64	0
32	MG	U	8073	1/1	0.79	0.08	-2.35	62,62,62,62	0
32	MG	A	8017	1/1	0.90	0.06	-2.57	42,42,42,42	0
32	MG	4	8078	1/1	0.91	0.06	-2.59	54,54,54,54	0
32	MG	D	8055	1/1	0.98	0.10	-2.68	51,51,51,51	0
34	NA	N	8347	1/1	0.98	0.12	-2.76	23,23,23,23	0
35	CL	K	8521	1/1	0.93	0.16	-2.91	64,64,64,64	0
34	NA	S	8338	1/1	0.98	0.09	-3.04	49,49,49,49	0
32	MG	A	8107	1/1	0.98	0.04	-3.08	60,60,60,60	0
32	MG	A	8012	1/1	0.95	0.10	-3.26	35,35,35,35	0
34	NA	A	8317	1/1	0.98	0.04	-3.27	43,43,43,43	0
32	MG	A	8080	1/1	0.97	0.13	-3.34	65,65,65,65	0
32	MG	A	8056	1/1	0.94	0.10	-3.39	61,61,61,61	0
32	MG	A	8033	1/1	0.95	0.11	-3.42	36,36,36,36	0
34	NA	R	8348	1/1	0.94	0.07	-3.49	39,39,39,39	0
32	MG	A	8027	1/1	0.96	0.05	-3.61	51,51,51,51	0
32	MG	A	8108	1/1	0.94	0.13	-3.65	85,85,85,85	0
32	MG	A	8074	1/1	0.95	0.04	-3.70	52,52,52,52	0
32	MG	A	8003	1/1	0.97	0.10	-3.95	26,26,26,26	0
32	MG	A	8018	1/1	0.98	0.11	-4.16	54,54,54,54	0
34	NA	A	8344	1/1	0.96	0.08	-4.26	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
32	MG	A	8001	1/1	0.87	0.10	-4.46	41,41,41,41	0
32	MG	A	8052	1/1	0.92	0.13	-4.65	58,58,58,58	0
32	MG	A	8019	1/1	0.99	0.06	-4.66	24,24,24,24	0
32	MG	A	8035	1/1	0.96	0.08	-4.83	60,60,60,60	0
32	MG	C	8065	1/1	0.99	0.05	-4.87	40,40,40,40	0
32	MG	A	8022	1/1	0.96	0.05	-4.93	55,55,55,55	0
32	MG	A	8007	1/1	0.98	0.09	-5.35	42,42,42,42	0
32	MG	A	8039	1/1	0.94	0.06	-5.39	67,67,67,67	0
32	MG	A	8038	1/1	0.96	0.08	-5.95	29,29,29,29	0
32	MG	A	8020	1/1	0.95	0.07	-6.61	36,36,36,36	0
34	NA	A	8320	1/1	0.97	0.12	-6.65	32,32,32,32	0
32	MG	A	8077	1/1	0.97	0.07	-6.82	37,37,37,37	0
32	MG	A	8054	1/1	0.95	0.06	-6.93	52,52,52,52	0
32	MG	A	8010	1/1	0.95	0.09	-7.46	43,43,43,43	0
32	MG	A	8002	1/1	0.96	0.07	-8.08	43,43,43,43	0
32	MG	A	8014	1/1	0.99	0.07	-8.88	24,24,24,24	0
34	NA	A	8327	1/1	0.95	0.09	-8.89	44,44,44,44	0
32	MG	A	8084	1/1	0.96	0.05	-9.79	41,41,41,41	0
32	MG	A	8110	1/1	0.95	0.08	-10.46	35,35,35,35	0
32	MG	A	8015	1/1	0.97	0.09	-11.06	57,57,57,57	0
32	MG	A	8006	1/1	0.96	0.04	-12.02	54,54,54,54	0
32	MG	A	8028	1/1	0.97	0.05	-12.79	57,57,57,57	0
34	NA	A	8339	1/1	0.98	0.06	-20.29	33,33,33,33	0
34	NA	A	8330	1/1	0.85	0.28	-	57,57,57,57	0
35	CL	K	8516	1/1	0.97	0.26	-	53,53,53,53	0
32	MG	A	8093	1/1	0.91	0.09	-	59,59,59,59	0
35	CL	A	8522	1/1	0.81	0.69	-	83,83,83,83	0
32	MG	A	8045	1/1	0.97	0.10	-	58,58,58,58	0
32	MG	A	8041	1/1	0.76	0.26	-	69,69,69,69	0
34	NA	A	8311	1/1	0.92	0.15	-	63,63,63,63	0
32	MG	A	8047	1/1	0.98	0.17	-	81,81,81,81	0
34	NA	A	8301	1/1	0.95	0.17	-	42,42,42,42	0
34	NA	A	8340	1/1	0.75	0.61	-	56,56,56,56	0
34	NA	B	8351	1/1	0.80	0.15	-	54,54,54,54	0
34	NA	A	8358	1/1	0.96	0.65	-	107,107,107,107	0
32	MG	1	8105	1/1	0.85	0.43	-	38,38,38,38	0
34	NA	A	8302	1/1	0.92	0.23	-	52,52,52,52	0
32	MG	A	8106	1/1	0.88	0.14	-	71,71,71,71	0
34	NA	A	8355	1/1	0.88	0.50	-	60,60,60,60	0
32	MG	A	8063	1/1	0.94	0.11	-	92,92,92,92	0
32	MG	A	8115	1/1	0.98	0.05	-	43,43,43,43	0
35	CL	A	8514	1/1	0.91	0.18	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
35	CL	A	8517	1/1	0.89	0.16	-	52,52,52,52	0
35	CL	C	8509	1/1	0.91	0.27	-	69,69,69,69	0
32	MG	A	8083	1/1	0.95	0.08	-	51,51,51,51	0
32	MG	A	8070	1/1	0.95	0.18	-	46,46,46,46	0
34	NA	A	8354	1/1	0.78	0.60	-	54,54,54,54	0
32	MG	A	8061	1/1	0.96	0.04	-	37,37,37,37	0
34	NA	A	8367	1/1	0.83	0.24	-	38,38,38,38	0
32	MG	A	8072	1/1	0.96	0.11	-	65,65,65,65	0
32	MG	A	8099	1/1	0.86	0.17	-	55,55,55,55	0
34	NA	E	8304	1/1	0.90	0.20	-	32,32,32,32	0
34	NA	A	8385	1/1	0.75	0.67	-	73,73,73,73	0
34	NA	A	8306	1/1	0.95	0.53	-	41,41,41,41	0
34	NA	A	8352	1/1	0.87	0.32	-	56,56,56,56	0
32	MG	A	8117	1/1	0.99	0.10	-	33,33,33,33	0
35	CL	S	8506	1/1	0.91	0.27	-	69,69,69,69	0
34	NA	A	8360	1/1	0.91	0.85	-	59,59,59,59	0
34	NA	A	8316	1/1	0.84	0.41	-	61,61,61,61	0
32	MG	A	8011	1/1	0.81	0.08	-	44,44,44,44	0
34	NA	A	8329	1/1	0.27	0.45	-	70,70,70,70	0
32	MG	A	8029	1/1	0.98	0.12	-	50,50,50,50	0
34	NA	A	8308	1/1	0.86	0.23	-	53,53,53,53	0
32	MG	A	8043	1/1	0.94	0.14	-	56,56,56,56	0
32	MG	A	8103	1/1	0.94	0.20	-	76,76,76,76	0
34	NA	A	8349	1/1	0.91	0.31	-	57,57,57,57	0
32	MG	A	8036	1/1	0.97	0.07	-	46,46,46,46	0
32	MG	A	8068	1/1	0.95	0.05	-	56,56,56,56	0
34	NA	A	8315	1/1	0.97	0.30	-	62,62,62,62	0
34	NA	A	8336	1/1	0.90	0.16	-	85,85,85,85	0
32	MG	A	8031	1/1	1.00	0.03	-	44,44,44,44	0
32	MG	A	8021	1/1	0.94	0.09	-	32,32,32,32	0
34	NA	A	8313	1/1	0.88	0.21	-	66,66,66,66	0
32	MG	B	8095	1/1	0.95	0.08	-	98,98,98,98	0
34	NA	A	8342	1/1	0.86	0.37	-	51,51,51,51	0
32	MG	A	8101	1/1	0.91	0.14	-	60,60,60,60	0
35	CL	R	8511	1/1	0.60	0.59	-	102,102,102,102	0
35	CL	O	8507	1/1	0.71	0.52	-	84,84,84,84	0
32	MG	A	8076	1/1	0.95	0.09	-	75,75,75,75	0
32	MG	L	8069	1/1	0.91	0.16	-	79,79,79,79	0
32	MG	A	8085	1/1	0.97	0.15	-	68,68,68,68	0
32	MG	A	8051	1/1	0.96	0.13	-	66,66,66,66	0
32	MG	A	8009	1/1	0.95	0.05	-	46,46,46,46	0
32	MG	A	8016	1/1	0.96	0.13	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
32	MG	A	8111	1/1	0.90	0.08	-	62,62,62,62	0
35	CL	K	8501	1/1	0.96	0.33	-	81,81,81,81	0
34	NA	A	8341	1/1	0.58	0.30	-	63,63,63,63	0
35	CL	A	8503	1/1	0.80	0.51	-	74,74,74,74	0
35	CL	A	8513	1/1	0.83	0.15	-	67,67,67,67	0
32	MG	A	8100	1/1	0.90	0.15	-	88,88,88,88	0
32	MG	A	8090	1/1	0.93	0.16	-	47,47,47,47	0
32	MG	A	8030	1/1	0.99	0.10	-	40,40,40,40	0
32	MG	A	8104	1/1	0.97	0.07	-	50,50,50,50	0
34	NA	A	8375	1/1	0.68	0.28	-	86,86,86,86	0
32	MG	A	8088	1/1	0.84	0.13	-	64,64,64,64	0
32	MG	A	8079	1/1	0.97	0.08	-	42,42,42,42	0
32	MG	A	8114	1/1	0.88	0.27	-	47,47,47,47	0
32	MG	A	8098	1/1	0.99	0.25	-	52,52,52,52	0
35	CL	A	8520	1/1	0.84	0.19	-	65,65,65,65	0
34	NA	A	8307	1/1	0.87	0.42	-	48,48,48,48	0
34	NA	J	8322	1/1	0.71	0.43	-	62,62,62,62	0
32	MG	A	8025	1/1	0.98	0.05	-	54,54,54,54	0
36	CD	P	8405	1/1	0.91	0.09	-	152,152,152,152	0
34	NA	A	8319	1/1	0.99	0.14	-	57,57,57,57	0
35	CL	K	8502	1/1	0.95	0.15	-	87,87,87,87	0
34	NA	A	8363	1/1	0.56	0.91	-	79,79,79,79	0
32	MG	A	8081	1/1	0.96	0.12	-	67,67,67,67	0
34	NA	A	8318	1/1	0.90	0.69	-	45,45,45,45	0
32	MG	A	8040	1/1	0.90	0.09	-	63,63,63,63	0
32	MG	A	8113	1/1	0.90	0.15	-	53,53,53,53	0
34	NA	A	8328	1/1	0.70	0.29	-	61,61,61,61	0
32	MG	A	8026	1/1	0.97	0.09	-	49,49,49,49	0
32	MG	A	8062	1/1	0.97	0.09	-	61,61,61,61	0
32	MG	A	8087	1/1	0.84	0.10	-	75,75,75,75	0
32	MG	A	8089	1/1	0.90	0.11	-	70,70,70,70	0
32	MG	A	8042	1/1	0.93	0.23	-	52,52,52,52	0
32	MG	A	8097	1/1	0.92	0.30	-	45,45,45,45	0
32	MG	A	8116	1/1	0.83	0.10	-	54,54,54,54	0
32	MG	A	8034	1/1	0.97	0.03	-	32,32,32,32	0
34	NA	A	8357	1/1	0.79	0.07	-	64,64,64,64	0
32	MG	A	8046	1/1	0.96	0.10	-	72,72,72,72	0
32	MG	A	8082	1/1	0.89	0.22	-	83,83,83,83	0
32	MG	A	8091	1/1	0.94	0.06	-	58,58,58,58	0
34	NA	A	8334	1/1	0.94	0.20	-	45,45,45,45	0
32	MG	A	8037	1/1	0.95	0.12	-	61,61,61,61	0
32	MG	A	8005	1/1	0.96	0.13	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
34	NA	A	8370	1/1	0.95	0.20	-	42,42,42,42	0
34	NA	T	8312	1/1	0.79	0.25	-	51,51,51,51	0
32	MG	A	8023	1/1	0.98	0.03	-	33,33,33,33	0
32	MG	A	8102	1/1	0.95	0.28	-	75,75,75,75	0
32	MG	A	8050	1/1	0.88	0.26	-	67,67,67,67	0
32	MG	A	8048	1/1	0.96	0.08	-	41,41,41,41	0
32	MG	A	8075	1/1	0.94	0.11	-	56,56,56,56	0
34	NA	A	8384	1/1	0.40	1.14	-	90,90,90,90	0
34	NA	A	8310	1/1	0.81	0.20	-	29,29,29,29	0
32	MG	A	8094	1/1	0.96	0.09	-	66,66,66,66	0
32	MG	A	8092	1/1	0.84	0.32	-	95,95,95,95	0

6.5 Other polymers

There are no such residues in this entry.