



Full wwPDB EM Validation Report ⓘ

Nov 9, 2022 – 07:38 AM EST

PDB ID : 6PPK
EMDB ID : EMD-20441
Title : RbgA+45SRbgA complex
Authors : Ortega, J.
Deposited on : 2019-07-07
Resolution : 4.40 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

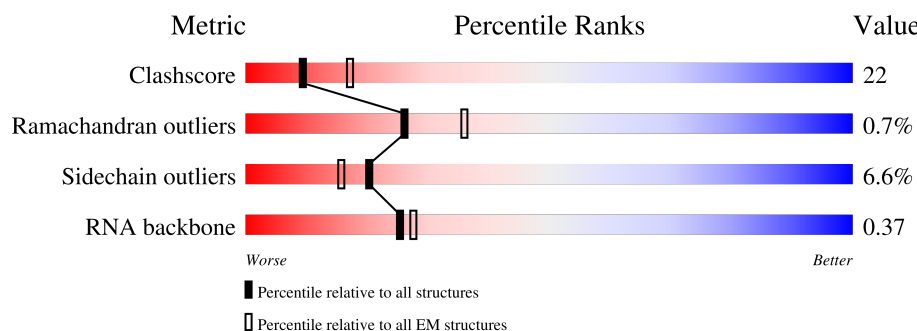
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 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.





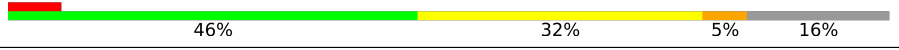

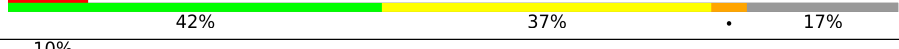
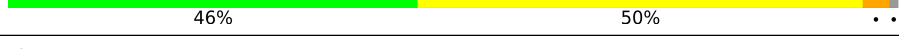

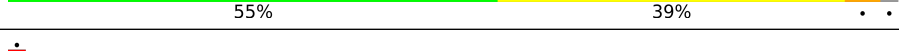
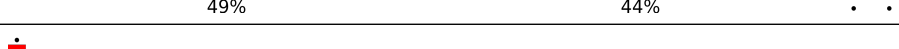
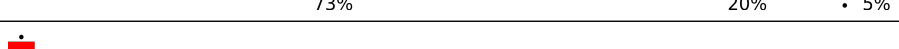




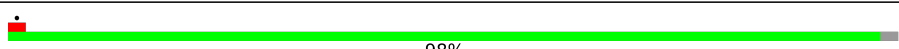


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2927	
2	B	119	
3	C	277	
4	D	209	
5	E	207	
6	F	179	
7	G	179	

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Mol	Chain	Length	Quality of chain
8	J	145	
9	K	122	
10	L	146	
11	N	120	
12	O	120	
13	P	115	
14	Q	118	
15	R	102	
16	S	113	
17	T	95	
18	U	103	
19	V	94	
20	Z	59	
21	b	59	
22	Y	66	
23	d	44	
24	W	282	

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
25	GNP	W	301	-	-	X	-

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 80451 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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					AltConf	Trace
1	A	2658	Total	C	N	O	P	0	0
			57112	25477	10569	18408	2658		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	260	Total	C	N	O	S	0	0
			2010	1253	392	359	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	206	Total	C	N	O	S	0	0
			1569	985	289	290	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	197	Total	C	N	O	S	0	0
			1511	951	280	278	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	139	Total	C	N	O	S	0	0
			1090	694	190	199	7		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	109	Total	C	N	O	S	0	0
			829	518	153	157	1		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	141	Total	C	N	O	S	0	0
			1119	708	205	201	5		

- Molecule 9 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	122	Total	C	N	O	S	0	0
			904	561	171	171	1		

- Molecule 11 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	118	Total	C	N	O	S	0	0
			947	580	185	178	4		

- Molecule 12 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	O	100	Total	C	N	O	0	0
			775	483	154	138		

- Molecule 13 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	P	114	Total	C	N	O	0	0
			936	595	184	157		

- Molecule 14 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 15 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	100	Total	C	N	O	S	0	0
			781	498	138	145			

- Molecule 16 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	90	Total	C	N	O	S	0	0
			724	452	133	136	3		

- Molecule 18 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	U	91	Total	C	N	O	S	0	0
			691	438	129	121	3		

- Molecule 19 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	V	78	Total	C	N	O	S	0	0
			604	375	118	111			

- Molecule 20 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	b	53	Total	C	N	O	S	0	0
			418	258	84	69	7		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Y	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

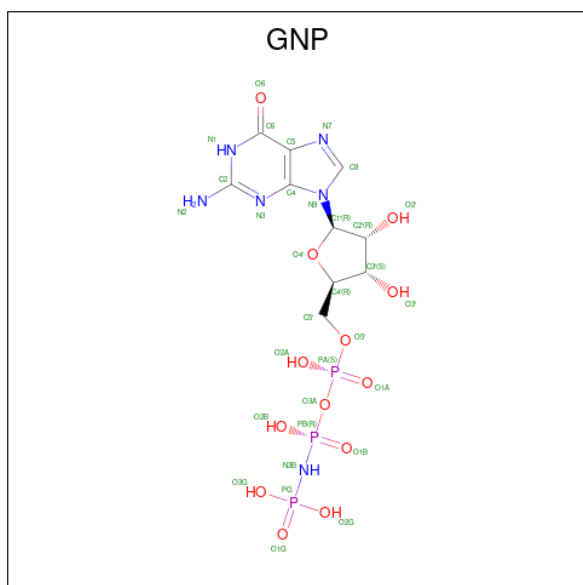
- Molecule 23 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	d	43	Total	C	N	O	S	0	0
			359	217	88	53	1		

- Molecule 24 is a protein called Ribosome biogenesis GTPase A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	252	Total	C	N	O	S	0	0
			1958	1250	343	359	6		

- Molecule 25 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).

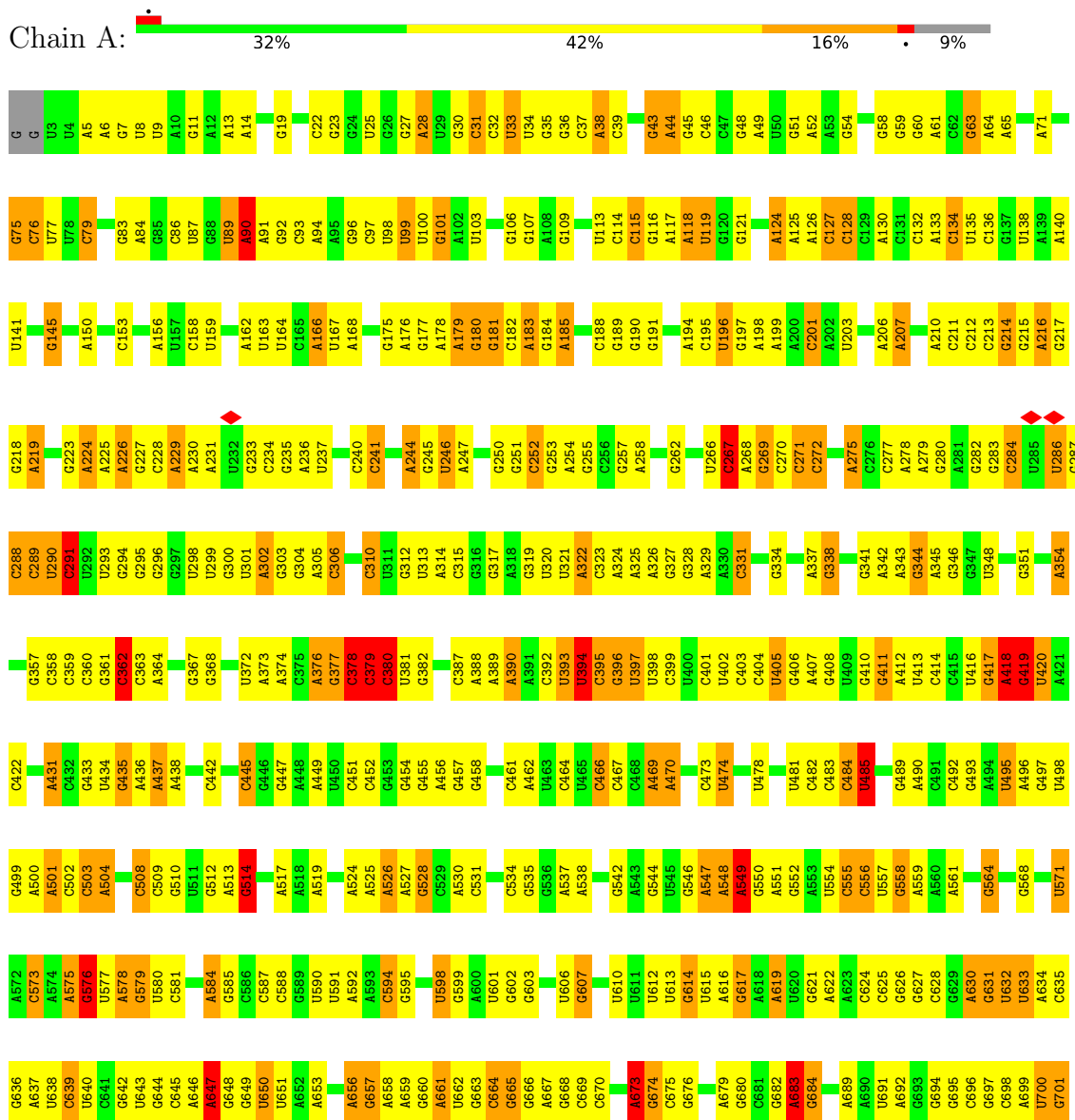


Mol	Chain	Residues	Atoms					AltConf
25	W	1	Total	C	N	O	P	0
			32	10	6	13	3	

3 Residue-property plots

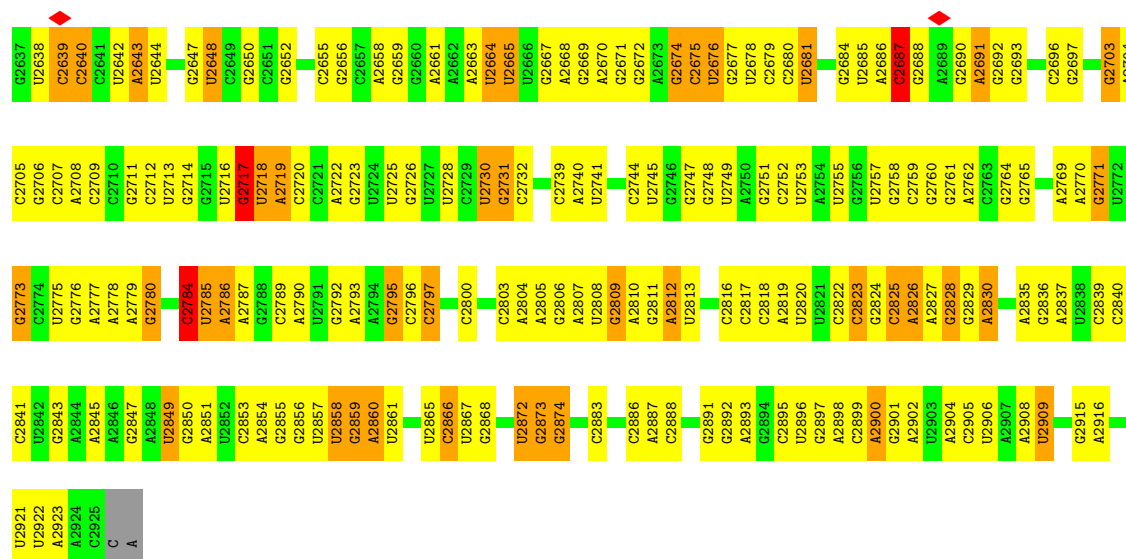
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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

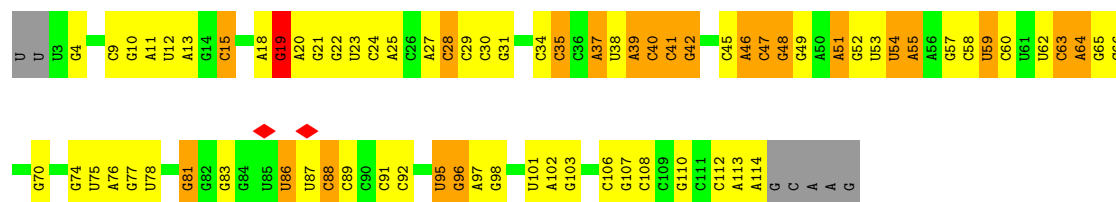




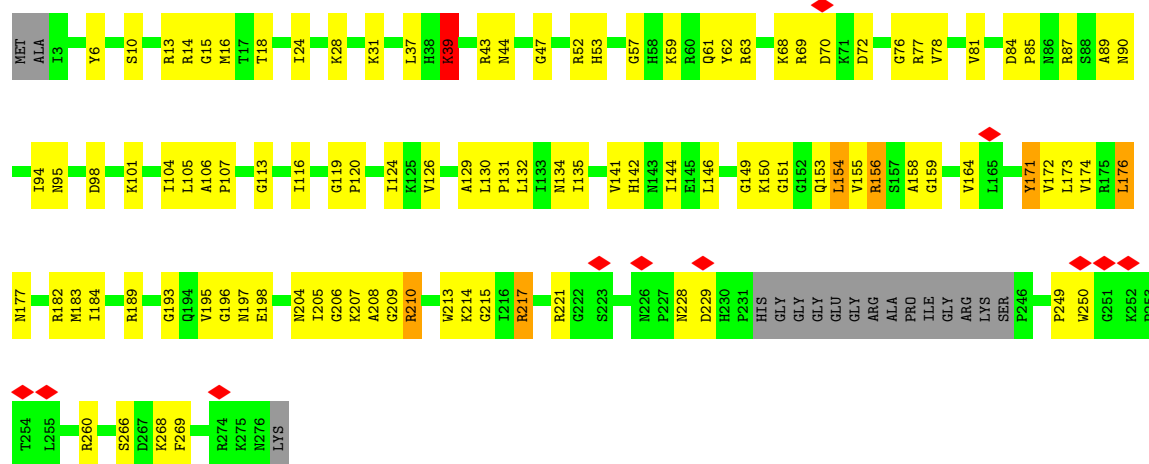


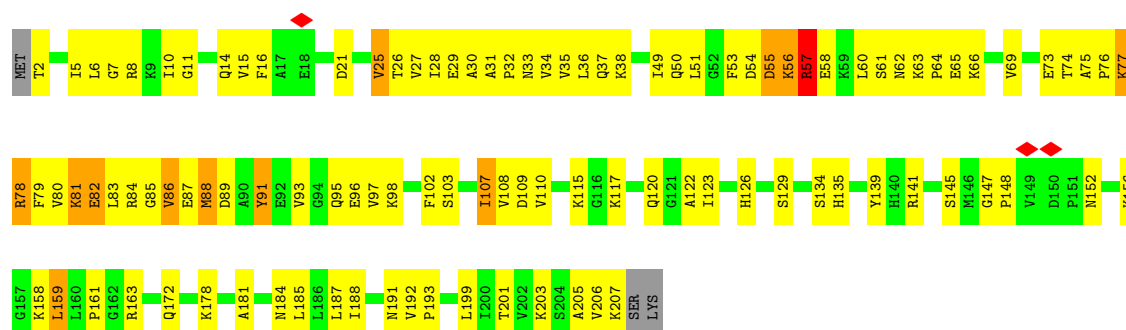


• Molecule 2: 5S rRNA

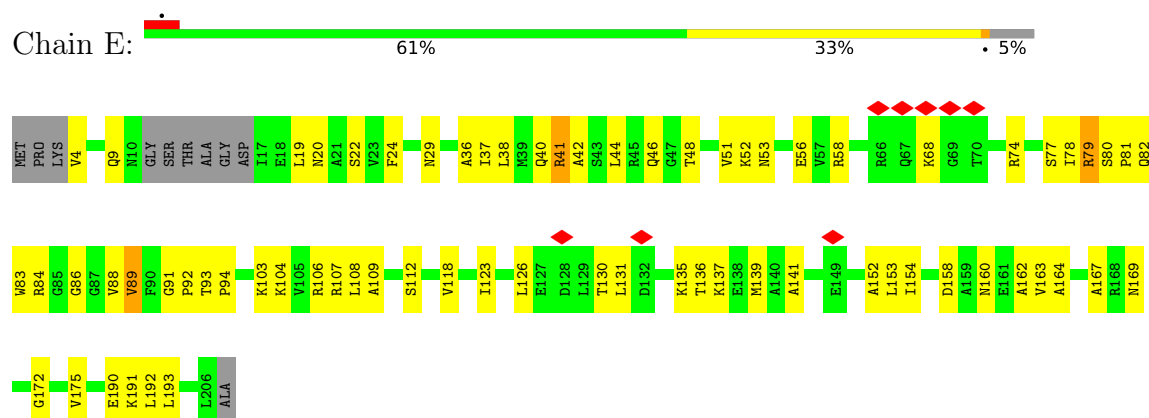


• Molecule 3: 50S ribosomal protein L2

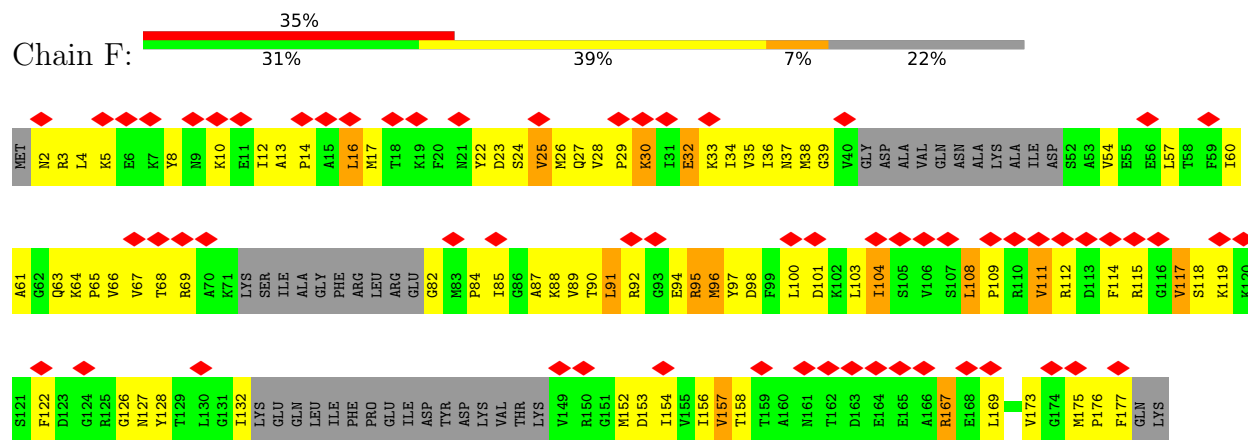




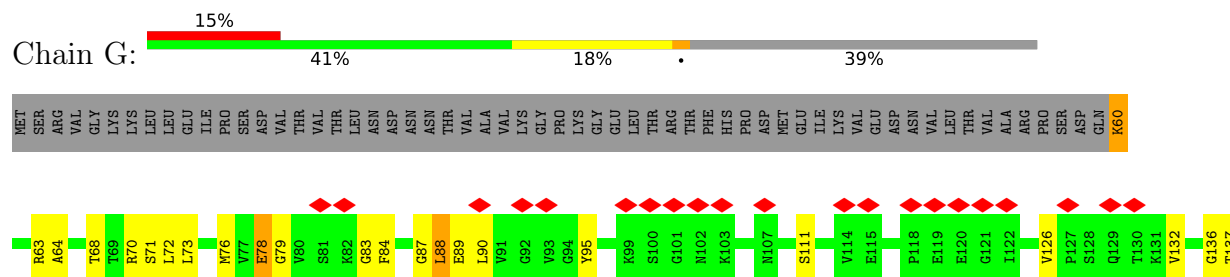
• Molecule 5: 50S ribosomal protein L4

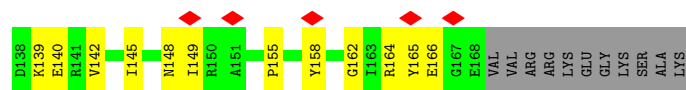


• Molecule 6: 50S ribosomal protein L5

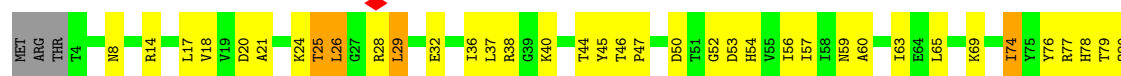


• Molecule 7: 50S ribosomal protein L6





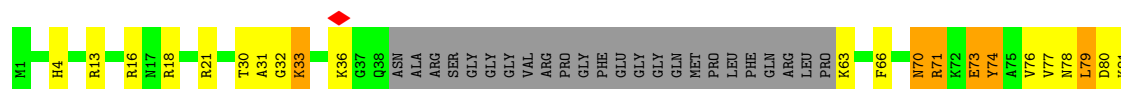
• Molecule 8: 50S ribosomal protein L13



• Molecule 9: 50S ribosomal protein L14



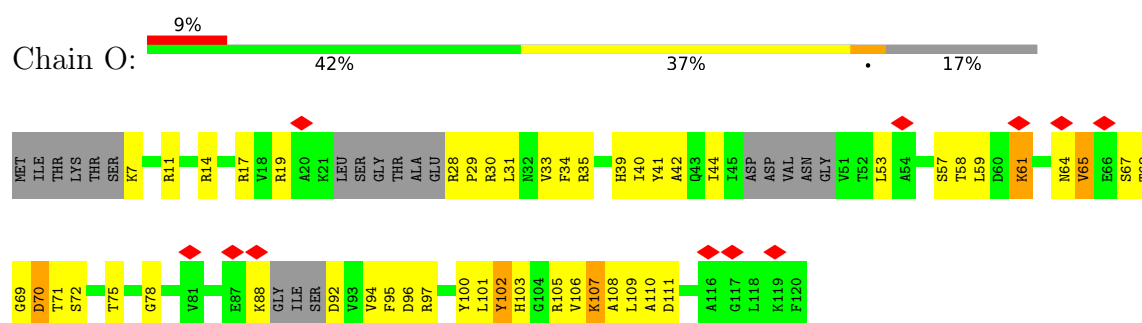
• Molecule 10: 50S ribosomal protein L15



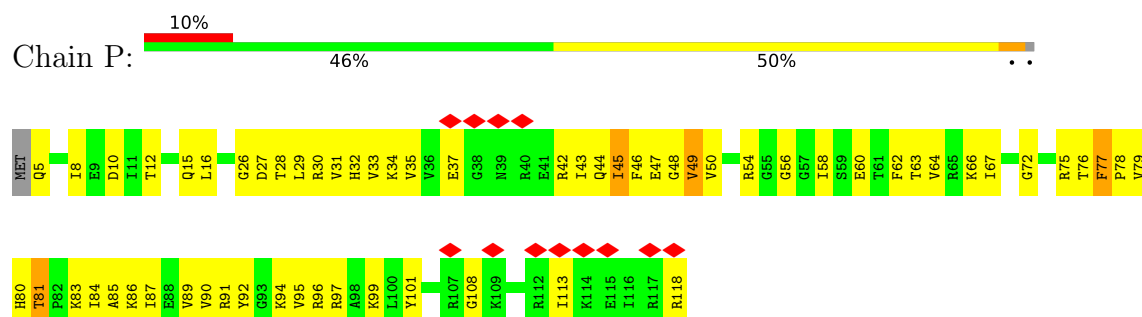
• Molecule 11: 50S ribosomal protein L17



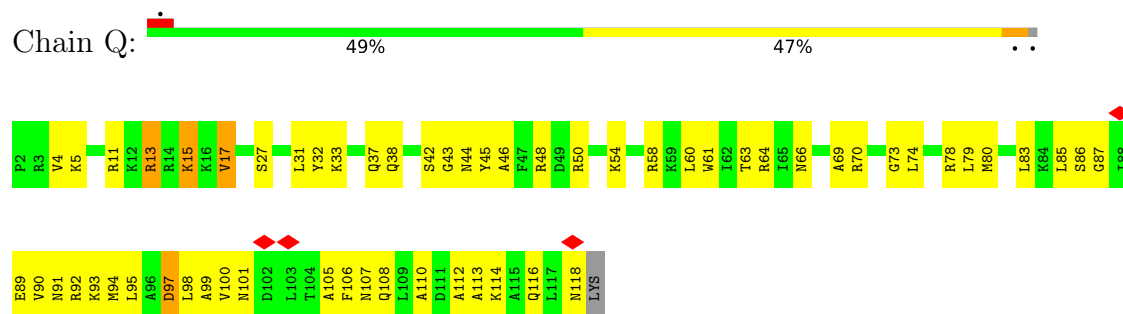
• Molecule 12: 50S ribosomal protein L18



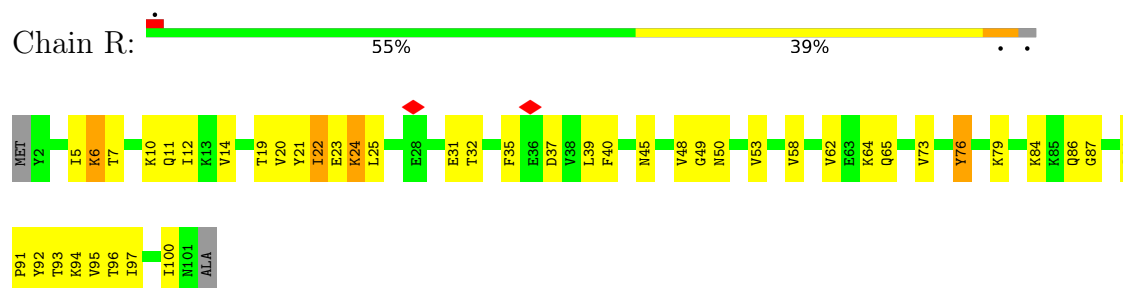
• Molecule 13: 50S ribosomal protein L19



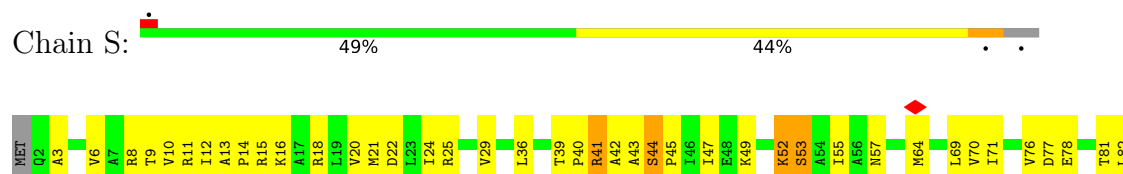
• Molecule 14: 50S ribosomal protein L20



• Molecule 15: 50S ribosomal protein L21



• Molecule 16: 50S ribosomal protein L22

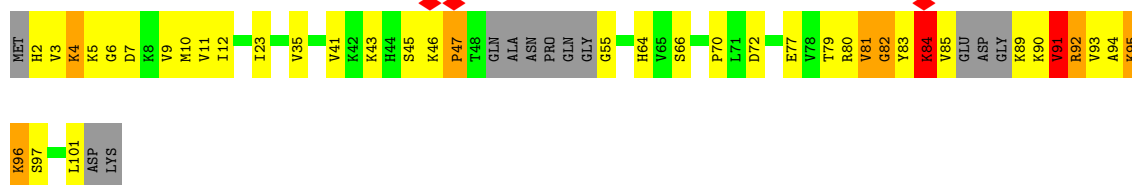




- Molecule 17: 50S ribosomal protein L23



- Molecule 18: 50S ribosomal protein L24



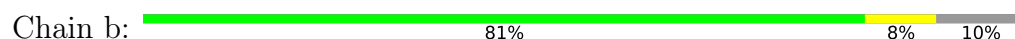
- Molecule 19: 50S ribosomal protein L27



- Molecule 20: 50S ribosomal protein L30

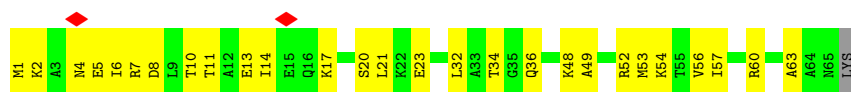


- Molecule 21: 50S ribosomal protein L32



- Molecule 22: 50S ribosomal protein L29

Chain Y:  58% 41%




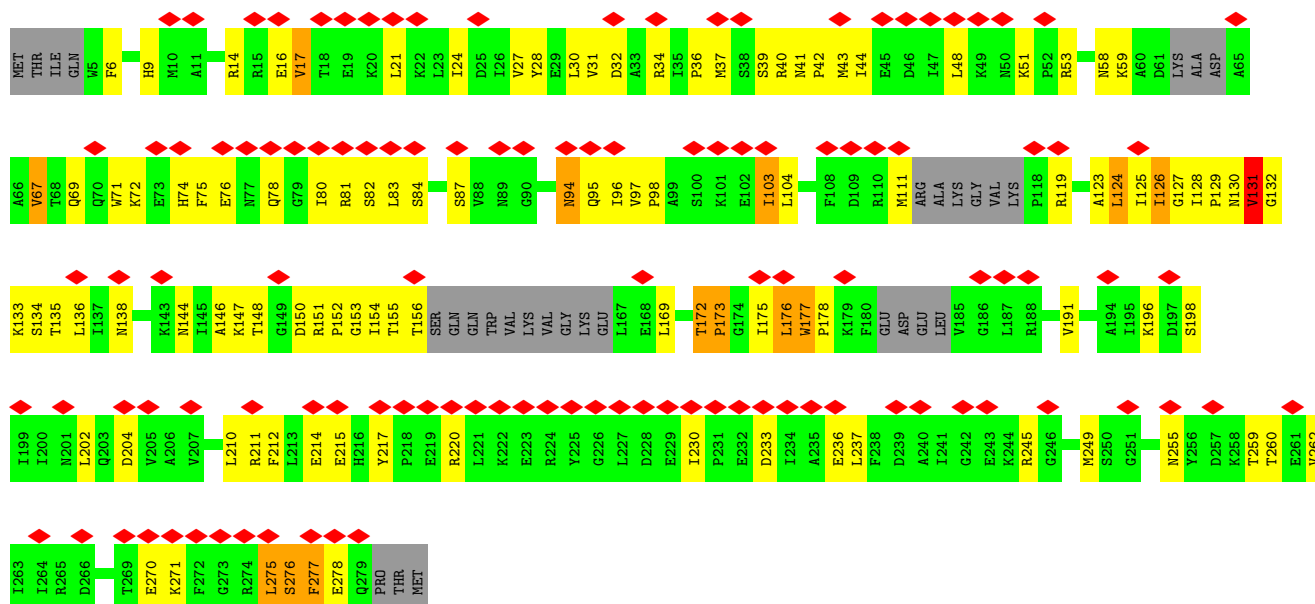
- Molecule 23: 50S ribosomal protein L34

Chain d:  98%



- Molecule 24: Ribosome biogenesis GTPase A

Chain W:  41% 50% 34% 5% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	81392	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.102	Depositor
Minimum map value	-0.047	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	348.0, 348.0, 348.0	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.45, 1.45, 1.45	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GNP

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	1.04	14/63968 (0.0%)	1.25	497/99771 (0.5%)
2	B	0.62	0/2678	1.18	21/4174 (0.5%)
3	C	0.41	0/2044	0.59	1/2741 (0.0%)
4	D	0.38	0/1591	0.59	2/2132 (0.1%)
5	E	0.43	0/1528	0.59	0/2061
6	F	0.21	0/1102	0.37	0/1476
7	G	0.30	0/841	0.54	1/1130 (0.1%)
8	J	0.36	0/1142	0.52	0/1537
9	K	0.38	0/927	0.81	7/1245 (0.6%)
10	L	0.33	0/910	0.47	0/1210
11	N	0.44	0/954	0.61	0/1276
12	O	0.26	0/781	0.48	0/1042
13	P	0.37	0/949	0.62	1/1269 (0.1%)
14	Q	0.51	0/952	0.56	0/1266
15	R	0.48	1/792 (0.1%)	0.56	0/1063
16	S	0.43	0/851	0.54	0/1146
17	T	0.46	0/730	0.60	0/974
18	U	0.34	0/698	0.60	2/929 (0.2%)
19	V	0.40	0/611	0.77	3/810 (0.4%)
20	Z	0.33	0/457	0.50	0/613
21	b	0.40	0/425	0.59	0/563
22	Y	0.35	0/531	0.51	0/707
23	d	0.54	0/362	0.56	0/473
24	W	0.29	0/1987	0.51	0/2680
All	All	0.91	15/87811 (0.0%)	1.14	535/132288 (0.4%)

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
5	E	0	1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	179	A	N9-C4	-6.73	1.33	1.37
1	A	830	A	N9-C4	-6.22	1.34	1.37
1	A	630	A	N9-C4	-6.14	1.34	1.37
1	A	2860	A	N9-C4	-5.97	1.34	1.37
1	A	1679	A	N9-C4	-5.71	1.34	1.37
1	A	1067	A	N9-C4	-5.70	1.34	1.37
1	A	1615	A	N9-C4	-5.65	1.34	1.37
15	R	76	TYR	C-N	-5.64	1.21	1.34
1	A	575	A	N9-C4	-5.60	1.34	1.37
1	A	1677	A	N7-C5	-5.43	1.35	1.39
1	A	847	A	N9-C4	-5.39	1.34	1.37
1	A	732	A	N7-C5	-5.12	1.36	1.39
1	A	1850	A	N9-C4	-5.05	1.34	1.37
1	A	1293	A	N9-C4	-5.03	1.34	1.37
1	A	500	A	N9-C4	-5.03	1.34	1.37

All (535) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	K	2	ILE	CB-CA-C	12.98	137.56	111.60
19	V	82	ARG	CB-CA-C	11.91	134.21	110.40
1	A	1352	U	C2-N1-C1'	11.62	131.65	117.70
1	A	2825	C	C2-N1-C1'	11.49	131.44	118.80
1	A	2825	C	N1-C2-O2	11.39	125.73	118.90
1	A	2225	C	N1-C2-O2	11.05	125.53	118.90
1	A	442	C	N1-C2-O2	10.79	125.37	118.90
1	A	2110	C	N1-C2-O2	10.66	125.30	118.90
13	P	29	LEU	CB-CA-C	10.53	130.20	110.20
1	A	556	C	N1-C2-O2	9.92	124.86	118.90
1	A	99	U	N1-C2-O2	9.78	129.64	122.80
1	A	1281	C	N1-C2-O2	9.52	124.61	118.90
1	A	442	C	N3-C2-O2	-9.38	115.33	121.90
1	A	1333	C	N1-C2-O2	9.24	124.45	118.90
1	A	2110	C	N3-C2-O2	-9.11	115.53	121.90
1	A	99	U	N3-C2-O2	-9.05	115.87	122.20
1	A	1352	U	N3-C2-O2	-9.03	115.88	122.20
1	A	2225	C	N3-C2-O2	-8.94	115.64	121.90
1	A	2035	C	N1-C2-O2	8.91	124.25	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	392	C	N1-C2-O2	8.77	124.16	118.90
1	A	1519	C	O5'-P-OP1	8.77	121.23	110.70
1	A	2883	C	N1-C2-O2	8.71	124.13	118.90
1	A	1333	C	C2-N1-C1'	8.60	128.25	118.80
1	A	2825	C	C5-C6-N1	8.52	125.26	121.00
1	A	1771	C	N1-C2-O2	8.49	124.00	118.90
1	A	1333	C	C6-N1-C2	-8.43	116.93	120.30
1	A	1281	C	N3-C2-O2	-8.42	116.01	121.90
1	A	1352	U	N1-C2-O2	8.41	128.69	122.80
1	A	2816	C	N1-C2-O2	8.35	123.91	118.90
1	A	2825	C	C6-N1-C2	-8.35	116.96	120.30
1	A	2825	C	N3-C2-O2	-8.33	116.07	121.90
1	A	1069	U	N3-C2-O2	-8.29	116.39	122.20
1	A	1795	C	N1-C2-O2	8.28	123.87	118.90
1	A	556	C	N3-C2-O2	-8.28	116.10	121.90
2	B	86	U	N1-C2-O2	8.28	128.59	122.80
3	C	176	LEU	CB-CA-C	-8.27	94.50	110.20
1	A	1281	C	C2-N1-C1'	8.23	127.85	118.80
1	A	115	C	N1-C2-O2	8.22	123.83	118.90
1	A	2797	C	N1-C2-O2	8.18	123.81	118.90
1	A	2147	U	C2-N1-C1'	8.17	127.50	117.70
1	A	442	C	C2-N1-C1'	8.16	127.78	118.80
1	A	571	U	C2-N1-C1'	8.12	127.44	117.70
1	A	716	G	C4-N9-C1'	8.08	137.01	126.50
1	A	1069	U	C2-N1-C1'	8.08	127.40	117.70
2	B	19	G	C4-N9-C1'	8.06	136.97	126.50
1	A	2393	C	N1-C2-O2	8.02	123.71	118.90
1	A	556	C	C2-N1-C1'	7.96	127.56	118.80
1	A	1352	U	C6-N1-C1'	-7.94	110.09	121.20
1	A	1333	C	N3-C2-O2	-7.90	116.37	121.90
1	A	8	U	N3-C2-O2	-7.86	116.70	122.20
1	A	2028	C	N1-C2-O2	7.83	123.60	118.90
1	A	380	C	N3-C2-O2	-7.77	116.46	121.90
1	A	1523	U	N3-C2-O2	-7.76	116.77	122.20
1	A	1715	C	C6-N1-C2	-7.75	117.20	120.30
1	A	2825	C	C6-N1-C1'	-7.74	111.51	120.80
1	A	228	C	N1-C2-O2	7.72	123.53	118.90
1	A	1028	C	N1-C2-O2	7.72	123.53	118.90
18	U	84	LYS	CB-CA-C	-7.68	95.04	110.40
1	A	445	C	N1-C2-O2	7.66	123.50	118.90
2	B	86	U	N3-C2-O2	-7.66	116.84	122.20
1	A	719	C	C6-N1-C2	-7.62	117.25	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	362	C	N1-C2-O2	7.60	123.46	118.90
2	B	19	G	C8-N9-C1'	-7.59	117.13	127.00
1	A	858	U	C2-N1-C1'	7.58	126.80	117.70
1	A	2079	C	N1-C2-O2	7.52	123.41	118.90
1	A	1333	C	C5-C6-N1	7.51	124.76	121.00
1	A	716	G	C8-N9-C1'	-7.50	117.24	127.00
2	B	86	U	C2-N1-C1'	7.50	126.70	117.70
1	A	99	U	C2-N1-C1'	7.49	126.69	117.70
1	A	2028	C	N3-C2-O2	-7.49	116.66	121.90
4	D	103	SER	CB-CA-C	-7.45	95.94	110.10
1	A	1523	U	N1-C2-O2	7.42	127.99	122.80
1	A	127	C	N1-C2-O2	7.41	123.35	118.90
9	K	97	ARG	CB-CA-C	-7.39	95.63	110.40
1	A	2035	C	C2-N1-C1'	7.38	126.92	118.80
2	B	19	G	N3-C4-N9	7.37	130.42	126.00
1	A	2393	C	N3-C2-O2	-7.35	116.76	121.90
1	A	1529	G	C4-C5-N7	7.35	113.74	110.80
1	A	1728	C	N1-C2-O2	7.34	123.31	118.90
1	A	380	C	N1-C2-O2	7.34	123.30	118.90
1	A	1069	U	N1-C2-O2	7.34	127.94	122.80
2	B	108	C	N1-C2-O2	7.32	123.29	118.90
1	A	1107	U	P-O3'-C3'	7.31	128.47	119.70
1	A	1033	C	N1-C2-O2	7.31	123.28	118.90
1	A	2849	U	N3-C2-O2	-7.30	117.09	122.20
1	A	2110	C	C2-N1-C1'	7.27	126.80	118.80
1	A	556	C	C6-N1-C2	-7.25	117.40	120.30
1	A	2866	C	N1-C2-O2	7.24	123.24	118.90
1	A	2028	C	C2-N1-C1'	7.22	126.74	118.80
4	D	57	ARG	CB-CA-C	-7.20	96.00	110.40
1	A	158	C	N1-C2-O2	7.18	123.21	118.90
1	A	127	C	N3-C2-O2	-7.12	116.92	121.90
1	A	442	C	C6-N1-C2	-7.11	117.46	120.30
1	A	1262	C	N1-C2-O2	7.08	123.15	118.90
1	A	2883	C	C2-N1-C1'	7.07	126.58	118.80
1	A	1673	G	C6-C5-N7	-7.07	126.16	130.40
1	A	2785	U	P-O3'-C3'	7.07	128.18	119.70
1	A	778	C	C6-N1-C2	-7.04	117.48	120.30
1	A	362	C	N3-C2-O2	-7.04	116.97	121.90
1	A	2147	U	C5-C6-N1	7.03	126.21	122.70
1	A	115	C	N3-C2-O2	-7.01	116.99	121.90
1	A	2883	C	N3-C2-O2	-6.98	117.01	121.90
9	K	2	ILE	N-CA-C	-6.97	92.19	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	K	37	ASP	CB-CA-C	6.97	124.33	110.40
9	K	43	VAL	CB-CA-C	-6.94	98.21	111.40
1	A	228	C	N3-C2-O2	-6.94	117.05	121.90
1	A	878	G	N3-C4-N9	6.92	130.15	126.00
1	A	2797	C	N3-C2-O2	-6.92	117.06	121.90
1	A	392	C	N3-C2-O2	-6.92	117.06	121.90
1	A	1245	G	P-O3'-C3'	6.91	127.99	119.70
1	A	2866	C	C2-N1-C1'	6.91	126.40	118.80
1	A	2816	C	N3-C2-O2	-6.87	117.09	121.90
1	A	508	C	N1-C2-O2	6.86	123.02	118.90
1	A	1529	G	C6-C5-N7	-6.85	126.29	130.40
1	A	2334	U	N1-C2-O2	6.83	127.58	122.80
1	A	2921	U	N1-C2-O2	6.82	127.58	122.80
1	A	2866	C	N3-C2-O2	-6.82	117.12	121.90
1	A	1771	C	N3-C2-O2	-6.80	117.14	121.90
1	A	732	A	C5-N7-C8	-6.80	100.50	103.90
1	A	1246	G	C4-N9-C1'	6.79	135.33	126.50
1	A	1596	U	C5-C6-N1	6.77	126.08	122.70
1	A	1028	C	N3-C2-O2	-6.77	117.16	121.90
1	A	2585	C	C6-N1-C2	-6.75	117.60	120.30
1	A	2541	C	C6-N1-C2	-6.74	117.61	120.30
1	A	1577	C	N1-C2-O2	6.73	122.94	118.90
1	A	2883	C	C6-N1-C2	-6.73	117.61	120.30
1	A	858	U	N3-C2-O2	-6.73	117.49	122.20
1	A	478	U	N3-C2-O2	-6.73	117.49	122.20
1	A	473	C	N1-C2-O2	6.72	122.93	118.90
1	A	31	C	N1-C2-O2	6.72	122.93	118.90
1	A	732	A	C4-C5-N7	6.72	114.06	110.70
1	A	831	U	N3-C2-O2	-6.72	117.50	122.20
19	V	88	SER	CB-CA-C	-6.70	97.38	110.10
1	A	331	C	N1-C2-O2	6.66	122.89	118.90
1	A	363	C	N1-C2-O2	6.66	122.89	118.90
1	A	2620	C	N1-C2-O2	6.64	122.89	118.90
1	A	2687	C	C6-N1-C2	-6.63	117.65	120.30
1	A	466	C	N3-C2-O2	-6.63	117.26	121.90
1	A	1148	C	N1-C2-O2	6.62	122.87	118.90
1	A	2849	U	N1-C2-O2	6.61	127.43	122.80
1	A	843	C	N1-C2-O2	6.61	122.87	118.90
1	A	571	U	C5-C6-N1	6.60	126.00	122.70
1	A	478	U	N1-C2-O2	6.59	127.42	122.80
1	A	8	U	N1-C2-O2	6.58	127.41	122.80
1	A	2035	C	N3-C2-O2	-6.57	117.30	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	778	C	C2-N1-C1'	6.57	126.03	118.80
1	A	2432	C	N3-C2-O2	-6.57	117.30	121.90
1	A	2780	G	C4-N9-C1'	6.57	135.03	126.50
1	A	508	C	C6-N1-C2	-6.56	117.68	120.30
1	A	392	C	C2-N1-C1'	6.56	126.02	118.80
1	A	473	C	N3-C2-O2	-6.56	117.31	121.90
1	A	1817	C	N3-C2-O2	-6.56	117.31	121.90
1	A	1817	C	N1-C2-O2	6.55	122.83	118.90
1	A	466	C	N1-C2-O2	6.53	122.82	118.90
1	A	1297	C	N3-C2-O2	-6.53	117.33	121.90
1	A	2921	U	C2-N1-C1'	6.52	125.53	117.70
1	A	492	C	N1-C2-O2	6.51	122.81	118.90
1	A	1515	C	C2-N1-C1'	6.50	125.95	118.80
1	A	571	U	N3-C2-O2	-6.50	117.65	122.20
1	A	127	C	C6-N1-C2	-6.47	117.71	120.30
1	A	1539	C	N1-C2-O2	6.47	122.78	118.90
1	A	1033	C	N3-C2-O2	-6.46	117.38	121.90
1	A	2225	C	C2-N1-C1'	6.46	125.91	118.80
2	B	63	C	N1-C2-O2	6.46	122.78	118.90
1	A	2921	U	N3-C2-O2	-6.46	117.68	122.20
1	A	8	U	C2-N1-C1'	6.45	125.44	117.70
1	A	359	C	N1-C2-O2	6.43	122.76	118.90
1	A	683	A	P-O3'-C3'	6.43	127.42	119.70
7	G	88	LEU	CB-CA-C	6.40	122.36	110.20
1	A	272	C	N1-C2-O2	6.40	122.74	118.90
1	A	842	C	N3-C2-O2	-6.39	117.43	121.90
1	A	2147	U	N1-C2-O2	6.39	127.27	122.80
1	A	1362	G	P-O3'-C3'	6.38	127.36	119.70
1	A	2255	C	C6-N1-C2	-6.38	117.75	120.30
1	A	1564	C	N1-C2-O2	6.37	122.72	118.90
1	A	1564	C	N3-C2-O2	-6.37	117.44	121.90
1	A	115	C	C2-N1-C1'	6.35	125.79	118.80
1	A	2432	C	N1-C2-O2	6.35	122.71	118.90
1	A	1796	C	N1-C2-O2	6.35	122.71	118.90
1	A	1351	U	P-O3'-C3'	6.34	127.31	119.70
1	A	1511	C	N3-C2-O2	-6.32	117.47	121.90
1	A	1728	C	N3-C2-O2	-6.32	117.48	121.90
1	A	1568	G	O4'-C1'-N9	6.29	113.23	108.20
1	A	624	C	N1-C2-O2	6.28	122.67	118.90
1	A	1805	G	C4-N9-C1'	6.28	134.67	126.50
1	A	2079	C	N3-C2-O2	-6.28	117.50	121.90
1	A	571	U	N1-C2-O2	6.26	127.18	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1568	G	C6-C5-N7	-6.26	126.65	130.40
2	B	59	U	P-O3'-C3'	6.25	127.20	119.70
1	A	843	C	N3-C2-O2	-6.25	117.53	121.90
1	A	2337	G	C4-N9-C1'	6.25	134.62	126.50
1	A	1519	C	O5'-P-OP2	-6.25	100.08	105.70
9	K	56	GLU	CB-CA-C	6.22	122.84	110.40
1	A	1506	A	C2-N3-C4	6.21	113.71	110.60
1	A	397	U	N1-C2-O2	6.21	127.14	122.80
1	A	1544	C	C2-N1-C1'	6.20	125.62	118.80
1	A	1495	C	N1-C2-O2	6.19	122.62	118.90
18	U	84	LYS	N-CA-C	6.18	127.69	111.00
1	A	878	G	C4-N9-C1'	6.18	134.53	126.50
1	A	394	U	N3-C2-O2	-6.18	117.88	122.20
1	A	2597	C	C6-N1-C2	-6.18	117.83	120.30
1	A	2664	U	N3-C2-O2	-6.17	117.88	122.20
1	A	878	G	C8-N9-C1'	-6.17	118.97	127.00
1	A	2687	C	C5-C6-N1	6.16	124.08	121.00
1	A	1795	C	N3-C2-O2	-6.15	117.60	121.90
1	A	725	C	N3-C2-O2	-6.14	117.60	121.90
1	A	134	C	N1-C2-O2	6.13	122.58	118.90
1	A	136	C	N1-C2-O2	6.13	122.58	118.90
1	A	556	C	C5-C6-N1	6.12	124.06	121.00
1	A	858	U	N1-C2-O2	6.12	127.08	122.80
1	A	1539	C	N3-C2-O2	-6.12	117.62	121.90
9	K	45	GLN	CB-CA-C	-6.11	98.17	110.40
1	A	613	U	N3-C2-O2	-6.10	117.93	122.20
1	A	717	A	P-O3'-C3'	6.10	127.02	119.70
1	A	158	C	N3-C2-O2	-6.09	117.64	121.90
1	A	1245	G	O4'-C1'-N9	6.08	113.06	108.20
1	A	508	C	N3-C2-O2	-6.07	117.65	121.90
1	A	31	C	C6-N1-C2	-6.07	117.87	120.30
1	A	716	G	N3-C4-N9	6.07	129.64	126.00
1	A	1281	C	C6-N1-C1'	-6.06	113.53	120.80
1	A	419	G	P-O3'-C3'	6.06	126.97	119.70
1	A	124	A	P-O3'-C3'	6.05	126.96	119.70
1	A	1327	U	N3-C2-O2	-6.04	117.97	122.20
1	A	1568	G	C4-C5-N7	6.04	113.22	110.80
1	A	2337	G	N3-C4-C5	-6.04	125.58	128.60
1	A	241	C	N3-C2-O2	-6.04	117.67	121.90
1	A	1327	U	N1-C2-O2	6.03	127.02	122.80
1	A	1715	C	C5-C6-N1	6.03	124.01	121.00
1	A	2349	A	N7-C8-N9	6.03	116.81	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2909	U	N3-C2-O2	-6.02	117.99	122.20
1	A	647	A	P-O3'-C3'	6.02	126.92	119.70
1	A	1150	C	C5-C6-N1	6.02	124.01	121.00
1	A	778	C	N3-C2-O2	-6.01	117.69	121.90
1	A	1551	C	N1-C2-O2	6.01	122.51	118.90
1	A	969	C	N3-C2-O2	-6.00	117.70	121.90
1	A	730	U	N3-C2-O2	-6.00	118.00	122.20
1	A	1146	C	C6-N1-C2	-6.00	117.90	120.30
1	A	1339	A	P-O3'-C3'	6.00	126.90	119.70
1	A	716	G	C6-C5-N7	-5.98	126.81	130.40
1	A	2337	G	N3-C4-N9	5.98	129.59	126.00
1	A	2350	G	C4-N9-C1'	5.97	134.27	126.50
1	A	2679	C	N1-C2-O2	5.97	122.48	118.90
1	A	2351	A	P-O3'-C3'	5.97	126.86	119.70
1	A	805	G	N3-C4-N9	5.96	129.57	126.00
1	A	1551	C	N3-C2-O2	-5.95	117.73	121.90
1	A	1246	G	O4'-C1'-N9	5.95	112.96	108.20
1	A	576	G	N3-C4-N9	5.93	129.56	126.00
1	A	467	C	N3-C2-O2	-5.93	117.75	121.90
1	A	1728	C	C2-N1-C1'	5.92	125.32	118.80
1	A	2086	G	N3-C4-N9	5.92	129.55	126.00
1	A	442	C	C5-C6-N1	5.91	123.96	121.00
1	A	878	G	C6-C5-N7	-5.91	126.86	130.40
1	A	2073	C	C5-C6-N1	5.90	123.95	121.00
1	A	1622	C	N1-C2-O2	5.90	122.44	118.90
2	B	19	G	C6-C5-N7	-5.90	126.86	130.40
1	A	2849	U	C2-N1-C1'	5.89	124.77	117.70
1	A	842	C	N1-C2-O2	5.89	122.43	118.90
1	A	237	U	N3-C2-O2	-5.89	118.08	122.20
1	A	482	C	C2-N1-C1'	5.88	125.27	118.80
1	A	158	C	C2-N1-C1'	5.88	125.26	118.80
1	A	492	C	N3-C2-O2	-5.87	117.79	121.90
1	A	414	C	N1-C2-O2	5.87	122.42	118.90
1	A	2797	C	C2-N1-C1'	5.86	125.25	118.80
1	A	1577	C	N3-C2-O2	-5.86	117.80	121.90
1	A	1595	U	N3-C2-O2	-5.86	118.10	122.20
1	A	90	A	P-O3'-C3'	5.85	126.72	119.70
1	A	788	G	C4-N9-C1'	5.84	134.09	126.50
1	A	831	U	N1-C2-O2	5.83	126.88	122.80
1	A	2784	C	N1-C2-O2	5.83	122.40	118.90
1	A	861	C	N1-C2-O2	5.82	122.39	118.90
1	A	1523	U	C2-N1-C1'	5.82	124.68	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1568	G	N7-C8-N9	5.82	116.01	113.10
1	A	2324	C	N1-C2-O2	5.82	122.39	118.90
1	A	272	C	N3-C2-O2	-5.81	117.83	121.90
1	A	732	A	N7-C8-N9	5.81	116.70	113.80
1	A	1297	C	N1-C2-O2	5.81	122.38	118.90
1	A	183	A	P-O3'-C3'	5.80	126.66	119.70
19	V	82	ARG	N-CA-C	-5.80	95.34	111.00
1	A	445	C	C2-N1-C1'	5.79	125.17	118.80
1	A	1293	A	O4'-C1'-N9	-5.79	103.57	108.20
1	A	2255	C	N3-C2-O2	-5.79	117.84	121.90
1	A	2681	U	N1-C2-O2	5.79	126.85	122.80
1	A	2883	C	C5-C6-N1	5.79	123.89	121.00
1	A	252	C	P-O3'-C3'	5.78	126.63	119.70
1	A	843	C	C2-N1-C1'	5.78	125.16	118.80
1	A	153	C	N1-C2-O2	5.77	122.36	118.90
1	A	1509	C	C5-C6-N1	5.77	123.89	121.00
1	A	1146	C	C5-C6-N1	5.77	123.88	121.00
1	A	387	C	C6-N1-C2	-5.76	118.00	120.30
1	A	856	G	C4-N9-C1'	5.76	134.00	126.50
1	A	2679	C	N3-C2-O2	-5.76	117.86	121.90
1	A	2255	C	N1-C2-O2	5.76	122.36	118.90
1	A	861	C	N3-C2-O2	-5.75	117.87	121.90
1	A	1148	C	C6-N1-C2	-5.75	118.00	120.30
1	A	1641	U	N3-C2-O2	-5.75	118.18	122.20
1	A	2110	C	C6-N1-C2	-5.75	118.00	120.30
1	A	598	U	N3-C2-O2	-5.74	118.18	122.20
1	A	2608	C	N1-C2-O2	5.74	122.34	118.90
1	A	2073	C	C6-N1-C2	-5.73	118.01	120.30
1	A	673	A	C8-N9-C4	5.72	108.09	105.80
1	A	1596	U	N1-C2-O2	5.72	126.81	122.80
1	A	1297	C	C2-N1-C1'	5.72	125.09	118.80
1	A	969	C	C6-N1-C2	-5.70	118.02	120.30
1	A	1529	G	N7-C8-N9	5.70	115.95	113.10
2	B	108	C	N3-C2-O2	-5.69	117.92	121.90
1	A	1771	C	C2-N1-C1'	5.69	125.06	118.80
1	A	2225	C	C6-N1-C2	-5.69	118.02	120.30
2	B	62	U	N1-C2-O2	5.68	126.78	122.80
1	A	856	G	C8-N9-C1'	-5.67	119.62	127.00
1	A	478	U	C2-N1-C1'	5.67	124.50	117.70
1	A	1674	G	C6-C5-N7	-5.67	127.00	130.40
1	A	2858	U	P-O3'-C3'	5.67	126.50	119.70
1	A	2780	G	N3-C4-N9	5.66	129.40	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1093	G	C4-N9-C1'	5.65	133.84	126.50
1	A	363	C	N3-C2-O2	-5.64	117.95	121.90
1	A	291	C	C5-C6-N1	5.64	123.82	121.00
1	A	2454	A	P-O3'-C3'	5.64	126.46	119.70
1	A	981	C	C5-C6-N1	5.63	123.82	121.00
1	A	1246	G	C8-N9-C1'	-5.63	119.68	127.00
1	A	1673	G	C4-C5-N7	5.63	113.05	110.80
1	A	2597	C	N1-C2-O2	5.63	122.28	118.90
1	A	732	A	C6-C5-N7	-5.62	128.36	132.30
1	A	1573	C	C6-N1-C2	-5.62	118.05	120.30
1	A	31	C	N3-C2-O2	-5.62	117.97	121.90
1	A	788	G	C4-C5-N7	5.61	113.05	110.80
1	A	271	C	C6-N1-C2	-5.61	118.06	120.30
1	A	872	C	C6-N1-C2	-5.61	118.06	120.30
1	A	1705	C	N1-C2-O2	5.61	122.27	118.90
1	A	2371	C	N1-C2-O2	5.61	122.26	118.90
1	A	485	U	N1-C2-O2	5.60	126.72	122.80
1	A	1370	C	N3-C2-O2	-5.60	117.98	121.90
1	A	1262	C	N3-C2-O2	-5.59	117.98	121.90
1	A	1529	G	C5-N7-C8	-5.59	101.50	104.30
1	A	229	A	P-O3'-C3'	5.59	126.41	119.70
1	A	1310	C	N3-C2-O2	-5.59	117.99	121.90
1	A	1368	U	C2-N1-C1'	5.59	124.41	117.70
1	A	2597	C	N3-C2-O2	-5.59	117.99	121.90
1	A	99	U	C6-N1-C1'	-5.57	113.41	121.20
1	A	2267	G	N3-C4-N9	5.56	129.34	126.00
1	A	719	C	N3-C2-O2	-5.56	118.01	121.90
1	A	1370	C	N1-C2-O2	5.55	122.23	118.90
1	A	1433	U	C2-N1-C1'	5.55	124.36	117.70
1	A	890	G	N3-C4-N9	5.54	129.32	126.00
1	A	380	C	C2-N1-C1'	5.54	124.89	118.80
1	A	359	C	N3-C2-O2	-5.54	118.03	121.90
1	A	1362	G	OP1-P-O3'	5.54	117.38	105.20
1	A	14	A	C8-N9-C4	-5.53	103.59	105.80
1	A	1069	U	C6-N1-C2	-5.52	117.69	121.00
1	A	1163	U	N1-C2-O2	5.52	126.66	122.80
1	A	240	C	N3-C2-O2	-5.52	118.04	121.90
1	A	1327	U	C2-N1-C1'	5.51	124.32	117.70
1	A	732	A	C4-N9-C1'	5.51	136.22	126.30
1	A	2608	C	N3-C2-O2	-5.51	118.04	121.90
1	A	1568	G	C5-N7-C8	-5.50	101.55	104.30
1	A	387	C	N1-C2-O2	5.50	122.20	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	9	C	N1-C2-O2	5.50	122.20	118.90
1	A	1622	C	N3-C2-O2	-5.49	118.06	121.90
2	B	35	C	C6-N1-C2	-5.49	118.10	120.30
1	A	2015	G	N3-C4-N9	5.49	129.29	126.00
1	A	348	U	N1-C2-O2	5.48	126.64	122.80
1	A	1148	C	N3-C2-O2	-5.48	118.07	121.90
1	A	725	C	N1-C2-O2	5.47	122.18	118.90
1	A	2816	C	C2-N1-C1'	5.47	124.81	118.80
1	A	2433	C	N3-C2-O2	-5.46	118.08	121.90
1	A	981	C	C2-N1-C1'	5.46	124.81	118.80
1	A	31	C	C5-C6-N1	5.46	123.73	121.00
1	A	2268	G	N3-C4-N9	5.45	129.27	126.00
1	A	2795	G	C5-C6-O6	-5.45	125.33	128.60
1	A	2664	U	N1-C2-O2	5.44	126.61	122.80
1	A	1652	C	P-O3'-C3'	5.44	126.22	119.70
1	A	1755	C	P-O3'-C3'	5.43	126.22	119.70
1	A	2158	C	C6-N1-C2	-5.43	118.13	120.30
1	A	228	C	C2-N1-C1'	5.43	124.78	118.80
1	A	613	U	N1-C2-O2	5.43	126.60	122.80
1	A	1805	G	C8-N9-C1'	-5.43	119.94	127.00
1	A	988	G	C4-N9-C1'	5.43	133.56	126.50
1	A	2035	C	C6-N1-C1'	-5.43	114.29	120.80
1	A	778	C	N1-C2-O2	5.42	122.15	118.90
1	A	2334	U	N3-C2-O2	-5.42	118.41	122.20
1	A	1622	C	C6-N1-C2	-5.42	118.13	120.30
1	A	413	U	N1-C2-O2	5.41	126.59	122.80
1	A	2095	C	N3-C2-O2	-5.41	118.11	121.90
1	A	1529	G	N9-C4-C5	-5.41	103.24	105.40
1	A	2780	G	C8-N9-C1'	-5.41	119.97	127.00
1	A	405	U	P-O3'-C3'	5.40	126.18	119.70
2	B	63	C	N3-C2-O2	-5.40	118.12	121.90
1	A	2349	A	C8-N9-C4	-5.40	103.64	105.80
1	A	571	U	C6-N1-C2	-5.40	117.76	121.00
1	A	2732	C	N1-C2-O2	5.40	122.14	118.90
1	A	1245	G	C4-N9-C1'	5.39	133.51	126.50
1	A	145	G	C8-N9-C1'	-5.39	119.99	127.00
1	A	485	U	N3-C2-O2	-5.39	118.42	122.20
1	A	2031	G	N3-C4-N9	5.39	129.24	126.00
1	A	1527	C	P-O3'-C3'	5.39	126.17	119.70
1	A	2797	C	C6-N1-C2	-5.39	118.14	120.30
1	A	2784	C	C6-N1-C2	-5.38	118.15	120.30
1	A	730	U	N1-C2-O2	5.38	126.56	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1150	C	C6-N1-C2	-5.38	118.15	120.30
1	A	445	C	N3-C2-O2	-5.37	118.14	121.90
1	A	1366	C	C6-N1-C2	-5.37	118.15	120.30
1	A	1452	C	C6-N1-C2	-5.36	118.16	120.30
1	A	2780	G	N3-C4-C5	-5.36	125.92	128.60
1	A	788	G	C8-N9-C1'	-5.36	120.04	127.00
1	A	624	C	N3-C2-O2	-5.36	118.15	121.90
1	A	1506	A	C4-N9-C1'	5.36	135.94	126.30
1	A	37	C	N3-C2-O2	-5.35	118.15	121.90
1	A	632	U	N1-C2-O2	5.35	126.55	122.80
1	A	473	C	C2-N1-C1'	5.34	124.68	118.80
1	A	1756	U	N1-C2-O2	5.34	126.54	122.80
1	A	805	G	C4-N9-C1'	5.34	133.44	126.50
1	A	2812	A	P-O3'-C3'	5.34	126.10	119.70
1	A	1339	A	OP2-P-O3'	5.33	116.93	105.20
1	A	1568	G	C4-N9-C1'	5.33	133.43	126.50
1	A	22	C	N1-C2-O2	5.33	122.10	118.90
1	A	1495	C	N3-C2-O2	-5.32	118.17	121.90
1	A	1495	C	C2-N1-C1'	5.32	124.65	118.80
1	A	76	C	N1-C2-O2	5.31	122.09	118.90
1	A	241	C	N1-C2-O2	5.31	122.08	118.90
1	A	1240	U	N3-C2-O2	-5.31	118.48	122.20
1	A	632	U	C2-N1-C1'	5.31	124.07	117.70
1	A	397	U	N3-C2-O2	-5.29	118.50	122.20
1	A	1595	U	P-O3'-C3'	5.28	126.03	119.70
1	A	2678	U	N1-C2-O2	5.27	126.49	122.80
1	A	726	C	C6-N1-C2	-5.27	118.19	120.30
1	A	1759	U	N1-C2-O2	5.27	126.49	122.80
1	A	188	C	C5-C4-N4	-5.26	116.52	120.20
1	A	183	A	OP1-P-O3'	5.26	116.76	105.20
1	A	1198	C	N3-C2-O2	-5.25	118.22	121.90
1	A	1246	G	C6-C5-N7	-5.25	127.25	130.40
1	A	331	C	N3-C2-O2	-5.25	118.22	121.90
1	A	1668	G	N3-C4-N9	5.25	129.15	126.00
1	A	214	G	C4-C5-N7	5.25	112.90	110.80
1	A	310	C	N1-C2-O2	5.24	122.05	118.90
1	A	2597	C	C5-C6-N1	5.24	123.62	121.00
1	A	2647	G	C4-N9-C1'	5.24	133.31	126.50
1	A	31	C	C2-N1-C1'	5.23	124.56	118.80
1	A	115	C	C6-N1-C1'	-5.23	114.52	120.80
1	A	2647	G	C6-C5-N7	-5.23	127.26	130.40
1	A	1596	U	N3-C2-O2	-5.22	118.55	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2334	U	P-O3'-C3'	5.22	125.96	119.70
1	A	726	C	N3-C2-O2	-5.22	118.25	121.90
1	A	503	C	N1-C2-O2	5.21	122.03	118.90
1	A	508	C	C5-C6-N1	5.21	123.61	121.00
1	A	1711	G	C6-C5-N7	-5.21	127.28	130.40
1	A	145	G	C4-N9-C1'	5.20	133.26	126.50
1	A	418	A	O5'-P-OP2	-5.20	101.02	105.70
1	A	76	C	N3-C2-O2	-5.20	118.26	121.90
1	A	1326	A	N1-C6-N6	5.20	121.72	118.60
1	A	1564	C	C2-N1-C1'	5.20	124.52	118.80
1	A	895	G	C4-N9-C1'	5.20	133.26	126.50
1	A	2472	C	N1-C2-O2	5.20	122.02	118.90
1	A	1368	U	N1-C2-O2	5.20	126.44	122.80
1	A	2712	C	N1-C2-O2	5.20	122.02	118.90
1	A	394	U	N1-C2-O2	5.19	126.44	122.80
1	A	267	C	N1-C2-O2	5.19	122.01	118.90
1	A	1321	U	N3-C2-O2	-5.19	118.57	122.20
1	A	378	C	C6-N1-C1'	5.19	127.02	120.80
1	A	379	C	N3-C4-C5	5.18	123.97	121.90
1	A	271	C	P-O3'-C3'	5.18	125.91	119.70
2	B	35	C	C5-C6-N1	5.17	123.59	121.00
1	A	1715	C	C2-N1-C1'	5.17	124.48	118.80
1	A	1780	C	N1-C2-O2	5.17	122.00	118.90
1	A	2822	C	N1-C2-O2	5.17	122.00	118.90
1	A	464	C	N1-C2-O2	5.16	122.00	118.90
1	A	805	G	C8-N9-C1'	-5.16	120.29	127.00
1	A	1577	C	C6-N1-C2	-5.15	118.24	120.30
1	A	2337	G	C8-N9-C1'	-5.15	120.30	127.00
1	A	2147	U	C6-N1-C1'	-5.15	113.99	121.20
1	A	422	C	N3-C2-O2	-5.15	118.30	121.90
1	A	2691	A	C5-N7-C8	-5.15	101.32	103.90
1	A	1164	C	N1-C2-O2	5.15	121.99	118.90
1	A	2064	G	C8-N9-C4	5.15	108.46	106.40
1	A	1581	A	C4-N9-C1'	5.14	135.56	126.30
1	A	2349	A	C4-N9-C1'	5.14	135.56	126.30
1	A	1705	C	N3-C2-O2	-5.14	118.30	121.90
2	B	62	U	N3-C2-O2	-5.13	118.61	122.20
1	A	1016	U	N3-C2-O2	-5.13	118.61	122.20
1	A	1715	C	N3-C2-O2	-5.13	118.31	121.90
1	A	2129	G	C6-C5-N7	-5.13	127.33	130.40
1	A	1184	G	C6-C5-N7	-5.12	127.33	130.40
1	A	1509	C	C6-N1-C2	-5.12	118.25	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	969	C	N1-C2-O2	5.12	121.97	118.90
1	A	2841	C	N1-C2-O2	5.11	121.97	118.90
1	A	2158	C	C5-C6-N1	5.11	123.55	121.00
1	A	696	C	N3-C2-O2	-5.11	118.33	121.90
2	B	19	G	C4-C5-N7	5.11	112.84	110.80
1	A	1670	C	C6-N1-C2	-5.10	118.26	120.30
1	A	903	G	N3-C4-N9	5.10	129.06	126.00
1	A	1770	C	N3-C2-O2	-5.10	118.33	121.90
1	A	1372	C	N3-C2-O2	-5.10	118.33	121.90
1	A	2795	G	C4-C5-N7	5.10	112.84	110.80
1	A	514	G	C5-C6-O6	-5.09	125.55	128.60
1	A	788	G	C6-C5-N7	-5.09	127.35	130.40
1	A	1438	C	P-O3'-C3'	5.09	125.80	119.70
1	A	1720	C	C6-N1-C2	-5.08	118.27	120.30
1	A	1452	C	N3-C2-O2	-5.08	118.34	121.90
1	A	153	C	N3-C2-O2	-5.07	118.35	121.90
1	A	2640	C	C6-N1-C2	-5.07	118.27	120.30
1	A	1433	U	N1-C2-O2	5.07	126.35	122.80
1	A	2866	C	C6-N1-C2	-5.07	118.27	120.30
1	A	892	U	N3-C2-O2	-5.07	118.65	122.20
1	A	1241	C	C6-N1-C2	-5.07	118.27	120.30
1	A	1652	C	OP2-P-O3'	5.07	116.34	105.20
1	A	442	C	C6-N1-C1'	-5.06	114.72	120.80
1	A	1333	C	C6-N1-C1'	-5.06	114.72	120.80
1	A	2028	C	C6-N1-C2	-5.06	118.28	120.30
1	A	1521	G	N3-C2-N2	-5.06	116.36	119.90
1	A	1527	C	C6-N1-C2	-5.06	118.28	120.30
1	A	469	A	C4-N9-C1'	5.06	135.41	126.30
1	A	549	A	P-O3'-C3'	5.06	125.77	119.70
1	A	201	C	N1-C2-O2	5.06	121.93	118.90
1	A	1683	C	N3-C2-O2	-5.06	118.36	121.90
1	A	1832	A	N7-C8-N9	5.05	116.32	113.80
1	A	732	A	N9-C4-C5	-5.04	103.78	105.80
1	A	1673	G	N1-C6-O6	5.04	122.92	119.90
1	A	1368	U	N3-C2-O2	-5.04	118.67	122.20
1	A	2031	G	C6-C5-N7	-5.04	127.38	130.40
1	A	2789	C	N1-C2-O2	5.04	121.92	118.90
1	A	1372	C	N1-C2-O2	5.04	121.92	118.90
1	A	1550	C	N1-C2-O2	5.04	121.92	118.90
1	A	1211	C	N3-C2-O2	-5.03	118.38	121.90
1	A	2031	G	C4-C5-N7	5.03	112.81	110.80
2	B	81	G	C5-C6-O6	-5.03	125.58	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	492	C	C6-N1-C2	-5.03	118.29	120.30
1	A	854	U	N1-C2-O2	5.03	126.32	122.80
1	A	878	G	N3-C4-C5	-5.02	126.09	128.60
1	A	1600	G	N7-C8-N9	5.02	115.61	113.10
2	B	15	C	N1-C2-O2	5.02	121.91	118.90
1	A	492	C	C2-N1-C1'	5.02	124.32	118.80
1	A	1148	C	C2-N1-C1'	5.01	124.31	118.80
1	A	2717	G	C6-C5-N7	-5.01	127.39	130.40
1	A	419	G	OP2-P-O3'	5.01	116.22	105.20
2	B	19	G	N3-C4-C5	-5.01	126.10	128.60
1	A	698	C	N1-C2-O2	5.00	121.90	118.90
1	A	1715	C	N1-C2-O2	5.00	121.90	118.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	E	41	ARG	Peptide

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	57112	0	28735	1143	0
2	B	2395	0	1212	66	0
3	C	2010	0	2100	138	0
4	D	1569	0	1635	190	0
5	E	1511	0	1598	59	0
6	F	1090	0	1136	203	0
7	G	829	0	851	51	0
8	J	1119	0	1159	94	0
9	K	920	0	977	75	0
10	L	904	0	957	77	0
11	N	947	0	978	33	0
12	O	775	0	807	79	0
13	P	936	0	1008	92	0
14	Q	940	0	1005	76	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	R	781	0	820	66	0
16	S	842	0	899	71	0
17	T	724	0	768	15	0
18	U	691	0	755	87	0
19	V	604	0	614	59	0
20	Z	455	0	491	19	0
21	b	418	0	439	0	0
22	Y	530	0	568	34	0
23	d	359	0	398	0	0
24	W	1958	0	1979	203	0
25	W	32	0	13	10	0
All	All	80451	0	51902	2529	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 22.

All (2529) 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)
10:L:117:LEU:CD2	10:L:136:VAL:HA	1.29	1.58
6:F:122:PHE:CE2	6:F:167:ARG:NH2	1.69	1.57
8:J:26:LEU:HA	8:J:29:LEU:CD1	1.40	1.50
13:P:33:VAL:HG21	13:P:77:PHE:CZ	1.48	1.47
24:W:81:ARG:NH1	24:W:103:ILE:CG1	1.79	1.45
13:P:94:LYS:HD2	13:P:118:ARG:NH2	1.18	1.42
7:G:87:GLY:CA	7:G:166:GLU:HG3	1.49	1.39
18:U:84:LYS:O	18:U:84:LYS:CE	1.69	1.39
24:W:58:ASN:ND2	24:W:132:GLY:CA	1.88	1.37
6:F:68:THR:CG2	6:F:88:LYS:HG3	1.54	1.36
6:F:122:PHE:HE2	6:F:167:ARG:NH2	0.85	1.34
2:B:55:A:C5'	6:F:23:ASP:CB	2.06	1.34
12:O:95:PHE:CE2	12:O:106:VAL:CG1	2.11	1.34
1:A:2280:G:O6	19:V:12:LYS:HB3	1.19	1.34
2:B:55:A:H5''	6:F:23:ASP:CB	1.55	1.33
1:A:1397:G:N2	1:A:1411:U:C5	1.95	1.33
1:A:1527:C:O2	1:A:1558:G:N2	1.60	1.33
2:B:55:A:C5'	6:F:23:ASP:HB3	1.59	1.32
1:A:2126:G:N2	1:A:2221:C:O2	1.60	1.32
24:W:58:ASN:ND2	24:W:132:GLY:HA3	0.99	1.31
1:A:2687:C:O2	1:A:2692:G:N2	1.65	1.30
10:L:137:GLU:OE1	10:L:143:ALA:HB2	1.13	1.30

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:76:TYR:CD1	8:J:85:LEU:HD11	1.67	1.29
13:P:33:VAL:CG2	13:P:77:PHE:CZ	2.14	1.29
12:O:95:PHE:HE2	12:O:106:VAL:CG1	1.41	1.29
4:D:83:LEU:CD2	4:D:203:LYS:HD2	1.60	1.28
10:L:79:LEU:CD2	10:L:117:LEU:HB2	1.64	1.27
12:O:35:ARG:HH12	12:O:105:ARG:NE	1.31	1.27
7:G:87:GLY:HA3	7:G:166:GLU:CG	1.65	1.27
8:J:126:TYR:CE2	8:J:132:PRO:HD2	1.69	1.26
6:F:8:TYR:CE1	6:F:30:LYS:NZ	2.03	1.26
4:D:10:ILE:HD11	4:D:29:GLU:OE1	1.28	1.26
1:A:2280:G:O6	19:V:12:LYS:CB	1.85	1.25
24:W:31:VAL:HG13	24:W:39:SER:OG	1.33	1.25
1:A:495:U:O2	5:E:84:ARG:HD2	1.29	1.25
1:A:2777:A:O2'	7:G:64:ALA:CA	1.83	1.25
13:P:94:LYS:CD	13:P:118:ARG:NH2	1.98	1.25
16:S:36:LEU:HD11	16:S:47:ILE:CG2	1.67	1.24
14:Q:95:LEU:HD12	15:R:11:GLN:CB	1.68	1.23
14:Q:95:LEU:HD11	15:R:11:GLN:O	1.37	1.23
6:F:122:PHE:HE2	6:F:167:ARG:CZ	1.52	1.22
24:W:154:ILE:HD11	24:W:172:THR:CG2	1.70	1.21
10:L:117:LEU:CD2	10:L:136:VAL:CA	2.19	1.20
24:W:67:VAL:HG21	24:W:276:SER:CB	1.69	1.20
6:F:108:LEU:CD1	6:F:176:PRO:HG3	1.72	1.18
1:A:2777:A:O2'	7:G:64:ALA:HA	1.37	1.18
3:C:94:ILE:HD11	3:C:104:ILE:CD1	1.74	1.17
24:W:67:VAL:HG21	24:W:276:SER:OG	1.40	1.17
20:Z:6:ILE:HG22	20:Z:28:LEU:HD11	1.26	1.17
10:L:117:LEU:HD23	10:L:136:VAL:HA	1.17	1.17
4:D:16:PHE:CZ	13:P:80:HIS:O	1.98	1.16
12:O:35:ARG:NH1	12:O:105:ARG:HG3	1.58	1.16
8:J:26:LEU:CA	8:J:29:LEU:HD11	1.76	1.16
9:K:76:TYR:HB2	13:P:76:THR:HB	1.27	1.16
10:L:117:LEU:HD21	10:L:136:VAL:HA	1.17	1.16
14:Q:92:ARG:HB2	15:R:11:GLN:CG	1.74	1.16
7:G:78:GLU:HB3	7:G:84:PHE:HZ	1.08	1.16
1:A:673:A:C8	10:L:76:VAL:HG11	1.81	1.15
2:B:41:C:H5''	6:F:63:GLN:OE1	1.43	1.14
1:A:1659:A:N6	16:S:91:GLY:HA2	1.62	1.14
1:A:2280:G:C5	19:V:12:LYS:HE3	1.83	1.14
2:B:55:A:C5'	6:F:23:ASP:HB2	1.78	1.14
4:D:27:VAL:HG21	13:P:8:ILE:HD11	1.30	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Y:21:LEU:CD1	22:Y:53:MET:HE1	1.78	1.14
12:O:95:PHE:CE2	12:O:106:VAL:HG12	1.75	1.13
9:K:62:ILE:HA	9:K:84:CYS:SG	1.88	1.13
14:Q:92:ARG:CB	15:R:11:GLN:HG3	1.77	1.13
24:W:154:ILE:CD1	24:W:172:THR:HG21	1.78	1.12
6:F:3:ARG:NH2	6:F:101:ASP:OD2	1.82	1.12
18:U:45:SER:HG	18:U:55:GLY:N	1.46	1.12
4:D:30:ALA:HB1	4:D:53:PHE:CZ	1.84	1.12
16:S:86:ARG:NH2	16:S:96:ILE:HD11	1.64	1.12
18:U:41:VAL:HG12	18:U:43:LYS:HG3	1.32	1.12
1:A:738:C:C5'	3:C:217:ARG:HH22	1.62	1.12
24:W:67:VAL:CG2	24:W:276:SER:OG	1.98	1.12
24:W:81:ARG:NH1	24:W:103:ILE:HG12	1.64	1.12
24:W:127:GLY:O	24:W:175:ILE:HB	1.48	1.11
1:A:2282:G:H1	19:V:13:LYS:HG3	1.00	1.11
4:D:7:GLY:HA3	4:D:30:ALA:HB2	1.32	1.11
1:A:787:C:H1'	1:A:2010:A:N7	1.66	1.11
1:A:2342:C:H5''	6:F:88:LYS:HD3	1.33	1.10
1:A:702:A:H4'	1:A:703:G:H5'	1.16	1.10
2:B:53:U:O2'	6:F:26:MET:HG2	1.49	1.10
1:A:699:A:H5''	1:A:700:U:OP2	1.50	1.10
1:A:1527:C:O2	1:A:1558:G:C2	2.05	1.10
18:U:80:ARG:O	18:U:94:ALA:CB	1.98	1.10
1:A:2282:G:O6	19:V:13:LYS:HA	1.52	1.09
5:E:51:VAL:HG21	5:E:91:GLY:HA3	1.34	1.09
10:L:79:LEU:HD21	10:L:117:LEU:CB	1.81	1.09
1:A:920:G:C6	1:A:946:G:O6	2.05	1.09
4:D:10:ILE:HB	4:D:27:VAL:HG11	1.25	1.09
6:F:63:GLN:HG2	6:F:91:LEU:HB3	1.16	1.09
4:D:55:ASP:HA	4:D:77:LYS:HA	1.19	1.09
6:F:68:THR:HG22	6:F:88:LYS:HE2	1.09	1.09
24:W:81:ARG:HH12	24:W:103:ILE:HG13	0.94	1.09
3:C:94:ILE:HD11	3:C:104:ILE:HD11	1.33	1.08
18:U:84:LYS:HE3	18:U:84:LYS:C	1.73	1.08
24:W:126:ILE:CG2	24:W:175:ILE:HD11	1.82	1.08
1:A:738:C:H5'	3:C:217:ARG:NH2	1.66	1.08
2:B:53:U:H1'	6:F:26:MET:SD	1.91	1.08
24:W:81:ARG:HH11	24:W:103:ILE:CD1	1.66	1.08
22:Y:21:LEU:HD12	22:Y:53:MET:HE1	1.18	1.07
16:S:36:LEU:HD11	16:S:47:ILE:HG21	1.29	1.07
1:A:1288:G:H21	5:E:88:VAL:HG21	0.98	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:41:C:C5'	6:F:63:GLN:OE1	2.02	1.07
2:B:55:A:H5'	6:F:23:ASP:CB	1.84	1.06
4:D:50:GLN:HG2	4:D:82:GLU:OE1	1.52	1.06
14:Q:95:LEU:HD12	15:R:11:GLN:HB3	1.27	1.06
14:Q:108:GLN:OE1	15:R:45:ASN:ND2	1.88	1.06
1:A:2342:C:C5'	6:F:88:LYS:HD3	1.85	1.06
4:D:10:ILE:CD1	4:D:29:GLU:OE1	2.02	1.06
18:U:82:GLY:N	18:U:93:VAL:O	1.89	1.06
7:G:78:GLU:HB3	7:G:84:PHE:CZ	1.91	1.05
9:K:22:ILE:HD12	9:K:40:VAL:HG12	1.33	1.05
13:P:33:VAL:CG2	13:P:77:PHE:CE2	2.38	1.05
8:J:24:LYS:O	8:J:29:LEU:HD21	1.55	1.05
4:D:11:GLY:H	4:D:27:VAL:HB	1.16	1.05
4:D:83:LEU:HD22	4:D:203:LYS:HD2	1.13	1.05
1:A:2667:G:OP2	4:D:84:ARG:NH1	1.90	1.05
11:N:28:GLU:HG3	11:N:119:LEU:HD12	1.38	1.05
24:W:81:ARG:NH1	24:W:103:ILE:HG13	1.50	1.05
15:R:48:VAL:HG22	15:R:53:VAL:HG23	1.06	1.04
14:Q:95:LEU:HD11	15:R:11:GLN:C	1.76	1.04
6:F:63:GLN:HG2	6:F:91:LEU:CB	1.86	1.04
6:F:126:GLY:O	6:F:158:THR:OG1	1.74	1.04
9:K:25:LEU:CB	9:K:38:VAL:HG13	1.88	1.04
16:S:36:LEU:CD1	16:S:47:ILE:HG22	1.88	1.04
1:A:2342:C:O2'	6:F:37:ASN:ND2	1.91	1.04
8:J:76:TYR:HD1	8:J:85:LEU:HD11	0.90	1.04
19:V:39:VAL:CG2	19:V:75:VAL:HG23	1.88	1.04
12:O:95:PHE:CZ	12:O:106:VAL:HG13	1.93	1.03
1:A:1527:C:C2	1:A:1558:G:N2	2.26	1.03
19:V:53:ILE:HG13	19:V:67:LEU:HD11	1.36	1.03
1:A:673:A:H8	10:L:76:VAL:HG11	1.23	1.02
1:A:2777:A:O2'	7:G:64:ALA:C	1.98	1.02
6:F:4:LEU:CD2	6:F:97:TYR:O	2.07	1.02
1:A:2703:G:H4'	9:K:30:ARG:HD3	1.37	1.02
2:B:53:U:O2'	6:F:26:MET:CG	2.07	1.02
22:Y:21:LEU:CD1	22:Y:53:MET:CE	2.37	1.02
1:A:2592:U:H4'	9:K:28:SER:OG	1.58	1.02
6:F:63:GLN:CB	6:F:90:THR:O	2.06	1.02
6:F:69:ARG:HA	6:F:84:PRO:HA	1.38	1.02
6:F:108:LEU:HD12	6:F:176:PRO:HG3	1.42	1.02
1:A:1288:G:N2	5:E:88:VAL:HG21	1.74	1.02
6:F:68:THR:HG22	6:F:88:LYS:CE	1.89	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:84:LYS:H	18:U:93:VAL:CG1	1.72	1.02
12:O:95:PHE:CE2	12:O:106:VAL:HG13	1.91	1.01
1:A:342:A:O5'	18:U:95:LYS:NZ	1.93	1.01
1:A:1397:G:C2	1:A:1411:U:H5	1.78	1.01
4:D:10:ILE:HB	4:D:27:VAL:CG1	1.91	1.01
4:D:30:ALA:CA	4:D:53:PHE:HZ	1.73	1.01
16:S:36:LEU:CD1	16:S:47:ILE:CG2	2.39	1.01
22:Y:21:LEU:HD12	22:Y:53:MET:CE	1.89	1.01
1:A:2282:G:N1	19:V:13:LYS:HG3	1.73	1.01
1:A:2777:A:O2'	7:G:64:ALA:O	1.77	1.01
1:A:342:A:C5'	18:U:95:LYS:NZ	2.24	1.00
1:A:2342:C:H5''	6:F:88:LYS:CD	1.90	1.00
1:A:2280:G:C6	19:V:12:LYS:HE3	1.94	1.00
1:A:1861:C:O2	1:A:2002:G:N2	1.94	1.00
6:F:8:TYR:HE1	6:F:30:LYS:NZ	1.48	1.00
19:V:39:VAL:HG21	19:V:75:VAL:CG2	1.91	1.00
1:A:669:C:H2'	1:A:670:C:C6	1.97	1.00
6:F:68:THR:CG2	6:F:88:LYS:CG	2.38	1.00
20:Z:8:LEU:HD23	20:Z:54:VAL:HG13	1.42	0.99
2:B:53:U:O2'	6:F:26:MET:SD	2.20	0.99
1:A:2282:G:H1	19:V:13:LYS:CG	1.74	0.99
8:J:26:LEU:CA	8:J:29:LEU:CD1	2.37	0.99
8:J:76:TYR:HD1	8:J:85:LEU:CD1	1.75	0.99
6:F:68:THR:HG23	6:F:88:LYS:HG3	1.43	0.99
1:A:2823:C:O2	1:A:2828:G:N2	1.93	0.99
8:J:126:TYR:CE2	8:J:132:PRO:CD	2.45	0.99
6:F:68:THR:HG21	6:F:88:LYS:HG3	1.41	0.99
10:L:117:LEU:HD23	10:L:136:VAL:CA	1.87	0.99
1:A:683:A:H8	10:L:114:ASN:OD1	1.45	0.98
24:W:127:GLY:H	24:W:175:ILE:CG1	1.76	0.98
4:D:30:ALA:CB	4:D:53:PHE:CZ	2.46	0.98
6:F:4:LEU:HD23	6:F:97:TYR:O	1.63	0.98
13:P:33:VAL:HG21	13:P:77:PHE:CE2	1.98	0.98
19:V:39:VAL:HG21	19:V:75:VAL:HG23	1.01	0.98
1:A:1858:A:N7	1:A:1859:C:C4	2.32	0.98
19:V:80:PHE:CZ	19:V:86:LYS:HD2	1.99	0.98
24:W:31:VAL:CG1	24:W:39:SER:OG	2.12	0.98
6:F:4:LEU:HD23	6:F:97:TYR:HA	1.46	0.98
18:U:82:GLY:CA	18:U:93:VAL:O	2.11	0.98
2:B:55:A:H5''	6:F:23:ASP:HB3	1.02	0.97
10:L:137:GLU:OE1	10:L:143:ALA:CB	2.10	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:67:VAL:HG21	24:W:276:SER:HB2	1.46	0.97
15:R:7:THR:HG21	15:R:35:PHE:CD1	2.00	0.97
24:W:81:ARG:HH11	24:W:103:ILE:CG1	1.58	0.97
1:A:342:A:H5''	18:U:95:LYS:NZ	1.80	0.97
24:W:31:VAL:HG13	24:W:39:SER:HG	1.16	0.97
1:A:2552:G:O6	1:A:2569:C:N4	1.97	0.97
2:B:28:C:O2	2:B:52:G:N2	1.96	0.97
8:J:26:LEU:HB2	8:J:63:ILE:CG2	1.93	0.97
8:J:26:LEU:HD12	8:J:102:LEU:HD13	1.46	0.97
24:W:125:ILE:HD13	24:W:136:LEU:HD23	1.44	0.97
1:A:2557:U:H3	1:A:2564:G:H22	1.11	0.96
15:R:22:ILE:HD11	15:R:95:VAL:HB	1.45	0.96
4:D:30:ALA:HA	4:D:53:PHE:HZ	1.27	0.96
1:A:2280:G:N7	19:V:12:LYS:CE	2.29	0.96
12:O:95:PHE:CZ	12:O:106:VAL:CG1	2.48	0.96
1:A:683:A:OP2	10:L:112:LEU:HD22	1.66	0.96
4:D:49:ILE:HD13	4:D:91:TYR:CG	2.01	0.96
14:Q:95:LEU:HD12	15:R:11:GLN:HB2	1.47	0.95
6:F:4:LEU:HD23	6:F:97:TYR:CA	1.96	0.95
24:W:81:ARG:HH11	24:W:103:ILE:HD11	1.31	0.95
1:A:1553:A:N3	1:A:1555:A:N6	2.14	0.95
15:R:48:VAL:HG22	15:R:53:VAL:CG2	1.96	0.95
8:J:32:GLU:HG2	8:J:143:LEU:HG	1.49	0.95
2:B:41:C:H1'	6:F:92:ARG:HB2	1.48	0.95
6:F:34:ILE:CD1	6:F:96:MET:SD	2.54	0.95
24:W:126:ILE:HG21	24:W:175:ILE:HD11	1.48	0.94
1:A:1397:G:N2	1:A:1411:U:H5	1.44	0.94
4:D:35:VAL:HG21	4:D:91:TYR:HD1	1.31	0.94
24:W:126:ILE:HB	24:W:175:ILE:CG1	1.96	0.94
6:F:63:GLN:HG3	6:F:91:LEU:HA	1.48	0.94
10:L:125:ALA:HB3	10:L:128:PHE:CE1	2.01	0.94
1:A:77:U:H4'	22:Y:2:LYS:HG3	1.49	0.94
1:A:925:A:H62	1:A:947:A:C1'	1.79	0.94
6:F:132:ILE:HD13	6:F:154:ILE:HG13	1.50	0.94
8:J:26:LEU:HB2	8:J:63:ILE:HG21	1.46	0.94
1:A:920:G:O6	1:A:946:G:O6	1.86	0.94
1:A:925:A:H62	1:A:947:A:H1'	1.32	0.94
15:R:31:GLU:HG2	15:R:32:THR:H	1.29	0.94
16:S:86:ARG:HH21	16:S:96:ILE:CD1	1.79	0.94
19:V:67:LEU:HD13	19:V:87:VAL:HG11	1.49	0.94
24:W:81:ARG:NH1	24:W:103:ILE:CD1	2.27	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:87:GLY:CA	7:G:166:GLU:CG	2.33	0.93
10:L:117:LEU:HD23	10:L:135:ALA:O	1.68	0.93
4:D:7:GLY:HA2	4:D:53:PHE:CE2	2.04	0.93
8:J:126:TYR:HE2	8:J:132:PRO:HD2	1.13	0.93
1:A:2361:C:OP1	19:V:84:ARG:NH1	2.02	0.93
1:A:2823:C:N3	1:A:2828:G:N1	2.17	0.93
4:D:29:GLU:HB3	4:D:185:LEU:CD2	1.98	0.93
3:C:173:LEU:CD2	3:C:183:MET:HG2	1.99	0.92
24:W:58:ASN:HD21	24:W:132:GLY:CA	1.59	0.92
4:D:32:PRO:HG3	4:D:98:LYS:HG2	1.51	0.92
13:P:94:LYS:CD	13:P:118:ARG:HH21	1.71	0.92
18:U:41:VAL:CG1	18:U:43:LYS:HG3	1.99	0.92
16:S:86:ARG:NH2	16:S:96:ILE:CD1	2.33	0.92
19:V:80:PHE:CE2	19:V:86:LYS:HG3	2.05	0.92
1:A:1397:G:N2	1:A:1411:U:C6	2.37	0.92
6:F:34:ILE:HD12	6:F:96:MET:SD	2.09	0.92
6:F:68:THR:HG21	6:F:88:LYS:CG	1.99	0.92
24:W:74:HIS:O	24:W:78:GLN:HG3	1.69	0.92
1:A:495:U:O2	5:E:84:ARG:CD	2.16	0.91
6:F:63:GLN:CG	6:F:91:LEU:HA	2.00	0.91
15:R:24:LYS:HD2	15:R:91:PRO:HG3	1.50	0.91
9:K:58:VAL:HG12	9:K:59:LYS:N	1.83	0.91
1:A:2777:A:O4'	7:G:68:THR:CG2	2.19	0.91
9:K:58:VAL:HG12	9:K:59:LYS:H	1.35	0.91
12:O:35:ARG:NH1	12:O:105:ARG:NE	2.17	0.91
1:A:2230:C:O2	1:A:2251:G:N2	2.03	0.91
12:O:35:ARG:NH1	12:O:105:ARG:CG	2.33	0.91
1:A:2039:G:OP2	16:S:41:ARG:NH1	2.04	0.91
4:D:83:LEU:CD2	4:D:203:LYS:CD	2.48	0.91
12:O:35:ARG:HH11	12:O:105:ARG:HG3	1.23	0.91
24:W:126:ILE:CB	24:W:175:ILE:HD11	2.01	0.91
1:A:1659:A:H62	16:S:91:GLY:HA2	1.31	0.90
5:E:51:VAL:CG2	5:E:91:GLY:HA3	2.02	0.90
1:A:1529:G:N1	1:A:1552:C:N3	2.19	0.90
6:F:38:MET:HE1	6:F:57:LEU:HD13	1.54	0.90
6:F:108:LEU:HD11	6:F:176:PRO:HG3	1.50	0.90
4:D:27:VAL:HG21	13:P:8:ILE:CD1	2.02	0.90
1:A:2093:C:H42	1:A:2475:G:H1	1.20	0.90
24:W:172:THR:N	24:W:173:PRO:CD	2.34	0.90
4:D:83:LEU:HD22	4:D:203:LYS:CD	2.02	0.89
14:Q:95:LEU:CD1	15:R:11:GLN:CB	2.49	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:S:12:ILE:HD13	16:S:43:ALA:HB2	1.55	0.89
18:U:84:LYS:O	18:U:84:LYS:HE3	0.72	0.89
1:A:2777:A:O4'	7:G:68:THR:HG22	1.71	0.89
1:A:683:A:C8	10:L:114:ASN:OD1	2.25	0.89
9:K:76:TYR:HB2	13:P:76:THR:CB	2.03	0.89
12:O:53:LEU:O	12:O:88:LYS:NZ	2.05	0.89
11:N:37:ALA:HB1	11:N:117:ILE:HD11	1.52	0.89
1:A:738:C:H5'	3:C:217:ARG:HH22	1.25	0.88
6:F:122:PHE:CE2	6:F:167:ARG:CZ	2.39	0.88
13:P:33:VAL:HG22	13:P:77:PHE:CZ	2.07	0.88
8:J:26:LEU:HA	8:J:29:LEU:HD11	0.89	0.88
8:J:57:ILE:HD12	8:J:125:VAL:HG22	1.52	0.88
1:A:1830:G:OP2	3:C:153:GLN:NE2	2.06	0.88
1:A:2592:U:C4'	9:K:28:SER:OG	2.22	0.88
14:Q:92:ARG:HB2	15:R:11:GLN:HG3	0.91	0.88
10:L:117:LEU:HD22	10:L:136:VAL:HG12	1.56	0.87
15:R:48:VAL:HG12	15:R:50:ASN:O	1.75	0.87
15:R:48:VAL:CG2	15:R:53:VAL:HG23	1.99	0.87
4:D:55:ASP:HA	4:D:77:LYS:CA	2.02	0.87
9:K:25:LEU:HB3	9:K:38:VAL:HG13	1.53	0.87
13:P:33:VAL:HG21	13:P:77:PHE:HZ	0.90	0.87
16:S:86:ARG:HH21	16:S:96:ILE:HD11	1.32	0.87
1:A:787:C:H1'	1:A:2010:A:C8	2.09	0.87
1:A:673:A:C8	10:L:76:VAL:CG1	2.57	0.87
4:D:30:ALA:CA	4:D:53:PHE:CZ	2.57	0.87
13:P:12:THR:HG22	13:P:58:ILE:HD11	1.56	0.87
1:A:1353:C:H42	1:A:1377:G:H1	1.23	0.87
1:A:1858:A:N7	1:A:1859:C:N4	2.23	0.87
1:A:2809:G:OP2	8:J:121:LYS:HE2	1.75	0.87
6:F:4:LEU:HG	6:F:97:TYR:HD1	1.37	0.87
4:D:49:ILE:CD1	4:D:91:TYR:CG	2.58	0.86
8:J:24:LYS:O	8:J:29:LEU:CD2	2.23	0.86
24:W:154:ILE:HD11	24:W:172:THR:HG21	0.89	0.86
8:J:25:THR:O	8:J:29:LEU:HG	1.75	0.86
6:F:5:LYS:NZ	6:F:94:GLU:OE2	2.07	0.86
12:O:35:ARG:HH12	12:O:105:ARG:HE	1.20	0.86
1:A:702:A:H4'	1:A:703:G:C5'	2.04	0.85
5:E:81:PRO:HB3	5:E:89:VAL:HG22	1.56	0.85
10:L:79:LEU:HD21	10:L:117:LEU:HB2	0.89	0.85
18:U:80:ARG:O	18:U:94:ALA:HB2	1.76	0.85
1:A:2284:G:H1	1:A:2304:C:H42	1.20	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:49:ILE:HD13	4:D:91:TYR:CD1	2.11	0.85
8:J:44:THR:HG22	14:Q:100:VAL:HG12	1.59	0.85
12:O:69:GLY:O	12:O:105:ARG:NH1	2.09	0.85
1:A:1659:A:N6	16:S:91:GLY:CA	2.39	0.85
1:A:2342:C:H4'	6:F:37:ASN:OD1	1.77	0.85
1:A:2777:A:C1'	7:G:68:THR:CG2	2.55	0.85
2:B:55:A:H8	6:F:24:SER:OG	1.59	0.85
7:G:87:GLY:C	7:G:166:GLU:HG2	1.97	0.85
24:W:127:GLY:H	24:W:175:ILE:HG13	1.39	0.85
18:U:80:ARG:O	18:U:94:ALA:HB1	1.75	0.85
24:W:172:THR:H	24:W:173:PRO:CD	1.89	0.85
8:J:26:LEU:HA	8:J:29:LEU:HD12	1.59	0.85
1:A:2280:G:C6	19:V:12:LYS:HB3	2.11	0.85
1:A:377:G:O2'	1:A:378:C:H6	1.60	0.84
1:A:84:A:OP2	18:U:4:LYS:HD3	1.76	0.84
1:A:2126:G:C2	1:A:2221:C:O2	2.29	0.84
4:D:54:ASP:O	4:D:78:ARG:HG3	1.76	0.84
1:A:342:A:C5'	18:U:95:LYS:HZ2	1.84	0.84
1:A:740:A:OP1	3:C:39:LYS:HE3	1.77	0.84
24:W:191:VAL:HG11	24:W:277:PHE:HZ	1.42	0.84
6:F:69:ARG:HA	6:F:84:PRO:CA	2.05	0.84
1:A:2280:G:C5	19:V:12:LYS:CE	2.60	0.84
6:F:69:ARG:HE	6:F:82:GLY:HA2	1.43	0.84
10:L:117:LEU:HD23	10:L:135:ALA:C	1.98	0.84
12:O:101:LEU:HD23	12:O:101:LEU:H	1.41	0.84
4:D:31:ALA:N	4:D:53:PHE:CE1	2.45	0.84
24:W:58:ASN:HD21	24:W:132:GLY:HA3	1.10	0.84
4:D:11:GLY:H	4:D:27:VAL:CB	1.91	0.83
4:D:49:ILE:O	4:D:82:GLU:HA	1.77	0.83
24:W:125:ILE:HD13	24:W:136:LEU:CD2	2.08	0.83
1:A:738:C:H5''	3:C:217:ARG:HH22	1.39	0.83
1:A:920:G:O6	1:A:946:G:C6	2.31	0.83
1:A:2687:C:O2	1:A:2692:G:C2	2.31	0.83
24:W:58:ASN:CG	24:W:131:VAL:O	2.16	0.83
1:A:1858:A:C5	1:A:1859:C:C4	2.66	0.83
2:B:55:A:N6	6:F:26:MET:CE	2.40	0.83
3:C:94:ILE:HD11	3:C:104:ILE:HD13	1.60	0.83
1:A:341:G:OP1	18:U:82:GLY:O	1.97	0.83
1:A:787:C:C1'	1:A:2010:A:N7	2.41	0.83
1:A:699:A:C5'	1:A:700:U:OP2	2.26	0.83
24:W:37:MET:CE	24:W:71:TRP:CZ3	2.61	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:126:ILE:HB	24:W:175:ILE:CD1	2.09	0.83
1:A:342:A:C5'	18:U:95:LYS:HZ1	1.91	0.83
4:D:107:ILE:HG22	4:D:205:ALA:CB	2.08	0.83
1:A:580:U:H2'	1:A:581:C:H6	1.43	0.83
14:Q:108:GLN:OE1	15:R:45:ASN:CG	2.16	0.83
2:B:35:C:O2'	12:O:103:HIS:NE2	2.11	0.82
6:F:4:LEU:HD23	6:F:97:TYR:C	1.99	0.82
12:O:28:ARG:HA	12:O:92:ASP:O	1.78	0.82
12:O:75:THR:HG21	12:O:108:ALA:CB	2.09	0.82
1:A:343:A:OP2	18:U:95:LYS:NZ	2.12	0.82
1:A:1390:C:H2'	1:A:1391:U:C6	2.13	0.82
7:G:87:GLY:C	7:G:166:GLU:CG	2.48	0.82
1:A:920:G:C5	1:A:946:G:O6	2.31	0.82
18:U:82:GLY:HA3	18:U:93:VAL:O	1.77	0.82
1:A:2777:A:C1'	7:G:68:THR:HG23	2.10	0.82
1:A:2340:A:C8	6:F:85:ILE:HD13	2.14	0.82
14:Q:95:LEU:CD1	15:R:11:GLN:O	2.26	0.82
1:A:1847:U:C6	3:C:153:GLN:O	2.33	0.81
19:V:80:PHE:CZ	19:V:86:LYS:CD	2.63	0.81
3:C:173:LEU:HD21	3:C:183:MET:HG2	1.59	0.81
6:F:122:PHE:CE2	6:F:167:ARG:NE	2.47	0.81
11:N:37:ALA:CB	11:N:117:ILE:HD11	2.11	0.81
1:A:647:A:N6	1:A:702:A:C8	2.49	0.81
3:C:94:ILE:CD1	3:C:104:ILE:CD1	2.59	0.81
13:P:64:VAL:HB	13:P:75:ARG:HB3	1.61	0.81
4:D:30:ALA:HA	4:D:53:PHE:CZ	2.15	0.81
9:K:2:ILE:HD13	9:K:8:LEU:HD21	1.63	0.81
15:R:14:VAL:CG1	15:R:97:ILE:HG13	2.11	0.81
6:F:68:THR:CG2	6:F:88:LYS:HE2	2.03	0.81
9:K:25:LEU:HB2	9:K:38:VAL:O	1.80	0.81
24:W:58:ASN:OD1	24:W:131:VAL:O	1.99	0.81
24:W:126:ILE:HB	24:W:175:ILE:HD11	1.60	0.81
1:A:2359:G:N2	1:A:2414:C:O2	2.12	0.81
8:J:59:ASN:OD1	8:J:129:SER:HB3	1.80	0.81
1:A:2536:C:N4	1:A:2611:G:C6	2.49	0.80
6:F:63:GLN:HB3	6:F:90:THR:O	1.81	0.80
1:A:380:C:H5'	18:U:2:HIS:CE1	2.16	0.80
4:D:34:VAL:HG11	4:D:74:THR:HG21	1.64	0.80
1:A:77:U:H4'	22:Y:2:LYS:CG	2.12	0.80
4:D:35:VAL:CG2	4:D:91:TYR:HD1	1.95	0.80
6:F:104:ILE:HA	6:F:108:LEU:HB2	1.61	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:43:MET:HB2	24:W:178:PRO:HG3	1.64	0.80
24:W:126:ILE:HB	24:W:175:ILE:HG13	1.64	0.80
1:A:2681:U:H3	1:A:2697:G:H1	1.30	0.80
10:L:79:LEU:CD2	10:L:117:LEU:CB	2.49	0.80
13:P:94:LYS:CD	13:P:118:ARG:HH22	1.91	0.79
1:A:1527:C:H1'	1:A:1558:G:N2	1.96	0.79
1:A:2703:G:C4'	9:K:30:ARG:HD3	2.12	0.79
4:D:55:ASP:HB3	4:D:77:LYS:HG2	1.63	0.79
6:F:8:TYR:CD1	6:F:30:LYS:NZ	2.49	0.79
6:F:61:ALA:HB1	6:F:91:LEU:CD2	2.11	0.79
6:F:104:ILE:HG23	6:F:108:LEU:HD12	1.62	0.79
24:W:71:TRP:HE1	24:W:278:GLU:C	1.85	0.79
1:A:317:G:H1	1:A:403:C:H42	1.31	0.79
1:A:2093:C:N4	1:A:2475:G:H1	1.80	0.79
9:K:25:LEU:HB2	9:K:38:VAL:HG13	1.62	0.79
9:K:58:VAL:CG1	9:K:59:LYS:H	1.95	0.79
1:A:783:C:H42	1:A:807:G:H1	1.31	0.79
1:A:1858:A:C8	1:A:1859:C:C5	2.69	0.79
1:A:1517:A:H61	1:A:1567:U:H3	1.30	0.79
1:A:2280:G:O6	19:V:12:LYS:HB2	1.80	0.79
6:F:118:SER:OG	6:F:177:PHE:CD1	2.35	0.79
1:A:377:G:O2'	1:A:378:C:C6	2.33	0.79
1:A:580:U:H2'	1:A:581:C:C6	2.17	0.79
24:W:153:GLY:HA3	25:W:301:GNP:O2G	1.82	0.79
1:A:1554:U:H5''	1:A:1555:A:C8	2.17	0.79
4:D:32:PRO:CG	4:D:98:LYS:HG2	2.12	0.79
24:W:127:GLY:H	24:W:175:ILE:HG12	1.48	0.79
1:A:2777:A:H1'	7:G:68:THR:CG2	2.13	0.78
6:F:4:LEU:HG	6:F:97:TYR:CD1	2.16	0.78
1:A:2684:G:HO2'	1:A:2693:G:H1	1.31	0.78
1:A:1554:U:H5'	1:A:1555:A:N7	1.99	0.78
1:A:2557:U:H3	1:A:2564:G:N2	1.82	0.78
6:F:29:PRO:O	6:F:169:LEU:HD22	1.84	0.78
1:A:2280:G:N7	19:V:12:LYS:HE2	1.97	0.78
3:C:205:ILE:HG23	3:C:210:ARG:HB3	1.64	0.78
12:O:75:THR:HG21	12:O:108:ALA:HB3	1.65	0.78
6:F:8:TYR:HA	6:F:12:ILE:HB	1.66	0.78
12:O:107:LYS:O	12:O:111:ASP:CG	2.22	0.78
4:D:35:VAL:CG2	4:D:91:TYR:CD1	2.67	0.78
14:Q:95:LEU:CD1	15:R:11:GLN:HB2	2.12	0.78
1:A:1362:G:H1	1:A:1370:C:H42	1.28	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:53:U:C1'	6:F:26:MET:SD	2.70	0.77
4:D:50:GLN:CG	4:D:82:GLU:OE1	2.30	0.77
6:F:69:ARG:NE	6:F:82:GLY:HA2	1.97	0.77
1:A:1551:C:H2'	1:A:1552:C:C6	2.20	0.77
24:W:156:THR:HG22	24:W:172:THR:HB	1.67	0.77
3:C:171:TYR:HE1	3:C:183:MET:SD	2.07	0.77
6:F:69:ARG:CA	6:F:84:PRO:HB3	2.14	0.77
18:U:84:LYS:H	18:U:93:VAL:HG11	1.47	0.77
18:U:84:LYS:H	18:U:93:VAL:HG12	1.50	0.77
1:A:2342:C:H1'	6:F:37:ASN:ND2	1.99	0.77
4:D:33:ASN:HB2	4:D:97:VAL:HG23	1.67	0.77
24:W:220:ARG:CZ	24:W:275:LEU:HD23	2.15	0.77
24:W:172:THR:H	24:W:173:PRO:HD3	1.48	0.77
6:F:4:LEU:HD22	6:F:97:TYR:O	1.83	0.76
1:A:77:U:O3'	22:Y:2:LYS:HG3	1.85	0.76
1:A:1526:G:N2	1:A:1558:G:N2	2.33	0.76
8:J:26:LEU:HA	8:J:29:LEU:CG	2.14	0.76
1:A:2280:G:N7	19:V:12:LYS:HE3	1.95	0.76
1:A:2777:A:H1'	7:G:68:THR:HG23	1.68	0.76
6:F:63:GLN:CG	6:F:90:THR:O	2.34	0.76
6:F:63:GLN:CG	6:F:91:LEU:HB3	2.09	0.76
1:A:925:A:N6	1:A:947:A:C1'	2.48	0.76
2:B:55:A:C8	6:F:24:SER:OG	2.39	0.76
3:C:94:ILE:CD1	3:C:104:ILE:HD13	2.15	0.76
4:D:29:GLU:CB	4:D:185:LEU:CD2	2.62	0.76
1:A:77:U:C4'	22:Y:2:LYS:HG3	2.15	0.76
3:C:171:TYR:CZ	3:C:269:PHE:CE1	2.74	0.76
10:L:137:GLU:CD	10:L:143:ALA:HB2	2.07	0.76
24:W:81:ARG:NH1	24:W:103:ILE:HD11	1.94	0.76
1:A:402:U:H2'	1:A:403:C:C6	2.21	0.75
1:A:1847:U:OP2	3:C:156:ARG:HD2	1.86	0.75
4:D:31:ALA:N	4:D:53:PHE:CZ	2.53	0.75
12:O:78:GLY:O	12:O:109:LEU:CD1	2.34	0.75
1:A:2129:G:N1	1:A:2218:U:O2	2.19	0.75
1:A:2777:A:HO2'	7:G:64:ALA:C	1.85	0.75
2:B:55:A:H5'	6:F:23:ASP:C	2.07	0.75
9:K:17:ARG:HB2	9:K:45:GLN:O	1.86	0.75
15:R:14:VAL:HG11	15:R:97:ILE:HG13	1.68	0.75
6:F:122:PHE:CZ	6:F:167:ARG:HB2	2.21	0.75
16:S:21:MET:HA	16:S:24:ILE:HD12	1.67	0.75
18:U:11:VAL:HG12	18:U:12:ILE:N	2.02	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:495:U:H1'	5:E:84:ARG:HG3	1.69	0.75
4:D:16:PHE:CE1	13:P:80:HIS:O	2.39	0.75
24:W:58:ASN:ND2	24:W:131:VAL:O	2.19	0.75
4:D:2:THR:O	4:D:86:VAL:HG13	1.86	0.75
4:D:108:VAL:O	4:D:205:ALA:HB2	1.86	0.75
24:W:151:ARG:N	24:W:152:PRO:HD2	2.02	0.75
1:A:2900:A:HO2'	13:P:5:GLN:N	1.84	0.75
4:D:6:LEU:H	4:D:33:ASN:HD21	1.35	0.75
15:R:5:ILE:HG22	15:R:7:THR:HG23	1.67	0.75
6:F:108:LEU:HD11	6:F:176:PRO:CG	2.17	0.74
15:R:7:THR:HG21	15:R:35:PHE:CG	2.21	0.74
16:S:29:VAL:HG12	16:S:55:ILE:HD11	1.69	0.74
4:D:11:GLY:N	4:D:27:VAL:HB	1.99	0.74
4:D:38:LYS:NZ	4:D:88:MET:HG2	2.02	0.74
8:J:36:ILE:CD1	8:J:141:TYR:HE2	2.00	0.74
1:A:673:A:N7	10:L:112:LEU:HD12	2.02	0.74
12:O:35:ARG:HH12	12:O:105:ARG:CD	2.01	0.74
16:S:100:THR:HG22	16:S:101:SER:N	2.02	0.74
4:D:32:PRO:CB	4:D:98:LYS:HG2	2.16	0.74
16:S:39:THR:OG1	16:S:44:SER:OG	2.05	0.74
20:Z:6:ILE:CG2	20:Z:28:LEU:HD11	2.14	0.74
24:W:58:ASN:HD22	24:W:132:GLY:CA	1.77	0.74
1:A:2132:A:H61	1:A:2215:U:H3	1.34	0.74
6:F:17:MET:SD	6:F:22:TYR:CD2	2.80	0.74
6:F:122:PHE:CD2	6:F:167:ARG:NH2	2.50	0.74
9:K:58:VAL:CG1	9:K:59:LYS:N	2.50	0.74
24:W:127:GLY:N	24:W:175:ILE:HG13	2.02	0.74
1:A:683:A:N7	10:L:114:ASN:ND2	2.35	0.74
6:F:111:VAL:HB	6:F:114:PHE:HB3	1.69	0.74
19:V:67:LEU:CD1	19:V:87:VAL:HG11	2.18	0.74
24:W:154:ILE:CD1	24:W:172:THR:CG2	2.48	0.74
4:D:55:ASP:CB	4:D:77:LYS:HG2	2.18	0.74
24:W:220:ARG:HD2	24:W:275:LEU:HD21	1.69	0.74
24:W:172:THR:N	24:W:173:PRO:HD2	2.00	0.73
9:K:69:ALA:HB1	9:K:105:GLU:OE2	1.88	0.73
6:F:63:GLN:HG2	6:F:91:LEU:CA	2.18	0.73
1:A:738:C:C5'	3:C:217:ARG:NH2	2.34	0.73
24:W:150:ASP:HB3	24:W:152:PRO:HD2	1.70	0.73
4:D:32:PRO:HB3	4:D:98:LYS:CG	2.19	0.73
24:W:129:PRO:CG	24:W:176:LEU:HD23	2.19	0.73
4:D:49:ILE:CD1	4:D:91:TYR:CD2	2.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:55:ASP:CA	4:D:77:LYS:HA	2.10	0.73
13:P:33:VAL:HG22	13:P:77:PHE:CE2	2.19	0.73
1:A:925:A:N6	1:A:947:A:N9	2.36	0.73
16:S:29:VAL:CG1	16:S:55:ILE:HD11	2.18	0.73
18:U:84:LYS:N	18:U:93:VAL:CG1	2.51	0.73
24:W:37:MET:HE3	24:W:71:TRP:HZ3	1.54	0.73
1:A:643:U:H3	1:A:705:A:H61	1.32	0.73
1:A:2670:A:H5''	8:J:79:THR:HG21	1.71	0.73
8:J:36:ILE:HD11	8:J:141:TYR:HE2	1.54	0.73
6:F:95:ARG:HG3	6:F:95:ARG:O	1.87	0.72
15:R:19:THR:HG22	15:R:96:THR:HB	1.71	0.72
15:R:31:GLU:HG2	15:R:32:THR:N	2.01	0.72
24:W:58:ASN:HD22	24:W:132:GLY:HA3	0.93	0.72
8:J:36:ILE:HD13	8:J:141:TYR:CE2	2.24	0.72
8:J:50:ASP:HB2	8:J:115:LEU:HD13	1.70	0.72
9:K:64:ARG:HB2	9:K:83:ALA:H	1.54	0.72
2:B:55:A:C4'	6:F:23:ASP:HB2	2.19	0.72
13:P:50:VAL:HG13	13:P:63:THR:O	1.89	0.72
22:Y:21:LEU:CD1	22:Y:53:MET:HE2	2.18	0.72
9:K:10:VAL:HG21	9:K:16:ALA:C	2.10	0.72
1:A:702:A:H2'	1:A:702:A:OP2	1.90	0.72
1:A:1793:G:H2'	1:A:1794:C:C6	2.24	0.72
1:A:2220:A:H2'	1:A:2221:C:C6	2.24	0.72
2:B:41:C:H5'	6:F:63:GLN:OE1	1.87	0.72
24:W:37:MET:HE3	24:W:71:TRP:CZ3	2.24	0.72
24:W:37:MET:SD	24:W:71:TRP:CH2	2.83	0.72
9:K:62:ILE:CA	9:K:84:CYS:SG	2.74	0.72
19:V:80:PHE:CE1	19:V:86:LYS:HD2	2.25	0.72
1:A:1573:C:O2	1:A:1594:G:N2	2.16	0.72
4:D:35:VAL:HG21	4:D:91:TYR:CD1	2.20	0.72
6:F:10:LYS:HG3	6:F:10:LYS:O	1.89	0.72
1:A:2342:C:C2'	6:F:37:ASN:HD21	2.01	0.72
3:C:171:TYR:CE1	3:C:183:MET:SD	2.83	0.72
6:F:61:ALA:HB1	6:F:91:LEU:HD23	1.71	0.72
6:F:63:GLN:HB2	6:F:90:THR:O	1.89	0.72
10:L:74:TYR:CZ	10:L:127:LYS:HG3	2.25	0.71
6:F:63:GLN:CG	6:F:91:LEU:CA	2.69	0.71
14:Q:90:VAL:O	14:Q:90:VAL:HG12	1.90	0.71
14:Q:95:LEU:CD1	15:R:11:GLN:C	2.57	0.71
24:W:210:LEU:HD13	24:W:237:LEU:HD22	1.70	0.71
4:D:50:GLN:HG2	4:D:82:GLU:CD	2.10	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:132:ILE:HD11	6:F:154:ILE:HB	1.71	0.71
8:J:99:GLU:OE2	8:J:127:ARG:HB2	1.89	0.71
24:W:129:PRO:CD	24:W:176:LEU:HD23	2.20	0.71
1:A:1529:G:N2	1:A:1552:C:O2	2.19	0.71
4:D:7:GLY:HA3	4:D:30:ALA:CB	2.16	0.71
14:Q:17:VAL:HG21	14:Q:32:TYR:HE1	1.55	0.71
24:W:151:ARG:N	24:W:152:PRO:CD	2.53	0.71
1:A:1858:A:C8	1:A:1859:C:C4	2.78	0.71
1:A:925:A:N6	1:A:947:A:H1'	2.05	0.71
24:W:150:ASP:CB	24:W:152:PRO:HD2	2.21	0.71
24:W:191:VAL:HG11	24:W:277:PHE:CZ	2.24	0.71
4:D:5:ILE:CG2	4:D:33:ASN:ND2	2.54	0.71
15:R:31:GLU:CG	15:R:32:THR:H	2.03	0.71
4:D:30:ALA:HB1	4:D:53:PHE:CE1	2.25	0.70
10:L:117:LEU:HD23	10:L:136:VAL:N	2.05	0.70
3:C:210:ARG:HA	3:C:213:TRP:HD1	1.55	0.70
7:G:60:LYS:NZ	7:G:60:LYS:HB3	2.05	0.70
10:L:91:VAL:HB	10:L:122:THR:O	1.91	0.70
24:W:153:GLY:N	25:W:301:GNP:O1G	2.24	0.70
1:A:795:G:H5''	16:S:89:ALA:HB2	1.73	0.70
4:D:7:GLY:HA2	4:D:53:PHE:CD2	2.26	0.70
1:A:2039:G:P	16:S:41:ARG:NH1	2.63	0.70
1:A:343:A:OP2	18:U:95:LYS:HD3	1.90	0.70
1:A:559:A:N3	14:Q:11:ARG:NH2	2.39	0.70
14:Q:95:LEU:CD1	15:R:11:GLN:HB3	2.16	0.70
2:B:55:A:N6	6:F:26:MET:HE1	2.05	0.70
3:C:205:ILE:CG2	3:C:210:ARG:HB3	2.20	0.70
24:W:129:PRO:HG3	24:W:176:LEU:HG	1.74	0.70
1:A:2039:G:H5''	16:S:42:ALA:HB2	1.74	0.70
14:Q:58:ARG:HE	14:Q:93:LYS:HE3	1.56	0.69
4:D:5:ILE:HG23	4:D:33:ASN:ND2	2.07	0.69
10:L:74:TYR:CD1	10:L:110:LYS:HB2	2.27	0.69
24:W:31:VAL:CG1	24:W:36:PRO:O	2.40	0.69
1:A:1564:C:C2	1:A:1565:U:C5	2.79	0.69
7:G:87:GLY:HA3	7:G:166:GLU:HG3	0.74	0.69
10:L:79:LEU:HD22	10:L:117:LEU:N	2.06	0.69
13:P:94:LYS:HB2	13:P:118:ARG:CZ	2.23	0.69
24:W:37:MET:CE	24:W:71:TRP:CH2	2.76	0.69
1:A:2298:A:C6	1:A:2299:G:C6	2.80	0.69
18:U:41:VAL:HG12	18:U:43:LYS:CG	2.18	0.69
1:A:2667:G:P	4:D:84:ARG:HH22	2.15	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2536:C:N4	1:A:2611:G:N1	2.41	0.69
10:L:74:TYR:OH	10:L:127:LYS:HG3	1.92	0.69
1:A:2290:C:C5	19:V:24:SER:HB2	2.28	0.69
4:D:29:GLU:HG3	4:D:29:GLU:O	1.91	0.69
4:D:29:GLU:CB	4:D:185:LEU:HD23	2.23	0.69
9:K:63:VAL:CG2	9:K:85:VAL:HG23	2.22	0.69
13:P:30:ARG:NE	13:P:47:GLU:OE1	2.26	0.69
8:J:36:ILE:CD1	8:J:141:TYR:CE2	2.76	0.68
24:W:31:VAL:HG11	24:W:36:PRO:O	1.92	0.68
1:A:1847:U:C5	3:C:153:GLN:O	2.46	0.68
24:W:220:ARG:CZ	24:W:275:LEU:CD2	2.71	0.68
1:A:2786:A:N1	7:G:68:THR:HG21	2.08	0.68
6:F:13:ALA:HB3	6:F:14:PRO:HD3	1.74	0.68
24:W:37:MET:CE	24:W:71:TRP:HZ3	2.02	0.68
13:P:94:LYS:CE	13:P:118:ARG:HH22	2.06	0.68
1:A:787:C:C2	1:A:2010:A:N7	2.62	0.68
6:F:69:ARG:HB2	6:F:84:PRO:HB3	1.76	0.68
1:A:925:A:H3'	1:A:925:A:N3	2.09	0.68
1:A:2823:C:N4	1:A:2828:G:O6	2.27	0.68
1:A:380:C:H5'	18:U:2:HIS:NE2	2.08	0.68
4:D:7:GLY:CA	4:D:53:PHE:CE2	2.78	0.68
4:D:15:VAL:O	4:D:15:VAL:HG12	2.75	0.68
4:D:28:ILE:HD12	4:D:188:ILE:CD1	2.24	0.68
1:A:2859:G:OP1	4:D:57:ARG:NH1	2.27	0.67
4:D:31:ALA:N	4:D:53:PHE:HE1	1.90	0.67
9:K:87:ILE:HD11	9:K:91:LYS:C	2.15	0.67
9:K:63:VAL:HG12	9:K:64:ARG:HG3	1.76	0.67
19:V:53:ILE:CG1	19:V:67:LEU:HD11	2.21	0.67
4:D:29:GLU:HB3	4:D:185:LEU:HD22	1.76	0.67
24:W:153:GLY:HA3	25:W:301:GNP:PG	2.35	0.67
1:A:343:A:OP2	18:U:95:LYS:CE	2.42	0.67
1:A:925:A:N3	1:A:925:A:H5'	2.09	0.67
14:Q:44:ASN:HD22	15:R:76:TYR:H	1.42	0.67
1:A:2777:A:O4'	7:G:68:THR:HG23	1.94	0.67
6:F:60:ILE:HD13	6:F:152:MET:SD	2.34	0.67
16:S:100:THR:HG22	16:S:101:SER:H	1.60	0.67
1:A:343:A:OP2	18:U:95:LYS:CD	2.43	0.67
1:A:631:G:H22	10:L:33:LYS:HE2	1.59	0.67
1:A:2298:A:H2'	1:A:2299:G:C8	2.30	0.67
4:D:54:ASP:HB3	4:D:78:ARG:HD2	1.76	0.67
1:A:607:G:H1	1:A:622:A:H61	1.40	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:635:C:C2	1:A:636:G:N7	2.63	0.67
1:A:1242:U:H2'	1:A:1243:A:H8	1.59	0.67
1:A:1711:G:H4'	9:K:6:THR:HG23	1.77	0.67
22:Y:2:LYS:C	22:Y:2:LYS:HD3	2.16	0.67
1:A:224:A:H1'	1:A:236:A:H1'	1.76	0.66
1:A:998:G:H1	1:A:1011:C:H42	1.43	0.66
1:A:77:U:C3'	22:Y:2:LYS:HG3	2.25	0.66
4:D:2:THR:OG1	4:D:85:GLY:O	2.11	0.66
1:A:738:C:OP1	3:C:217:ARG:NH1	2.28	0.66
1:A:897:G:H1	1:A:975:C:H42	1.42	0.66
13:P:97:ARG:HG3	13:P:99:LYS:H	1.60	0.66
24:W:135:THR:HA	24:W:138:ASN:HD21	1.60	0.66
6:F:64:LYS:HD2	6:F:65:PRO:HD2	1.77	0.66
24:W:97:VAL:N	24:W:98:PRO:HD2	2.11	0.66
1:A:1811:C:N3	1:A:2615:C:N4	2.44	0.66
1:A:2548:U:C5	1:A:2570:A:C6	2.84	0.66
8:J:113:GLY:O	8:J:117:ARG:NH1	2.28	0.66
12:O:78:GLY:HA3	12:O:109:LEU:HD13	1.77	0.66
18:U:79:THR:HG21	18:U:96:LYS:HG2	1.78	0.66
24:W:39:SER:O	24:W:128:ILE:HG12	1.95	0.66
1:A:1793:G:H2'	1:A:1794:C:H6	1.59	0.66
12:O:28:ARG:CG	12:O:92:ASP:O	2.44	0.66
17:T:3:ASP:N	17:T:3:ASP:OD1	2.27	0.66
24:W:220:ARG:CD	24:W:275:LEU:HD21	2.25	0.66
1:A:342:A:P	18:U:95:LYS:CE	2.83	0.66
1:A:647:A:C6	1:A:702:A:C8	2.84	0.66
5:E:93:THR:OG1	5:E:94:PRO:HD2	1.95	0.66
1:A:758:A:H61	1:A:767:U:H3	1.43	0.66
1:A:2000:A:H2'	1:A:2000:A:N3	2.10	0.66
2:B:41:C:H5''	6:F:63:GLN:CD	2.17	0.66
9:K:87:ILE:HG13	9:K:93:PRO:HA	1.79	0.66
9:K:104:ARG:NH2	13:P:37:GLU:HA	2.10	0.66
1:A:1759:U:O2	1:A:1759:U:H2'	1.96	0.65
12:O:95:PHE:HZ	12:O:106:VAL:HG13	1.60	0.65
18:U:92:ARG:NH1	18:U:101:LEU:O	2.26	0.65
6:F:16:LEU:O	6:F:16:LEU:HG	1.94	0.65
6:F:118:SER:OG	6:F:177:PHE:HD1	1.78	0.65
1:A:2704:A:H61	1:A:2761:G:H1	1.44	0.65
4:D:83:LEU:O	4:D:86:VAL:HG23	1.97	0.65
24:W:125:ILE:HG21	24:W:136:LEU:HD23	1.79	0.65
3:C:16:MET:HB3	3:C:206:GLY:HA3	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:44:THR:HG22	14:Q:100:VAL:CG1	2.27	0.65
1:A:1178:U:H5'	8:J:85:LEU:HD21	1.77	0.65
12:O:39:HIS:HB2	12:O:58:THR:OG1	1.97	0.65
16:S:70:VAL:HG12	16:S:71:ILE:N	2.11	0.65
1:A:1395:C:H42	1:A:1414:G:H1	1.42	0.65
9:K:17:ARG:N	9:K:45:GLN:O	2.29	0.65
1:A:2342:C:H5'	6:F:88:LYS:HD3	1.79	0.64
3:C:159:GLY:HA2	3:C:198:GLU:HG2	1.79	0.64
1:A:1554:U:C5'	1:A:1555:A:C8	2.80	0.64
3:C:53:HIS:HB2	3:C:217:ARG:O	1.97	0.64
24:W:37:MET:HE1	24:W:71:TRP:CH2	2.32	0.64
1:A:1554:U:C5'	1:A:1555:A:N7	2.59	0.64
3:C:57:GLY:HA3	3:C:214:LYS:O	1.96	0.64
24:W:31:VAL:CG1	24:W:39:SER:HG	1.98	0.64
24:W:125:ILE:CG2	24:W:136:LEU:HD23	2.27	0.64
1:A:785:C:H42	1:A:805:G:H1	1.45	0.64
1:A:1757:G:N7	1:A:1759:U:C5	2.66	0.64
1:A:2364:A:OP1	12:O:17:ARG:NE	2.30	0.64
5:E:190:GLU:O	5:E:191:LYS:HG3	1.97	0.64
24:W:37:MET:HE1	24:W:71:TRP:CZ3	2.33	0.64
1:A:1267:G:OP2	14:Q:13:ARG:HG3	1.97	0.64
6:F:4:LEU:CD2	6:F:100:LEU:HB2	2.28	0.64
7:G:72:LEU:CD2	7:G:140:GLU:OE2	2.46	0.64
13:P:94:LYS:CG	13:P:118:ARG:NH2	2.61	0.64
3:C:142:HIS:HA	3:C:155:VAL:HG11	1.78	0.64
12:O:95:PHE:HE2	12:O:106:VAL:HG12	1.19	0.64
1:A:635:C:N3	1:A:636:G:N7	2.46	0.64
3:C:131:PRO:HA	3:C:189:ARG:HA	1.80	0.64
1:A:2111:A:N6	1:A:2266:G:O2'	2.30	0.64
6:F:29:PRO:O	6:F:169:LEU:CD2	2.44	0.64
1:A:1573:C:N3	1:A:1594:G:N1	2.37	0.64
1:A:2559:U:H6	1:A:2559:U:O5'	1.80	0.64
2:B:29:C:H1'	2:B:51:A:H61	1.62	0.64
24:W:97:VAL:N	24:W:98:PRO:CD	2.60	0.63
18:U:45:SER:OG	18:U:55:GLY:N	2.26	0.63
1:A:2282:G:C6	19:V:13:LYS:HA	2.33	0.63
9:K:25:LEU:HD12	9:K:38:VAL:HG11	1.81	0.63
10:L:77:VAL:O	10:L:112:LEU:N	2.28	0.63
24:W:34:ARG:O	24:W:277:PHE:HB2	1.98	0.63
1:A:920:G:H8	1:A:920:G:O5'	1.81	0.63
12:O:95:PHE:HE2	12:O:106:VAL:HG11	1.51	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:495:U:C2	5:E:84:ARG:HD2	2.27	0.63
1:A:2667:G:P	4:D:84:ARG:HH12	2.18	0.63
18:U:41:VAL:CG1	18:U:43:LYS:CG	2.75	0.63
1:A:504:A:N7	1:A:519:A:N6	2.46	0.63
1:A:949:U:OP1	1:A:949:U:H4'	1.99	0.63
1:A:2002:G:H8	1:A:2002:G:O5'	1.82	0.63
3:C:87:ARG:HG3	3:C:89:ALA:H	1.62	0.63
6:F:13:ALA:HB3	6:F:14:PRO:CD	2.29	0.63
6:F:69:ARG:N	6:F:84:PRO:HB3	2.14	0.63
1:A:1820:A:N6	1:A:1857:G:O2'	2.31	0.63
4:D:32:PRO:HB3	4:D:98:LYS:HG3	1.81	0.63
1:A:1861:C:O5'	1:A:1861:C:H6	1.81	0.63
1:A:2359:G:N1	1:A:2414:C:N3	2.35	0.63
12:O:71:THR:OG1	12:O:72:SER:N	2.30	0.63
1:A:776:G:OP2	3:C:13:ARG:NH2	2.32	0.63
1:A:2778:A:O4'	7:G:64:ALA:HB2	1.99	0.63
7:G:83:GLY:HA2	7:G:137:THR:HA	1.81	0.63
1:A:1847:U:O2'	3:C:154:LEU:HA	1.98	0.62
1:A:1656:C:H42	1:A:1666:U:H3	1.46	0.62
4:D:79:PHE:CG	4:D:199:LEU:HD22	2.33	0.62
6:F:33:LYS:HA	6:F:96:MET:HE1	1.81	0.62
24:W:134:SER:N	25:W:301:GNP:O1A	2.30	0.62
1:A:398:U:H2'	1:A:399:C:H6	1.64	0.62
1:A:927:G:H8	1:A:927:G:O5'	1.82	0.62
13:P:33:VAL:CG2	13:P:77:PHE:HZ	1.74	0.62
15:R:25:LEU:HD11	15:R:93:THR:HG21	1.80	0.62
1:A:1659:A:H62	16:S:91:GLY:CA	2.04	0.62
1:A:2218:U:O2	1:A:2218:U:H2'	2.00	0.62
7:G:78:GLU:CB	7:G:84:PHE:HZ	1.98	0.62
15:R:22:ILE:HD11	15:R:95:VAL:CB	2.25	0.62
19:V:54:TYR:CE1	19:V:84:ARG:HD3	2.35	0.62
1:A:2291:U:O2'	1:A:2292:C:H5'	1.99	0.62
8:J:77:ARG:NH1	8:J:86:LYS:HD3	2.15	0.62
3:C:195:VAL:HG12	3:C:196:GLY:N	2.15	0.62
4:D:25:VAL:HG11	4:D:187:LEU:HB3	1.82	0.62
1:A:732:A:H8	1:A:735:U:H3	1.48	0.62
12:O:29:PRO:HB2	12:O:44:ILE:HG23	1.81	0.62
14:Q:92:ARG:CG	15:R:11:GLN:HG3	2.30	0.62
18:U:11:VAL:CG1	18:U:12:ILE:N	2.63	0.62
1:A:886:U:H2'	1:A:887:C:C6	2.34	0.62
1:A:1631:A:H4'	1:A:1632:G:H4'	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2674:G:N2	1:A:2796:C:OP2	2.33	0.62
1:A:2853:C:H2'	1:A:2854:A:H8	1.65	0.62
16:S:89:ALA:C	16:S:91:GLY:H	2.04	0.62
1:A:634:A:C5	1:A:635:C:C5	2.88	0.62
1:A:1527:C:H1'	1:A:1558:G:H21	1.63	0.62
1:A:1846:G:OP2	3:C:156:ARG:NH1	2.33	0.62
2:B:53:U:C2'	6:F:26:MET:SD	2.87	0.62
16:S:21:MET:SD	16:S:24:ILE:HD12	2.39	0.62
1:A:2289:C:O5'	1:A:2289:C:H6	1.83	0.61
1:A:2809:G:OP2	8:J:121:LYS:CE	2.47	0.61
1:A:1513:U:H3	1:A:1572:G:H1	1.48	0.61
7:G:89:GLU:N	7:G:164:ARG:O	2.17	0.61
10:L:117:LEU:HD21	10:L:136:VAL:CA	2.08	0.61
1:A:531:C:OP2	18:U:47:PRO:HG3	1.99	0.61
1:A:2342:C:C1'	6:F:37:ASN:ND2	2.62	0.61
3:C:142:HIS:ND1	3:C:193:GLY:O	2.33	0.61
6:F:132:ILE:CD1	6:F:154:ILE:HG13	2.29	0.61
24:W:135:THR:O	24:W:135:THR:HG22	2.00	0.61
1:A:1529:G:O6	1:A:1552:C:N4	2.27	0.61
1:A:2537:G:H8	1:A:2537:G:O5'	1.83	0.61
1:A:2560:A:H1'	1:A:2688:G:H5'	1.81	0.61
2:B:39:A:H2'	6:F:66:VAL:HG21	1.83	0.61
4:D:16:PHE:HZ	13:P:80:HIS:O	1.73	0.61
4:D:38:LYS:HZ3	4:D:88:MET:HG2	1.64	0.61
22:Y:8:ASP:HB2	22:Y:13:GLU:HB2	1.83	0.61
2:B:55:A:H1'	6:F:27:GLN:NE2	1.86	0.61
3:C:68:LYS:HD3	3:C:149:GLY:O	2.01	0.61
4:D:178:LYS:HB3	4:D:187:LEU:HD12	1.81	0.61
15:R:65:GLN:HG2	15:R:93:THR:HG23	1.82	0.61
24:W:126:ILE:CG2	24:W:175:ILE:CD1	2.70	0.61
6:F:37:ASN:HB2	6:F:153:ASP:HB2	1.81	0.61
8:J:25:THR:C	8:J:29:LEU:HD21	2.21	0.61
24:W:39:SER:O	24:W:128:ILE:CG1	2.49	0.61
3:C:132:LEU:HB3	3:C:172:VAL:HG21	1.81	0.61
4:D:107:ILE:HB	4:D:205:ALA:HB3	1.83	0.61
24:W:129:PRO:HG3	24:W:176:LEU:CG	2.31	0.61
1:A:2298:A:C5	1:A:2299:G:C5	2.89	0.61
1:A:2777:A:O2'	7:G:64:ALA:CB	2.49	0.61
3:C:94:ILE:CG1	3:C:104:ILE:HD13	2.31	0.61
9:K:10:VAL:HG21	9:K:16:ALA:O	2.01	0.61
9:K:63:VAL:HG21	9:K:85:VAL:HG23	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:80:ARG:O	18:U:94:ALA:CA	2.48	0.61
24:W:36:PRO:HB3	24:W:75:PHE:HE2	1.66	0.61
1:A:357:G:H2'	1:A:358:C:H6	1.66	0.60
1:A:530:A:H5''	18:U:47:PRO:HD3	1.82	0.60
10:L:71:ARG:HG2	10:L:73:GLU:OE1	2.01	0.60
22:Y:21:LEU:HD11	22:Y:53:MET:CE	2.31	0.60
1:A:77:U:H5'	22:Y:2:LYS:HB2	1.81	0.60
1:A:418:A:N6	1:A:449:A:OP2	2.35	0.60
1:A:2291:U:H2'	1:A:2292:C:C6	2.36	0.60
1:A:2324:C:OP1	12:O:14:ARG:NH1	2.34	0.60
6:F:4:LEU:HB3	6:F:97:TYR:HB3	1.83	0.60
6:F:68:THR:CG2	6:F:88:LYS:CD	2.79	0.60
12:O:29:PRO:CB	12:O:44:ILE:HG23	2.30	0.60
1:A:319:G:H1	1:A:401:C:H42	1.49	0.60
4:D:16:PHE:H	13:P:15:GLN:HE22	1.49	0.60
4:D:108:VAL:C	4:D:205:ALA:HB2	2.22	0.60
6:F:68:THR:HG22	6:F:88:LYS:HG3	1.75	0.60
10:L:117:LEU:HD22	10:L:136:VAL:CG1	2.28	0.60
13:P:30:ARG:HG2	13:P:47:GLU:HB2	1.83	0.60
1:A:607:G:H21	14:Q:37:GLN:HE22	1.47	0.60
1:A:790:A:C2	1:A:802:G:C2	2.89	0.60
1:A:1859:C:H2'	1:A:1860:G:H8	1.66	0.60
7:G:126:VAL:HG13	7:G:132:VAL:HG22	1.84	0.60
12:O:28:ARG:HG2	12:O:92:ASP:O	2.01	0.60
15:R:5:ILE:CG2	15:R:7:THR:HG23	2.31	0.60
1:A:1497:G:H1	1:A:1505:U:H3	1.50	0.60
1:A:1706:G:N2	1:A:2717:G:OP1	2.35	0.60
1:A:2132:A:N1	1:A:2215:U:O2	2.34	0.60
12:O:31:LEU:N	12:O:94:VAL:O	2.33	0.60
1:A:306:C:O2	1:A:411:G:N2	2.33	0.60
1:A:751:G:O2'	1:A:774:A:N6	2.34	0.60
1:A:998:G:H21	1:A:2296:A:H2	1.50	0.60
6:F:69:ARG:CB	6:F:84:PRO:HB3	2.30	0.60
12:O:28:ARG:N	12:O:29:PRO:HD3	2.16	0.60
24:W:32:ASP:HB2	24:W:131:VAL:HG21	1.82	0.60
1:A:644:G:OP1	5:E:29:ASN:ND2	2.34	0.60
1:A:743:U:H2'	1:A:744:C:H6	1.67	0.60
1:A:2342:C:H5''	6:F:88:LYS:HD2	1.81	0.60
1:A:2773:G:OP2	1:A:2784:C:N4	2.34	0.60
5:E:9:GLN:NE2	5:E:130:THR:O	2.33	0.60
5:E:81:PRO:HB3	5:E:89:VAL:CG2	2.28	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:25:THR:HG22	8:J:28:ARG:HB2	1.83	0.60
24:W:202:LEU:HB2	24:W:260:THR:HG21	1.84	0.60
1:A:417:G:OP2	1:A:470:A:N6	2.35	0.60
1:A:911:G:H1	1:A:959:C:H42	1.48	0.60
1:A:2343:A:H4'	6:F:35:VAL:HG21	1.84	0.60
9:K:62:ILE:HA	9:K:84:CYS:HG	1.65	0.60
14:Q:100:VAL:HG12	14:Q:100:VAL:O	2.01	0.60
1:A:528:G:H1	1:A:555:C:H42	1.49	0.60
1:A:1354:C:H42	1:A:1376:G:H1	1.48	0.60
1:A:1460:G:O2'	1:A:1631:A:N6	2.35	0.60
1:A:2132:A:N6	1:A:2215:U:H3	1.99	0.60
3:C:130:LEU:HD12	3:C:134:ASN:HB2	1.83	0.60
4:D:8:ARG:HH21	4:D:78:ARG:NH1	1.99	0.60
3:C:171:TYR:HH	3:C:269:PHE:HE1	1.48	0.60
5:E:164:ALA:HA	5:E:175:VAL:HG11	1.83	0.59
19:V:53:ILE:HG13	19:V:67:LEU:CD1	2.21	0.59
1:A:578:A:OP2	14:Q:38:GLN:NE2	2.35	0.59
1:A:1337:C:H42	1:A:1687:G:H1	1.49	0.59
1:A:2566:U:H2'	1:A:2567:C:C6	2.37	0.59
6:F:69:ARG:HA	6:F:84:PRO:CB	2.32	0.59
6:F:69:ARG:CA	6:F:84:PRO:CB	2.80	0.59
6:F:132:ILE:HD13	6:F:154:ILE:CG1	2.28	0.59
6:F:132:ILE:HB	6:F:152:MET:O	2.02	0.59
24:W:156:THR:HG22	24:W:172:THR:CB	2.31	0.59
1:A:634:A:C4	1:A:635:C:C6	2.91	0.59
1:A:673:A:O2'	1:A:674:G:O4'	2.20	0.59
1:A:1055:A:OP1	8:J:40:LYS:NZ	2.35	0.59
9:K:63:VAL:HG13	9:K:102:VAL:HG13	1.84	0.59
9:K:64:ARG:NH2	9:K:99:PHE:O	2.36	0.59
20:Z:6:ILE:HG22	20:Z:28:LEU:CD1	2.18	0.59
1:A:1213:G:H1	1:A:1223:C:H42	1.48	0.59
4:D:110:VAL:HG11	4:D:192:VAL:HG13	1.84	0.59
5:E:24:PHE:HB3	5:E:118:VAL:HG21	1.84	0.59
1:A:601:U:O3'	8:J:114:SER:OG	2.15	0.59
1:A:787:C:O2	1:A:2010:A:N7	2.36	0.59
1:A:1599:U:H3'	1:A:1600:G:H21	1.66	0.59
1:A:1858:A:C5	1:A:1859:C:N3	2.70	0.59
1:A:2010:A:H2'	1:A:2010:A:N3	2.17	0.59
1:A:2291:U:O2'	1:A:2292:C:O4'	2.19	0.59
2:B:83:G:H1	2:B:89:C:H42	1.49	0.59
10:L:125:ALA:HB3	10:L:128:PHE:HE1	1.59	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:R:90:GLN:NE2	15:R:91:PRO:O	2.35	0.59
1:A:30:G:OP2	14:Q:5:LYS:NZ	2.34	0.59
1:A:84:A:N6	1:A:101:G:O2'	2.36	0.59
1:A:217:G:H21	1:A:219:A:H1'	1.67	0.59
1:A:1252:G:H21	1:A:1277:A:H62	1.51	0.59
1:A:2291:U:H2'	1:A:2292:C:H6	1.67	0.59
1:A:2655:C:H2'	1:A:2656:G:H8	1.66	0.59
6:F:122:PHE:CZ	6:F:167:ARG:NE	2.70	0.59
12:O:69:GLY:O	12:O:105:ARG:CZ	2.51	0.59
16:S:100:THR:CG2	16:S:101:SER:H	2.16	0.59
19:V:80:PHE:CZ	19:V:86:LYS:CG	2.86	0.59
1:A:54:G:N2	1:A:115:C:O2	2.35	0.59
4:D:117:LYS:O	4:D:120:GLN:NE2	2.36	0.59
1:A:342:A:O5'	18:U:95:LYS:CE	2.51	0.59
1:A:364:A:N3	5:E:169:ASN:ND2	2.50	0.59
1:A:701:G:H8	1:A:701:G:O5'	1.85	0.59
1:A:1578:G:N2	1:A:1587:U:OP2	2.36	0.59
1:A:1828:G:OP1	3:C:260:ARG:NH1	2.35	0.59
4:D:83:LEU:HD21	4:D:203:LYS:HD2	1.76	0.59
4:D:83:LEU:HB3	4:D:86:VAL:CG2	2.33	0.59
16:S:44:SER:N	16:S:45:PRO:HD2	2.18	0.59
1:A:647:A:C5	1:A:702:A:C5	2.91	0.59
1:A:740:A:OP1	3:C:39:LYS:CE	2.49	0.59
1:A:2128:U:H2'	1:A:2129:G:H8	1.68	0.59
1:A:917:A:H8	1:A:917:A:O5'	1.86	0.59
4:D:49:ILE:HD11	4:D:91:TYR:CG	2.38	0.59
4:D:79:PHE:HB3	4:D:199:LEU:HD22	1.85	0.59
1:A:530:A:H4'	18:U:45:SER:O	2.03	0.58
1:A:866:A:OP2	1:A:1228:G:N2	2.35	0.58
1:A:1801:G:N2	1:A:2008:C:O2	2.34	0.58
1:A:2112:G:N2	1:A:2265:U:O2	2.34	0.58
2:B:40:C:H4'	6:F:64:LYS:HB3	1.85	0.58
3:C:146:LEU:HD12	3:C:153:GLN:OE1	2.01	0.58
6:F:68:THR:CG2	6:F:88:LYS:CE	2.74	0.58
1:A:1526:G:N1	1:A:1558:G:N1	2.49	0.58
3:C:94:ILE:HG13	3:C:104:ILE:HG21	1.85	0.58
6:F:38:MET:HG2	6:F:87:ALA:O	2.03	0.58
6:F:169:LEU:O	6:F:173:VAL:HG23	2.02	0.58
10:L:79:LEU:CD2	10:L:117:LEU:CA	2.81	0.58
13:P:62:PHE:CD2	13:P:79:VAL:HG22	2.38	0.58
24:W:44:ILE:HG12	24:W:126:ILE:HD12	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1397:G:O6	1:A:1410:G:C8	2.56	0.58
1:A:2169:G:N1	1:A:2181:C:O2	2.36	0.58
6:F:108:LEU:N	6:F:109:PRO:HD2	2.18	0.58
22:Y:21:LEU:HD11	22:Y:53:MET:HE1	1.77	0.58
1:A:2873:G:O2'	1:A:2893:A:N6	2.36	0.58
8:J:25:THR:O	8:J:29:LEU:CG	2.49	0.58
10:L:116:LYS:HG3	10:L:116:LYS:O	2.02	0.58
24:W:130:ASN:N	25:W:301:GNP:O1B	2.36	0.58
1:A:2038:G:C5'	16:S:40:PRO:HB2	2.34	0.58
4:D:134:SER:OG	4:D:135:HIS:N	2.36	0.58
24:W:42:PRO:HD2	24:W:177:TRP:NE1	2.18	0.58
1:A:830:A:H2'	1:A:831:U:H4'	1.86	0.58
1:A:1563:G:C5	1:A:1564:C:C5	2.91	0.58
1:A:1738:U:O2	3:C:14:ARG:NH2	2.37	0.58
1:A:2426:G:H1	1:A:2448:U:H3	1.50	0.58
12:O:69:GLY:O	12:O:105:ARG:NH2	2.36	0.58
1:A:1338:G:H21	1:A:1686:A:H62	1.51	0.58
1:A:1711:G:N2	1:A:2023:C:N3	2.52	0.58
24:W:94:ASN:OD1	24:W:94:ASN:N	2.28	0.58
1:A:1231:G:H5''	10:L:32:GLY:HA2	1.86	0.58
1:A:2186:G:N2	1:A:2187:A:N7	2.52	0.58
1:A:2669:G:H1	1:A:2803:C:H42	1.51	0.58
4:D:34:VAL:O	4:D:34:VAL:HG13	2.03	0.58
6:F:127:ASN:OD1	6:F:157:VAL:HG13	2.04	0.58
1:A:1246:G:O6	1:A:1281:C:N4	2.36	0.58
1:A:1521:G:H22	1:A:1563:G:H1	1.52	0.58
1:A:1801:G:O6	1:A:2005:C:N4	2.37	0.58
1:A:2164:A:H62	1:A:2185:G:H21	1.51	0.58
1:A:2420:G:H22	1:A:2456:C:H1'	1.69	0.58
1:A:2592:U:H4'	9:K:28:SER:CB	2.33	0.58
4:D:5:ILE:HA	4:D:33:ASN:ND2	2.18	0.58
4:D:28:ILE:HD12	4:D:188:ILE:HD11	1.85	0.58
6:F:63:GLN:HG3	6:F:90:THR:O	2.03	0.58
6:F:108:LEU:CD1	6:F:176:PRO:CG	2.64	0.58
1:A:1390:C:H2'	1:A:1391:U:H6	1.65	0.58
1:A:2030:A:OP1	11:N:5:LYS:NZ	2.37	0.58
1:A:2549:C:H42	1:A:2574:G:H1	1.52	0.58
1:A:2847:G:H5''	4:D:163:ARG:HE	1.68	0.58
8:J:111:PRO:O	8:J:116:GLY:HA3	2.03	0.58
11:N:24:LEU:HD23	11:N:44:VAL:HG11	1.85	0.58
11:N:45:GLU:OE2	11:N:98:TYR:N	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:O:30:ARG:HB2	12:O:96:ASP:OD2	2.03	0.58
24:W:59:LYS:N	25:W:301:GNP:O6	2.36	0.58
1:A:1245:G:O4'	10:L:4:HIS:NE2	2.36	0.57
1:A:1264:G:O2'	15:R:86:GLN:NE2	2.37	0.57
1:A:1322:G:N2	1:A:1325:A:OP2	2.37	0.57
1:A:1387:G:O6	1:A:1643:C:N4	2.37	0.57
1:A:1525:G:HO2'	1:A:1608:A:HO2'	1.50	0.57
1:A:2298:A:H2'	1:A:2299:G:H8	1.66	0.57
3:C:107:PRO:HA	3:C:195:VAL:HA	1.85	0.57
4:D:109:ASP:N	4:D:203:LYS:O	2.32	0.57
13:P:32:HIS:HB2	13:P:85:ALA:HB3	1.86	0.57
1:A:1651:G:O2'	1:A:1653:A:N6	2.37	0.57
1:A:2719:A:OP1	11:N:13:ARG:NH1	2.37	0.57
19:V:80:PHE:CE2	19:V:86:LYS:CG	2.85	0.57
1:A:1102:G:N2	1:A:1150:C:N3	2.52	0.57
2:B:41:C:Cl'	6:F:92:ARG:HB2	2.30	0.57
6:F:8:TYR:HE1	6:F:30:LYS:HZ1	0.71	0.57
8:J:24:LYS:C	8:J:29:LEU:HD21	2.24	0.57
9:K:71:ARG:HH12	9:K:104:ARG:HH11	1.52	0.57
15:R:24:LYS:HD2	15:R:91:PRO:CG	2.30	0.57
15:R:62:VAL:HA	15:R:95:VAL:HG22	1.86	0.57
16:S:36:LEU:HD12	16:S:47:ILE:HG22	1.82	0.57
16:S:78:GLU:OE1	16:S:99:ARG:NH1	2.37	0.57
18:U:4:LYS:H	18:U:92:ARG:HH21	1.51	0.57
1:A:635:C:N4	1:A:636:G:O6	2.38	0.57
6:F:24:SER:O	6:F:26:MET:N	2.33	0.57
6:F:34:ILE:HD11	6:F:96:MET:SD	2.44	0.57
1:A:517:A:OP1	5:E:79:ARG:NH2	2.37	0.57
1:A:684:G:C6	1:A:697:G:N1	2.73	0.57
1:A:1177:G:C5	8:J:78:HIS:CE1	2.92	0.57
3:C:210:ARG:CA	3:C:213:TRP:HD1	2.15	0.57
1:A:740:A:OP1	3:C:39:LYS:HG2	2.05	0.57
1:A:2294:U:O5'	1:A:2294:U:H6	1.87	0.57
1:A:2752:C:C4	1:A:2753:U:C5	2.93	0.57
1:A:65:A:N1	1:A:90:A:N6	2.52	0.57
1:A:1563:G:H2'	1:A:1564:C:H6	1.69	0.57
1:A:2026:A:H2'	1:A:2027:A:H8	1.70	0.57
1:A:2322:C:OP1	12:O:97:ARG:NH1	2.37	0.57
1:A:2559:U:OP1	1:A:2564:G:N2	2.38	0.57
9:K:87:ILE:HA	9:K:93:PRO:HA	1.87	0.57
15:R:48:VAL:CG1	15:R:50:ASN:O	2.51	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:148:THR:HG22	24:W:150:ASP:H	1.69	0.57
1:A:455:G:H1	1:A:466:C:H42	1.52	0.57
1:A:1069:U:H3'	1:A:1070:G:H8	1.69	0.57
1:A:2298:A:C6	1:A:2299:G:C5	2.92	0.57
18:U:85:VAL:HG21	18:U:91:VAL:H	1.69	0.57
1:A:1314:A:N7	1:A:1335:A:O2'	2.36	0.57
1:A:2281:G:H8	1:A:2281:G:O5'	1.88	0.57
2:B:30:C:H42	2:B:48:G:H1	1.53	0.57
4:D:33:ASN:N	4:D:97:VAL:O	2.37	0.57
14:Q:4:VAL:HG12	14:Q:5:LYS:N	2.19	0.57
1:A:1526:G:C2	1:A:1558:G:N2	2.73	0.57
11:N:55:ASP:HB3	11:N:58:ALA:H	1.69	0.57
1:A:28:A:HO2'	1:A:626:G:HO2'	1.53	0.56
1:A:166:A:H2'	1:A:167:U:C6	2.39	0.56
3:C:70:ASP:OD1	3:C:70:ASP:N	2.37	0.56
6:F:108:LEU:N	6:F:109:PRO:CD	2.67	0.56
12:O:78:GLY:O	12:O:109:LEU:HD12	2.04	0.56
13:P:28:THR:HA	13:P:48:GLY:O	2.05	0.56
15:R:58:VAL:HG13	15:R:100:ILE:HD13	1.85	0.56
16:S:12:ILE:HD13	16:S:43:ALA:CB	2.33	0.56
16:S:100:THR:CG2	16:S:101:SER:N	2.66	0.56
24:W:111:MET:SD	24:W:119:ARG:CB	2.93	0.56
1:A:138:U:N3	1:A:141:U:OP2	2.38	0.56
1:A:636:G:N2	1:A:712:C:O2	2.34	0.56
1:A:2325:U:O2	1:A:2366:G:N2	2.38	0.56
16:S:6:VAL:HG22	16:S:104:THR:HG22	1.87	0.56
24:W:129:PRO:HD2	24:W:176:LEU:HD23	1.85	0.56
1:A:38:A:OP1	5:E:52:LYS:NZ	2.38	0.56
1:A:286:U:H3'	1:A:287:G:H8	1.70	0.56
1:A:342:A:H5''	18:U:95:LYS:HZ1	1.57	0.56
1:A:398:U:H2'	1:A:399:C:C6	2.40	0.56
1:A:683:A:C8	10:L:114:ASN:CG	2.78	0.56
1:A:2380:G:O2'	1:A:2395:A:N6	2.39	0.56
3:C:6:TYR:HD2	3:C:13:ARG:HD2	1.71	0.56
3:C:171:TYR:CE2	3:C:269:PHE:CE1	2.93	0.56
4:D:49:ILE:O	4:D:82:GLU:CA	2.53	0.56
6:F:69:ARG:CD	6:F:82:GLY:HA2	2.34	0.56
8:J:17:LEU:HD22	8:J:141:TYR:HB2	1.86	0.56
12:O:34:PHE:HB3	12:O:41:TYR:HB2	1.87	0.56
15:R:19:THR:HA	15:R:96:THR:HA	1.86	0.56
1:A:1342:G:HO2'	1:A:1687:G:HO2'	1.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:155:PRO:HA	7:G:162:GLY:HA3	1.86	0.56
13:P:34:LYS:O	13:P:83:LYS:NZ	2.37	0.56
16:S:13:ALA:HB3	16:S:16:LYS:HG3	1.86	0.56
19:V:80:PHE:CZ	19:V:86:LYS:HG3	2.40	0.56
1:A:2560:A:N6	1:A:2690:G:O6	2.38	0.56
2:B:101:U:H2'	2:B:102:A:H8	1.70	0.56
12:O:59:LEU:HG	12:O:59:LEU:O	2.04	0.56
1:A:1657:C:N4	1:A:1664:G:O6	2.32	0.56
1:A:2703:G:H4'	9:K:30:ARG:CD	2.23	0.56
1:A:2722:A:H2'	1:A:2723:G:H8	1.69	0.56
11:N:107:ARG:NE	11:N:110:ASP:OD2	2.30	0.56
14:Q:79:LEU:HD21	14:Q:106:PHE:HZ	1.70	0.56
1:A:2277:C:O5'	1:A:2277:C:H6	1.88	0.56
6:F:63:GLN:HG2	6:F:91:LEU:HA	1.78	0.56
8:J:77:ARG:CZ	8:J:86:LYS:HD3	2.35	0.56
9:K:17:ARG:CB	9:K:45:GLN:O	2.52	0.56
9:K:87:ILE:HG13	9:K:92:SER:O	2.05	0.56
1:A:1243:A:O2'	5:E:41:ARG:NH1	2.38	0.56
1:A:1313:A:N6	1:A:1691:A:N7	2.53	0.56
10:L:117:LEU:HD22	10:L:136:VAL:CA	2.31	0.56
12:O:95:PHE:CE2	12:O:102:TYR:HE1	2.23	0.56
1:A:226:A:H8	1:A:454:G:H21	1.52	0.56
1:A:673:A:H61	1:A:682:G:H2'	1.71	0.56
1:A:776:G:OP2	3:C:207:LYS:NZ	2.39	0.56
1:A:861:C:H2'	1:A:862:U:H6	1.70	0.56
1:A:2066:A:H2'	1:A:2067:G:H8	1.69	0.56
4:D:107:ILE:CG2	4:D:205:ALA:CB	2.82	0.56
4:D:122:ALA:HB2	4:D:161:PRO:HD3	1.87	0.56
12:O:58:THR:O	12:O:68:THR:HB	2.06	0.56
15:R:24:LYS:HB2	15:R:91:PRO:HG2	1.88	0.56
19:V:53:ILE:HG22	19:V:85:LYS:HB2	1.87	0.56
1:A:344:G:OP2	18:U:80:ARG:NH2	2.39	0.56
1:A:1002:G:O2'	1:A:1005:A:N6	2.35	0.56
1:A:1614:A:P	3:C:210:ARG:HH22	2.29	0.56
1:A:2340:A:H8	6:F:85:ILE:HD13	1.68	0.56
18:U:85:VAL:O	18:U:85:VAL:HG12	2.06	0.56
1:A:77:U:O3'	22:Y:2:LYS:CG	2.54	0.55
1:A:2548:U:C4	1:A:2570:A:C6	2.94	0.55
5:E:79:ARG:HG3	5:E:86:GLY:HA2	1.87	0.55
7:G:90:LEU:HD12	7:G:132:VAL:HG21	1.88	0.55
1:A:893:A:O2'	1:A:978:A:N6	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1673:G:H1	1:A:1683:C:H42	1.54	0.55
6:F:34:ILE:HG13	6:F:96:MET:SD	2.45	0.55
9:K:13:ASN:ND2	9:K:96:THR:OG1	2.33	0.55
9:K:104:ARG:HG2	9:K:104:ARG:O	2.06	0.55
11:N:90:ARG:NH1	11:N:91:TYR:OH	2.39	0.55
24:W:81:ARG:HH11	24:W:103:ILE:HG12	1.40	0.55
1:A:2906:U:O2'	11:N:99:THR:O	2.24	0.55
5:E:80:SER:HB3	5:E:83:TRP:CD1	2.41	0.55
5:E:152:ALA:N	5:E:172:GLY:O	2.38	0.55
9:K:13:ASN:HD22	9:K:96:THR:HG1	1.54	0.55
1:A:656:A:H61	1:A:662:U:H3	1.52	0.55
1:A:719:C:C2	1:A:856:G:C2	2.94	0.55
1:A:2130:G:H22	1:A:2217:U:H3	1.53	0.55
1:A:2895:C:C5'	11:N:61:GLN:HE22	2.20	0.55
2:B:34:C:N4	2:B:47:C:O2'	2.39	0.55
1:A:1200:G:OP2	14:Q:58:ARG:NH2	2.36	0.55
6:F:69:ARG:N	6:F:84:PRO:CB	2.70	0.55
6:F:132:ILE:CD1	6:F:154:ILE:HB	2.35	0.55
13:P:66:LYS:NZ	13:P:67:ILE:O	2.40	0.55
24:W:58:ASN:HD21	24:W:132:GLY:N	2.04	0.55
1:A:546:G:N1	1:A:549:A:OP2	2.39	0.55
1:A:1707:U:C4	1:A:1708:U:C5	2.95	0.55
1:A:2301:U:O2	1:A:2301:U:H2'	2.07	0.55
1:A:2474:G:OP1	5:E:74:ARG:NH2	2.40	0.55
4:D:145:SER:O	4:D:158:LYS:NZ	2.40	0.55
12:O:35:ARG:NH1	12:O:105:ARG:CD	2.67	0.55
15:R:7:THR:HG22	15:R:37:ASP:OD2	2.06	0.55
1:A:223:G:H22	1:A:474:U:H2'	1.71	0.55
1:A:659:A:N1	5:E:46:GLN:NE2	2.54	0.55
1:A:1519:C:H42	1:A:1565:U:H3	1.53	0.55
1:A:2029:G:H2'	1:A:2030:A:H8	1.72	0.55
1:A:2684:G:O2'	1:A:2693:G:N1	2.35	0.55
1:A:2696:C:N3	7:G:111:SER:OG	2.39	0.55
3:C:78:VAL:HB	3:C:113:GLY:H	1.71	0.55
13:P:94:LYS:HD2	13:P:118:ARG:HH21	0.75	0.55
16:S:22:ASP:OD1	16:S:25:ARG:NH2	2.38	0.55
1:A:63:G:H2'	1:A:64:A:H8	1.71	0.55
1:A:557:U:H4'	1:A:1275:G:H4'	1.89	0.55
1:A:1757:G:C8	1:A:1759:U:C6	2.94	0.55
1:A:2171:G:N2	1:A:2179:U:O2	2.40	0.55
1:A:2231:C:H42	1:A:2250:G:H1	1.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2342:C:C1'	6:F:37:ASN:HD21	2.20	0.55
1:A:2718:U:OP2	1:A:2748:G:N2	2.38	0.55
2:B:55:A:H5'	6:F:23:ASP:CA	2.37	0.55
4:D:11:GLY:O	4:D:27:VAL:HG23	2.05	0.55
18:U:81:VAL:C	18:U:94:ALA:HA	2.27	0.55
1:A:564:G:O3'	16:S:18:ARG:NH1	2.40	0.55
1:A:765:A:H5''	1:A:766:C:H5	1.72	0.55
1:A:2357:A:C6	1:A:2358:A:C6	2.95	0.55
2:B:42:G:N3	2:B:45:C:N4	2.42	0.55
9:K:35:ILE:HG21	9:K:105:GLU:OE1	2.07	0.55
14:Q:114:LYS:O	14:Q:118:ASN:ND2	2.39	0.55
1:A:2537:G:C6	1:A:2611:G:N1	2.75	0.55
4:D:181:ALA:O	4:D:184:ASN:ND2	2.40	0.55
16:S:18:ARG:NH2	16:S:76:VAL:O	2.35	0.55
22:Y:6:ILE:O	22:Y:6:ILE:HG13	2.07	0.55
1:A:376:A:C2	1:A:379:C:C5	2.95	0.54
3:C:15:GLY:O	3:C:204:ASN:ND2	2.40	0.54
4:D:27:VAL:O	4:D:27:VAL:HG12	2.06	0.54
4:D:93:VAL:O	4:D:93:VAL:HG13	2.08	0.54
9:K:7:ARG:HD3	9:K:18:GLU:OE1	2.07	0.54
12:O:39:HIS:CE1	12:O:59:LEU:HD13	2.42	0.54
24:W:58:ASN:ND2	24:W:132:GLY:C	2.58	0.54
1:A:1314:A:OP2	11:N:12:GLN:NE2	2.41	0.54
1:A:1546:G:N2	3:C:98:ASP:O	2.40	0.54
1:A:2291:U:O2'	1:A:2292:C:C5'	2.55	0.54
4:D:96:GLU:OE1	4:D:96:GLU:N	2.40	0.54
6:F:104:ILE:HD11	6:F:175:MET:SD	2.47	0.54
1:A:377:G:HO2'	1:A:378:C:H6	0.76	0.54
3:C:132:LEU:HD23	3:C:135:ILE:HD12	1.89	0.54
9:K:104:ARG:HH21	13:P:37:GLU:HA	1.72	0.54
13:P:27:ASP:OD1	13:P:27:ASP:N	2.40	0.54
13:P:67:ILE:HA	13:P:72:GLY:HA2	1.89	0.54
1:A:1585:A:N6	1:A:1587:U:O2	2.40	0.54
5:E:20:ASN:OD1	5:E:22:SER:OG	2.26	0.54
6:F:34:ILE:CG1	6:F:96:MET:SD	2.95	0.54
8:J:36:ILE:O	8:J:36:ILE:HG22	2.06	0.54
15:R:21:TYR:CZ	15:R:94:LYS:HD2	2.43	0.54
1:A:304:G:H2'	1:A:305:A:H8	1.73	0.54
1:A:2049:A:OP1	14:Q:27:SER:OG	2.26	0.54
3:C:77:ARG:HB3	3:C:95:ASN:HB3	1.89	0.54
3:C:94:ILE:HG13	3:C:104:ILE:HD13	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:24:LYS:C	8:J:29:LEU:CD2	2.74	0.54
12:O:97:ARG:HG2	12:O:100:TYR:O	2.07	0.54
22:Y:10:THR:OG1	22:Y:11:THR:N	2.40	0.54
1:A:1059:A:O2'	14:Q:78:ARG:NH2	2.41	0.54
2:B:35:C:H42	2:B:46:A:H2	1.55	0.54
3:C:173:LEU:HD23	3:C:183:MET:HA	1.90	0.54
5:E:38:LEU:HD22	10:L:13:ARG:HH22	1.72	0.54
9:K:25:LEU:HB3	9:K:38:VAL:CG1	2.33	0.54
22:Y:49:ALA:HA	22:Y:52:ARG:HG2	1.89	0.54
24:W:58:ASN:HB2	25:W:301:GNP:O6	2.07	0.54
24:W:75:PHE:O	24:W:78:GLN:HB2	2.07	0.54
24:W:128:ILE:HG23	24:W:129:PRO:HD2	1.90	0.54
24:W:204:ASP:OD1	24:W:204:ASP:N	2.39	0.54
1:A:644:G:N2	1:A:650:U:OP1	2.38	0.54
1:A:2598:G:H2'	1:A:2599:G:H8	1.72	0.54
6:F:38:MET:CE	6:F:57:LEU:HD22	2.38	0.54
1:A:250:G:OP1	1:A:435:G:N2	2.40	0.54
1:A:1133:G:H22	1:A:1148:C:H42	1.56	0.54
1:A:1713:A:H61	1:A:1721:A:H61	1.56	0.54
1:A:1858:A:C6	1:A:1859:C:N3	2.76	0.54
1:A:2308:G:N7	19:V:22:ARG:NH2	2.55	0.54
9:K:7:ARG:HH21	9:K:20:LEU:HD11	1.71	0.54
1:A:1334:C:OP1	11:N:67:ARG:NH2	2.40	0.54
2:B:77:G:H1	2:B:95:U:H3	1.56	0.54
7:G:79:GLY:O	7:G:83:GLY:N	2.41	0.54
1:A:967:G:N2	1:A:2298:A:OP2	2.40	0.54
1:A:1563:G:C4	1:A:1564:C:C6	2.95	0.54
4:D:5:ILE:HA	4:D:33:ASN:HD22	1.73	0.54
9:K:63:VAL:HG23	9:K:85:VAL:HG23	1.90	0.54
24:W:217:TYR:HB3	24:W:220:ARG:HG3	1.89	0.54
1:A:510:G:N2	1:A:513:A:OP2	2.38	0.53
1:A:527:A:H4'	18:U:43:LYS:HG2	1.89	0.53
1:A:726:C:H2'	1:A:727:A:C8	2.43	0.53
1:A:2344:U:O2	1:A:2344:U:H2'	2.07	0.53
1:A:2895:C:H5''	11:N:61:GLN:HE22	1.72	0.53
13:P:50:VAL:CG1	13:P:63:THR:O	2.57	0.53
1:A:118:A:H4'	1:A:119:U:H5'	1.89	0.53
1:A:767:U:H2'	1:A:768:G:H8	1.73	0.53
1:A:2015:G:O2'	24:W:198:SER:O	2.22	0.53
1:A:2872:U:OP1	13:P:99:LYS:NZ	2.40	0.53
4:D:51:LEU:O	4:D:80:VAL:HA	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:4:VAL:HG11	5:E:123:ILE:HD11	1.90	0.53
6:F:8:TYR:HH	6:F:97:TYR:HE2	1.56	0.53
8:J:26:LEU:HB2	8:J:63:ILE:HG22	1.86	0.53
10:L:90:GLU:O	10:L:92:THR:HG23	2.08	0.53
1:A:719:C:C2	1:A:856:G:N2	2.76	0.53
1:A:724:A:O2'	1:A:2099:G:O2'	2.25	0.53
1:A:1474:C:OP2	3:C:28:LYS:NZ	2.41	0.53
5:E:158:ASP:N	5:E:158:ASP:OD1	2.40	0.53
8:J:65:LEU:HD13	8:J:69:LYS:HB2	1.89	0.53
13:P:89:VAL:HG12	13:P:90:VAL:N	2.24	0.53
13:P:94:LYS:CE	13:P:118:ARG:NH2	2.64	0.53
24:W:134:SER:CB	25:W:301:GNP:O1A	2.56	0.53
1:A:342:A:P	18:U:95:LYS:NZ	2.80	0.53
1:A:1862:C:H3'	1:A:1862:C:H6	1.74	0.53
4:D:21:ASP:OD1	4:D:21:ASP:N	2.38	0.53
15:R:25:LEU:HD12	15:R:25:LEU:O	2.08	0.53
24:W:67:VAL:CB	24:W:276:SER:OG	2.57	0.53
1:A:211:C:C2	1:A:212:C:C5	2.96	0.53
1:A:362:C:H42	1:A:377:G:H1	1.57	0.53
1:A:950:U:C4	1:A:951:C:C2	2.96	0.53
1:A:1572:G:O2'	1:A:1573:C:H6	1.91	0.53
1:A:2281:G:N7	19:V:12:LYS:NZ	2.56	0.53
1:A:2922:U:O2'	8:J:135:ALA:O	2.25	0.53
11:N:25:ILE:HD13	11:N:83:LEU:HD21	1.90	0.53
15:R:6:LYS:O	15:R:6:LYS:HD2	2.07	0.53
18:U:11:VAL:CG1	18:U:12:ILE:H	2.20	0.53
1:A:1587:U:H2'	1:A:1588:A:H8	1.73	0.53
1:A:1616:G:H4'	3:C:59:LYS:HD2	1.90	0.53
1:A:2713:U:OP2	13:P:54:ARG:NH1	2.41	0.53
2:B:75:U:O2	2:B:75:U:H2'	2.09	0.53
3:C:171:TYR:HB2	3:C:184:ILE:O	2.09	0.53
7:G:73:LEU:HA	7:G:76:MET:HE2	1.90	0.53
7:G:78:GLU:HA	7:G:78:GLU:OE1	2.06	0.53
12:O:31:LEU:HB3	12:O:95:PHE:HA	1.91	0.53
1:A:683:A:OP1	10:L:131:SER:OG	2.25	0.53
1:A:1104:U:N3	1:A:1127:U:O2	2.42	0.53
1:A:1446:C:H2'	1:A:1447:C:C6	2.44	0.53
1:A:1613:C:H5''	3:C:18:THR:HG21	1.89	0.53
1:A:610:U:O4	15:R:79:LYS:NZ	2.41	0.53
1:A:662:U:H2'	1:A:663:G:H8	1.74	0.53
1:A:2561:G:H1'	1:A:2692:G:H21	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2709:C:O2'	4:D:191:ASN:ND2	2.42	0.53
3:C:89:ALA:HA	3:C:158:ALA:HB2	1.90	0.53
4:D:102:PHE:HE2	4:D:108:VAL:HG12	1.73	0.53
13:P:89:VAL:HG11	13:P:92:TYR:CE1	2.44	0.53
1:A:266:U:H2'	1:A:267:C:H4'	1.90	0.53
1:A:275:A:N7	1:A:296:G:N2	2.56	0.53
1:A:1296:G:N2	5:E:82:GLN:O	2.41	0.53
16:S:89:ALA:O	16:S:91:GLY:N	2.41	0.53
24:W:177:TRP:HD1	24:W:178:PRO:HD2	1.73	0.53
8:J:46:THR:OG1	14:Q:64:ARG:NH2	2.42	0.53
10:L:92:THR:HA	10:L:124:LYS:HB2	1.90	0.53
12:O:95:PHE:CZ	12:O:106:VAL:HG12	2.24	0.53
20:Z:57:LYS:HG3	20:Z:57:LYS:O	2.08	0.53
24:W:28:TYR:HB2	24:W:125:ILE:HG12	1.91	0.53
24:W:41:ASN:OD1	24:W:44:ILE:N	2.38	0.53
1:A:1103:A:O2'	1:A:1132:A:N6	2.42	0.52
1:A:1572:G:O2'	1:A:1573:C:O4'	2.27	0.52
6:F:2:ASN:N	6:F:98:ASP:OD1	2.43	0.52
6:F:132:ILE:CD1	6:F:154:ILE:CG1	2.86	0.52
11:N:99:THR:OG1	11:N:100:ARG:N	2.41	0.52
14:Q:44:ASN:ND2	15:R:76:TYR:O	2.41	0.52
18:U:79:THR:CG2	18:U:96:LYS:HG2	2.37	0.52
1:A:1835:C:O2	3:C:44:ASN:ND2	2.41	0.52
1:A:2298:A:C4	1:A:2299:G:N7	2.77	0.52
1:A:2353:U:C2	1:A:2414:C:C5	2.97	0.52
4:D:83:LEU:HD21	4:D:203:LYS:CG	2.39	0.52
13:P:35:VAL:HG21	13:P:44:GLN:HE21	1.74	0.52
24:W:30:LEU:HD11	24:W:133:LYS:HA	1.89	0.52
1:A:342:A:P	18:U:95:LYS:HE3	2.48	0.52
1:A:925:A:C6	1:A:947:A:C4	2.97	0.52
1:A:1029:A:N6	1:A:1030:G:O6	2.43	0.52
1:A:1043:G:H1	1:A:1204:C:H42	1.57	0.52
1:A:1178:U:O4'	8:J:76:TYR:CZ	2.62	0.52
1:A:2281:G:O6	19:V:12:LYS:HD2	2.08	0.52
1:A:2886:C:H2'	1:A:2887:A:H8	1.73	0.52
3:C:120:PRO:O	3:C:134:ASN:ND2	2.42	0.52
4:D:29:GLU:HB2	4:D:185:LEU:HD23	1.91	0.52
4:D:83:LEU:HD21	4:D:203:LYS:CD	2.36	0.52
7:G:89:GLU:HB3	7:G:164:ARG:HB2	1.91	0.52
24:W:71:TRP:NE1	24:W:278:GLU:O	2.39	0.52
1:A:512:G:H21	1:A:731:G:H1'	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1614:A:OP1	3:C:210:ARG:NH2	2.40	0.52
1:A:1615:A:H5'	3:C:85:PRO:HB3	1.91	0.52
1:A:2066:A:H2'	1:A:2067:G:C8	2.44	0.52
1:A:2849:U:H3'	1:A:2850:G:H21	1.75	0.52
1:A:580:U:C2	1:A:581:C:C5	2.98	0.52
1:A:2093:C:O2	1:A:2093:C:H2'	2.09	0.52
1:A:2828:G:H2'	1:A:2829:G:H8	1.74	0.52
4:D:108:VAL:N	4:D:205:ALA:HB2	2.25	0.52
6:F:36:ILE:HB	6:F:89:VAL:O	2.10	0.52
6:F:38:MET:SD	6:F:57:LEU:HD22	2.50	0.52
10:L:70:ASN:OD1	10:L:70:ASN:N	2.43	0.52
14:Q:99:ALA:HB1	14:Q:105:ALA:HB3	1.92	0.52
1:A:19:G:N1	1:A:568:G:C6	2.77	0.52
1:A:1425:C:H2'	1:A:1426:A:H8	1.75	0.52
1:A:1762:G:H2'	1:A:1763:G:H8	1.74	0.52
1:A:2112:G:H1	1:A:2265:U:H3	1.58	0.52
1:A:2163:A:N7	1:A:2185:G:N1	2.46	0.52
1:A:2558:G:P	1:A:2558:G:H21	2.33	0.52
1:A:2717:G:N1	1:A:2749:U:OP2	2.41	0.52
3:C:72:ASP:OD1	3:C:72:ASP:N	2.41	0.52
12:O:75:THR:HG21	12:O:108:ALA:HB1	1.89	0.52
1:A:789:C:H2'	1:A:790:A:C8	2.44	0.52
1:A:1231:G:OP1	10:L:30:THR:OG1	2.26	0.52
1:A:2224:U:H2'	1:A:2225:C:H6	1.74	0.52
4:D:55:ASP:HB3	4:D:77:LYS:NZ	2.25	0.52
13:P:45:ILE:O	13:P:45:ILE:HG23	2.10	0.52
13:P:46:PHE:CZ	13:P:66:LYS:HD3	2.44	0.52
14:Q:42:SER:OG	14:Q:43:GLY:N	2.42	0.52
16:S:70:VAL:CG1	16:S:71:ILE:N	2.72	0.52
18:U:79:THR:HG21	18:U:96:LYS:HB2	1.90	0.52
19:V:35:ASP:N	19:V:35:ASP:OD1	2.40	0.52
24:W:87:SER:OG	25:W:301:GNP:C6	2.58	0.52
24:W:210:LEU:HD13	24:W:237:LEU:CD2	2.40	0.52
1:A:342:A:P	18:U:95:LYS:HZ1	2.33	0.52
1:A:602:G:H2'	1:A:603:G:H8	1.74	0.52
1:A:1526:G:N2	1:A:1558:G:C2	2.78	0.52
1:A:1616:G:OP2	3:C:63:ARG:NH1	2.43	0.52
1:A:2670:A:H5''	8:J:79:THR:CG2	2.40	0.52
1:A:2675:C:C5	1:A:2676:U:C5	2.98	0.52
24:W:21:LEU:O	24:W:51:LYS:NZ	2.42	0.52
1:A:269:G:O2'	1:A:322:A:N6	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1616:G:O3'	3:C:59:LYS:NZ	2.40	0.52
1:A:2688:G:N2	1:A:2691:A:OP2	2.42	0.52
4:D:109:ASP:HB2	4:D:205:ALA:HA	1.92	0.52
12:O:78:GLY:O	12:O:109:LEU:HD11	2.10	0.52
18:U:84:LYS:N	18:U:93:VAL:HG11	2.19	0.52
24:W:74:HIS:NE2	24:W:78:GLN:OE1	2.43	0.52
1:A:77:U:OP1	22:Y:52:ARG:NH1	2.43	0.52
1:A:732:A:O5'	1:A:835:A:N6	2.43	0.52
1:A:1257:C:O2	1:A:1272:G:N2	2.35	0.52
1:A:2084:C:O2	1:A:2601:A:N6	2.43	0.52
1:A:2607:G:N7	4:D:145:SER:OG	2.41	0.52
4:D:15:VAL:O	4:D:15:VAL:CG1	3.33	0.52
6:F:33:LYS:O	6:F:157:VAL:HG23	2.10	0.52
11:N:119:LEU:C	11:N:120:VAL:HG23	2.30	0.52
18:U:45:SER:OG	18:U:55:GLY:O	2.28	0.52
24:W:75:PHE:HA	24:W:78:GLN:HG3	1.92	0.52
1:A:376:A:C2	1:A:379:C:C6	2.98	0.51
1:A:1364:C:N3	16:S:86:ARG:NH1	2.57	0.51
1:A:1382:G:O6	1:A:1442:A:N6	2.43	0.51
1:A:1708:U:O4	1:A:2027:A:N6	2.43	0.51
1:A:2298:A:N6	1:A:2299:G:C6	2.78	0.51
12:O:40:ILE:O	12:O:57:SER:OG	2.28	0.51
14:Q:66:ASN:OD1	14:Q:70:ARG:NH1	2.44	0.51
18:U:11:VAL:HG12	18:U:12:ILE:H	1.73	0.51
1:A:861:C:H2'	1:A:862:U:C6	2.45	0.51
1:A:2326:C:H42	1:A:2350:G:H1	1.58	0.51
4:D:63:LYS:HA	4:D:66:LYS:HB2	1.93	0.51
4:D:123:ILE:HD11	4:D:141:ARG:HA	1.91	0.51
1:A:5:A:H61	1:A:2922:U:H3	1.58	0.51
1:A:2298:A:C4	1:A:2299:G:C8	2.99	0.51
1:A:2357:A:H61	1:A:2416:U:H3	1.58	0.51
4:D:32:PRO:HG3	4:D:98:LYS:CG	2.32	0.51
4:D:55:ASP:CA	4:D:77:LYS:HB3	2.39	0.51
6:F:96:MET:HG3	6:F:96:MET:O	2.11	0.51
7:G:60:LYS:NZ	7:G:60:LYS:CB	2.73	0.51
1:A:198:A:N6	1:A:201:C:OP2	2.43	0.51
4:D:49:ILE:HD11	4:D:91:TYR:CD2	2.45	0.51
18:U:80:ARG:O	18:U:94:ALA:HA	2.10	0.51
1:A:559:A:O2'	1:A:1257:C:OP1	2.28	0.51
1:A:948:A:C5'	1:A:948:A:N3	2.73	0.51
1:A:970:A:O3'	19:V:37:GLN:NE2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1469:G:HO2'	1:A:1545:C:HO2'	1.51	0.51
1:A:1695:A:OP1	11:N:8:ARG:NH2	2.44	0.51
3:C:172:VAL:HG12	3:C:174:VAL:HG23	1.93	0.51
10:L:76:VAL:O	10:L:76:VAL:HG12	2.09	0.51
24:W:24:ILE:HG21	24:W:124:LEU:HB2	1.93	0.51
24:W:37:MET:SD	24:W:71:TRP:HH2	2.32	0.51
1:A:380:C:H2'	1:A:381:U:H6	1.76	0.51
1:A:719:C:N3	1:A:856:G:N1	2.57	0.51
1:A:1554:U:H3'	1:A:1555:A:C5'	2.39	0.51
1:A:2280:G:O6	19:V:12:LYS:HE3	2.09	0.51
7:G:72:LEU:HD22	7:G:140:GLU:OE2	2.09	0.51
10:L:74:TYR:CE1	10:L:127:LYS:HG3	2.44	0.51
19:V:53:ILE:CD1	19:V:67:LEU:CD1	2.89	0.51
24:W:39:SER:CA	24:W:128:ILE:HG13	2.41	0.51
1:A:1578:G:O2'	1:A:1587:U:O4	2.20	0.51
4:D:79:PHE:CG	4:D:199:LEU:CD2	2.94	0.51
1:A:1099:C:H42	1:A:1152:G:H1	1.58	0.51
1:A:1306:G:OP2	16:S:15:ARG:NH2	2.44	0.51
1:A:1437:C:O3'	17:T:25:LYS:NZ	2.44	0.51
1:A:1554:U:H3'	1:A:1555:A:H5'	1.93	0.51
1:A:2082:G:O2'	4:D:152:ASN:ND2	2.39	0.51
1:A:2094:C:H2'	1:A:2095:C:H6	1.76	0.51
1:A:2824:G:C2	1:A:2826:A:H5''	2.46	0.51
10:L:91:VAL:CB	10:L:122:THR:O	2.59	0.51
12:O:69:GLY:C	12:O:105:ARG:HH12	2.13	0.51
16:S:53:SER:O	16:S:57:ASN:N	2.41	0.51
1:A:568:G:O2'	1:A:587:C:O2'	2.26	0.51
1:A:925:A:N3	1:A:925:A:C5'	2.74	0.51
1:A:947:A:H3'	1:A:948:A:C2	2.45	0.51
1:A:1129:U:N3	1:A:1132:A:OP2	2.42	0.51
1:A:1231:G:H2'	1:A:1232:G:H8	1.74	0.51
1:A:2230:C:H2'	1:A:2231:C:C6	2.46	0.51
1:A:2334:U:O4	6:F:39:GLY:HA3	2.10	0.51
4:D:156:LYS:O	8:J:81:HIS:ND1	2.34	0.51
5:E:139:MET:N	5:E:139:MET:SD	2.84	0.51
10:L:77:VAL:O	10:L:111:ILE:HA	2.11	0.51
16:S:29:VAL:HG12	16:S:29:VAL:O	2.10	0.51
1:A:1500:U:OP2	11:N:81:GLN:NE2	2.44	0.51
4:D:62:ASN:O	4:D:65:GLU:N	2.44	0.51
1:A:52:A:OP2	1:A:116:G:N1	2.44	0.50
1:A:1038:C:OP1	15:R:84:LYS:NZ	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2003:C:OP1	24:W:144:ASN:ND2	2.39	0.50
3:C:68:LYS:O	3:C:69:ARG:C	2.50	0.50
3:C:171:TYR:CE2	3:C:269:PHE:CZ	2.99	0.50
1:A:573:C:N4	1:A:2072:C:OP2	2.44	0.50
1:A:615:U:O2'	1:A:617:G:OP2	2.27	0.50
1:A:948:A:N3	1:A:948:A:H5''	2.26	0.50
1:A:2153:G:N2	1:A:2203:C:N3	2.58	0.50
1:A:2688:G:O2'	1:A:2690:G:N7	2.38	0.50
5:E:103:LYS:HG3	5:E:106:ARG:HH21	1.77	0.50
6:F:69:ARG:HE	6:F:82:GLY:CA	2.20	0.50
24:W:67:VAL:HG23	24:W:276:SER:OG	2.07	0.50
1:A:357:G:C5	1:A:358:C:C5	3.00	0.50
1:A:455:G:H2'	1:A:456:A:H8	1.76	0.50
1:A:745:C:H5''	1:A:746:A:H5'	1.93	0.50
1:A:1831:A:HO2'	1:A:1832:A:H8	1.58	0.50
1:A:2065:C:H2'	1:A:2066:A:H8	1.76	0.50
1:A:2777:A:C2'	7:G:64:ALA:HA	2.36	0.50
1:A:2847:G:O3'	4:D:163:ARG:NH2	2.44	0.50
1:A:2922:U:H2'	1:A:2923:A:C8	2.47	0.50
4:D:107:ILE:CB	4:D:205:ALA:HB3	2.41	0.50
8:J:25:THR:O	8:J:29:LEU:CD2	2.59	0.50
14:Q:92:ARG:HH12	14:Q:93:LYS:HE2	1.76	0.50
16:S:9:THR:OG1	16:S:102:HIS:NE2	2.44	0.50
24:W:191:VAL:CG1	24:W:277:PHE:HZ	2.19	0.50
1:A:638:U:H2'	1:A:639:C:C6	2.46	0.50
1:A:869:U:O4	1:A:882:A:N6	2.42	0.50
1:A:1370:C:O2'	1:A:1371:G:N2	2.41	0.50
1:A:1444:C:H2'	1:A:1445:A:H8	1.76	0.50
1:A:1847:U:HO2'	3:C:154:LEU:HA	1.74	0.50
1:A:2218:U:O2	1:A:2218:U:C2'	2.60	0.50
1:A:2810:A:H5''	1:A:2811:G:H5'	1.93	0.50
8:J:47:PRO:O	8:J:115:LEU:HD11	2.11	0.50
13:P:56:GLY:N	13:P:60:GLU:OE2	2.44	0.50
13:P:63:THR:HA	13:P:75:ARG:O	2.11	0.50
16:S:53:SER:O	16:S:57:ASN:HB2	2.11	0.50
1:A:19:G:C6	1:A:568:G:C6	3.00	0.50
1:A:1381:A:O2'	1:A:1383:U:OP2	2.29	0.50
1:A:1397:G:C2	1:A:1411:U:C5	2.66	0.50
1:A:1481:G:H1	1:A:1605:C:H42	1.60	0.50
1:A:2038:G:H5''	16:S:40:PRO:HB2	1.92	0.50
3:C:61:GLN:O	3:C:63:ARG:NH2	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:195:VAL:CG1	3:C:196:GLY:N	2.74	0.50
4:D:69:VAL:O	4:D:73:GLU:N	2.44	0.50
8:J:44:THR:CG2	14:Q:100:VAL:HG12	2.36	0.50
9:K:93:PRO:HD2	9:K:113:LYS:HD3	1.92	0.50
16:S:89:ALA:C	16:S:91:GLY:N	2.65	0.50
1:A:657:G:H21	1:A:661:A:H62	1.59	0.50
1:A:2152:A:H62	1:A:2200:A:H4'	1.76	0.50
3:C:72:ASP:HB2	3:C:119:GLY:HA2	1.94	0.50
3:C:77:ARG:NH1	3:C:113:GLY:O	2.45	0.50
7:G:145:ILE:HA	7:G:148:ASN:HB2	1.94	0.50
24:W:31:VAL:HG13	24:W:39:SER:CB	2.37	0.50
1:A:75:G:O3'	22:Y:48:LYS:NZ	2.40	0.50
1:A:504:A:H62	1:A:519:A:H62	1.60	0.50
1:A:635:C:C2	1:A:636:G:C8	2.99	0.50
1:A:997:C:OP1	2:B:88:C:N4	2.45	0.50
1:A:1421:A:O3'	1:A:1621:G:N2	2.43	0.50
1:A:2541:C:OP1	4:D:129:SER:N	2.44	0.50
1:A:2610:G:N2	1:A:2639:C:OP2	2.45	0.50
1:A:2829:G:H2'	1:A:2830:A:O4'	2.11	0.50
10:L:73:GLU:HG2	10:L:73:GLU:O	2.11	0.50
12:O:102:TYR:OH	12:O:110:ALA:CB	2.60	0.50
16:S:8:ARG:HD3	16:S:102:HIS:CE1	2.47	0.50
16:S:20:VAL:O	16:S:20:VAL:HG12	2.12	0.50
16:S:81:THR:OG1	16:S:82:LEU:N	2.44	0.50
17:T:62:LYS:H	17:T:73:THR:HG22	1.75	0.50
1:A:380:C:H2'	1:A:381:U:C6	2.46	0.50
1:A:735:U:H2'	1:A:736:A:H8	1.77	0.50
1:A:1745:A:H3'	1:A:1746:A:H8	1.76	0.50
1:A:2542:A:H3'	1:A:2543:U:H6	1.76	0.50
3:C:105:LEU:HD11	3:C:156:ARG:HG2	1.94	0.50
3:C:172:VAL:HG12	3:C:173:LEU:N	2.27	0.50
8:J:88:ARG:HH22	8:J:96:ASN:HD22	1.58	0.50
18:U:3:VAL:HG21	18:U:70:PRO:HD3	1.92	0.50
1:A:634:A:N7	1:A:635:C:C5	2.80	0.50
1:A:703:G:C2	1:A:704:U:C2	3.00	0.50
1:A:1023:G:H2'	1:A:1024:G:H8	1.77	0.50
1:A:1419:G:H21	1:A:1617:A:H61	1.60	0.50
4:D:38:LYS:HZ1	4:D:88:MET:HG2	1.73	0.50
15:R:39:LEU:HB2	15:R:48:VAL:HG21	1.94	0.50
24:W:41:ASN:ND2	24:W:176:LEU:O	2.43	0.50
24:W:41:ASN:CG	24:W:175:ILE:HG22	2.32	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:211:ARG:HA	24:W:214:GLU:HB2	1.94	0.50
1:A:342:A:H5''	18:U:95:LYS:HZ2	1.57	0.49
1:A:2039:G:OP1	16:S:41:ARG:HA	2.12	0.49
6:F:60:ILE:CD1	6:F:152:MET:SD	2.99	0.49
14:Q:79:LEU:HD21	14:Q:106:PHE:CZ	2.47	0.49
24:W:156:THR:CG2	24:W:172:THR:OG1	2.59	0.49
1:A:106:G:H4'	1:A:337:A:H5''	1.95	0.49
1:A:531:C:P	18:U:47:PRO:HG3	2.51	0.49
1:A:796:A:N7	1:A:1663:A:N6	2.60	0.49
1:A:1332:U:H2'	1:A:1333:C:H6	1.77	0.49
1:A:1493:C:H2'	1:A:1494:G:C8	2.47	0.49
1:A:1782:G:OP1	13:P:96:ARG:NH2	2.41	0.49
1:A:2292:C:O2'	1:A:2293:C:H5'	2.12	0.49
2:B:55:A:H62	6:F:26:MET:CE	2.17	0.49
6:F:68:THR:HG21	6:F:88:LYS:CD	2.40	0.49
12:O:35:ARG:NH1	12:O:105:ARG:HE	1.97	0.49
20:Z:39:ASP:OD1	20:Z:44:ARG:NH2	2.45	0.49
24:W:76:GLU:HA	24:W:80:ILE:O	2.12	0.49
24:W:123:ALA:HB3	24:W:169:LEU:HD21	1.94	0.49
24:W:220:ARG:NE	24:W:275:LEU:CD2	2.75	0.49
1:A:361:G:H1	1:A:378:C:H42	1.60	0.49
1:A:1246:G:H1'	1:A:1247:G:H5'	1.93	0.49
1:A:1301:U:H2'	1:A:1302:A:H8	1.76	0.49
1:A:1496:G:H1	1:A:1507:U:H3	1.60	0.49
1:A:1528:U:H4'	1:A:1529:G:H5'	1.94	0.49
1:A:1858:A:C8	1:A:1859:C:N4	2.80	0.49
1:A:1858:A:C6	1:A:1859:C:C2	3.00	0.49
1:A:2082:G:H2'	1:A:2083:A:H8	1.76	0.49
1:A:2573:G:N2	1:A:2675:C:O2'	2.37	0.49
1:A:2777:A:C2'	7:G:64:ALA:HB1	2.41	0.49
6:F:67:VAL:HA	6:F:87:ALA:HA	1.93	0.49
8:J:14:ARG:HH12	8:J:122:LYS:HE3	1.75	0.49
9:K:12:ASP:OD1	9:K:12:ASP:N	2.40	0.49
20:Z:7:THR:O	20:Z:54:VAL:HG12	2.12	0.49
24:W:40:ARG:O	24:W:128:ILE:HD11	2.11	0.49
24:W:191:VAL:CG1	24:W:277:PHE:CZ	2.95	0.49
1:A:19:G:N2	1:A:568:G:C4	2.80	0.49
1:A:621:G:H2'	1:A:622:A:C8	2.47	0.49
1:A:673:A:N7	10:L:76:VAL:HG13	2.27	0.49
1:A:727:A:H2'	1:A:728:G:H8	1.76	0.49
1:A:2326:C:O2	1:A:2327:A:H1'	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2711:G:O2'	4:D:14:GLN:NE2	2.45	0.49
1:A:925:A:N3	1:A:925:A:C3'	2.73	0.49
1:A:1478:G:H2'	1:A:1479:G:C8	2.48	0.49
5:E:58:ARG:O	5:E:79:ARG:NH1	2.45	0.49
1:A:284:C:O2'	1:A:287:G:O6	2.31	0.49
1:A:796:A:H61	1:A:800:G:H21	1.60	0.49
1:A:1672:A:H2'	1:A:1673:G:H8	1.78	0.49
4:D:107:ILE:CG2	4:D:205:ALA:HB3	2.43	0.49
8:J:26:LEU:HD12	8:J:102:LEU:CD1	2.30	0.49
14:Q:94:MET:O	14:Q:97:ASP:OD1	2.30	0.49
24:W:249:MET:HB3	24:W:255:ASN:HB2	1.94	0.49
1:A:2309:G:N7	19:V:22:ARG:NH2	2.61	0.49
1:A:2839:C:H3'	1:A:2840:C:H6	1.77	0.49
6:F:17:MET:CE	6:F:25:VAL:O	2.61	0.49
8:J:57:ILE:HD12	8:J:125:VAL:CG2	2.34	0.49
9:K:11:ALA:O	9:K:99:PHE:N	2.35	0.49
20:Z:22:THR:HG21	20:Z:49:LYS:HD3	1.93	0.49
24:W:31:VAL:CG1	24:W:36:PRO:HA	2.43	0.49
1:A:1557:G:H8	1:A:1557:G:O5'	1.95	0.49
1:A:2290:C:O4'	1:A:2417:A:H1'	2.13	0.49
1:A:2536:C:O5'	1:A:2536:C:H6	1.95	0.49
2:B:64:A:H2	2:B:66:C:H41	1.59	0.49
9:K:43:VAL:O	9:K:43:VAL:HG12	2.09	0.49
16:S:14:PRO:HG3	16:S:78:GLU:HB3	1.93	0.49
1:A:634:A:C8	1:A:635:C:C5	3.01	0.49
1:A:1518:G:H1	1:A:1566:G:H1	1.61	0.49
1:A:2024:U:O2	9:K:3:GLN:NE2	2.45	0.49
4:D:49:ILE:O	4:D:82:GLU:HB3	2.12	0.49
12:O:28:ARG:N	12:O:29:PRO:CD	2.74	0.49
24:W:31:VAL:HG12	24:W:36:PRO:HA	1.94	0.49
1:A:337:A:O2'	1:A:338:G:O4'	2.31	0.49
1:A:761:U:N3	1:A:764:C:OP2	2.35	0.49
1:A:1557:G:H2'	1:A:1558:G:C8	2.48	0.49
3:C:126:VAL:HG23	3:C:193:GLY:HA3	1.95	0.49
8:J:25:THR:C	8:J:29:LEU:CD2	2.81	0.49
14:Q:44:ASN:ND2	15:R:76:TYR:H	2.09	0.49
14:Q:86:SER:HB3	14:Q:116:GLN:HE21	1.78	0.49
1:A:527:A:O2'	18:U:43:LYS:HG2	2.13	0.48
1:A:869:U:H5	1:A:990:C:H1'	1.78	0.48
1:A:1471:G:N7	3:C:31:LYS:NZ	2.61	0.48
1:A:1616:G:H5''	3:C:61:GLN:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2000:A:OP2	1:A:2000:A:H4'	2.13	0.48
1:A:2111:A:H3'	1:A:2112:G:H8	1.77	0.48
4:D:5:ILE:HG22	4:D:33:ASN:ND2	2.27	0.48
8:J:25:THR:HG23	8:J:28:ARG:H	1.76	0.48
8:J:26:LEU:CA	8:J:29:LEU:CG	2.87	0.48
15:R:86:GLN:NE2	15:R:87:GLY:O	2.41	0.48
18:U:79:THR:HB	18:U:94:ALA:HB1	1.95	0.48
22:Y:4:ASN:HA	22:Y:7:ARG:HH21	1.77	0.48
1:A:65:A:H5'	17:T:71:GLY:HA3	1.95	0.48
1:A:739:C:H2'	1:A:740:A:H8	1.77	0.48
1:A:2576:U:HO2'	1:A:2577:G:H8	1.59	0.48
1:A:2684:G:N2	1:A:2685:U:O4	2.37	0.48
13:P:35:VAL:HB	13:P:42:ARG:HG3	1.95	0.48
14:Q:85:LEU:HB2	14:Q:116:GLN:HG3	1.95	0.48
24:W:129:PRO:HG3	24:W:176:LEU:CD2	2.43	0.48
1:A:279:A:H2'	1:A:280:G:H8	1.77	0.48
1:A:568:G:HO2'	1:A:587:C:HO2'	1.61	0.48
1:A:907:U:HO2'	1:A:908:A:H8	1.61	0.48
1:A:1554:U:C5'	1:A:1555:A:C5	2.96	0.48
1:A:2420:G:N1	1:A:2453:C:O2'	2.46	0.48
1:A:2554:G:HO2'	1:A:2771:G:HO2'	1.57	0.48
1:A:2850:G:H3'	1:A:2851:A:H8	1.79	0.48
6:F:38:MET:HE3	6:F:57:LEU:HD22	1.95	0.48
10:L:125:ALA:HB3	10:L:128:PHE:CZ	2.45	0.48
24:W:81:ARG:HH12	24:W:103:ILE:CG1	1.66	0.48
1:A:357:G:C4	1:A:358:C:C5	3.01	0.48
1:A:1673:G:H2'	1:A:1674:G:C8	2.48	0.48
1:A:2233:C:H4'	3:C:150:LYS:HE2	1.95	0.48
1:A:2800:C:O2'	4:D:172:GLN:NE2	2.37	0.48
2:B:74:G:H2'	2:B:75:U:H6	1.78	0.48
8:J:26:LEU:CB	8:J:63:ILE:CG2	2.81	0.48
14:Q:110:ALA:O	14:Q:113:ALA:N	2.46	0.48
18:U:72:ASP:N	18:U:77:GLU:O	2.41	0.48
1:A:614:G:OP1	1:A:1018:G:O2'	2.25	0.48
1:A:910:A:O2'	2:B:98:G:N3	2.46	0.48
1:A:2342:C:C5'	6:F:88:LYS:CD	2.64	0.48
1:A:2605:G:O2'	1:A:2608:C:OP2	2.30	0.48
3:C:171:TYR:OH	3:C:269:PHE:HE1	1.95	0.48
4:D:27:VAL:CG2	13:P:8:ILE:HD11	2.21	0.48
1:A:435:G:O2'	1:A:437:A:OP2	2.24	0.48
1:A:743:U:H2'	1:A:744:C:C6	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1482:G:O2'	1:A:1523:U:O2	2.30	0.48
1:A:2103:U:H3	1:A:2464:A:H61	1.61	0.48
1:A:2285:G:H2'	1:A:2286:U:C6	2.48	0.48
1:A:2291:U:O2	1:A:2307:A:H2	1.96	0.48
1:A:2344:U:O2	1:A:2344:U:C2'	2.60	0.48
1:A:2353:U:O2	1:A:2414:C:C5	2.67	0.48
1:A:2664:U:O2'	4:D:82:GLU:OE2	2.25	0.48
8:J:18:VAL:N	8:J:139:GLU:O	2.46	0.48
12:O:65:VAL:HB	12:O:68:THR:H	1.79	0.48
13:P:27:ASP:O	13:P:49:VAL:CG1	2.62	0.48
22:Y:2:LYS:HD3	22:Y:2:LYS:O	2.13	0.48
1:A:288:C:OP2	1:A:289:C:N4	2.46	0.48
1:A:760:G:O2'	1:A:766:C:N3	2.47	0.48
1:A:833:C:H2'	1:A:834:C:H6	1.79	0.48
1:A:1178:U:H5''	8:J:85:LEU:CD2	2.44	0.48
1:A:1417:A:O2'	1:A:1419:G:OP2	2.29	0.48
1:A:1580:A:OP2	1:A:1581:A:N6	2.47	0.48
2:B:22:G:H22	2:B:57:G:H1	1.61	0.48
10:L:81:LYS:HB3	10:L:101:VAL:CG1	2.44	0.48
13:P:58:ILE:O	13:P:80:HIS:CD2	2.67	0.48
13:P:60:GLU:O	13:P:79:VAL:HG23	2.14	0.48
18:U:84:LYS:CE	18:U:84:LYS:C	2.54	0.48
19:V:46:TYR:HB3	19:V:67:LEU:HD12	1.95	0.48
1:A:594:C:OP1	15:R:92:TYR:OH	2.27	0.48
1:A:833:C:C2	1:A:834:C:C5	3.02	0.48
1:A:948:A:OP2	1:A:948:A:H2	1.97	0.48
1:A:2607:G:OP1	1:A:2643:A:N6	2.46	0.48
3:C:94:ILE:HG13	3:C:104:ILE:CG2	2.44	0.48
4:D:35:VAL:CG2	4:D:91:TYR:CE1	2.96	0.48
14:Q:79:LEU:O	14:Q:83:LEU:N	2.47	0.48
24:W:72:LYS:HG3	24:W:82:SER:OG	2.13	0.48
1:A:334:G:C2	1:A:394:U:C2	3.01	0.48
1:A:617:G:O2'	1:A:619:A:OP1	2.32	0.48
1:A:775:G:H5''	3:C:13:ARG:HH22	1.78	0.48
1:A:1519:C:O2	1:A:1566:G:N2	2.47	0.48
1:A:2062:A:O2'	1:A:2064:G:OP2	2.32	0.48
1:A:2290:C:H5	19:V:24:SER:HB2	1.78	0.48
1:A:2293:C:N4	19:V:23:ASP:OD2	2.47	0.48
1:A:2369:A:H2'	1:A:2370:G:H8	1.77	0.48
1:A:2552:G:H2'	1:A:2553:G:H8	1.79	0.48
5:E:153:LEU:HB3	5:E:192:LEU:HB2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:P:78:PRO:O	13:P:84:ILE:HD12	2.14	0.48
24:W:129:PRO:HD3	24:W:176:LEU:HA	1.96	0.48
1:A:206:A:N1	1:A:207:A:N6	2.62	0.48
1:A:302:A:H2'	1:A:303:G:C8	2.49	0.48
1:A:527:A:H4'	18:U:43:LYS:CD	2.44	0.48
1:A:673:A:N7	10:L:76:VAL:CG1	2.77	0.48
1:A:950:U:C4	1:A:951:C:N3	2.82	0.48
1:A:1160:G:H2'	1:A:1161:A:H8	1.79	0.48
1:A:2076:C:H2'	1:A:2077:G:C8	2.48	0.48
1:A:2313:C:O2'	1:A:2317:A:N6	2.46	0.48
2:B:27:A:N6	2:B:52:G:O6	2.46	0.48
11:N:21:THR:HG22	11:N:44:VAL:HG22	1.96	0.48
16:S:3:ALA:N	16:S:107:VAL:O	2.45	0.48
1:A:241:C:H42	1:A:262:G:H1	1.60	0.47
1:A:1433:U:H4'	1:A:1648:A:H4'	1.96	0.47
1:A:1546:G:O3'	3:C:101:LYS:NZ	2.42	0.47
1:A:1673:G:H2'	1:A:1674:G:H8	1.79	0.47
2:B:37:A:O2'	2:B:45:C:O2	2.28	0.47
2:B:102:A:H3'	2:B:103:G:H8	1.79	0.47
8:J:90:ALA:O	8:J:94:ARG:N	2.46	0.47
9:K:113:LYS:O	9:K:116:SER:OG	2.26	0.47
12:O:70:ASP:OD1	12:O:70:ASP:N	2.30	0.47
14:Q:86:SER:OG	14:Q:112:ALA:O	2.31	0.47
1:A:167:U:H2'	1:A:168:A:H8	1.79	0.47
1:A:909:G:H22	1:A:963:G:H1'	1.79	0.47
1:A:2267:G:H1'	1:A:2269:C:H5	1.79	0.47
1:A:2320:U:OP1	1:A:2409:U:O2'	2.32	0.47
1:A:2853:C:H2'	1:A:2854:A:C8	2.47	0.47
6:F:38:MET:HE1	6:F:57:LEU:CD1	2.36	0.47
9:K:87:ILE:HD11	9:K:92:SER:N	2.29	0.47
10:L:79:LEU:HD22	10:L:117:LEU:CA	2.44	0.47
13:P:90:VAL:HG12	13:P:91:ARG:HG3	1.96	0.47
1:A:351:G:N1	1:A:354:A:OP2	2.47	0.47
1:A:1827:U:O2	1:A:1831:A:H2	1.96	0.47
1:A:2469:C:H2'	1:A:2470:C:H4'	1.96	0.47
2:B:41:C:C5'	6:F:63:GLN:CD	2.78	0.47
3:C:84:ASP:OD2	3:C:87:ARG:N	2.33	0.47
4:D:51:LEU:N	4:D:81:LYS:O	2.36	0.47
12:O:11:ARG:NH1	12:O:33:VAL:O	2.37	0.47
14:Q:90:VAL:O	14:Q:90:VAL:CG1	2.62	0.47
1:A:1054:A:OP2	8:J:38:ARG:NH1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1446:C:O2	1:A:1640:G:N2	2.41	0.47
4:D:37:GLN:H	4:D:50:GLN:HB2	1.79	0.47
4:D:55:ASP:N	4:D:77:LYS:HB3	2.29	0.47
11:N:119:LEU:O	11:N:120:VAL:HG23	2.15	0.47
13:P:58:ILE:HA	13:P:80:HIS:HD2	1.78	0.47
1:A:746:A:H62	1:A:780:G:H21	1.62	0.47
1:A:776:G:C8	3:C:207:LYS:HE2	2.50	0.47
1:A:2364:A:OP1	12:O:17:ARG:HG3	2.14	0.47
1:A:2839:C:C6	1:A:2840:C:C5	3.02	0.47
2:B:40:C:C4'	6:F:64:LYS:HB3	2.44	0.47
3:C:72:ASP:OD2	3:C:189:ARG:NH2	2.44	0.47
10:L:74:TYR:CZ	10:L:127:LYS:CG	2.96	0.47
13:P:26:GLY:HA3	13:P:95:VAL:HG21	1.96	0.47
24:W:42:PRO:CD	24:W:177:TRP:HE1	2.28	0.47
1:A:744:C:H42	1:A:812:G:H1	1.63	0.47
1:A:2001:G:H8	1:A:2001:G:O5'	1.97	0.47
1:A:2015:G:H4'	24:W:198:SER:HB3	1.97	0.47
1:A:2113:C:H42	1:A:2264:G:H1	1.62	0.47
1:A:2275:G:C2	1:A:2455:A:C4	3.02	0.47
1:A:2357:A:N6	1:A:2416:U:H3	2.12	0.47
1:A:2537:G:N1	1:A:2611:G:C6	2.82	0.47
3:C:37:LEU:HB2	3:C:62:TYR:HB2	1.96	0.47
14:Q:45:TYR:HD1	14:Q:48:ARG:HH21	1.62	0.47
15:R:14:VAL:HG13	15:R:97:ILE:HG13	1.91	0.47
1:A:213:C:H2'	1:A:214:G:H8	1.79	0.47
1:A:379:C:C2	1:A:380:C:C5	3.02	0.47
1:A:1307:U:H2'	1:A:1308:A:H8	1.79	0.47
1:A:1446:C:H2'	1:A:1447:C:H6	1.80	0.47
1:A:1472:G:H5''	1:A:1473:A:H2'	1.96	0.47
1:A:1850:A:H2'	1:A:1851:G:H8	1.79	0.47
1:A:2261:C:H2'	1:A:2262:A:H8	1.80	0.47
4:D:32:PRO:CB	4:D:98:LYS:CG	2.83	0.47
4:D:55:ASP:HB2	4:D:77:LYS:HG2	1.94	0.47
5:E:4:VAL:HG22	5:E:19:LEU:HD11	1.97	0.47
8:J:88:ARG:NH1	8:J:97:TYR:OH	2.48	0.47
10:L:90:GLU:N	10:L:122:THR:OG1	2.47	0.47
12:O:78:GLY:CA	12:O:109:LEU:HD13	2.44	0.47
13:P:16:LEU:HG	13:P:80:HIS:CE1	2.49	0.47
24:W:58:ASN:OD1	24:W:58:ASN:N	2.44	0.47
24:W:83:LEU:HD22	24:W:95:GLN:HG3	1.96	0.47
24:W:211:ARG:O	24:W:215:GLU:N	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:632:U:C2	1:A:633:U:C5	3.03	0.47
1:A:912:C:O2	1:A:913:A:N6	2.47	0.47
1:A:2026:A:H2'	1:A:2027:A:C8	2.49	0.47
1:A:2342:C:O2'	6:F:37:ASN:CG	2.53	0.47
2:B:74:G:C4	2:B:75:U:C5	3.03	0.47
3:C:210:ARG:HA	3:C:213:TRP:CD1	2.42	0.47
10:L:91:VAL:N	10:L:122:THR:O	2.45	0.47
12:O:61:LYS:HD3	12:O:61:LYS:HA	1.36	0.47
20:Z:45:GLY:HA2	20:Z:48:ASN:HB2	1.97	0.47
1:A:302:A:H2'	1:A:303:G:H8	1.80	0.47
1:A:1384:C:H2'	1:A:1385:G:C8	2.50	0.47
1:A:1476:C:H2'	1:A:1477:A:C8	2.50	0.47
1:A:2874:G:O2'	1:A:2891:G:N2	2.48	0.47
1:A:2900:A:O2'	13:P:5:GLN:N	2.45	0.47
6:F:57:LEU:HD23	6:F:65:PRO:HB3	1.96	0.47
14:Q:60:LEU:O	14:Q:63:THR:OG1	2.28	0.47
15:R:96:THR:O	15:R:96:THR:HG23	2.15	0.47
22:Y:34:THR:OG1	22:Y:36:GLN:NE2	2.48	0.47
1:A:196:U:H2'	1:A:197:G:H8	1.80	0.47
1:A:635:C:O2	1:A:636:G:C8	2.68	0.47
1:A:1068:G:N2	1:A:1069:U:O4	2.48	0.47
1:A:1674:G:H2'	1:A:1675:A:C8	2.50	0.47
1:A:2703:G:C5'	9:K:30:ARG:HD3	2.44	0.47
9:K:22:ILE:CD1	9:K:40:VAL:HG12	2.24	0.47
11:N:9:THR:OG1	11:N:10:SER:N	2.46	0.47
13:P:28:THR:HG22	13:P:49:VAL:HG22	1.97	0.47
13:P:94:LYS:HB2	13:P:118:ARG:NE	2.29	0.47
22:Y:20:SER:HA	22:Y:23:GLU:HB2	1.96	0.47
1:A:293:U:H2'	1:A:294:G:H8	1.80	0.46
1:A:455:G:H2'	1:A:456:A:C8	2.50	0.46
1:A:1527:C:C1'	1:A:1558:G:N2	2.72	0.46
1:A:1819:C:H2'	1:A:1820:A:C4	2.50	0.46
1:A:2342:C:C4'	6:F:37:ASN:OD1	2.58	0.46
1:A:2384:C:OP1	19:V:33:ARG:NH2	2.47	0.46
5:E:163:VAL:HG12	5:E:175:VAL:HG12	1.97	0.46
6:F:28:VAL:HG13	6:F:28:VAL:O	2.14	0.46
7:G:60:LYS:HB3	7:G:60:LYS:HZ1	1.76	0.46
8:J:60:ALA:HB2	8:J:126:TYR:O	2.14	0.46
8:J:106:ILE:HG21	8:J:123:LEU:HD13	1.96	0.46
16:S:10:VAL:HG12	16:S:11:ARG:N	2.30	0.46
16:S:70:VAL:CG1	16:S:71:ILE:H	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:V:48:GLN:NE2	19:V:53:ILE:H	2.13	0.46
1:A:679:A:O2'	1:A:2433:C:OP1	2.29	0.46
1:A:787:C:O2	1:A:2010:A:C8	2.68	0.46
1:A:1044:C:OP2	14:Q:93:LYS:NZ	2.39	0.46
1:A:1765:G:N2	1:A:1768:A:OP2	2.40	0.46
9:K:122:ILE:HD13	13:P:46:PHE:HE1	1.80	0.46
22:Y:6:ILE:HG22	22:Y:56:VAL:CG1	2.45	0.46
1:A:290:U:H1'	1:A:291:C:H5'	1.97	0.46
1:A:625:C:H2'	1:A:626:G:C8	2.50	0.46
1:A:984:G:H2'	1:A:985:G:H8	1.80	0.46
1:A:1581:A:O2'	1:A:1584:U:N3	2.49	0.46
1:A:1828:G:O2'	3:C:182:ARG:NH1	2.48	0.46
1:A:1849:U:OP1	3:C:177:ASN:ND2	2.48	0.46
1:A:2827:A:C5	1:A:2828:G:H1'	2.51	0.46
1:A:2828:G:H2'	1:A:2829:G:C8	2.51	0.46
1:A:2922:U:H2'	1:A:2923:A:H8	1.80	0.46
5:E:160:ASN:HB2	5:E:163:VAL:HG23	1.97	0.46
1:A:114:C:H2'	1:A:115:C:H6	1.79	0.46
1:A:461:C:H2'	1:A:462:A:C8	2.50	0.46
1:A:920:G:N7	1:A:946:G:O6	2.48	0.46
1:A:1595:U:H2'	1:A:1596:U:H6	1.81	0.46
1:A:1656:C:O2'	1:A:1657:C:O4'	2.34	0.46
1:A:2394:G:OP1	19:V:63:GLY:N	2.43	0.46
1:A:2423:C:N4	1:A:2450:G:O6	2.48	0.46
4:D:55:ASP:HB3	4:D:77:LYS:HZ3	1.80	0.46
4:D:58:GLU:HA	4:D:61:SER:HB3	1.98	0.46
9:K:25:LEU:HD12	9:K:38:VAL:CG1	2.44	0.46
10:L:79:LEU:HD22	10:L:117:LEU:HB2	1.80	0.46
24:W:32:ASP:CB	24:W:131:VAL:HG21	2.45	0.46
1:A:121:G:O6	1:A:128:C:N4	2.46	0.46
1:A:664:C:O2'	1:A:665:G:O4'	2.34	0.46
1:A:919:U:H6	1:A:919:U:H5''	1.81	0.46
1:A:1818:A:OP2	3:C:221:ARG:NE	2.48	0.46
1:A:2704:A:H5'	9:K:30:ARG:HB3	1.97	0.46
10:L:21:ARG:HD3	10:L:21:ARG:HA	1.78	0.46
1:A:2471:C:H2'	1:A:2472:C:H6	1.81	0.46
6:F:4:LEU:CG	6:F:97:TYR:HD1	2.18	0.46
1:A:185:A:H61	1:A:218:G:H1	1.63	0.46
1:A:1355:U:H2'	1:A:1356:G:C8	2.51	0.46
4:D:35:VAL:HG22	4:D:91:TYR:CD1	2.48	0.46
9:K:11:ALA:HB2	9:K:83:ALA:HB1	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:9:THR:O	11:N:13:ARG:N	2.49	0.46
13:P:94:LYS:HB2	13:P:118:ARG:NH2	2.30	0.46
14:Q:15:LYS:HD3	14:Q:15:LYS:HA	1.54	0.46
14:Q:69:ALA:O	14:Q:73:GLY:N	2.48	0.46
15:R:19:THR:HG22	15:R:96:THR:CB	2.45	0.46
17:T:52:ASP:HB2	17:T:84:THR:HG22	1.97	0.46
19:V:57:GLU:O	19:V:88:SER:OG	2.30	0.46
1:A:211:C:H2'	1:A:212:C:H6	1.81	0.46
1:A:684:G:C6	1:A:697:G:C2	3.04	0.46
1:A:709:G:H2'	1:A:710:G:H8	1.80	0.46
1:A:776:G:O6	3:C:208:ALA:N	2.42	0.46
1:A:1058:U:OP2	14:Q:70:ARG:NH2	2.49	0.46
1:A:1577:C:H3'	1:A:1578:G:H8	1.80	0.46
1:A:2286:U:O5'	1:A:2286:U:H6	1.99	0.46
1:A:2562:U:H4'	1:A:2693:G:H4'	1.98	0.46
4:D:83:LEU:HB3	4:D:86:VAL:HG22	1.96	0.46
24:W:129:PRO:CG	24:W:176:LEU:CD2	2.91	0.46
1:A:1537:G:H2'	1:A:1538:G:C8	2.50	0.46
1:A:1598:C:OP1	1:A:1764:U:O2'	2.27	0.46
1:A:1828:G:N2	3:C:154:LEU:HB3	2.30	0.46
1:A:2628:G:H2'	1:A:2629:A:H8	1.80	0.46
4:D:25:VAL:CG1	4:D:187:LEU:HB3	2.44	0.46
4:D:79:PHE:CB	4:D:199:LEU:HD22	2.46	0.46
6:F:33:LYS:CA	6:F:96:MET:HE1	2.45	0.46
8:J:53:ASP:OD1	8:J:53:ASP:N	2.47	0.46
10:L:81:LYS:HB3	10:L:101:VAL:HG13	1.98	0.46
15:R:64:LYS:O	15:R:94:LYS:N	2.49	0.46
24:W:74:HIS:O	24:W:78:GLN:CG	2.53	0.46
1:A:925:A:C5	1:A:947:A:N3	2.84	0.46
1:A:1027:A:O2'	1:A:2065:C:O2'	2.34	0.46
1:A:1043:G:OP1	14:Q:92:ARG:NH1	2.49	0.46
1:A:1090:U:HO2'	1:A:1157:A:H61	1.61	0.46
1:A:2895:C:H2'	1:A:2896:U:C6	2.51	0.46
8:J:32:GLU:CG	8:J:143:LEU:HG	2.33	0.46
8:J:78:HIS:HD2	8:J:85:LEU:HB2	1.81	0.46
14:Q:38:GLN:O	14:Q:42:SER:N	2.49	0.46
16:S:44:SER:N	16:S:45:PRO:CD	2.79	0.46
17:T:58:ASN:OD1	17:T:58:ASN:N	2.46	0.46
24:W:32:ASP:HB2	24:W:131:VAL:CG2	2.46	0.46
1:A:694:G:H2'	1:A:695:G:H8	1.81	0.45
1:A:956:A:H3'	1:A:959:C:H41	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1151:U:N3	1:A:1152:G:N7	2.63	0.45
8:J:37:LEU:HD11	8:J:123:LEU:HD12	1.98	0.45
13:P:64:VAL:O	13:P:75:ARG:N	2.46	0.45
16:S:29:VAL:HG11	16:S:55:ILE:HD11	1.96	0.45
16:S:64:MET:HB3	16:S:69:LEU:HD21	1.97	0.45
20:Z:8:LEU:HG	20:Z:28:LEU:HD13	1.97	0.45
22:Y:34:THR:HG23	22:Y:36:GLN:H	1.81	0.45
1:A:277:C:H2'	1:A:278:A:H8	1.80	0.45
1:A:638:U:H2'	1:A:639:C:H6	1.81	0.45
1:A:663:G:OP1	5:E:107:ARG:NH2	2.42	0.45
1:A:706:C:N4	1:A:707:G:O6	2.49	0.45
1:A:927:G:H2'	1:A:928:G:H8	1.82	0.45
1:A:950:U:H2'	1:A:951:C:O4'	2.15	0.45
1:A:1384:C:H2'	1:A:1385:G:H8	1.80	0.45
1:A:1458:U:O2	1:A:1460:G:N1	2.50	0.45
1:A:1618:A:OP1	3:C:61:GLN:NE2	2.49	0.45
1:A:2094:C:H2'	1:A:2095:C:C6	2.51	0.45
1:A:2469:C:C4	1:A:2470:C:H1'	2.51	0.45
4:D:28:ILE:HD12	4:D:188:ILE:HD12	1.98	0.45
5:E:137:LYS:O	5:E:141:ALA:N	2.46	0.45
14:Q:4:VAL:CG1	14:Q:5:LYS:N	2.79	0.45
14:Q:61:TRP:CD1	14:Q:97:ASP:OD1	2.69	0.45
15:R:40:PHE:H	15:R:48:VAL:HG23	1.81	0.45
24:W:39:SER:HA	24:W:128:ILE:HG13	1.97	0.45
24:W:59:LYS:HA	25:W:301:GNP:HN1	1.82	0.45
1:A:372:U:O2'	18:U:66:SER:OG	2.27	0.45
1:A:484:C:N3	1:A:485:U:C4	2.84	0.45
1:A:534:C:H2'	1:A:535:G:H8	1.80	0.45
1:A:726:C:H2'	1:A:727:A:H8	1.82	0.45
1:A:2353:U:O2	1:A:2414:C:C6	2.69	0.45
3:C:76:GLY:N	3:C:116:ILE:O	2.44	0.45
4:D:83:LEU:CB	4:D:86:VAL:CG2	2.95	0.45
13:P:78:PRO:HG2	13:P:81:THR:HG21	1.97	0.45
16:S:86:ARG:NH2	16:S:96:ILE:HD13	2.27	0.45
1:A:395:C:H2'	1:A:396:G:C8	2.51	0.45
1:A:416:U:H5''	1:A:417:G:H5''	1.99	0.45
1:A:547:A:H2'	1:A:548:A:H8	1.81	0.45
1:A:999:A:H2'	1:A:1000:G:H8	1.81	0.45
1:A:1478:G:H2'	1:A:1479:G:H8	1.82	0.45
1:A:1619:A:H2'	1:A:1620:A:C8	2.52	0.45
2:B:27:A:H2	2:B:54:U:H3	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:207:LYS:HG3	3:C:209:GLY:H	1.82	0.45
4:D:201:THR:HG22	4:D:203:LYS:HG3	1.96	0.45
6:F:8:TYR:CD1	6:F:8:TYR:C	2.89	0.45
8:J:29:LEU:HD11	8:J:63:ILE:CG2	2.46	0.45
8:J:37:LEU:O	8:J:52:GLY:HA3	2.16	0.45
8:J:98:PRO:HD2	8:J:127:ARG:HE	1.82	0.45
16:S:52:LYS:HD3	16:S:52:LYS:HA	1.45	0.45
17:T:31:ASP:OD1	17:T:32:VAL:N	2.49	0.45
24:W:129:PRO:CD	24:W:176:LEU:HA	2.47	0.45
1:A:1573:C:N4	1:A:1594:G:O6	2.42	0.45
1:A:1644:C:H2'	1:A:1645:C:H6	1.82	0.45
1:A:1847:U:O5'	3:C:156:ARG:HB3	2.16	0.45
1:A:2106:A:N3	1:A:2463:A:O2'	2.43	0.45
7:G:87:GLY:O	7:G:166:GLU:HG2	2.17	0.45
24:W:34:ARG:NH1	24:W:270:GLU:OE1	2.46	0.45
24:W:40:ARG:HH22	24:W:78:GLN:HE22	1.64	0.45
1:A:626:G:H2'	1:A:627:G:C8	2.51	0.45
1:A:669:C:C2'	1:A:670:C:C6	2.86	0.45
1:A:1160:G:H2'	1:A:1161:A:C8	2.51	0.45
1:A:1527:C:C2	1:A:1558:G:N1	2.84	0.45
1:A:2021:G:N2	1:A:2025:C:O2'	2.50	0.45
1:A:2717:G:N2	1:A:2751:G:O6	2.50	0.45
1:A:2770:A:H62	1:A:2792:G:H21	1.65	0.45
3:C:260:ARG:NH2	3:C:266:SER:OG	2.42	0.45
10:L:66:PHE:CD1	10:L:66:PHE:N	2.85	0.45
19:V:79:ARG:HA	19:V:85:LYS:HA	1.99	0.45
22:Y:32:LEU:HD12	22:Y:32:LEU:HA	1.85	0.45
1:A:719:C:N3	1:A:856:G:C2	2.85	0.45
1:A:1207:C:O2'	15:R:23:GLU:OE1	2.31	0.45
1:A:1232:G:H2'	1:A:1233:A:H8	1.81	0.45
1:A:1734:A:H2'	1:A:1735:A:C8	2.51	0.45
1:A:2291:U:OP1	1:A:2416:U:O2'	2.34	0.45
1:A:2302:A:H2'	1:A:2303:A:C8	2.52	0.45
4:D:62:ASN:HB3	4:D:64:PRO:HG2	1.97	0.45
4:D:147:GLY:HA3	4:D:148:PRO:HD3	1.83	0.45
4:D:203:LYS:HE2	4:D:203:LYS:HB3	1.63	0.45
6:F:33:LYS:HA	6:F:96:MET:CE	2.47	0.45
6:F:128:TYR:CD2	6:F:156:ILE:HD12	2.51	0.45
7:G:84:PHE:N	7:G:136:GLY:O	2.47	0.45
9:K:122:ILE:HD13	13:P:46:PHE:CE1	2.51	0.45
1:A:140:A:H1'	1:A:1448:U:H5'	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:A:O2'	18:U:55:GLY:HA2	2.17	0.45
1:A:787:C:N1	1:A:2010:A:N7	2.64	0.45
1:A:1026:A:N6	1:A:1027:A:N1	2.64	0.45
1:A:1359:G:N2	1:A:1370:C:H41	2.15	0.45
1:A:2312:C:OP2	1:A:2418:G:O2'	2.34	0.45
1:A:2730:U:H5'	1:A:2731:G:H5''	1.97	0.45
1:A:2739:C:H2'	1:A:2740:A:C8	2.52	0.45
2:B:27:A:H3'	2:B:28:C:C6	2.51	0.45
3:C:146:LEU:HD21	3:C:154:LEU:HD21	1.99	0.45
6:F:8:TYR:O	6:F:8:TYR:HD1	1.99	0.45
11:N:20:LEU:O	11:N:24:LEU:N	2.50	0.45
12:O:101:LEU:H	12:O:101:LEU:CD2	2.18	0.45
13:P:89:VAL:CG1	13:P:90:VAL:N	2.80	0.45
1:A:106:G:H2'	1:A:107:G:H8	1.81	0.45
1:A:784:C:N4	1:A:806:G:O6	2.50	0.45
1:A:1512:G:H1'	1:A:1593:A:H2	1.81	0.45
1:A:2744:C:H2'	1:A:2745:U:C6	2.52	0.45
4:D:55:ASP:HA	4:D:77:LYS:CB	2.45	0.45
4:D:55:ASP:OD2	4:D:75:ALA:CB	2.64	0.45
10:L:31:ALA:O	10:L:33:LYS:NZ	2.44	0.45
22:Y:54:LYS:HD3	22:Y:57:ILE:HD12	1.99	0.45
1:A:1326:A:H5'	11:N:107:ARG:HD2	1.99	0.45
1:A:1523:U:H5''	1:A:1524:A:C8	2.52	0.45
2:B:55:A:H4'	6:F:23:ASP:HB2	1.96	0.45
3:C:77:ARG:N	3:C:95:ASN:O	2.49	0.45
5:E:38:LEU:O	5:E:42:ALA:N	2.50	0.45
5:E:190:GLU:O	5:E:191:LYS:CG	2.64	0.45
14:Q:89:GLU:HG3	14:Q:91:ASN:HB2	1.97	0.45
20:Z:5:GLU:O	20:Z:57:LYS:HB3	2.17	0.45
24:W:212:PHE:CZ	24:W:276:SER:O	2.70	0.45
1:A:833:C:H2'	1:A:834:C:C6	2.52	0.44
1:A:1060:U:H2'	1:A:1061:A:C8	2.53	0.44
1:A:1385:G:H1	1:A:1645:C:H42	1.65	0.44
1:A:2356:A:O2'	1:A:2357:A:C8	2.70	0.44
1:A:2703:G:H5''	9:K:30:ARG:HD3	1.99	0.44
2:B:112:C:H2'	2:B:113:A:C8	2.52	0.44
1:A:79:C:O2'	1:A:390:A:N3	2.43	0.44
1:A:918:U:H6	1:A:918:U:H5''	1.82	0.44
1:A:2349:A:O2'	1:A:2362:A:N6	2.51	0.44
3:C:205:ILE:O	3:C:210:ARG:HG2	2.17	0.44
5:E:131:LEU:HB2	5:E:162:ALA:HB1	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:O:102:TYR:OH	12:O:110:ALA:HB3	2.17	0.44
24:W:37:MET:HE1	24:W:71:TRP:HH2	1.82	0.44
1:A:675:C:N4	1:A:676:G:O6	2.51	0.44
1:A:888:A:H2'	1:A:889:A:H8	1.82	0.44
1:A:1042:A:H5'	14:Q:92:ARG:HH21	1.82	0.44
1:A:1476:C:H2'	1:A:1477:A:H8	1.82	0.44
1:A:1508:C:H2'	1:A:1509:C:H6	1.82	0.44
1:A:1614:A:H4'	3:C:214:LYS:HG2	1.99	0.44
1:A:2094:C:O5'	1:A:2094:C:H6	2.00	0.44
1:A:2292:C:C2'	1:A:2293:C:H5'	2.48	0.44
1:A:2539:C:O2	1:A:2607:G:N2	2.43	0.44
1:A:2748:G:H5'	13:P:99:LYS:HZ1	1.82	0.44
10:L:33:LYS:HD3	10:L:33:LYS:HA	1.59	0.44
12:O:103:HIS:CD2	12:O:103:HIS:O	2.70	0.44
14:Q:33:LYS:HE2	14:Q:33:LYS:HB3	1.74	0.44
18:U:84:LYS:CB	18:U:93:VAL:HG11	2.48	0.44
20:Z:5:GLU:OE2	20:Z:59:GLN:NE2	2.50	0.44
24:W:16:GLU:OE1	24:W:16:GLU:HA	2.17	0.44
1:A:304:G:H2'	1:A:305:A:C8	2.51	0.44
1:A:704:U:H2'	1:A:705:A:C8	2.52	0.44
1:A:950:U:O5'	1:A:950:U:H6	2.01	0.44
1:A:1572:G:O2'	1:A:1573:C:C6	2.71	0.44
1:A:1859:C:H2'	1:A:1860:G:C8	2.48	0.44
3:C:69:ARG:HE	3:C:129:ALA:HB2	1.82	0.44
9:K:26:GLY:HA3	9:K:30:ARG:HH21	1.82	0.44
10:L:91:VAL:HB	10:L:123:VAL:HA	1.99	0.44
1:A:776:G:OP1	3:C:10:SER:OG	2.30	0.44
1:A:2099:G:H2'	1:A:2100:A:H8	1.83	0.44
1:A:2163:A:H2'	1:A:2164:A:H8	1.82	0.44
12:O:29:PRO:HB3	12:O:44:ILE:HG23	1.97	0.44
18:U:84:LYS:C	18:U:84:LYS:CD	2.85	0.44
1:A:897:G:H1'	20:Z:25:THR:HG21	2.00	0.44
1:A:1564:C:O2	1:A:1564:C:H2'	2.16	0.44
1:A:1847:U:O4	3:C:153:GLN:HG2	2.18	0.44
1:A:2374:G:H5'	1:A:2376:C:H5'	2.00	0.44
1:A:2703:G:O3'	9:K:30:ARG:HB3	2.17	0.44
1:A:2747:G:O2'	1:A:2872:U:OP1	2.29	0.44
1:A:2865:U:H5'	11:N:49:THR:HG21	1.99	0.44
4:D:126:HIS:CG	4:D:159:LEU:HB3	2.52	0.44
14:Q:50:ARG:HH21	15:R:73:VAL:HG22	1.83	0.44
1:A:431:A:N6	1:A:458:G:O6	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:738:C:O2'	3:C:43:ARG:NE	2.51	0.44
1:A:1214:U:O4	1:A:1221:A:N6	2.51	0.44
1:A:1587:U:H2'	1:A:1588:A:C8	2.53	0.44
1:A:2835:A:H62	1:A:2915:G:H21	1.66	0.44
6:F:69:ARG:HD3	6:F:82:GLY:HA2	1.99	0.44
11:N:22:THR:HG21	11:N:67:ARG:HB2	1.99	0.44
12:O:95:PHE:CD2	12:O:102:TYR:HE1	2.35	0.44
16:S:9:THR:HG23	16:S:100:THR:HG21	2.00	0.44
18:U:9:VAL:HG22	18:U:70:PRO:HA	2.00	0.44
1:A:627:G:H2'	1:A:628:C:C6	2.52	0.44
1:A:684:G:C4	1:A:697:G:N2	2.86	0.44
1:A:1735:A:H4'	24:W:245:ARG:HH12	1.82	0.44
1:A:2280:G:OP2	1:A:2280:G:H8	2.00	0.44
1:A:2539:C:H41	1:A:2604:C:N4	2.15	0.44
1:A:2581:U:OP1	24:W:196:LYS:NZ	2.51	0.44
1:A:2705:C:H2'	1:A:2706:G:H8	1.82	0.44
6:F:65:PRO:HB3	6:F:89:VAL:HG22	1.99	0.44
18:U:83:TYR:N	18:U:93:VAL:HG13	2.33	0.44
19:V:48:GLN:O	19:V:49:ARG:NH1	2.51	0.44
24:W:176:LEU:HD13	24:W:177:TRP:H	1.83	0.44
1:A:372:U:H4'	18:U:64:HIS:HD2	1.81	0.44
1:A:526:A:H1'	1:A:527:A:H5''	2.00	0.44
1:A:578:A:H4'	1:A:579:G:C8	2.53	0.44
1:A:925:A:N6	1:A:947:A:C4	2.86	0.44
1:A:1656:C:N4	1:A:1665:G:O6	2.51	0.44
1:A:2041:G:N7	16:S:16:LYS:NZ	2.61	0.44
1:A:2540:U:O2'	4:D:139:TYR:OH	2.31	0.44
1:A:2548:U:C4	1:A:2570:A:C5	3.05	0.44
4:D:29:GLU:HB2	4:D:185:LEU:CD2	2.44	0.44
4:D:54:ASP:O	4:D:78:ARG:CG	2.55	0.44
4:D:55:ASP:CB	4:D:77:LYS:CG	2.93	0.44
6:F:17:MET:HE1	6:F:25:VAL:O	2.18	0.44
6:F:54:VAL:O	6:F:54:VAL:HG12	2.18	0.44
8:J:74:ILE:H	8:J:74:ILE:HG13	1.48	0.44
10:L:117:LEU:HD11	10:L:119:LYS:O	2.17	0.44
12:O:94:VAL:HG12	12:O:95:PHE:N	2.31	0.44
13:P:76:THR:O	13:P:76:THR:HG22	2.18	0.44
1:A:244:A:H5'	1:A:246:U:H1'	1.99	0.43
1:A:1232:G:H2'	1:A:1233:A:C8	2.53	0.43
1:A:1508:C:H2'	1:A:1509:C:C6	2.53	0.43
1:A:1806:U:H2'	1:A:1807:U:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2154:G:O6	1:A:2192:U:O2'	2.33	0.43
1:A:2753:U:P	4:D:117:LYS:HZ2	2.41	0.43
11:N:20:LEU:HD13	11:N:40:LEU:HD22	1.98	0.43
13:P:32:HIS:HD2	13:P:86:LYS:HB3	1.83	0.43
18:U:79:THR:HG21	18:U:96:LYS:CG	2.46	0.43
24:W:9:HIS:CD2	24:W:9:HIS:O	2.70	0.43
24:W:58:ASN:HD21	24:W:131:VAL:C	2.20	0.43
24:W:96:ILE:O	24:W:96:ILE:HG13	2.17	0.43
24:W:220:ARG:NE	24:W:275:LEU:HD21	2.33	0.43
1:A:393:U:C2	1:A:394:U:C5	3.06	0.43
1:A:1177:G:O2'	1:A:1179:A:N7	2.49	0.43
1:A:2376:C:H42	1:A:2399:G:H1	1.66	0.43
2:B:4:G:O2'	2:B:25:A:O2'	2.33	0.43
2:B:18:A:C4	2:B:19:G:H1'	2.53	0.43
12:O:35:ARG:HH12	12:O:105:ARG:CG	2.13	0.43
15:R:12:ILE:HG21	15:R:20:VAL:HG11	1.98	0.43
17:T:50:LYS:HE2	17:T:50:LYS:HB3	1.76	0.43
22:Y:60:ARG:HA	22:Y:63:ALA:HB3	1.99	0.43
24:W:58:ASN:ND2	24:W:131:VAL:C	2.71	0.43
1:A:827:G:N2	1:A:832:G:N7	2.65	0.43
1:A:2542:A:H3'	1:A:2543:U:C6	2.53	0.43
13:P:32:HIS:HB3	13:P:43:ILE:HD11	1.99	0.43
18:U:23:ILE:HA	18:U:35:VAL:HG22	2.00	0.43
1:A:888:A:H2'	1:A:889:A:C8	2.54	0.43
1:A:1717:C:H2'	1:A:1718:G:H8	1.82	0.43
1:A:2298:A:C5	1:A:2299:G:N7	2.86	0.43
1:A:2307:A:OP2	19:V:20:ASN:ND2	2.51	0.43
1:A:2342:C:HO2'	6:F:37:ASN:CG	2.21	0.43
1:A:2708:A:H4'	4:D:193:PRO:HB3	2.00	0.43
1:A:2823:C:C2	1:A:2828:G:N2	2.75	0.43
8:J:40:LYS:HA	8:J:40:LYS:HD3	1.72	0.43
12:O:42:ALA:CB	12:O:109:LEU:HD21	2.48	0.43
18:U:4:LYS:H	18:U:92:ARG:NH2	2.15	0.43
19:V:88:SER:OG	19:V:89:VAL:N	2.51	0.43
1:A:89:U:H3'	1:A:90:A:H2'	2.00	0.43
1:A:419:G:H22	1:A:447:G:H2'	1.83	0.43
1:A:635:C:N3	1:A:636:G:C5	2.87	0.43
1:A:892:U:H1'	1:A:894:A:H2	1.83	0.43
1:A:1646:G:OP2	17:T:58:ASN:ND2	2.34	0.43
1:A:2049:A:N1	1:A:2064:G:N2	2.67	0.43
1:A:2320:U:O2'	1:A:2403:C:O2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2757:U:H2'	1:A:2758:G:C8	2.53	0.43
3:C:68:LYS:HG2	3:C:151:GLY:N	2.34	0.43
5:E:37:ILE:HD13	5:E:37:ILE:HA	1.85	0.43
15:R:39:LEU:CB	15:R:48:VAL:HG21	2.48	0.43
18:U:2:HIS:ND1	18:U:2:HIS:N	2.66	0.43
18:U:7:ASP:OD1	18:U:7:ASP:N	2.50	0.43
1:A:875:U:H2'	1:A:876:A:C8	2.54	0.43
1:A:929:G:H8	1:A:929:G:OP2	2.02	0.43
1:A:1178:U:O4'	8:J:76:TYR:CE2	2.71	0.43
1:A:1774:A:H3'	1:A:1775:G:H8	1.84	0.43
1:A:2126:G:N1	1:A:2221:C:C2	2.79	0.43
6:F:128:TYR:CD2	6:F:156:ILE:CD1	3.02	0.43
1:A:357:G:C4	1:A:358:C:C6	3.07	0.43
1:A:638:U:C2	1:A:639:C:C5	3.07	0.43
1:A:1081:U:H2'	1:A:1082:G:H8	1.84	0.43
1:A:1289:U:H2'	10:L:18:ARG:HH22	1.83	0.43
1:A:1412:A:H3'	1:A:1413:G:H8	1.83	0.43
1:A:2318:G:H2'	1:A:2319:G:H8	1.84	0.43
1:A:2595:A:H4'	1:A:2596:G:H5''	2.00	0.43
1:A:2759:C:H2'	1:A:2760:G:C8	2.54	0.43
2:B:24:C:H3'	2:B:25:A:H8	1.83	0.43
3:C:141:VAL:HG13	3:C:144:ILE:HD11	2.00	0.43
4:D:83:LEU:CD2	4:D:203:LYS:CG	2.95	0.43
5:E:46:GLN:HG2	5:E:48:THR:HG23	1.99	0.43
8:J:8:ASN:OD1	8:J:8:ASN:N	2.46	0.43
17:T:91:GLU:HG3	17:T:92:ILE:HG12	2.00	0.43
19:V:49:ARG:HA	19:V:49:ARG:HD3	1.77	0.43
24:W:9:HIS:O	24:W:9:HIS:HD2	2.01	0.43
24:W:27:VAL:HG11	24:W:48:LEU:HD13	2.01	0.43
24:W:32:ASP:HA	24:W:131:VAL:CG2	2.48	0.43
1:A:342:A:OP1	18:U:95:LYS:CE	2.66	0.43
1:A:1575:A:N6	1:A:1591:G:O2'	2.52	0.43
1:A:1630:G:O2'	1:A:1631:A:O5'	2.28	0.43
2:B:21:G:H1	2:B:58:C:H42	1.67	0.43
2:B:40:C:H5''	6:F:64:LYS:HB3	2.00	0.43
3:C:44:ASN:HB3	3:C:47:GLY:H	1.82	0.43
3:C:90:ASN:HD21	3:C:197:ASN:HB2	1.83	0.43
4:D:31:ALA:O	4:D:53:PHE:HE1	2.00	0.43
5:E:104:LYS:O	5:E:108:LEU:N	2.52	0.43
5:E:137:LYS:HA	5:E:137:LYS:HD2	1.88	0.43
22:Y:21:LEU:HD13	22:Y:53:MET:HE2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:G:H2'	1:A:190:G:H8	1.83	0.43
1:A:2376:C:N4	1:A:2399:G:H1	2.16	0.43
4:D:10:ILE:HB	4:D:27:VAL:HG12	1.92	0.43
6:F:167:ARG:HB2	6:F:167:ARG:HE	1.55	0.43
8:J:26:LEU:CA	8:J:29:LEU:HG	2.49	0.43
11:N:55:ASP:OD1	11:N:56:LEU:N	2.52	0.43
24:W:156:THR:HG21	24:W:172:THR:OG1	2.18	0.43
1:A:683:A:C8	10:L:114:ASN:ND2	2.86	0.43
1:A:796:A:H2'	1:A:797:A:H8	1.83	0.43
1:A:1626:U:H2'	1:A:1627:A:H8	1.84	0.43
1:A:2038:G:H2'	1:A:2039:G:H8	1.83	0.43
1:A:2342:C:HO2'	6:F:37:ASN:ND2	2.08	0.43
10:L:132:ALA:O	10:L:136:VAL:HG13	2.19	0.43
13:P:78:PRO:HG2	13:P:81:THR:CG2	2.49	0.43
16:S:86:ARG:HH21	16:S:96:ILE:HD13	1.76	0.43
20:Z:7:THR:O	20:Z:54:VAL:CG1	2.66	0.43
1:A:342:A:OP1	18:U:95:LYS:HE2	2.19	0.42
1:A:749:G:C2	1:A:778:C:C2	3.07	0.42
1:A:1042:A:H5'	14:Q:92:ARG:NH2	2.33	0.42
1:A:1518:G:H1	1:A:1566:G:H22	1.67	0.42
3:C:164:VAL:HG13	3:C:174:VAL:HG22	2.00	0.42
4:D:62:ASN:O	4:D:66:LYS:N	2.48	0.42
5:E:154:ILE:HG12	5:E:193:LEU:HD12	2.00	0.42
6:F:68:THR:HG22	6:F:88:LYS:CD	2.38	0.42
18:U:41:VAL:HG11	18:U:43:LYS:CG	2.49	0.42
20:Z:8:LEU:HD21	20:Z:28:LEU:CD1	2.49	0.42
20:Z:47:ILE:H	20:Z:47:ILE:HG13	1.70	0.42
24:W:40:ARG:NH2	24:W:75:PHE:CE1	2.87	0.42
1:A:77:U:C5'	22:Y:2:LYS:HB2	2.47	0.42
1:A:210:A:C8	1:A:211:C:C5	3.07	0.42
1:A:1129:U:H3	1:A:1131:A:H3'	1.84	0.42
1:A:1288:G:N2	5:E:88:VAL:CG2	2.64	0.42
1:A:1388:A:H5'	1:A:1389:C:H5''	2.00	0.42
1:A:1858:A:N9	1:A:1859:C:C5	2.87	0.42
1:A:2120:U:H5''	1:A:2121:U:H2'	2.02	0.42
1:A:2148:A:H61	1:A:2200:A:H1'	1.84	0.42
1:A:2360:G:HO2'	19:V:51:THR:HG1	1.64	0.42
1:A:2537:G:N1	1:A:2611:G:N1	2.67	0.42
1:A:2725:U:H2'	1:A:2726:G:C8	2.53	0.42
1:A:2901:G:H2'	1:A:2902:A:H8	1.82	0.42
2:B:55:A:C1'	6:F:27:GLN:NE2	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:164:VAL:HA	3:C:174:VAL:HG13	2.01	0.42
1:A:5:A:H2'	1:A:6:A:C8	2.54	0.42
1:A:1183:G:H2'	1:A:1184:G:C8	2.54	0.42
1:A:1733:U:N3	1:A:1745:A:OP1	2.53	0.42
1:A:2472:C:H2'	1:A:2473:G:C8	2.54	0.42
1:A:2566:U:H2'	1:A:2567:C:H6	1.82	0.42
1:A:2752:C:OP2	4:D:115:LYS:NZ	2.41	0.42
5:E:136:THR:HG22	5:E:167:ALA:H	1.84	0.42
10:L:129:SER:HB3	10:L:132:ALA:HB3	2.01	0.42
13:P:12:THR:HG22	13:P:58:ILE:CD1	2.38	0.42
13:P:30:ARG:HG2	13:P:47:GLU:CB	2.48	0.42
19:V:78:GLU:HB2	19:V:86:LYS:HD3	2.02	0.42
24:W:220:ARG:CZ	24:W:275:LEU:HD21	2.49	0.42
1:A:816:U:H2'	1:A:817:G:C8	2.54	0.42
1:A:1069:U:H3'	1:A:1070:G:C8	2.52	0.42
1:A:1315:G:H2'	1:A:1316:A:H8	1.85	0.42
1:A:1757:G:N7	1:A:1759:U:C6	2.87	0.42
1:A:2253:G:OP1	3:C:268:LYS:NZ	2.39	0.42
1:A:2282:G:O6	19:V:13:LYS:CA	2.45	0.42
1:A:2321:U:OP1	1:A:2408:G:N2	2.45	0.42
1:A:2687:C:N3	1:A:2692:G:N1	2.60	0.42
3:C:90:ASN:HB2	3:C:106:ALA:HB3	2.01	0.42
4:D:31:ALA:HB1	4:D:32:PRO:HD2	2.01	0.42
4:D:55:ASP:CA	4:D:77:LYS:CB	2.96	0.42
6:F:13:ALA:N	6:F:14:PRO:HD2	2.34	0.42
9:K:15:GLY:O	9:K:47:THR:N	2.42	0.42
24:W:14:ARG:HA	24:W:17:VAL:HG12	2.02	0.42
24:W:277:PHE:HD1	24:W:277:PHE:HA	1.74	0.42
1:A:419:G:N2	1:A:420:U:O4	2.52	0.42
1:A:1117:G:H4'	1:A:1135:G:H2'	2.01	0.42
1:A:1759:U:H3	1:A:1774:A:H62	1.67	0.42
1:A:1850:A:H2'	1:A:1851:G:C8	2.55	0.42
1:A:1862:C:C3'	1:A:1862:C:C6	3.02	0.42
1:A:2072:C:H2'	1:A:2073:C:H6	1.85	0.42
1:A:2253:G:H4'	1:A:2255:C:C2	2.54	0.42
1:A:2299:G:H2'	1:A:2300:G:C8	2.55	0.42
6:F:128:TYR:HD2	6:F:156:ILE:HD12	1.84	0.42
10:L:16:ARG:HG2	10:L:18:ARG:HD2	2.02	0.42
13:P:27:ASP:O	13:P:49:VAL:HG12	2.19	0.42
13:P:28:THR:HA	13:P:49:VAL:HA	2.01	0.42
14:Q:80:MET:HA	14:Q:83:LEU:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:A:H2'	1:A:195:C:C6	2.55	0.42
1:A:1058:U:P	8:J:144:ARG:HH22	2.42	0.42
1:A:1489:U:N3	1:A:1597:C:O2	2.52	0.42
1:A:1564:C:N3	1:A:1565:U:C5	2.87	0.42
1:A:2392:U:H2'	1:A:2393:C:H6	1.82	0.42
1:A:2548:U:C5	1:A:2570:A:N6	2.88	0.42
1:A:2888:C:OP1	13:P:94:LYS:NZ	2.53	0.42
4:D:26:THR:HG21	4:D:192:VAL:HB	2.01	0.42
11:N:119:LEU:O	11:N:120:VAL:CG2	2.67	0.42
14:Q:86:SER:HB3	14:Q:116:GLN:HG2	2.02	0.42
20:Z:40:ASN:O	20:Z:44:ARG:N	2.51	0.42
24:W:127:GLY:O	24:W:175:ILE:CB	2.42	0.42
1:A:510:G:N1	1:A:514:G:O6	2.53	0.42
1:A:776:G:C5	3:C:207:LYS:HB2	2.55	0.42
1:A:802:G:H2'	1:A:803:C:C6	2.55	0.42
1:A:929:G:OP2	1:A:929:G:C8	2.72	0.42
1:A:1529:G:H3'	1:A:1530:G:C8	2.55	0.42
1:A:2247:C:H2'	1:A:2248:G:H8	1.85	0.42
1:A:2709:C:H5'	4:D:193:PRO:HA	2.01	0.42
1:A:2873:G:H5''	13:P:97:ARG:HA	2.01	0.42
4:D:107:ILE:HG22	4:D:205:ALA:HB1	1.98	0.42
5:E:77:SER:OG	5:E:78:ILE:N	2.52	0.42
6:F:115:ARG:HE	6:F:115:ARG:HB2	1.74	0.42
6:F:132:ILE:CD1	6:F:154:ILE:CB	2.98	0.42
8:J:26:LEU:CD1	8:J:102:LEU:HD13	2.33	0.42
8:J:29:LEU:HD11	8:J:63:ILE:HG23	2.02	0.42
12:O:35:ARG:HD3	12:O:100:TYR:CZ	2.55	0.42
17:T:14:THR:HG1	17:T:17:SER:H	1.61	0.42
17:T:53:LYS:HB3	17:T:82:LYS:HB3	2.01	0.42
24:W:220:ARG:NE	24:W:275:LEU:HD23	2.35	0.42
1:A:27:G:H21	1:A:558:G:H2'	1.85	0.42
1:A:987:A:H3'	1:A:988:G:H8	1.85	0.42
1:A:1553:A:H1'	1:A:1555:A:N1	2.35	0.42
1:A:1735:A:H5'	24:W:245:ARG:HH22	1.85	0.42
1:A:2295:A:C6	1:A:2301:U:C2	3.08	0.42
3:C:176:LEU:O	3:C:177:ASN:C	2.56	0.42
4:D:56:LYS:HB2	4:D:57:ARG:H	1.66	0.42
5:E:139:MET:HG3	5:E:167:ALA:HB2	2.01	0.42
8:J:20:ASP:OD1	8:J:21:ALA:N	2.53	0.42
24:W:42:PRO:HD2	24:W:177:TRP:HE1	1.82	0.42
1:A:132:C:H2'	1:A:133:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:738:C:H42	1:A:818:G:H1	1.68	0.42
1:A:751:G:H2'	1:A:773:G:H22	1.85	0.42
1:A:790:A:O2'	1:A:1704:U:OP1	2.30	0.42
1:A:1046:A:OP2	1:A:1200:G:N1	2.37	0.42
1:A:1425:C:H2'	1:A:1426:A:C8	2.54	0.42
1:A:1614:A:P	3:C:210:ARG:NH2	2.92	0.42
1:A:2282:G:H2'	1:A:2283:C:H5'	2.01	0.42
1:A:2561:G:O4'	1:A:2687:C:O2'	2.34	0.42
1:A:2635:C:N4	1:A:2636:G:O6	2.52	0.42
2:B:64:A:OP2	2:B:106:C:N4	2.51	0.42
3:C:210:ARG:HA	3:C:210:ARG:HD2	1.63	0.42
6:F:8:TYR:CD1	6:F:8:TYR:O	2.73	0.42
7:G:139:LYS:HA	7:G:142:VAL:HG12	2.02	0.42
9:K:40:VAL:HG22	9:K:59:LYS:HG2	2.01	0.42
11:N:50:LEU:HD23	11:N:50:LEU:HA	1.88	0.42
12:O:39:HIS:HD2	12:O:41:TYR:HE1	1.68	0.42
13:P:30:ARG:HA	13:P:47:GLU:HA	2.00	0.42
14:Q:110:ALA:O	14:Q:113:ALA:HB3	2.20	0.42
15:R:40:PHE:H	15:R:48:VAL:CG2	2.33	0.42
19:V:48:GLN:HE22	19:V:53:ILE:H	1.68	0.42
22:Y:17:LYS:HD3	22:Y:17:LYS:HA	1.87	0.42
24:W:30:LEU:CD1	24:W:133:LYS:HA	2.49	0.42
24:W:41:ASN:CG	24:W:175:ILE:CG2	2.88	0.42
24:W:129:PRO:HD3	24:W:176:LEU:CA	2.50	0.42
1:A:134:C:H2'	1:A:135:U:C6	2.55	0.42
1:A:247:A:H62	1:A:257:G:H21	1.67	0.42
1:A:407:A:H2'	1:A:408:G:H8	1.85	0.42
1:A:456:A:H2'	1:A:457:G:C8	2.55	0.42
1:A:575:A:O2'	1:A:576:G:N2	2.53	0.42
1:A:639:C:C2	1:A:640:U:C5	3.07	0.42
1:A:827:G:H21	1:A:830:A:H62	1.67	0.42
1:A:1060:U:H2'	1:A:1061:A:H8	1.85	0.42
1:A:1240:U:H2'	1:A:1241:C:C6	2.55	0.42
1:A:1564:C:C2	1:A:1565:U:H5	2.36	0.42
1:A:2151:U:H2'	1:A:2152:A:C8	2.55	0.42
1:A:2539:C:H41	1:A:2604:C:H42	1.68	0.42
1:A:2664:U:C4	1:A:2665:U:C5	3.08	0.42
1:A:2671:G:H2'	1:A:2672:G:H8	1.85	0.42
2:B:112:C:H2'	2:B:113:A:H8	1.85	0.42
3:C:94:ILE:CG1	3:C:104:ILE:CD1	2.98	0.42
5:E:109:ALA:O	5:E:112:SER:OG	2.25	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:35:ILE:HD13	9:K:35:ILE:HA	1.90	0.42
12:O:107:LYS:O	12:O:111:ASP:OD2	2.38	0.42
13:P:62:PHE:CE2	13:P:79:VAL:HG22	2.55	0.42
13:P:78:PRO:HG2	13:P:81:THR:HB	2.02	0.42
14:Q:27:SER:HB3	14:Q:31:LEU:HD13	2.01	0.42
17:T:54:VAL:HG22	17:T:81:VAL:HG13	2.02	0.42
24:W:233:ASP:HB3	24:W:236:GLU:HB3	2.02	0.42
1:A:43:G:H3'	1:A:44:A:C8	2.55	0.41
1:A:86:C:HO2'	1:A:103:U:HO2'	1.66	0.41
1:A:303:G:H2'	1:A:304:G:C8	2.54	0.41
1:A:1108:G:H1'	1:A:1134:A:C6	2.54	0.41
1:A:1808:U:H5''	1:A:1809:A:H5'	2.01	0.41
1:A:2128:U:H2'	1:A:2129:G:C8	2.52	0.41
8:J:103:GLU:HG2	8:J:120:PHE:HE1	1.85	0.41
13:P:31:VAL:HG22	13:P:87:ILE:HG12	2.01	0.41
14:Q:74:LEU:HD23	14:Q:74:LEU:HA	1.92	0.41
22:Y:10:THR:O	22:Y:14:ILE:N	2.48	0.41
1:A:190:G:C2	1:A:213:C:O2	2.73	0.41
1:A:1027:A:HO2'	1:A:2065:C:HO2'	1.61	0.41
1:A:1554:U:H5'	1:A:1555:A:C5	2.55	0.41
1:A:1846:G:OP1	3:C:87:ARG:NH2	2.50	0.41
1:A:2298:A:C2'	1:A:2299:G:H8	2.32	0.41
1:A:2434:G:H2'	1:A:2440:A:H61	1.85	0.41
1:A:2557:U:H2'	1:A:2558:G:H2'	2.02	0.41
1:A:2769:A:N6	1:A:2770:A:N1	2.68	0.41
2:B:76:A:H62	2:B:96:G:H21	1.67	0.41
5:E:51:VAL:CG1	5:E:92:PRO:HD2	2.49	0.41
5:E:135:LYS:HD2	5:E:135:LYS:HA	1.90	0.41
10:L:79:LEU:HD22	10:L:117:LEU:CB	2.43	0.41
13:P:31:VAL:O	13:P:46:PHE:N	2.52	0.41
14:Q:54:LYS:HB2	14:Q:54:LYS:HE3	1.83	0.41
16:S:83:LYS:O	16:S:84:ARG:NH1	2.44	0.41
1:A:5:A:H2'	1:A:6:A:H8	1.86	0.41
1:A:213:C:H2'	1:A:214:G:C8	2.55	0.41
1:A:992:G:H2'	1:A:993:A:H8	1.85	0.41
1:A:1858:A:H2'	1:A:1859:C:C6	2.56	0.41
1:A:2667:G:P	4:D:84:ARG:NH2	2.87	0.41
3:C:52:ARG:HH12	3:C:249:PRO:HG3	1.85	0.41
6:F:5:LYS:HZ3	6:F:94:GLU:CD	2.17	0.41
24:W:39:SER:O	24:W:128:ILE:HG13	2.21	0.41
24:W:44:ILE:HD12	24:W:44:ILE:HA	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:U:OP2	1:A:90:A:O2'	2.30	0.41
1:A:527:A:H4'	18:U:43:LYS:CG	2.50	0.41
1:A:528:G:O2'	1:A:552:G:N2	2.53	0.41
1:A:626:G:H2'	1:A:627:G:H8	1.85	0.41
1:A:1072:A:H61	1:A:1173:A:H3'	1.84	0.41
1:A:1177:G:N7	8:J:78:HIS:CE1	2.89	0.41
1:A:2072:C:OP1	1:A:2806:G:O2'	2.38	0.41
1:A:2559:U:O2	7:G:158:TYR:OH	2.38	0.41
5:E:53:ASN:HB3	5:E:56:GLU:HG2	2.03	0.41
6:F:38:MET:HB2	6:F:87:ALA:H	1.86	0.41
9:K:87:ILE:HG13	9:K:93:PRO:CA	2.50	0.41
14:Q:87:GLY:HA2	15:R:49:GLY:HA2	2.01	0.41
24:W:31:VAL:HG12	24:W:32:ASP:N	2.34	0.41
1:A:33:U:H2'	1:A:493:G:N2	2.35	0.41
1:A:705:A:C5	1:A:706:C:C6	3.08	0.41
1:A:925:A:N7	1:A:947:A:H1'	2.36	0.41
1:A:1090:U:HO2'	1:A:1157:A:N6	2.18	0.41
1:A:1178:U:H2'	1:A:1179:A:C8	2.55	0.41
1:A:1205:U:H2'	1:A:1206:G:H8	1.86	0.41
1:A:1324:G:N2	1:A:1367:G:O3'	2.46	0.41
1:A:1711:G:N2	1:A:2023:C:C2	2.89	0.41
1:A:2132:A:C2	1:A:2215:U:O2	2.74	0.41
3:C:57:GLY:CA	3:C:214:LYS:O	2.65	0.41
5:E:36:ALA:O	5:E:40:GLN:N	2.45	0.41
7:G:60:LYS:HB3	7:G:60:LYS:HE3	1.71	0.41
7:G:88:LEU:HD13	7:G:149:ILE:HG21	2.02	0.41
16:S:86:ARG:HH22	16:S:96:ILE:HD11	1.70	0.41
24:W:41:ASN:HB3	24:W:44:ILE:HG22	2.03	0.41
1:A:1711:G:H4'	9:K:6:THR:CG2	2.47	0.41
1:A:2836:G:H2'	1:A:2837:A:C8	2.55	0.41
1:A:2886:C:H2'	1:A:2887:A:C8	2.53	0.41
3:C:228:ASN:OD1	3:C:229:ASP:N	2.54	0.41
8:J:56:ILE:HG22	8:J:124:ASN:HD22	1.85	0.41
10:L:104:LYS:HE3	10:L:106:ASN:ND2	2.35	0.41
24:W:214:GLU:HG2	24:W:230:ILE:HG21	2.03	0.41
1:A:180:G:H2'	1:A:181:G:C8	2.56	0.41
1:A:653:A:H62	1:A:665:G:N2	2.18	0.41
1:A:727:A:H2'	1:A:728:G:C8	2.54	0.41
1:A:1094:A:OP2	1:A:1156:G:N2	2.54	0.41
1:A:2082:G:H2'	1:A:2083:A:C8	2.53	0.41
1:A:2292:C:H2'	1:A:2293:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2295:A:C4	1:A:2301:U:N3	2.88	0.41
1:A:2648:U:H5'	4:D:156:LYS:HG3	2.03	0.41
8:J:29:LEU:HG	8:J:29:LEU:H	1.53	0.41
10:L:74:TYR:OH	10:L:127:LYS:CG	2.65	0.41
13:P:32:HIS:CE1	13:P:45:ILE:HG13	2.56	0.41
14:Q:43:GLY:HA2	14:Q:46:ALA:HB3	2.02	0.41
16:S:83:LYS:HE2	16:S:83:LYS:HB3	1.93	0.41
18:U:79:THR:HB	18:U:94:ALA:CB	2.50	0.41
20:Z:5:GLU:HB2	20:Z:57:LYS:HG2	2.03	0.41
24:W:32:ASP:CB	24:W:131:VAL:CG2	2.98	0.41
24:W:32:ASP:HA	24:W:131:VAL:HG22	2.02	0.41
1:A:286:U:H3'	1:A:287:G:C8	2.52	0.41
1:A:861:C:C2	1:A:862:U:C5	3.09	0.41
1:A:1298:C:H2'	1:A:1299:G:C8	2.56	0.41
1:A:2234:C:H2'	1:A:2235:G:C8	2.55	0.41
1:A:2280:G:H8	1:A:2280:G:P	2.44	0.41
1:A:2302:A:O2'	1:A:2303:A:H5'	2.21	0.41
12:O:28:ARG:HG3	12:O:92:ASP:O	2.19	0.41
16:S:77:ASP:N	16:S:77:ASP:OD1	2.53	0.41
17:T:91:GLU:HG3	17:T:92:ILE:H	1.86	0.41
24:W:36:PRO:O	24:W:39:SER:OG	2.33	0.41
1:A:96:G:H2'	1:A:97:C:C6	2.56	0.41
1:A:216:A:H2'	1:A:217:G:C8	2.56	0.41
1:A:303:G:H2'	1:A:304:G:H8	1.85	0.41
1:A:497:G:H1	1:A:501:A:P	2.44	0.41
1:A:584:A:H3'	1:A:585:G:H8	1.86	0.41
1:A:794:U:H4'	16:S:89:ALA:HB3	2.03	0.41
1:A:908:A:H2'	1:A:909:G:O4'	2.20	0.41
1:A:1241:C:H42	1:A:1285:G:H1	1.67	0.41
1:A:1439:U:H2'	1:A:1440:G:C8	2.56	0.41
1:A:1497:G:H2'	1:A:1504:A:H61	1.86	0.41
1:A:1735:A:O3'	24:W:271:LYS:NZ	2.54	0.41
1:A:1843:G:H3'	1:A:1844:A:H2'	2.02	0.41
1:A:2247:C:H2'	1:A:2248:G:C8	2.56	0.41
1:A:2281:G:O5'	1:A:2281:G:C8	2.71	0.41
1:A:2473:G:OP2	5:E:68:LYS:NZ	2.36	0.41
1:A:2620:C:N4	1:A:2621:G:O6	2.53	0.41
1:A:2777:A:C2'	7:G:64:ALA:CB	2.99	0.41
2:B:70:G:H21	2:B:102:A:H62	1.67	0.41
4:D:16:PHE:O	13:P:15:GLN:NE2	2.54	0.41
4:D:36:LEU:HD23	4:D:36:LEU:HA	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:50:GLN:HG2	4:D:82:GLU:OE2	2.19	0.41
4:D:56:LYS:HD2	4:D:60:LEU:HB2	2.02	0.41
4:D:86:VAL:HG11	4:D:91:TYR:CE2	2.55	0.41
5:E:44:LEU:HD23	5:E:44:LEU:HA	1.83	0.41
6:F:13:ALA:CB	6:F:14:PRO:CD	2.95	0.41
6:F:67:VAL:CG2	6:F:84:PRO:CG	2.99	0.41
6:F:117:VAL:HB	6:F:118:SER:H	1.58	0.41
9:K:87:ILE:HG13	9:K:92:SER:C	2.41	0.41
9:K:87:ILE:CG1	9:K:92:SER:O	2.69	0.41
12:O:75:THR:OG1	12:O:108:ALA:HB1	2.21	0.41
14:Q:69:ALA:O	14:Q:74:LEU:N	2.54	0.41
17:T:5:ARG:HH11	17:T:5:ARG:HG3	1.86	0.41
24:W:36:PRO:HB3	24:W:75:PHE:CE2	2.52	0.41
24:W:128:ILE:CG2	24:W:129:PRO:HD2	2.51	0.41
1:A:1314:A:N3	1:A:1315:G:H1'	2.36	0.41
1:A:1644:C:C2	1:A:1645:C:C5	3.08	0.41
1:A:1672:A:H2'	1:A:1673:G:C8	2.55	0.41
1:A:1834:C:O3'	3:C:250:TRP:NE1	2.54	0.41
1:A:2536:C:C4	1:A:2611:G:N1	2.89	0.41
3:C:53:HIS:CB	3:C:217:ARG:O	2.66	0.41
3:C:68:LYS:O	3:C:69:ARG:O	2.38	0.41
7:G:90:LEU:HD22	7:G:95:TYR:HB3	2.02	0.41
8:J:45:TYR:O	14:Q:64:ARG:NE	2.38	0.41
24:W:75:PHE:HA	24:W:75:PHE:HD1	1.79	0.41
1:A:89:U:H3'	1:A:90:A:H8	1.85	0.40
1:A:217:G:N3	1:A:219:A:O2'	2.53	0.40
1:A:789:C:H42	1:A:802:G:H1	1.69	0.40
1:A:1326:A:N6	11:N:109:GLY:O	2.44	0.40
1:A:1572:G:O2'	1:A:1573:C:O5'	2.36	0.40
1:A:1694:G:H2'	1:A:1695:A:H8	1.86	0.40
1:A:2293:C:H2'	1:A:2294:U:C6	2.56	0.40
1:A:2707:C:H2'	1:A:2708:A:H8	1.86	0.40
4:D:55:ASP:CA	4:D:77:LYS:CA	2.87	0.40
4:D:75:ALA:HA	4:D:76:PRO:HD3	1.93	0.40
5:E:126:LEU:HD23	5:E:126:LEU:HA	1.87	0.40
8:J:14:ARG:HD3	8:J:14:ARG:HA	1.85	0.40
14:Q:5:LYS:HD2	14:Q:5:LYS:HA	1.91	0.40
16:S:70:VAL:HG12	16:S:71:ILE:H	1.81	0.40
20:Z:51:SER:O	20:Z:54:VAL:O	2.39	0.40
1:A:217:G:H2'	1:A:218:G:C8	2.56	0.40
1:A:527:A:C4'	18:U:43:LYS:HE2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1073:A:N6	1:A:1172:A:O4'	2.54	0.40
1:A:1359:G:H22	1:A:1370:C:H5	1.69	0.40
1:A:2103:U:O2'	1:A:2626:G:N3	2.55	0.40
1:A:2536:C:O5'	1:A:2536:C:C6	2.74	0.40
1:A:2705:C:H2'	1:A:2706:G:C8	2.56	0.40
4:D:2:THR:OG1	4:D:86:VAL:HA	2.21	0.40
6:F:30:LYS:HE3	6:F:30:LYS:HB3	1.26	0.40
12:O:95:PHE:CD1	12:O:110:ALA:HB2	2.56	0.40
13:P:77:PHE:HD1	13:P:77:PHE:HA	1.74	0.40
13:P:99:LYS:HD2	13:P:101:TYR:HE1	1.84	0.40
1:A:201:C:HO2'	1:A:2272:U:HO2'	1.62	0.40
1:A:684:G:C6	1:A:697:G:C6	3.10	0.40
1:A:783:C:O2	1:A:783:C:H2'	2.22	0.40
1:A:999:A:H2'	1:A:1000:G:C8	2.57	0.40
1:A:1176:U:N3	1:A:2055:U:OP2	2.54	0.40
1:A:1649:C:O2'	1:A:1655:A:N6	2.54	0.40
1:A:1862:C:H3'	1:A:1862:C:C6	2.56	0.40
1:A:2275:G:N2	1:A:2455:A:H1'	2.36	0.40
1:A:2777:A:H2'	7:G:64:ALA:HB1	2.02	0.40
1:A:2901:G:H2'	1:A:2902:A:C8	2.57	0.40
2:B:55:A:O2'	6:F:27:GLN:NE2	2.53	0.40
3:C:24:ILE:HG13	3:C:81:VAL:HG12	2.03	0.40
3:C:154:LEU:H	3:C:154:LEU:HG	1.55	0.40
6:F:38:MET:CE	6:F:57:LEU:HD13	2.37	0.40
6:F:118:SER:HB2	6:F:128:TYR:HE1	1.87	0.40
12:O:31:LEU:HD12	12:O:31:LEU:HA	1.99	0.40
13:P:10:ASP:N	13:P:10:ASP:OD1	2.53	0.40
24:W:6:PHE:CD2	24:W:176:LEU:HD11	2.56	0.40
1:A:211:C:N3	1:A:212:C:C5	2.89	0.40
1:A:509:C:H2'	1:A:510:G:H8	1.86	0.40
1:A:1314:A:H8	1:A:1314:A:H5''	1.86	0.40
1:A:1537:G:H2'	1:A:1538:G:H8	1.86	0.40
1:A:1601:A:N6	1:A:1603:U:O2	2.54	0.40
1:A:2008:C:H2'	1:A:2009:G:C8	2.56	0.40
3:C:37:LEU:HD12	3:C:37:LEU:HA	1.96	0.40
3:C:124:ILE:HG22	3:C:124:ILE:O	2.21	0.40
9:K:19:VAL:HG13	9:K:41:CYS:HB2	2.03	0.40
18:U:96:LYS:HA	18:U:96:LYS:HD3	1.60	0.40
19:V:53:ILE:CD1	19:V:67:LEU:HD12	2.50	0.40
24:W:259:THR:HA	24:W:262:VAL:HG22	2.02	0.40
1:A:293:U:H2'	1:A:294:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:C:H4'	18:U:2:HIS:CE1	2.57	0.40
1:A:1507:U:H2'	1:A:1508:C:H6	1.87	0.40
4:D:11:GLY:C	4:D:27:VAL:HG23	2.42	0.40
12:O:35:ARG:HH12	12:O:105:ARG:CZ	2.19	0.40
16:S:20:VAL:O	16:S:20:VAL:CG1	2.69	0.40
24:W:146:ALA:O	24:W:147:LYS:HG3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	256/277 (92%)	230 (90%)	24 (9%)	2 (1%)	19	60
4	D	204/209 (98%)	176 (86%)	27 (13%)	1 (0%)	29	68
5	E	193/207 (93%)	167 (86%)	26 (14%)	0	100	100
6	F	131/179 (73%)	114 (87%)	14 (11%)	3 (2%)	6	37
7	G	107/179 (60%)	93 (87%)	14 (13%)	0	100	100
8	J	139/145 (96%)	122 (88%)	17 (12%)	0	100	100
9	K	120/122 (98%)	100 (83%)	20 (17%)	0	100	100
10	L	118/146 (81%)	101 (86%)	16 (14%)	1 (1%)	19	60
11	N	116/120 (97%)	108 (93%)	8 (7%)	0	100	100
12	O	92/120 (77%)	84 (91%)	8 (9%)	0	100	100
13	P	112/115 (97%)	98 (88%)	13 (12%)	1 (1%)	17	56
14	Q	115/118 (98%)	105 (91%)	10 (9%)	0	100	100
15	R	98/102 (96%)	82 (84%)	15 (15%)	1 (1%)	15	54
16	S	107/113 (95%)	97 (91%)	9 (8%)	1 (1%)	17	56
17	T	88/95 (93%)	77 (88%)	11 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	U	85/103 (82%)	62 (73%)	19 (22%)	4 (5%)	2	24
19	V	74/94 (79%)	67 (90%)	7 (10%)	0	100	100
20	Z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
21	b	51/59 (86%)	42 (82%)	9 (18%)	0	100	100
22	Y	63/66 (96%)	55 (87%)	8 (13%)	0	100	100
23	d	41/44 (93%)	38 (93%)	3 (7%)	0	100	100
24	W	242/282 (86%)	213 (88%)	26 (11%)	3 (1%)	13	50
All	All	2608/2954 (88%)	2283 (88%)	308 (12%)	17 (1%)	26	62

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	R	24	LYS
16	S	90	MET
18	U	82	GLY
24	W	172	THR
3	C	215	GLY
4	D	206	VAL
6	F	117	VAL
18	U	47	PRO
24	W	173	PRO
3	C	39	LYS
6	F	32	GLU
24	W	131	VAL
13	P	108	GLY
18	U	6	GLY
18	U	91	VAL
6	F	25	VAL
10	L	84	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	215/225 (96%)	209 (97%)	6 (3%)	43	65
4	D	167/170 (98%)	150 (90%)	17 (10%)	7	27
5	E	164/170 (96%)	162 (99%)	2 (1%)	71	84
6	F	120/154 (78%)	106 (88%)	14 (12%)	5	23
7	G	88/151 (58%)	82 (93%)	6 (7%)	16	43
8	J	120/123 (98%)	112 (93%)	8 (7%)	16	43
9	K	101/101 (100%)	98 (97%)	3 (3%)	41	63
10	L	93/110 (84%)	75 (81%)	18 (19%)	1	9
11	N	98/100 (98%)	98 (100%)	0	100	100
12	O	77/93 (83%)	68 (88%)	9 (12%)	5	23
13	P	99/100 (99%)	94 (95%)	5 (5%)	24	50
14	Q	96/97 (99%)	89 (93%)	7 (7%)	14	41
15	R	83/84 (99%)	80 (96%)	3 (4%)	35	60
16	S	90/93 (97%)	85 (94%)	5 (6%)	21	48
17	T	81/85 (95%)	78 (96%)	3 (4%)	34	59
18	U	78/87 (90%)	65 (83%)	13 (17%)	2	14
19	V	61/74 (82%)	59 (97%)	2 (3%)	38	61
20	Z	52/53 (98%)	50 (96%)	2 (4%)	33	58
21	b	47/53 (89%)	42 (89%)	5 (11%)	6	26
22	Y	56/57 (98%)	54 (96%)	2 (4%)	35	60
23	d	38/39 (97%)	38 (100%)	0	100	100
24	W	205/244 (84%)	188 (92%)	17 (8%)	11	37
All	All	2229/2463 (90%)	2082 (93%)	147 (7%)	20	43

All (147) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	39	LYS
3	C	154	LEU
3	C	156	ARG
3	C	171	TYR
3	C	210	ARG
3	C	217	ARG
4	D	25	VAL
4	D	55	ASP

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Mol	Chain	Res	Type
4	D	56	LYS
4	D	57	ARG
4	D	77	LYS
4	D	78	ARG
4	D	81	LYS
4	D	82	GLU
4	D	86	VAL
4	D	87	GLU
4	D	88	MET
4	D	89	ASP
4	D	91	TYR
4	D	95	GLN
4	D	107	ILE
4	D	159	LEU
4	D	207	LYS
5	E	79	ARG
5	E	89	VAL
6	F	16	LEU
6	F	30	LYS
6	F	32	GLU
6	F	91	LEU
6	F	95	ARG
6	F	96	MET
6	F	103	LEU
6	F	104	ILE
6	F	108	LEU
6	F	111	VAL
6	F	112	ARG
6	F	119	LYS
6	F	157	VAL
6	F	167	ARG
7	G	60	LYS
7	G	63	ARG
7	G	70	ARG
7	G	71	SER
7	G	78	GLU
7	G	165	TYR
8	J	25	THR
8	J	26	LEU
8	J	29	LEU
8	J	54	HIS
8	J	74	ILE

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Mol	Chain	Res	Type
8	J	80	GLN
8	J	115	LEU
8	J	121	LYS
9	K	25	LEU
9	K	28	SER
9	K	84	CYS
10	L	33	LYS
10	L	36	LYS
10	L	63	LYS
10	L	70	ASN
10	L	71	ARG
10	L	73	GLU
10	L	74	TYR
10	L	78	ASN
10	L	79	LEU
10	L	80	ASP
10	L	87	GLU
10	L	89	THR
10	L	90	GLU
10	L	99	THR
10	L	118	GLU
10	L	120	LYS
10	L	121	LEU
10	L	137	GLU
12	O	7	LYS
12	O	19	ARG
12	O	61	LYS
12	O	64	ASN
12	O	65	VAL
12	O	67	SER
12	O	70	ASP
12	O	102	TYR
12	O	107	LYS
13	P	45	ILE
13	P	49	VAL
13	P	77	PHE
13	P	81	THR
13	P	113	ILE
14	Q	13	ARG
14	Q	15	LYS
14	Q	17	VAL
14	Q	97	ASP

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Mol	Chain	Res	Type
14	Q	98	LEU
14	Q	101	ASN
14	Q	107	ASN
15	R	6	LYS
15	R	10	LYS
15	R	22	ILE
16	S	41	ARG
16	S	44	SER
16	S	49	LYS
16	S	52	LYS
16	S	53	SER
17	T	3	ASP
17	T	5	ARG
17	T	6	ASP
18	U	4	LYS
18	U	5	LYS
18	U	10	MET
18	U	46	LYS
18	U	81	VAL
18	U	84	LYS
18	U	89	LYS
18	U	90	LYS
18	U	91	VAL
18	U	92	ARG
18	U	95	LYS
18	U	96	LYS
18	U	97	SER
19	V	48	GLN
19	V	83	ASP
20	Z	24	ARG
20	Z	54	VAL
21	b	29	GLU
21	b	30	CYS
21	b	32	SER
21	b	37	LYS
21	b	52	LYS
22	Y	1	MET
22	Y	5	GLU
24	W	17	VAL
24	W	53	ARG
24	W	67	VAL
24	W	69	GLN

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Mol	Chain	Res	Type
24	W	84	SER
24	W	94	ASN
24	W	103	ILE
24	W	104	LEU
24	W	124	LEU
24	W	126	ILE
24	W	131	VAL
24	W	155	THR
24	W	176	LEU
24	W	177	TRP
24	W	275	LEU
24	W	276	SER
24	W	277	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	264	ASN
4	D	14	GLN
4	D	33	ASN
4	D	120	GLN
4	D	135	HIS
4	D	152	ASN
4	D	184	ASN
6	F	37	ASN
8	J	124	ASN
9	K	3	GLN
11	N	61	GLN
11	N	81	GLN
13	P	32	HIS
13	P	44	GLN
13	P	80	HIS
14	Q	37	GLN
14	Q	44	ASN
14	Q	107	ASN
14	Q	116	GLN
14	Q	118	ASN
15	R	81	ASN
15	R	86	GLN
16	S	60	HIS
20	Z	59	GLN
22	Y	36	GLN

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Mol	Chain	Res	Type
23	d	6	GLN
23	d	26	ASN
24	W	9	HIS
24	W	144	ASN
24	W	216	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2643/2927 (90%)	955 (36%)	55 (2%)
2	B	111/119 (93%)	38 (34%)	3 (2%)
All	All	2754/3046 (90%)	993 (36%)	58 (2%)

All (993) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	9	U
1	A	11	G
1	A	13	A
1	A	23	G
1	A	25	U
1	A	28	A
1	A	31	C
1	A	32	C
1	A	33	U
1	A	34	U
1	A	35	G
1	A	36	G
1	A	38	A
1	A	39	C
1	A	43	G
1	A	44	A
1	A	45	G
1	A	46	C
1	A	48	G
1	A	49	A
1	A	51	G
1	A	59	G
1	A	60	G
1	A	61	A

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Mol	Chain	Res	Type
1	A	63	G
1	A	71	A
1	A	75	G
1	A	76	C
1	A	79	C
1	A	83	G
1	A	87	U
1	A	89	U
1	A	90	A
1	A	91	A
1	A	92	G
1	A	93	C
1	A	94	A
1	A	98	U
1	A	100	U
1	A	101	G
1	A	109	G
1	A	113	U
1	A	117	A
1	A	118	A
1	A	119	U
1	A	124	A
1	A	125	A
1	A	126	A
1	A	127	C
1	A	128	C
1	A	130	A
1	A	145	G
1	A	150	A
1	A	156	A
1	A	159	U
1	A	162	A
1	A	163	U
1	A	164	U
1	A	166	A
1	A	175	G
1	A	176	A
1	A	177	G
1	A	178	A
1	A	179	A
1	A	180	G
1	A	181	G

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Mol	Chain	Res	Type
1	A	182	C
1	A	184	G
1	A	185	A
1	A	191	G
1	A	196	U
1	A	199	A
1	A	203	U
1	A	207	A
1	A	215	G
1	A	216	A
1	A	219	A
1	A	224	A
1	A	225	A
1	A	226	A
1	A	227	G
1	A	230	A
1	A	231	A
1	A	233	G
1	A	234	C
1	A	235	G
1	A	244	A
1	A	245	G
1	A	246	U
1	A	251	G
1	A	252	C
1	A	253	G
1	A	254	A
1	A	255	G
1	A	258	A
1	A	267	C
1	A	268	A
1	A	269	G
1	A	270	C
1	A	271	C
1	A	272	C
1	A	275	A
1	A	282	G
1	A	283	G
1	A	284	C
1	A	286	U
1	A	289	C
1	A	290	U

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Mol	Chain	Res	Type
1	A	291	C
1	A	295	G
1	A	298	U
1	A	299	U
1	A	300	G
1	A	301	U
1	A	302	A
1	A	306	C
1	A	310	C
1	A	312	G
1	A	313	U
1	A	314	A
1	A	315	C
1	A	320	U
1	A	321	U
1	A	322	A
1	A	323	C
1	A	324	A
1	A	325	A
1	A	326	A
1	A	327	G
1	A	328	G
1	A	329	A
1	A	331	C
1	A	338	G
1	A	344	G
1	A	345	A
1	A	346	G
1	A	354	A
1	A	360	C
1	A	362	C
1	A	367	G
1	A	368	G
1	A	373	A
1	A	374	A
1	A	376	A
1	A	378	C
1	A	379	C
1	A	380	C
1	A	382	G
1	A	388	A
1	A	389	A

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Mol	Chain	Res	Type
1	A	390	A
1	A	393	U
1	A	394	U
1	A	395	C
1	A	396	G
1	A	397	U
1	A	404	C
1	A	405	U
1	A	406	G
1	A	410	G
1	A	411	G
1	A	412	A
1	A	417	G
1	A	418	A
1	A	419	G
1	A	420	U
1	A	431	A
1	A	433	G
1	A	434	U
1	A	435	G
1	A	436	A
1	A	437	A
1	A	438	A
1	A	445	C
1	A	451	C
1	A	452	C
1	A	469	A
1	A	470	A
1	A	474	U
1	A	481	U
1	A	483	C
1	A	484	C
1	A	485	U
1	A	489	G
1	A	490	A
1	A	495	U
1	A	496	A
1	A	498	U
1	A	499	G
1	A	501	A
1	A	502	C
1	A	503	C

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Mol	Chain	Res	Type
1	A	504	A
1	A	508	C
1	A	514	G
1	A	524	A
1	A	525	A
1	A	526	A
1	A	528	G
1	A	537	A
1	A	538	A
1	A	542	G
1	A	544	G
1	A	547	A
1	A	548	A
1	A	550	G
1	A	551	A
1	A	554	U
1	A	555	C
1	A	556	C
1	A	558	G
1	A	561	A
1	A	564	G
1	A	571	U
1	A	573	C
1	A	576	G
1	A	577	U
1	A	578	A
1	A	579	G
1	A	584	A
1	A	588	C
1	A	590	U
1	A	591	U
1	A	592	A
1	A	594	C
1	A	595	G
1	A	598	U
1	A	599	G
1	A	606	U
1	A	607	G
1	A	612	U
1	A	614	G
1	A	616	A
1	A	617	G

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Mol	Chain	Res	Type
1	A	619	A
1	A	630	A
1	A	631	G
1	A	633	U
1	A	637	A
1	A	639	C
1	A	642	G
1	A	645	C
1	A	646	A
1	A	648	G
1	A	649	G
1	A	650	U
1	A	651	U
1	A	656	A
1	A	657	G
1	A	658	A
1	A	660	G
1	A	661	A
1	A	665	G
1	A	666	G
1	A	667	A
1	A	668	G
1	A	673	A
1	A	674	G
1	A	680	G
1	A	683	A
1	A	684	G
1	A	689	A
1	A	691	U
1	A	692	A
1	A	700	U
1	A	701	G
1	A	702	A
1	A	703	G
1	A	706	C
1	A	711	U
1	A	713	G
1	A	716	G
1	A	717	A
1	A	718	C
1	A	724	A
1	A	729	G

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Mol	Chain	Res	Type
1	A	731	G
1	A	732	A
1	A	733	U
1	A	734	C
1	A	742	G
1	A	747	G
1	A	758	A
1	A	764	C
1	A	765	A
1	A	766	C
1	A	769	A
1	A	773	G
1	A	774	A
1	A	775	G
1	A	776	G
1	A	777	C
1	A	782	A
1	A	783	C
1	A	784	C
1	A	785	C
1	A	787	C
1	A	788	G
1	A	792	G
1	A	793	U
1	A	794	U
1	A	795	G
1	A	796	A
1	A	799	A
1	A	811	A
1	A	812	G
1	A	817	G
1	A	822	G
1	A	823	G
1	A	825	G
1	A	829	A
1	A	830	A
1	A	831	U
1	A	832	G
1	A	835	A
1	A	836	A
1	A	838	C
1	A	843	C

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Mol	Chain	Res	Type
1	A	847	A
1	A	852	G
1	A	853	C
1	A	856	G
1	A	858	U
1	A	859	C
1	A	866	A
1	A	872	C
1	A	874	U
1	A	877	G
1	A	878	G
1	A	881	U
1	A	882	A
1	A	886	U
1	A	890	G
1	A	892	U
1	A	895	G
1	A	896	A
1	A	898	U
1	A	899	C
1	A	903	G
1	A	906	G
1	A	907	U
1	A	908	A
1	A	909	G
1	A	910	A
1	A	912	C
1	A	914	C
1	A	918	U
1	A	919	U
1	A	921	G
1	A	924	U
1	A	925	A
1	A	927	G
1	A	949	U
1	A	951	C
1	A	954	U
1	A	956	A
1	A	957	A
1	A	959	C
1	A	964	A
1	A	970	A

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Mol	Chain	Res	Type
1	A	972	U
1	A	974	A
1	A	975	C
1	A	976	U
1	A	978	A
1	A	981	C
1	A	987	A
1	A	988	G
1	A	990	C
1	A	991	A
1	A	992	G
1	A	1004	U
1	A	1005	A
1	A	1007	G
1	A	1008	A
1	A	1016	U
1	A	1019	A
1	A	1020	A
1	A	1028	C
1	A	1029	A
1	A	1030	G
1	A	1031	C
1	A	1034	A
1	A	1035	G
1	A	1037	C
1	A	1042	A
1	A	1043	G
1	A	1054	A
1	A	1055	A
1	A	1056	A
1	A	1058	U
1	A	1059	A
1	A	1063	G
1	A	1067	A
1	A	1068	G
1	A	1069	U
1	A	1070	G
1	A	1071	G
1	A	1072	A
1	A	1073	A
1	A	1074	A
1	A	1079	U

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Mol	Chain	Res	Type
1	A	1092	A
1	A	1093	G
1	A	1096	A
1	A	1098	C
1	A	1102	G
1	A	1104	U
1	A	1107	U
1	A	1108	G
1	A	1117	G
1	A	1128	U
1	A	1129	U
1	A	1130	A
1	A	1131	A
1	A	1134	A
1	A	1135	G
1	A	1148	C
1	A	1151	U
1	A	1153	G
1	A	1154	U
1	A	1158	G
1	A	1159	U
1	A	1168	G
1	A	1173	A
1	A	1174	A
1	A	1175	A
1	A	1176	U
1	A	1177	G
1	A	1178	U
1	A	1179	A
1	A	1180	C
1	A	1181	C
1	A	1182	G
1	A	1185	G
1	A	1188	A
1	A	1189	A
1	A	1190	A
1	A	1193	U
1	A	1194	A
1	A	1201	A
1	A	1202	A
1	A	1208	G
1	A	1209	G

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Mol	Chain	Res	Type
1	A	1215	U
1	A	1222	A
1	A	1223	C
1	A	1227	G
1	A	1236	G
1	A	1246	G
1	A	1247	G
1	A	1248	C
1	A	1250	G
1	A	1251	U
1	A	1252	G
1	A	1258	A
1	A	1259	G
1	A	1267	G
1	A	1269	A
1	A	1278	G
1	A	1279	C
1	A	1286	A
1	A	1288	G
1	A	1289	U
1	A	1293	A
1	A	1295	U
1	A	1296	G
1	A	1299	G
1	A	1305	A
1	A	1306	G
1	A	1311	G
1	A	1312	A
1	A	1313	A
1	A	1314	A
1	A	1315	G
1	A	1317	G
1	A	1326	A
1	A	1327	U
1	A	1335	A
1	A	1339	A
1	A	1340	A
1	A	1341	U
1	A	1342	G
1	A	1344	C
1	A	1345	U
1	A	1346	A

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Mol	Chain	Res	Type
1	A	1350	U
1	A	1352	U
1	A	1353	C
1	A	1360	A
1	A	1363	G
1	A	1364	C
1	A	1367	G
1	A	1368	U
1	A	1369	C
1	A	1372	C
1	A	1376	G
1	A	1380	U
1	A	1384	C
1	A	1388	A
1	A	1398	A
1	A	1404	A
1	A	1406	A
1	A	1417	A
1	A	1418	U
1	A	1423	A
1	A	1424	A
1	A	1427	G
1	A	1430	U
1	A	1431	G
1	A	1434	A
1	A	1435	U
1	A	1436	U
1	A	1439	U
1	A	1441	U
1	A	1442	A
1	A	1448	U
1	A	1449	C
1	A	1450	C
1	A	1455	C
1	A	1456	A
1	A	1459	U
1	A	1460	G
1	A	1462	G
1	A	1464	A
1	A	1466	U
1	A	1472	G
1	A	1473	A

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Mol	Chain	Res	Type
1	A	1474	C
1	A	1490	A
1	A	1495	C
1	A	1497	G
1	A	1498	U
1	A	1499	A
1	A	1500	U
1	A	1501	U
1	A	1502	G
1	A	1503	G
1	A	1505	U
1	A	1506	A
1	A	1507	U
1	A	1512	G
1	A	1513	U
1	A	1516	A
1	A	1519	C
1	A	1520	A
1	A	1521	G
1	A	1528	U
1	A	1529	G
1	A	1530	G
1	A	1535	U
1	A	1536	A
1	A	1539	C
1	A	1540	A
1	A	1541	A
1	A	1543	U
1	A	1544	C
1	A	1545	C
1	A	1553	A
1	A	1554	U
1	A	1555	A
1	A	1556	A
1	A	1561	G
1	A	1562	A
1	A	1565	U
1	A	1570	U
1	A	1573	C
1	A	1576	G
1	A	1578	G
1	A	1582	U

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Mol	Chain	Res	Type
1	A	1584	U
1	A	1585	A
1	A	1586	G
1	A	1587	U
1	A	1589	G
1	A	1592	A
1	A	1596	U
1	A	1601	A
1	A	1606	A
1	A	1607	C
1	A	1608	A
1	A	1615	A
1	A	1617	A
1	A	1626	U
1	A	1629	C
1	A	1631	A
1	A	1632	G
1	A	1634	U
1	A	1636	A
1	A	1638	A
1	A	1643	C
1	A	1644	C
1	A	1651	G
1	A	1652	C
1	A	1653	A
1	A	1654	A
1	A	1655	A
1	A	1656	C
1	A	1657	C
1	A	1658	G
1	A	1660	C
1	A	1661	A
1	A	1667	A
1	A	1668	G
1	A	1674	G
1	A	1685	A
1	A	1688	G
1	A	1690	G
1	A	1692	U
1	A	1693	C
1	A	1696	G
1	A	1697	A

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Mol	Chain	Res	Type
1	A	1707	U
1	A	1708	U
1	A	1712	G
1	A	1713	A
1	A	1714	A
1	A	1719	G
1	A	1726	G
1	A	1727	A
1	A	1739	C
1	A	1745	A
1	A	1752	G
1	A	1756	U
1	A	1758	U
1	A	1759	U
1	A	1762	G
1	A	1763	G
1	A	1771	C
1	A	1774	A
1	A	1776	A
1	A	1777	G
1	A	1778	A
1	A	1779	G
1	A	1780	C
1	A	1782	G
1	A	1785	G
1	A	1787	G
1	A	1788	A
1	A	1790	U
1	A	1791	A
1	A	1792	G
1	A	1793	G
1	A	1796	C
1	A	1797	A
1	A	1802	A
1	A	1803	C
1	A	1805	G
1	A	1808	U
1	A	1810	G
1	A	1811	C
1	A	1813	A
1	A	1815	A
1	A	1816	A

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Mol	Chain	Res	Type
1	A	1818	A
1	A	1829	C
1	A	1830	G
1	A	1831	A
1	A	1832	A
1	A	1834	C
1	A	1837	U
1	A	1838	A
1	A	1839	A
1	A	1844	A
1	A	1849	U
1	A	2001	G
1	A	2006	A
1	A	2009	G
1	A	2010	A
1	A	2011	U
1	A	2014	G
1	A	2015	G
1	A	2021	G
1	A	2022	U
1	A	2024	U
1	A	2026	A
1	A	2031	G
1	A	2032	A
1	A	2052	A
1	A	2059	A
1	A	2060	A
1	A	2062	A
1	A	2064	G
1	A	2065	C
1	A	2068	G
1	A	2072	C
1	A	2081	G
1	A	2084	C
1	A	2085	G
1	A	2086	G
1	A	2092	C
1	A	2093	C
1	A	2096	G
1	A	2097	U
1	A	2098	G
1	A	2105	U

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Mol	Chain	Res	Type
1	A	2109	G
1	A	2111	A
1	A	2116	G
1	A	2121	U
1	A	2122	G
1	A	2124	A
1	A	2128	U
1	A	2131	U
1	A	2132	A
1	A	2135	G
1	A	2136	C
1	A	2146	A
1	A	2147	U
1	A	2148	A
1	A	2149	G
1	A	2151	U
1	A	2155	A
1	A	2156	G
1	A	2157	C
1	A	2158	C
1	A	2159	U
1	A	2161	G
1	A	2162	G
1	A	2163	A
1	A	2165	A
1	A	2166	C
1	A	2168	G
1	A	2169	G
1	A	2178	C
1	A	2183	G
1	A	2187	A
1	A	2188	G
1	A	2190	C
1	A	2199	G
1	A	2200	A
1	A	2201	U
1	A	2202	A
1	A	2203	C
1	A	2217	U
1	A	2221	C
1	A	2222	C
1	A	2223	U

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Mol	Chain	Res	Type
1	A	2227	A
1	A	2232	G
1	A	2233	C
1	A	2235	G
1	A	2240	U
1	A	2241	A
1	A	2242	U
1	A	2243	C
1	A	2244	G
1	A	2246	G
1	A	2253	G
1	A	2254	A
1	A	2255	C
1	A	2260	U
1	A	2264	G
1	A	2267	G
1	A	2268	G
1	A	2274	U
1	A	2276	A
1	A	2283	C
1	A	2288	G
1	A	2291	U
1	A	2297	A
1	A	2301	U
1	A	2303	A
1	A	2304	C
1	A	2308	G
1	A	2311	G
1	A	2312	C
1	A	2315	A
1	A	2325	U
1	A	2328	G
1	A	2334	U
1	A	2335	U
1	A	2336	G
1	A	2337	G
1	A	2339	A
1	A	2340	A
1	A	2341	U
1	A	2342	C
1	A	2343	A
1	A	2344	U

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Mol	Chain	Res	Type
1	A	2345	U
1	A	2346	C
1	A	2347	G
1	A	2348	C
1	A	2349	A
1	A	2351	A
1	A	2352	G
1	A	2356	A
1	A	2357	A
1	A	2363	C
1	A	2364	A
1	A	2365	A
1	A	2373	U
1	A	2374	G
1	A	2375	A
1	A	2376	C
1	A	2377	U
1	A	2379	C
1	A	2387	A
1	A	2400	G
1	A	2401	G
1	A	2411	G
1	A	2412	G
1	A	2414	C
1	A	2420	G
1	A	2421	A
1	A	2430	U
1	A	2431	U
1	A	2435	C
1	A	2448	U
1	A	2452	U
1	A	2453	C
1	A	2454	A
1	A	2455	A
1	A	2456	C
1	A	2457	G
1	A	2458	G
1	A	2459	A
1	A	2460	U
1	A	2464	A
1	A	2468	A
1	A	2470	C

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Mol	Chain	Res	Type
1	A	2541	C
1	A	2542	A
1	A	2543	U
1	A	2546	C
1	A	2547	A
1	A	2548	U
1	A	2549	C
1	A	2554	G
1	A	2556	C
1	A	2557	U
1	A	2558	G
1	A	2559	U
1	A	2560	A
1	A	2561	G
1	A	2569	C
1	A	2572	G
1	A	2573	G
1	A	2575	U
1	A	2576	U
1	A	2579	G
1	A	2580	C
1	A	2581	U
1	A	2582	G
1	A	2583	U
1	A	2585	C
1	A	2593	A
1	A	2594	A
1	A	2595	A
1	A	2596	G
1	A	2597	C
1	A	2602	C
1	A	2603	G
1	A	2607	G
1	A	2610	G
1	A	2611	G
1	A	2616	A
1	A	2618	A
1	A	2619	A
1	A	2620	C
1	A	2621	G
1	A	2628	G
1	A	2631	A

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Mol	Chain	Res	Type
1	A	2638	U
1	A	2639	C
1	A	2640	C
1	A	2642	U
1	A	2643	A
1	A	2644	U
1	A	2648	U
1	A	2650	G
1	A	2652	G
1	A	2658	A
1	A	2659	G
1	A	2661	A
1	A	2663	A
1	A	2665	U
1	A	2668	A
1	A	2674	G
1	A	2675	C
1	A	2676	U
1	A	2677	G
1	A	2680	C
1	A	2686	A
1	A	2687	C
1	A	2703	G
1	A	2714	G
1	A	2717	G
1	A	2718	U
1	A	2719	A
1	A	2720	C
1	A	2728	U
1	A	2730	U
1	A	2731	G
1	A	2741	U
1	A	2755	U
1	A	2762	A
1	A	2764	G
1	A	2765	G
1	A	2771	G
1	A	2773	G
1	A	2775	U
1	A	2776	G
1	A	2779	A
1	A	2780	G

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Mol	Chain	Res	Type
1	A	2784	C
1	A	2785	U
1	A	2786	A
1	A	2787	A
1	A	2790	A
1	A	2793	A
1	A	2795	G
1	A	2797	C
1	A	2804	A
1	A	2805	A
1	A	2807	A
1	A	2808	U
1	A	2809	G
1	A	2813	U
1	A	2817	C
1	A	2818	C
1	A	2819	A
1	A	2820	U
1	A	2823	C
1	A	2825	C
1	A	2826	A
1	A	2828	G
1	A	2830	A
1	A	2843	G
1	A	2845	A
1	A	2855	G
1	A	2856	G
1	A	2857	U
1	A	2858	U
1	A	2859	G
1	A	2860	A
1	A	2861	U
1	A	2866	C
1	A	2867	U
1	A	2868	G
1	A	2872	U
1	A	2873	G
1	A	2874	G
1	A	2892	G
1	A	2897	G
1	A	2898	A
1	A	2899	C

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Mol	Chain	Res	Type
1	A	2900	A
1	A	2904	A
1	A	2905	C
1	A	2908	A
1	A	2909	U
1	A	2916	A
2	B	10	G
2	B	11	A
2	B	12	U
2	B	13	A
2	B	15	C
2	B	19	G
2	B	20	A
2	B	23	U
2	B	28	C
2	B	31	G
2	B	37	A
2	B	38	U
2	B	39	A
2	B	40	C
2	B	41	C
2	B	42	G
2	B	46	A
2	B	48	G
2	B	49	G
2	B	51	A
2	B	55	A
2	B	60	C
2	B	63	C
2	B	64	A
2	B	65	G
2	B	78	U
2	B	81	G
2	B	86	U
2	B	87	U
2	B	88	C
2	B	91	C
2	B	92	C
2	B	95	U
2	B	96	G
2	B	97	A
2	B	107	G

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Mol	Chain	Res	Type
2	B	110	G
2	B	114	A

All (58) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	43	G
1	A	58	G
1	A	90	A
1	A	99	U
1	A	124	A
1	A	163	U
1	A	175	G
1	A	183	A
1	A	229	A
1	A	252	C
1	A	271	C
1	A	288	C
1	A	377	G
1	A	405	U
1	A	417	G
1	A	419	G
1	A	549	A
1	A	647	A
1	A	649	G
1	A	664	C
1	A	666	G
1	A	683	A
1	A	717	A
1	A	733	U
1	A	837	U
1	A	1066	A
1	A	1103	A
1	A	1107	U
1	A	1245	G
1	A	1250	G
1	A	1314	A
1	A	1325	A
1	A	1339	A
1	A	1351	U
1	A	1362	G
1	A	1438	C

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Mol	Chain	Res	Type
1	A	1455	C
1	A	1527	C
1	A	1535	U
1	A	1595	U
1	A	1630	G
1	A	1652	C
1	A	1656	C
1	A	1755	C
1	A	1779	G
1	A	1784	A
1	A	2267	G
1	A	2334	U
1	A	2351	A
1	A	2454	A
1	A	2716	U
1	A	2784	C
1	A	2785	U
1	A	2812	A
1	A	2858	U
2	B	47	C
2	B	54	U
2	B	59	U

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
25	GNP	W	301	-	29,34,34	1.78	4 (13%)	33,54,54	2.04	8 (24%)

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
25	GNP	W	301	-	-	3/14/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	W	301	GNP	PG-N3B	4.63	1.75	1.63
25	W	301	GNP	PB-N3B	4.60	1.75	1.63
25	W	301	GNP	C5-C6	4.21	1.48	1.41
25	W	301	GNP	C5-C4	2.47	1.47	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	W	301	GNP	C2-N3-C4	4.95	121.02	115.36
25	W	301	GNP	C2-N1-C6	4.02	122.32	115.93
25	W	301	GNP	C5-C6-N1	-3.98	117.99	123.43
25	W	301	GNP	C4-C5-C6	-3.75	117.21	120.80
25	W	301	GNP	PB-O3A-PA	-3.47	120.41	132.62
25	W	301	GNP	C3'-C2'-C1'	3.44	106.16	100.98
25	W	301	GNP	N3-C2-N1	-3.29	122.84	127.22
25	W	301	GNP	C4-C5-N7	-2.69	106.60	109.40

There are no chirality outliers.

All (3) torsion outliers are listed below:

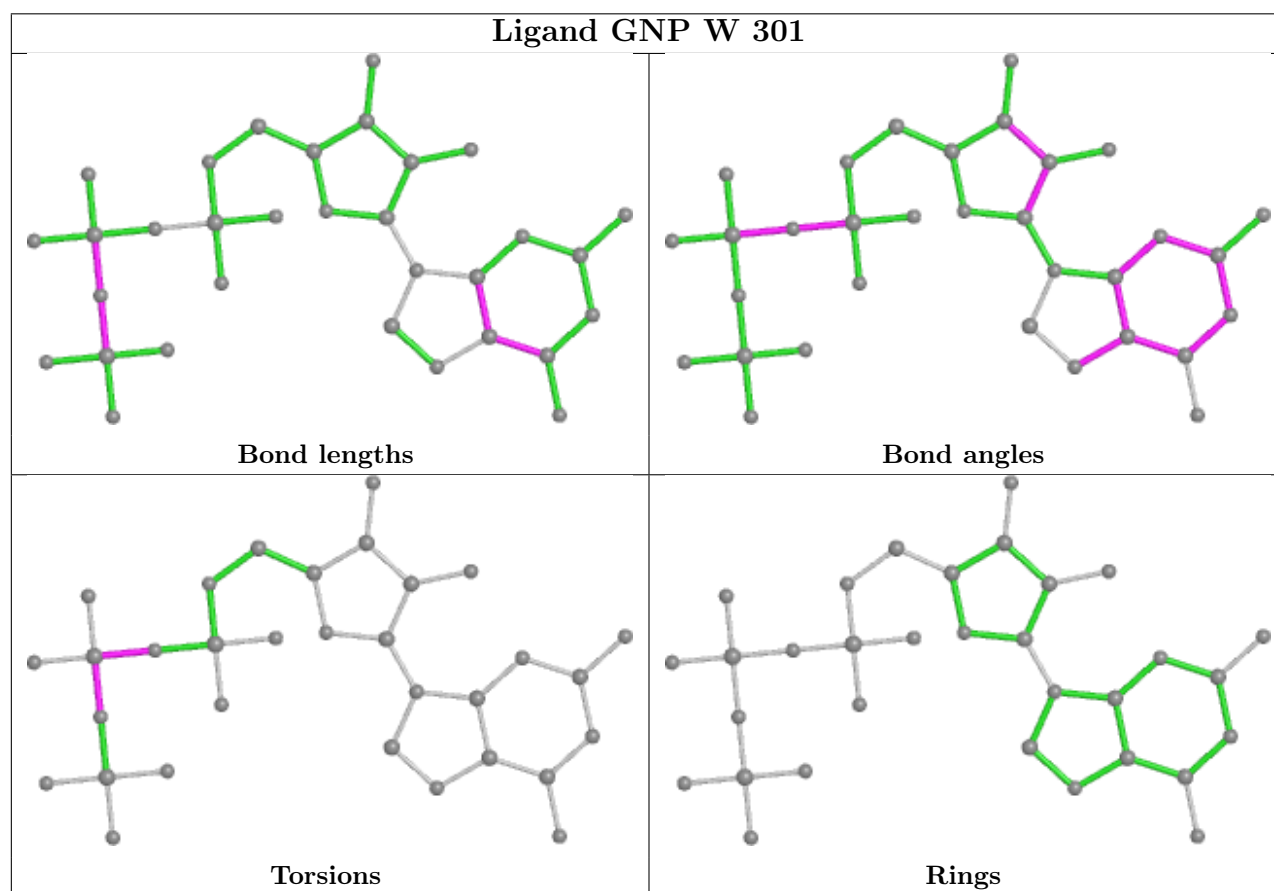
Mol	Chain	Res	Type	Atoms
25	W	301	GNP	PG-N3B-PB-O1B
25	W	301	GNP	PA-O3A-PB-O1B
25	W	301	GNP	PA-O3A-PB-O2B

There are no ring outliers.

1 monomer is involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	W	301	GNP	10	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

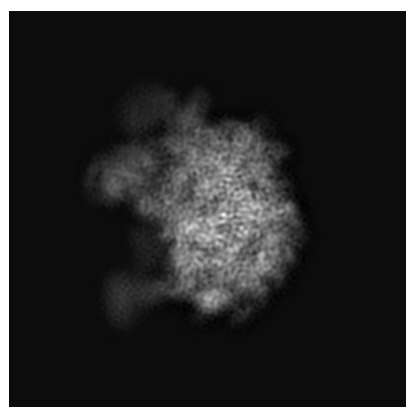
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20441. These allow visual inspection of the internal detail of the map and identification of artifacts.

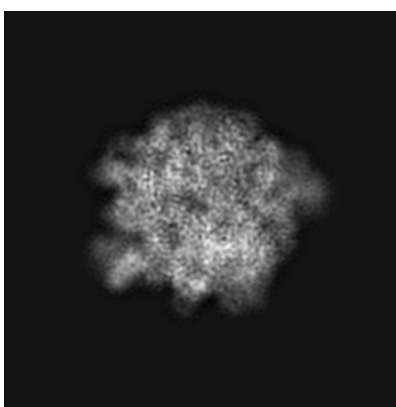
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

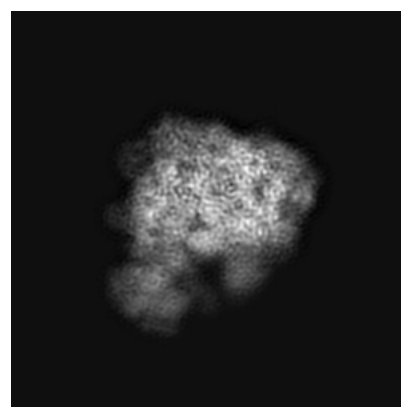
6.1.1 Primary map



X



Y

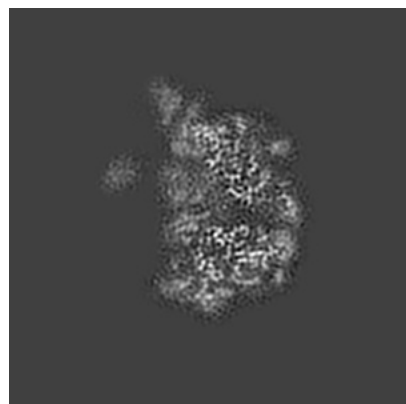


Z

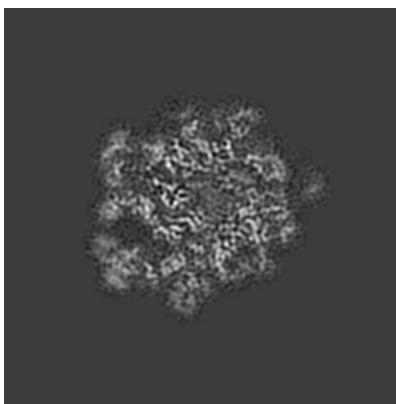
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

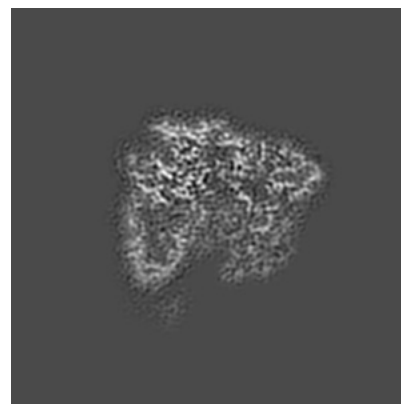
6.2.1 Primary map



X Index: 120



Y Index: 120

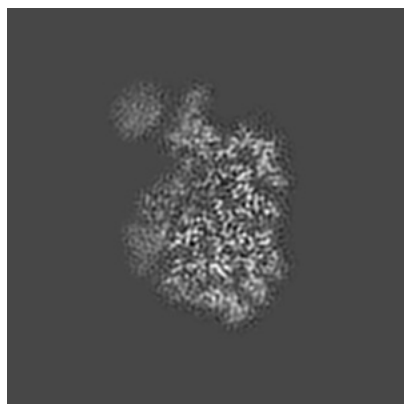


Z Index: 120

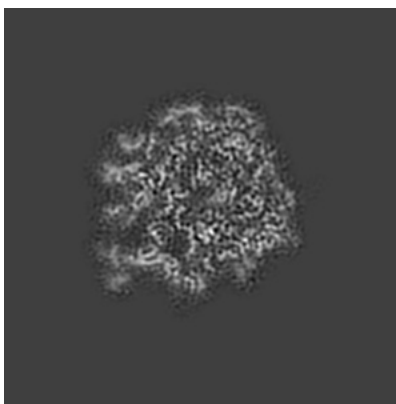
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

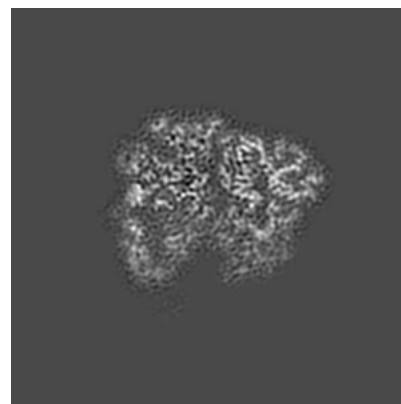
6.3.1 Primary map



X Index: 140



Y Index: 127



Z Index: 117

The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

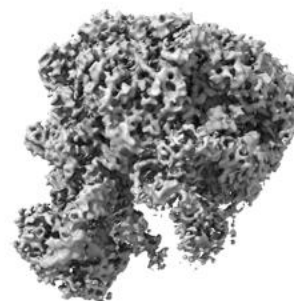
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.017. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

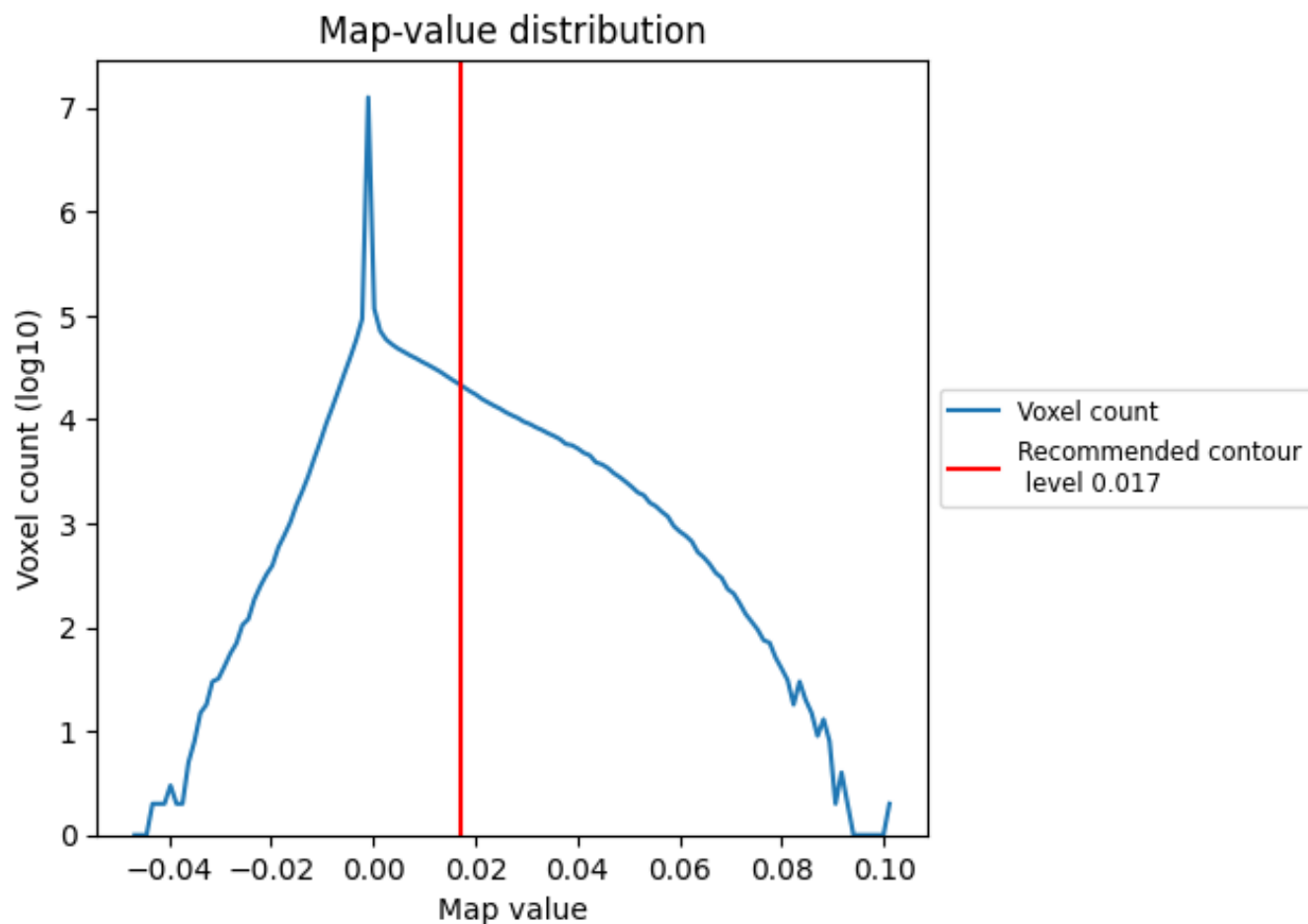
6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

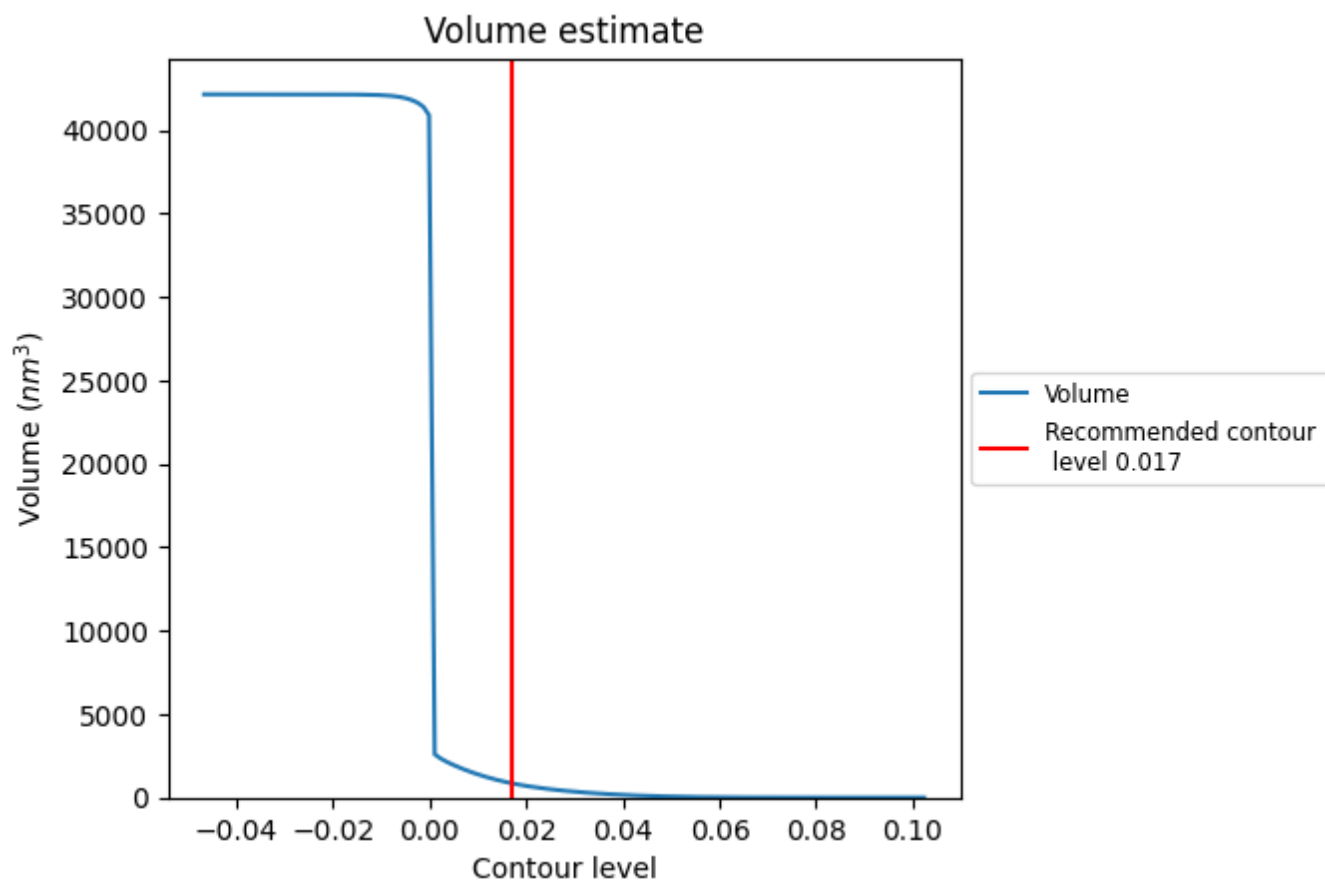
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

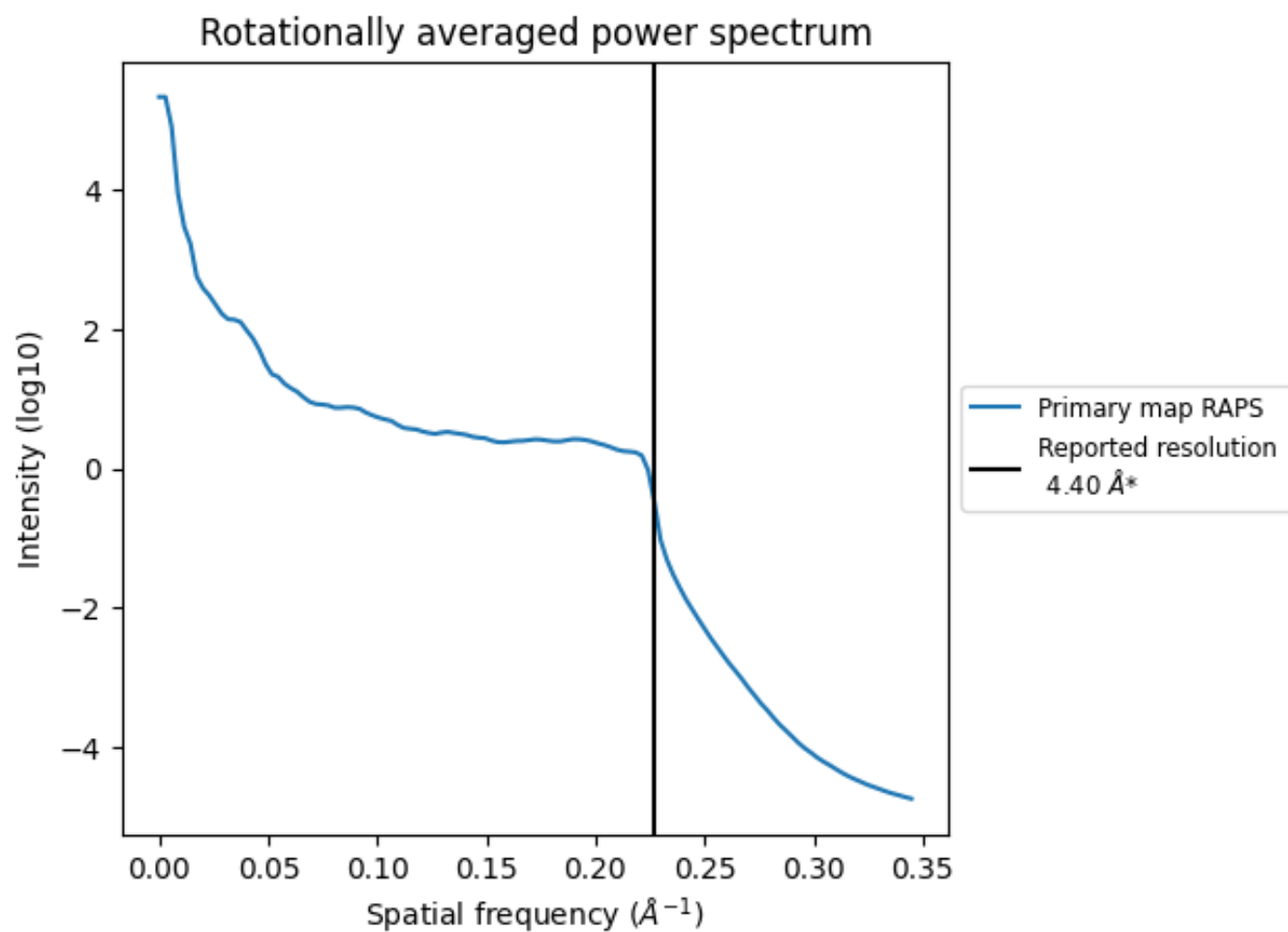
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 855 nm^3 ; this corresponds to an approximate mass of 772 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

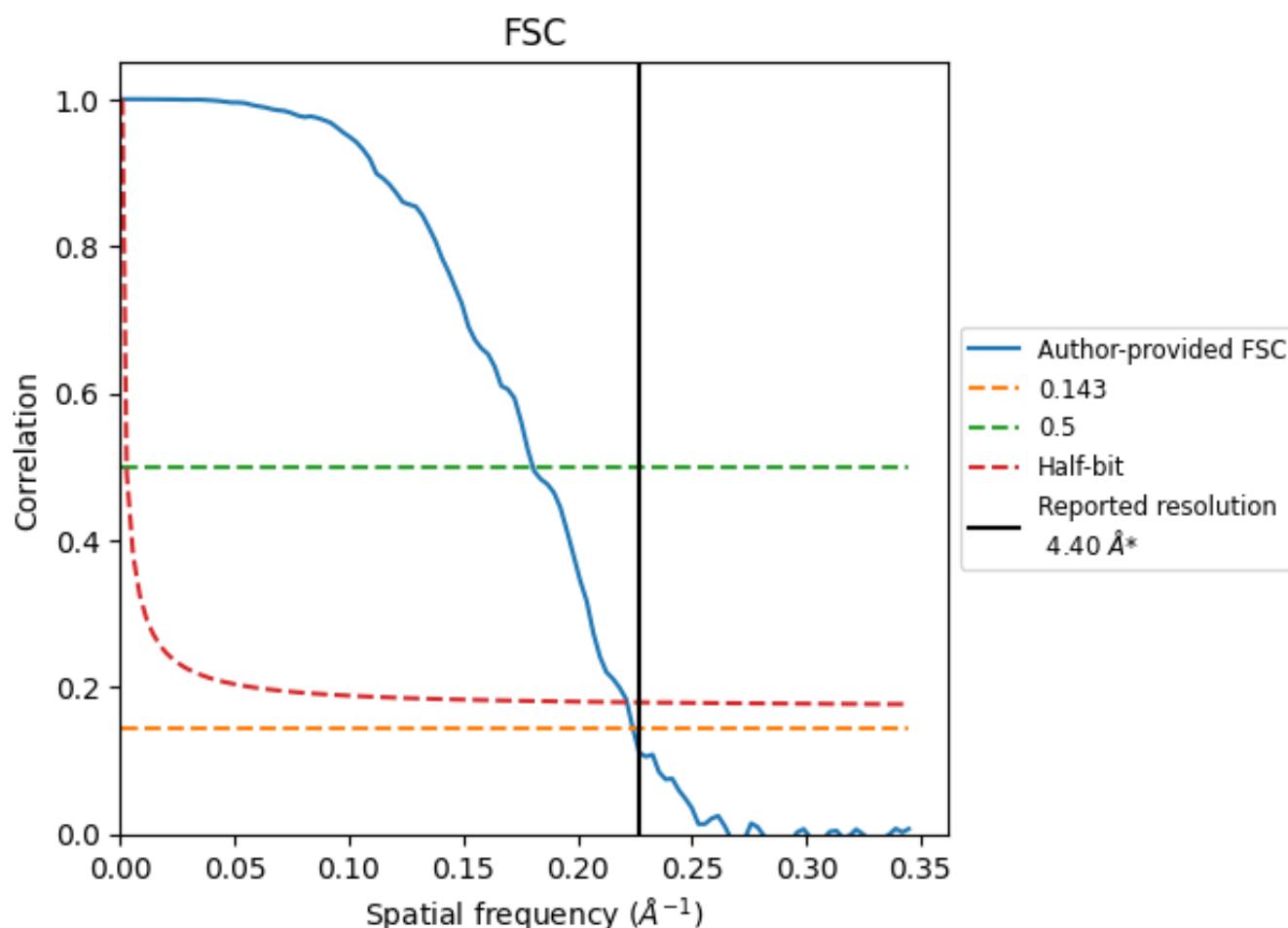


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.227 \AA^{-1}

8.2 Resolution estimates [i](#)

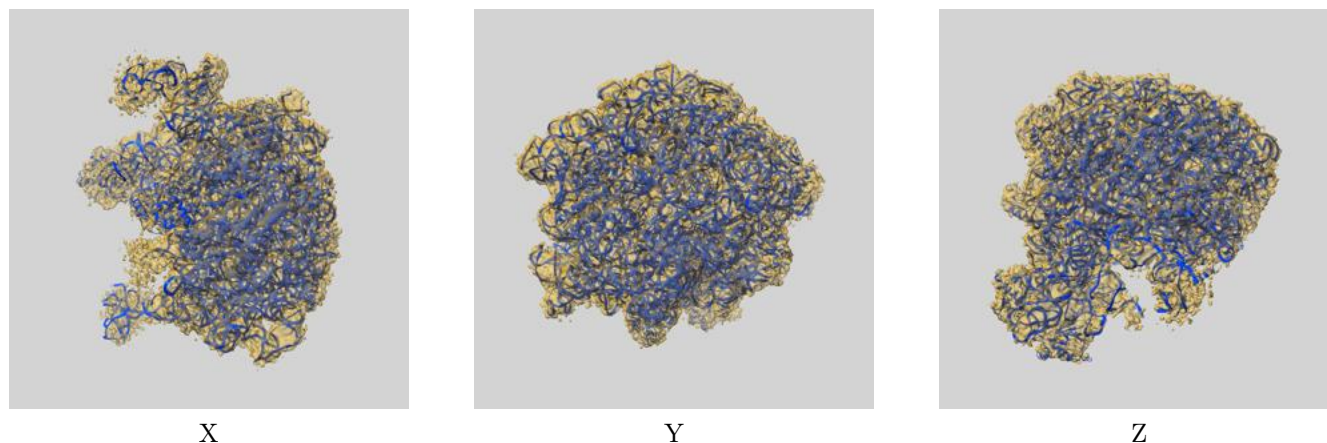
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.46	5.54	4.51
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

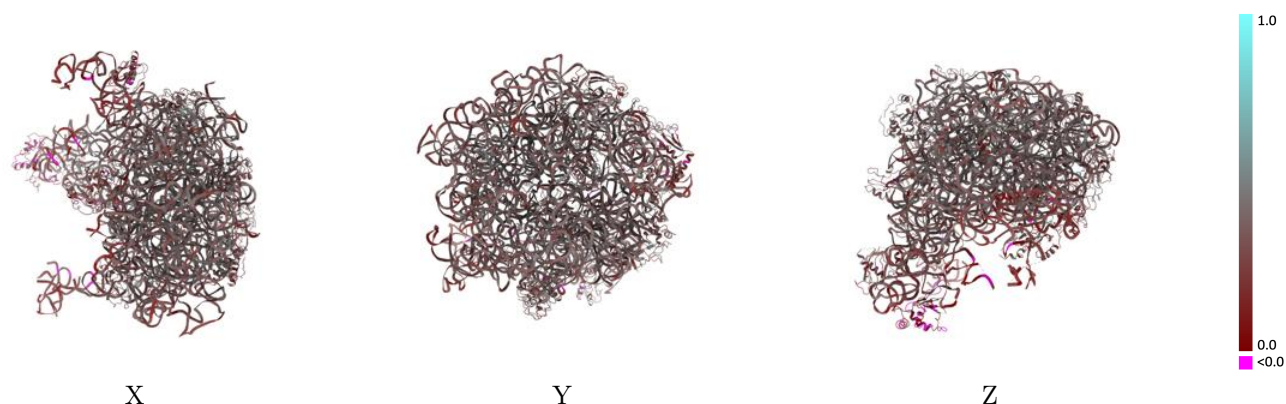
This section contains information regarding the fit between EMDB map EMD-20441 and PDB model 6PPK. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



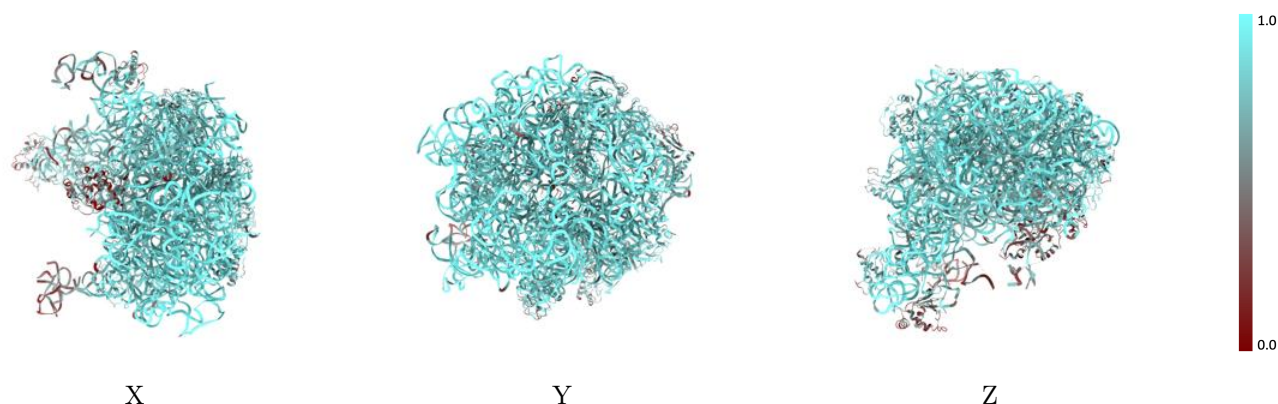
The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



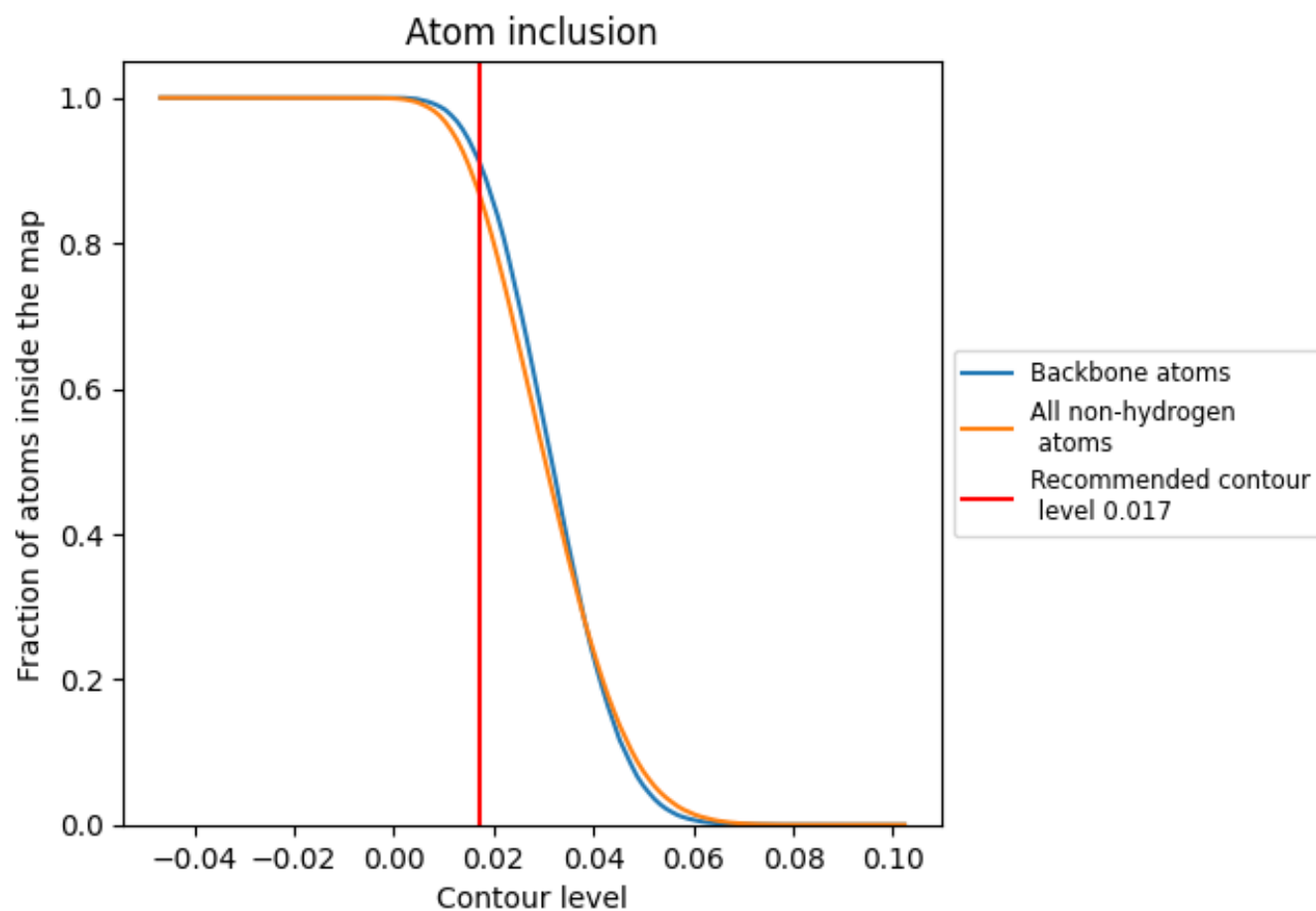
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.017).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8707	 0.3540
A	 0.9208	 0.3570
B	 0.8965	 0.3060
C	 0.7983	 0.3770
D	 0.7782	 0.3900
E	 0.7889	 0.3850
F	 0.4268	 0.1090
G	 0.5909	 0.2660
J	 0.7925	 0.3700
K	 0.8027	 0.3930
L	 0.7508	 0.3500
N	 0.8211	 0.3890
O	 0.6907	 0.2740
P	 0.7439	 0.3450
Q	 0.8493	 0.3740
R	 0.8301	 0.4010
S	 0.8059	 0.3960
T	 0.8393	 0.4080
U	 0.7822	 0.3500
V	 0.6981	 0.3630
W	 0.4275	 0.3160
Y	 0.7996	 0.3440
Z	 0.7326	 0.3500
b	 0.8198	 0.3980
d	 0.8754	 0.4290

