wwPDB EM Map/Model Validation Report (i)

Sep 27, 2016 – 03:56 PM EDT

PDB ID	:	5LMU
EMDB ID:	:	EMD-4080
Title	:	Structure of bacterial 30S-IF3-mRNA-tRNA translation pre-initiation complex, closed form (state-4)
Authors	:	Hussain, T.; Llacer, J.L.; Wimberly, B.T.; Ramakrishnan, V.
Deposited on	:	2016-08-01
Resolution	:	4.00 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

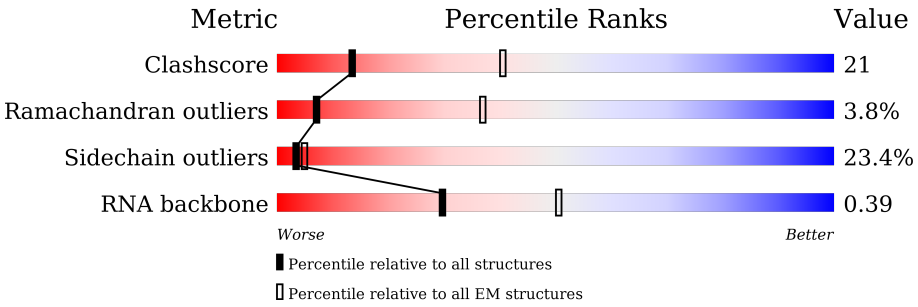
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027939

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	1522	22% 55% 22% •
2	B	256	45% 34% 11% • 9%
3	C	239	49% 31% 6% 14%
4	D	209	49% 39% 11%
5	E	162	58% 23% 12% 7%
6	F	101	51% 39% 8% •
7	G	156	69% 30% ••
8	H	138	63% 29% 7% •

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Mol	Chain	Length	Quality of chain
9	I	128	56% 36% 7%
10	J	105	38% 41% 13% 7%
11	K	129	55% 32% 5% 8%
12	L	132	53% 34% 6% 6%
13	M	126	60% 33% 6%
14	N	61	54% 36% 8%
15	O	89	56% 36% 6%
16	P	88	65% 22% 8% 6%
17	Q	105	52% 33% 8% 6%
18	R	88	47% 27% 9% 17%
19	S	93	46% 24% 16% 12%
20	T	106	45% 35% 13% 7%
21	V	27	41% 37% 7% 11%
22	X	171	37% 46% 12%
23	Y	42	10% 21% 17% 52%
24	Z	77	22% 44% 34%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
26	ZN	D	300	-	-	X	-

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 55195 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1515	32548	14490	6022	10523	1513	0	0

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	234	1900	1213	341	341	5	0	0

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	206	1612	1016	314	281	1	0	0

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	208	1703	1066	339	291	7	0	0

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	150	1146	724	217	201	4	0	0

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	101	843	531	155	154	3	0	0

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	127	Total	C	N	O	0	0
			1010	639	197	174		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	98	Total	C	N	O	S	0	0
			792	498	156	137	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	119	Total	C	N	O	S	0	0
			885	549	168	165	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	124	Total	C	N	O	S	0	0
			970	611	195	163	1		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	118	Total	C	N	O	S	0	0
			937	579	193	163	2		

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	60	Total 492	C 312	N 104	O 72	S 4	0	0

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	88	Total 734	C 459	N 147	O 126	S 2	0	0

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	83	Total 700	C 443	N 139	O 117	S 1	0	0

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	99	Total 823	C 528	N 151	O 142	S 2	0	0

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	73	Total 598	C 381	N 118	O 99	0	0

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	82	Total 655	C 419	N 120	O 114	S 2	0	0

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	99	Total 763	C 470	N 162	O 129	S 2	0	0

- Molecule 21 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	V	24	Total 208	C 128	N 50	O 30	0	0

- Molecule 22 is a protein called Translation initiation factor IF-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	164	Total 1336	C 841	N 245	O 241	S 9	0	0

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	20	Total 439	C 196	N 89	O 134	P 20	0	0

- Molecule 24 is a RNA chain called tRNAi.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Z	77	Total 1646	C 735	N 297	O 536	P 77	S 1	0	0

- Molecule 25 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
25	Z	1	Total 1	Mg 1	0
25	A	78	Total 78	Mg 78	0
25	L	1	Total 1	Mg 1	0

- Molecule 26 is ZINC ION (three-letter code: ZN) (formula: Zn).

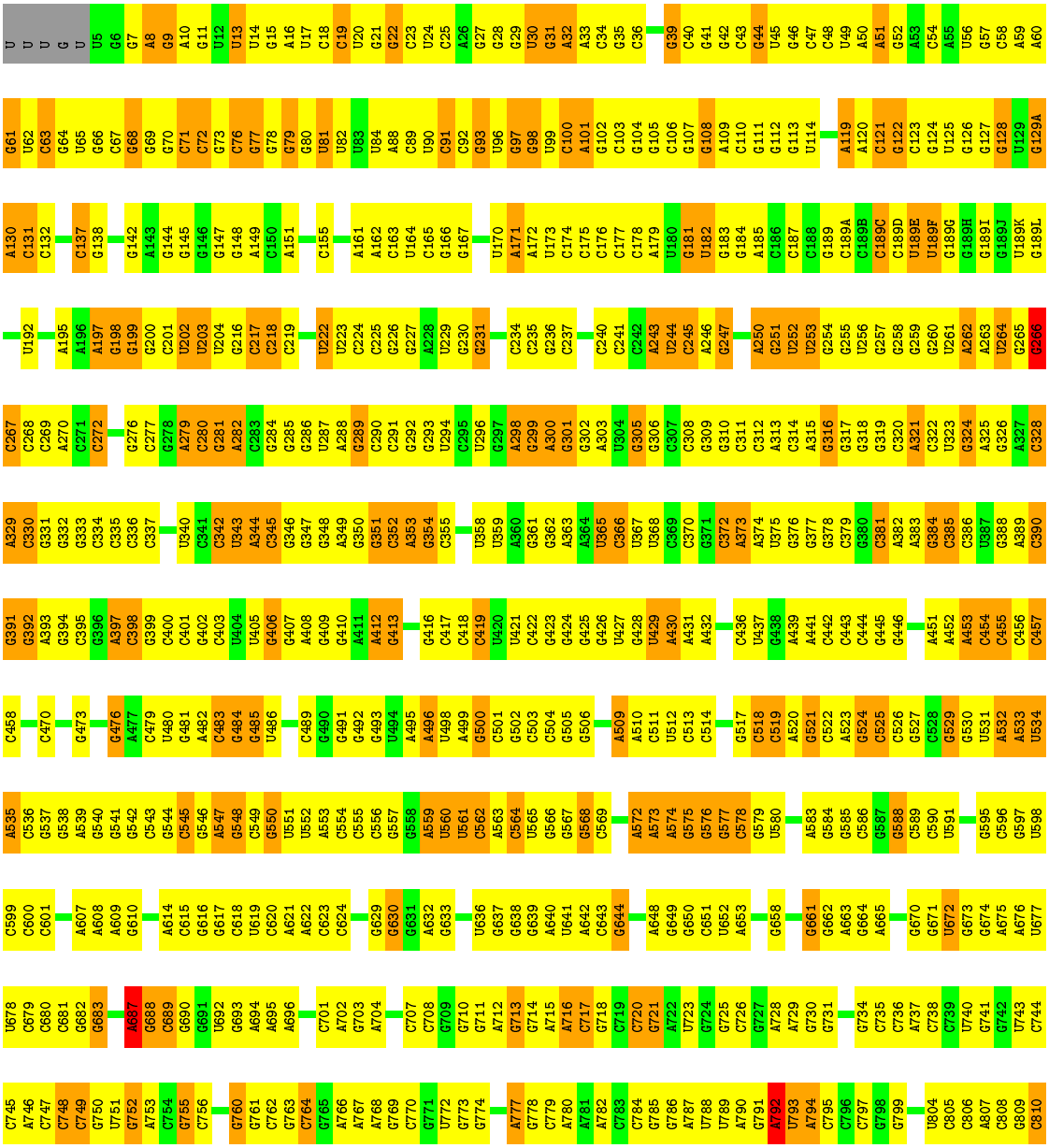
Mol	Chain	Residues	Atoms		AltConf
26	D	1	Total 1	Zn 1	0
26	N	1	Total 1	Zn 1	0

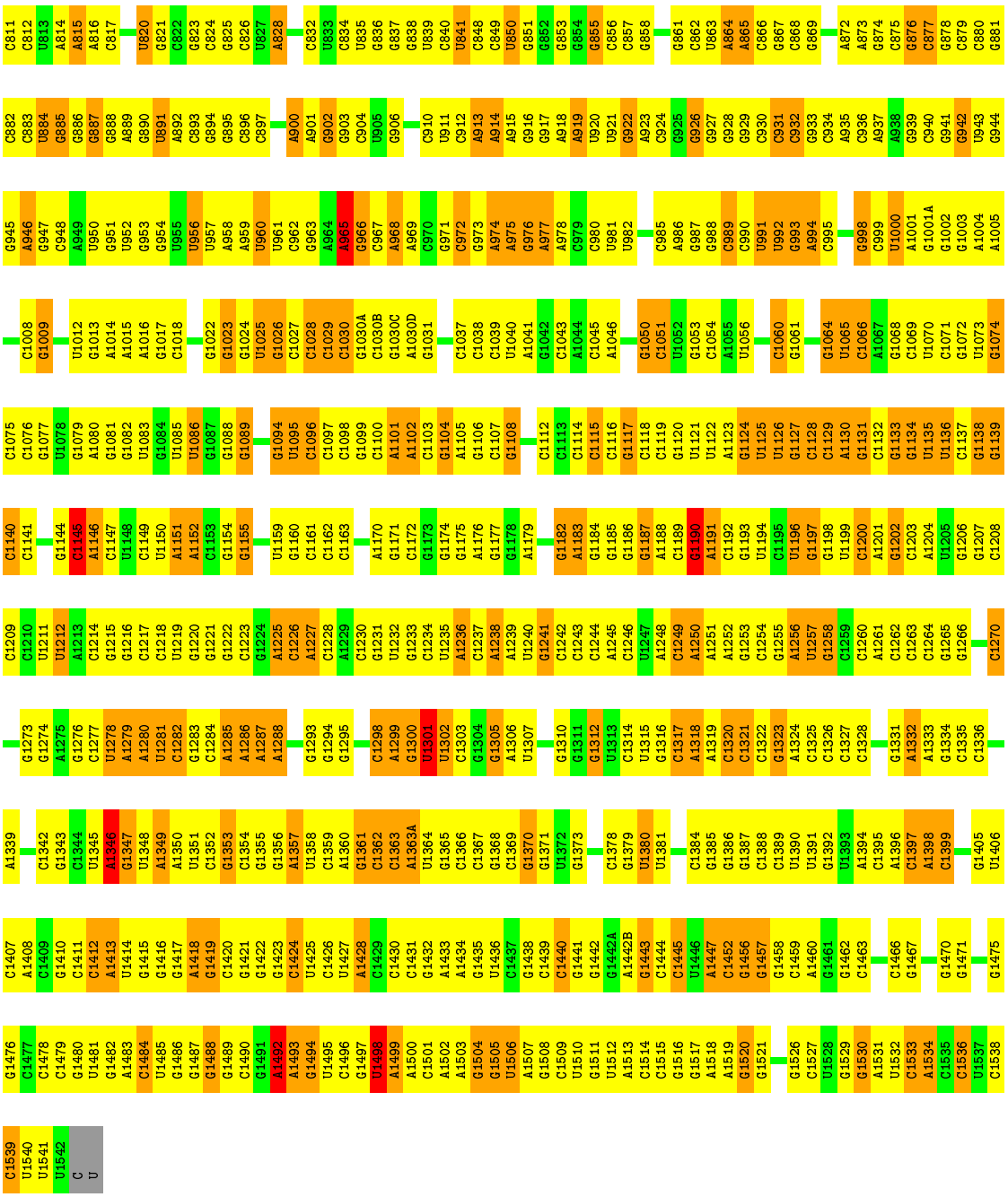
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: 16S ribosomal RNA

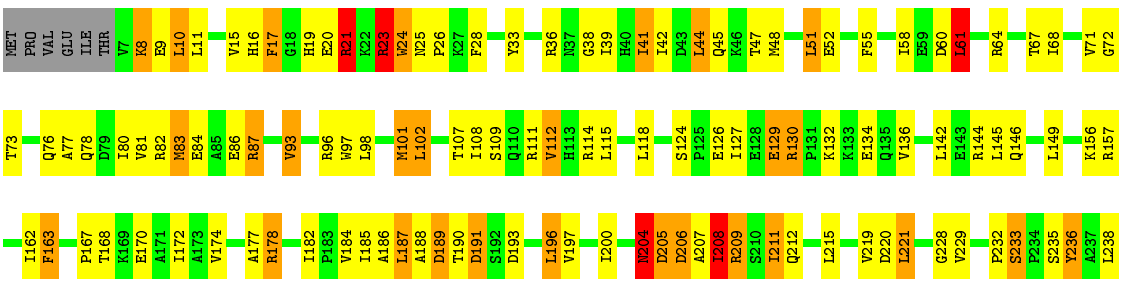
Chain A: 22% 55% 22%





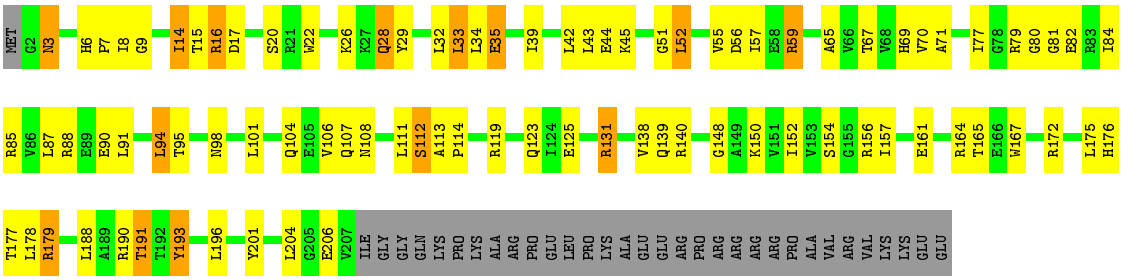
• Molecule 2: 30S ribosomal protein S2

Chain B:



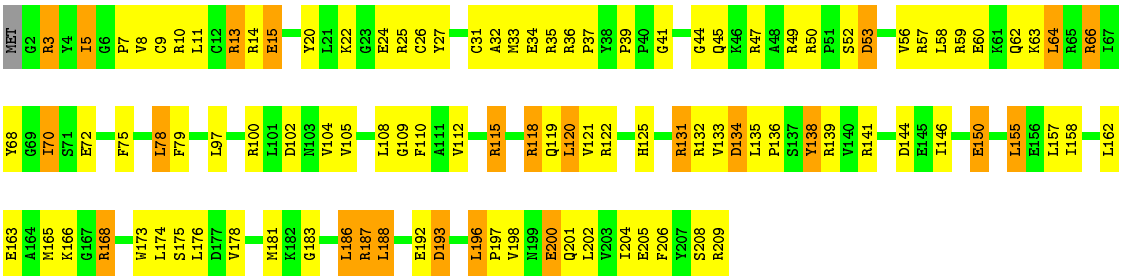
- Molecule 3: 30S ribosomal protein S3

Chain C:



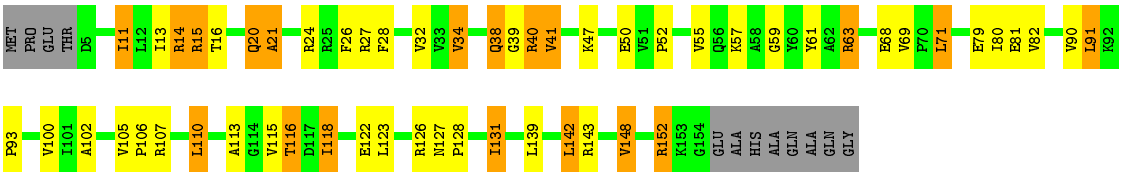
- Molecule 4: 30S ribosomal protein S4

Chain D:



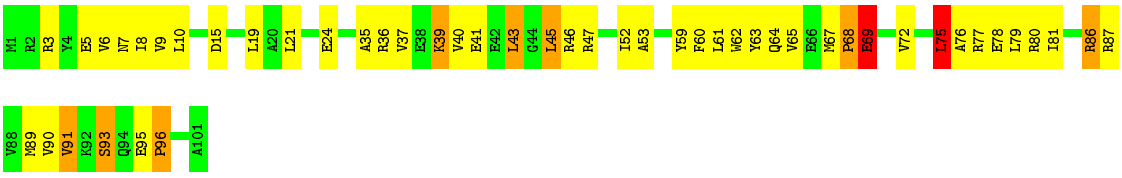
- Molecule 5: 30S ribosomal protein S5

Chain E:



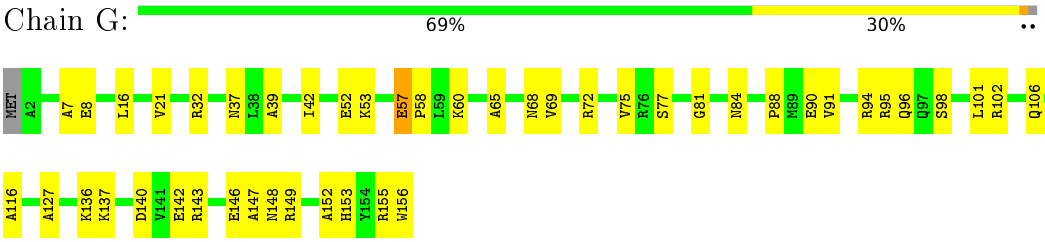
- Molecule 6: 30S ribosomal protein S6

Chain F:



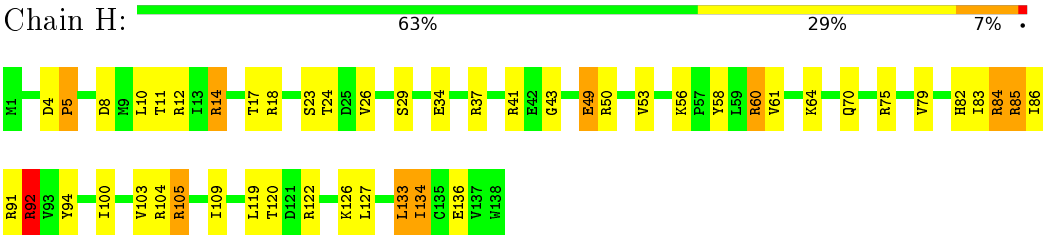
- Molecule 7: 30S ribosomal protein S7

Chain G:



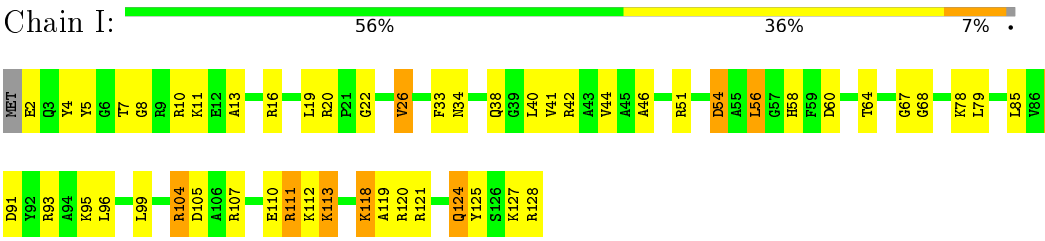
• Molecule 8: 30S ribosomal protein S8

Chain H:



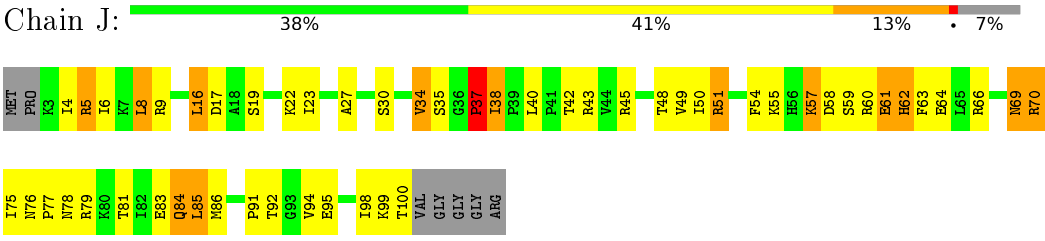
• Molecule 9: 30S ribosomal protein S9

Chain I:



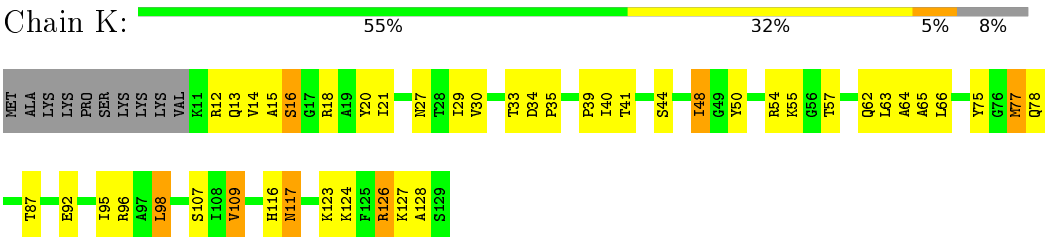
• Molecule 10: 30S ribosomal protein S10

Chain J:



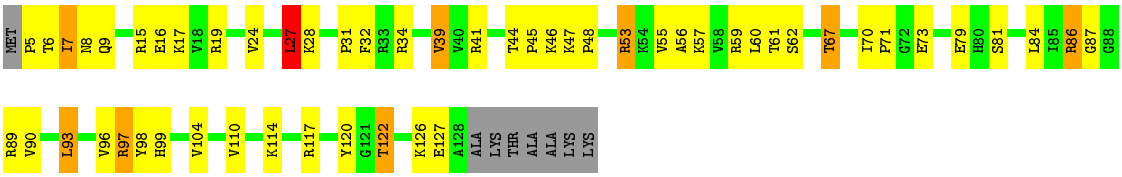
• Molecule 11: 30S ribosomal protein S11

Chain K:



• Molecule 12: 30S ribosomal protein S12

Chain L:



• Molecule 13: 30S ribosomal protein S13

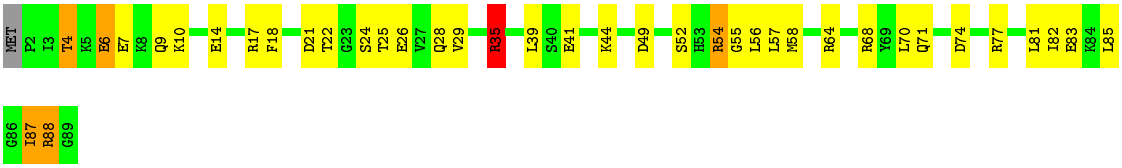
Chain M:

• Molecule 14: 30S ribosomal protein S14 type Z

Chain N:

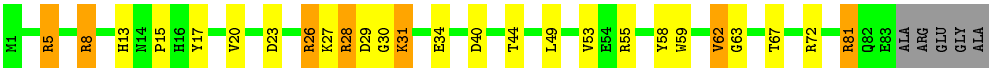
• Molecule 15: 30S ribosomal protein S15

Chain O:



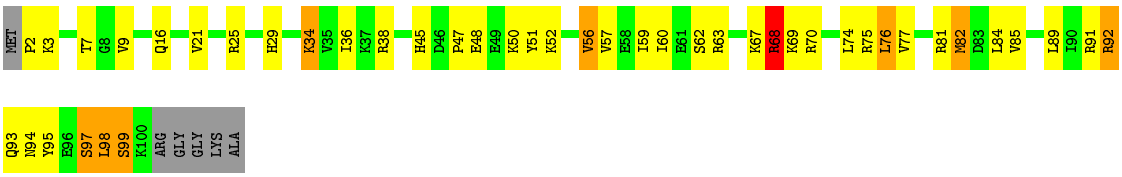
• Molecule 16: 30S ribosomal protein S16

Chain P:



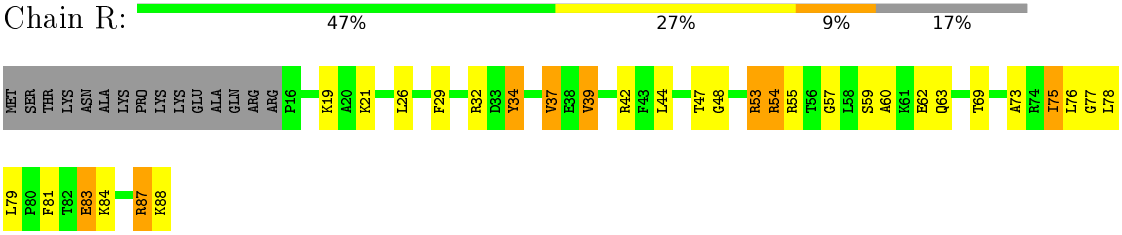
• Molecule 17: 30S ribosomal protein S17

Chain Q:



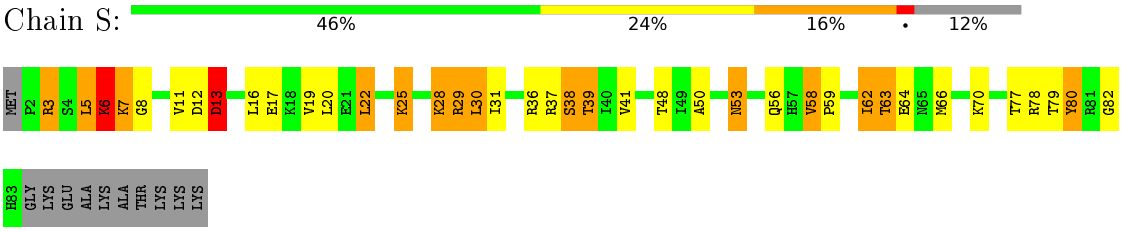
• Molecule 18: 30S ribosomal protein S18

Chain R:



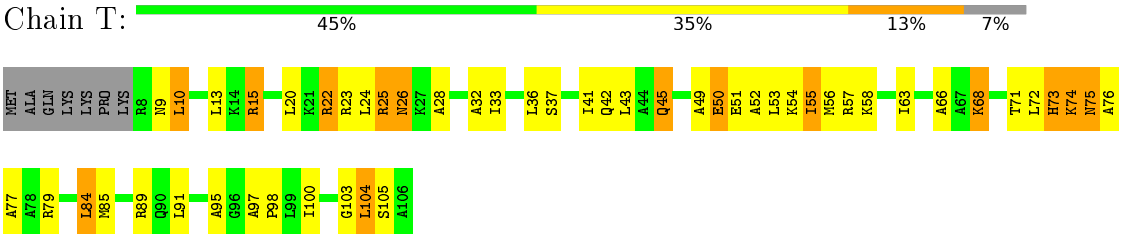
- Molecule 19: 30S ribosomal protein S19

Chain S:



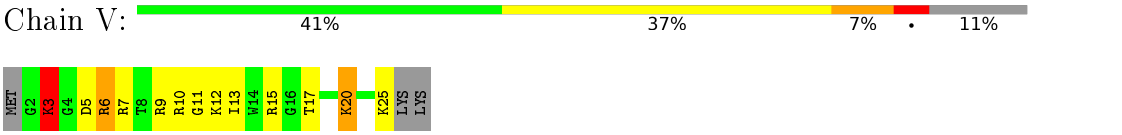
- Molecule 20: 30S ribosomal protein S20

Chain T:



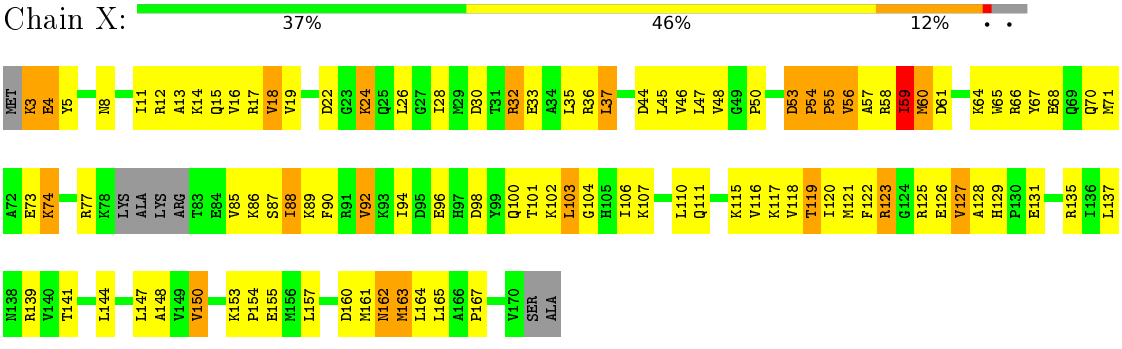
- Molecule 21: 30S ribosomal protein Thx

Chain V:



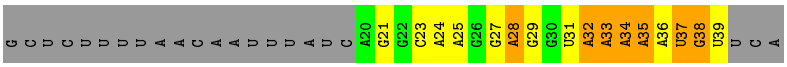
- Molecule 22: Translation initiation factor IF-3

Chain X:



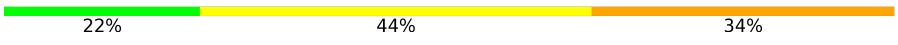
- Molecule 23: mRNA

Chain Y:



- Molecule 24: tRNAi

Chain Z:



4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	26949	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	Not provided	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	78000	Depositor
Image detector	Not provided	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, OMC, ZN, G7M, MG, 4SU, PSU

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>2$	RMSZ	#$\|Z\|>2$
1	A	0.32	1/36426 (0.0%)	0.75	13/56837 (0.0%)
10	J	0.43	0/805	0.78	1/1082 (0.1%)
11	K	0.45	0/900	0.78	0/1213
12	L	0.37	0/986	0.82	0/1320
13	M	0.43	0/947	0.80	0/1270
14	N	0.41	0/501	0.83	1/664 (0.2%)
15	O	0.46	0/745	0.93	1/992 (0.1%)
16	P	0.44	0/716	0.79	0/963
17	Q	0.40	0/836	0.80	0/1117
18	R	0.44	0/604	0.83	0/801
19	S	0.43	0/670	0.81	0/903
2	B	0.52	0/1935	0.92	4/2609 (0.2%)
20	T	0.43	0/765	0.92	1/1007 (0.1%)
21	V	0.42	0/212	0.83	0/277
22	X	0.57	0/1354	1.00	6/1813 (0.3%)
23	Y	0.34	0/493	0.74	0/766
24	Z	0.42	0/1721	0.79	1/2682 (0.0%)
3	C	0.47	0/1636	0.82	1/2205 (0.0%)
4	D	0.41	0/1733	0.84	0/2318
5	E	0.43	0/1162	0.83	0/1564
6	F	0.43	0/856	0.86	2/1154 (0.2%)
7	G	0.43	0/1276	0.81	0/1709
8	H	0.42	0/1136	0.81	0/1527
9	I	0.44	0/1029	0.77	0/1379
All	All	0.37	1/59444 (0.0%)	0.78	31/88172 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
19	S	0	1
22	X	0	2
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	71	C	O3'-P	-5.67	1.54	1.61

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	X	4	GLU	N-CA-CB	-14.85	83.86	110.60
1	A	266	G	C2'-C3'-O3'	7.90	126.87	109.50
1	A	1145	C	C2'-C3'-O3'	7.31	125.58	109.50
1	A	1498	U	C2'-C3'-O3'	7.03	124.96	109.50
22	X	35	LEU	CA-CB-CG	6.98	131.34	115.30
2	B	187	LEU	CA-CB-CG	6.97	131.32	115.30
1	A	1346	A	C2'-C3'-O3'	6.86	124.67	113.70
1	A	509	A	C4'-C3'-O3'	6.84	126.69	113.00
22	X	4	GLU	CB-CA-C	-6.81	96.78	110.40
1	A	792	A	C2'-C3'-O3'	6.80	124.58	113.70
1	A	1301	U	C2'-C3'-O3'	6.62	124.29	113.70
6	F	75	LEU	CA-CB-CG	6.36	129.93	115.30
1	A	1190	G	C2'-C3'-O3'	6.10	123.46	113.70
14	N	44	LEU	CA-CB-CG	5.93	128.93	115.30
2	B	221	LEU	CA-CB-CG	5.91	128.89	115.30
1	A	1492	A	C4'-C3'-O3'	5.74	124.47	113.00
1	A	687	A	C2'-C3'-O3'	5.70	122.82	113.70
3	C	33	LEU	CA-CB-CG	5.69	128.39	115.30
15	O	35	ARG	NE-CZ-NH1	5.63	123.11	120.30
22	X	37	LEU	CA-CB-CG	5.62	128.22	115.30
10	J	37	PRO	N-CA-C	-5.60	97.53	112.10
22	X	103	LEU	CA-CB-CG	5.59	128.16	115.30
20	T	10	LEU	CA-CB-CG	5.53	128.01	115.30
1	A	372	C	C2'-C3'-O3'	5.49	122.49	113.70
1	A	1380	U	C2'-C3'-O3'	5.49	122.49	113.70
1	A	965	A	C2'-C3'-O3'	5.42	122.36	113.70
24	Z	47	U	C2'-C3'-O3'	5.23	122.06	113.70
2	B	196	LEU	CA-CB-CG	5.18	127.20	115.30
2	B	61	LEU	CA-CB-CG	5.11	127.06	115.30
6	F	43	LEU	CA-CB-CG	5.08	126.98	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	X	4	GLU	N-CA-C	5.08	124.71	111.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1445	C	Sidechain
1	A	218	C	Sidechain
19	S	3	ARG	Peptide
22	X	3	LYS	Peptide
22	X	53	ASP	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	32548	0	16440	1268	0
2	B	1900	0	1951	72	0
3	C	1612	0	1675	61	0
4	D	1703	0	1767	92	0
5	E	1146	0	1207	46	0
6	F	843	0	857	25	0
7	G	1257	0	1296	14	0
8	H	1116	0	1177	20	0
9	I	1010	0	1037	30	0
10	J	792	0	834	99	0
11	K	885	0	904	16	0
12	L	970	0	1057	31	0
13	M	937	0	995	18	0
14	N	492	0	531	15	0
15	O	734	0	771	14	0
16	P	700	0	720	17	0
17	Q	823	0	891	24	0
18	R	598	0	670	17	0
19	S	655	0	672	26	0
20	T	763	0	861	46	0
21	V	208	0	221	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	X	1336	0	1388	85	0
23	Y	439	0	219	18	0
24	Z	1646	0	843	57	0
25	A	78	0	0	3	0
25	L	1	0	0	0	0
25	Z	1	0	0	0	0
26	D	1	0	0	2	0
26	N	1	0	0	1	0
All	All	55195	0	38984	1968	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 21.

All (1968) 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:J:38:ILE:HG23	10:J:71:LEU:CB	1.24	1.66
10:J:38:ILE:CG2	10:J:71:LEU:HB3	1.04	1.50
1:A:412:A:N3	4:D:35:ARG:NH1	1.66	1.44
1:A:1358:U:H3	1:A:1363(A):A:N6	1.13	1.43
1:A:1061:G:C5'	10:J:59:SER:OG	1.68	1.39
1:A:262:A:H5'	20:T:73:HIS:CE1	1.59	1.37
4:D:13:ARG:NH2	4:D:36:ARG:NH2	1.69	1.36
1:A:439:A:OP2	1:A:493:G:N2	1.57	1.34
10:J:48:THR:CG2	10:J:60:ARG:HD3	1.58	1.34
3:C:8:ILE:CD1	3:C:16:ARG:HH21	1.41	1.32
4:D:13:ARG:NH2	4:D:36:ARG:HH21	1.19	1.30
10:J:38:ILE:HG22	10:J:71:LEU:O	1.27	1.29
4:D:13:ARG:HH21	4:D:36:ARG:NH2	1.31	1.23
1:A:1358:U:O4	1:A:1363(A):A:N1	1.71	1.22
1:A:1061:G:H5'	10:J:59:SER:OG	1.18	1.19
10:J:38:ILE:CG2	10:J:71:LEU:CB	1.95	1.16
10:J:38:ILE:HG21	10:J:71:LEU:HB3	1.24	1.15
3:C:8:ILE:HD13	3:C:16:ARG:NH2	1.62	1.14
10:J:6:ILE:HG13	10:J:72:VAL:HB	1.31	1.12
1:A:1348:U:H2'	1:A:1349:A:H8	1.10	1.12
1:A:439:A:OP2	1:A:493:G:C2	2.02	1.12
10:J:38:ILE:HG23	10:J:71:LEU:CA	1.81	1.10
1:A:412:A:C4	4:D:35:ARG:NH1	2.19	1.09
4:D:13:ARG:CZ	4:D:36:ARG:HH21	1.65	1.08
1:A:1458:G:H5"	20:T:32:ALA:HB2	1.37	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:38:ILE:CG2	10:J:71:LEU:O	2.03	1.06
10:J:8:LEU:CB	10:J:70:ARG:HB2	1.86	1.05
10:J:8:LEU:HB3	10:J:70:ARG:HB2	1.12	1.04
3:C:8:ILE:HG12	3:C:16:ARG:HE	1.20	1.04
10:J:48:THR:HG22	10:J:60:ARG:CD	1.88	1.04
10:J:48:THR:HG22	10:J:60:ARG:HD3	1.08	1.04
1:A:413:G:N7	4:D:35:ARG:NH2	2.08	1.02
1:A:262:A:C5'	20:T:73:HIS:HE1	1.76	0.99
3:C:8:ILE:CD1	3:C:16:ARG:NH2	2.19	0.98
16:P:59:TRP:O	16:P:62:VAL:HG23	1.61	0.98
24:Z:71:C:H2'	24:Z:72:A:H8	1.25	0.98
1:A:96:U:H2'	1:A:97:G:C8	2.00	0.97
1:A:1398:A:N6	5:E:21:ALA:O	1.97	0.97
3:C:8:ILE:HD13	3:C:16:ARG:HH21	0.83	0.97
1:A:1391:U:H2'	1:A:1392:G:H8	1.31	0.96
10:J:16:LEU:HD23	10:J:70:ARG:HG2	1.48	0.96
10:J:49:VAL:O	10:J:60:ARG:HG3	1.65	0.95
1:A:436:C:H2'	1:A:437:U:H6	1.32	0.94
10:J:6:ILE:N	10:J:72:VAL:O	2.00	0.94
10:J:48:THR:HG21	10:J:60:ARG:HD3	1.50	0.93
1:A:1061:G:H5"	10:J:59:SER:OG	1.66	0.93
1:A:262:A:C5'	20:T:73:HIS:CE1	2.50	0.93
1:A:1038:C:H2'	1:A:1039:C:H6	1.31	0.93
1:A:1080:A:O3'	5:E:16:THR:CG2	2.16	0.93
4:D:13:ARG:HH21	4:D:36:ARG:HH22	1.01	0.93
10:J:38:ILE:HG21	10:J:71:LEU:HD12	1.50	0.93
1:A:664:G:H22	1:A:741:G:H1	0.98	0.93
1:A:1348:U:H2'	1:A:1349:A:C8	2.02	0.93
1:A:1391:U:H2'	1:A:1392:G:C8	2.04	0.92
1:A:1533:C:H4'	1:A:1533:C:OP1	1.69	0.92
1:A:576:G:H3'	1:A:577:G:H5"	1.51	0.91
10:J:38:ILE:CG2	10:J:71:LEU:C	2.39	0.91
9:I:26:VAL:HB	9:I:33:PHE:HB2	1.51	0.91
10:J:8:LEU:HB3	10:J:70:ARG:CB	2.00	0.90
15:O:35:ARG:HH11	15:O:35:ARG:HG2	1.34	0.90
1:A:920:U:H2'	1:A:921:U:C6	2.06	0.89
1:A:148:G:H2'	1:A:149:A:C8	2.07	0.89
1:A:439:A:OP2	1:A:493:G:N1	2.05	0.89
1:A:1458:G:OP1	20:T:32:ALA:HA	1.74	0.87
16:P:59:TRP:O	16:P:62:VAL:CG2	2.23	0.87
6:F:35:ALA:HA	6:F:67:MET:HB3	1.57	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1507:A:H2'	1:A:1508:G:C8	2.10	0.86
22:X:111:GLN:HG3	22:X:147:LEU:HD21	1.55	0.86
1:A:398:C:H2'	1:A:399:G:H8	1.39	0.86
9:I:5:TYR:OH	9:I:7:THR:OG1	1.88	0.86
10:J:61:GLU:OE1	10:J:63:PHE:CZ	2.29	0.86
10:J:38:ILE:HG21	10:J:71:LEU:CD1	2.05	0.85
1:A:946:A:H2'	1:A:947:G:C8	2.11	0.85
9:I:51:ARG:HG2	9:I:56:LEU:HD11	1.59	0.85
9:I:8:GLY:HA2	9:I:79:LEU:HD12	1.59	0.85
10:J:6:ILE:CG1	10:J:72:VAL:HB	2.06	0.85
1:A:1219:U:H2'	1:A:1220:G:H8	1.41	0.85
22:X:3:LYS:HB3	22:X:66:ARG:HH22	1.41	0.85
1:A:1061:G:H5'	10:J:59:SER:CB	2.07	0.84
22:X:3:LYS:HB3	22:X:66:ARG:NH2	1.92	0.84
1:A:1305:G:HO2'	1:A:1306:A:H8	1.25	0.84
1:A:1457:G:H5"	1:A:1457:G:C8	2.12	0.83
1:A:436:C:H2'	1:A:437:U:C6	2.12	0.83
1:A:674:G:H2'	1:A:675:A:H8	1.42	0.83
22:X:58:ARG:HH22	24:Z:19:G:H2'	1.40	0.83
1:A:564:C:O2	1:A:564:C:H2'	1.77	0.83
2:B:19:HIS:O	2:B:190:THR:HG22	1.79	0.82
1:A:262:A:H5'	20:T:73:HIS:HE1	1.07	0.82
1:A:658:G:C2	1:A:749:C:N3	2.48	0.82
10:J:38:ILE:HG22	10:J:71:LEU:C	1.98	0.82
1:A:71:C:H2'	1:A:72:C:O4'	1.79	0.82
1:A:97:G:H2'	1:A:98:G:C8	2.14	0.82
1:A:1219:U:H2'	1:A:1220:G:C8	2.16	0.81
24:Z:71:C:H2'	24:Z:72:A:C8	2.14	0.81
22:X:19:VAL:O	22:X:58:ARG:HA	1.81	0.81
1:A:30:U:H3'	1:A:31:G:H5"	1.63	0.81
20:T:15:ARG:HH11	20:T:15:ARG:HG2	1.46	0.80
24:Z:36:U:H2'	24:Z:37:A:H8	1.45	0.80
18:R:37:VAL:HG21	18:R:78:LEU:HB3	1.62	0.80
2:B:215:LEU:O	2:B:219:VAL:HG23	1.82	0.80
1:A:1507:A:H2'	1:A:1508:G:H8	1.44	0.80
1:A:553:A:H2'	1:A:554:C:C6	2.16	0.80
1:A:1356:G:H2'	1:A:1357:A:C8	2.16	0.80
1:A:10:A:H2'	1:A:11:G:H8	1.47	0.80
11:K:15:ALA:HA	11:K:77:MET:HA	1.64	0.80
1:A:750:G:H1'	15:O:22:THR:OG1	1.82	0.79
2:B:212:GLN:HG3	2:B:239:VAL:CG2	2.12	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1513:A:H2'	1:A:1514:C:C6	2.17	0.79
1:A:745:C:H2'	1:A:746:A:C8	2.17	0.79
3:C:8:ILE:HG12	3:C:16:ARG:NE	1.96	0.79
9:I:5:TYR:HH	9:I:7:THR:HG1	1.14	0.79
10:J:38:ILE:CB	10:J:71:LEU:HB3	2.09	0.79
1:A:1080:A:O3'	5:E:16:THR:HG21	1.83	0.79
10:J:48:THR:CG2	10:J:60:ARG:CD	2.50	0.79
1:A:17:U:H2'	1:A:18:C:C6	2.17	0.78
1:A:946:A:H2'	1:A:947:G:H8	1.47	0.78
10:J:6:ILE:HG13	10:J:72:VAL:CB	2.12	0.78
1:A:977:A:H2'	1:A:978:A:H5"	1.66	0.78
1:A:373:A:H2'	1:A:374:A:H8	1.49	0.78
22:X:106:ILE:HG12	22:X:116:VAL:HG11	1.66	0.78
1:A:262:A:H5'	20:T:73:HIS:NE2	1.99	0.77
13:M:22:ILE:HG22	13:M:24:GLY:H	1.48	0.77
1:A:1327:C:H5"	21:V:20:LYS:HB2	1.66	0.77
1:A:1347:G:C8	9:I:107:ARG:HB3	2.19	0.77
9:I:46:ALA:HA	9:I:78:LYS:HB2	1.67	0.77
10:J:8:LEU:CB	10:J:70:ARG:CB	2.61	0.77
1:A:1264:C:H2'	1:A:1265:G:H8	1.50	0.77
4:D:165:MET:HA	4:D:168:ARG:HG2	1.66	0.77
1:A:20:U:H2'	1:A:21:G:O4'	1.84	0.77
1:A:24:U:H2'	1:A:25:C:C6	2.20	0.76
10:J:35:SER:HB2	10:J:73:ASP:HB3	1.67	0.76
1:A:880:C:H2'	1:A:881:G:H8	1.49	0.76
1:A:1255:G:H2'	1:A:1279:A:N6	2.01	0.76
1:A:737:A:H2'	1:A:738:C:C6	2.21	0.76
18:R:32:ARG:HA	18:R:69:THR:HG21	1.68	0.76
1:A:1399:C:C2	1:A:1502:A:N6	2.54	0.76
1:A:1095:U:OP1	1:A:1108:G:N1	2.18	0.75
1:A:1293:G:H2'	1:A:1294:G:H8	1.51	0.75
1:A:81:U:O2'	1:A:88:A:N6	2.19	0.75
1:A:1228:C:H5'	13:M:108:ARG:HH22	1.51	0.75
1:A:148:G:H2'	1:A:149:A:H8	1.50	0.75
1:A:263:A:OP1	20:T:79:ARG:HD3	1.86	0.75
24:Z:23:C:H2'	24:Z:24:U:C6	2.21	0.75
1:A:1121:U:H2'	1:A:1122:U:C6	2.21	0.75
1:A:351:G:H4'	1:A:352:C:OP1	1.87	0.75
10:J:51:ARG:N	10:J:59:SER:O	2.19	0.75
10:J:49:VAL:O	10:J:60:ARG:CG	2.35	0.75
1:A:1038:C:H2'	1:A:1039:C:C6	2.19	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:G:H2'	1:A:125:U:O4'	1.87	0.74
1:A:714:G:H2'	1:A:715:A:C8	2.21	0.74
1:A:559:A:H4'	1:A:560:U:H5"	1.69	0.74
1:A:1458:G:C5'	20:T:32:ALA:HB2	2.15	0.74
24:Z:33:U:N3	24:Z:36:U:OP2	2.21	0.74
1:A:343:U:O2'	1:A:346:G:O6	2.04	0.74
1:A:121:C:N4	1:A:236:G:N7	2.35	0.74
1:A:266:G:C8	1:A:266:G:H5"	2.22	0.74
24:Z:55:PSU:O2'	24:Z:57:A:N7	2.18	0.74
1:A:81:U:OP1	1:A:81:U:H4'	1.88	0.73
3:C:22:TRP:CZ3	3:C:29:TYR:CD1	2.77	0.73
22:X:67:TYR:O	22:X:71:MET:HG3	1.88	0.73
24:Z:63:G:H2'	24:Z:64:G:H8	1.52	0.73
1:A:524:G:C6	1:A:525:C:N4	2.56	0.73
1:A:922:G:H2'	1:A:923:A:C8	2.24	0.73
1:A:184:G:H2'	1:A:185:A:H8	1.53	0.73
1:A:728:A:H2'	1:A:729:A:C8	2.23	0.73
1:A:302:G:H2'	1:A:303:A:C8	2.24	0.73
1:A:736:C:H2'	1:A:737:A:C8	2.24	0.73
1:A:101:A:H2'	1:A:102:G:H8	1.53	0.72
1:A:78:G:H2'	1:A:79:G:O4'	1.89	0.72
1:A:600:C:H2'	1:A:601:C:C6	2.24	0.72
17:Q:94:ASN:O	17:Q:97:SER:HB3	1.89	0.72
19:S:28:LYS:HD3	19:S:29:ARG:H	1.53	0.72
1:A:1281:U:H3	10:J:5:ARG:HH12	1.35	0.72
1:A:1014:A:H2'	1:A:1015:A:C8	2.24	0.72
1:A:1135:U:H4'	1:A:1136:U:C5	2.23	0.72
1:A:917:G:H2'	1:A:918:A:C8	2.23	0.72
5:E:14:ARG:HG3	5:E:14:ARG:NH1	2.05	0.72
4:D:15:GLU:HG2	4:D:63:LYS:HG3	1.72	0.72
1:A:1445:C:C2	1:A:1458:G:C2	2.78	0.72
1:A:576:G:H3'	1:A:577:G:C5'	2.20	0.72
19:S:13:ASP:HA	19:S:16:LEU:HB3	1.71	0.72
1:A:664:G:N2	1:A:741:G:H1	1.81	0.71
3:C:14:ILE:HD13	3:C:14:ILE:N	2.04	0.71
23:Y:38:G:H1	24:Z:34:C:H42	1.38	0.71
5:E:14:ARG:HG3	5:E:14:ARG:HH11	1.56	0.71
6:F:7:ASN:HB2	6:F:89:MET:HB3	1.70	0.71
1:A:92:C:H2'	1:A:93:G:C8	2.24	0.71
20:T:63:ILE:HG23	20:T:72:LEU:HD13	1.73	0.71
1:A:109:A:H2'	1:A:326:G:N2	2.05	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1475:G:H2'	1:A:1476:G:C8	2.26	0.71
2:B:93:VAL:HG11	2:B:97:TRP:HD1	1.56	0.71
5:E:105:VAL:HB	5:E:106:PRO:HD3	1.73	0.70
10:J:60:ARG:HB3	10:J:60:ARG:HH21	1.55	0.70
12:L:53:ARG:HH11	12:L:53:ARG:HG2	1.54	0.70
1:A:920:U:H2'	1:A:921:U:H6	1.52	0.70
1:A:1016:A:H2'	1:A:1017:G:O4'	1.91	0.70
1:A:1293:G:H2'	1:A:1294:G:C8	2.26	0.70
1:A:72:C:H42	1:A:97:G:H1	1.39	0.70
2:B:212:GLN:HG3	2:B:239:VAL:HG21	1.72	0.70
4:D:9:CYS:SG	26:D:300:ZN:ZN	1.79	0.70
4:D:201:GLN:HG2	4:D:205:GLU:OE1	1.91	0.70
1:A:769:G:N2	1:A:770:C:C2	2.60	0.70
1:A:1121:U:H2'	1:A:1122:U:H6	1.57	0.70
1:A:10:A:H2'	1:A:11:G:C8	2.27	0.70
1:A:1518:A:H2'	1:A:1519:A:C8	2.26	0.70
1:A:658:G:N2	1:A:749:C:C2	2.60	0.70
1:A:914:A:H2'	1:A:915:A:H8	1.55	0.70
1:A:544:G:OP1	4:D:62:GLN:HG3	1.91	0.70
22:X:64:LYS:O	22:X:68:GLU:HG2	1.92	0.70
1:A:224:C:H2'	1:A:225:C:C6	2.27	0.69
1:A:575:G:H4'	1:A:576:G:H5"	1.74	0.69
1:A:662:G:H2'	1:A:663:A:C8	2.26	0.69
1:A:728:A:H2'	1:A:729:A:H8	1.57	0.69
1:A:864:A:H2'	1:A:865:A:C8	2.26	0.69
1:A:1097:C:H2'	1:A:1098:C:C6	2.27	0.69
8:H:91:ARG:HD3	12:L:7:ILE:HG21	1.73	0.69
1:A:335:C:H2'	1:A:336:C:C6	2.27	0.69
23:Y:27:G:H2'	23:Y:28:A:O4'	1.91	0.69
1:A:1354:C:H2'	1:A:1355:G:H8	1.57	0.69
22:X:137:LEU:HD12	22:X:154:PRO:HB3	1.74	0.69
1:A:1287:A:H2'	1:A:1288:A:C8	2.27	0.69
2:B:112:VAL:HG23	2:B:149:LEU:HB3	1.75	0.69
1:A:1256:A:N6	1:A:1278:U:C2	2.61	0.69
1:A:585:G:H4'	12:L:8:ASN:HD21	1.58	0.69
1:A:973:G:H3'	1:A:974:A:H5"	1.73	0.69
8:H:12:ARG:HD3	8:H:26:VAL:HG12	1.74	0.69
10:J:61:GLU:OE1	10:J:63:PHE:CE2	2.45	0.69
19:S:11:VAL:HA	19:S:38:SER:HB3	1.75	0.69
22:X:61:ASP:HB3	22:X:64:LYS:HB3	1.75	0.69
1:A:1106:G:H5"	3:C:172:ARG:HG2	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:578:C:OP1	25:A:1668:MG:MG	1.36	0.68
1:A:841:U:H5"	1:A:841:U:H6	1.56	0.68
10:J:23:ILE:HG21	10:J:72:VAL:HG11	1.74	0.68
1:A:1358:U:C4	1:A:1363(A):A:N1	2.59	0.68
1:A:579:G:H2'	1:A:580:U:C6	2.29	0.68
1:A:736:C:H2'	1:A:737:A:H8	1.58	0.68
1:A:772:U:H2'	1:A:773:G:C8	2.29	0.68
2:B:8:LYS:HD2	2:B:9:GLU:H	1.58	0.68
24:Z:36:U:H2'	24:Z:37:A:C8	2.28	0.68
1:A:975:A:H4'	1:A:976:G:H5'	1.75	0.68
1:A:1281:U:H5'	1:A:1282:C:H5	1.59	0.68
1:A:24:U:H2'	1:A:25:C:H6	1.57	0.68
1:A:99:U:H2'	1:A:100:C:C6	2.28	0.68
1:A:412:A:C2	4:D:35:ARG:NH1	2.60	0.68
1:A:1513:A:H2'	1:A:1514:C:H6	1.57	0.68
1:A:1518:A:H2'	1:A:1519:A:H8	1.58	0.68
1:A:322:C:H2'	1:A:323:U:H6	1.58	0.68
1:A:674:G:H2'	1:A:675:A:C8	2.28	0.68
1:A:568:G:N2	1:A:883:C:C2	2.61	0.68
1:A:914:A:H2'	1:A:915:A:C8	2.28	0.68
1:A:222:U:H2'	1:A:223:U:C6	2.29	0.68
6:F:52:ILE:HD11	18:R:77:GLY:HA3	1.75	0.68
1:A:216:G:H2'	1:A:217:C:C6	2.29	0.68
10:J:6:ILE:HD11	10:J:72:VAL:HG11	1.75	0.68
1:A:352:C:H4'	1:A:354:G:OP1	1.94	0.67
10:J:40:LEU:HB2	10:J:69:ASN:HB3	1.77	0.67
1:A:797:C:OP1	11:K:124:LYS:HG3	1.94	0.67
1:A:1488:G:H2'	1:A:1489:G:H8	1.58	0.67
1:A:299:G:H2'	1:A:300:A:C8	2.30	0.67
1:A:84:U:H2'	1:A:88:A:O4'	1.94	0.67
1:A:1263:C:H2'	1:A:1264:C:C6	2.30	0.67
1:A:729:A:H2'	1:A:730:G:H8	1.59	0.67
10:J:49:VAL:HG22	10:J:61:GLU:O	1.94	0.67
1:A:302:G:H2'	1:A:303:A:H8	1.60	0.67
1:A:524:G:C2	1:A:525:C:N3	2.62	0.67
20:T:42:GLN:O	20:T:45:GLN:HB2	1.95	0.67
1:A:1099:G:C6	1:A:1100:C:N3	2.63	0.67
1:A:1349:A:H3'	1:A:1350:A:H8	1.60	0.67
1:A:413:G:N7	4:D:35:ARG:CZ	2.57	0.67
3:C:22:TRP:CH2	3:C:29:TYR:CE1	2.82	0.67
13:M:97:PRO:HG2	13:M:103:THR:HG22	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:28:GLN:O	3:C:32:LEU:HG	1.95	0.67
2:B:212:GLN:HG3	2:B:239:VAL:HG22	1.77	0.67
1:A:632:A:H2'	1:A:633:G:O4'	1.94	0.66
15:O:35:ARG:HG2	15:O:35:ARG:NH1	2.09	0.66
22:X:127:VAL:HG23	22:X:128:ALA:H	1.60	0.66
1:A:1126:U:H1'	1:A:1280:A:C6	2.29	0.66
3:C:22:TRP:CH2	3:C:29:TYR:HE1	2.12	0.66
12:L:73:GLU:H	12:L:110:VAL:HG11	1.60	0.66
22:X:88:ILE:HG22	22:X:118:VAL:HG13	1.77	0.66
10:J:62:HIS:HB2	14:N:59:ALA:HB3	1.77	0.66
1:A:197:A:H4'	1:A:198:G:O5'	1.94	0.66
1:A:568:G:C2	1:A:883:C:N3	2.63	0.66
1:A:1218:C:H2'	1:A:1219:U:C6	2.30	0.66
19:S:56:GLN:HB3	19:S:58:VAL:HG13	1.78	0.66
1:A:96:U:H2'	1:A:97:G:H8	1.55	0.66
5:E:15:ARG:HG3	5:E:15:ARG:O	1.94	0.66
1:A:1161:C:H2'	1:A:1162:C:C6	2.31	0.66
18:R:48:GLY:H	18:R:83:GLU:HB2	1.61	0.66
22:X:11:ILE:HG12	22:X:47:LEU:HD22	1.78	0.66
24:Z:63:G:H2'	24:Z:64:G:C8	2.30	0.66
1:A:1040:U:H2'	1:A:1041:A:C8	2.31	0.66
1:A:1363(A):A:H1'	1:A:1365:G:C5	2.31	0.66
1:A:33:A:H2'	1:A:34:C:C6	2.31	0.66
1:A:491:G:H2'	1:A:492:G:O4'	1.96	0.65
1:A:499:A:C6	1:A:547:A:C8	2.84	0.65
1:A:1151:A:O2'	1:A:1152:A:H8	1.79	0.65
1:A:1312:G:N2	1:A:1326:C:C2	2.65	0.65
1:A:69:G:H1	1:A:100:C:H42	1.43	0.65
1:A:874:G:N2	1:A:875:C:C2	2.65	0.65
4:D:173:TRP:HB2	4:D:187:ARG:O	1.96	0.65
1:A:1264:C:H2'	1:A:1265:G:C8	2.29	0.65
15:O:82:ILE:HG21	15:O:88:ARG:HE	1.61	0.65
22:X:110:LEU:HD22	22:X:148:ALA:HB2	1.79	0.65
22:X:48:VAL:HG21	22:X:58:ARG:HE	1.62	0.65
23:Y:28:A:H3'	23:Y:29:G:C8	2.32	0.65
1:A:1361:G:C6	1:A:1362:C:N3	2.65	0.65
3:C:44:GLU:HG2	3:C:52:LEU:HD11	1.78	0.65
3:C:77:ILE:HA	3:C:84:ILE:HB	1.79	0.65
1:A:1504:G:H4'	1:A:1505:G:O5'	1.97	0.65
1:A:1353:G:N2	1:A:1354:C:C2	2.64	0.65
1:A:354:G:N2	1:A:355:C:C2	2.65	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:61:GLU:OE2	14:N:45:ARG:NH1	2.29	0.65
1:A:1151:A:O2'	1:A:1152:A:C8	2.50	0.65
5:E:100:VAL:HG13	5:E:118:ILE:HD11	1.79	0.65
22:X:15:GLN:HB3	22:X:28:ILE:HG22	1.79	0.65
22:X:88:ILE:HG23	22:X:102:LYS:HD3	1.79	0.65
1:A:1095:U:H2'	1:A:1096:C:C6	2.31	0.64
1:A:397:A:N3	1:A:397:A:H3'	2.12	0.64
1:A:442:C:H2'	1:A:443:C:C6	2.33	0.64
1:A:97:G:H2'	1:A:98:G:H8	1.58	0.64
1:A:409:G:OP2	4:D:22:LYS:HB3	1.97	0.64
1:A:1151:A:HO2'	1:A:1152:A:H8	1.44	0.64
1:A:416:G:C6	1:A:417:C:N3	2.65	0.64
1:A:1128:C:H1'	1:A:1146:A:H61	1.63	0.64
1:A:539:A:H2'	1:A:540:G:C8	2.32	0.64
3:C:22:TRP:HZ3	3:C:29:TYR:HD1	1.45	0.64
22:X:157:LEU:HB2	22:X:160:ASP:HB2	1.78	0.64
1:A:1456:G:H3'	1:A:1457:G:O4'	1.97	0.64
2:B:71:VAL:HA	2:B:93:VAL:HG12	1.79	0.64
3:C:22:TRP:CZ3	3:C:29:TYR:CE1	2.85	0.64
4:D:13:ARG:CZ	4:D:36:ARG:NH2	2.39	0.64
9:I:112:LYS:HG2	9:I:118:LYS:HA	1.79	0.64
24:Z:48:C:H4'	24:Z:49:G:H5"	1.80	0.64
1:A:1354:C:H2'	1:A:1355:G:C8	2.32	0.64
1:A:772:U:H2'	1:A:773:G:H8	1.63	0.63
3:C:22:TRP:CZ3	3:C:29:TYR:HD1	2.15	0.63
3:C:8:ILE:HD11	3:C:16:ARG:NH2	2.12	0.63
13:M:108:ARG:HE	13:M:114:ARG:HG2	1.62	0.63
1:A:744:C:H2'	1:A:745:C:C6	2.34	0.63
1:A:34:C:H2'	1:A:35:G:H8	1.64	0.63
24:Z:43:A:H2'	24:Z:44:A:C8	2.33	0.63
1:A:505:G:H5'	1:A:534:U:H2'	1.80	0.63
1:A:725:G:N2	1:A:726:C:C2	2.67	0.63
4:D:3:ARG:CZ	4:D:3:ARG:HA	2.28	0.63
9:I:10:ARG:HA	9:I:104:ARG:HH12	1.63	0.63
22:X:90:PHE:HB2	22:X:120:ILE:HD13	1.79	0.63
1:A:588:G:N2	1:A:589:C:C2	2.67	0.63
1:A:965:A:H8	1:A:965:A:O5'	1.82	0.63
1:A:585:G:H4'	12:L:8:ASN:ND2	2.13	0.63
1:A:107:G:C2	1:A:108:G:H1'	2.34	0.63
1:A:1492:A:H2'	1:A:1493:A:H5"	1.80	0.63
6:F:41:GLU:HB2	6:F:62:TRP:HE3	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:38:ILE:HG23	10:J:71:LEU:C	2.12	0.63
20:T:63:ILE:HG12	20:T:72:LEU:HD11	1.80	0.63
1:A:352:C:OP2	25:A:1639:MG:MG	1.42	0.62
2:B:84:GLU:HA	2:B:87:ARG:HB2	1.80	0.62
1:A:1443:G:C6	1:A:1444:C:N4	2.66	0.62
4:D:33:MET:HA	4:D:36:ARG:O	1.99	0.62
1:A:170:U:H2'	1:A:171:A:H8	1.64	0.62
18:R:59:SER:HB3	18:R:62:GLU:HB2	1.80	0.62
1:A:110:C:H2'	1:A:111:G:O4'	1.99	0.62
1:A:1355:G:H2'	1:A:1356:G:H8	1.64	0.62
10:J:38:ILE:HG21	10:J:71:LEU:CB	1.99	0.62
10:J:48:THR:HG22	10:J:60:ARG:CG	2.29	0.62
1:A:1456:G:C4	1:A:1457:G:H1'	2.34	0.62
1:A:1492:A:H8	1:A:1492:A:H3'	1.65	0.62
14:N:27:CYS:SG	26:N:101:ZN:ZN	1.88	0.62
1:A:598:U:H2'	1:A:599:C:H6	1.65	0.62
1:A:79:G:H2'	1:A:80:G:C8	2.34	0.62
10:J:38:ILE:HG23	10:J:71:LEU:HB3	0.64	0.62
22:X:96:GLU:O	22:X:100:GLN:HG3	2.00	0.62
1:A:663:A:H2'	1:A:664:G:O4'	1.99	0.62
1:A:34:C:H2'	1:A:35:G:C8	2.34	0.62
2:B:162:ILE:HD12	2:B:177:ALA:HB2	1.81	0.62
15:O:17:ARG:HE	15:O:77:ARG:HD2	1.65	0.62
1:A:1004:A:H5"	1:A:1025:U:C5	2.35	0.62
1:A:1342:C:H2'	1:A:1343:G:H8	1.65	0.62
1:A:1425:U:H2'	1:A:1426:C:C6	2.34	0.62
1:A:322:C:H2'	1:A:323:U:C6	2.34	0.62
4:D:78:LEU:HD22	4:D:97:LEU:HG	1.81	0.62
1:A:198:G:H1	1:A:219:C:N4	1.98	0.62
1:A:21:G:H2'	1:A:22:G:C8	2.34	0.62
1:A:999:C:O2	1:A:1043:C:O2	2.17	0.62
4:D:11:LEU:HD13	4:D:66:ARG:HG2	1.82	0.62
5:E:40:ARG:HH11	5:E:40:ARG:HG2	1.64	0.62
1:A:376:G:H2'	1:A:377:G:H8	1.65	0.61
1:A:543:C:H2'	1:A:544:G:C8	2.35	0.61
1:A:681:C:C2	1:A:710:G:N2	2.68	0.61
1:A:1305:G:O2'	1:A:1306:A:H8	1.82	0.61
1:A:216:G:C6	1:A:217:C:N4	2.68	0.61
1:A:413:G:C5	4:D:35:ARG:NH2	2.68	0.61
3:C:131:ARG:NH1	5:E:50:GLU:HB3	2.14	0.61
1:A:1536:C:H42	23:Y:29:G:H1	1.47	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:A:H2'	1:A:374:A:C8	2.34	0.61
1:A:583:A:O2'	17:Q:91:ARG:HG3	2.00	0.61
1:A:952:U:H2'	1:A:953:G:H8	1.65	0.61
1:A:269:C:H2'	1:A:270:A:C8	2.36	0.61
1:A:1333:A:H2'	1:A:1334:G:O4'	2.00	0.61
2:B:177:ALA:HB1	2:B:182:ILE:O	2.01	0.61
1:A:1368:G:N2	1:A:1369:C:C2	2.68	0.61
1:A:262:A:H2'	1:A:263:A:C8	2.35	0.61
1:A:824:C:H42	1:A:876:G:H1	1.48	0.61
1:A:1106:G:N2	1:A:1107:C:C2	2.68	0.61
1:A:1323:G:H2'	1:A:1324:A:C8	2.36	0.61
1:A:1361:G:C2	1:A:1362:C:O2	2.53	0.61
1:A:259:G:H2'	1:A:260:G:C8	2.36	0.61
1:A:712:A:H2'	1:A:713:G:O4'	2.00	0.61
4:D:133:VAL:HG11	4:D:138:TYR:HD2	1.66	0.61
5:E:14:ARG:CG	5:E:14:ARG:HH11	2.14	0.61
1:A:1287:A:H5'	1:A:1287:A:H8	1.65	0.61
1:A:187:C:C2	20:T:105:SER:HB2	2.36	0.61
4:D:196:LEU:HB3	4:D:198:VAL:HG12	1.81	0.61
3:C:131:ARG:HH12	5:E:52:PRO:HD2	1.64	0.61
10:J:78:ASN:HB2	10:J:81:THR:H	1.65	0.61
22:X:16:VAL:HB	22:X:57:ALA:HB2	1.82	0.61
4:D:201:GLN:HA	4:D:204:ILE:HD12	1.81	0.61
1:A:1003:G:N2	1:A:1038:C:C2	2.69	0.60
1:A:222:U:H2'	1:A:223:U:H6	1.65	0.60
1:A:68:G:H5"	1:A:68:G:C8	2.35	0.60
1:A:662:G:H2'	1:A:663:A:H8	1.64	0.60
1:A:975:A:H5'	1:A:975:A:C8	2.37	0.60
10:J:16:LEU:CD2	10:J:70:ARG:HG2	2.28	0.60
22:X:157:LEU:HD12	22:X:160:ASP:HB2	1.82	0.60
1:A:1127:G:N2	1:A:1145:C:C2	2.69	0.60
1:A:122:G:N1	1:A:123:C:C2	2.70	0.60
1:A:1342:C:H2'	1:A:1343:G:C8	2.36	0.60
1:A:184:G:H2'	1:A:185:A:C8	2.35	0.60
2:B:118:LEU:HB3	2:B:142:LEU:HD11	1.82	0.60
10:J:5:ARG:HA	10:J:73:ASP:HA	1.83	0.60
1:A:1182:G:H4'	1:A:1183:A:O5'	2.01	0.60
1:A:1025:U:H2'	1:A:1026:G:C8	2.37	0.60
1:A:1126:U:H2'	1:A:1126:U:O2	2.00	0.60
1:A:746:A:H2'	1:A:747:C:C6	2.36	0.60
1:A:598:U:H2'	1:A:599:C:C6	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:G:H2'	1:A:79:G:C1'	2.31	0.60
20:T:15:ARG:CG	20:T:15:ARG:HH11	2.14	0.60
1:A:1056:U:H2'	1:A:1056:U:O2	2.00	0.60
1:A:181:G:H4'	1:A:182:U:H5'	1.84	0.60
1:A:524:G:C2	1:A:525:C:C4	2.90	0.60
1:A:584:G:H2'	1:A:585:G:H8	1.67	0.60
1:A:865:A:O5'	1:A:865:A:H8	1.84	0.60
1:A:992:U:H4'	1:A:993:G:O5'	2.02	0.60
2:B:19:HIS:HB2	2:B:204:ASN:HA	1.84	0.60
19:S:12:ASP:H	19:S:38:SER:HB3	1.66	0.60
1:A:320:C:H2'	1:A:321:A:C8	2.36	0.60
3:C:29:TYR:OH	14:N:54:PRO:HD2	2.02	0.60
1:A:1001(A):G:N2	1:A:1040:U:C2	2.69	0.59
1:A:1248:A:H2'	1:A:1249:C:C6	2.37	0.59
1:A:600:C:H2'	1:A:601:C:H6	1.67	0.59
1:A:658:G:C2	1:A:749:C:C2	2.90	0.59
1:A:127:G:C2	1:A:235:C:N3	2.70	0.59
1:A:344:A:H4'	1:A:345:C:OP2	2.02	0.59
1:A:365:U:O2	1:A:365:U:H2'	2.01	0.59
2:B:15:VAL:HG21	2:B:209:ARG:HG3	1.82	0.59
3:C:6:HIS:HD2	3:C:9:GLY:H	1.49	0.59
1:A:1128:C:H2'	1:A:1139:G:N7	2.16	0.59
1:A:755:G:N2	1:A:756:C:C2	2.70	0.59
1:A:1163:C:C2	1:A:1174:G:N2	2.71	0.59
1:A:289:G:N2	1:A:290:C:C2	2.70	0.59
20:T:53:LEU:HB3	20:T:100:ILE:HG22	1.83	0.59
22:X:111:GLN:HG3	22:X:147:LEU:CD2	2.28	0.59
1:A:683:G:N2	1:A:708:C:C2	2.70	0.59
2:B:21:ARG:HA	2:B:39:ILE:HA	1.84	0.59
2:B:82:ARG:O	2:B:86:GLU:HB2	2.01	0.59
10:J:27:ALA:HB1	10:J:34:VAL:HG21	1.85	0.59
10:J:51:ARG:HB2	10:J:59:SER:O	2.01	0.59
5:E:81:GLU:HG3	5:E:90:VAL:HG22	1.85	0.59
1:A:1125:U:H5'	1:A:1126:U:H5	1.67	0.59
1:A:127:G:N2	1:A:235:C:C2	2.71	0.59
1:A:517:G:N1	1:A:533:A:OP2	2.29	0.59
1:A:552:U:H2'	1:A:553:A:C8	2.38	0.59
7:G:39:ALA:HA	7:G:42:ILE:HD12	1.83	0.59
1:A:1530:G:H2'	1:A:1531:A:C8	2.38	0.59
1:A:766:A:OP2	25:A:1629:MG:MG	1.44	0.59
1:A:412:A:H1'	4:D:35:ARG:NH1	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:975:A:H4'	1:A:976:G:C5'	2.32	0.59
1:A:555:C:H2'	1:A:556:C:C6	2.37	0.59
1:A:564:C:O2	1:A:564:C:C2'	2.50	0.59
10:J:38:ILE:CG2	10:J:71:LEU:CA	2.58	0.59
1:A:1232:U:H5"	9:I:124:GLN:O	2.03	0.58
20:T:54:LYS:HA	20:T:57:ARG:HD3	1.85	0.58
20:T:72:LEU:HD22	20:T:77:ALA:HA	1.84	0.58
22:X:87:SER:HA	22:X:117:LYS:O	2.03	0.58
1:A:1312:G:C2	1:A:1326:C:C2	2.92	0.58
1:A:198:G:H2'	1:A:199:G:C8	2.38	0.58
1:A:19:C:H2'	1:A:20:U:C6	2.39	0.58
1:A:1492:A:C8	1:A:1492:A:H3'	2.37	0.58
11:K:48:ILE:HD11	11:K:64:ALA:HB2	1.84	0.58
1:A:1216:G:N2	1:A:1217:C:C2	2.72	0.58
1:A:584:G:H2'	1:A:585:G:C8	2.39	0.58
1:A:98:G:H2'	1:A:99:U:O4'	2.03	0.58
1:A:518:C:H5"	1:A:519:C:C6	2.39	0.58
1:A:914:A:C4	1:A:915:A:N7	2.71	0.58
22:X:86:LYS:O	22:X:116:VAL:HA	2.04	0.58
1:A:1355:G:H2'	1:A:1356:G:C8	2.39	0.58
1:A:145:G:C2	1:A:178:C:N3	2.72	0.58
2:B:174:VAL:HG13	2:B:184:VAL:HG21	1.86	0.58
10:J:38:ILE:HG21	10:J:71:LEU:CG	2.34	0.58
10:J:23:ILE:CG2	10:J:72:VAL:HG11	2.33	0.58
1:A:975:A:C8	1:A:975:A:C5'	2.86	0.58
1:A:1203:C:H2'	1:A:1204:A:H8	1.68	0.58
1:A:202:U:H4'	1:A:203:U:OP1	2.03	0.58
1:A:312:C:H2'	1:A:313:A:C8	2.39	0.58
2:B:209:ARG:HA	2:B:239:VAL:CG1	2.34	0.58
1:A:761:G:C6	1:A:762:C:N3	2.72	0.58
1:A:767:A:H2'	1:A:768:A:O4'	2.03	0.58
6:F:5:GLU:HB2	6:F:91:VAL:HG12	1.86	0.58
1:A:1439:C:O2	1:A:1463:C:O2	2.22	0.58
2:B:178:ARG:HA	2:B:178:ARG:HH11	1.68	0.58
2:B:200:ILE:H	2:B:200:ILE:HD12	1.68	0.58
10:J:6:ILE:CD1	10:J:72:VAL:HB	2.34	0.58
24:Z:8:4SU:O2	24:Z:21:A:H2	1.86	0.58
1:A:1134:G:H1	1:A:1140:C:H42	1.52	0.57
1:A:198:G:H1	1:A:219:C:H42	1.51	0.57
4:D:133:VAL:HG11	4:D:138:TYR:CD2	2.39	0.57
3:C:29:TYR:OH	14:N:54:PRO:CD	2.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1488:G:H2'	1:A:1489:G:C8	2.38	0.57
1:A:1512:U:H2'	1:A:1513:A:H8	1.69	0.57
1:A:174:C:H2'	1:A:175:C:H6	1.69	0.57
1:A:269:C:H2'	1:A:270:A:H8	1.68	0.57
5:E:20:GLN:OE1	5:E:20:GLN:HA	2.02	0.57
1:A:1114:C:C2	1:A:1187:G:C2	2.93	0.57
1:A:1456:G:H2'	1:A:1457:G:O4'	2.05	0.57
1:A:1392:G:N2	1:A:1502:A:H8	2.02	0.57
1:A:128:G:C2	1:A:234:C:C2	2.92	0.57
1:A:589:C:O2	1:A:651:C:O2	2.22	0.57
1:A:769:G:N1	1:A:770:C:C4	2.71	0.57
20:T:51:GLU:HA	20:T:54:LYS:HE3	1.87	0.57
1:A:1039:C:H2'	1:A:1040:U:C6	2.39	0.57
1:A:308:C:H2'	1:A:309:G:H8	1.70	0.57
1:A:392:G:H2'	1:A:393:A:C8	2.39	0.57
3:C:85:ARG:NH1	3:C:88:ARG:HB3	2.20	0.57
4:D:35:ARG:HG2	4:D:36:ARG:HG3	1.87	0.57
18:R:21:LYS:HE3	18:R:57:GLY:HA3	1.86	0.57
1:A:1002:G:H2'	1:A:1003:G:O4'	2.05	0.57
1:A:174:C:H2'	1:A:175:C:C6	2.39	0.57
1:A:777:A:H2'	1:A:778:G:C8	2.39	0.57
1:A:838:G:C2	1:A:849:C:C2	2.92	0.57
2:B:73:THR:HB	2:B:170:GLU:HG2	1.86	0.57
1:A:1281:U:H5'	1:A:1282:C:C5	2.39	0.57
1:A:67:C:H2'	1:A:68:G:C8	2.40	0.57
1:A:1435:G:H2'	1:A:1436:U:C6	2.40	0.57
1:A:1457:G:C5'	1:A:1457:G:C8	2.85	0.57
1:A:216:G:C2	1:A:217:C:N3	2.73	0.57
2:B:114:ARG:HH11	2:B:118:LEU:HD11	1.69	0.57
5:E:69:VAL:HG11	5:E:113:ALA:HB1	1.86	0.57
1:A:1097:C:H2'	1:A:1098:C:H6	1.70	0.57
1:A:652:U:O4	1:A:752:G:O2'	2.17	0.57
1:A:131:C:H2'	1:A:132:C:C6	2.39	0.57
1:A:1512:U:H2'	1:A:1513:A:C8	2.40	0.57
1:A:128:G:N2	1:A:234:C:C2	2.72	0.57
1:A:419:C:H42	1:A:424:G:H1	1.52	0.57
1:A:629:G:H2'	1:A:630:G:O4'	2.05	0.57
18:R:48:GLY:N	18:R:83:GLU:HB2	2.19	0.57
1:A:1105:A:H2'	1:A:1106:G:H8	1.69	0.56
1:A:1222:G:N2	1:A:1223:C:C2	2.73	0.56
1:A:1315:U:O2'	1:A:1360:A:N3	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:G:H2'	1:A:256:U:C6	2.40	0.56
1:A:662:G:C2	1:A:744:C:O2	2.58	0.56
2:B:115:LEU:HD11	2:B:146:GLN:HG3	1.87	0.56
17:Q:82:MET:O	17:Q:85:VAL:HB	2.05	0.56
19:S:28:LYS:CD	19:S:29:ARG:H	2.18	0.56
20:T:43:LEU:HB3	20:T:52:ALA:HB2	1.86	0.56
1:A:1218:C:H2'	1:A:1219:U:H6	1.70	0.56
1:A:1414:U:H2'	1:A:1415:G:C8	2.39	0.56
1:A:35:G:H2'	1:A:36:C:C6	2.40	0.56
1:A:806:C:H2'	1:A:807:A:C8	2.41	0.56
5:E:28:PHE:HD2	5:E:50:GLU:HA	1.71	0.56
1:A:30:U:H3'	1:A:31:G:C5'	2.33	0.56
1:A:794:A:H2'	1:A:795:C:C6	2.40	0.56
4:D:200:GLU:O	4:D:204:ILE:HG13	2.05	0.56
1:A:1416:G:H2'	1:A:1417:G:O4'	2.05	0.56
1:A:279:A:OP2	17:Q:95:TYR:OH	2.21	0.56
1:A:864:A:C2	1:A:865:A:C2	2.94	0.56
4:D:201:GLN:HE21	5:E:100:VAL:HG23	1.69	0.56
5:E:91:LEU:HD11	5:E:110:LEU:HD11	1.88	0.56
5:E:148:VAL:HG22	5:E:152:ARG:HE	1.71	0.56
13:M:4:ILE:HA	13:M:57:ARG:HG3	1.87	0.56
1:A:1256:A:H1'	1:A:1258:G:C4	2.40	0.56
1:A:880:C:H2'	1:A:881:G:C8	2.36	0.56
23:Y:38:G:H1	24:Z:34:C:N4	2.02	0.56
1:A:1233:G:C6	1:A:1234:C:N4	2.73	0.56
1:A:29:G:N2	1:A:555:C:C2	2.74	0.56
1:A:814:A:H2'	1:A:816:A:H5"	1.87	0.56
1:A:259:G:C2	1:A:268:C:C2	2.93	0.56
1:A:401:C:H2'	1:A:402:G:H8	1.71	0.56
24:Z:49:G:C2	24:Z:66:C:C2	2.94	0.56
1:A:21:G:C2	1:A:22:G:C5	2.93	0.56
1:A:834:C:C2	1:A:853:G:C2	2.94	0.56
1:A:1023:G:N3	1:A:1023:G:H2'	2.21	0.56
1:A:954:G:H21	1:A:1227:A:H62	1.53	0.56
4:D:33:MET:CA	4:D:36:ARG:O	2.52	0.56
5:E:11:ILE:HG21	5:E:105:VAL:HG13	1.88	0.56
11:K:84:VAL:HG11	11:K:95:ILE:HD11	1.88	0.56
1:A:280:C:O2	17:Q:38:ARG:HG3	2.06	0.56
1:A:543:C:H2'	1:A:544:G:H8	1.70	0.56
2:B:61:LEU:HD11	2:B:68:ILE:HG13	1.87	0.56
7:G:146:GLU:HA	7:G:149:ARG:HG2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:89:ARG:HH12	20:T:105:SER:H	1.54	0.56
1:A:1314:C:H2'	1:A:1315:U:C6	2.41	0.55
1:A:68:G:C5'	1:A:68:G:C8	2.88	0.55
1:A:79:G:H2'	1:A:80:G:H8	1.68	0.55
1:A:913:A:H4'	1:A:914:A:O5'	2.06	0.55
1:A:398:C:H2'	1:A:399:G:C8	2.31	0.55
1:A:1438:G:N2	1:A:1439:C:C2	2.74	0.55
1:A:397:A:H5"	1:A:398:C:OP1	2.06	0.55
1:A:671:G:C2	1:A:736:C:N3	2.74	0.55
1:A:891:U:H2'	1:A:892:A:H8	1.72	0.55
15:O:35:ARG:HH11	15:O:35:ARG:CG	2.11	0.55
22:X:33:GLU:O	22:X:37:LEU:HG	2.06	0.55
24:Z:35:A:H2'	24:Z:36:U:C6	2.41	0.55
1:A:1050:G:C2	1:A:1209:C:O2	2.60	0.55
1:A:1310:G:N2	1:A:1328:C:C2	2.74	0.55
1:A:301:G:H2'	1:A:302:G:H8	1.71	0.55
1:A:690:G:OP2	11:K:27:ASN:HB3	2.06	0.55
18:R:34:TYR:N	18:R:34:TYR:CD1	2.74	0.55
1:A:512:U:H2'	1:A:513:C:C6	2.42	0.55
1:A:725:G:N1	1:A:726:C:C4	2.75	0.55
1:A:917:G:H2'	1:A:918:A:H8	1.71	0.55
1:A:316:G:H2'	1:A:317:G:H8	1.71	0.55
1:A:774:G:C2	1:A:806:C:C2	2.94	0.55
1:A:991:U:C4	1:A:1212:U:H1'	2.42	0.55
2:B:102:LEU:HD21	2:B:162:ILE:HD11	1.88	0.55
1:A:1327:C:H5"	21:V:20:LYS:CB	2.36	0.55
22:X:45:LEU:HD12	22:X:59:ILE:HG12	1.88	0.55
1:A:1317:C:H2'	1:A:1318:A:O4'	2.07	0.55
1:A:1484:C:H2'	1:A:1485:U:O4'	2.06	0.55
1:A:1533:C:C4'	1:A:1533:C:OP1	2.50	0.55
1:A:279:A:H5"	1:A:280:C:H3'	1.89	0.55
1:A:878:G:H2'	1:A:879:C:C6	2.41	0.55
23:Y:34:A:H3'	23:Y:35:A:H8	1.72	0.55
1:A:385:C:H2'	1:A:386:C:O4'	2.07	0.55
1:A:482:A:C2	1:A:483:C:H1'	2.42	0.55
2:B:126:GLU:HA	2:B:129:GLU:HB3	1.88	0.55
13:M:39:ILE:HD13	13:M:56:LEU:HG	1.89	0.55
21:V:6:ARG:HB3	21:V:15:ARG:HH11	1.72	0.55
1:A:100:C:H2'	1:A:101:A:C8	2.42	0.55
1:A:1060:C:O2	1:A:1198:G:C2	2.60	0.55
1:A:35:G:C6	1:A:36:C:N4	2.75	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:786:G:C2	1:A:797:C:C2	2.94	0.55
11:K:34:ASP:HB2	11:K:35:PRO:CD	2.37	0.55
19:S:30:LEU:HD22	19:S:50:ALA:HB2	1.88	0.55
20:T:63:ILE:HG23	20:T:72:LEU:CD1	2.37	0.55
1:A:36:C:O2'	1:A:501:C:OP1	2.25	0.55
1:A:542:G:C6	1:A:543:C:N4	2.74	0.55
1:A:90:U:H2'	1:A:91:C:C6	2.42	0.55
20:T:56:MET:SD	20:T:103:GLY:HA3	2.47	0.55
1:A:1124:G:H1	1:A:1149:C:H42	1.54	0.54
1:A:1284:C:H2'	1:A:1285:A:C8	2.42	0.54
1:A:46:G:O2'	1:A:365:U:H1'	2.07	0.54
1:A:403:C:H5"	4:D:136:PRO:HD2	1.88	0.54
1:A:743:U:H2'	1:A:744:C:C6	2.42	0.54
4:D:9:CYS:HG	26:D:300:ZN:ZN	1.20	0.54
1:A:1459:C:OP1	20:T:28:ALA:HA	2.07	0.54
22:X:18:VAL:HG12	22:X:59:ILE:HD11	1.89	0.54
1:A:1534:A:H61	23:Y:31:U:H3	1.54	0.54
1:A:1237:C:H5"	1:A:1238:A:O4'	2.08	0.54
1:A:1369:C:H2'	1:A:1370:G:C8	2.43	0.54
1:A:255:G:C2	1:A:272:C:C2	2.94	0.54
4:D:157:LEU:HG	4:D:158:ILE:HD12	1.90	0.54
10:J:6:ILE:HD11	10:J:23:ILE:HG21	1.87	0.54
22:X:141:THR:HG21	22:X:163:MET:HE1	1.90	0.54
22:X:45:LEU:HG	22:X:57:ALA:HB1	1.89	0.54
1:A:1000:U:H2'	1:A:1001:A:O4'	2.07	0.54
1:A:381:C:H2'	1:A:382:A:O4'	2.07	0.54
18:R:73:ALA:HA	18:R:76:LEU:HD12	1.89	0.54
3:C:57:ILE:HA	3:C:65:ALA:O	2.08	0.54
4:D:163:GLU:HA	4:D:166:LYS:HD2	1.89	0.54
9:I:111:ARG:HD3	9:I:113:LYS:HG2	1.89	0.54
1:A:1106:G:N1	1:A:1107:C:C4	2.75	0.54
1:A:977:A:H8	1:A:1223:C:N3	2.06	0.54
1:A:1287:A:H2'	1:A:1288:A:H8	1.73	0.54
1:A:1358:U:N3	1:A:1363(A):A:N6	1.95	0.54
1:A:617:G:N1	1:A:618:C:C4	2.76	0.54
1:A:952:U:H2'	1:A:953:G:C8	2.43	0.54
3:C:150:LYS:HE2	3:C:152:ILE:HD11	1.90	0.54
5:E:14:ARG:O	5:E:14:ARG:HG2	2.07	0.54
19:S:17:GLU:HA	19:S:20:LEU:HG	1.89	0.54
1:A:1484:C:H6	1:A:1484:C:O5'	1.90	0.54
1:A:61:G:H2'	1:A:62:U:O4'	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:942:G:N3	1:A:942:G:H2'	2.22	0.54
15:O:87:ILE:HG22	15:O:88:ARG:H	1.72	0.54
1:A:1536:C:N4	23:Y:29:G:H1	2.05	0.54
1:A:1283:G:N2	1:A:1284:C:C2	2.76	0.54
1:A:70:G:C2	1:A:100:C:C2	2.95	0.54
1:A:806:C:H2'	1:A:807:A:H8	1.73	0.54
1:A:88:A:H3'	1:A:89:C:C6	2.43	0.54
7:G:88:PRO:HG3	7:G:148:ASN:O	2.08	0.54
8:H:89:PRO:HA	8:H:92:ARG:HD2	1.89	0.54
24:Z:16:C:H2'	24:Z:17:C:C6	2.42	0.54
1:A:1410:G:H2'	1:A:1411:C:C6	2.43	0.54
1:A:333:G:N2	1:A:334:C:C2	2.75	0.54
1:A:680:C:H2'	1:A:681:C:C6	2.42	0.54
2:B:20:GLU:HB3	2:B:23:ARG:HD2	1.88	0.54
8:H:10:LEU:HD13	8:H:83:ILE:HG12	1.90	0.54
14:N:27:CYS:SG	14:N:29:ARG:HB2	2.48	0.54
22:X:137:LEU:HB3	22:X:163:MET:SD	2.48	0.54
1:A:1323:G:H2'	1:A:1324:A:H8	1.72	0.54
1:A:444:C:H2'	1:A:445:G:H8	1.72	0.54
1:A:563:A:H2'	1:A:567:G:C8	2.43	0.54
1:A:945:G:H2'	1:A:945:G:N3	2.23	0.54
6:F:67:MET:HB2	6:F:68:PRO:HD2	1.89	0.54
1:A:132:C:N3	1:A:231:G:C2	2.76	0.54
1:A:874:G:N1	1:A:875:C:C4	2.75	0.54
2:B:77:ALA:HA	2:B:80:ILE:HD12	1.90	0.54
4:D:209:ARG:HB3	4:D:209:ARG:HH11	1.73	0.54
1:A:28:G:O2'	1:A:296:U:OP1	2.26	0.53
1:A:343:U:O3'	1:A:344:A:H8	1.92	0.53
1:A:45:U:H2'	1:A:46:G:C8	2.43	0.53
1:A:521:G:N2	1:A:522:C:C2	2.77	0.53
1:A:67:C:H2'	1:A:68:G:H8	1.72	0.53
1:A:1250:A:H4'	9:I:67:GLY:HA2	1.90	0.53
16:P:59:TRP:CE3	16:P:62:VAL:HG21	2.43	0.53
1:A:931:C:O2	1:A:1387:G:C2	2.61	0.53
1:A:22:G:C6	1:A:23:C:C4	2.96	0.53
1:A:525:C:H2'	1:A:526:C:C6	2.44	0.53
1:A:81:U:H2'	1:A:84:U:O4	2.07	0.53
1:A:972:C:O2	1:A:972:C:H2'	2.07	0.53
1:A:1456:G:N2	1:A:1457:G:C5	2.77	0.53
1:A:877:C:H2'	1:A:878:G:C8	2.43	0.53
1:A:877:C:H2'	1:A:878:G:H8	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:10:ARG:HG3	4:D:10:ARG:HH11	1.73	0.53
10:J:8:LEU:HB2	10:J:70:ARG:CB	2.37	0.53
1:A:1029:C:H2'	1:A:1030:C:C6	2.44	0.53
1:A:122:G:C2	1:A:123:C:C2	2.96	0.53
1:A:1475:G:H2'	1:A:1476:G:H8	1.73	0.53
1:A:164:U:H2'	1:A:165:C:C6	2.43	0.53
15:O:85:LEU:HB2	15:O:87:ILE:HD11	1.90	0.53
1:A:1217:C:H2'	1:A:1218:C:O4'	2.09	0.53
1:A:129(A):G:H4'	1:A:130:A:O5'	2.08	0.53
1:A:1511:G:H2'	1:A:1512:U:O4'	2.09	0.53
1:A:200:G:C2	1:A:218:C:C2	2.96	0.53
1:A:358:U:H2'	1:A:359:U:O4'	2.09	0.53
1:A:455:C:H2'	1:A:456:C:C6	2.43	0.53
4:D:3:ARG:NE	4:D:3:ARG:HA	2.23	0.53
24:Z:51:C:H42	24:Z:63:G:H1	1.56	0.53
24:Z:64:G:C2	24:Z:65:C:C2	2.97	0.53
1:A:1361:G:C5	1:A:1362:C:N3	2.77	0.53
1:A:1422:G:H1	1:A:1478:C:N4	2.07	0.53
1:A:92:C:H2'	1:A:93:G:H8	1.73	0.53
1:A:1030(B):C:H2'	1:A:1030(C):G:O4'	2.09	0.53
1:A:1234:C:H2'	1:A:1235:U:C6	2.44	0.53
1:A:1235:U:H2'	1:A:1236:A:O4'	2.09	0.53
5:E:115:VAL:HG11	5:E:118:ILE:HG23	1.90	0.53
10:J:4:ILE:HB	10:J:74:ILE:HD12	1.90	0.53
11:K:13:GLN:HE21	11:K:75:TYR:HA	1.73	0.53
22:X:16:VAL:HG12	22:X:55:PRO:HB2	1.91	0.53
1:A:122:G:C6	1:A:123:C:C4	2.97	0.53
1:A:500:G:C6	1:A:501:C:N4	2.77	0.53
1:A:671:G:N2	1:A:736:C:C2	2.77	0.53
3:C:16:ARG:HB3	3:C:16:ARG:HH11	1.74	0.53
6:F:95:GLU:HB3	6:F:96:PRO:HD2	1.90	0.53
12:L:86:ARG:HG2	12:L:99:HIS:HB2	1.91	0.53
1:A:1015:A:H2'	1:A:1016:A:C8	2.44	0.53
1:A:102:G:N2	1:A:103:C:C2	2.77	0.53
1:A:313:A:H2'	1:A:314:C:C6	2.44	0.53
1:A:392:G:H2'	1:A:393:A:H8	1.73	0.53
1:A:823:G:N2	1:A:824:C:C2	2.77	0.53
10:J:27:ALA:HB2	10:J:85:LEU:HD11	1.89	0.53
1:A:1030:C:H42	1:A:1031:G:H1	1.56	0.53
1:A:1105:A:H2'	1:A:1106:G:C8	2.44	0.53
1:A:1363(A):A:H1'	1:A:1365:G:N7	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:502:G:H2'	1:A:503:C:O4'	2.09	0.53
1:A:810:C:H2'	1:A:811:C:O4'	2.09	0.53
1:A:872:A:C8	1:A:874:G:C8	2.97	0.53
1:A:974:A:H8	1:A:974:A:OP1	1.92	0.53
1:A:72:C:N4	1:A:97:G:H1	2.06	0.53
1:A:1190:G:H5'	3:C:176:HIS:CE1	2.44	0.53
17:Q:69:LYS:H	17:Q:70:ARG:HD2	1.73	0.53
1:A:1130:A:H2'	1:A:1131:G:C8	2.43	0.52
16:P:5:ARG:HH21	16:P:28:ARG:HA	1.73	0.52
1:A:1386:G:H2'	1:A:1387:G:H8	1.74	0.52
1:A:173:U:H5'	1:A:197:A:O4'	2.09	0.52
1:A:262:A:H5"	20:T:76:ALA:HB2	1.90	0.52
8:H:49:GLU:HG3	8:H:60:ARG:HB2	1.90	0.52
17:Q:92:ARG:O	17:Q:95:TYR:HB2	2.09	0.52
1:A:1095:U:P	1:A:1108:G:H1	2.29	0.52
1:A:788:U:H2'	1:A:789:U:O4'	2.08	0.52
1:A:985:C:C2	1:A:1221:G:N2	2.78	0.52
4:D:109:GLY:HA3	4:D:165:MET:HG3	1.89	0.52
17:Q:81:ARG:HH21	17:Q:84:LEU:HB2	1.75	0.52
1:A:1351:U:H2'	1:A:1352:C:H6	1.74	0.52
1:A:998:G:N2	1:A:999:C:C2	2.77	0.52
12:L:39:VAL:HG23	12:L:57:LYS:HB2	1.91	0.52
1:A:165:C:H2'	1:A:166:G:H8	1.74	0.52
1:A:258:G:N2	1:A:269:C:C2	2.77	0.52
1:A:872:A:C4	1:A:874:G:N7	2.78	0.52
3:C:157:ILE:HD12	3:C:164:ARG:HB3	1.91	0.52
1:A:1225:A:H4'	19:S:78:ARG:HD3	1.92	0.52
1:A:1405:G:H1	1:A:1496:C:H42	1.57	0.52
1:A:1434:A:H2'	1:A:1435:G:O4'	2.10	0.52
1:A:145:G:N2	1:A:178:C:C2	2.78	0.52
2:B:10:LEU:HG	2:B:48:MET:HG3	1.92	0.52
22:X:144:LEU:HD11	22:X:165:LEU:HD13	1.91	0.52
1:A:291:C:H2'	1:A:292:G:H8	1.74	0.52
1:A:550:G:H2'	1:A:551:U:C6	2.45	0.52
1:A:777:A:H2'	1:A:778:G:H8	1.75	0.52
1:A:77:G:C8	1:A:77:G:H3'	2.44	0.52
1:A:838:G:N2	1:A:849:C:C2	2.78	0.52
1:A:884:U:H4'	1:A:885:G:H5"	1.90	0.52
1:A:988:G:N1	1:A:989:C:C2	2.77	0.52
4:D:32:ALA:O	4:D:36:ARG:O	2.28	0.52
10:J:60:ARG:CB	10:J:60:ARG:NH2	2.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:59:ALA:HB1	14:N:61:TRP:HZ3	1.75	0.52
20:T:66:ALA:HB3	20:T:72:LEU:HD12	1.90	0.52
1:A:99:U:H2'	1:A:100:C:H6	1.75	0.52
1:A:1017:G:C2	1:A:1018:C:C2	2.97	0.52
1:A:560:U:H5"	1:A:561:U:H5'	1.92	0.52
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.92	0.52
4:D:121:VAL:O	4:D:134:ASP:HA	2.10	0.52
10:J:60:ARG:HB3	10:J:60:ARG:NH2	2.23	0.52
20:T:72:LEU:HB3	20:T:77:ALA:HB2	1.91	0.52
1:A:1478:C:H2'	1:A:1479:C:C6	2.44	0.52
1:A:281:G:O2'	1:A:282:A:OP2	2.25	0.52
1:A:354:G:C6	1:A:355:C:N4	2.78	0.52
1:A:416:G:H2'	1:A:417:C:O4'	2.10	0.52
1:A:696:A:N3	1:A:786:G:O2'	2.39	0.52
24:Z:50:U:H2'	24:Z:51:C:C6	2.45	0.52
1:A:1129:C:O5'	1:A:1130:A:H5'	2.09	0.52
1:A:1233:G:N2	1:A:1234:C:C2	2.78	0.52
1:A:738:C:H5"	6:F:69:GLU:HB2	1.92	0.52
1:A:761:G:C2	1:A:762:C:C2	2.98	0.52
1:A:76:C:H2'	1:A:77:G:H5'	1.91	0.52
1:A:966:G:N3	24:Z:34:C:H5'	2.23	0.52
10:J:6:ILE:HD11	10:J:72:VAL:CG1	2.40	0.52
1:A:407:G:C2	1:A:436:C:C2	2.98	0.51
3:C:15:THR:HG21	3:C:178:LEU:O	2.10	0.51
6:F:45:LEU:HA	6:F:59:TYR:HA	1.92	0.51
24:Z:18:G:H21	24:Z:57:A:H2'	1.74	0.51
1:A:1144:G:C2	1:A:1145:C:N3	2.78	0.51
1:A:1222:G:N1	1:A:1223:C:C4	2.78	0.51
1:A:234:C:H2'	1:A:235:C:C6	2.45	0.51
1:A:376:G:H2'	1:A:377:G:C8	2.45	0.51
3:C:22:TRP:HB3	3:C:59:ARG:H	1.75	0.51
5:E:102:ALA:HB1	5:E:106:PRO:HB2	1.91	0.51
24:Z:52:G:H2'	24:Z:53:G:C8	2.46	0.51
24:Z:49:G:N2	24:Z:66:C:C2	2.78	0.51
1:A:1114:C:C2	1:A:1187:G:N2	2.79	0.51
1:A:399:G:C6	1:A:400:C:N4	2.79	0.51
1:A:883:C:H2'	1:A:884:U:C6	2.45	0.51
17:Q:21:VAL:HG21	17:Q:59:ILE:HD11	1.92	0.51
1:A:1074:G:C2	1:A:1075:C:C2	2.98	0.51
1:A:1082:G:H2'	1:A:1083:U:O4'	2.10	0.51
1:A:481:G:O2'	1:A:483:C:N4	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:536:C:H2'	1:A:537:G:C8	2.45	0.51
1:A:913:A:O2'	1:A:914:A:OP2	2.24	0.51
14:N:24:CYS:HB2	14:N:40:CYS:HB3	1.91	0.51
20:T:84:LEU:HD23	20:T:85:MET:HG3	1.92	0.51
9:I:127:LYS:HE2	24:Z:34:C:OP2	2.10	0.51
24:Z:70:G:H2'	24:Z:71:C:C6	2.45	0.51
1:A:1070:U:H2'	1:A:1071:C:H6	1.75	0.51
1:A:198:G:H2'	1:A:199:G:H8	1.76	0.51
1:A:672:U:H3	1:A:734:G:H1	1.59	0.51
2:B:72:GLY:HA3	2:B:81:VAL:HG21	1.92	0.51
1:A:1520:G:H2'	1:A:1521:G:C8	2.46	0.51
1:A:427:U:O2'	1:A:541:G:OP1	2.28	0.51
1:A:609:A:C4	1:A:610:G:C8	2.98	0.51
1:A:681:C:N3	1:A:710:G:C2	2.79	0.51
3:C:94:LEU:HB3	3:C:95:THR:HG23	1.92	0.51
4:D:102:ASP:HB3	4:D:136:PRO:HB3	1.92	0.51
1:A:1256:A:H4'	1:A:1258:G:O4'	2.11	0.51
1:A:132:C:C2	1:A:231:G:N2	2.79	0.51
1:A:1373:G:N7	9:I:11:LYS:NZ	2.59	0.51
1:A:172:A:H2'	1:A:174:C:H5	1.76	0.51
5:E:40:ARG:NH1	5:E:40:ARG:HG2	2.23	0.51
6:F:45:LEU:HD12	6:F:59:TYR:HD2	1.75	0.51
11:K:21:ILE:HG12	11:K:30:VAL:HG22	1.92	0.51
17:Q:48:GLU:HB2	17:Q:50:LYS:HB2	1.92	0.51
1:A:1486:G:H2'	1:A:1486:G:N3	2.25	0.51
1:A:725:G:C2	1:A:726:C:C4	2.98	0.51
2:B:189:ASP:OD1	2:B:189:ASP:N	2.44	0.51
13:M:23:TYR:HB3	13:M:67:GLU:HA	1.93	0.51
1:A:1252:A:H2'	1:A:1253:G:O4'	2.10	0.51
1:A:1300:G:HO2'	1:A:1301:U:P	2.34	0.51
1:A:1441:G:O2'	1:A:1460:A:N6	2.43	0.51
17:Q:45:HIS:HA	17:Q:69:LYS:HE2	1.92	0.51
22:X:122:PHE:CE2	22:X:161:MET:HB2	2.46	0.51
1:A:1353:G:N1	1:A:1354:C:C4	2.79	0.51
1:A:236:G:C2	1:A:237:C:C2	2.99	0.51
1:A:69:G:H1	1:A:100:C:N4	2.09	0.51
1:A:1225:A:N3	1:A:1225:A:H2'	2.26	0.50
1:A:1431:C:C2	1:A:1470:G:N2	2.79	0.50
1:A:616:G:H2'	1:A:617:G:H8	1.75	0.50
1:A:568:G:C2	1:A:883:C:C2	2.99	0.50
1:A:887:G:H3'	1:A:888:G:H8	1.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:718:G:H5'	11:K:117:ASN:HB2	1.93	0.50
3:C:77:ILE:HD13	3:C:84:ILE:HD12	1.93	0.50
9:I:16:ARG:HH21	9:I:64:THR:HG21	1.76	0.50
10:J:83:GLU:HA	10:J:86:MET:HB2	1.93	0.50
22:X:126:GLU:HA	22:X:129:HIS:HB2	1.94	0.50
1:A:1038:C:C6	1:A:1039:C:H5	2.30	0.50
1:A:1064:G:H21	1:A:1190:G:H2'	1.77	0.50
1:A:1118:C:H1'	1:A:1179:A:C5	2.47	0.50
1:A:1255:G:O2'	1:A:1258:G:N3	2.43	0.50
1:A:1412:C:H2'	1:A:1413:A:O4'	2.10	0.50
1:A:250:A:H4'	1:A:251:G:O5'	2.11	0.50
1:A:354:G:C2	1:A:355:C:C4	2.99	0.50
2:B:167:PRO:HG3	2:B:186:ALA:HB1	1.94	0.50
22:X:90:PHE:HD1	22:X:94:ILE:HD11	1.75	0.50
1:A:1068:G:N2	1:A:1069:C:C2	2.80	0.50
1:A:1103:C:H2'	1:A:1104:G:O4'	2.11	0.50
1:A:1189:C:OP1	10:J:51:ARG:NH2	2.44	0.50
1:A:1060:C:C2	1:A:1198:G:N1	2.80	0.50
1:A:316:G:H2'	1:A:317:G:C8	2.45	0.50
1:A:539:A:H2'	1:A:540:G:H8	1.73	0.50
1:A:597:G:H2'	1:A:598:U:H5'	1.94	0.50
1:A:910:C:H2'	1:A:911:U:O4'	2.12	0.50
2:B:15:VAL:HG11	2:B:209:ARG:HG3	1.93	0.50
4:D:187:ARG:CZ	4:D:188:LEU:O	2.59	0.50
5:E:127:ASN:O	5:E:131:ILE:HB	2.10	0.50
7:G:16:LEU:HD11	9:I:42:ARG:HD2	1.94	0.50
13:M:3:ARG:HB3	13:M:7:VAL:HA	1.94	0.50
1:A:101:A:H2'	1:A:102:G:C8	2.41	0.50
1:A:1134:G:N2	1:A:1141:C:C2	2.79	0.50
1:A:1198:G:H2'	1:A:1199:U:C6	2.47	0.50
1:A:407:G:C2	1:A:436:C:O2	2.65	0.50
1:A:965:A:C8	1:A:965:A:O5'	2.63	0.50
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.93	0.50
5:E:139:LEU:HA	5:E:142:LEU:HD12	1.94	0.50
12:L:67:THR:HB	12:L:96:VAL:HG22	1.93	0.50
1:A:137:C:H1'	16:P:63:GLY:HA3	1.94	0.50
1:A:1074:G:C6	1:A:1075:C:N3	2.80	0.50
1:A:1462:G:N2	1:A:1463:C:C2	2.80	0.50
1:A:1417:G:H22	1:A:1482:G:H2'	1.76	0.50
1:A:590:C:N3	1:A:650:G:C2	2.79	0.50
24:Z:64:G:C5	24:Z:65:C:C4	3.00	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1410:G:C6	1:A:1411:C:N4	2.80	0.50
1:A:500:G:H2'	1:A:501:C:C6	2.47	0.50
1:A:57:G:C6	1:A:58:C:N3	2.80	0.50
1:A:975:A:H5'	1:A:975:A:H8	1.76	0.50
3:C:131:ARG:NH1	5:E:52:PRO:HD2	2.27	0.50
4:D:60:GLU:HG2	4:D:202:LEU:HB2	1.93	0.50
1:A:1390:U:H2'	1:A:1391:U:C6	2.47	0.50
1:A:183:G:H2'	1:A:184:G:O4'	2.11	0.50
1:A:572:A:N1	1:A:864:A:C5	2.79	0.50
1:A:56:U:H2'	1:A:57:G:C8	2.47	0.50
1:A:64:G:H4'	1:A:65:U:H5"	1.94	0.50
1:A:678:U:H2'	1:A:679:C:C6	2.47	0.50
1:A:947:G:H2'	1:A:948:C:O4'	2.11	0.50
1:A:1408:A:OP1	22:X:123:ARG:HB3	2.12	0.50
1:A:1251:A:H2'	1:A:1252:A:O4'	2.12	0.50
1:A:1365:G:C2	1:A:1366:C:C2	3.00	0.50
1:A:680:C:H2'	1:A:681:C:H6	1.77	0.50
4:D:20:TYR:HA	4:D:26:CYS:HB3	1.94	0.50
4:D:58:LEU:HD23	4:D:206:PHE:CE2	2.47	0.50
19:S:30:LEU:HA	19:S:48:THR:O	2.12	0.50
22:X:150:VAL:HG23	22:X:165:LEU:HG	1.92	0.50
1:A:1008:C:H2'	1:A:1009:G:O4'	2.12	0.49
1:A:1121:U:O5'	1:A:1121:U:H6	1.94	0.49
1:A:1485:U:H2'	1:A:1486:G:H8	1.77	0.49
1:A:259:G:H2'	1:A:260:G:H8	1.76	0.49
1:A:260:G:H2'	1:A:261:U:C6	2.47	0.49
1:A:333:G:C6	1:A:334:C:N4	2.80	0.49
1:A:648:A:H2'	1:A:649:G:H8	1.77	0.49
3:C:106:VAL:HG11	3:C:112:SER:HB2	1.94	0.49
22:X:28:ILE:HG12	22:X:54:PRO:HG3	1.94	0.49
1:A:1241:G:N2	1:A:1242:C:C2	2.81	0.49
1:A:1420:C:H2'	1:A:1421:G:H8	1.76	0.49
1:A:953:G:H2'	1:A:954:G:O4'	2.11	0.49
4:D:68:TYR:HD2	4:D:97:LEU:HD13	1.78	0.49
4:D:70:ILE:HD13	4:D:75:PHE:HD2	1.77	0.49
1:A:1368:G:OP1	10:J:62:HIS:NE2	2.43	0.49
1:A:375:U:H4'	16:P:17:TYR:CE2	2.47	0.49
20:T:37:SER:O	20:T:41:ILE:HG13	2.12	0.49
22:X:118:VAL:HG12	22:X:137:LEU:HD22	1.94	0.49
1:A:1001(A):G:N1	1:A:1002:G:C6	2.80	0.49
1:A:370:C:C2	1:A:392:G:N2	2.80	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:499:A:N6	1:A:547:A:C8	2.80	0.49
1:A:761:G:C6	1:A:762:C:C4	3.00	0.49
1:A:412:A:H1'	4:D:35:ARG:HH12	1.74	0.49
8:H:87:SER:HB2	8:H:133:LEU:O	2.11	0.49
1:A:734:G:H21	18:R:75:ILE:HD11	1.78	0.49
24:Z:55:PSU:C6	24:Z:57:A:OP2	2.65	0.49
1:A:1073:U:OP2	5:E:57:LYS:HE2	2.11	0.49
1:A:768:A:C4	1:A:769:G:C8	3.00	0.49
1:A:828:A:H4'	1:A:828:A:OP1	2.11	0.49
2:B:83:MET:HG3	2:B:238:LEU:HD22	1.94	0.49
1:A:1074:G:C6	1:A:1075:C:C4	3.00	0.49
1:A:1104:G:H4'	2:B:111:ARG:CZ	2.42	0.49
1:A:588:G:N1	1:A:589:C:C4	2.80	0.49
1:A:902:G:H2'	1:A:903:G:H8	1.78	0.49
1:A:947:G:C2	1:A:948:C:C2	3.00	0.49
3:C:85:ARG:HH11	3:C:88:ARG:HB3	1.78	0.49
4:D:201:GLN:NE2	5:E:116:THR:OG1	2.46	0.49
1:A:1443:G:C2	1:A:1444:C:N3	2.81	0.49
1:A:354:G:N1	1:A:355:C:C4	2.81	0.49
1:A:439:A:C8	1:A:496:A:N1	2.79	0.49
1:A:876:G:C6	1:A:877:C:N4	2.81	0.49
2:B:15:VAL:HG21	2:B:209:ARG:CG	2.42	0.49
5:E:57:LYS:O	5:E:61:TYR:HD1	1.96	0.49
12:L:55:VAL:HG12	12:L:56:ALA:H	1.78	0.49
23:Y:28:A:H3'	23:Y:29:G:H8	1.76	0.49
1:A:1074:G:C5	1:A:1075:C:C4	3.01	0.49
1:A:1266:G:N2	1:A:1270:C:C2	2.81	0.49
1:A:945:G:C2	1:A:946:A:C8	3.01	0.49
1:A:994:A:N7	1:A:1216:G:H4'	2.28	0.49
1:A:1508:G:C2	1:A:1509:C:C2	3.01	0.49
1:A:18:C:H2'	1:A:19:C:O4'	2.13	0.49
1:A:22:G:C2	1:A:23:C:C2	3.00	0.49
1:A:658:G:C6	1:A:749:C:N4	2.81	0.49
1:A:77:G:C3'	1:A:77:G:C8	2.96	0.49
3:C:39:ILE:O	3:C:43:LEU:HG	2.13	0.49
4:D:58:LEU:HD23	4:D:206:PHE:HE2	1.77	0.49
7:G:65:ALA:O	7:G:69:VAL:HG23	2.13	0.49
10:J:19:SER:HA	10:J:22:LYS:HB2	1.95	0.49
1:A:1244:C:H2'	1:A:1245:A:C8	2.48	0.49
1:A:1365:G:C6	1:A:1366:C:C4	3.00	0.49
1:A:19:C:H2'	1:A:20:U:H6	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:688:G:C6	1:A:689:C:N4	2.81	0.49
1:A:84:U:O5'	1:A:84:U:H6	1.95	0.49
1:A:1407:C:H5"	22:X:123:ARG:HG3	1.94	0.49
1:A:1191:A:H2'	1:A:1192:C:C6	2.48	0.49
1:A:439:A:C8	1:A:496:A:C2	3.01	0.49
2:B:111:ARG:HD3	2:B:145:LEU:HD21	1.94	0.49
7:G:98:SER:HA	7:G:101:LEU:HD12	1.95	0.49
22:X:45:LEU:CG	22:X:57:ALA:HB1	2.43	0.49
1:A:1392:G:H21	1:A:1502:A:H8	1.59	0.48
1:A:189(D):C:H3'	1:A:189(E):U:C6	2.48	0.48
1:A:32:A:H2'	1:A:33:A:C8	2.47	0.48
1:A:584:G:C4	1:A:585:G:C8	3.01	0.48
1:A:792:A:H4'	1:A:793:U:H5'	1.95	0.48
1:A:939:G:H2'	1:A:940:C:C6	2.48	0.48
1:A:1281:U:H4'	1:A:1282:C:OP2	2.13	0.48
1:A:976:G:C8	1:A:1358:U:C2	3.01	0.48
1:A:189:G:C2	1:A:189(A):C:C2	3.01	0.48
1:A:942:G:C6	1:A:1342:C:N3	2.81	0.48
13:M:39:ILE:HG13	13:M:55:ARG:HH21	1.78	0.48
1:A:192:U:H1'	20:T:103:GLY:HA2	1.95	0.48
1:A:1217:C:N4	1:A:1218:C:N4	2.61	0.48
1:A:1320:C:H2'	1:A:1321:C:O4'	2.13	0.48
1:A:1399:C:N3	1:A:1502:A:N6	2.61	0.48
1:A:243:A:H4'	1:A:244:U:O5'	2.13	0.48
1:A:444:C:H2'	1:A:445:G:C8	2.49	0.48
1:A:729:A:H2'	1:A:730:G:C8	2.45	0.48
18:R:37:VAL:HG22	18:R:79:LEU:HG	1.94	0.48
22:X:5:TYR:HB2	22:X:46:VAL:HG12	1.96	0.48
1:A:402:G:N2	1:A:403:C:C2	2.81	0.48
1:A:505:G:H1	1:A:526:C:H42	1.60	0.48
1:A:548:G:C6	1:A:549:C:N4	2.80	0.48
1:A:867:G:N2	1:A:868:C:C2	2.81	0.48
7:G:65:ALA:HB1	7:G:127:ALA:HB3	1.95	0.48
10:J:4:ILE:HA	10:J:100:THR:HA	1.94	0.48
1:A:1123:A:H4'	10:J:37:PRO:HD2	1.95	0.48
17:Q:57:VAL:HG12	17:Q:76:LEU:HA	1.94	0.48
19:S:62:ILE:HG13	19:S:66:MET:SD	2.53	0.48
1:A:1001(A):G:C6	1:A:1002:G:O6	2.66	0.48
1:A:112:G:C2	1:A:113:G:C8	3.00	0.48
1:A:1511:G:C6	1:A:1512:U:N3	2.81	0.48
1:A:15:G:H2'	1:A:16:A:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:G:O2'	1:A:267:C:OP2	2.22	0.48
1:A:309:G:H2'	1:A:310:G:H8	1.78	0.48
1:A:542:G:N2	1:A:543:C:C2	2.82	0.48
1:A:881:G:C2	1:A:882:C:C2	3.02	0.48
2:B:44:LEU:HA	2:B:47:THR:HB	1.95	0.48
1:A:546:G:OP2	4:D:72:GLU:HB3	2.14	0.48
4:D:97:LEU:HD23	4:D:100:ARG:HD3	1.94	0.48
5:E:139:LEU:O	5:E:142:LEU:HB2	2.14	0.48
8:H:85:ARG:HH21	8:H:134:ILE:HG22	1.77	0.48
1:A:1086:U:O5'	1:A:1086:U:H6	1.96	0.48
1:A:1163:C:N3	1:A:1174:G:C2	2.82	0.48
1:A:1233:G:H2'	1:A:1234:C:C6	2.49	0.48
1:A:1306:A:H2'	1:A:1307:U:O4'	2.14	0.48
1:A:287:U:H2'	1:A:288:A:H8	1.77	0.48
1:A:453:A:H2'	1:A:454:C:C6	2.48	0.48
1:A:532:A:O2'	1:A:533:A:H5'	2.14	0.48
1:A:836:G:H1	1:A:850:U:H3	1.62	0.48
4:D:162:LEU:O	4:D:166:LYS:N	2.46	0.48
6:F:43:LEU:HB2	6:F:60:PHE:HB2	1.96	0.48
19:S:63:THR:HG22	19:S:64:GLU:H	1.79	0.48
1:A:170:U:H2'	1:A:171:A:C8	2.46	0.48
1:A:405:U:H5"	1:A:406:G:O4'	2.14	0.48
3:C:69:HIS:HA	3:C:104:GLN:O	2.14	0.48
1:A:1081:G:P	5:E:16:THR:CG2	3.01	0.48
22:X:115:LYS:HD3	22:X:164:LEU:HD11	1.96	0.48
1:A:549:C:H2'	1:A:550:G:H8	1.79	0.48
10:J:60:ARG:CB	10:J:60:ARG:HH21	2.25	0.48
11:K:83:ILE:HG12	11:K:109:VAL:HG12	1.96	0.48
18:R:34:TYR:H	18:R:34:TYR:HD1	1.58	0.48
1:A:105:G:C2	1:A:106:C:C2	3.01	0.48
1:A:1286:A:H3'	1:A:1286:A:C8	2.49	0.48
1:A:256:U:H2'	1:A:257:G:C8	2.49	0.48
1:A:590:C:H2'	1:A:591:U:C6	2.48	0.48
1:A:648:A:H2'	1:A:649:G:C8	2.49	0.48
1:A:966:G:OP1	1:A:966:G:H8	1.96	0.48
2:B:101:MET:HG3	2:B:108:ILE:HD13	1.95	0.48
1:A:1358:U:O4	1:A:1363(A):A:C2	2.59	0.48
1:A:362:G:H5"	12:L:61:THR:HB	1.96	0.48
3:C:148:GLY:HA3	3:C:172:ARG:O	2.14	0.48
4:D:57:ARG:HB3	4:D:206:PHE:HB2	1.95	0.48
6:F:78:GLU:HA	6:F:81:ILE:HD12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:20:TYR:HE2	11:K:33:THR:HG21	1.78	0.48
18:R:53:ARG:HE	18:R:60:ALA:HA	1.78	0.48
20:T:45:GLN:HA	20:T:91:LEU:HD22	1.95	0.48
1:A:1147:C:H4'	9:I:5:TYR:CE2	2.49	0.47
1:A:1244:C:H2'	1:A:1245:A:H8	1.79	0.47
1:A:1492:A:C8	1:A:1492:A:C3'	2.97	0.47
1:A:15:G:H2'	1:A:16:A:H8	1.78	0.47
1:A:276:G:C2	1:A:277:C:C2	3.02	0.47
1:A:293:G:C4	1:A:305:G:N2	2.82	0.47
1:A:418:C:C2	1:A:426:G:C2	3.02	0.47
1:A:521:G:N1	1:A:522:C:C4	2.82	0.47
5:E:152:ARG:HB2	8:H:43:GLY:HA3	1.96	0.47
12:L:89:ARG:HA	12:L:97:ARG:HA	1.96	0.47
1:A:1216:G:N1	1:A:1217:C:C4	2.82	0.47
1:A:177:C:H2'	1:A:178:C:C6	2.49	0.47
1:A:229:U:H2'	1:A:230:G:H8	1.79	0.47
1:A:328:C:H4'	1:A:329:A:O5'	2.15	0.47
1:A:365:U:O2	1:A:365:U:C2'	2.62	0.47
1:A:585:G:C2	1:A:586:C:C2	3.02	0.47
1:A:720:C:H2'	1:A:721:G:N7	2.29	0.47
4:D:66:ARG:HB2	4:D:66:ARG:HH11	1.79	0.47
1:A:223:U:H5'	20:T:68:LYS:HZ1	1.80	0.47
21:V:3:LYS:O	21:V:11:GLY:HA2	2.14	0.47
22:X:45:LEU:HD11	22:X:57:ALA:HB1	1.95	0.47
1:A:1079:G:N2	1:A:1080:A:C2	2.82	0.47
1:A:1144:G:C6	1:A:1145:C:N4	2.82	0.47
1:A:1427:U:H2'	1:A:1428:A:C8	2.49	0.47
1:A:390:C:H2'	1:A:391:G:H8	1.79	0.47
1:A:399:G:N2	1:A:400:C:C2	2.83	0.47
1:A:680:C:C2	1:A:711:G:N2	2.82	0.47
1:A:778:G:C2	1:A:779:C:C2	3.03	0.47
1:A:109:A:H2'	1:A:326:G:H21	1.78	0.47
1:A:1266:G:C2	1:A:1270:C:N3	2.83	0.47
1:A:1287:A:H5'	1:A:1287:A:C8	2.47	0.47
1:A:1301:U:H1'	1:A:1302:U:OP1	2.15	0.47
1:A:1397:C:O2	1:A:1397:C:H2'	2.13	0.47
1:A:178:C:H2'	1:A:179:A:H8	1.79	0.47
1:A:128:G:C2	1:A:234:C:N3	2.81	0.47
1:A:416:G:C6	1:A:417:C:C4	3.02	0.47
1:A:579:G:H5'	1:A:728:A:H1'	1.95	0.47
1:A:80:G:H3'	1:A:81:U:H5"	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1112:C:O2	3:C:179:ARG:HB2	2.15	0.47
6:F:76:ALA:HB2	6:F:90:VAL:HG21	1.96	0.47
24:Z:43:A:H2'	24:Z:44:A:O4'	2.13	0.47
24:Z:64:G:C6	24:Z:65:C:C4	3.03	0.47
1:A:1406:U:H2'	1:A:1407:C:H6	1.80	0.47
1:A:312:C:H2'	1:A:313:A:H8	1.79	0.47
1:A:79:G:C2'	1:A:80:G:H8	2.28	0.47
1:A:928:G:H1	1:A:1389:C:H42	1.62	0.47
4:D:39:PRO:O	4:D:44:GLY:HA3	2.14	0.47
5:E:15:ARG:HD3	5:E:26:PHE:CD1	2.49	0.47
16:P:13:HIS:C	16:P:15:PRO:HD3	2.34	0.47
22:X:45:LEU:CD1	22:X:57:ALA:HB1	2.44	0.47
1:A:1039:C:H2'	1:A:1040:U:H6	1.76	0.47
1:A:1479:C:H2'	1:A:1480:G:H8	1.79	0.47
1:A:1505:G:H4'	1:A:1506:U:H5"	1.97	0.47
1:A:373:A:OP2	1:A:373:A:H3'	2.15	0.47
1:A:601:C:C2	1:A:638:G:N2	2.83	0.47
2:B:33:TYR:HB2	2:B:42:ILE:C	2.35	0.47
4:D:155:LEU:HB3	4:D:158:ILE:HD13	1.96	0.47
13:M:25:ILE:HG12	13:M:29:ARG:HB3	1.96	0.47
22:X:5:TYR:HD2	22:X:65:TRP:HH2	1.63	0.47
24:Z:36:U:C2	24:Z:37:A:C8	3.02	0.47
1:A:1017:G:C6	1:A:1018:C:C4	3.02	0.47
1:A:1050:G:N2	1:A:1051:C:C2	2.83	0.47
1:A:1133:G:H1	1:A:1141:C:H42	1.63	0.47
1:A:1312:G:C2	1:A:1326:C:N3	2.82	0.47
1:A:1456:G:C3'	1:A:1457:G:O4'	2.63	0.47
1:A:155:C:H42	1:A:166:G:H1	1.62	0.47
1:A:33:A:H2'	1:A:34:C:H6	1.76	0.47
1:A:43:C:H2'	1:A:44:G:C8	2.49	0.47
1:A:585:G:C6	1:A:586:C:C4	3.03	0.47
1:A:768:A:C5	1:A:769:G:C8	3.03	0.47
1:A:942:G:C2	1:A:1342:C:O2	2.68	0.47
7:G:143:ARG:O	7:G:147:ALA:N	2.43	0.47
1:A:67:C:H42	1:A:102:G:H1	1.61	0.47
1:A:689:C:H2'	1:A:690:G:C8	2.50	0.47
1:A:784:C:C2	1:A:799:G:N2	2.83	0.47
1:A:815:A:O2'	1:A:1527:C:H1'	2.15	0.47
1:A:998:G:N1	1:A:999:C:C4	2.83	0.47
2:B:188:ALA:HB3	2:B:200:ILE:HG23	1.96	0.47
2:B:87:ARG:HB3	2:B:219:VAL:HG11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:25:ARG:C	4:D:27:TYR:H	2.17	0.47
17:Q:51:TYR:HE1	17:Q:76:LEU:HB2	1.80	0.47
22:X:17:ARG:HB2	22:X:54:PRO:O	2.14	0.47
23:Y:37:U:H2'	23:Y:37:U:O2	2.14	0.47
24:Z:10:G:N2	24:Z:26:G:H1'	2.30	0.47
1:A:113:G:H2'	1:A:114:U:C6	2.49	0.47
1:A:122:G:C6	1:A:123:C:N3	2.82	0.47
1:A:1532:U:O5'	1:A:1532:U:H6	1.98	0.47
1:A:189:G:C6	1:A:189(A):C:C4	3.03	0.47
1:A:394:G:N2	1:A:395:C:C2	2.83	0.47
1:A:505:G:H2'	1:A:506:G:C8	2.49	0.47
1:A:962:C:H2'	1:A:963:G:O4'	2.14	0.47
3:C:45:LYS:HD3	3:C:45:LYS:HA	1.65	0.47
1:A:636:U:H5'	17:Q:2:PRO:HG3	1.97	0.47
20:T:74:LYS:HD2	20:T:74:LYS:HA	1.52	0.47
22:X:11:ILE:HD11	22:X:45:LEU:O	2.14	0.47
1:A:1223:C:P	19:S:78:ARG:HH22	2.37	0.47
1:A:1255:G:O2'	1:A:1258:G:H1'	2.15	0.47
1:A:412:A:C1'	4:D:35:ARG:NH1	2.78	0.47
1:A:484:G:H4'	1:A:485:G:O5'	2.15	0.47
1:A:68:G:H8	1:A:68:G:C5'	2.28	0.47
11:K:126:ARG:C	11:K:128:ALA:N	2.68	0.47
22:X:103:LEU:HA	22:X:106:ILE:HD12	1.96	0.47
24:Z:16:C:H5'	24:Z:17:C:H2'	1.97	0.47
1:A:1128:C:H1'	1:A:1146:A:N6	2.28	0.47
1:A:1116:C:C2	1:A:1185:G:C2	3.03	0.47
1:A:1452:C:H4'	1:A:1456:G:O4'	2.15	0.47
1:A:1539:C:C2	23:Y:27:G:N2	2.83	0.47
1:A:19:C:O2	1:A:917:G:C2	2.68	0.47
1:A:225:C:H2'	1:A:226:G:H8	1.80	0.47
1:A:27:G:H2'	1:A:28:G:O4'	2.14	0.47
1:A:70:G:C2	1:A:100:C:O2	2.68	0.47
1:A:778:G:C6	1:A:779:C:C4	3.03	0.47
1:A:807:A:H2'	1:A:808:C:C6	2.50	0.47
1:A:868:C:H2'	1:A:869:G:O4'	2.14	0.47
1:A:391:G:H5"	16:P:8:ARG:NH1	2.30	0.47
22:X:106:ILE:O	22:X:110:LEU:HG	2.14	0.47
1:A:200:G:N2	1:A:218:C:C2	2.83	0.46
1:A:577:G:C2	1:A:578:C:C2	3.03	0.46
1:A:601:C:H42	1:A:637:G:H1	1.63	0.46
2:B:51:LEU:HD23	2:B:55:PHE:CZ	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:83:MET:SD	2:B:235:SER:HB2	2.54	0.46
9:I:5:TYR:CZ	9:I:7:THR:OG1	2.68	0.46
22:X:155:GLU:HB2	22:X:162:ASN:ND2	2.30	0.46
22:X:85:VAL:HG22	22:X:115:LYS:HD2	1.96	0.46
1:A:1276:G:H2'	1:A:1277:C:O4'	2.15	0.46
6:F:9:VAL:HG12	6:F:86:ARG:HG3	1.97	0.46
9:I:13:ALA:HB2	9:I:68:GLY:HA3	1.98	0.46
1:A:453:A:H4'	16:P:72:ARG:HD2	1.97	0.46
20:T:55:ILE:HA	20:T:58:LYS:HD2	1.97	0.46
22:X:13:ALA:HB3	22:X:47:LEU:HD21	1.97	0.46
1:A:1125:U:H5'	1:A:1126:U:C5	2.48	0.46
1:A:1456:G:C2	1:A:1457:G:C4	3.03	0.46
1:A:794:A:H2'	1:A:795:C:H6	1.78	0.46
1:A:857:C:H2'	1:A:858:G:C8	2.50	0.46
1:A:886:G:C2	1:A:912:C:O2	2.69	0.46
1:A:1070:U:OP1	5:E:20:GLN:HG3	2.15	0.46
1:A:1325:C:H4'	21:V:17:THR:HG21	1.98	0.46
1:A:1384:C:H2'	1:A:1385:G:C8	2.50	0.46
1:A:1509:C:H2'	1:A:1510:U:O4'	2.16	0.46
1:A:439:A:C6	1:A:441:A:H1'	2.50	0.46
1:A:931:C:C2	1:A:1387:G:C2	3.03	0.46
1:A:1356:G:N2	1:A:1357:A:C2	2.83	0.46
1:A:1447:A:OP2	1:A:1452:C:H5	1.99	0.46
1:A:390:C:O5'	1:A:390:C:H6	1.98	0.46
3:C:154:SER:HA	3:C:165:THR:HA	1.96	0.46
9:I:10:ARG:HD3	9:I:105:ASP:HB3	1.96	0.46
22:X:102:LYS:O	22:X:106:ILE:HG13	2.16	0.46
22:X:18:VAL:HB	22:X:26:LEU:HB2	1.97	0.46
1:A:1119:C:H2'	1:A:1120:G:H8	1.81	0.46
1:A:253:U:H2'	1:A:254:G:H8	1.79	0.46
1:A:473:G:H5"	16:P:81:ARG:NH2	2.30	0.46
1:A:617:G:N2	1:A:618:C:C2	2.83	0.46
1:A:734:G:C2	1:A:735:C:C2	3.03	0.46
1:A:790:A:O5'	1:A:790:A:H8	1.98	0.46
1:A:568:G:N1	1:A:883:C:C4	2.84	0.46
1:A:985:C:C2	1:A:1221:G:C2	3.04	0.46
2:B:207:ALA:O	2:B:209:ARG:N	2.48	0.46
3:C:8:ILE:CG1	3:C:16:ARG:HH21	2.19	0.46
3:C:125:GLU:HA	3:C:191:THR:HG23	1.97	0.46
8:H:24:THR:HG22	8:H:61:VAL:HB	1.98	0.46
20:T:74:LYS:HE2	20:T:75:ASN:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:54:5MU:N3	24:Z:58:A:C8	2.83	0.46
1:A:1283:G:C6	1:A:1284:C:N4	2.84	0.46
1:A:236:G:C6	1:A:237:C:C4	3.04	0.46
1:A:377:G:H2'	1:A:378:G:C8	2.50	0.46
1:A:524:G:N2	1:A:525:C:C2	2.84	0.46
1:A:553:A:H2'	1:A:554:C:H6	1.74	0.46
1:A:745:C:H2'	1:A:746:A:H8	1.78	0.46
3:C:56:ASP:HB2	3:C:67:THR:HB	1.97	0.46
9:I:89:ASN:HD21	9:I:91:ASP:HB2	1.79	0.46
12:L:60:LEU:HB3	12:L:62:SER:H	1.80	0.46
22:X:47:LEU:HD23	22:X:50:PRO:HB3	1.98	0.46
23:Y:32:A:H4'	23:Y:33:A:OP2	2.14	0.46
1:A:1094:G:O2'	1:A:1095:U:P	2.74	0.46
1:A:1129:C:H4'	1:A:1130:A:H3'	1.97	0.46
1:A:1060:C:N3	1:A:1198:G:C6	2.84	0.46
1:A:416:G:C2	1:A:417:C:C2	3.03	0.46
1:A:513:C:H2'	1:A:514:C:C6	2.51	0.46
1:A:51:A:C6	1:A:353:A:C2	3.04	0.46
1:A:658:G:C2	1:A:749:C:C4	3.03	0.46
6:F:72:VAL:O	6:F:75:LEU:HG	2.16	0.46
22:X:32:ARG:O	22:X:36:ARG:HG3	2.15	0.46
22:X:5:TYR:HD2	22:X:65:TRP:CH2	2.34	0.46
1:A:1003:G:N2	1:A:1038:C:O2	2.48	0.46
1:A:662:G:C6	1:A:744:C:N3	2.84	0.46
1:A:688:G:H2'	1:A:689:C:C6	2.50	0.46
1:A:825:G:C6	1:A:826:C:C4	3.04	0.46
11:K:16:SER:HB2	11:K:79:SER:HB3	1.97	0.46
13:M:86:CYS:SG	13:M:87:TYR:N	2.89	0.46
1:A:1245:A:H2'	1:A:1246:C:C6	2.50	0.46
1:A:1339:A:H1'	24:Z:41:C:H1'	1.97	0.46
1:A:1487:G:H2'	1:A:1488:G:C8	2.51	0.46
1:A:308:C:H2'	1:A:309:G:C8	2.51	0.46
1:A:399:G:C2	1:A:400:C:C2	3.04	0.46
1:A:573:A:C5	1:A:574:A:C2	3.04	0.46
1:A:57:G:C5	1:A:58:C:C4	3.04	0.46
1:A:98:G:H2'	1:A:99:U:C6	2.51	0.46
10:J:40:LEU:HB2	10:J:69:ASN:CB	2.45	0.46
1:A:1056:U:C2'	1:A:1056:U:O2	2.64	0.45
1:A:1257:U:H4'	1:A:1258:G:O5'	2.16	0.45
1:A:1305:G:H1'	1:A:1332:A:N6	2.31	0.45
1:A:1368:G:N1	1:A:1369:C:C4	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:G:C2	1:A:175:C:C2	3.05	0.45
1:A:299:G:C6	1:A:300:A:C6	3.04	0.45
1:A:109:A:C2'	1:A:326:G:N2	2.79	0.45
1:A:377:G:H2'	1:A:378:G:H8	1.80	0.45
1:A:473:G:OP1	16:P:81:ARG:NH1	2.49	0.45
1:A:562:C:H41	1:A:884:U:H2'	1.81	0.45
1:A:88:A:O5'	1:A:88:A:H8	1.99	0.45
1:A:13:U:N3	1:A:915:A:N6	2.64	0.45
1:A:957:U:H2'	1:A:959:A:OP2	2.16	0.45
3:C:156:ARG:HH21	3:C:161:GLU:HA	1.81	0.45
1:A:8:A:C4	4:D:209:ARG:HD3	2.50	0.45
15:O:74:ASP:OD2	15:O:77:ARG:HB2	2.16	0.45
17:Q:74:LEU:HG	17:Q:75:ARG:HG2	1.96	0.45
24:Z:70:G:H2'	24:Z:71:C:O4'	2.16	0.45
1:A:1191:A:H2'	1:A:1192:C:H6	1.81	0.45
1:A:182:U:OP2	1:A:183:G:C8	2.69	0.45
1:A:348:G:H2'	1:A:349:A:H8	1.80	0.45
1:A:500:G:N2	1:A:501:C:C2	2.85	0.45
1:A:502:G:C2	1:A:503:C:C2	3.04	0.45
1:A:568:G:C6	1:A:883:C:N4	2.85	0.45
3:C:35:GLU:HB3	3:C:59:ARG:HH22	1.82	0.45
9:I:16:ARG:HB2	9:I:64:THR:HB	1.96	0.45
16:P:27:LYS:C	16:P:29:ASP:H	2.20	0.45
22:X:141:THR:HG22	22:X:165:LEU:HD21	1.99	0.45
1:A:1119:C:C2	1:A:1155:G:N2	2.84	0.45
1:A:128:G:H4'	17:Q:3:LYS:HG3	1.98	0.45
1:A:1508:G:C6	1:A:1509:C:C4	3.04	0.45
1:A:14:U:N3	1:A:17:U:OP2	2.47	0.45
1:A:416:G:C5	1:A:417:C:C4	3.04	0.45
1:A:429:U:H4'	1:A:430:A:O5'	2.16	0.45
1:A:500:G:C2	1:A:501:C:N3	2.84	0.45
1:A:682:G:H1	1:A:708:C:H42	1.64	0.45
1:A:76:C:C2'	1:A:77:G:H5'	2.46	0.45
1:A:841:U:H5'	1:A:848:C:O4'	2.17	0.45
6:F:39:LYS:HD2	6:F:39:LYS:H	1.80	0.45
6:F:9:VAL:HB	6:F:87:ARG:HB2	1.98	0.45
10:J:38:ILE:CG1	10:J:71:LEU:HB3	2.46	0.45
17:Q:9:VAL:O	17:Q:21:VAL:HA	2.17	0.45
22:X:17:ARG:HE	22:X:56:VAL:HG22	1.82	0.45
24:Z:48:C:C4'	24:Z:49:G:H5"	2.44	0.45
24:Z:70:G:C6	24:Z:71:C:N4	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1220:G:H2'	1:A:1221:G:O4'	2.17	0.45
1:A:1327:C:H2'	1:A:1328:C:C6	2.51	0.45
1:A:1515:C:H2'	1:A:1516:G:C8	2.52	0.45
1:A:165:C:H2'	1:A:166:G:C8	2.50	0.45
1:A:318:G:N2	1:A:336:C:C2	2.85	0.45
1:A:419:C:N4	1:A:424:G:H1	2.13	0.45
1:A:505:G:C6	1:A:535:A:C2	3.04	0.45
1:A:769:G:H2'	1:A:769:G:N3	2.29	0.45
1:A:916:G:H2'	1:A:917:G:H8	1.81	0.45
1:A:947:G:C6	1:A:948:C:C4	3.04	0.45
1:A:760:G:O2'	17:Q:98:LEU:HB3	2.15	0.45
19:S:6:LYS:HD2	19:S:7:LYS:H	1.80	0.45
1:A:1070:U:H2'	1:A:1071:C:C6	2.51	0.45
1:A:1086:U:H3	1:A:1099:G:H22	1.62	0.45
1:A:986:A:C6	1:A:1220:G:N1	2.85	0.45
1:A:1256:A:H62	1:A:1278:U:H1'	1.82	0.45
1:A:42:G:C6	1:A:43:C:C4	3.05	0.45
1:A:893:C:H2'	1:A:894:G:O4'	2.17	0.45
12:L:53:ARG:NH1	12:L:53:ARG:HG2	2.28	0.45
1:A:1171:G:C2	1:A:1172:C:C2	3.05	0.45
1:A:1207:G:C2	1:A:1208:C:C2	3.05	0.45
1:A:129(A):G:O2'	1:A:130:A:OP2	2.34	0.45
1:A:1353:G:C2	1:A:1354:C:C4	3.05	0.45
1:A:790:A:H2'	1:A:791:G:C8	2.52	0.45
2:B:189:ASP:HB3	2:B:205:ASP:H	1.81	0.45
2:B:28:PHE:CD2	2:B:190:THR:HA	2.52	0.45
1:A:407:G:H5"	4:D:115:ARG:HD3	1.99	0.45
4:D:64:LEU:HG	4:D:198:VAL:HG21	1.99	0.45
1:A:1080:A:H5"	5:E:16:THR:HG21	1.98	0.45
8:H:85:ARG:C	8:H:85:ARG:HD3	2.37	0.45
1:A:1466:C:H2'	1:A:1467:G:O4'	2.17	0.45
1:A:1489:G:C2	1:A:1490:C:C2	3.05	0.45
1:A:431:A:H2'	1:A:432:A:O4'	2.17	0.45
1:A:692:U:H2'	1:A:694:A:OP2	2.17	0.45
3:C:6:HIS:CD2	3:C:9:GLY:H	2.30	0.45
24:Z:11:A:H2'	24:Z:12:G:H8	1.82	0.45
1:A:1216:G:H5"	14:N:5:ALA:CB	2.47	0.45
1:A:1282:C:H2'	1:A:1282:C:O2	2.17	0.45
1:A:161:A:H2'	1:A:162:A:O4'	2.17	0.45
1:A:623:C:H2'	1:A:624:C:O4'	2.17	0.45
1:A:643:C:H2'	1:A:644:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:661:G:C2	1:A:745:C:N3	2.85	0.45
1:A:683:G:C2	1:A:708:C:N3	2.85	0.45
1:A:885:G:H1	1:A:912:C:H42	1.64	0.45
1:A:903:G:C2	1:A:904:C:C2	3.05	0.45
2:B:187:LEU:CD1	2:B:205:ASP:HA	2.47	0.45
9:I:4:TYR:HA	9:I:87:GLN:NE2	2.32	0.45
1:A:1081:G:P	5:E:16:THR:HG22	2.57	0.45
1:A:1207:G:C6	1:A:1208:C:C4	3.05	0.45
4:D:138:TYR:C	4:D:138:TYR:CD1	2.90	0.45
5:E:71:LEU:HD11	5:E:115:VAL:HG22	1.99	0.45
10:J:38:ILE:HG12	10:J:71:LEU:CB	2.47	0.45
19:S:6:LYS:HB2	19:S:7:LYS:HE3	1.99	0.45
23:Y:23:C:H2'	23:Y:24:A:O4'	2.17	0.45
1:A:1012:U:H2'	1:A:1013:G:O4'	2.17	0.45
1:A:1050:G:C6	1:A:1051:C:N4	2.85	0.45
1:A:1486:G:C2	1:A:1487:G:O4'	2.70	0.45
1:A:725:G:C6	1:A:726:C:N4	2.85	0.45
1:A:885:G:C2	1:A:913:A:C2	3.05	0.45
17:Q:68:ARG:HG3	17:Q:68:ARG:O	2.17	0.45
17:Q:91:ARG:O	17:Q:94:ASN:HB2	2.17	0.45
23:Y:23:C:H2'	23:Y:24:A:C8	2.52	0.45
1:A:1099:G:C2	1:A:1100:C:O2	2.71	0.44
1:A:1196:U:O2'	1:A:1197:G:OP2	2.24	0.44
1:A:1241:G:C2	1:A:1242:C:C2	3.04	0.44
1:A:1406:U:H2'	1:A:1407:C:C6	2.52	0.44
1:A:284:G:H2'	1:A:285:G:C8	2.53	0.44
1:A:316:G:H1	1:A:337:C:H42	1.64	0.44
1:A:41:G:H2'	1:A:42:G:H8	1.82	0.44
1:A:568:G:C6	1:A:569:C:N4	2.85	0.44
1:A:740:U:H2'	1:A:741:G:H8	1.82	0.44
1:A:928:G:H1	1:A:1389:C:N4	2.15	0.44
1:A:936:C:H2'	1:A:937:A:O4'	2.16	0.44
1:A:976:G:C5	1:A:1362:C:H5	2.35	0.44
10:J:57:LYS:HG2	10:J:58:ASP:N	2.32	0.44
19:S:11:VAL:HA	19:S:38:SER:CB	2.45	0.44
24:Z:24:U:H2'	24:Z:25:C:H6	1.81	0.44
1:A:1230:C:H5'	24:Z:30:G:H5"	1.99	0.44
1:A:1038:C:C5	1:A:1039:C:H5	2.35	0.44
1:A:1348:U:C2	1:A:1349:A:C8	3.05	0.44
1:A:19:C:N3	1:A:917:G:C6	2.85	0.44
1:A:237:C:H5"	17:Q:25:ARG:CZ	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:A:C2	1:A:482:A:C6	3.04	0.44
1:A:769:G:H4'	1:A:1513:A:H4'	1.99	0.44
6:F:8:ILE:CD1	6:F:63:TYR:HD2	2.30	0.44
10:J:70:ARG:HA	10:J:70:ARG:HD3	1.61	0.44
11:K:33:THR:HA	11:K:39:PRO:HA	1.98	0.44
19:S:22:LEU:HA	19:S:25:LYS:HB2	1.99	0.44
22:X:88:ILE:HG21	22:X:106:ILE:HD11	1.99	0.44
1:A:113:G:H1'	1:A:354:G:H5'	1.99	0.44
12:L:90:VAL:HG11	12:L:93:LEU:HD12	2.00	0.44
12:L:6:THR:O	12:L:9:GLN:HB2	2.17	0.44
15:O:4:THR:HB	15:O:6:GLU:OE2	2.17	0.44
20:T:22:ARG:HA	20:T:25:ARG:HG2	2.00	0.44
23:Y:36:A:H2'	23:Y:37:U:O4'	2.17	0.44
1:A:1030:C:N4	1:A:1031:G:H1	2.15	0.44
1:A:105:G:H2'	1:A:106:C:C6	2.51	0.44
1:A:1076:C:N3	1:A:1082:G:C2	2.85	0.44
1:A:1222:G:C2	1:A:1223:C:C2	3.06	0.44
1:A:42:G:N1	1:A:43:C:C2	2.86	0.44
1:A:590:C:C2	1:A:650:G:C2	3.05	0.44
1:A:881:G:C6	1:A:882:C:C4	3.05	0.44
1:A:91:C:C6	1:A:91:C:OP2	2.70	0.44
1:A:989:C:H2'	1:A:990:C:H6	1.82	0.44
1:A:413:G:N1	4:D:36:ARG:NH1	2.65	0.44
4:D:201:GLN:HE22	5:E:116:THR:HA	1.83	0.44
7:G:115:ARG:HG2	7:G:116:ALA:H	1.82	0.44
11:K:65:ALA:HB1	11:K:98:LEU:HD12	1.99	0.44
15:O:54:ARG:HG3	15:O:55:GLY:N	2.31	0.44
20:T:43:LEU:HB3	20:T:52:ALA:CB	2.47	0.44
20:T:72:LEU:HD22	20:T:77:ALA:CA	2.48	0.44
22:X:89:LYS:HG2	22:X:119:THR:HB	1.98	0.44
24:Z:11:A:H2'	24:Z:12:G:C8	2.53	0.44
1:A:1028:C:H2'	1:A:1029:C:O4'	2.18	0.44
1:A:1187:G:C6	1:A:1188:A:C6	3.06	0.44
1:A:1462:G:N1	1:A:1463:C:C4	2.86	0.44
1:A:291:C:O2	1:A:310:G:C2	2.71	0.44
1:A:409:G:H3'	1:A:410:G:H8	1.83	0.44
1:A:42:G:C2	1:A:43:C:C2	3.06	0.44
1:A:734:G:C6	1:A:735:C:C4	3.06	0.44
1:A:774:G:N2	1:A:806:C:C2	2.86	0.44
1:A:841:U:H5"	1:A:841:U:C6	2.45	0.44
1:A:861:G:C2	1:A:862:C:C2	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:922:G:C2	1:A:923:A:C4	3.06	0.44
4:D:138:TYR:C	4:D:138:TYR:HD1	2.21	0.44
1:A:430:A:P	4:D:8:VAL:H	2.40	0.44
7:G:37:ASN:HD21	9:I:42:ARG:H	1.64	0.44
13:M:108:ARG:O	13:M:112:GLY:N	2.50	0.44
19:S:5:LEU:HD23	19:S:6:LYS:HE3	1.99	0.44
24:Z:31:G:H2'	24:Z:32:OMC:O4'	2.18	0.44
24:Z:49:G:C2	24:Z:66:C:N3	2.86	0.44
1:A:1115:C:C2	1:A:1186:G:N2	2.86	0.44
1:A:1060:C:C2	1:A:1198:G:C2	3.06	0.44
1:A:1418:A:H3'	1:A:1419:G:H8	1.83	0.44
1:A:1456:G:C2'	1:A:1457:G:O4'	2.64	0.44
1:A:284:G:H2'	1:A:285:G:H8	1.83	0.44
1:A:344:A:H5"	1:A:345:C:H5	1.83	0.44
1:A:408:A:H2'	1:A:409:G:O4'	2.18	0.44
1:A:500:G:C2	1:A:501:C:C2	3.06	0.44
1:A:501:C:H2'	1:A:502:G:C8	2.52	0.44
1:A:548:G:C2	1:A:549:C:C2	3.06	0.44
1:A:577:G:N2	1:A:578:C:C2	2.85	0.44
1:A:608:A:C4	1:A:609:A:C8	3.06	0.44
1:A:763:G:C2	1:A:764:C:C2	3.05	0.44
4:D:173:TRP:CZ3	4:D:193:ASP:HB3	2.53	0.44
5:E:91:LEU:HD21	5:E:110:LEU:HD21	2.00	0.44
6:F:37:VAL:HG13	6:F:65:VAL:HG12	1.99	0.44
8:H:86:ILE:HD11	8:H:136:GLU:HB2	1.99	0.44
1:A:1371:G:OP1	9:I:11:LYS:O	2.35	0.44
1:A:1225:A:H5"	1:A:1226:C:OP2	2.17	0.44
1:A:276:G:C6	1:A:277:C:C4	3.06	0.44
1:A:329:A:H4'	1:A:330:C:OP1	2.17	0.44
1:A:373:A:P	1:A:373:A:H3'	2.58	0.44
1:A:456:C:C2	1:A:476:G:C2	3.05	0.44
1:A:446:G:N2	1:A:489:C:C2	2.86	0.44
4:D:186:LEU:HB2	4:D:187:ARG:H	1.57	0.44
22:X:135:ARG:O	22:X:139:ARG:HB2	2.18	0.44
1:A:1064:G:N2	1:A:1190:G:H2'	2.33	0.44
1:A:1515:C:H2'	1:A:1516:G:H8	1.82	0.44
1:A:301:G:C4	1:A:302:G:C8	3.06	0.44
1:A:715:A:H2'	1:A:716:A:C8	2.53	0.44
1:A:862:C:H2'	1:A:863:U:O4'	2.17	0.44
1:A:926:G:H3'	1:A:1505:G:H21	1.83	0.44
2:B:19:HIS:HB3	2:B:189:ASP:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:97:TRP:CH2	2:B:101:MET:HB2	2.53	0.44
3:C:35:GLU:HG2	3:C:95:THR:HG22	1.99	0.44
4:D:120:LEU:HD11	4:D:157:LEU:HD11	1.99	0.44
1:A:751:U:H4'	15:O:24:SER:HA	2.00	0.44
22:X:3:LYS:CB	22:X:66:ARG:HH22	2.21	0.44
24:Z:67:C:H2'	24:Z:68:C:C6	2.53	0.44
1:A:1200:C:O2	1:A:1200:C:H2'	2.17	0.44
1:A:324:G:OP2	1:A:324:G:H8	2.01	0.44
1:A:792:A:H4'	1:A:793:U:C5'	2.48	0.44
1:A:79:G:H3'	1:A:80:G:H8	1.83	0.44
1:A:820:U:H4'	1:A:821:G:OP2	2.17	0.44
1:A:836:G:H2'	1:A:837:G:C8	2.53	0.44
1:A:865:A:C2	1:A:866:C:C2	3.06	0.44
1:A:975:A:H4'	1:A:976:G:O5'	2.18	0.44
3:C:113:ALA:N	3:C:114:PRO:CD	2.81	0.44
4:D:25:ARG:C	4:D:27:TYR:N	2.71	0.44
8:H:14:ARG:NH2	8:H:83:ILE:O	2.51	0.44
12:L:7:ILE:HG12	12:L:8:ASN:H	1.83	0.44
23:Y:31:U:H2'	23:Y:32:A:O4'	2.18	0.44
24:Z:56:C:H2'	24:Z:57:A:C8	2.53	0.44
1:A:1022:G:H2'	1:A:1023:G:C8	2.53	0.43
1:A:1233:G:C2	1:A:1234:C:C2	3.06	0.43
1:A:504:C:C2	1:A:542:G:C2	3.06	0.43
1:A:544:G:H2'	1:A:545:C:O4'	2.17	0.43
1:A:616:G:H2'	1:A:617:G:C8	2.52	0.43
1:A:825:G:C2	1:A:826:C:C2	3.06	0.43
1:A:886:G:C4	1:A:887:G:C8	3.06	0.43
6:F:3:ARG:HG3	6:F:93:SER:HB3	1.99	0.43
10:J:45:ARG:O	10:J:64:GLU:HA	2.18	0.43
10:J:9:ARG:HG3	10:J:95:GLU:HB3	2.00	0.43
12:L:117:ARG:HD2	12:L:122:THR:HB	2.00	0.43
19:S:30:LEU:HD21	19:S:59:PRO:HB3	1.99	0.43
1:A:262:A:H4'	20:T:75:ASN:OD1	2.18	0.43
22:X:5:TYR:CD2	22:X:48:VAL:HG12	2.53	0.43
22:X:90:PHE:HD1	22:X:94:ILE:CD1	2.30	0.43
24:Z:22:G:N2	24:Z:23:C:C2	2.86	0.43
1:A:1228:C:H6	1:A:1228:C:H5"	1.83	0.43
1:A:1498:U:H1'	1:A:1499:A:N7	2.32	0.43
1:A:374:A:C6	1:A:375:U:C4	3.05	0.43
1:A:383:A:C5	1:A:384:G:H1'	2.53	0.43
1:A:643:C:H2'	1:A:644:G:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:673:G:H2'	1:A:674:G:C8	2.52	0.43
1:A:80:G:H3'	1:A:81:U:C5'	2.48	0.43
2:B:132:LYS:O	2:B:136:VAL:HB	2.18	0.43
2:B:73:THR:HG23	2:B:96:ARG:HA	2.00	0.43
3:C:154:SER:HB3	3:C:165:THR:HG23	1.99	0.43
1:A:413:G:H1	4:D:36:ARG:NH1	2.16	0.43
24:Z:70:G:C5	24:Z:71:C:C4	3.06	0.43
1:A:1418:A:H8	1:A:1482:G:H21	1.66	0.43
1:A:148:G:C2	1:A:149:A:C5	3.06	0.43
1:A:1501:C:N4	1:A:1504:G:C2	2.85	0.43
1:A:391:G:H2'	1:A:392:G:O4'	2.18	0.43
1:A:538:G:H5"	12:L:114:LYS:HB2	2.00	0.43
1:A:542:G:H2'	1:A:543:C:C6	2.53	0.43
1:A:670:G:H1	1:A:736:C:H42	1.65	0.43
1:A:923:A:H2'	1:A:924:C:O4'	2.19	0.43
1:A:941:G:H2'	1:A:942:G:O4'	2.17	0.43
1:A:974:A:H4'	1:A:975:A:H3'	2.00	0.43
1:A:987:G:H2'	1:A:988:G:C8	2.53	0.43
16:P:26:ARG:HH21	16:P:31:LYS:HB3	1.83	0.43
20:T:63:ILE:HG23	20:T:77:ALA:HB1	2.00	0.43
22:X:147:LEU:O	22:X:167:PRO:HA	2.18	0.43
1:A:1231:G:C6	1:A:1232:U:C4	3.06	0.43
1:A:941:G:N1	1:A:1343:G:C6	2.86	0.43
1:A:333:G:C2	1:A:334:C:C4	3.06	0.43
1:A:549:C:H2'	1:A:550:G:C8	2.54	0.43
1:A:577:G:C6	1:A:578:C:C4	3.06	0.43
1:A:766:A:C2	1:A:814:A:C2	3.07	0.43
6:F:43:LEU:HB3	6:F:46:ARG:HD2	2.00	0.43
3:C:26:LYS:NZ	10:J:45:ARG:HE	2.16	0.43
16:P:59:TRP:HA	16:P:62:VAL:CG2	2.49	0.43
22:X:104:GLY:HA2	22:X:107:LYS:HD2	1.99	0.43
1:A:1445:C:O2	1:A:1458:G:C2	2.71	0.43
1:A:1447:A:OP2	1:A:1452:C:C5	2.71	0.43
1:A:171:A:H2'	1:A:172:A:C8	2.54	0.43
1:A:109:A:C2'	1:A:326:G:H21	2.32	0.43
1:A:529:G:H5'	1:A:530:G:OP2	2.19	0.43
1:A:35:G:C6	1:A:550:G:N1	2.87	0.43
1:A:639:G:H2'	1:A:640:A:H8	1.83	0.43
1:A:761:G:C5	1:A:762:C:C4	3.07	0.43
1:A:900:A:H2'	1:A:901:A:C8	2.54	0.43
2:B:87:ARG:HH12	2:B:233:SER:H	1.64	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:76:ALA:O	6:F:80:ARG:HG3	2.19	0.43
1:A:1061:G:P	10:J:59:SER:OG	2.76	0.43
1:A:1233:G:C2	1:A:1234:C:C4	3.06	0.43
1:A:1262:C:H2'	1:A:1263:C:C6	2.53	0.43
1:A:147:G:C2	1:A:176:C:C2	3.07	0.43
1:A:1487:G:C2'	1:A:1488:G:C8	3.02	0.43
1:A:189(K):U:H2'	1:A:189(L):G:C8	2.53	0.43
1:A:264:U:H2'	1:A:265:G:O4'	2.18	0.43
12:L:27:LEU:HG	12:L:28:LYS:N	2.34	0.43
17:Q:56:VAL:HG13	17:Q:77:VAL:HB	2.01	0.43
1:A:1076:C:H2'	1:A:1077:G:C8	2.53	0.43
1:A:1438:G:N1	1:A:1439:C:C4	2.86	0.43
1:A:259:G:N2	1:A:268:C:C2	2.86	0.43
1:A:972:C:OP1	10:J:57:LYS:HD2	2.19	0.43
13:M:96:LEU:HD23	13:M:97:PRO:HD2	2.01	0.43
1:A:1327:C:C5'	21:V:20:LYS:HB2	2.44	0.43
1:A:1126:U:C2'	1:A:1126:U:O2	2.66	0.43
1:A:13:U:H3	1:A:915:A:N6	2.16	0.43
1:A:1440:C:C2	1:A:1462:G:N2	2.87	0.43
1:A:286:G:H2'	1:A:287:U:O4'	2.18	0.43
1:A:298:A:C6	1:A:299:G:C2	3.07	0.43
1:A:310:G:C6	1:A:311:C:C4	3.06	0.43
1:A:317:G:P	1:A:353:A:H61	2.41	0.43
1:A:551:U:H2'	1:A:552:U:C6	2.54	0.43
1:A:755:G:N1	1:A:756:C:C4	2.86	0.43
1:A:855:G:C6	1:A:856:C:C4	3.07	0.43
1:A:902:G:H2'	1:A:903:G:C8	2.54	0.43
1:A:977:A:H1'	1:A:982:U:O4	2.18	0.43
1:A:977:A:C2'	1:A:978:A:H5"	2.42	0.43
2:B:193:ASP:HB3	2:B:196:LEU:HD12	2.00	0.43
3:C:152:ILE:HG12	3:C:167:TRP:HD1	1.84	0.43
1:A:972:C:P	10:J:57:LYS:HD2	2.59	0.43
8:H:91:ARG:CD	12:L:7:ILE:HG21	2.46	0.43
22:X:120:ILE:HG22	22:X:121:MET:N	2.33	0.43
22:X:14:LYS:HG3	22:X:14:LYS:H	1.43	0.43
1:A:1134:G:H1	1:A:1140:C:N4	2.15	0.43
1:A:1135:U:O2'	1:A:1138:G:O6	2.37	0.43
1:A:1315:U:H2'	1:A:1316:G:O4'	2.19	0.43
1:A:1526:G:C6	1:A:1527:C:N4	2.87	0.43
1:A:293:G:C6	1:A:294:U:C4	3.07	0.43
1:A:59:A:H3'	1:A:331:G:H22	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:C:C4	1:A:72:C:C5	3.07	0.43
4:D:206:PHE:C	4:D:206:PHE:CD1	2.92	0.43
1:A:412:A:C1'	4:D:35:ARG:HH12	2.31	0.43
10:J:27:ALA:CB	10:J:34:VAL:HG21	2.48	0.43
12:L:46:LYS:HB3	12:L:48:PRO:HD2	1.99	0.43
19:S:53:ASN:HD22	19:S:53:ASN:HA	1.60	0.43
1:A:1176:A:H2'	1:A:1177:G:C8	2.53	0.43
1:A:119:A:H2'	1:A:240:C:H41	1.84	0.43
1:A:246:A:N3	1:A:247:G:H1'	2.33	0.43
1:A:289:G:N1	1:A:290:C:C4	2.87	0.43
1:A:707:C:H4'	11:K:20:TYR:CG	2.54	0.43
3:C:6:HIS:NE2	3:C:8:ILE:HB	2.34	0.43
4:D:120:LEU:O	4:D:125:HIS:HB2	2.19	0.43
8:H:64:LYS:HB3	8:H:79:VAL:HG11	2.01	0.43
9:I:2:GLU:HG2	9:I:20:ARG:HG2	2.00	0.43
10:J:50:ILE:HD13	14:N:41:ARG:HH11	1.84	0.43
10:J:6:ILE:CG1	10:J:72:VAL:CB	2.86	0.43
1:A:1492:A:N7	12:L:47:LYS:HA	2.34	0.43
12:L:5:PRO:HB2	12:L:6:THR:H	1.65	0.43
22:X:118:VAL:HG12	22:X:137:LEU:CD2	2.49	0.43
22:X:11:ILE:HD13	22:X:45:LEU:HD23	2.00	0.43
22:X:54:PRO:HA	22:X:55:PRO:HD2	1.89	0.43
1:A:63:C:H42	1:A:104:G:H1	1.66	0.42
1:A:1358:U:H2'	1:A:1359:C:O4'	2.19	0.42
1:A:235:C:H2'	1:A:236:G:H8	1.84	0.42
1:A:390:C:H2'	1:A:391:G:C8	2.54	0.42
2:B:25:ASN:HA	2:B:26:PRO:HD3	1.75	0.42
2:B:93:VAL:HG11	2:B:97:TRP:CD1	2.45	0.42
1:A:1347:G:H8	9:I:107:ARG:HB3	1.79	0.42
10:J:62:HIS:HB2	14:N:59:ALA:CB	2.46	0.42
24:Z:51:C:N4	24:Z:63:G:H1	2.17	0.42
1:A:105:G:C6	1:A:106:C:C4	3.06	0.42
1:A:109:A:H5'	1:A:110:C:H5	1.83	0.42
1:A:1499:A:C4	1:A:1500:A:C8	3.07	0.42
1:A:189(C):C:C2	1:A:189(I):G:N2	2.87	0.42
1:A:299:G:H2'	1:A:300:A:H8	1.82	0.42
1:A:319:G:C2	1:A:320:C:C2	3.07	0.42
1:A:542:G:C2	1:A:543:C:C2	3.07	0.42
1:A:58:C:H6	1:A:58:C:O5'	2.02	0.42
1:A:824:C:N4	1:A:876:G:H1	2.16	0.42
1:A:916:G:H2'	1:A:917:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:951:G:C6	1:A:1231:G:C6	3.08	0.42
15:O:26:GLU:HB3	15:O:81:LEU:HD21	2.01	0.42
1:A:1030(A):G:N2	1:A:1030(C):G:H3'	2.34	0.42
1:A:1220:G:H2'	1:A:1221:G:C8	2.55	0.42
1:A:1363:C:H5'	1:A:1363(A):A:O5'	2.19	0.42
1:A:931:C:C2	1:A:1387:G:N1	2.87	0.42
1:A:244:U:H4'	1:A:245:C:H5"	2.01	0.42
1:A:809:G:N1	1:A:810:C:C2	2.87	0.42
4:D:100:ARG:HH22	4:D:118:ARG:HH22	1.65	0.42
5:E:105:VAL:HB	5:E:106:PRO:CD	2.46	0.42
5:E:41:VAL:HG13	5:E:113:ALA:HA	2.02	0.42
7:G:81:GLY:N	23:Y:32:A:OP1	2.52	0.42
12:L:24:VAL:HG13	12:L:98:TYR:HE1	1.84	0.42
1:A:1050:G:N1	1:A:1051:C:C4	2.88	0.42
1:A:108:G:H5'	1:A:109:A:H5"	2.02	0.42
1:A:1106:G:C2	1:A:1107:C:C4	3.08	0.42
1:A:1206:G:H2'	1:A:1207:G:C8	2.55	0.42
1:A:234:C:H2'	1:A:235:C:H6	1.85	0.42
1:A:39:G:C6	1:A:40:C:C4	3.08	0.42
1:A:514:C:H42	1:A:537:G:H1	1.66	0.42
1:A:504:C:N3	1:A:542:G:C2	2.87	0.42
1:A:573:A:C6	1:A:574:A:N1	2.87	0.42
1:A:598:U:H4'	8:H:94:TYR:CG	2.55	0.42
24:Z:40:C:H2'	24:Z:41:C:C6	2.54	0.42
24:Z:18:G:N2	24:Z:57:A:H2'	2.35	0.42
1:A:1218:C:H2'	1:A:1219:U:C5	2.53	0.42
1:A:1356:G:C2	1:A:1367:C:C2	3.07	0.42
1:A:1540:U:H3	23:Y:25:A:H61	1.66	0.42
1:A:67:C:OP1	1:A:199:G:H4'	2.20	0.42
1:A:903:G:C6	1:A:904:C:C4	3.08	0.42
1:A:967:C:C4	1:A:968:A:C6	3.07	0.42
10:J:49:VAL:CG2	10:J:61:GLU:O	2.64	0.42
24:Z:18:G:H1'	24:Z:57:A:C2	2.55	0.42
24:Z:34:C:H2'	24:Z:35:A:C8	2.54	0.42
1:A:1171:G:H2'	1:A:1172:C:C6	2.55	0.42
1:A:932:C:C2	1:A:1386:G:C2	3.08	0.42
1:A:21:G:C2	1:A:22:G:C6	3.07	0.42
1:A:366:C:H1'	1:A:394:G:H22	1.85	0.42
2:B:186:ALA:CB	2:B:197:VAL:HG11	2.49	0.42
12:L:110:VAL:HG23	12:L:120:TYR:HB3	2.01	0.42
20:T:63:ILE:HA	20:T:72:LEU:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:53:G:N2	24:Z:62:C:C2	2.87	0.42
1:A:1081:G:H2'	1:A:1082:G:O4'	2.19	0.42
1:A:1228:C:H5'	13:M:108:ARG:NH2	2.27	0.42
1:A:1281:U:H3'	1:A:1282:C:C5	2.54	0.42
1:A:301:G:H2'	1:A:302:G:C8	2.52	0.42
4:D:53:ASP:O	4:D:57:ARG:HD2	2.19	0.42
12:L:87:GLY:HA2	12:L:98:TYR:HA	2.02	0.42
13:M:22:ILE:HB	13:M:25:ILE:HB	2.02	0.42
16:P:59:TRP:O	16:P:62:VAL:HG22	2.13	0.42
19:S:50:ALA:HA	19:S:58:VAL:O	2.19	0.42
1:A:1082:G:C2	1:A:1083:U:C2	3.08	0.42
1:A:1284:C:H2'	1:A:1285:A:N7	2.35	0.42
1:A:284:G:C2	1:A:285:G:C5	3.07	0.42
1:A:333:G:C2	1:A:334:C:C2	3.08	0.42
1:A:333:G:N1	1:A:334:C:C4	2.88	0.42
1:A:763:G:C6	1:A:764:C:C4	3.08	0.42
1:A:786:G:N2	1:A:797:C:C2	2.87	0.42
1:A:814:A:C8	1:A:816:A:C8	3.07	0.42
1:A:956:U:H2'	1:A:957:U:O4'	2.19	0.42
5:E:59:GLY:O	5:E:63:ARG:HD3	2.19	0.42
6:F:8:ILE:HD13	6:F:63:TYR:HD2	1.84	0.42
1:A:939:G:H5"	7:G:102:ARG:CZ	2.49	0.42
9:I:26:VAL:HB	9:I:33:PHE:CB	2.36	0.42
10:J:83:GLU:CA	10:J:86:MET:HB2	2.50	0.42
1:A:1081:G:C4	1:A:1082:G:C8	3.07	0.42
1:A:1419:G:C6	1:A:1420:C:C4	3.08	0.42
1:A:1423:G:C6	1:A:1424:C:C4	3.08	0.42
1:A:310:G:C2	1:A:311:C:C2	3.08	0.42
1:A:457:C:H2'	1:A:458:C:H6	1.85	0.42
1:A:501:C:H2'	1:A:502:G:H8	1.84	0.42
1:A:57:G:C6	1:A:58:C:C4	3.08	0.42
1:A:583:A:H2'	1:A:584:G:O4'	2.19	0.42
1:A:614:A:H2'	1:A:615:C:C6	2.55	0.42
1:A:620:C:N3	4:D:135:LEU:HD22	2.35	0.42
1:A:70:G:N1	1:A:100:C:N3	2.68	0.42
1:A:890:G:O2'	1:A:906:G:O6	2.28	0.42
8:H:100:ILE:HG13	8:H:100:ILE:H	1.60	0.42
1:A:1243:C:H2'	1:A:1244:C:O4'	2.20	0.42
1:A:1306:A:C2	1:A:1307:U:H1'	2.55	0.42
1:A:1494:G:C6	1:A:1495:U:C4	3.08	0.42
1:A:424:G:H2'	1:A:425:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:502:G:C6	1:A:503:C:C4	3.08	0.42
1:A:505:G:H2'	1:A:506:G:H8	1.84	0.42
1:A:559:A:H4'	1:A:560:U:C5'	2.44	0.42
1:A:823:G:C2	1:A:824:C:C2	3.07	0.42
6:F:6:VAL:HB	6:F:63:TYR:HB2	2.02	0.42
1:A:34:C:H1'	12:L:32:PHE:CZ	2.55	0.42
20:T:50:GLU:HG2	20:T:100:ILE:HB	2.02	0.42
21:V:10:ARG:HA	21:V:13:ILE:HD12	2.02	0.42
22:X:45:LEU:HA	22:X:59:ILE:HA	2.01	0.42
22:X:44:ASP:O	22:X:60:MET:O	2.37	0.42
22:X:70:GLN:O	22:X:74:LYS:HD2	2.19	0.42
1:A:1162:C:C2	1:A:1175:G:C2	3.08	0.41
1:A:1050:G:N1	1:A:1209:C:C2	2.88	0.41
1:A:129(A):G:N3	1:A:189(F):U:H5"	2.35	0.41
1:A:1353:G:C6	1:A:1354:C:N4	2.88	0.41
1:A:1514:C:H2'	1:A:1515:C:C6	2.55	0.41
1:A:216:G:C2	1:A:217:C:C2	3.08	0.41
1:A:399:G:C6	1:A:400:C:C4	3.08	0.41
1:A:402:G:C6	1:A:403:C:N4	2.88	0.41
1:A:774:G:C2	1:A:806:C:N3	2.88	0.41
1:A:823:G:N1	1:A:824:C:C4	2.88	0.41
2:B:80:ILE:HD11	2:B:208:ILE:HG22	2.02	0.41
1:A:412:A:N9	4:D:35:ARG:NH1	2.65	0.41
7:G:152:ALA:HB1	7:G:155:ARG:HH21	1.85	0.41
10:J:38:ILE:HG12	10:J:71:LEU:HB3	2.01	0.41
18:R:54:ARG:NH1	18:R:54:ARG:HB2	2.34	0.41
20:T:15:ARG:NH1	20:T:15:ARG:CG	2.80	0.41
1:A:1276:G:C2	1:A:1277:C:C2	3.09	0.41
1:A:1489:G:C6	1:A:1490:C:C4	3.08	0.41
1:A:456:C:H2'	1:A:457:C:C6	2.55	0.41
1:A:524:G:N2	1:A:525:C:N3	2.67	0.41
1:A:563:A:O2'	1:A:566:G:O2'	2.27	0.41
1:A:57:G:C2	1:A:58:C:C2	3.08	0.41
1:A:922:G:H2'	1:A:923:A:H8	1.83	0.41
1:A:929:G:C6	1:A:930:C:C4	3.08	0.41
6:F:8:ILE:HD13	6:F:63:TYR:CD2	2.55	0.41
15:O:17:ARG:HE	15:O:77:ARG:CD	2.31	0.41
21:V:3:LYS:HZ2	21:V:3:LYS:HG2	1.80	0.41
22:X:106:ILE:HA	22:X:116:VAL:HG21	2.01	0.41
1:A:102:G:N1	1:A:103:C:C4	2.88	0.41
1:A:1346:A:C8	1:A:1348:U:C2	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:542:G:O3'	4:D:14:ARG:NH2	2.52	0.41
1:A:548:G:N2	1:A:549:C:C2	2.87	0.41
1:A:673:G:H1	1:A:717:C:H42	1.68	0.41
1:A:911:U:OP2	12:L:97:ARG:NH2	2.52	0.41
1:A:985:C:H2'	1:A:986:A:C8	2.55	0.41
19:S:39:THR:HA	19:S:70:LYS:HA	2.01	0.41
20:T:72:LEU:HD13	20:T:77:ALA:CB	2.50	0.41
1:A:229:U:H2'	1:A:230:G:C8	2.55	0.41
1:A:256:U:H2'	1:A:257:G:H8	1.85	0.41
1:A:319:G:C6	1:A:320:C:C4	3.08	0.41
1:A:500:G:C2	1:A:501:C:C4	3.09	0.41
1:A:601:C:C2	1:A:638:G:C2	3.09	0.41
1:A:621:A:H2'	1:A:622:A:C8	2.56	0.41
1:A:867:G:C2	1:A:868:C:C2	3.08	0.41
1:A:929:G:C2	1:A:930:C:C2	3.09	0.41
2:B:163:PHE:HA	2:B:185:ILE:HB	2.01	0.41
4:D:105:VAL:HG13	4:D:110:PHE:HB2	2.02	0.41
4:D:62:GLN:HB3	4:D:66:ARG:NH1	2.35	0.41
10:J:34:VAL:H	10:J:75:ILE:HB	1.85	0.41
1:A:1076:C:H2'	1:A:1077:G:H8	1.86	0.41
1:A:1202:G:H2'	1:A:1203:C:O4'	2.21	0.41
1:A:1485:U:H2'	1:A:1486:G:C8	2.55	0.41
1:A:1526:G:C2	1:A:1527:C:C2	3.08	0.41
1:A:109:A:C6	1:A:326:G:C6	3.08	0.41
1:A:39:G:C2	1:A:40:C:C2	3.08	0.41
1:A:584:G:C5	1:A:585:G:N7	2.88	0.41
1:A:689:C:H2'	1:A:690:G:O4'	2.21	0.41
2:B:142:LEU:O	2:B:146:GLN:HB2	2.21	0.41
2:B:48:MET:HA	2:B:51:LEU:HD12	2.02	0.41
3:C:150:LYS:HB3	3:C:201:TYR:HB2	2.02	0.41
13:M:78:ILE:O	13:M:82:MET:N	2.49	0.41
1:A:391:G:H4'	16:P:8:ARG:HH22	1.86	0.41
1:A:1132:C:H2'	1:A:1133:G:C8	2.55	0.41
1:A:1162:C:C2	1:A:1175:G:N2	2.89	0.41
1:A:1186:G:H4'	9:I:110:GLU:HG3	2.02	0.41
1:A:342:C:H42	1:A:347:G:H1	1.69	0.41
1:A:725:G:C2	1:A:726:C:C2	3.09	0.41
2:B:55:PHE:HD1	2:B:58:ILE:HD12	1.85	0.41
3:C:123:GLN:HE22	3:C:140:ARG:HH22	1.67	0.41
3:C:6:HIS:HA	3:C:7:PRO:HD3	1.74	0.41
22:X:22:ASP:HB2	22:X:24:LYS:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1030(A):G:N2	1:A:1030(D):A:C8	2.88	0.41
1:A:1233:G:C2	1:A:1234:C:N3	2.89	0.41
1:A:125:U:H2'	1:A:126:G:C8	2.55	0.41
1:A:1286:A:H3'	1:A:1286:A:H8	1.85	0.41
1:A:109:A:C4	1:A:326:G:C2	3.08	0.41
1:A:363:A:C6	12:L:31:PRO:HD2	2.55	0.41
1:A:556:C:H2'	1:A:557:G:O4'	2.20	0.41
1:A:918:A:H2'	1:A:919:A:C8	2.56	0.41
1:A:922:G:C2'	1:A:923:A:C8	2.99	0.41
1:A:939:G:C2	1:A:940:C:C2	3.08	0.41
1:A:99:U:C2	1:A:100:C:C5	3.08	0.41
4:D:9:CYS:SG	4:D:26:CYS:SG	3.18	0.41
5:E:93:PRO:HG3	8:H:105:ARG:HD3	2.03	0.41
7:G:57:GLU:HA	7:G:58:PRO:HD2	1.90	0.41
9:I:4:TYR:CZ	9:I:88:TYR:HD1	2.39	0.41
18:R:44:LEU:HD23	18:R:48:GLY:HA2	2.03	0.41
22:X:92:VAL:HG11	22:X:129:HIS:CD2	2.55	0.41
1:A:1101:A:H4'	1:A:1102:A:O5'	2.20	0.41
1:A:542:G:N1	1:A:543:C:C4	2.88	0.41
1:A:567:G:H2'	1:A:568:G:O4'	2.21	0.41
1:A:687:A:H4'	1:A:688:G:O5'	2.20	0.41
1:A:832:C:O2	1:A:855:G:C2	2.74	0.41
4:D:138:TYR:HD1	4:D:139:ARG:N	2.19	0.41
10:J:79:ARG:O	10:J:83:GLU:HB2	2.21	0.41
10:J:84:GLN:HB2	10:J:84:GLN:HE21	1.64	0.41
10:J:92:THR:H	10:J:94:VAL:HG23	1.86	0.41
13:M:22:ILE:HG22	13:M:24:GLY:N	2.26	0.41
17:Q:29:HIS:HD2	17:Q:36:ILE:HD11	1.86	0.41
24:Z:54:5MU:N3	24:Z:58:A:N7	2.69	0.41
24:Z:71:C:C2'	24:Z:72:A:H8	2.13	0.41
1:A:1106:G:C2	1:A:1107:C:C2	3.09	0.41
1:A:1144:G:H21	1:A:1146:A:H62	1.69	0.41
1:A:1410:G:C5	1:A:1411:C:C4	3.09	0.41
1:A:402:G:C2	1:A:403:C:C2	3.09	0.41
1:A:524:G:N1	1:A:525:C:N4	2.69	0.41
1:A:70:G:N1	1:A:100:C:C2	2.89	0.41
1:A:861:G:C6	1:A:862:C:C4	3.09	0.41
2:B:109:SER:O	2:B:112:VAL:HG12	2.21	0.41
2:B:178:ARG:NE	2:B:196:LEU:O	2.47	0.41
3:C:9:GLY:HA3	14:N:49:HIS:HA	2.03	0.41
10:J:30:SER:HB3	10:J:84:GLN:HE22	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:27:ALA:CB	10:J:85:LEU:HD11	2.50	0.41
19:S:6:LYS:CD	19:S:7:LYS:H	2.33	0.41
1:A:103:C:H2'	1:A:104:G:H8	1.86	0.41
1:A:1050:G:C2	1:A:1051:C:C2	3.09	0.41
1:A:1088:G:C6	1:A:1089:G:C5	3.09	0.41
1:A:1253:G:C2	1:A:1254:C:C2	3.09	0.41
1:A:1387:G:C2	1:A:1388:C:C2	3.09	0.41
1:A:746:A:H2'	1:A:747:C:H6	1.84	0.41
1:A:748:C:H1'	1:A:749:C:C5	2.55	0.41
1:A:886:G:C6	1:A:912:C:N3	2.89	0.41
1:A:895:G:C2	1:A:896:C:C2	3.08	0.41
1:A:957:U:O2	1:A:960:U:C2	2.73	0.41
2:B:19:HIS:CE1	2:B:206:ASP:HB2	2.56	0.41
1:A:532:A:H62	3:C:193:TYR:HB3	1.86	0.41
13:M:15:VAL:O	13:M:19:LEU:HG	2.21	0.41
18:R:26:LEU:HD11	18:R:39:VAL:HG22	2.03	0.41
18:R:32:ARG:HA	18:R:69:THR:CG2	2.45	0.41
1:A:70:G:C6	1:A:100:C:N3	2.89	0.41
1:A:1327:C:H2'	1:A:1328:C:H6	1.86	0.41
1:A:1368:G:H5"	14:N:61:TRP:HZ2	1.86	0.41
1:A:137:C:H2'	1:A:138:G:H8	1.86	0.41
1:A:1419:G:C2	1:A:1420:C:C2	3.09	0.41
1:A:378:G:C2	1:A:379:C:C2	3.08	0.41
1:A:677:U:H3	1:A:713:G:H22	1.69	0.41
2:B:87:ARG:NH1	2:B:233:SER:H	2.19	0.41
4:D:26:CYS:HA	4:D:31:CYS:HB2	2.03	0.41
8:H:82:HIS:NE2	8:H:84:ARG:HB2	2.35	0.41
10:J:76:ASN:HA	10:J:77:PRO:HD2	1.96	0.41
22:X:119:THR:HG22	22:X:160:ASP:HB3	2.01	0.41
1:A:1102:A:H2'	1:A:1103:C:C6	2.56	0.40
1:A:1116:C:H3'	1:A:1117:G:H5"	2.02	0.40
1:A:1193:G:N2	1:A:1194:U:C2	2.89	0.40
1:A:1298:C:H4'	1:A:1299:A:O5'	2.22	0.40
1:A:1456:G:C2	1:A:1457:G:N9	2.88	0.40
1:A:245:C:C2	1:A:284:G:C2	3.08	0.40
1:A:252:U:H2'	1:A:253:U:C6	2.56	0.40
1:A:35:G:C2	1:A:36:C:N3	2.89	0.40
1:A:522:C:H2'	1:A:523:A:C8	2.56	0.40
1:A:575:G:H4'	1:A:576:G:C5'	2.48	0.40
1:A:779:C:N4	1:A:780:A:N1	2.69	0.40
1:A:943:U:H2'	1:A:944:G:H8	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:25:ASN:H	2:B:191:ASP:HA	1.86	0.40
4:D:175:SER:O	4:D:183:GLY:HA2	2.20	0.40
4:D:196:LEU:HD13	4:D:197:PRO:HD2	2.03	0.40
1:A:9:G:H5'	5:E:122:GLU:CD	2.41	0.40
10:J:38:ILE:O	10:J:71:LEU:N	2.49	0.40
16:P:58:TYR:O	16:P:62:VAL:HG22	2.21	0.40
1:A:1031:G:O5'	1:A:1031:G:H8	2.04	0.40
1:A:1065:U:O2'	1:A:1066:C:OP2	2.30	0.40
1:A:1071:C:H2'	1:A:1072:G:C8	2.57	0.40
1:A:976:G:C4	1:A:1363(A):A:N6	2.89	0.40
1:A:91:C:H6	1:A:91:C:OP2	2.03	0.40
1:A:980:C:C5	1:A:981:U:C2	3.10	0.40
2:B:208:ILE:HA	2:B:211:ILE:HD12	2.03	0.40
2:B:236:TYR:HA	2:B:239:VAL:HG23	2.04	0.40
4:D:79:PHE:CZ	4:D:204:ILE:HA	2.57	0.40
5:E:34:VAL:HG21	5:E:63:ARG:NE	2.36	0.40
12:L:71:PRO:HB2	12:L:120:TYR:HE1	1.85	0.40
14:N:7:ILE:O	14:N:7:ILE:HG22	2.21	0.40
19:S:58:VAL:HA	19:S:59:PRO:HD3	1.87	0.40
22:X:110:LEU:HD13	22:X:148:ALA:CB	2.51	0.40
1:A:1027:C:C2'	1:A:1028:C:H5'	2.51	0.40
1:A:1251:A:O5'	1:A:1251:A:H8	2.05	0.40
1:A:1261:A:N6	1:A:1274:G:O2'	2.55	0.40
1:A:932:C:C2	1:A:1386:G:N2	2.90	0.40
1:A:240:C:H2'	1:A:241:C:C6	2.57	0.40
1:A:457:C:H2'	1:A:458:C:C6	2.56	0.40
1:A:520:A:N1	1:A:536:C:H1'	2.36	0.40
2:B:36:ARG:HB2	2:B:41:ILE:HD13	2.02	0.40
1:A:363:A:OP2	12:L:34:ARG:HB3	2.21	0.40
8:H:91:ARG:HA	17:Q:34:LYS:HB3	2.03	0.40
19:S:80:TYR:CE2	19:S:82:GLY:HA3	2.56	0.40
20:T:26:ASN:ND2	20:T:71:THR:HA	2.36	0.40
22:X:17:ARG:HB2	22:X:54:PRO:HB2	2.03	0.40
1:A:1064:G:C4	1:A:1066:C:C4	3.09	0.40
1:A:1253:G:C6	1:A:1254:C:C4	3.09	0.40
1:A:1432:G:HO2'	1:A:1433:A:H8	1.67	0.40
1:A:199:G:C2	1:A:219:C:N3	2.90	0.40
1:A:361:G:H2'	1:A:362:G:O4'	2.21	0.40
3:C:26:LYS:H	3:C:26:LYS:HG2	1.64	0.40
3:C:70:VAL:HB	3:C:71:ALA:H	1.81	0.40
10:J:51:ARG:HG3	14:N:45:ARG:NH1	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:31:ILE:HD13	19:S:31:ILE:HA	1.87	0.40
22:X:120:ILE:HG13	22:X:161:MET:HB3	2.03	0.40
1:A:104:G:C2	1:A:105:G:C5	3.09	0.40
1:A:1197:G:OP1	1:A:1198:G:OP2	2.40	0.40
1:A:1384:C:H2'	1:A:1385:G:H8	1.86	0.40
1:A:1430:C:C2	1:A:1471:G:N2	2.89	0.40
1:A:675:A:C4	1:A:676:A:C8	3.09	0.40
1:A:79:G:C3'	1:A:80:G:H8	2.34	0.40
1:A:876:G:C2	1:A:877:C:N3	2.89	0.40
1:A:985:C:N3	1:A:1221:G:C2	2.90	0.40
4:D:131:ARG:HB2	4:D:131:ARG:HH11	1.87	0.40
8:H:4:ASP:HA	8:H:5:PRO:HD3	1.80	0.40
10:J:6:ILE:HG22	10:J:98:ILE:HA	2.03	0.40
20:T:89:ARG:HG3	20:T:104:LEU:HD22	2.03	0.40
1:A:1305:G:OP2	21:V:5:ASP:HB2	2.22	0.40
22:X:5:TYR:CD2	22:X:65:TRP:HH2	2.40	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
2	B	232/256 (91%)	184 (79%)	33 (14%)	15 (6%)	1 26
3	C	204/239 (85%)	174 (85%)	26 (13%)	4 (2%)	9 54
4	D	206/209 (99%)	176 (85%)	26 (13%)	4 (2%)	10 54
5	E	148/162 (91%)	125 (84%)	19 (13%)	4 (3%)	6 47
6	F	99/101 (98%)	87 (88%)	7 (7%)	5 (5%)	2 31
7	G	153/156 (98%)	132 (86%)	18 (12%)	3 (2%)	9 54
8	H	136/138 (99%)	125 (92%)	9 (7%)	2 (2%)	13 58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	125/128 (98%)	104 (83%)	14 (11%)	7 (6%)	2	29
10	J	96/105 (91%)	79 (82%)	12 (12%)	5 (5%)	2	31
11	K	117/129 (91%)	94 (80%)	17 (14%)	6 (5%)	2	31
12	L	122/132 (92%)	95 (78%)	24 (20%)	3 (2%)	7	49
13	M	116/126 (92%)	100 (86%)	13 (11%)	3 (3%)	7	48
14	N	58/61 (95%)	44 (76%)	9 (16%)	5 (9%)	1	17
15	O	86/89 (97%)	77 (90%)	7 (8%)	2 (2%)	8	51
16	P	81/88 (92%)	71 (88%)	8 (10%)	2 (2%)	7	49
17	Q	97/105 (92%)	82 (84%)	10 (10%)	5 (5%)	2	31
18	R	71/88 (81%)	62 (87%)	8 (11%)	1 (1%)	14	59
19	S	80/93 (86%)	63 (79%)	12 (15%)	5 (6%)	2	27
20	T	97/106 (92%)	81 (84%)	11 (11%)	5 (5%)	2	31
21	V	22/27 (82%)	19 (86%)	1 (4%)	2 (9%)	1	16
22	X	160/171 (94%)	137 (86%)	17 (11%)	6 (4%)	4	39
All	All	2506/2709 (92%)	2111 (84%)	301 (12%)	94 (4%)	7	39

All (94) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	21	ARG
2	B	24	TRP
2	B	229	VAL
4	D	37	PRO
5	E	21	ALA
6	F	69	GLU
6	F	96	PRO
12	L	27	LEU
14	N	15	LYS
19	S	6	LYS
20	T	98	PRO
21	V	3	LYS
22	X	54	PRO
22	X	127	VAL
2	B	134	GLU
3	C	81	GLY
4	D	5	ILE
7	G	7	ALA

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Mol	Chain	Res	Type
7	G	153	HIS
9	I	41	VAL
9	I	58	HIS
9	I	119	ALA
10	J	34	VAL
10	J	55	LYS
11	K	14	VAL
11	K	50	TYR
11	K	55	LYS
11	K	126	ARG
12	L	16	GLU
12	L	45	PRO
14	N	14	PRO
17	Q	67	LYS
19	S	30	LEU
22	X	8	ASN
2	B	17	PHE
2	B	38	GLY
2	B	204	ASN
2	B	228	GLY
2	B	233	SER
3	C	3	ASN
3	C	51	GLY
6	F	93	SER
7	G	53	LYS
8	H	92	ARG
9	I	54	ASP
10	J	54	PHE
11	K	123	LYS
13	M	100	GLY
14	N	22	THR
15	O	88	ARG
17	Q	68	ARG
19	S	13	ASP
20	T	9	ASN
20	T	97	ALA
2	B	130	ARG
6	F	53	ALA
8	H	5	PRO
9	I	56	LEU
11	K	127	LYS
13	M	10	PRO

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Mol	Chain	Res	Type
14	N	23	ARG
16	P	30	GLY
17	Q	97	SER
17	Q	99	SER
20	T	95	ALA
21	V	6	ARG
2	B	23	ARG
4	D	150	GLU
16	P	31	LYS
18	R	87	ARG
20	T	49	ALA
22	X	55	PRO
22	X	56	VAL
2	B	78	GLN
5	E	38	GLN
6	F	68	PRO
14	N	17	LYS
15	O	18	PHE
19	S	80	TYR
4	D	41	GLY
22	X	59	ILE
2	B	208	ILE
2	B	232	PRO
5	E	128	PRO
9	I	22	GLY
9	I	44	VAL
10	J	37	PRO
10	J	91	PRO
13	M	113	PRO
19	S	8	GLY
3	C	80	GLY
17	Q	47	PRO
2	B	127	ILE
5	E	39	GLY

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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
2	B	202/220 (92%)	154 (76%)	48 (24%)	1 8
3	C	160/188 (85%)	121 (76%)	39 (24%)	1 7
4	D	180/181 (99%)	132 (73%)	48 (27%)	0 5
5	E	115/123 (94%)	83 (72%)	32 (28%)	0 4
6	F	90/90 (100%)	72 (80%)	18 (20%)	1 13
7	G	126/127 (99%)	103 (82%)	23 (18%)	2 16
8	H	119/119 (100%)	86 (72%)	33 (28%)	0 4
9	I	98/99 (99%)	76 (78%)	22 (22%)	1 10
10	J	87/92 (95%)	69 (79%)	18 (21%)	1 11
11	K	90/99 (91%)	67 (74%)	23 (26%)	0 6
12	L	104/109 (95%)	82 (79%)	22 (21%)	1 11
13	M	94/101 (93%)	79 (84%)	15 (16%)	3 23
14	N	49/50 (98%)	35 (71%)	14 (29%)	0 4
15	O	79/80 (99%)	53 (67%)	26 (33%)	0 3
16	P	72/74 (97%)	57 (79%)	15 (21%)	1 11
17	Q	94/97 (97%)	78 (83%)	16 (17%)	2 20
18	R	64/77 (83%)	47 (73%)	17 (27%)	0 5
19	S	71/80 (89%)	50 (70%)	21 (30%)	0 4
20	T	76/82 (93%)	56 (74%)	20 (26%)	0 6
21	V	19/22 (86%)	13 (68%)	6 (32%)	0 3
22	X	145/150 (97%)	121 (83%)	24 (17%)	3 21
All	All	2134/2260 (94%)	1634 (77%)	500 (23%)	3 8

All (500) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	8	LYS
2	B	10	LEU
2	B	11	LEU
2	B	16	HIS
2	B	17	PHE
2	B	21	ARG
2	B	23	ARG
2	B	24	TRP
2	B	41	ILE
2	B	44	LEU

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Mol	Chain	Res	Type
2	B	45	GLN
2	B	51	LEU
2	B	52	GLU
2	B	60	ASP
2	B	61	LEU
2	B	64	ARG
2	B	67	THR
2	B	76	GLN
2	B	83	MET
2	B	87	ARG
2	B	93	VAL
2	B	98	LEU
2	B	101	MET
2	B	102	LEU
2	B	107	THR
2	B	112	VAL
2	B	124	SER
2	B	129	GLU
2	B	130	ARG
2	B	144	ARG
2	B	156	LYS
2	B	157	ARG
2	B	163	PHE
2	B	168	THR
2	B	172	ILE
2	B	178	ARG
2	B	189	ASP
2	B	191	ASP
2	B	204	ASN
2	B	205	ASP
2	B	206	ASP
2	B	208	ILE
2	B	209	ARG
2	B	211	ILE
2	B	220	ASP
2	B	221	LEU
2	B	236	TYR
2	B	240	GLN
3	C	3	ASN
3	C	14	ILE
3	C	16	ARG
3	C	17	ASP

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Mol	Chain	Res	Type
3	C	20	SER
3	C	28	GLN
3	C	33	LEU
3	C	34	LEU
3	C	35	GLU
3	C	42	LEU
3	C	52	LEU
3	C	55	VAL
3	C	59	ARG
3	C	79	ARG
3	C	82	GLU
3	C	87	LEU
3	C	90	GLU
3	C	91	LEU
3	C	94	LEU
3	C	98	ASN
3	C	101	LEU
3	C	107	GLN
3	C	108	ASN
3	C	111	LEU
3	C	112	SER
3	C	119	ARG
3	C	131	ARG
3	C	138	VAL
3	C	139	GLN
3	C	175	LEU
3	C	177	THR
3	C	179	ARG
3	C	188	LEU
3	C	190	ARG
3	C	191	THR
3	C	193	TYR
3	C	196	LEU
3	C	204	LEU
3	C	206	GLU
4	D	3	ARG
4	D	5	ILE
4	D	13	ARG
4	D	15	GLU
4	D	24	GLU
4	D	34	GLU
4	D	45	GLN

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Mol	Chain	Res	Type
4	D	47	ARG
4	D	49	ARG
4	D	50	ARG
4	D	52	SER
4	D	53	ASP
4	D	56	VAL
4	D	59	ARG
4	D	64	LEU
4	D	66	ARG
4	D	70	ILE
4	D	78	LEU
4	D	104	VAL
4	D	108	LEU
4	D	112	VAL
4	D	115	ARG
4	D	118	ARG
4	D	119	GLN
4	D	120	LEU
4	D	122	ARG
4	D	131	ARG
4	D	132	ARG
4	D	134	ASP
4	D	138	TYR
4	D	141	ARG
4	D	144	ASP
4	D	146	ILE
4	D	150	GLU
4	D	155	LEU
4	D	168	ARG
4	D	174	LEU
4	D	176	LEU
4	D	178	VAL
4	D	181	MET
4	D	186	LEU
4	D	187	ARG
4	D	188	LEU
4	D	192	GLU
4	D	193	ASP
4	D	196	LEU
4	D	200	GLU
4	D	208	SER
5	E	11	ILE

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Mol	Chain	Res	Type
5	E	13	ILE
5	E	14	ARG
5	E	15	ARG
5	E	20	GLN
5	E	24	ARG
5	E	27	ARG
5	E	32	VAL
5	E	34	VAL
5	E	38	GLN
5	E	40	ARG
5	E	41	VAL
5	E	47	LYS
5	E	55	VAL
5	E	63	ARG
5	E	68	GLU
5	E	71	LEU
5	E	79	GLU
5	E	80	ILE
5	E	82	VAL
5	E	91	LEU
5	E	107	ARG
5	E	110	LEU
5	E	116	THR
5	E	118	ILE
5	E	123	LEU
5	E	126	ARG
5	E	131	ILE
5	E	142	LEU
5	E	143	ARG
5	E	148	VAL
5	E	152	ARG
6	F	10	LEU
6	F	15	ASP
6	F	19	LEU
6	F	21	LEU
6	F	24	GLU
6	F	36	ARG
6	F	39	LYS
6	F	40	VAL
6	F	45	LEU
6	F	47	ARG
6	F	61	LEU

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Mol	Chain	Res	Type
6	F	64	GLN
6	F	69	GLU
6	F	75	LEU
6	F	77	ARG
6	F	79	LEU
6	F	86	ARG
6	F	91	VAL
7	G	8	GLU
7	G	21	VAL
7	G	32	ARG
7	G	52	GLU
7	G	57	GLU
7	G	60	LYS
7	G	68	ASN
7	G	72	ARG
7	G	75	VAL
7	G	77	SER
7	G	84	ASN
7	G	90	GLU
7	G	91	VAL
7	G	94	ARG
7	G	95	ARG
7	G	96	GLN
7	G	106	GLN
7	G	113	GLU
7	G	136	LYS
7	G	137	LYS
7	G	140	ASP
7	G	142	GLU
7	G	156	TRP
8	H	8	ASP
8	H	11	THR
8	H	14	ARG
8	H	17	THR
8	H	18	ARG
8	H	23	SER
8	H	29	SER
8	H	34	GLU
8	H	37	ARG
8	H	41	ARG
8	H	49	GLU
8	H	50	ARG

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Mol	Chain	Res	Type
8	H	53	VAL
8	H	56	LYS
8	H	58	TYR
8	H	60	ARG
8	H	70	GLN
8	H	75	ARG
8	H	84	ARG
8	H	85	ARG
8	H	87	SER
8	H	92	ARG
8	H	103	VAL
8	H	104	ARG
8	H	105	ARG
8	H	109	ILE
8	H	119	LEU
8	H	120	THR
8	H	122	ARG
8	H	126	LYS
8	H	127	LEU
8	H	133	LEU
8	H	134	ILE
9	I	19	LEU
9	I	26	VAL
9	I	34	ASN
9	I	38	GLN
9	I	40	LEU
9	I	54	ASP
9	I	60	ASP
9	I	85	LEU
9	I	87	GLN
9	I	93	ARG
9	I	95	LYS
9	I	96	LEU
9	I	99	LEU
9	I	104	ARG
9	I	111	ARG
9	I	113	LYS
9	I	118	LYS
9	I	120	ARG
9	I	121	ARG
9	I	124	GLN
9	I	125	TYR

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Mol	Chain	Res	Type
9	I	128	ARG
10	J	5	ARG
10	J	8	LEU
10	J	16	LEU
10	J	17	ASP
10	J	38	ILE
10	J	42	THR
10	J	43	ARG
10	J	51	ARG
10	J	57	LYS
10	J	61	GLU
10	J	62	HIS
10	J	66	ARG
10	J	69	ASN
10	J	70	ARG
10	J	71	LEU
10	J	84	GLN
10	J	85	LEU
10	J	99	LYS
11	K	12	ARG
11	K	16	SER
11	K	18	ARG
11	K	29	ILE
11	K	40	ILE
11	K	41	THR
11	K	44	SER
11	K	48	ILE
11	K	54	ARG
11	K	57	THR
11	K	62	GLN
11	K	63	LEU
11	K	66	LEU
11	K	77	MET
11	K	78	GLN
11	K	87	THR
11	K	92	GLU
11	K	96	ARG
11	K	98	LEU
11	K	107	SER
11	K	109	VAL
11	K	116	HIS
11	K	117	ASN

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Mol	Chain	Res	Type
12	L	7	ILE
12	L	15	ARG
12	L	17	LYS
12	L	19	ARG
12	L	27	LEU
12	L	39	VAL
12	L	41	ARG
12	L	44	THR
12	L	53	ARG
12	L	59	ARG
12	L	67	THR
12	L	70	ILE
12	L	79	GLU
12	L	81	SER
12	L	84	LEU
12	L	86	ARG
12	L	93	LEU
12	L	97	ARG
12	L	104	VAL
12	L	122	THR
12	L	126	LYS
12	L	127	GLU
13	M	9	ILE
13	M	15	VAL
13	M	32	GLU
13	M	45	VAL
13	M	47	ASP
13	M	48	LEU
13	M	69	GLU
13	M	70	LEU
13	M	79	LYS
13	M	80	ARG
13	M	99	ARG
13	M	102	ARG
13	M	110	ARG
13	M	115	LYS
13	M	116	THR
14	N	4	LYS
14	N	8	GLU
14	N	9	LYS
14	N	12	ARG
14	N	17	LYS

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Mol	Chain	Res	Type
14	N	18	VAL
14	N	26	ARG
14	N	31	ARG
14	N	40	CYS
14	N	41	ARG
14	N	44	LEU
14	N	45	ARG
14	N	50	LYS
14	N	53	LEU
15	O	4	THR
15	O	6	GLU
15	O	7	GLU
15	O	9	GLN
15	O	10	LYS
15	O	14	GLU
15	O	21	ASP
15	O	25	THR
15	O	28	GLN
15	O	29	VAL
15	O	35	ARG
15	O	39	LEU
15	O	41	GLU
15	O	44	LYS
15	O	49	ASP
15	O	52	SER
15	O	54	ARG
15	O	56	LEU
15	O	57	LEU
15	O	58	MET
15	O	64	ARG
15	O	68	ARG
15	O	70	LEU
15	O	71	GLN
15	O	83	GLU
15	O	87	ILE
16	P	5	ARG
16	P	8	ARG
16	P	20	VAL
16	P	23	ASP
16	P	26	ARG
16	P	28	ARG
16	P	34	GLU

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Mol	Chain	Res	Type
16	P	40	ASP
16	P	44	THR
16	P	49	LEU
16	P	53	VAL
16	P	55	ARG
16	P	62	VAL
16	P	67	THR
16	P	81	ARG
17	Q	7	THR
17	Q	16	GLN
17	Q	34	LYS
17	Q	52	LYS
17	Q	56	VAL
17	Q	60	ILE
17	Q	62	SER
17	Q	63	ARG
17	Q	68	ARG
17	Q	76	LEU
17	Q	82	MET
17	Q	89	LEU
17	Q	92	ARG
17	Q	93	GLN
17	Q	98	LEU
17	Q	99	SER
18	R	19	LYS
18	R	29	PHE
18	R	34	TYR
18	R	37	VAL
18	R	39	VAL
18	R	42	ARG
18	R	47	THR
18	R	53	ARG
18	R	54	ARG
18	R	55	ARG
18	R	63	GLN
18	R	75	ILE
18	R	81	PHE
18	R	83	GLU
18	R	84	LYS
18	R	87	ARG
18	R	88	LYS
19	S	3	ARG

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Mol	Chain	Res	Type
19	S	5	LEU
19	S	6	LYS
19	S	7	LYS
19	S	13	ASP
19	S	19	VAL
19	S	22	LEU
19	S	25	LYS
19	S	28	LYS
19	S	29	ARG
19	S	36	ARG
19	S	37	ARG
19	S	38	SER
19	S	39	THR
19	S	41	VAL
19	S	53	ASN
19	S	58	VAL
19	S	62	ILE
19	S	63	THR
19	S	77	THR
19	S	79	THR
20	T	10	LEU
20	T	13	LEU
20	T	15	ARG
20	T	20	LEU
20	T	22	ARG
20	T	23	ARG
20	T	24	LEU
20	T	25	ARG
20	T	26	ASN
20	T	33	ILE
20	T	36	LEU
20	T	45	GLN
20	T	50	GLU
20	T	55	ILE
20	T	68	LYS
20	T	73	HIS
20	T	74	LYS
20	T	75	ASN
20	T	84	LEU
20	T	104	LEU
21	V	3	LYS
21	V	7	ARG

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Mol	Chain	Res	Type
21	V	9	ARG
21	V	12	LYS
21	V	20	LYS
21	V	25	LYS
22	X	4	GLU
22	X	12	ARG
22	X	18	VAL
22	X	24	LYS
22	X	30	ASP
22	X	32	ARG
22	X	53	ASP
22	X	59	ILE
22	X	60	MET
22	X	73	GLU
22	X	74	LYS
22	X	77	ARG
22	X	88	ILE
22	X	92	VAL
22	X	98	ASP
22	X	101	THR
22	X	119	THR
22	X	123	ARG
22	X	125	ARG
22	X	131	GLU
22	X	150	VAL
22	X	153	LYS
22	X	162	ASN
22	X	163	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	16	HIS
2	B	25	ASN
2	B	94	ASN
2	B	212	GLN
2	B	224	GLN
3	C	6	HIS
3	C	108	ASN
3	C	123	GLN
3	C	176	HIS
4	D	45	GLN

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Mol	Chain	Res	Type
4	D	129	ASN
4	D	161	ASN
4	D	201	GLN
6	F	18	GLN
6	F	64	GLN
6	F	100	ASN
7	G	68	ASN
9	I	87	GLN
9	I	89	ASN
10	J	56	HIS
10	J	78	ASN
10	J	84	GLN
11	K	13	GLN
12	L	8	ASN
12	L	49	ASN
12	L	99	HIS
13	M	12	ASN
14	N	52	GLN
15	O	37	ASN
16	P	13	HIS
17	Q	16	GLN
18	R	63	GLN
19	S	53	ASN
20	T	26	ASN
22	X	129	HIS
22	X	138	ASN
22	X	162	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1509/1522 (99%)	452 (29%)	109 (7%)
23	Y	18/42 (42%)	9 (50%)	1 (5%)
24	Z	76/77 (98%)	37 (48%)	5 (6%)
All	All	1603/1641 (97%)	498 (31%)	115 (7%)

All (498) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	A
1	A	9	G

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Mol	Chain	Res	Type
1	A	13	U
1	A	19	C
1	A	22	G
1	A	30	U
1	A	31	G
1	A	32	A
1	A	39	G
1	A	44	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	52	G
1	A	54	C
1	A	60	A
1	A	61	G
1	A	63	C
1	A	66	G
1	A	68	G
1	A	72	C
1	A	73	G
1	A	76	C
1	A	77	G
1	A	79	G
1	A	81	U
1	A	82	U
1	A	91	C
1	A	93	G
1	A	97	G
1	A	98	G
1	A	100	C
1	A	101	A
1	A	108	G
1	A	120	A
1	A	121	C
1	A	122	G
1	A	128	G
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	137	C

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Mol	Chain	Res	Type
1	A	142	G
1	A	144	G
1	A	151	A
1	A	163	C
1	A	167	G
1	A	171	A
1	A	181	G
1	A	182	U
1	A	189(C)	C
1	A	189(E)	U
1	A	189(F)	U
1	A	189(G)	G
1	A	195	A
1	A	197	A
1	A	198	G
1	A	199	G
1	A	201	C
1	A	202	U
1	A	203	U
1	A	204	U
1	A	217	C
1	A	222	U
1	A	227	G
1	A	231	G
1	A	244	U
1	A	245	C
1	A	247	G
1	A	250	A
1	A	251	G
1	A	252	U
1	A	253	U
1	A	262	A
1	A	264	U
1	A	266	G
1	A	267	C
1	A	272	C
1	A	279	A
1	A	280	C
1	A	281	G
1	A	282	A
1	A	289	G
1	A	298	A

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Mol	Chain	Res	Type
1	A	299	G
1	A	300	A
1	A	301	G
1	A	305	G
1	A	306	G
1	A	315	A
1	A	316	G
1	A	321	A
1	A	324	G
1	A	325	A
1	A	328	C
1	A	329	A
1	A	330	C
1	A	332	G
1	A	340	U
1	A	342	C
1	A	343	U
1	A	344	A
1	A	345	C
1	A	350	G
1	A	351	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	365	U
1	A	367	U
1	A	368	U
1	A	373	A
1	A	381	C
1	A	384	G
1	A	385	C
1	A	388	G
1	A	389	A
1	A	390	C
1	A	392	G
1	A	397	A
1	A	398	C
1	A	406	G
1	A	412	A
1	A	413	G
1	A	419	C
1	A	421	U

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Mol	Chain	Res	Type
1	A	422	C
1	A	423	G
1	A	428	G
1	A	429	U
1	A	430	A
1	A	451	A
1	A	452	A
1	A	453	A
1	A	454	C
1	A	455	C
1	A	457	C
1	A	470	C
1	A	476	G
1	A	479	C
1	A	480	U
1	A	483	C
1	A	484	G
1	A	485	G
1	A	486	U
1	A	495	A
1	A	496	A
1	A	498	U
1	A	500	G
1	A	510	A
1	A	511	C
1	A	518	C
1	A	519	C
1	A	521	G
1	A	524	G
1	A	525	C
1	A	527	G
1	A	529	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	535	A
1	A	545	C
1	A	547	A
1	A	548	G
1	A	550	G
1	A	559	A

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Mol	Chain	Res	Type
1	A	560	U
1	A	561	U
1	A	562	C
1	A	564	C
1	A	565	U
1	A	568	G
1	A	572	A
1	A	573	A
1	A	574	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	578	C
1	A	588	G
1	A	596	C
1	A	607	A
1	A	619	U
1	A	630	G
1	A	641	U
1	A	642	A
1	A	644	G
1	A	653	A
1	A	665	A
1	A	672	U
1	A	683	G
1	A	688	G
1	A	689	C
1	A	693	G
1	A	695	A
1	A	701	C
1	A	702	A
1	A	703	G
1	A	704	A
1	A	713	G
1	A	716	A
1	A	717	C
1	A	720	C
1	A	721	G
1	A	723	U
1	A	731	G
1	A	748	C
1	A	749	C

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Mol	Chain	Res	Type
1	A	752	G
1	A	753	A
1	A	755	G
1	A	760	G
1	A	764	C
1	A	777	A
1	A	782	A
1	A	785	G
1	A	787	A
1	A	792	A
1	A	793	U
1	A	794	A
1	A	804	U
1	A	805	C
1	A	810	C
1	A	812	C
1	A	815	A
1	A	817	C
1	A	820	U
1	A	828	A
1	A	835	U
1	A	839	U
1	A	840	C
1	A	841	U
1	A	851	G
1	A	855	G
1	A	864	A
1	A	865	A
1	A	873	A
1	A	876	G
1	A	877	C
1	A	885	G
1	A	887	G
1	A	889	A
1	A	891	U
1	A	900	A
1	A	902	G
1	A	914	A
1	A	919	A
1	A	922	G
1	A	926	G
1	A	927	G

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Mol	Chain	Res	Type
1	A	931	C
1	A	932	C
1	A	933	G
1	A	934	C
1	A	935	A
1	A	942	G
1	A	946	A
1	A	950	U
1	A	956	U
1	A	958	A
1	A	960	U
1	A	961	U
1	A	966	G
1	A	968	A
1	A	969	A
1	A	971	G
1	A	972	C
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	989	C
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	995	C
1	A	998	G
1	A	1000	U
1	A	1005	A
1	A	1009	G
1	A	1023	G
1	A	1024	G
1	A	1025	U
1	A	1026	G
1	A	1028	C
1	A	1029	C
1	A	1030	C
1	A	1037	C
1	A	1045	C
1	A	1046	A
1	A	1050	G

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Mol	Chain	Res	Type
1	A	1051	C
1	A	1053	G
1	A	1054	C
1	A	1060	C
1	A	1065	U
1	A	1066	C
1	A	1074	G
1	A	1085	U
1	A	1086	U
1	A	1089	G
1	A	1094	G
1	A	1095	U
1	A	1096	C
1	A	1101	A
1	A	1102	A
1	A	1104	G
1	A	1108	G
1	A	1115	C
1	A	1117	G
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1128	C
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1133	G
1	A	1134	G
1	A	1135	U
1	A	1136	U
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1145	C
1	A	1146	A
1	A	1150	U
1	A	1151	A
1	A	1152	A
1	A	1154	G
1	A	1155	G

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Mol	Chain	Res	Type
1	A	1159	U
1	A	1160	G
1	A	1170	A
1	A	1183	A
1	A	1184	G
1	A	1187	G
1	A	1191	A
1	A	1196	U
1	A	1197	G
1	A	1200	C
1	A	1201	A
1	A	1202	G
1	A	1211	U
1	A	1212	U
1	A	1214	C
1	A	1215	G
1	A	1225	A
1	A	1227	A
1	A	1236	A
1	A	1238	A
1	A	1240	U
1	A	1241	G
1	A	1249	C
1	A	1250	A
1	A	1256	A
1	A	1257	U
1	A	1258	G
1	A	1260	C
1	A	1270	C
1	A	1273	G
1	A	1278	U
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1288	A
1	A	1295	G
1	A	1299	A
1	A	1300	G

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Mol	Chain	Res	Type
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1305	G
1	A	1312	G
1	A	1317	C
1	A	1318	A
1	A	1319	A
1	A	1320	C
1	A	1321	C
1	A	1322	C
1	A	1323	G
1	A	1332	A
1	A	1335	C
1	A	1336	C
1	A	1345	U
1	A	1346	A
1	A	1347	G
1	A	1349	A
1	A	1353	G
1	A	1357	A
1	A	1361	G
1	A	1362	C
1	A	1363	C
1	A	1363(A)	A
1	A	1364	U
1	A	1370	G
1	A	1378	C
1	A	1379	G
1	A	1381	U
1	A	1394	A
1	A	1395	C
1	A	1396	A
1	A	1397	C
1	A	1398	A
1	A	1399	C
1	A	1412	C
1	A	1413	A
1	A	1418	A
1	A	1419	G
1	A	1424	C
1	A	1428	A

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Mol	Chain	Res	Type
1	A	1440	C
1	A	1442	G
1	A	1443	G
1	A	1447	A
1	A	1452	C
1	A	1456	G
1	A	1457	G
1	A	1481	U
1	A	1483	A
1	A	1484	C
1	A	1488	G
1	A	1492	A
1	A	1493	A
1	A	1494	G
1	A	1497	G
1	A	1499	A
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G
1	A	1533	C
1	A	1534	A
1	A	1536	C
1	A	1538	C
1	A	1539	C
1	A	1541	U
23	Y	21	G
23	Y	28	A
23	Y	32	A
23	Y	33	A
23	Y	34	A
23	Y	35	A
23	Y	37	U
23	Y	38	G
23	Y	39	U
24	Z	2	G
24	Z	3	C
24	Z	5	G

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Mol	Chain	Res	Type
24	Z	8	4SU
24	Z	9	G
24	Z	10	G
24	Z	13	C
24	Z	14	A
24	Z	16	C
24	Z	17	C
24	Z	17(A)	U
24	Z	18	G
24	Z	19	G
24	Z	21	A
24	Z	22	G
24	Z	23	C
24	Z	26	G
24	Z	32	OMC
24	Z	34	C
24	Z	42	G
24	Z	43	A
24	Z	44	A
24	Z	47	U
24	Z	48	C
24	Z	49	G
24	Z	52	G
24	Z	54	5MU
24	Z	55	PSU
24	Z	57	A
24	Z	59	A
24	Z	64	G
24	Z	65	C
24	Z	67	C
24	Z	68	C
24	Z	69	C
24	Z	70	G
24	Z	76	A

All (115) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	8	A
1	A	30	U
1	A	48	C

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Mol	Chain	Res	Type
1	A	51	A
1	A	60	A
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	197	A
1	A	202	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	279	A
1	A	281	G
1	A	305	G
1	A	328	C
1	A	329	A
1	A	344	A
1	A	351	G
1	A	366	C
1	A	367	U
1	A	372	C
1	A	389	A
1	A	391	G
1	A	397	A
1	A	412	A
1	A	428	G
1	A	429	U
1	A	484	G
1	A	485	G
1	A	495	A
1	A	496	A
1	A	509	A
1	A	518	C
1	A	524	G
1	A	531	U
1	A	559	A
1	A	560	U
1	A	562	C
1	A	595	G
1	A	641	U
1	A	653	A
1	A	661	G

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Mol	Chain	Res	Type
1	A	687	A
1	A	701	C
1	A	703	G
1	A	748	C
1	A	792	A
1	A	839	U
1	A	850	U
1	A	864	A
1	A	884	U
1	A	897	C
1	A	913	A
1	A	932	C
1	A	960	U
1	A	965	A
1	A	968	A
1	A	975	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	1028	C
1	A	1030	C
1	A	1064	G
1	A	1065	U
1	A	1101	A
1	A	1128	C
1	A	1145	C
1	A	1151	A
1	A	1182	G
1	A	1190	G
1	A	1196	U
1	A	1200	C
1	A	1201	A
1	A	1212	U
1	A	1226	C
1	A	1239	A
1	A	1240	U
1	A	1257	U
1	A	1278	U
1	A	1279	A
1	A	1285	A
1	A	1287	A
1	A	1298	C

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Mol	Chain	Res	Type
1	A	1299	A
1	A	1300	G
1	A	1301	U
1	A	1322	C
1	A	1331	G
1	A	1335	C
1	A	1345	U
1	A	1346	A
1	A	1364	U
1	A	1380	U
1	A	1419	G
1	A	1442(B)	A
1	A	1447	A
1	A	1452	C
1	A	1457	G
1	A	1483	A
1	A	1492	A
1	A	1498	U
1	A	1503	A
1	A	1504	G
1	A	1533	C
23	Y	32	A
24	Z	3	C
24	Z	9	G
24	Z	47	U
24	Z	48	C
24	Z	60	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
24	OMC	Z	32	24	15,22,23	0.77	1 (6%)	20,31,34	1.50	3 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
24	G7M	Z	46	24	18,26,27	2.81	3 (16%)	21,39,42	2.84	7 (33%)
24	5MU	Z	54	24	13,22,23	0.82	0	16,32,35	3.32	4 (25%)
24	PSU	Z	55	24	15,21,22	0.88	0	16,30,33	2.56	5 (31%)
24	4SU	Z	8	24	12,21,22	1.01	1 (8%)	15,30,33	1.80	3 (20%)

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
24	OMC	Z	32	24	-	0/5/27/28	0/2/2/2
24	G7M	Z	46	24	-	0/3/25/26	0/3/3/3
24	5MU	Z	54	24	-	0/3/25/26	0/2/2/2
24	PSU	Z	55	24	-	0/7/25/26	0/2/2/2
24	4SU	Z	8	24	-	0/3/25/26	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	Z	32	OMC	O4'-C1'	2.04	1.44	1.41
24	Z	8	4SU	O4'-C1'	2.56	1.44	1.41
24	Z	46	G7M	C6-C5	3.90	1.49	1.41
24	Z	46	G7M	C8-N7	7.30	1.46	1.33
24	Z	46	G7M	C8-N9	8.01	1.48	1.33

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	Z	54	5MU	C5-C4-N3	-8.42	118.28	125.35
24	Z	46	G7M	N7-C8-N9	-8.24	96.51	108.67
24	Z	46	G7M	C5-C6-N1	-5.39	116.47	123.52
24	Z	8	4SU	C5-C4-N3	-4.44	118.85	123.56
24	Z	55	PSU	C5-C1'-C2'	-4.29	108.15	115.44
24	Z	8	4SU	C6-N1-C2	-2.99	116.46	121.33
24	Z	46	G7M	N3-C2-N1	-2.77	123.79	127.56
24	Z	46	G7M	CN7-N7-C8	-2.51	112.22	125.31
24	Z	46	G7M	O4'-C4'-C3'	-2.38	100.32	105.16
24	Z	32	OMC	C6-N1-C2	-2.07	117.95	121.33
24	Z	46	G7M	C6-C5-C4	-2.01	118.56	120.86
24	Z	32	OMC	N4-C4-N3	2.03	120.06	116.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	Z	55	PSU	C3'-C2'-C1'	2.14	104.25	101.71
24	Z	54	5MU	O4'-C1'-N1	2.17	112.22	108.10
24	Z	55	PSU	C4-C5-C1'	2.19	124.91	121.22
24	Z	55	PSU	O3'-C3'-C4'	2.69	119.05	111.01
24	Z	54	5MU	C4'-O4'-C1'	2.78	112.59	109.64
24	Z	8	4SU	C4'-O4'-C1'	2.88	112.69	109.64
24	Z	32	OMC	C6-C5-C4	4.43	119.17	117.44
24	Z	46	G7M	C6-N1-C2	5.71	122.57	115.88
24	Z	55	PSU	C4-N3-C2	7.59	121.49	115.16
24	Z	54	5MU	C4-N3-C2	9.08	122.73	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	Z	32	OMC	1	0
24	Z	54	5MU	2	0
24	Z	55	PSU	2	0
24	Z	8	4SU	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 82 ligands modelled in this entry, 82 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	5
23	Y	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1442(A):G	O3'	1442(B):A	P	5.11
1	A	84:U	O3'	88:A	P	5.07
1	A	93:G	O3'	96:U	P	4.99
1	A	204:U	O3'	216:G	P	4.97
1	A	841:U	O3'	848:C	P	4.05
1	Y	28:A	O3'	29:G	P	3.21