



Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 04:40 AM GMT

PDB ID : 3DF3
Title : Crystal structure of the bacterial ribosome from Escherichia coli in complex with hygromycin B. This file contains the 30S subunit of the second 70S ribosome, with hygromycin B bound. The entire crystal structure contains two 70S ribosomes.
Authors : Borovinskaya, M.A.; Shoji, S.; Fredrick, K.; Cate, J.H.D.
Deposited on : 2008-06-11
Resolution : 3.50 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

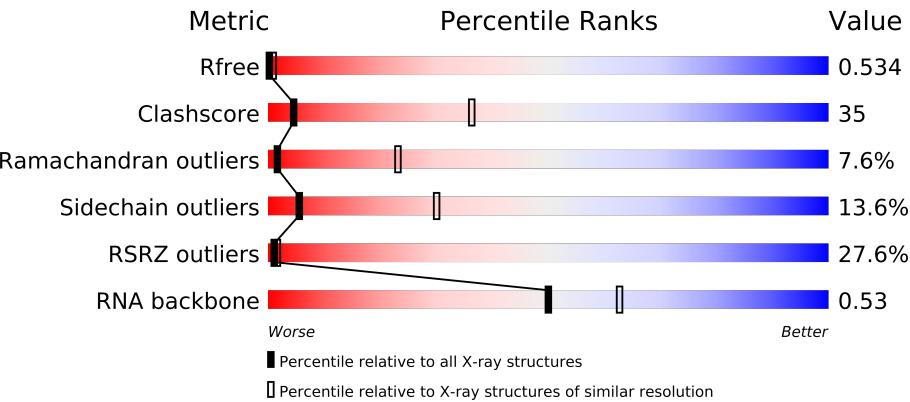
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance i

The reported resolution of this entry is 3.50 Å.

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



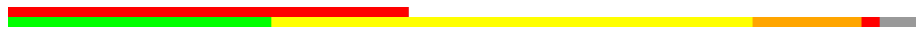



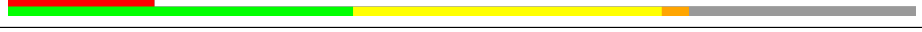
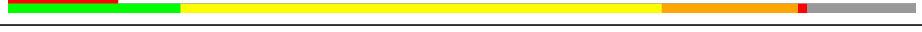



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	66092	1243 (3.70-3.30)
Clashscore	79885	1039 (3.66-3.34)
Ramachandran outliers	78287	1000 (3.66-3.34)
Sidechain outliers	78261	1000 (3.66-3.34)
RSRZ outliers	66119	1243 (3.70-3.30)
RNA backbone	1838	1007 (4.22-2.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	1542	<div><div></div><div></div></div>
2	C	232	<div><div></div><div></div></div>
3	D	205	<div><div></div><div></div></div>
4	E	166	<div><div></div><div></div></div>
5	F	135	<div><div></div><div></div></div>
6	G	178	<div><div></div><div></div></div>
7	H	129	<div><div></div><div></div></div>
8	I	129	<div><div></div><div></div></div>
9	J	103	<div><div></div><div></div></div>
10	K	128	<div><div></div><div></div></div>
11	L	123	<div><div></div><div></div></div>
12	M	117	<div><div></div><div></div></div>

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Mol	Chain	Length	Quality of chain
13	N	100	
14	O	89	
15	P	82	
16	Q	83	
17	R	74	
18	S	91	
19	T	86	
20	B	240	
21	U	71	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
22	MG	A	2042	-	X
22	MG	A	2062	-	X
22	MG	A	2168	-	X
22	MG	A	2182	-	X
22	MG	A	2346	-	X
22	MG	A	2360	-	X

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 51794 atoms, of which 0 are hydrogen and 0 are deuterium.

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

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1530	Total	C	N	O	P	0	0	0
			32831	14642	6024	10635	1530			

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	206	Total	C	N	O	S	0	0	0
			1624	1028	305	288	3			

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	205	Total	C	N	O	S	0	0	0
			1643	1026	315	298	4			

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	150	Total	C	N	O	S	0	0	0
			1105	687	211	201	6			

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	100	Total	C	N	O	S	0	0	0
			817	515	148	148	6			

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	152	Total	C	N	O	S	0	0	0
			1196	745	230	217	4			

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	127	Total	C	N	O	S	0	0	0
			1022	634	206	179	3			

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	J	98	Total	C	N	O	S	0	0	0
			786	493	150	142	1			

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	K	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	L	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	M	113	Total	C	N	O	S	0	0	0
			876	541	177	155	3			

- Molecule 13 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	N	96	Total	C	N	O	S	0	0	0
			774	483	160	128	3			

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	O	88	Total	C	N	O	S	0	0	0
			715	440	146	128	1			

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	P	80	Total	C	N	O	S	0	0	0
			638	400	126	111	1			

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	Q	81	Total	C	N	O	S	0	0	0
			656	417	122	114	3			

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	R	55	Total	C	N	O	0	0	0
			455	288	86	81			

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	S	80	Total	C	N	O	S	0	0	0
			644	413	121	108	2			

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	T	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			

- Molecule 20 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	B	218	Total	C	N	O	S	0	0	0
			1704	1081	305	311	7			

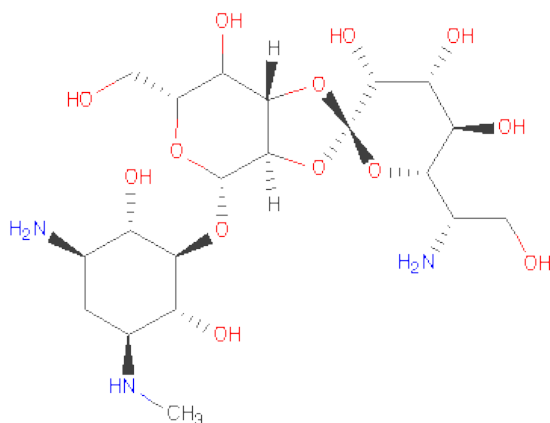
- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	U	51	Total	C	N	O	S	0	0	0
			425	265	86	73	1			

- Molecule 22 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	61	Total	Mg	0	0
			61	61		
22	E	1	Total	Mg	0	0
			1	1		

- Molecule 23 is HYGROMYCIN B (three-letter code: HYG) (formula: C₂₀H₃₇N₃O₁₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
23	A	1	Total	C	N	O	0	0
			36	20	3	13		

- Molecule 24 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	A	299	Total	O	0	0
			299	299		
24	E	5	Total	O	0	0
			5	5		
24	L	1	Total	O	0	0
			1	1		

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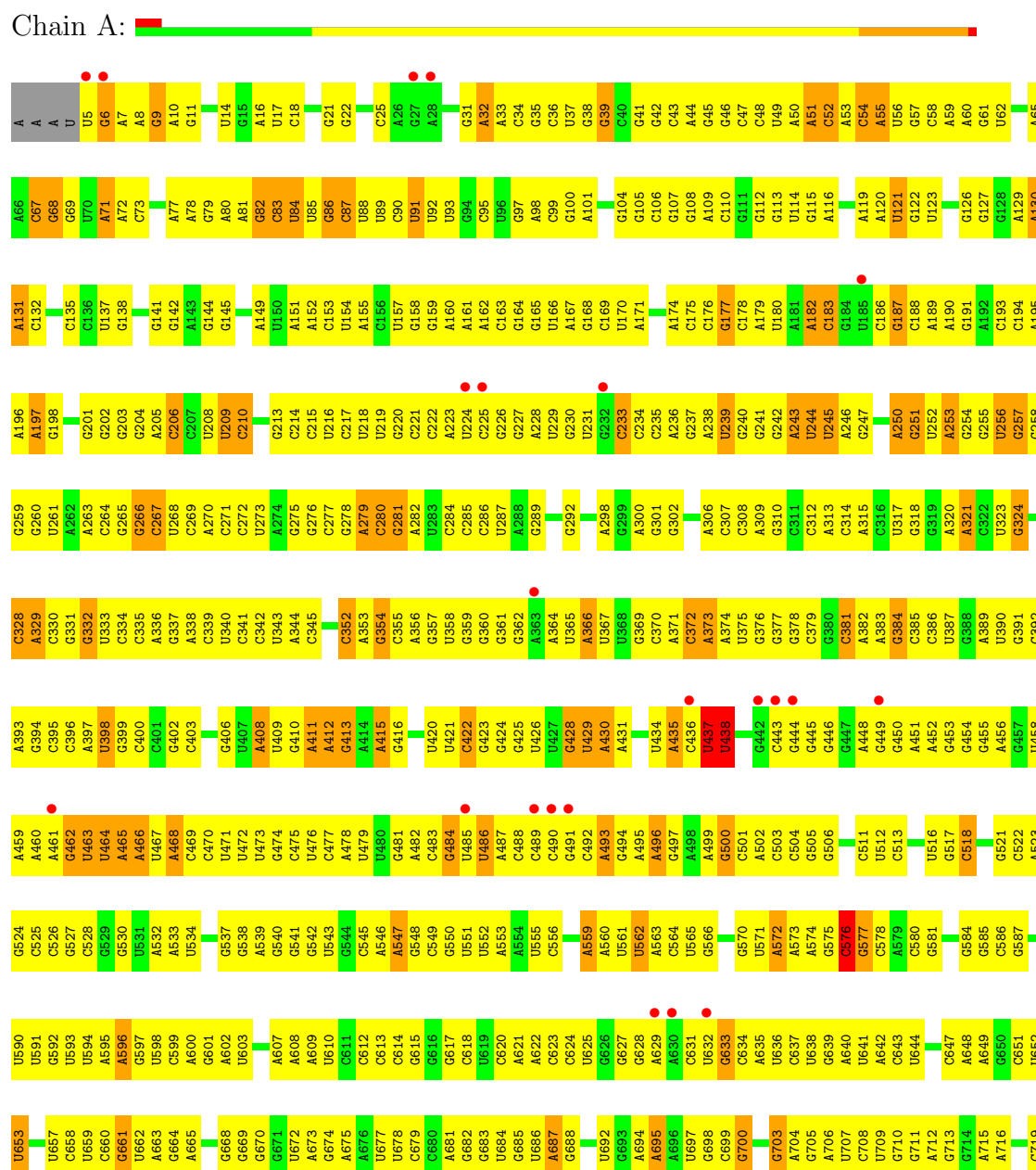
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	N	4	Total	O	0	0
			4	4		

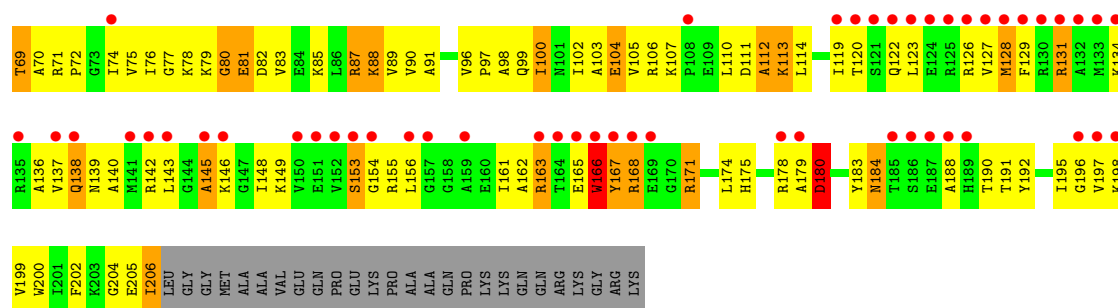
3 Residue-property plots

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

• Molecule 1: 16S ribosomal RNA

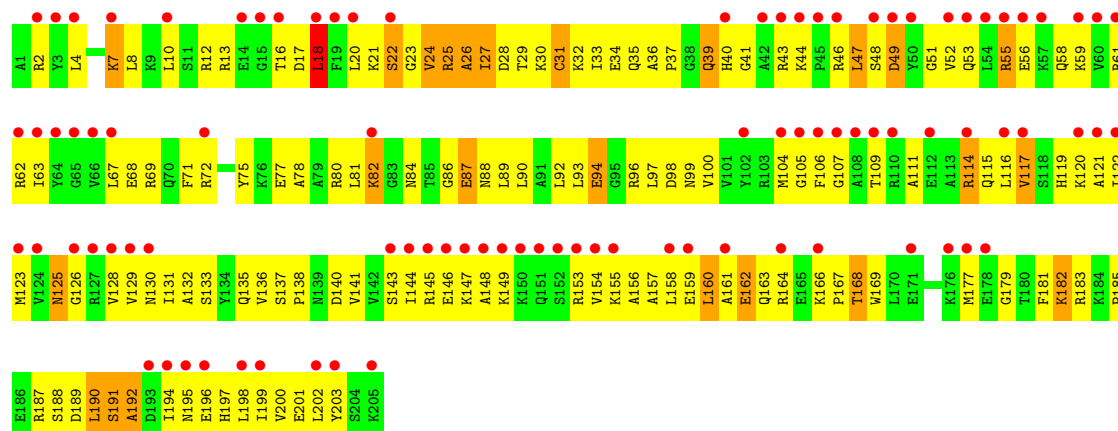






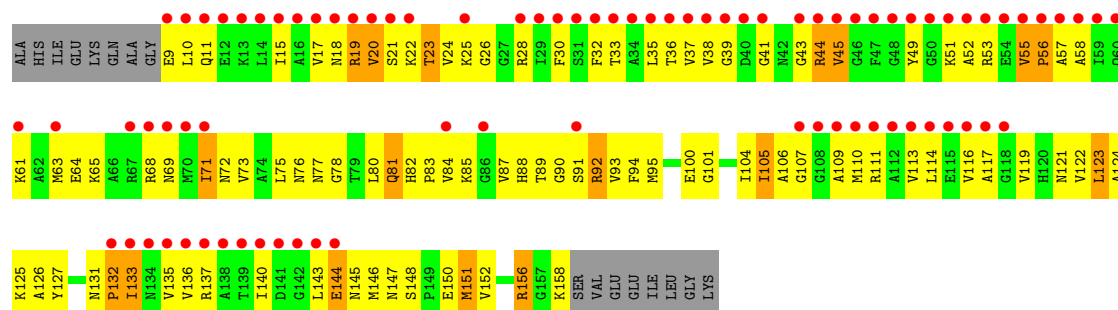
• Molecule 3: 30S ribosomal protein S4

Chain D:



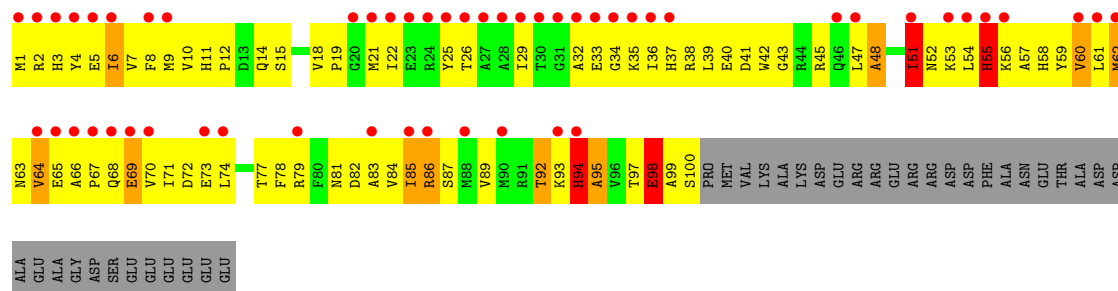
• Molecule 4: 30S ribosomal protein S5

Chain E:

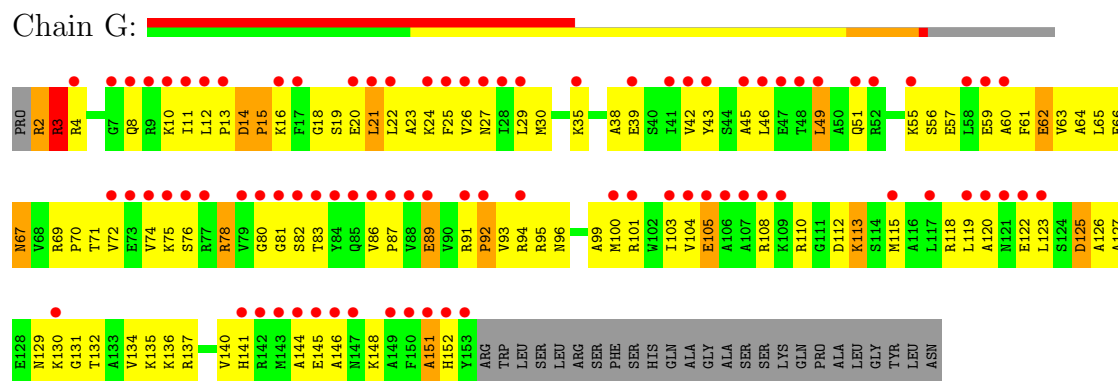


• Molecule 5: 30S ribosomal protein S6

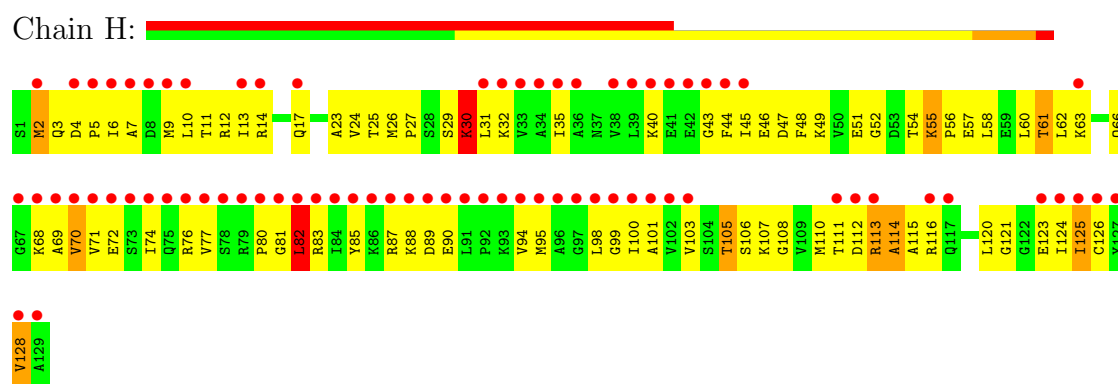
Chain F:



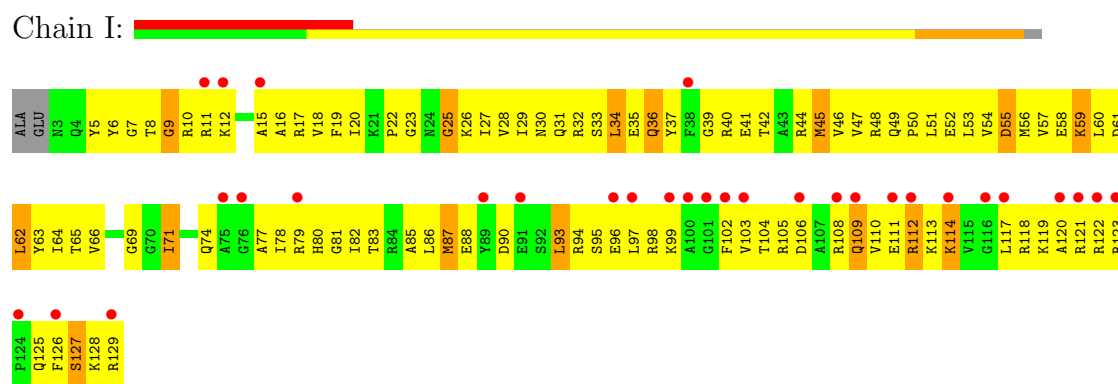
- Molecule 6: 30S ribosomal protein S7



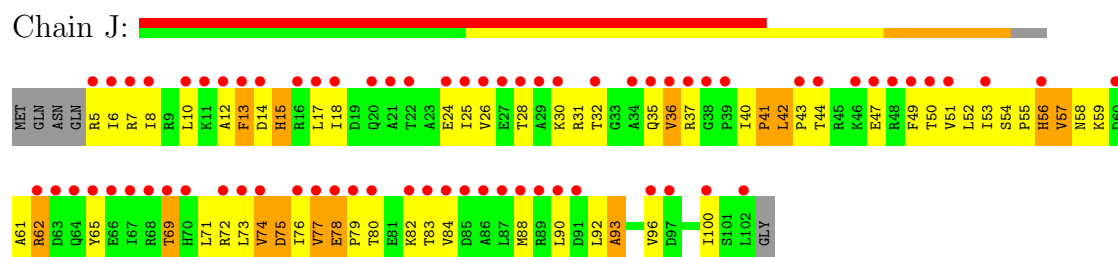
- Molecule 7: 30S ribosomal protein S8



- Molecule 8: 30S ribosomal protein S9

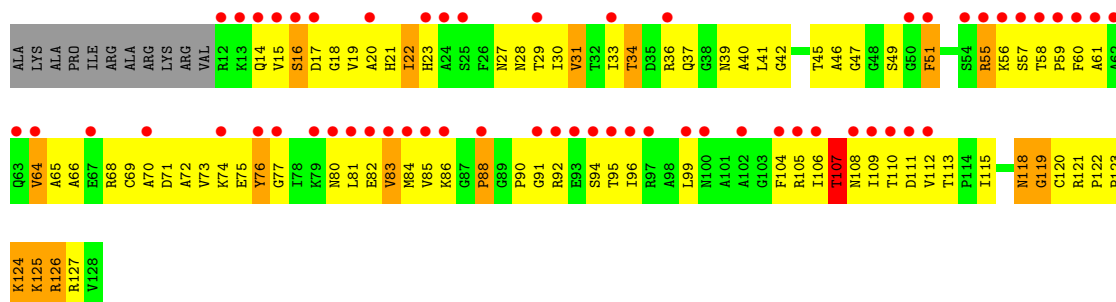


- Molecule 9: 30S ribosomal protein S10



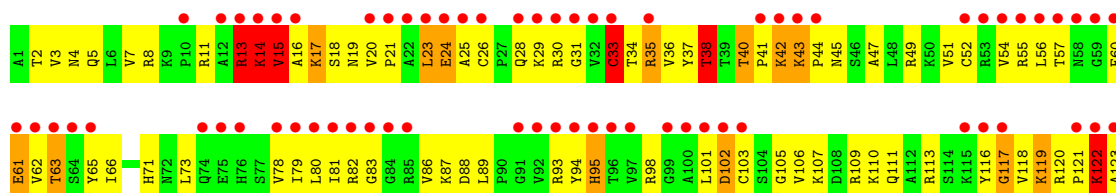
- Molecule 10: 30S ribosomal protein S11

Chain K:



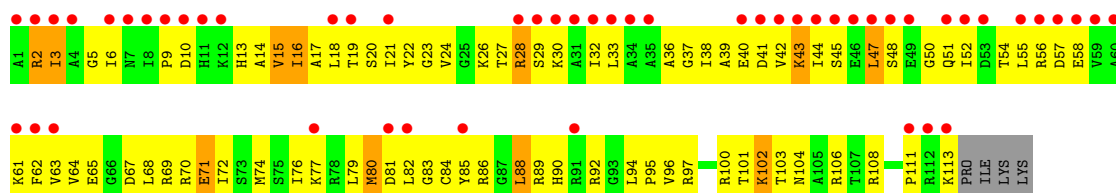
- Molecule 11: 30S ribosomal protein S12

Chain L:



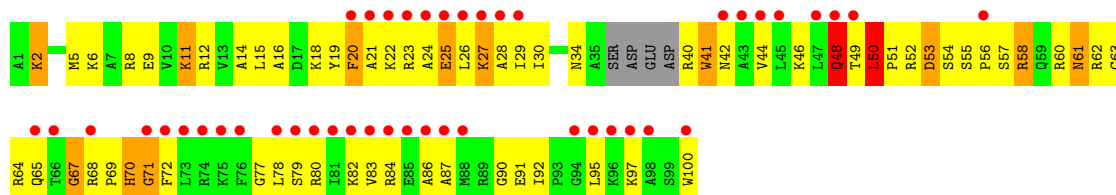
- Molecule 12: 30S ribosomal protein S13

Chain M:



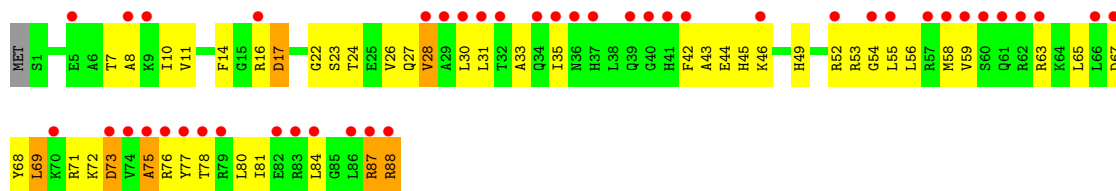
- Molecule 13: 30S ribosomal protein S14

Chain N:



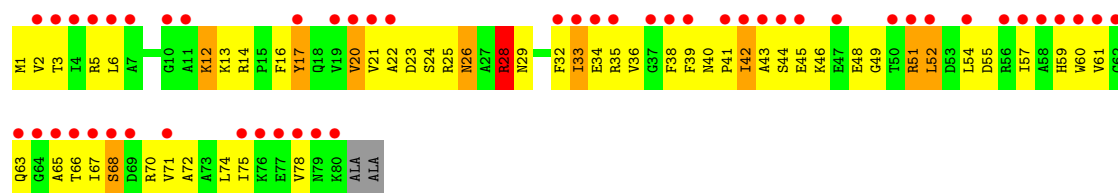
- Molecule 14: 30S ribosomal protein S15

Chain O:



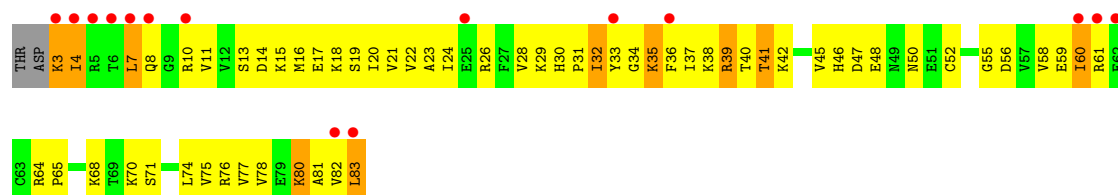
- Molecule 15: 30S ribosomal protein S16

Chain P:



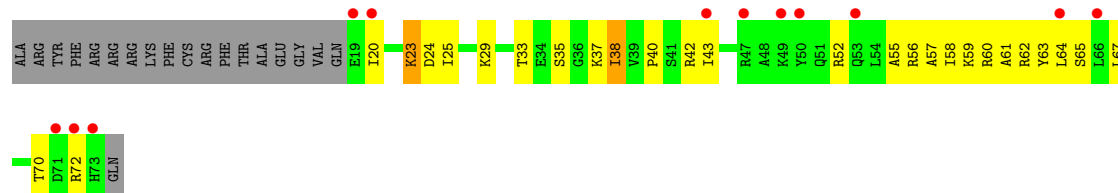
- Molecule 16: 30S ribosomal protein S17

Chain Q:



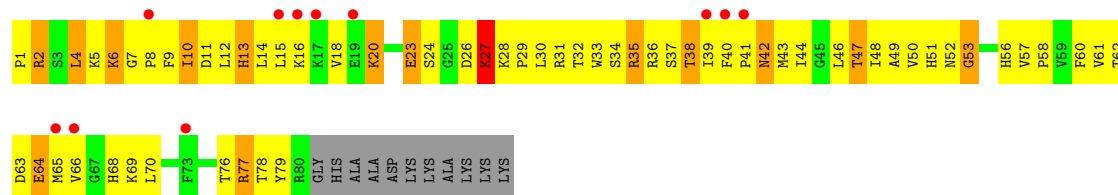
- Molecule 17: 30S ribosomal protein S18

Chain R:



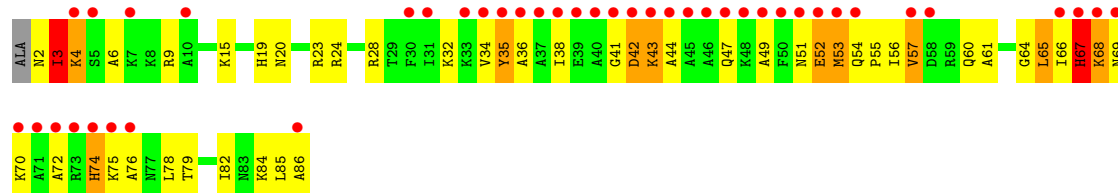
- Molecule 18: 30S ribosomal protein S19

Chain S:



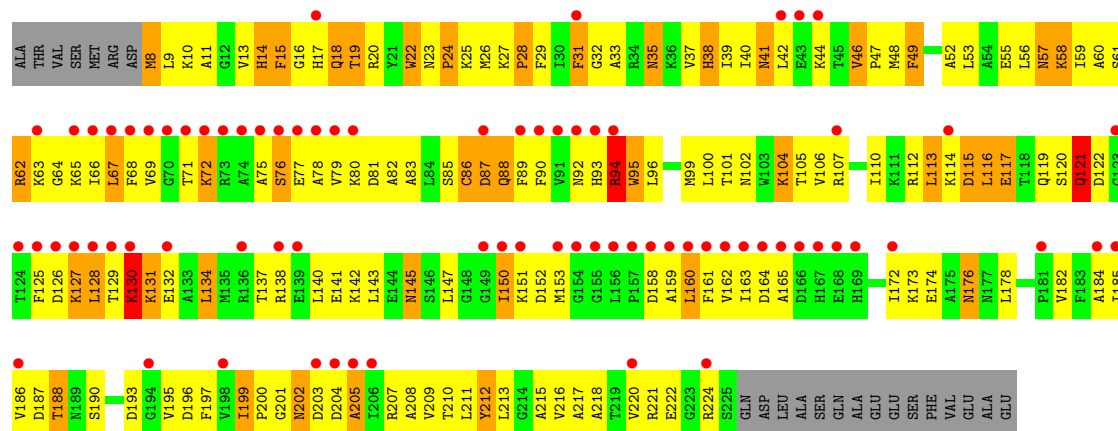
- Molecule 19: 30S ribosomal protein S20

Chain T:



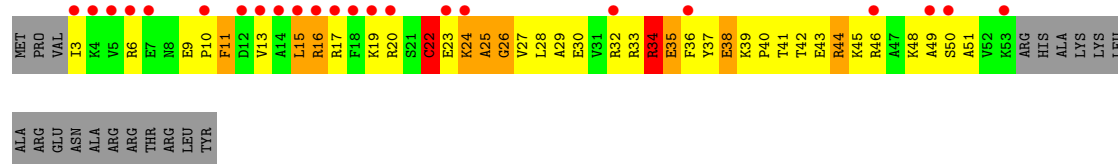
- Molecule 20: 30S ribosomal protein S2

Chain B:



- Molecule 21: 30S ribosomal protein S21

Chain U: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	208.70Å 379.50Å 739.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.00 – 3.50 137.77 – 3.50	Depositor EDS
% Data completeness (in resolution range)	62.1 (70.00-3.50) 62.3 (137.77-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 3.49Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.269 , 0.318 0.526 , 0.534	Depositor DCC
R_{free} test set	22206 reflections (4.89%)	DCC
Wilson B-factor (Å ²)	117.9	Xtriage
Anisotropy	0.294	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 20.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 454411 reflections	Xtriage
F_o, F_c correlation	0.58	EDS
Total number of atoms	51794	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.26	1/36762 (0.0%)	0.77	17/57350 (0.0%)
2	C	0.23	0/1651	0.44	0/2225
3	D	0.23	0/1665	0.43	0/2227
4	E	0.23	0/1118	0.45	0/1504
5	F	0.24	0/835	0.44	0/1128
6	G	0.23	0/1211	0.44	0/1624
7	H	0.23	0/989	0.45	0/1326
8	I	0.24	0/1034	0.44	0/1375
9	J	0.22	0/796	0.47	0/1077
10	K	0.24	0/893	0.46	0/1205
11	L	0.22	0/969	0.47	0/1300
12	M	0.21	0/884	0.45	0/1181
13	N	0.24	0/785	0.43	0/1043
14	O	0.22	0/723	0.44	0/966
15	P	0.25	0/648	0.44	0/870
16	Q	0.24	0/665	0.48	0/892
17	R	0.23	0/462	0.44	0/621
18	S	0.25	0/660	0.46	0/888
19	T	0.24	0/671	0.41	0/888
20	B	0.25	0/1735	0.44	0/2338
21	U	0.26	0/430	0.46	0/570
All	All	0.25	1/55586 (0.0%)	0.68	17/82598 (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	13

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	495	A	N3-C4	-5.48	1.31	1.34

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1213	A	O5'-P-OP1	-26.18	79.28	110.70
1	A	1213	A	O5'-P-OP2	17.64	131.86	110.70
1	A	1212	U	OP1-P-O3'	15.45	139.18	105.20
1	A	1049	U	O5'-P-OP1	-7.79	98.69	105.70
1	A	975	A	C5'-C4'-C3'	-7.25	104.41	116.00
1	A	1212	U	O3'-P-O5'	-6.43	91.78	104.00
1	A	1424	U	C5'-C4'-C3'	-6.11	106.23	116.00
1	A	1534	A	C2'-C3'-O3'	-5.99	96.33	109.50
1	A	1213	A	C5'-C4'-O4'	5.84	116.11	109.10
1	A	576	C	O5'-P-OP1	-5.80	100.48	105.70
1	A	1213	A	C1'-O4'-C4'	-5.54	105.47	109.90
1	A	765	G	N9-C1'-C2'	-5.51	105.94	112.00
1	A	67	C	C5'-C4'-C3'	-5.42	107.33	116.00
1	A	437	U	N1-C1'-C2'	5.28	120.86	114.00
1	A	1362	A	C5'-C4'-O4'	5.23	115.38	109.10
1	A	1362	A	C5'-C4'-C3'	5.18	124.30	116.00
1	A	1301	U	N1-C1'-C2'	5.02	120.52	114.00

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1006	G	Sidechain
1	A	1047	G	Sidechain
1	A	1441	A	Sidechain
1	A	187	G	Sidechain
1	A	281	G	Sidechain
1	A	324	G	Sidechain
1	A	437	U	Sidechain
1	A	438	U	Sidechain
1	A	496	A	Sidechain
1	A	703	G	Sidechain
1	A	82	G	Sidechain
1	A	832	G	Sidechain
1	A	992	U	Sidechain

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32831	0	16521	1375	0
2	C	1624	0	1699	136	0
3	D	1643	0	1710	156	0
4	E	1105	0	1148	115	0
5	F	817	0	808	88	0
6	G	1196	0	1246	110	0
7	H	979	0	1034	93	0
8	I	1022	0	1070	151	0
9	J	786	0	828	82	0
10	K	877	0	887	101	0
11	L	955	0	1019	94	0
12	M	876	0	937	107	0
13	N	774	0	827	90	0
14	O	715	0	742	40	0
15	P	638	0	656	55	0
16	Q	656	0	702	73	0
17	R	455	0	478	34	0
18	S	644	0	675	98	0
19	T	665	0	714	49	0
20	B	1704	0	1732	208	0
21	U	425	0	449	68	0
22	A	61	0	0	0	0
22	E	1	0	0	0	0
23	A	36	0	37	1	0
24	A	299	0	0	0	0
24	E	5	0	0	0	0
24	L	1	0	0	0	0
24	N	4	0	0	0	0
All	All	51794	0	35919	3069	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 35.

All (3069) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1533:C:H2'	1:A:1534:A:H3'	1.34	1.08
1:A:1221:G:H4'	18:S:76:THR:HG21	1.41	1.02
21:U:16:ARG:HA	21:U:16:ARG:HE	1.23	1.02
8:I:20:ILE:HA	8:I:62:LEU:HD12	1.37	1.01
20:B:202:ASN:HD22	20:B:204:ASP:H	1.06	1.00
5:F:92:THR:HG22	5:F:94:HIS:H	1.26	1.00
10:K:33:ILE:HB	10:K:73:VAL:HG11	1.42	0.99
20:B:46:VAL:HG13	20:B:47:PRO:HD3	1.45	0.98
1:A:1086:U:H3	1:A:1099:G:H22	1.11	0.98
13:N:51:PRO:HB2	13:N:54:SER:HB3	1.45	0.98
2:C:48:LYS:HE2	2:C:48:LYS:H	1.29	0.97
1:A:465:A:H2'	1:A:466:A:H3'	1.46	0.96
2:C:69:THR:HG21	2:C:75:VAL:HG21	1.48	0.96
5:F:29:ILE:HG21	5:F:64:VAL:HG11	1.48	0.95
1:A:1399:C:H4'	1:A:1400:C:H5''	1.48	0.94
2:C:128:MET:HB2	2:C:131:ARG:HB2	1.46	0.94
21:U:24:LYS:HZ3	21:U:25:ALA:H	1.17	0.93
20:B:65:LYS:HB2	20:B:158:ASP:H	1.34	0.93
3:D:116:LEU:HB3	3:D:122:ILE:HD11	1.50	0.93
1:A:1003:G:H21	1:A:1005:A:H5'	1.33	0.92
12:M:21:ILE:HB	12:M:24:VAL:HG22	1.48	0.92
10:K:88:PRO:HD3	21:U:28:LEU:HD11	1.50	0.92
15:P:28:ARG:HD2	15:P:29:ASN:H	1.33	0.92
3:D:90:LEU:HA	3:D:93:LEU:HD12	1.50	0.92
5:F:38:ARG:HH21	5:F:63:ASN:ND2	1.69	0.91
8:I:5:TYR:HB2	8:I:20:ILE:HB	1.51	0.90
5:F:3:HIS:ND1	5:F:92:THR:HG23	1.86	0.90
1:A:1003:G:N2	1:A:1005:A:H5'	1.87	0.90
20:B:85:SER:HB3	20:B:221:ARG:HD3	1.54	0.90
18:S:18:VAL:HG21	18:S:43:MET:HG2	1.51	0.89
3:D:160:LEU:HD13	3:D:160:LEU:H	1.36	0.89
4:E:21:SER:HB2	4:E:28:ARG:HE	1.37	0.89
1:A:812:G:HO2'	1:A:813:U:H6	0.94	0.89
16:Q:74:LEU:HD22	16:Q:75:VAL:H	1.38	0.89
5:F:3:HIS:HB2	5:F:92:THR:HA	1.55	0.88
20:B:112:ARG:HD2	20:B:116:LEU:HD12	1.55	0.88
1:A:699:C:H2'	1:A:700:G:H5''	1.53	0.88
6:G:14:ASP:H	6:G:23:ALA:HB2	1.38	0.88
6:G:46:LEU:HG	6:G:57:GLU:HB3	1.56	0.88
8:I:34:LEU:HD21	8:I:48:ARG:HH21	1.37	0.87
19:T:24:ARG:HG3	19:T:65:LEU:HD11	1.55	0.87
1:A:817:C:H1'	1:A:819:A:H5'	1.57	0.86
1:A:600:A:H5''	7:H:88:LYS:HD2	1.57	0.86

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:G:129:ASN:HA	6:G:134:VAL:HG11	1.57	0.86
1:A:981:U:H4'	13:N:60:ARG:HD2	1.58	0.86
1:A:1328:C:H5''	12:M:27:THR:HG21	1.56	0.86
1:A:426:U:H4'	3:D:39:GLN:HA	1.59	0.85
15:P:40:ASN:HD21	15:P:43:ALA:N	1.74	0.85
1:A:429:U:H5'	3:D:8:LEU:HG	1.56	0.85
8:I:26:LYS:H	8:I:61:ASP:HB3	1.42	0.85
1:A:120:A:H2'	1:A:121:U:H5''	1.57	0.85
1:A:1323:G:H2'	1:A:1324:A:C8	2.12	0.85
3:D:105:GLY:HA3	3:D:158:LEU:HD23	1.58	0.84
9:J:42:LEU:HD11	9:J:73:LEU:HB2	1.59	0.84
20:B:221:ARG:HG3	20:B:222:GLU:HG2	1.58	0.84
15:P:61:VAL:HA	15:P:65:ALA:HB3	1.58	0.84
21:U:36:PHE:HB3	21:U:40:PRO:HD3	1.59	0.83
1:A:1060:U:H4'	9:J:54:SER:HB2	1.59	0.83
10:K:105:ARG:HH21	21:U:10:PRO:HD3	1.43	0.83
20:B:116:LEU:HD22	20:B:140:LEU:HD11	1.61	0.83
16:Q:16:MET:HB2	16:Q:19:SER:HB2	1.59	0.83
3:D:138:PRO:HA	3:D:181:PHE:HD2	1.42	0.83
4:E:81:GLN:HG2	4:E:148:SER:HA	1.60	0.83
1:A:18:C:H4'	1:A:1078:U:O2	1.78	0.82
20:B:19:THR:HG23	20:B:20:ARG:H	1.44	0.82
12:M:52:ILE:HD12	12:M:55:LEU:HD12	1.58	0.82
17:R:40:PRO:HD2	17:R:43:ILE:HD12	1.61	0.82
14:O:88:ARG:HA	14:O:88:ARG:HH11	1.42	0.82
2:C:70:ALA:HA	2:C:105:VAL:HG21	1.59	0.82
1:A:841:C:H3'	1:A:843:U:OP2	1.79	0.82
10:K:124:LYS:HA	21:U:34:ARG:HB3	1.61	0.82
10:K:86:LYS:HB3	10:K:112:VAL:HG23	1.60	0.81
3:D:29:THR:H	3:D:33:ILE:HG21	1.45	0.81
11:L:13:ARG:HD2	11:L:13:ARG:H	1.43	0.81
10:K:31:VAL:HG21	10:K:66:ALA:HA	1.60	0.81
1:A:1361:G:H2'	1:A:1362:A:H5''	1.61	0.81
5:F:86:ARG:NH1	17:R:63:TYR:HB3	1.95	0.81
12:M:47:LEU:HD13	12:M:51:GLN:HB3	1.63	0.81
12:M:2:ARG:HB2	12:M:56:ARG:HH22	1.46	0.81
18:S:51:HIS:HA	18:S:56:HIS:HA	1.63	0.81
1:A:1343:G:H1'	8:I:122:ARG:HH12	1.46	0.80
6:G:2:ARG:HB3	6:G:2:ARG:NH1	1.97	0.80
2:C:137:VAL:HA	2:C:148:ILE:HD13	1.61	0.80
20:B:32:GLY:H	20:B:39:ILE:HB	1.46	0.80
13:N:15:LEU:HB3	13:N:54:SER:HB2	1.64	0.79

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:I:29:ILE:HG12	8:I:64:ILE:HB	1.63	0.79
8:I:39:GLY:HA2	8:I:44:ARG:HD3	1.64	0.79
13:N:87:ALA:HB2	13:N:92:ILE:HD12	1.65	0.79
1:A:1032:G:H2'	1:A:1033:G:O4'	1.83	0.79
19:T:34:VAL:HG11	19:T:78:LEU:HD22	1.63	0.79
6:G:62:GLU:HG2	6:G:69:ARG:HH21	1.48	0.78
6:G:91:ARG:HD2	6:G:91:ARG:H	1.46	0.78
15:P:3:THR:HG22	15:P:66:THR:HB	1.65	0.78
2:C:122:GLN:HB3	2:C:127:VAL:HG21	1.64	0.78
1:A:781:A:H2'	1:A:782:A:H5'	1.63	0.78
7:H:103:VAL:HG22	7:H:124:ILE:HA	1.65	0.78
1:A:1144:G:N2	1:A:1146:A:H62	1.82	0.78
11:L:20:VAL:HG12	11:L:93:ARG:HB3	1.65	0.78
1:A:83:C:O2'	1:A:84:U:H3'	1.85	0.77
12:M:44:ILE:HD12	12:M:44:ILE:H	1.48	0.77
1:A:1057:G:H4'	2:C:196:GLY:H	1.50	0.77
18:S:30:LEU:HB2	18:S:48:ILE:HG23	1.66	0.77
20:B:202:ASN:ND2	20:B:204:ASP:H	1.81	0.77
1:A:1078:U:H4'	4:E:137:ARG:NH1	2.00	0.77
7:H:17:GLN:HG2	7:H:62:LEU:HD23	1.65	0.77
1:A:1160:G:H4'	20:B:130:LYS:HB2	1.65	0.76
15:P:25:ARG:HD3	15:P:25:ARG:H	1.50	0.76
8:I:27:ILE:HD12	8:I:34:LEU:HD22	1.67	0.76
14:O:35:ILE:HD11	14:O:58:MET:HG3	1.66	0.76
2:C:77:GLY:HA3	2:C:81:GLU:HB3	1.68	0.76
6:G:21:LEU:HD23	6:G:21:LEU:H	1.49	0.76
1:A:1306:A:H61	1:A:1331:G:H1'	1.50	0.76
6:G:14:ASP:HB3	6:G:19:SER:H	1.51	0.76
1:A:238:A:H2'	1:A:239:U:H5''	1.67	0.76
8:I:46:VAL:HA	8:I:49:GLN:HG3	1.68	0.76
1:A:243:A:H4'	1:A:244:U:H5'	1.66	0.76
10:K:106:ILE:HG13	10:K:107:THR:H	1.51	0.76
3:D:13:ARG:HA	3:D:37:PRO:HB3	1.67	0.76
1:A:423:G:H2'	1:A:424:G:O4'	1.85	0.76
15:P:52:LEU:HD21	15:P:75:ILE:HG12	1.67	0.76
19:T:85:LEU:HD23	19:T:86:ALA:H	1.51	0.76
2:C:26:LYS:HG3	2:C:27:GLU:HG3	1.68	0.76
6:G:2:ARG:HB3	6:G:2:ARG:HH11	1.51	0.76
10:K:22:ILE:HD13	10:K:85:VAL:HG22	1.68	0.76
1:A:437:U:H2'	1:A:438:U:O4'	1.86	0.75
1:A:264:C:H4'	16:Q:64:ARG:HD2	1.67	0.75
4:E:44:ARG:HA	4:E:71:ILE:O	1.87	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:24:VAL:HA	3:D:27:ILE:HD11	1.68	0.75
1:A:812:G:O2'	1:A:813:U:H6	1.70	0.75
9:J:10:LEU:HD11	9:J:25:ILE:HD12	1.68	0.75
21:U:16:ARG:NE	21:U:16:ARG:HA	2.01	0.74
20:B:163:ILE:HG23	20:B:164:ASP:H	1.52	0.74
1:A:979:C:H1'	1:A:1317:C:H41	1.51	0.74
1:A:946:A:H2'	1:A:947:G:C8	2.22	0.74
13:N:68:ARG:HH12	13:N:70:HIS:HB2	1.53	0.74
1:A:108:G:H5'	1:A:109:A:H5''	1.69	0.74
9:J:36:VAL:HG22	9:J:76:ILE:HG22	1.67	0.74
1:A:269:C:H2'	1:A:270:A:C8	2.23	0.74
4:E:105:ILE:HG13	4:E:123:LEU:HA	1.70	0.74
1:A:674:G:H2'	1:A:675:A:H8	1.50	0.74
20:B:61:SER:HB2	20:B:62:ARG:HH11	1.52	0.74
10:K:22:ILE:HG21	10:K:95:THR:HG21	1.69	0.74
9:J:51:VAL:HG23	13:N:80:ARG:HB2	1.69	0.74
10:K:20:ALA:HB2	10:K:81:LEU:HD12	1.70	0.74
19:T:43:LYS:HE2	19:T:44:ALA:H	1.50	0.74
17:R:38:ILE:HD13	17:R:38:ILE:H	1.51	0.74
1:A:410:G:OP2	3:D:25:ARG:HD2	1.88	0.74
19:T:47:GLN:HG2	19:T:82:ILE:HD12	1.70	0.74
6:G:74:VAL:HA	6:G:87:PRO:HA	1.70	0.73
2:C:57:GLU:HB2	2:C:64:ARG:HB2	1.69	0.73
1:A:1323:G:H2'	1:A:1324:A:H8	1.54	0.73
19:T:38:ILE:HD11	19:T:82:ILE:HG22	1.68	0.73
13:N:52:ARG:HH11	13:N:58:ARG:HH21	1.37	0.73
13:N:50:LEU:H	13:N:51:PRO:HD2	1.53	0.73
1:A:842:U:H3'	1:A:843:U:H4'	1.69	0.73
1:A:1391:U:H2'	1:A:1392:G:C8	2.23	0.73
20:B:61:SER:HB2	20:B:62:ARG:NH1	2.03	0.73
20:B:19:THR:HA	20:B:37:VAL:HA	1.70	0.73
1:A:957:U:H4'	18:S:78:THR:HB	1.70	0.73
1:A:1026:G:H2'	1:A:1027:C:H6	1.54	0.73
12:M:19:THR:HA	12:M:24:VAL:HG23	1.69	0.73
14:O:7:THR:O	14:O:10:ILE:HG22	1.88	0.73
1:A:1320:C:H41	18:S:36:ARG:HG2	1.54	0.73
9:J:12:ALA:HB2	9:J:96:VAL:HG12	1.69	0.73
1:A:17:U:H2'	1:A:18:C:C6	2.24	0.73
12:M:89:ARG:HH22	12:M:94:LEU:HD12	1.54	0.73
4:E:104:ILE:HG23	4:E:111:ARG:HH12	1.53	0.72
11:L:37:TYR:HB2	11:L:51:VAL:HB	1.71	0.72
6:G:110:ARG:HD2	6:G:122:GLU:HB2	1.70	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:15:PHE:HA	20:B:42:LEU:HD21	1.71	0.72
1:A:337:G:H2'	1:A:338:A:C8	2.24	0.72
13:N:63:CYS:HB2	13:N:79:SER:HB3	1.71	0.72
9:J:8:ILE:HG13	9:J:100:ILE:HG22	1.71	0.72
1:A:859:G:H2'	1:A:860:A:C8	2.23	0.72
1:A:1472:U:H2'	1:A:1473:G:C8	2.25	0.72
21:U:36:PHE:CB	21:U:40:PRO:HD3	2.19	0.72
20:B:66:ILE:HD13	20:B:159:ALA:HB3	1.71	0.72
2:C:149:LYS:HB3	2:C:200:TRP:HB2	1.72	0.72
1:A:193:C:H2'	1:A:194:C:C6	2.25	0.72
1:A:1348:U:H4'	8:I:121:ARG:HG3	1.70	0.72
20:B:99:MET:HA	20:B:106:VAL:HG21	1.72	0.72
1:A:279:A:H5''	1:A:280:C:H3'	1.71	0.72
20:B:59:ILE:H	20:B:59:ILE:HD12	1.54	0.72
1:A:1004:A:H3'	1:A:1024:G:H22	1.53	0.72
1:A:1133:G:H2'	1:A:1134:G:O4'	1.89	0.72
4:E:76:ASN:HB2	4:E:81:GLN:NE2	2.05	0.72
2:C:104:GLU:HG2	2:C:105:VAL:H	1.53	0.72
1:A:462:G:H5'	1:A:463:U:OP2	1.90	0.72
1:A:1292:G:H2'	1:A:1293:C:C6	2.25	0.72
8:I:33:SER:HB3	8:I:36:GLN:HB2	1.72	0.71
1:A:1142:G:H2'	1:A:1143:G:O4'	1.90	0.71
1:A:882:C:O2'	1:A:883:C:H5'	1.91	0.71
1:A:408:A:OP1	3:D:111:ALA:HB3	1.90	0.71
6:G:115:MET:HA	6:G:118:ARG:HD2	1.72	0.71
1:A:797:C:OP1	10:K:125:LYS:HE3	1.91	0.71
1:A:1472:U:H2'	1:A:1473:G:H8	1.53	0.71
1:A:764:C:H2'	1:A:765:G:H5'	1.72	0.71
9:J:57:VAL:HG22	9:J:58:ASN:H	1.56	0.71
13:N:30:ILE:HB	13:N:44:VAL:HG11	1.71	0.71
21:U:43:GLU:HG3	21:U:44:ARG:HH21	1.56	0.71
10:K:91:GLY:HA2	10:K:94:SER:HB3	1.72	0.71
1:A:764:C:C2'	1:A:765:G:H5'	2.21	0.71
1:A:1118:U:H2'	1:A:1119:C:C6	2.25	0.71
8:I:93:LEU:HD13	8:I:97:LEU:HD11	1.71	0.70
1:A:617:G:H4'	15:P:46:LYS:HE2	1.73	0.70
1:A:1132:C:H2'	1:A:1133:G:H8	1.55	0.70
1:A:695:A:H61	1:A:797:C:H1'	1.56	0.70
1:A:522:C:H41	11:L:49:ARG:HH22	1.39	0.70
15:P:57:ILE:O	15:P:61:VAL:HG23	1.90	0.70
12:M:86:ARG:HG3	12:M:96:VAL:HG11	1.73	0.70
12:M:90:HIS:HA	12:M:108:ARG:NH2	2.06	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:137:THR:O	20:B:141:GLU:HG3	1.92	0.70
8:I:64:ILE:HD12	8:I:64:ILE:H	1.57	0.70
20:B:53:LEU:HA	20:B:56:LEU:HD13	1.72	0.70
13:N:30:ILE:HG22	13:N:41:TRP:HB2	1.74	0.70
1:A:235:C:H2'	1:A:236:A:C8	2.27	0.70
2:C:112:ALA:HB1	2:C:184:ASN:HB2	1.73	0.70
10:K:33:ILE:HG13	10:K:73:VAL:HG21	1.72	0.70
3:D:197:HIS:O	3:D:200:VAL:HG22	1.91	0.70
2:C:63:ILE:HD12	2:C:98:ALA:HB2	1.72	0.70
3:D:47:LEU:HB2	3:D:51:GLY:HA3	1.72	0.70
13:N:86:ALA:HB1	13:N:91:GLU:HB2	1.73	0.70
21:U:42:THR:O	21:U:46:ARG:HG3	1.92	0.70
2:C:156:LEU:HD12	2:C:163:ARG:HD2	1.72	0.70
1:A:974:A:H4'	1:A:975:A:H5'	1.74	0.70
1:A:522:C:H41	11:L:49:ARG:NH2	1.90	0.70
20:B:60:ALA:HA	20:B:64:GLY:HA3	1.73	0.70
20:B:76:SER:HA	20:B:92:ASN:HB2	1.74	0.70
3:D:137:SER:HB2	3:D:138:PRO:HD2	1.73	0.70
5:F:26:THR:HA	5:F:29:ILE:HD12	1.73	0.70
16:Q:45:VAL:HG12	16:Q:46:HIS:H	1.56	0.70
7:H:44:PHE:HA	7:H:70:VAL:HG11	1.72	0.70
3:D:196:GLU:O	3:D:199:ILE:HG13	1.91	0.70
11:L:122:LYS:HD2	11:L:123:ALA:N	2.06	0.70
6:G:66:GLU:HA	6:G:69:ARG:HD2	1.74	0.69
11:L:51:VAL:HG12	11:L:52:CYS:H	1.57	0.69
11:L:66:ILE:HG21	11:L:71:HIS:HB3	1.72	0.69
12:M:92:ARG:HH12	18:S:79:TYR:HD2	1.40	0.69
20:B:205:ALA:HB3	20:B:208:ALA:HB3	1.73	0.69
2:C:148:ILE:HA	2:C:200:TRP:O	1.92	0.69
7:H:124:ILE:HG22	7:H:125:ILE:H	1.55	0.69
12:M:67:ASP:O	12:M:71:GLU:HB2	1.92	0.69
12:M:28:ARG:NH2	12:M:62:PHE:HB2	2.08	0.69
18:S:62:THR:HB	18:S:64:GLU:OE1	1.90	0.69
11:L:86:VAL:HG11	11:L:89:LEU:HD23	1.74	0.69
4:E:36:THR:HG21	4:E:63:MET:HG2	1.73	0.69
4:E:84:VAL:HG11	4:E:146:MET:HB3	1.75	0.69
1:A:964:A:H2'	1:A:965:U:H5''	1.74	0.69
8:I:25:GLY:HA2	8:I:60:LEU:O	1.93	0.69
1:A:229:U:H2'	1:A:230:G:H8	1.58	0.69
3:D:58:GLN:O	3:D:62:ARG:HG2	1.92	0.69
20:B:88:GLN:OE1	20:B:221:ARG:HB3	1.93	0.69
1:A:920:U:H2'	1:A:921:U:C6	2.27	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:119:ILE:HG21	2:C:197:VAL:HG11	1.72	0.69
8:I:126:PHE:HE1	8:I:129:ARG:HD3	1.57	0.69
1:A:475:C:H2'	1:A:476:U:C6	2.28	0.69
20:B:69:VAL:HB	20:B:162:VAL:HG23	1.74	0.69
8:I:26:LYS:H	8:I:61:ASP:CB	2.05	0.69
15:P:28:ARG:HD2	15:P:29:ASN:N	2.08	0.69
1:A:337:G:H2'	1:A:338:A:H8	1.58	0.69
1:A:677:U:H2'	1:A:678:U:C6	2.27	0.69
8:I:71:ILE:HD12	8:I:71:ILE:H	1.56	0.69
16:Q:77:VAL:HG11	16:Q:80:LYS:HB3	1.74	0.68
8:I:51:LEU:HD13	8:I:56:MET:HG2	1.75	0.68
9:J:7:ARG:O	9:J:100:ILE:HA	1.93	0.68
1:A:195:A:H1'	1:A:222:C:O2'	1.93	0.68
7:H:74:ILE:HG13	7:H:128:VAL:HG22	1.74	0.68
1:A:449:G:H2'	1:A:450:G:C8	2.28	0.68
1:A:1220:G:H3'	18:S:36:ARG:HH21	1.56	0.68
1:A:1026:G:H2'	1:A:1027:C:C6	2.27	0.68
2:C:2:GLN:H	2:C:2:GLN:NE2	1.92	0.68
16:Q:30:HIS:CE1	16:Q:32:ILE:HG22	2.27	0.68
16:Q:83:LEU:HD22	16:Q:83:LEU:H	1.57	0.68
12:M:10:ASP:HA	12:M:44:ILE:HD13	1.73	0.68
1:A:17:U:H2'	1:A:18:C:H6	1.57	0.68
1:A:176:C:H2'	1:A:177:G:N3	2.07	0.68
2:C:16:PRO:HG2	2:C:53:ARG:HH12	1.58	0.68
14:O:28:VAL:HG11	14:O:80:LEU:HD21	1.75	0.68
1:A:451:A:H5'	15:P:70:ARG:HH22	1.58	0.68
2:C:149:LYS:HA	2:C:168:ARG:HB2	1.76	0.68
20:B:145:ASN:HD22	20:B:145:ASN:N	1.90	0.68
2:C:51:VAL:HA	2:C:69:THR:HA	1.74	0.68
1:A:108:G:C6	19:T:9:ARG:HG2	2.29	0.68
1:A:89:U:H2'	1:A:90:C:C6	2.28	0.68
1:A:559:A:H4'	1:A:560:A:H3'	1.76	0.68
1:A:1238:A:H5'	1:A:1336:C:H41	1.59	0.68
19:T:61:ALA:HA	19:T:67:HIS:H	1.59	0.68
1:A:1134:G:C2	1:A:1135:U:H1'	2.29	0.68
1:A:1505:G:H4'	1:A:1506:U:H5''	1.73	0.68
1:A:97:G:H2'	1:A:98:A:O4'	1.94	0.68
5:F:64:VAL:HG12	5:F:65:GLU:H	1.57	0.68
1:A:344:A:H4'	1:A:345:C:OP2	1.93	0.68
16:Q:16:MET:CB	16:Q:19:SER:HB2	2.23	0.68
18:S:31:ARG:HA	18:S:49:ALA:HB3	1.76	0.68
6:G:91:ARG:HB3	6:G:92:PRO:HD2	1.76	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:239:U:OP1	1:A:239:U:H4'	1.92	0.68
11:L:49:ARG:HG2	11:L:89:LEU:HD21	1.75	0.68
1:A:1412:C:H2'	1:A:1413:A:H8	1.59	0.68
1:A:1414:U:H2'	1:A:1415:G:H8	1.60	0.68
1:A:1234:C:O2'	1:A:1235:U:H5'	1.94	0.68
1:A:1306:A:N6	1:A:1331:G:H1'	2.09	0.67
3:D:56:GLU:HG2	3:D:198:LEU:HD12	1.77	0.67
1:A:973:G:H3'	1:A:974:A:H5''	1.76	0.67
1:A:1513:A:H2'	1:A:1514:G:C8	2.29	0.67
1:A:810:C:O2'	1:A:811:C:H5'	1.93	0.67
12:M:70:ARG:O	12:M:74:MET:HG2	1.94	0.67
21:U:38:GLU:C	21:U:40:PRO:HD2	2.14	0.67
1:A:1060:U:C4'	9:J:54:SER:HB2	2.24	0.67
20:B:199:ILE:HD13	20:B:212:TYR:HE2	1.59	0.67
8:I:29:ILE:HA	8:I:64:ILE:O	1.95	0.67
3:D:153:ARG:HG3	3:D:154:VAL:N	2.07	0.67
1:A:376:G:H5''	15:P:5:ARG:HB2	1.76	0.67
1:A:108:G:O6	19:T:9:ARG:HG2	1.95	0.67
16:Q:20:ILE:HD13	16:Q:47:ASP:HB3	1.76	0.67
1:A:1314:C:H3'	18:S:5:LYS:HZ2	1.58	0.67
18:S:38:THR:HA	18:S:69:LYS:HA	1.77	0.67
6:G:23:ALA:O	6:G:26:VAL:HG22	1.95	0.67
13:N:68:ARG:NH1	13:N:71:GLY:H	1.92	0.67
20:B:113:LEU:HD13	20:B:147:LEU:HB2	1.75	0.67
2:C:171:ARG:HB2	2:C:171:ARG:HH11	1.58	0.67
1:A:865:A:H2	1:A:918:A:H4'	1.60	0.67
1:A:157:U:O2'	1:A:158:G:H5'	1.94	0.67
8:I:87:MET:HA	8:I:93:LEU:HD11	1.77	0.66
1:A:229:U:H2'	1:A:230:G:C8	2.30	0.66
1:A:415:A:H3'	1:A:416:G:H8	1.60	0.66
15:P:34:GLU:CD	15:P:60:TRP:HE1	1.99	0.66
1:A:706:A:H4'	10:K:30:ILE:HD11	1.77	0.66
1:A:21:G:H2'	1:A:22:G:C8	2.30	0.66
1:A:1388:C:H2'	1:A:1389:C:H6	1.60	0.66
10:K:83:VAL:HG21	10:K:109:ILE:HG12	1.76	0.66
13:N:52:ARG:NH1	13:N:58:ARG:HH21	1.92	0.66
1:A:6:G:H3'	1:A:6:G:N3	2.09	0.66
1:A:1382:C:H4'	6:G:78:ARG:CZ	2.25	0.66
6:G:72:VAL:HG12	6:G:89:GLU:HB3	1.78	0.66
20:B:212:TYR:HA	20:B:215:ALA:HB3	1.78	0.66
1:A:1288:A:N1	1:A:1371:G:H1'	2.10	0.66
15:P:28:ARG:CD	15:P:29:ASN:H	2.05	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:68:PHE:HA	20:B:161:PHE:O	1.96	0.66
1:A:1078:U:H4'	4:E:137:ARG:HH12	1.57	0.66
1:A:1080:A:H2'	1:A:1081:A:H5'	1.78	0.66
1:A:1412:C:H2'	1:A:1413:A:C8	2.29	0.66
1:A:1342:C:H2'	1:A:1343:G:C8	2.30	0.66
3:D:96:ARG:HB3	3:D:98:ASP:OD2	1.95	0.66
1:A:208:U:H2'	1:A:210:C:C4	2.30	0.66
4:E:32:PHE:O	4:E:51:LYS:HB2	1.94	0.66
1:A:266:G:O2'	1:A:267:C:H3'	1.96	0.66
1:A:1095:U:H2'	1:A:1096:C:C6	2.30	0.66
1:A:384:G:H2'	1:A:385:C:C6	2.30	0.66
1:A:1417:G:H22	1:A:1482:G:H2'	1.60	0.66
1:A:673:A:H2'	1:A:674:G:C8	2.31	0.66
8:I:10:ARG:HA	8:I:77:ALA:HB1	1.76	0.66
1:A:1152:A:H2'	1:A:1153:G:H8	1.61	0.66
16:Q:74:LEU:HD22	16:Q:75:VAL:N	2.08	0.66
1:A:575:G:H4'	1:A:576:C:O5'	1.96	0.66
4:E:45:VAL:HG12	4:E:116:VAL:HG23	1.78	0.66
16:Q:75:VAL:HG23	16:Q:76:ARG:HG2	1.77	0.66
1:A:1343:G:H1'	8:I:122:ARG:NH1	2.10	0.66
12:M:89:ARG:HG3	12:M:96:VAL:HG13	1.77	0.66
1:A:1149:C:H2'	1:A:1150:A:H8	1.61	0.65
20:B:209:VAL:HG23	20:B:210:THR:H	1.60	0.65
1:A:1513:A:H2'	1:A:1514:G:H8	1.60	0.65
4:E:152:VAL:HG21	7:H:98:LEU:HB3	1.78	0.65
6:G:56:SER:HB3	6:G:59:GLU:HG3	1.77	0.65
1:A:825:A:H2'	1:A:826:C:H6	1.60	0.65
1:A:841:C:O5'	1:A:842:U:H5''	1.96	0.65
12:M:64:VAL:HA	12:M:68:LEU:HD11	1.77	0.65
12:M:63:VAL:O	12:M:68:LEU:HD21	1.97	0.65
1:A:1070:U:H2'	1:A:1071:C:C6	2.31	0.65
1:A:1297:G:H1'	1:A:1298:U:H5	1.61	0.65
20:B:195:VAL:HG12	20:B:197:PHE:H	1.61	0.65
1:A:1085:U:H3'	1:A:1086:U:C5	2.31	0.65
12:M:2:ARG:HD3	12:M:2:ARG:H	1.59	0.65
18:S:30:LEU:HD12	18:S:48:ILE:HG12	1.78	0.65
1:A:373:A:H2'	1:A:374:A:H8	1.61	0.65
20:B:14:HIS:HB2	20:B:208:ALA:HB2	1.79	0.65
16:Q:59:GLU:O	16:Q:75:VAL:HG22	1.96	0.65
20:B:114:LYS:HE2	20:B:151:LYS:HZ1	1.62	0.65
14:O:7:THR:O	14:O:11:VAL:HG23	1.96	0.65
1:A:1103:C:H5''	20:B:96:LEU:HD12	1.79	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:473:U:H2'	1:A:474:G:C8	2.31	0.65
1:A:834:U:H2'	1:A:835:U:C6	2.31	0.65
3:D:122:ILE:O	3:D:128:VAL:HG23	1.96	0.65
13:N:58:ARG:HH11	13:N:58:ARG:HB3	1.62	0.65
18:S:42:ASN:N	18:S:42:ASN:HD22	1.95	0.65
18:S:41:PRO:O	18:S:44:ILE:HG22	1.97	0.65
1:A:1391:U:H2'	1:A:1392:G:H8	1.60	0.65
1:A:678:U:H2'	1:A:679:C:C6	2.32	0.65
3:D:36:ALA:HA	3:D:41:GLY:HA3	1.77	0.65
1:A:51:A:H5''	1:A:52:C:H5''	1.78	0.65
5:F:38:ARG:HH21	5:F:63:ASN:HD21	1.43	0.65
8:I:25:GLY:HA3	8:I:57:VAL:CA	2.27	0.65
7:H:63:LYS:HD2	7:H:70:VAL:HG21	1.78	0.65
11:L:106:VAL:HG23	11:L:116:TYR:HB3	1.79	0.65
16:Q:13:SER:HB3	16:Q:21:VAL:HB	1.78	0.65
1:A:662:U:H2'	1:A:663:A:C8	2.31	0.64
6:G:45:ALA:HB1	6:G:120:ALA:HB2	1.79	0.64
4:E:85:LYS:HG3	4:E:93:VAL:O	1.96	0.64
8:I:20:ILE:H	8:I:20:ILE:HD12	1.62	0.64
2:C:48:LYS:HE2	2:C:48:LYS:N	2.07	0.64
1:A:1258:G:H2'	1:A:1259:C:C6	2.33	0.64
21:U:16:ARG:CA	21:U:16:ARG:HE	2.01	0.64
10:K:108:ASN:ND2	21:U:6:ARG:HB2	2.12	0.64
1:A:1132:C:H2'	1:A:1133:G:C8	2.32	0.64
1:A:1270:G:H2'	1:A:1271:A:H8	1.62	0.64
1:A:707:U:H2'	1:A:708:C:C6	2.33	0.64
5:F:40:GLU:HB2	5:F:61:LEU:HB2	1.80	0.64
1:A:658:C:H2'	1:A:659:U:H6	1.62	0.64
8:I:79:ARG:NH2	8:I:102:PHE:HA	2.11	0.64
10:K:75:GLU:CD	10:K:75:GLU:H	1.98	0.64
1:A:927:G:H4'	1:A:1503:A:N7	2.12	0.64
1:A:71:A:O2'	1:A:72:A:H5''	1.98	0.64
1:A:825:A:H2'	1:A:826:C:C6	2.33	0.64
11:L:113:ARG:HG2	11:L:118:VAL:HB	1.80	0.64
1:A:735:C:O2'	1:A:736:C:H5'	1.97	0.64
1:A:763:G:H2'	1:A:764:C:H6	1.62	0.64
3:D:106:PHE:CD1	3:D:144:ILE:HD11	2.32	0.64
1:A:131:A:H2'	1:A:132:C:H6	1.62	0.64
20:B:115:ASP:O	20:B:119:GLN:HG2	1.97	0.64
3:D:29:THR:HB	3:D:30:LYS:NZ	2.12	0.64
1:A:1008:U:H5''	13:N:23:ARG:NH2	2.13	0.64
4:E:125:LYS:HD2	4:E:126:ALA:N	2.12	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:845:A:H5''	1:A:846:G:N7	2.13	0.64
7:H:6:ILE:HD11	7:H:31:LEU:HD23	1.79	0.64
20:B:186:VAL:HB	20:B:190:SER:CB	2.28	0.64
4:E:105:ILE:HD11	4:E:123:LEU:HB3	1.80	0.64
10:K:28:ASN:ND2	10:K:46:ALA:HB3	2.12	0.64
7:H:51:GLU:HG2	7:H:52:GLY:H	1.61	0.64
1:A:1320:C:N4	18:S:36:ARG:HG2	2.13	0.64
12:M:3:ILE:O	12:M:56:ARG:HG3	1.98	0.64
3:D:25:ARG:CZ	3:D:26:ALA:HB2	2.26	0.64
1:A:1323:G:H4'	1:A:1362:A:C4	2.33	0.64
1:A:69:G:N2	1:A:71:A:H62	1.96	0.64
1:A:412:A:H4'	1:A:413:G:OP1	1.98	0.64
20:B:62:ARG:H	20:B:62:ARG:HD2	1.63	0.64
8:I:42:THR:HA	8:I:45:MET:SD	2.37	0.64
1:A:129:A:H1'	1:A:130:A:C8	2.33	0.64
5:F:47:LEU:HD21	5:F:57:ALA:HB3	1.80	0.64
3:D:153:ARG:HG3	3:D:154:VAL:H	1.63	0.64
9:J:52:LEU:HA	9:J:62:ARG:HA	1.80	0.64
1:A:131:A:H2'	1:A:132:C:C6	2.33	0.64
1:A:524:G:H2'	1:A:525:C:C6	2.33	0.64
1:A:1404:C:H2'	1:A:1405:G:C8	2.33	0.64
1:A:958:A:H61	18:S:53:GLY:HA3	1.64	0.63
1:A:1148:U:H5'	8:I:6:TYR:OH	1.98	0.63
1:A:1004:A:H3'	1:A:1024:G:N2	2.12	0.63
1:A:1347:G:N2	1:A:1373:G:H2'	2.13	0.63
3:D:25:ARG:NH1	3:D:26:ALA:HB2	2.12	0.63
6:G:49:LEU:HD21	6:G:60:ALA:HB3	1.79	0.63
1:A:1330:U:H4'	12:M:69:ARG:HH12	1.63	0.63
1:A:437:U:H4'	3:D:153:ARG:HH12	1.63	0.63
1:A:859:G:H2'	1:A:860:A:H8	1.61	0.63
11:L:40:THR:HG22	11:L:41:PRO:HD2	1.79	0.63
1:A:370:C:O2'	1:A:371:A:H5'	1.99	0.63
2:C:62:SER:HA	2:C:97:PRO:O	1.98	0.63
20:B:101:THR:HG22	20:B:174:GLU:OE1	1.98	0.63
1:A:492:C:H2'	1:A:493:A:N3	2.12	0.63
1:A:1342:C:H2'	1:A:1343:G:H8	1.63	0.63
11:L:122:LYS:HD2	11:L:123:ALA:H	1.64	0.63
18:S:5:LYS:O	18:S:6:LYS:HD2	1.97	0.63
1:A:1307:U:H2'	1:A:1308:U:C6	2.33	0.63
13:N:42:ASN:O	13:N:46:LYS:HG2	1.99	0.63
3:D:160:LEU:HA	3:D:163:GLN:HG3	1.80	0.63
1:A:1380:U:O4	6:G:2:ARG:HB2	1.99	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:U:48:LYS:HA	21:U:51:ALA:HB3	1.80	0.63
8:I:23:GLY:H	8:I:60:LEU:HA	1.62	0.63
9:J:56:HIS:O	9:J:57:VAL:HG12	1.99	0.63
17:R:55:ALA:HA	17:R:58:ILE:HD13	1.80	0.63
10:K:28:ASN:HD21	10:K:46:ALA:HB3	1.62	0.63
1:A:950:U:H2'	1:A:951:G:C8	2.34	0.63
3:D:29:THR:HG22	3:D:30:LYS:H	1.64	0.63
4:E:158:LYS:HZ3	7:H:63:LYS:HD3	1.62	0.63
1:A:462:G:H2'	1:A:462:G:N3	2.13	0.63
1:A:677:U:H2'	1:A:678:U:H6	1.63	0.63
7:H:94:VAL:HG23	7:H:101:ALA:HB2	1.80	0.63
1:A:376:G:H2'	1:A:377:G:H8	1.64	0.63
1:A:620:C:C2	3:D:131:ILE:HD13	2.33	0.63
1:A:204:G:H2'	1:A:205:A:C8	2.34	0.63
8:I:25:GLY:HA3	8:I:57:VAL:N	2.13	0.62
9:J:52:LEU:HD12	9:J:52:LEU:H	1.64	0.62
9:J:28:THR:O	9:J:32:THR:HG22	1.98	0.62
1:A:600:A:H2'	1:A:601:G:H8	1.63	0.62
1:A:978:A:HO2'	1:A:1322:C:H5	1.46	0.62
6:G:14:ASP:CB	6:G:19:SER:H	2.12	0.62
6:G:86:VAL:HG13	6:G:151:ALA:O	1.98	0.62
9:J:24:GLU:HG3	9:J:90:LEU:HD11	1.81	0.62
18:S:10:ILE:HD12	18:S:15:LEU:HG	1.81	0.62
1:A:1144:G:H21	1:A:1146:A:H62	1.46	0.62
1:A:750:C:O2	14:O:22:GLY:HA3	1.98	0.62
1:A:946:A:H2'	1:A:947:G:H8	1.63	0.62
2:C:59:PRO:HG2	2:C:62:SER:OG	2.00	0.62
1:A:1053:G:H4'	1:A:1054:C:H5'	1.81	0.62
8:I:18:VAL:HG11	8:I:82:ILE:HG12	1.81	0.62
20:B:205:ALA:O	20:B:209:VAL:HG22	1.98	0.62
4:E:37:VAL:HG11	4:E:113:VAL:HG12	1.82	0.62
1:A:763:G:H2'	1:A:764:C:C6	2.34	0.62
13:N:26:LEU:HA	13:N:29:ILE:HD12	1.82	0.62
1:A:162:A:H2'	1:A:163:C:O4'	2.00	0.62
1:A:482:A:H2'	1:A:483:C:O4'	2.00	0.62
13:N:63:CYS:HB3	13:N:67:GLY:H	1.63	0.62
12:M:63:VAL:HG13	12:M:67:ASP:HB2	1.82	0.62
1:A:154:U:H2'	1:A:155:A:C8	2.35	0.62
3:D:84:ASN:ND2	4:E:101:GLY:HA3	2.14	0.62
1:A:1092:A:H5''	6:G:3:ARG:HH11	1.64	0.62
1:A:865:A:C2	1:A:918:A:H4'	2.34	0.62
11:L:14:LYS:HG2	11:L:16:ALA:H	1.63	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:71:THR:CG2	20:B:94:ARG:H	2.12	0.62
19:T:4:LYS:HZ1	19:T:6:ALA:HB2	1.63	0.62
5:F:3:HIS:CE1	5:F:95:ALA:H	2.18	0.62
1:A:487:A:H2'	1:A:488:C:O4'	2.00	0.62
1:A:1149:C:H2'	1:A:1150:A:C8	2.35	0.62
6:G:14:ASP:N	6:G:23:ALA:HB2	2.14	0.62
1:A:255:G:H2'	1:A:256:U:C6	2.34	0.62
1:A:1141:C:H2'	1:A:1142:G:H8	1.65	0.62
1:A:678:U:H2'	1:A:679:C:H6	1.64	0.62
1:A:539:A:H2'	1:A:540:G:C8	2.35	0.62
1:A:909:A:H2'	1:A:910:C:O4'	1.99	0.62
1:A:1432:G:H1'	1:A:1468:A:N6	2.14	0.62
3:D:123:MET:HB3	3:D:128:VAL:HA	1.82	0.61
9:J:53:ILE:HG22	9:J:61:ALA:HB1	1.82	0.61
6:G:2:ARG:HH11	6:G:2:ARG:CB	2.13	0.61
4:E:93:VAL:HG13	4:E:126:ALA:HB2	1.82	0.61
5:F:36:ILE:HG13	5:F:64:VAL:HG13	1.81	0.61
16:Q:58:VAL:HG12	16:Q:77:VAL:HA	1.82	0.61
21:U:33:ARG:HG2	21:U:34:ARG:H	1.65	0.61
19:T:79:THR:HA	19:T:82:ILE:HG12	1.82	0.61
1:A:46:G:O2'	1:A:365:U:H1'	2.00	0.61
1:A:1244:G:H2'	1:A:1245:C:C6	2.35	0.61
1:A:410:G:P	3:D:25:ARG:HD2	2.40	0.61
21:U:40:PRO:HA	21:U:44:ARG:HB2	1.82	0.61
8:I:17:ARG:O	8:I:64:ILE:HA	2.00	0.61
19:T:66:ILE:HG22	19:T:67:HIS:N	2.15	0.61
1:A:1029:U:H1'	1:A:1032:G:O6	2.00	0.61
1:A:1382:C:H4'	6:G:78:ARG:NH2	2.15	0.61
1:A:1463:U:H2'	1:A:1464:U:C6	2.36	0.61
13:N:9:GLU:HB2	13:N:62:ARG:NE	2.15	0.61
8:I:29:ILE:HD13	8:I:78:ILE:HD13	1.81	0.61
18:S:62:THR:HG22	18:S:63:ASP:H	1.66	0.61
1:A:978:A:H5'	1:A:1362:A:N6	2.14	0.61
4:E:81:GLN:H	4:E:146:MET:CE	2.14	0.61
1:A:335:C:H2'	1:A:336:A:H8	1.64	0.61
1:A:41:G:H2'	1:A:42:G:C8	2.35	0.61
1:A:987:G:O2'	1:A:988:G:H5'	2.00	0.61
5:F:42:TRP:HB2	5:F:59:TYR:HB2	1.82	0.61
18:S:30:LEU:H	18:S:48:ILE:HA	1.66	0.61
1:A:792:A:H1'	1:A:794:A:N7	2.15	0.61
1:A:1213:A:H2'	1:A:1215:G:N7	2.16	0.61
1:A:668:G:O2'	14:O:45:HIS:HB3	2.00	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:20:ARG:HA	20:B:38:HIS:HE1	1.65	0.61
12:M:79:LEU:HD21	12:M:86:ARG:HH21	1.65	0.61
1:A:335:C:H2'	1:A:336:A:C8	2.36	0.61
1:A:1210:C:H1'	1:A:1214:C:H2'	1.83	0.61
12:M:89:ARG:NH2	12:M:94:LEU:HD12	2.15	0.61
1:A:1278:G:H4'	1:A:1279:G:C5'	2.29	0.61
5:F:100:SER:HA	17:R:23:LYS:CE	2.30	0.61
1:A:512:U:H2'	1:A:513:C:C6	2.36	0.61
20:B:221:ARG:HG3	20:B:222:GLU:N	2.15	0.61
14:O:72:LYS:O	14:O:73:ASP:HB2	2.01	0.61
7:H:11:THR:HG22	7:H:14:ARG:HH22	1.65	0.61
2:C:13:ILE:O	2:C:14:VAL:HG22	2.00	0.61
18:S:50:VAL:O	18:S:57:VAL:HG22	2.00	0.60
1:A:1296:C:H4'	1:A:1302:C:C4	2.36	0.60
13:N:41:TRP:HB3	13:N:44:VAL:HB	1.83	0.60
1:A:1071:C:H2'	1:A:1072:G:H8	1.65	0.60
8:I:7:GLY:HA2	8:I:85:ALA:HB2	1.82	0.60
1:A:1238:A:N3	1:A:1238:A:H2'	2.16	0.60
1:A:253:A:H2'	1:A:254:G:C8	2.36	0.60
10:K:70:ALA:O	10:K:74:LYS:HB2	2.01	0.60
10:K:81:LEU:HD11	10:K:99:LEU:HD23	1.81	0.60
1:A:195:A:H2'	1:A:196:A:C8	2.36	0.60
1:A:1388:C:H2'	1:A:1389:C:C6	2.35	0.60
1:A:218:U:H2'	1:A:219:U:C6	2.36	0.60
1:A:17:U:O2'	1:A:1079:G:H1'	2.01	0.60
20:B:20:ARG:HA	20:B:38:HIS:CE1	2.36	0.60
1:A:1343:G:H4'	8:I:123:ARG:O	2.01	0.60
7:H:46:GLU:HB2	7:H:61:THR:HB	1.82	0.60
10:K:81:LEU:HD21	10:K:104:PHE:HB3	1.83	0.60
12:M:95:PRO:N	12:M:108:ARG:HG2	2.16	0.60
19:T:19:HIS:O	19:T:23:ARG:HG2	2.01	0.60
5:F:18:VAL:HG21	5:F:58:HIS:ND1	2.16	0.60
8:I:25:GLY:HA3	8:I:57:VAL:H	1.65	0.60
6:G:145:GLU:HA	6:G:148:LYS:HB2	1.84	0.60
11:L:26:CYS:SG	11:L:29:LYS:HE2	2.41	0.60
20:B:72:LYS:HE3	20:B:203:ASP:O	2.02	0.60
18:S:16:LYS:O	18:S:20:LYS:HB2	2.01	0.60
6:G:62:GLU:O	6:G:66:GLU:HG3	2.01	0.60
13:N:30:ILE:HG21	13:N:44:VAL:HG21	1.83	0.60
1:A:1427:C:H2'	1:A:1428:A:C8	2.37	0.60
4:E:106:ALA:HB1	4:E:110:MET:HB3	1.84	0.60
6:G:26:VAL:HB	6:G:39:GLU:HG2	1.83	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:270:A:H2'	1:A:271:C:C6	2.35	0.60
1:A:473:U:H2'	1:A:474:G:H8	1.66	0.60
4:E:143:LEU:O	4:E:146:MET:HG2	2.02	0.60
1:A:91:U:H2'	1:A:92:U:C6	2.36	0.60
1:A:208:U:H2'	1:A:210:C:N3	2.16	0.60
1:A:1001:C:H2'	1:A:1002:G:C8	2.36	0.60
1:A:923:A:H2'	1:A:924:C:C6	2.37	0.60
1:A:276:G:H5'	16:Q:16:MET:SD	2.42	0.60
7:H:25:THR:HA	7:H:58:LEU:O	2.01	0.60
8:I:9:GLY:HA3	8:I:81:GLY:H	1.67	0.60
1:A:1437:A:H2'	1:A:1438:G:H8	1.67	0.60
6:G:24:LYS:HA	6:G:27:ASN:HD22	1.66	0.60
4:E:100:GLU:HA	4:E:121:ASN:ND2	2.16	0.60
20:B:202:ASN:HD22	20:B:204:ASP:N	1.88	0.60
20:B:187:ASP:HB3	20:B:201:GLY:O	2.02	0.60
1:A:1302:C:H5'	12:M:16:ILE:HG13	1.84	0.60
12:M:79:LEU:HD11	12:M:86:ARG:HH21	1.66	0.60
11:L:7:VAL:HG22	16:Q:33:TYR:HD1	1.66	0.60
1:A:1386:G:H2'	1:A:1387:G:H8	1.67	0.60
1:A:35:G:H2'	1:A:36:C:C6	2.37	0.60
1:A:1236:A:H4'	1:A:1304:G:H4'	1.81	0.60
1:A:190:A:H8	1:A:190:A:O5'	1.85	0.60
3:D:29:THR:HG22	3:D:30:LYS:HD3	1.83	0.60
1:A:1417:G:N2	1:A:1482:G:H2'	2.17	0.60
7:H:24:VAL:HG12	7:H:60:LEU:O	2.01	0.60
5:F:79:ARG:NH2	5:F:87:SER:HB3	2.17	0.60
20:B:31:PHE:N	20:B:39:ILE:O	2.34	0.59
3:D:138:PRO:HA	3:D:181:PHE:CD2	2.31	0.59
1:A:1271:A:H5'	1:A:1314:C:H5'	1.83	0.59
1:A:182:A:O2'	1:A:183:C:H3'	2.02	0.59
1:A:1151:A:HO2'	1:A:1152:A:H8	1.49	0.59
20:B:163:ILE:HG23	20:B:164:ASP:N	2.17	0.59
8:I:126:PHE:CE1	8:I:129:ARG:HD3	2.37	0.59
1:A:10:A:H2'	1:A:11:G:C8	2.37	0.59
10:K:51:PHE:HB2	10:K:55:ARG:HB3	1.84	0.59
1:A:1301:U:H2'	1:A:1301:U:O2	2.02	0.59
3:D:169:TRP:CE2	3:D:185:PRO:HB3	2.36	0.59
20:B:42:LEU:O	20:B:46:VAL:HG12	2.02	0.59
1:A:1296:C:H4'	1:A:1302:C:N3	2.18	0.59
8:I:27:ILE:HB	8:I:34:LEU:HB2	1.84	0.59
1:A:1179:A:H2'	1:A:1180:A:O4'	2.02	0.59
1:A:824:G:O2'	1:A:825:A:H5'	2.02	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1258:G:H2'	1:A:1259:C:H6	1.68	0.59
1:A:918:A:H2'	1:A:919:A:C8	2.38	0.59
1:A:806:C:H2'	1:A:807:A:C8	2.36	0.59
20:B:23:ASN:HD22	20:B:24:PRO:HD2	1.67	0.59
12:M:58:GLU:O	12:M:61:LYS:HG2	2.01	0.59
1:A:751:U:H4'	14:O:23:SER:HA	1.83	0.59
12:M:43:LYS:H	12:M:43:LYS:HD2	1.68	0.59
16:Q:45:VAL:HG12	16:Q:46:HIS:N	2.18	0.59
1:A:699:C:C2'	1:A:700:G:H5''	2.30	0.59
8:I:93:LEU:O	8:I:97:LEU:HG	2.02	0.59
1:A:336:A:O2'	1:A:337:G:H5'	2.03	0.59
1:A:239:U:C5'	1:A:239:U:H6	2.15	0.59
8:I:120:ALA:O	8:I:121:ARG:HG2	2.02	0.59
1:A:1058:G:OP1	2:C:198:LYS:HE3	2.03	0.59
12:M:22:TYR:HB2	12:M:65:GLU:HA	1.83	0.59
1:A:499:A:H4'	1:A:500:G:H5'	1.85	0.59
2:C:82:ASP:HA	2:C:85:LYS:HB3	1.85	0.59
1:A:1296:C:H4'	1:A:1302:C:N4	2.17	0.59
1:A:1239:A:H4'	1:A:1240:U:H5'	1.84	0.59
5:F:3:HIS:NE2	5:F:95:ALA:HB2	2.18	0.59
20:B:16:GLY:CA	20:B:40:ILE:H	2.16	0.59
12:M:79:LEU:HD11	12:M:86:ARG:NH2	2.17	0.59
1:A:72:A:H5'	1:A:73:C:OP2	2.02	0.59
1:A:501:C:H2'	1:A:502:A:C8	2.37	0.59
20:B:32:GLY:N	20:B:39:ILE:HB	2.16	0.59
12:M:21:ILE:HB	12:M:24:VAL:CG2	2.27	0.59
18:S:43:MET:HB2	18:S:61:VAL:HG11	1.84	0.59
7:H:17:GLN:HE21	7:H:62:LEU:HB3	1.68	0.59
1:A:621:A:H2'	1:A:622:A:C8	2.38	0.59
12:M:77:LYS:HG2	12:M:81:ASP:OD2	2.02	0.59
20:B:99:MET:HA	20:B:106:VAL:HG11	1.85	0.59
1:A:332:G:OP2	19:T:4:LYS:HB2	2.03	0.59
1:A:802:A:H2'	1:A:803:G:O4'	2.03	0.59
1:A:719:C:O2'	17:R:37:LYS:HB2	2.03	0.59
1:A:1478:U:H2'	1:A:1479:C:C6	2.38	0.59
16:Q:26:ARG:HG2	16:Q:39:ARG:O	2.03	0.59
20:B:16:GLY:HA3	20:B:39:ILE:HA	1.84	0.58
7:H:124:ILE:HG22	7:H:125:ILE:N	2.16	0.58
1:A:6:G:HO2'	1:A:7:A:H8	1.48	0.58
1:A:1249:C:H4'	8:I:37:TYR:OH	2.03	0.58
1:A:1270:G:H2'	1:A:1271:A:C8	2.38	0.58
1:A:545:C:H5''	3:D:68:GLU:HG2	1.85	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:L:35:ARG:HA	11:L:35:ARG:NH1	2.18	0.58
13:N:68:ARG:NH1	13:N:70:HIS:HB2	2.17	0.58
10:K:124:LYS:HA	21:U:34:ARG:CB	2.30	0.58
5:F:86:ARG:HH12	17:R:63:TYR:HB3	1.66	0.58
2:C:154:GLY:HA3	2:C:162:ALA:HB1	1.86	0.58
10:K:70:ALA:C	10:K:72:ALA:H	2.05	0.58
1:A:451:A:H5'	15:P:70:ARG:NH2	2.17	0.58
1:A:411:A:H62	1:A:413:G:H21	1.50	0.58
1:A:638:U:H2'	1:A:639:G:O4'	2.02	0.58
1:A:1218:C:H2'	1:A:1219:A:C8	2.37	0.58
5:F:67:PRO:HG2	5:F:70:VAL:HG22	1.85	0.58
20:B:15:PHE:O	20:B:40:ILE:HD12	2.03	0.58
3:D:123:MET:HB2	3:D:126:GLY:O	2.03	0.58
1:A:268:U:H2'	1:A:269:C:C6	2.38	0.58
1:A:845:A:H3'	1:A:846:G:C8	2.37	0.58
8:I:32:ARG:HH21	8:I:36:GLN:HG3	1.68	0.58
11:L:109:ARG:HB3	11:L:118:VAL:HG21	1.85	0.58
1:A:555:U:H2'	1:A:556:C:H6	1.68	0.58
1:A:685:G:O2'	1:A:686:U:H5'	2.02	0.58
20:B:117:GLU:HA	20:B:140:LEU:HD21	1.85	0.58
14:O:27:GLN:O	14:O:31:LEU:HD23	2.02	0.58
10:K:16:SER:HA	10:K:77:GLY:O	2.03	0.58
1:A:472:U:H2'	1:A:473:U:C6	2.39	0.58
1:A:576:C:OP2	1:A:576:C:H3'	2.03	0.58
4:E:82:HIS:HB2	4:E:83:PRO:HD2	1.85	0.58
11:L:35:ARG:HA	11:L:35:ARG:CZ	2.34	0.58
1:A:742:G:H2'	1:A:743:A:H8	1.68	0.58
1:A:746:A:H2'	1:A:747:A:C8	2.38	0.58
7:H:6:ILE:HB	7:H:76:ARG:NH1	2.18	0.58
1:A:1008:U:H5''	13:N:23:ARG:HH22	1.69	0.58
1:A:620:C:O2	3:D:131:ILE:HG21	2.03	0.58
1:A:728:A:H2'	1:A:729:A:C8	2.38	0.58
1:A:390:U:H2'	1:A:391:G:C8	2.39	0.58
20:B:44:LYS:C	20:B:47:PRO:HD2	2.24	0.58
1:A:921:U:H2'	1:A:922:G:C8	2.38	0.58
1:A:777:A:H2'	1:A:778:G:C8	2.37	0.58
1:A:950:U:H2'	1:A:951:G:H8	1.68	0.58
5:F:79:ARG:HH21	5:F:87:SER:HB3	1.69	0.58
20:B:80:LYS:HG3	20:B:81:ASP:H	1.69	0.58
1:A:628:G:H2'	1:A:629:A:C8	2.38	0.58
1:A:1090:U:H2'	1:A:1091:U:C6	2.37	0.58
1:A:1461:G:H2'	1:A:1462:C:H6	1.68	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:651:C:H2'	1:A:652:U:C6	2.39	0.58
13:N:60:ARG:NE	13:N:62:ARG:HG2	2.19	0.58
20:B:65:LYS:H	20:B:158:ASP:CG	2.07	0.58
3:D:123:MET:SD	3:D:145:ARG:HD2	2.43	0.58
12:M:39:ALA:HB3	12:M:42:VAL:HG13	1.86	0.58
20:B:217:ALA:O	20:B:221:ARG:HG2	2.03	0.58
1:A:16:A:O2'	1:A:17:U:H5'	2.03	0.58
1:A:1054:C:O2'	1:A:1055:A:H5''	2.04	0.58
3:D:22:SER:H	3:D:109:THR:HG22	1.68	0.58
13:N:79:SER:OG	13:N:82:LYS:HG2	2.04	0.58
18:S:62:THR:H	18:S:65:MET:HB2	1.69	0.58
1:A:922:G:H4'	4:E:24:VAL:HA	1.84	0.58
1:A:328:C:H4'	1:A:329:A:H5''	1.86	0.58
1:A:538:G:H5''	11:L:110:LYS:HG2	1.84	0.58
20:B:107:ARG:HA	20:B:110:ILE:HD12	1.86	0.58
1:A:501:C:H2'	1:A:502:A:H8	1.68	0.58
1:A:182:A:H1'	1:A:183:C:C5	2.38	0.58
1:A:1448:C:H2'	1:A:1449:C:C6	2.38	0.58
20:B:172:ILE:HG22	20:B:176:ASN:HD21	1.69	0.58
2:C:31:ASN:ND2	2:C:58:ARG:HE	2.01	0.58
19:T:43:LYS:HE2	19:T:44:ALA:N	2.18	0.58
2:C:13:ILE:HD13	2:C:13:ILE:H	1.68	0.58
1:A:747:A:H2'	1:A:748:G:O4'	2.04	0.58
1:A:518:C:H2'	1:A:530:G:H8	1.69	0.58
1:A:580:C:H2'	1:A:581:G:O4'	2.04	0.58
2:C:88:LYS:HE3	2:C:88:LYS:O	2.03	0.58
5:F:98:GLU:HG2	5:F:99:ALA:N	2.19	0.58
1:A:1004:A:N7	1:A:1025:U:H1'	2.19	0.57
3:D:24:VAL:HG13	3:D:160:LEU:HB3	1.86	0.57
1:A:920:U:H2'	1:A:921:U:H6	1.69	0.57
8:I:22:PRO:HA	8:I:60:LEU:HB2	1.87	0.57
19:T:24:ARG:HD2	19:T:28:ARG:NH2	2.19	0.57
1:A:1343:G:H2'	1:A:1344:C:C6	2.39	0.57
1:A:1160:G:H4'	20:B:130:LYS:CB	2.34	0.57
1:A:235:C:H2'	1:A:236:A:H8	1.67	0.57
7:H:10:LEU:HD22	7:H:74:ILE:HD11	1.86	0.57
3:D:44:LYS:HD2	3:D:46:ARG:HG2	1.86	0.57
1:A:285:C:H2'	1:A:286:C:H6	1.68	0.57
19:T:15:LYS:HE2	19:T:15:LYS:HA	1.84	0.57
11:L:82:ARG:HG2	11:L:82:ARG:HH11	1.68	0.57
8:I:18:VAL:HA	8:I:64:ILE:HG13	1.86	0.57
1:A:1004:A:H5'	1:A:1024:G:N2	2.18	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:112:ARG:HH11	20:B:116:LEU:HG	1.69	0.57
20:B:110:ILE:HG23	20:B:151:LYS:HA	1.85	0.57
21:U:36:PHE:HB3	21:U:39:LYS:HB2	1.86	0.57
1:A:777:A:H2'	1:A:778:G:H8	1.68	0.57
1:A:769:G:H4'	1:A:1513:A:H4'	1.86	0.57
4:E:11:GLN:HE22	4:E:41:GLY:HA3	1.69	0.57
14:O:43:ALA:O	14:O:46:LYS:HE3	2.04	0.57
6:G:64:ALA:HA	6:G:127:ALA:HA	1.85	0.57
12:M:48:SER:O	12:M:52:ILE:HG22	2.03	0.57
3:D:201:GLU:OE1	4:E:104:ILE:HG22	2.04	0.57
1:A:1405:G:O2'	1:A:1406:U:H5'	2.04	0.57
2:C:183:TYR:HA	2:C:199:VAL:O	2.04	0.57
20:B:58:LYS:HB3	20:B:58:LYS:NZ	2.19	0.57
19:T:68:LYS:NZ	19:T:68:LYS:HA	2.19	0.57
18:S:27:LYS:HB3	18:S:27:LYS:NZ	2.20	0.57
12:M:86:ARG:HA	12:M:96:VAL:HG11	1.87	0.57
20:B:93:HIS:CD2	20:B:145:ASN:HB3	2.39	0.57
1:A:709:U:H2'	1:A:710:G:H8	1.69	0.57
3:D:84:ASN:ND2	3:D:86:GLY:H	2.03	0.57
1:A:1351:U:O2'	1:A:1352:C:H5'	2.05	0.57
1:A:1152:A:H2'	1:A:1153:G:C8	2.39	0.57
9:J:40:ILE:HD12	9:J:73:LEU:HD12	1.87	0.57
5:F:29:ILE:HG23	5:F:66:ALA:HB2	1.85	0.57
13:N:16:ALA:HB2	13:N:55:SER:N	2.19	0.57
12:M:2:ARG:HB2	12:M:56:ARG:NH2	2.16	0.57
18:S:11:ASP:O	18:S:14:LEU:HG	2.04	0.57
15:P:68:SER:OG	15:P:71:VAL:HG12	2.04	0.57
12:M:89:ARG:HD3	12:M:95:PRO:O	2.05	0.57
1:A:1006:G:H2'	1:A:1007:U:H6	1.69	0.57
1:A:1007:U:H2'	1:A:1008:U:C6	2.40	0.57
6:G:78:ARG:HH11	6:G:81:GLY:H	1.50	0.57
4:E:39:GLY:HA2	4:E:45:VAL:HA	1.85	0.57
1:A:1162:C:H2'	1:A:1163:A:C8	2.39	0.57
1:A:1253:G:N1	1:A:1285:A:N6	2.52	0.57
13:N:60:ARG:HD3	13:N:62:ARG:CZ	2.35	0.57
1:A:194:C:O2'	1:A:195:A:H5'	2.04	0.57
1:A:778:G:H2'	1:A:779:C:C6	2.40	0.57
1:A:1446:A:H2'	1:A:1447:A:H5''	1.87	0.57
1:A:1213:A:O2'	1:A:1214:C:H5''	2.04	0.57
3:D:7:LYS:O	3:D:20:LEU:HD12	2.03	0.57
1:A:1173:U:H2'	1:A:1174:G:C8	2.39	0.57
1:A:928:G:H2'	1:A:929:G:H8	1.69	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1014:A:H4'	18:S:13:HIS:CE1	2.39	0.57
20:B:83:ALA:CB	20:B:90:PHE:HB3	2.34	0.57
18:S:18:VAL:CG2	18:S:43:MET:HG2	2.32	0.57
1:A:1057:G:H5'	2:C:153:SER:HB2	1.87	0.57
1:A:1512:U:H2'	1:A:1513:A:H8	1.68	0.57
9:J:80:THR:HG21	9:J:82:LYS:HZ2	1.70	0.57
8:I:19:PHE:O	8:I:62:LEU:HA	2.04	0.57
1:A:1081:A:P	4:E:22:LYS:HB2	2.44	0.57
2:C:70:ALA:HA	2:C:105:VAL:CG2	2.34	0.57
1:A:1379:G:N7	6:G:2:ARG:CZ	2.68	0.57
1:A:1508:A:H2'	1:A:1509:C:C6	2.39	0.57
1:A:505:G:H2'	1:A:506:G:H8	1.70	0.57
1:A:881:G:P	11:L:8:ARG:HH12	2.27	0.57
1:A:1486:G:H2'	1:A:1487:G:O4'	2.05	0.57
8:I:50:PRO:HB3	8:I:83:THR:HB	1.87	0.57
1:A:430:A:OP1	3:D:8:LEU:HB2	2.03	0.57
3:D:12:ARG:HA	3:D:33:ILE:HD12	1.87	0.57
1:A:275:G:H5'	16:Q:15:LYS:HD3	1.85	0.57
1:A:31:G:H5'	1:A:306:A:C2	2.40	0.57
1:A:996:A:H2'	1:A:997:U:C6	2.40	0.57
1:A:1492:A:H5'	1:A:1493:A:OP2	2.05	0.57
18:S:1:PRO:O	18:S:2:ARG:HB2	2.05	0.57
5:F:92:THR:HG22	5:F:93:LYS:N	2.19	0.57
6:G:25:PHE:HZ	6:G:119:LEU:HD11	1.70	0.57
1:A:600:A:H2'	1:A:601:G:C8	2.39	0.57
7:H:45:ILE:HG22	7:H:62:LEU:HA	1.87	0.57
1:A:32:A:H2'	1:A:33:A:C8	2.39	0.57
1:A:1038:C:H2'	1:A:1039:G:C8	2.40	0.57
2:C:71:ARG:O	2:C:74:ILE:HG22	2.05	0.56
20:B:140:LEU:HD12	20:B:140:LEU:H	1.68	0.56
1:A:253:A:H2'	1:A:254:G:H8	1.69	0.56
6:G:65:LEU:O	6:G:69:ARG:HG3	2.05	0.56
1:A:975:A:H4'	1:A:976:G:O5'	2.05	0.56
1:A:1294:G:H2'	1:A:1295:U:C6	2.40	0.56
3:D:100:VAL:O	3:D:104:MET:HG3	2.04	0.56
10:K:58:THR:HB	10:K:59:PRO:HD2	1.87	0.56
13:N:50:LEU:N	13:N:51:PRO:HD2	2.20	0.56
1:A:1338:G:H2'	1:A:1339:A:C8	2.40	0.56
1:A:920:U:O2'	1:A:1081:A:H4'	2.05	0.56
3:D:29:THR:HG22	3:D:30:LYS:N	2.20	0.56
16:Q:37:ILE:HG22	16:Q:38:LYS:H	1.70	0.56
3:D:77:GLU:HA	3:D:80:ARG:HG2	1.87	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1450:U:H2'	1:A:1452:C:C5	2.40	0.56
2:C:8:GLY:HA2	2:C:11:LEU:HG	1.87	0.56
1:A:1320:C:H42	18:S:35:ARG:HD3	1.70	0.56
21:U:24:LYS:NZ	21:U:25:ALA:H	1.98	0.56
1:A:251:G:H1	1:A:271:C:H41	1.53	0.56
15:P:40:ASN:ND2	15:P:42:ILE:H	2.04	0.56
9:J:53:ILE:CG2	9:J:61:ALA:HB1	2.36	0.56
11:L:20:VAL:HB	11:L:94:TYR:CE1	2.40	0.56
4:E:140:ILE:HG22	4:E:144:GLU:OE1	2.06	0.56
1:A:1512:U:H2'	1:A:1513:A:C8	2.40	0.56
8:I:10:ARG:HB3	8:I:15:ALA:HA	1.87	0.56
4:E:61:LYS:O	4:E:65:LYS:HG2	2.05	0.56
4:E:125:LYS:HD2	4:E:126:ALA:H	1.69	0.56
1:A:518:C:H2'	1:A:530:G:C8	2.41	0.56
10:K:34:THR:HA	10:K:41:LEU:HG	1.87	0.56
15:P:74:LEU:O	15:P:78:VAL:HG12	2.05	0.56
1:A:352:C:H4'	1:A:354:G:OP1	2.06	0.56
2:C:6:PRO:HA	2:C:9:ILE:HG22	1.88	0.56
8:I:18:VAL:HG13	8:I:64:ILE:HG13	1.87	0.56
1:A:1004:A:C8	1:A:1025:U:H1'	2.40	0.56
2:C:149:LYS:HB2	2:C:168:ARG:HG3	1.87	0.56
9:J:55:PRO:HA	13:N:80:ARG:NH2	2.20	0.56
1:A:1250:A:H4'	8:I:69:GLY:O	2.06	0.56
1:A:313:A:H2'	1:A:314:C:C6	2.41	0.56
8:I:109:GLN:NE2	8:I:110:VAL:H	2.03	0.56
1:A:135:C:O2	15:P:1:MET:HB2	2.06	0.56
2:C:33:ASP:O	2:C:37:LYS:HG3	2.05	0.56
13:N:71:GLY:O	13:N:79:SER:HA	2.05	0.56
4:E:28:ARG:NH1	4:E:30:PHE:HB3	2.21	0.56
1:A:230:G:H2'	1:A:231:U:O4'	2.06	0.56
1:A:370:C:H2'	1:A:371:A:H8	1.69	0.56
1:A:1349:A:H2'	1:A:1350:A:O4'	2.05	0.56
1:A:811:C:H4'	1:A:900:A:N6	2.21	0.56
1:A:1250:A:H2'	1:A:1251:A:C8	2.40	0.56
4:E:152:VAL:O	4:E:156:ARG:HG2	2.05	0.56
1:A:546:A:OP1	3:D:69:ARG:HB2	2.05	0.56
1:A:1508:A:H2'	1:A:1509:C:H6	1.70	0.56
13:N:9:GLU:HB2	13:N:62:ARG:CZ	2.35	0.56
1:A:1329:A:OP1	12:M:28:ARG:HB2	2.06	0.56
18:S:11:ASP:H	18:S:14:LEU:HD21	1.70	0.56
4:E:148:SER:OG	4:E:151:MET:HB2	2.06	0.56
1:A:474:G:H2'	1:A:475:C:C6	2.41	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:778:G:H2'	1:A:779:C:H6	1.70	0.56
6:G:78:ARG:HG2	6:G:83:THR:HG22	1.86	0.56
1:A:314:C:O2'	1:A:315:A:H5'	2.06	0.56
13:N:63:CYS:HB3	13:N:67:GLY:N	2.20	0.56
1:A:264:C:O2'	16:Q:65:PRO:HG2	2.06	0.56
20:B:145:ASN:ND2	20:B:145:ASN:N	2.54	0.56
4:E:82:HIS:CD2	7:H:95:MET:HG3	2.41	0.56
6:G:144:ALA:O	6:G:146:ALA:N	2.37	0.56
1:A:1091:U:H2'	1:A:1093:A:OP2	2.05	0.56
1:A:215:C:H2'	1:A:216:U:C6	2.41	0.56
3:D:88:ASN:O	3:D:92:LEU:HD23	2.05	0.56
1:A:1021:A:H2'	1:A:1022:A:O4'	2.06	0.56
1:A:812:G:H2'	1:A:812:G:N3	2.19	0.56
10:K:86:LYS:HA	10:K:113:THR:OG1	2.05	0.56
7:H:76:ARG:HG3	7:H:77:VAL:N	2.21	0.56
9:J:30:LYS:NZ	9:J:36:VAL:HB	2.21	0.56
1:A:373:A:H1'	1:A:481:G:N3	2.21	0.56
1:A:10:A:H2'	1:A:11:G:H8	1.69	0.56
1:A:796:C:OP1	10:K:127:ARG:HB3	2.06	0.56
1:A:1488:G:O2'	1:A:1489:G:H5'	2.06	0.56
1:A:1320:C:H5''	18:S:2:ARG:NH2	2.20	0.56
21:U:28:LEU:HD23	21:U:29:ALA:N	2.20	0.56
1:A:843:U:H5'	1:A:844:G:N7	2.21	0.56
6:G:91:ARG:HD2	6:G:91:ARG:N	2.19	0.56
1:A:672:U:H2'	1:A:673:A:C8	2.40	0.56
1:A:476:U:O2'	1:A:477:C:H5'	2.06	0.56
5:F:22:ILE:HD11	5:F:60:VAL:HG11	1.88	0.56
1:A:1430:A:H2'	1:A:1431:A:O4'	2.06	0.56
1:A:738:C:H2'	1:A:739:C:C6	2.41	0.56
19:T:53:MET:HA	19:T:56:ILE:HD12	1.88	0.56
1:A:1504:G:H4'	1:A:1505:G:C4	2.41	0.55
20:B:95:TRP:CH2	20:B:100:LEU:HB2	2.40	0.55
9:J:80:THR:HG21	9:J:82:LYS:NZ	2.21	0.55
1:A:434:U:H3'	1:A:435:A:H8	1.71	0.55
17:R:25:ILE:O	17:R:29:LYS:HG3	2.05	0.55
18:S:52:ASN:CG	18:S:53:GLY:H	2.09	0.55
1:A:1085:U:H3'	1:A:1086:U:H5	1.70	0.55
12:M:17:ALA:CB	12:M:44:ILE:HD11	2.36	0.55
1:A:1078:U:H2'	1:A:1079:G:O4'	2.07	0.55
20:B:33:ALA:HA	20:B:38:HIS:HA	1.87	0.55
1:A:663:A:O2'	1:A:664:G:H5'	2.06	0.55
1:A:1118:U:H2'	1:A:1119:C:H6	1.70	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:560:A:N1	1:A:566:G:H5'	2.21	0.55
1:A:168:G:O2'	1:A:169:C:H5'	2.07	0.55
3:D:169:TRP:HB2	3:D:183:ARG:O	2.06	0.55
1:A:555:U:H2'	1:A:556:C:C6	2.42	0.55
1:A:1448:C:H2'	1:A:1449:C:H6	1.71	0.55
1:A:1121:U:H2'	1:A:1122:U:O4'	2.07	0.55
1:A:1123:U:O2'	1:A:1124:G:H5'	2.07	0.55
10:K:30:ILE:HG22	10:K:45:THR:OG1	2.07	0.55
14:O:63:ARG:HH12	14:O:87:ARG:HH22	1.54	0.55
1:A:562:U:H1'	11:L:11:ARG:HD2	1.87	0.55
1:A:470:C:H2'	1:A:471:U:C6	2.41	0.55
12:M:33:LEU:HD13	12:M:39:ALA:O	2.06	0.55
1:A:1397:C:H4'	1:A:1398:A:OP2	2.05	0.55
3:D:55:ARG:HG3	3:D:55:ARG:HH11	1.72	0.55
1:A:625:U:H4'	15:P:16:PHE:CZ	2.42	0.55
2:C:39:ARG:HG3	2:C:56:ILE:HD11	1.88	0.55
19:T:72:ALA:HA	19:T:75:LYS:HD3	1.89	0.55
8:I:6:TYR:HB2	8:I:19:PHE:CE1	2.42	0.55
8:I:49:GLN:N	8:I:50:PRO:HD2	2.21	0.55
11:L:13:ARG:O	11:L:14:LYS:HB3	2.06	0.55
8:I:113:LYS:HA	8:I:120:ALA:HB2	1.89	0.55
16:Q:83:LEU:H	16:Q:83:LEU:HD13	1.71	0.55
6:G:78:ARG:NH1	6:G:81:GLY:H	2.04	0.55
3:D:77:GLU:O	3:D:81:LEU:HG	2.06	0.55
1:A:1127:G:H5'	1:A:1280:A:O2'	2.06	0.55
18:S:29:PRO:HA	18:S:47:THR:O	2.05	0.55
1:A:858:G:O6	1:A:869:G:H3'	2.07	0.55
8:I:55:ASP:CB	8:I:59:LYS:HG3	2.36	0.55
1:A:252:U:H2'	1:A:253:A:C8	2.42	0.55
7:H:31:LEU:O	7:H:35:ILE:HG13	2.06	0.55
1:A:284:C:H2'	1:A:285:C:H6	1.71	0.55
1:A:393:A:O2'	1:A:394:G:H5'	2.06	0.55
1:A:784:A:H2'	1:A:785:G:C8	2.42	0.55
13:N:20:PHE:C	13:N:22:LYS:H	2.10	0.55
4:E:23:THR:HA	4:E:28:ARG:HA	1.88	0.55
4:E:19:ARG:NH1	4:E:28:ARG:HH22	2.04	0.55
6:G:129:ASN:ND2	6:G:137:ARG:HH22	2.04	0.55
3:D:29:THR:HB	3:D:30:LYS:HZ3	1.71	0.55
1:A:1226:C:H4'	1:A:1227:A:OP1	2.06	0.55
16:Q:83:LEU:HD22	16:Q:83:LEU:N	2.21	0.55
14:O:80:LEU:HD21	14:O:84:LEU:HD22	1.89	0.55
4:E:18:ASN:HB2	4:E:33:THR:OG1	2.07	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:34:C:H2'	1:A:35:G:C8	2.42	0.55
10:K:34:THR:HB	10:K:40:ALA:HA	1.87	0.55
2:C:68:HIS:HA	2:C:103:ALA:HB3	1.88	0.55
14:O:78:THR:HA	14:O:81:ILE:HD12	1.87	0.55
1:A:845:A:H3'	1:A:846:G:H8	1.71	0.55
11:L:3:VAL:O	11:L:7:VAL:HG23	2.07	0.55
20:B:122:ASP:OD2	20:B:125:PHE:HB2	2.07	0.55
21:U:3:ILE:HD13	21:U:19:LYS:HA	1.89	0.55
18:S:63:ASP:O	18:S:66:VAL:HG22	2.07	0.55
21:U:39:LYS:N	21:U:40:PRO:HD2	2.21	0.55
1:A:782:A:H2'	1:A:783:C:O4'	2.06	0.55
1:A:522:C:H2'	1:A:523:A:O4'	2.07	0.55
6:G:72:VAL:HG12	6:G:89:GLU:HA	1.88	0.55
1:A:189:A:H2'	1:A:190:A:C8	2.41	0.55
21:U:3:ILE:HD12	21:U:3:ILE:N	2.21	0.55
3:D:2:ARG:HH22	3:D:132:ALA:HB3	1.72	0.55
12:M:18:LEU:HB2	12:M:29:SER:OG	2.05	0.55
18:S:24:SER:HB2	18:S:27:LYS:HE3	1.88	0.55
1:A:17:U:O2'	1:A:18:C:H5'	2.06	0.55
1:A:736:C:H2'	1:A:737:C:C6	2.42	0.55
1:A:674:G:H2'	1:A:675:A:C8	2.38	0.55
20:B:75:ALA:O	20:B:79:VAL:HG23	2.07	0.55
1:A:709:U:H2'	1:A:710:G:C8	2.41	0.55
1:A:484:G:H5'	1:A:486:U:H5'	1.88	0.55
9:J:40:ILE:HB	9:J:73:LEU:HB3	1.89	0.54
3:D:24:VAL:CG1	3:D:160:LEU:HB3	2.37	0.54
10:K:83:VAL:HB	10:K:109:ILE:HG23	1.90	0.54
1:A:41:G:H2'	1:A:42:G:H8	1.72	0.54
20:B:172:ILE:HD12	20:B:172:ILE:H	1.71	0.54
12:M:17:ALA:HB2	12:M:44:ILE:HD11	1.89	0.54
1:A:17:U:H4'	1:A:1079:G:O2'	2.08	0.54
1:A:734:G:H21	17:R:63:TYR:HE1	1.54	0.54
2:C:156:LEU:HD11	2:C:165:GLU:HB2	1.89	0.54
4:E:73:VAL:HB	4:E:75:LEU:HD21	1.88	0.54
1:A:1317:C:OP1	13:N:56:PRO:HD2	2.06	0.54
1:A:1275:A:H2'	1:A:1276:G:O4'	2.07	0.54
1:A:1053:G:HO2'	1:A:1199:U:H5	1.55	0.54
20:B:13:VAL:HG11	20:B:207:ARG:HG2	1.87	0.54
1:A:490:C:H2'	1:A:491:G:C8	2.42	0.54
13:N:5:MET:HE3	13:N:60:ARG:HH11	1.72	0.54
13:N:60:ARG:HD3	13:N:62:ARG:NH2	2.22	0.54
1:A:1326:U:H2'	1:A:1327:C:H6	1.72	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:H:123:GLU:HG2	7:H:124:ILE:O	2.07	0.54
10:K:22:ILE:HD12	10:K:84:MET:O	2.07	0.54
1:A:1261:A:H1'	1:A:1275:A:C2	2.43	0.54
17:R:58:ILE:HD12	17:R:58:ILE:H	1.72	0.54
1:A:1477:U:H2'	1:A:1478:U:C6	2.42	0.54
4:E:56:PRO:HG2	4:E:57:ALA:H	1.71	0.54
1:A:179:A:H2'	1:A:180:U:C6	2.42	0.54
1:A:272:C:H2'	1:A:273:U:C6	2.42	0.54
1:A:596:A:H2'	1:A:597:G:H8	1.73	0.54
10:K:124:LYS:CA	21:U:34:ARG:HB3	2.36	0.54
1:A:437:U:H4'	3:D:153:ARG:NH1	2.21	0.54
20:B:199:ILE:HG21	20:B:212:TYR:CE2	2.42	0.54
1:A:190:A:H2'	1:A:191:G:O4'	2.08	0.54
1:A:1525:G:O2'	1:A:1526:G:H5'	2.07	0.54
3:D:72:ARG:HD3	3:D:203:TYR:CZ	2.42	0.54
1:A:552:U:O2'	1:A:553:A:H5'	2.07	0.54
1:A:1147:C:H2'	1:A:1148:U:C6	2.42	0.54
18:S:41:PRO:HA	18:S:66:VAL:HG11	1.89	0.54
1:A:1081:A:OP1	4:E:22:LYS:HB2	2.06	0.54
11:L:7:VAL:HG22	16:Q:33:TYR:CD1	2.42	0.54
14:O:28:VAL:HB	14:O:80:LEU:HD11	1.88	0.54
1:A:1314:C:H3'	18:S:5:LYS:NZ	2.23	0.54
15:P:6:LEU:HB3	15:P:17:TYR:HB3	1.89	0.54
1:A:1062:U:H2'	1:A:1063:C:C6	2.41	0.54
1:A:265:G:H2'	1:A:267:C:H5	1.72	0.54
1:A:817:C:H1'	1:A:819:A:C5'	2.35	0.54
1:A:1171:A:H2'	1:A:1172:C:C6	2.42	0.54
1:A:968:A:C8	1:A:1062:U:H4'	2.42	0.54
1:A:1332:A:H2'	1:A:1333:A:H8	1.72	0.54
10:K:27:ASN:O	10:K:56:LYS:HE3	2.08	0.54
1:A:8:A:H61	3:D:53:GLN:HE22	1.56	0.54
6:G:129:ASN:HA	6:G:134:VAL:HG21	1.90	0.54
8:I:126:PHE:O	8:I:128:LYS:N	2.41	0.54
1:A:678:U:H4'	1:A:778:G:OP1	2.07	0.54
1:A:715:A:H2'	1:A:716:A:C8	2.43	0.54
1:A:961:U:O4'	1:A:961:U:O2	2.26	0.54
1:A:79:G:H2'	1:A:80:A:C8	2.42	0.54
1:A:1246:A:H2'	1:A:1247:U:O4'	2.08	0.54
4:E:19:ARG:HH11	4:E:28:ARG:HH22	1.56	0.54
4:E:92:ARG:HH11	4:E:92:ARG:HB3	1.73	0.54
1:A:1326:U:H2'	1:A:1327:C:C6	2.43	0.54
21:U:35:GLU:HB2	21:U:37:TYR:CE2	2.42	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:642:A:H2'	1:A:643:C:H6	1.73	0.54
1:A:238:A:C2'	1:A:239:U:H5''	2.38	0.54
10:K:14:GLN:HA	10:K:77:GLY:HA3	1.89	0.54
1:A:762:U:H2'	1:A:763:G:C8	2.43	0.54
7:H:94:VAL:CG2	7:H:101:ALA:HB2	2.37	0.54
2:C:18:ASN:OD1	2:C:53:ARG:HD2	2.07	0.54
1:A:811:C:H4'	1:A:900:A:H62	1.73	0.54
6:G:78:ARG:C	6:G:78:ARG:HD2	2.28	0.54
6:G:72:VAL:HA	6:G:89:GLU:HA	1.89	0.54
7:H:13:ILE:HD11	7:H:60:LEU:HD21	1.89	0.54
1:A:1300:G:H1'	1:A:1301:U:H5	1.73	0.54
17:R:35:SER:O	17:R:70:THR:HA	2.08	0.54
10:K:124:LYS:HA	21:U:34:ARG:HG2	1.89	0.54
1:A:1278:G:H4'	1:A:1279:G:H5'	1.89	0.54
20:B:101:THR:HA	20:B:178:LEU:HD21	1.90	0.54
1:A:1464:U:H2'	1:A:1465:A:H8	1.73	0.54
7:H:11:THR:HA	7:H:14:ARG:CZ	2.38	0.54
19:T:54:GLN:N	19:T:55:PRO:HD2	2.23	0.54
13:N:14:ALA:O	13:N:18:LYS:HG2	2.07	0.54
11:L:2:THR:HG22	11:L:5:GLN:NE2	2.23	0.54
1:A:1384:C:H2'	1:A:1385:G:H8	1.72	0.54
1:A:692:U:C2	1:A:694:A:H5''	2.42	0.54
1:A:692:U:O2	1:A:694:A:H5''	2.07	0.54
15:P:40:ASN:HD21	15:P:42:ILE:C	2.11	0.54
1:A:193:C:H2'	1:A:194:C:H6	1.71	0.54
1:A:89:U:H2'	1:A:90:C:O4'	2.08	0.54
1:A:1070:U:H2'	1:A:1071:C:H6	1.72	0.54
1:A:1438:G:O2'	1:A:1439:G:H5'	2.08	0.54
10:K:17:ASP:C	10:K:36:ARG:HH12	2.11	0.54
12:M:82:LEU:HD11	18:S:64:GLU:HB2	1.90	0.53
17:R:52:ARG:O	17:R:56:ARG:HG3	2.08	0.53
20:B:53:LEU:HD11	20:B:216:VAL:HA	1.88	0.53
1:A:1141:C:H2'	1:A:1142:G:C8	2.42	0.53
1:A:474:G:H2'	1:A:475:C:H6	1.72	0.53
1:A:208:U:H4'	1:A:209:U:C5	2.42	0.53
1:A:624:C:H2'	1:A:625:U:H6	1.73	0.53
3:D:40:HIS:HB3	3:D:43:ARG:HG2	1.88	0.53
1:A:1262:C:H2'	1:A:1263:C:C6	2.43	0.53
3:D:90:LEU:HD11	3:D:194:ILE:CD1	2.38	0.53
1:A:734:G:H2'	1:A:735:C:H6	1.72	0.53
8:I:33:SER:CB	8:I:36:GLN:HB2	2.37	0.53
1:A:1530:G:HO2'	1:A:1531:A:H8	1.56	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:343:U:O2'	1:A:344:A:H2'	2.07	0.53
1:A:512:U:O2'	1:A:513:C:H5'	2.08	0.53
1:A:1352:C:H2'	1:A:1353:G:C8	2.43	0.53
3:D:7:LYS:HB2	3:D:21:LYS:HE2	1.91	0.53
1:A:590:U:H2'	1:A:591:U:C6	2.43	0.53
1:A:95:C:O2	1:A:95:C:H2'	2.06	0.53
8:I:78:ILE:O	8:I:82:ILE:HG13	2.08	0.53
1:A:465:A:O2'	1:A:466:A:H5'	2.07	0.53
1:A:254:G:H4'	16:Q:19:SER:OG	2.07	0.53
7:H:17:GLN:NE2	7:H:62:LEU:HB3	2.23	0.53
10:K:81:LEU:HD23	10:K:81:LEU:N	2.23	0.53
1:A:860:A:H2'	1:A:861:G:O4'	2.07	0.53
7:H:9:MET:O	7:H:13:ILE:HG13	2.08	0.53
1:A:9:G:OP2	4:E:125:LYS:HD3	2.07	0.53
11:L:24:GLU:HB2	11:L:26:CYS:SG	2.48	0.53
3:D:10:LEU:HD12	3:D:20:LEU:HD11	1.89	0.53
2:C:146:LYS:HD3	2:C:204:GLY:HA2	1.91	0.53
12:M:15:VAL:O	12:M:19:THR:HG23	2.09	0.53
18:S:44:ILE:HG13	18:S:62:THR:HA	1.90	0.53
8:I:46:VAL:O	8:I:79:ARG:HG3	2.08	0.53
17:R:60:ARG:O	17:R:64:LEU:HD13	2.08	0.53
11:L:20:VAL:HG23	11:L:20:VAL:O	2.07	0.53
1:A:106:C:O2'	1:A:107:G:H5'	2.08	0.53
1:A:90:C:H2'	1:A:91:U:C6	2.44	0.53
5:F:15:SER:HA	5:F:18:VAL:HG23	1.90	0.53
1:A:499:A:H4'	1:A:500:G:OP1	2.08	0.53
1:A:652:U:H1'	1:A:653:U:C5	2.43	0.53
1:A:928:G:H2'	1:A:929:G:C8	2.44	0.53
3:D:94:GLU:HG3	3:D:99:ASN:HD21	1.73	0.53
15:P:38:PHE:CD2	15:P:51:ARG:HB2	2.43	0.53
6:G:113:LYS:HZ2	6:G:113:LYS:HB3	1.73	0.53
13:N:5:MET:HB3	13:N:62:ARG:HH12	1.73	0.53
1:A:82:G:H2'	1:A:83:C:O4'	2.08	0.53
9:J:8:ILE:N	9:J:8:ILE:HD12	2.24	0.53
11:L:98:ARG:HB2	11:L:116:TYR:HA	1.89	0.53
20:B:142:LYS:HA	20:B:145:ASN:OD1	2.09	0.53
1:A:620:C:C2	3:D:131:ILE:HG21	2.44	0.53
1:A:188:C:H2'	1:A:189:A:O4'	2.09	0.53
1:A:627:G:H2'	1:A:628:G:C8	2.42	0.53
13:N:2:LYS:O	13:N:6:LYS:HG3	2.09	0.53
1:A:922:G:N3	1:A:1398:A:H2	2.06	0.53
1:A:1097:C:H2'	1:A:1098:C:C6	2.44	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:33:A:H2'	1:A:34:C:C6	2.44	0.53
1:A:153:C:H2'	1:A:154:U:C6	2.43	0.53
1:A:1238:A:H2	1:A:1241:G:N3	2.06	0.53
18:S:14:LEU:O	18:S:18:VAL:HG12	2.08	0.53
18:S:43:MET:O	18:S:61:VAL:HB	2.08	0.53
2:C:50:SER:HB2	2:C:70:ALA:HB3	1.91	0.53
1:A:1291:U:H2'	1:A:1292:G:C8	2.44	0.53
1:A:98:A:H2'	1:A:99:C:H6	1.74	0.53
1:A:707:U:H2'	1:A:708:C:H6	1.71	0.53
1:A:33:A:H2'	1:A:34:C:H6	1.72	0.53
1:A:1432:G:H1'	1:A:1468:A:H61	1.72	0.53
19:T:53:MET:O	19:T:57:VAL:HG22	2.08	0.53
21:U:3:ILE:HB	21:U:19:LYS:HD2	1.90	0.53
20:B:102:ASN:ND2	20:B:105:THR:HB	2.22	0.53
1:A:1221:G:O2'	1:A:1222:G:H5'	2.09	0.53
4:E:158:LYS:NZ	7:H:63:LYS:HD3	2.23	0.53
2:C:2:GLN:H	2:C:2:GLN:HE21	1.55	0.53
1:A:384:G:H2'	1:A:385:C:H6	1.73	0.53
13:N:50:LEU:CD2	13:N:51:PRO:HD3	2.39	0.53
21:U:35:GLU:HB2	21:U:37:TYR:CZ	2.43	0.53
7:H:100:ILE:HG13	7:H:128:VAL:O	2.08	0.53
1:A:1277:C:O2'	1:A:1279:G:H1'	2.09	0.53
20:B:23:ASN:HD22	20:B:24:PRO:CD	2.21	0.53
3:D:22:SER:HB2	3:D:109:THR:HG22	1.91	0.53
1:A:1168:U:H4'	1:A:1169:A:OP2	2.08	0.53
1:A:1332:A:H2'	1:A:1333:A:C8	2.44	0.53
1:A:590:U:H2'	1:A:591:U:H6	1.72	0.53
5:F:4:TYR:CE2	5:F:71:ILE:HD13	2.44	0.53
1:A:1245:C:H2'	1:A:1246:A:C8	2.43	0.53
18:S:39:ILE:HB	18:S:65:MET:O	2.09	0.53
16:Q:24:ILE:O	16:Q:40:THR:HA	2.09	0.53
16:Q:7:LEU:O	16:Q:60:ILE:HD13	2.09	0.53
21:U:36:PHE:HA	21:U:39:LYS:HE2	1.91	0.53
2:C:57:GLU:O	2:C:63:ILE:HA	2.09	0.53
1:A:91:U:H2'	1:A:92:U:H6	1.72	0.53
1:A:312:C:H2'	1:A:313:A:C8	2.44	0.53
1:A:539:A:H2'	1:A:540:G:H8	1.72	0.53
1:A:505:G:H2'	1:A:506:G:C8	2.44	0.53
2:C:190:THR:HG22	2:C:191:THR:N	2.24	0.53
8:I:27:ILE:HG21	8:I:34:LEU:HD13	1.91	0.52
2:C:166:TRP:CE3	2:C:166:TRP:HA	2.44	0.52
1:A:546:A:OP2	3:D:67:LEU:HB3	2.09	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:55:A:OP2	1:A:352:C:N4	2.41	0.52
20:B:27:LYS:HB3	20:B:28:PRO:HD3	1.91	0.52
1:A:1018:G:H2'	1:A:1019:A:C8	2.45	0.52
19:T:49:ALA:HA	19:T:52:GLU:HB3	1.89	0.52
1:A:1124:G:H4'	9:J:40:ILE:HG12	1.91	0.52
13:N:50:LEU:HG	13:N:51:PRO:HD3	1.92	0.52
20:B:65:LYS:HG2	20:B:89:PHE:HE1	1.74	0.52
3:D:117:VAL:O	3:D:130:ASN:HA	2.10	0.52
16:Q:75:VAL:HG23	16:Q:76:ARG:N	2.25	0.52
1:A:1324:A:H2'	1:A:1325:C:O4'	2.10	0.52
2:C:155:ARG:NH2	2:C:192:TYR:HB2	2.24	0.52
1:A:370:C:H2'	1:A:371:A:C8	2.45	0.52
1:A:455:G:O2'	1:A:456:A:H5'	2.08	0.52
1:A:1521:C:H2'	1:A:1522:U:C6	2.44	0.52
1:A:657:U:O2'	1:A:658:C:H5'	2.09	0.52
1:A:1423:G:H2'	1:A:1424:U:H6	1.73	0.52
1:A:390:U:H2'	1:A:391:G:H8	1.74	0.52
6:G:104:VAL:O	6:G:108:ARG:HG3	2.09	0.52
1:A:1302:C:H4'	1:A:1303:C:OP2	2.09	0.52
3:D:157:ALA:O	3:D:160:LEU:HD22	2.09	0.52
1:A:1379:G:O2'	1:A:1380:U:H5'	2.09	0.52
8:I:32:ARG:NH1	8:I:37:TYR:HA	2.24	0.52
1:A:814:A:H5'	1:A:1511:G:H4'	1.90	0.52
1:A:900:A:H2'	1:A:901:A:C8	2.44	0.52
9:J:28:THR:O	9:J:31:ARG:HG2	2.10	0.52
1:A:45:G:H2'	1:A:46:G:H8	1.74	0.52
2:C:35:ASP:HB3	2:C:39:ARG:HH12	1.75	0.52
1:A:165:G:O2'	1:A:166:U:H5'	2.09	0.52
1:A:443:C:H2'	1:A:444:G:C8	2.44	0.52
6:G:15:PRO:HG2	6:G:43:TYR:OH	2.09	0.52
18:S:12:LEU:O	18:S:15:LEU:HB2	2.10	0.52
4:E:15:ILE:HD12	4:E:35:LEU:HG	1.90	0.52
6:G:126:ALA:HA	6:G:134:VAL:HG13	1.90	0.52
1:A:252:U:H2'	1:A:253:A:H8	1.74	0.52
20:B:186:VAL:HB	20:B:190:SER:HB2	1.90	0.52
10:K:74:LYS:C	10:K:76:TYR:H	2.12	0.52
1:A:1386:G:H2'	1:A:1387:G:C8	2.45	0.52
1:A:1434:A:H2'	1:A:1435:G:C8	2.44	0.52
1:A:562:U:H2'	1:A:562:U:OP2	2.09	0.52
16:Q:3:LYS:HE2	16:Q:3:LYS:HA	1.91	0.52
1:A:160:A:H2'	1:A:161:A:O4'	2.09	0.52
5:F:74:LEU:HG	5:F:78:PHE:CE1	2.45	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1207:G:O2'	1:A:1208:C:H5'	2.09	0.52
9:J:12:ALA:HB3	9:J:18:ILE:HB	1.91	0.52
1:A:1004:A:H5'	1:A:1024:G:H22	1.74	0.52
20:B:112:ARG:HA	20:B:115:ASP:OD2	2.09	0.52
8:I:44:ARG:O	8:I:47:VAL:HG22	2.09	0.52
6:G:61:PHE:O	6:G:65:LEU:HD13	2.10	0.52
1:A:5:U:H4'	1:A:6:G:H5'	1.91	0.52
3:D:75:TYR:HE1	3:D:200:VAL:HA	1.74	0.52
1:A:1384:C:H2'	1:A:1385:G:C8	2.44	0.52
8:I:46:VAL:HG23	8:I:47:VAL:H	1.74	0.52
15:P:25:ARG:N	15:P:25:ARG:HD3	2.21	0.52
14:O:35:ILE:CD1	14:O:58:MET:HG3	2.39	0.52
10:K:95:THR:HG23	10:K:96:ILE:N	2.25	0.52
1:A:1273:C:H2'	1:A:1274:A:O4'	2.09	0.52
7:H:55:LYS:HA	7:H:55:LYS:NZ	2.25	0.52
1:A:301:G:H2'	1:A:302:G:H8	1.75	0.52
15:P:59:HIS:O	15:P:63:GLN:HG3	2.08	0.52
9:J:93:ALA:HB3	9:J:96:VAL:HG22	1.91	0.52
13:N:16:ALA:HA	13:N:20:PHE:HB2	1.92	0.52
1:A:469:C:H2'	1:A:470:C:H6	1.75	0.52
4:E:113:VAL:HG23	4:E:114:LEU:N	2.25	0.52
8:I:46:VAL:HG23	8:I:47:VAL:N	2.25	0.52
1:A:818:G:C3'	1:A:819:A:H5''	2.40	0.52
9:J:76:ILE:HD13	9:J:79:PRO:HB3	1.91	0.52
11:L:41:PRO:HB3	11:L:49:ARG:NH1	2.24	0.52
3:D:187:ARG:NH1	3:D:191:SER:HB3	2.25	0.52
20:B:31:PHE:HB2	20:B:41:ASN:HA	1.91	0.52
6:G:21:LEU:HG	6:G:22:LEU:H	1.74	0.52
8:I:44:ARG:HE	8:I:48:ARG:HH22	1.57	0.52
3:D:33:ILE:O	3:D:35:GLN:HG3	2.10	0.52
21:U:40:PRO:HA	21:U:44:ARG:HD2	1.92	0.52
1:A:436:C:O2'	1:A:437:U:H5'	2.10	0.52
9:J:52:LEU:HB2	13:N:80:ARG:HE	1.74	0.52
10:K:28:ASN:HD21	10:K:47:GLY:H	1.56	0.52
17:R:58:ILE:O	17:R:62:ARG:HG3	2.10	0.52
1:A:1427:C:H2'	1:A:1428:A:H8	1.74	0.52
1:A:806:C:H2'	1:A:807:A:H8	1.74	0.52
1:A:803:G:H2'	1:A:804:U:O4'	2.09	0.52
5:F:37:HIS:O	5:F:97:THR:HG23	2.10	0.52
2:C:35:ASP:HB3	2:C:39:ARG:NH1	2.25	0.52
12:M:111:PRO:O	12:M:113:LYS:HG3	2.10	0.52
16:Q:29:LYS:HG3	16:Q:34:GLY:HA2	1.91	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:S:44:ILE:HG23	18:S:44:ILE:O	2.10	0.52
2:C:165:GLU:HG3	2:C:166:TRP:H	1.75	0.52
12:M:86:ARG:CG	12:M:96:VAL:HG11	2.40	0.52
1:A:151:A:H5'	1:A:152:A:OP2	2.09	0.52
1:A:1436:U:H2'	1:A:1437:A:H8	1.75	0.52
1:A:636:U:H2'	1:A:637:C:C6	2.45	0.52
19:T:68:LYS:HZ3	19:T:68:LYS:HA	1.75	0.52
1:A:1166:G:H2'	1:A:1168:U:OP2	2.09	0.52
1:A:1020:G:H2'	1:A:1021:A:H5'	1.91	0.52
2:C:19:SER:HB2	2:C:39:ARG:HH22	1.74	0.52
8:I:61:ASP:C	8:I:62:LEU:HD13	2.30	0.52
18:S:43:MET:O	18:S:46:LEU:HB2	2.09	0.52
6:G:13:PRO:O	6:G:14:ASP:O	2.27	0.52
20:B:18:GLN:O	20:B:37:VAL:HG23	2.09	0.52
18:S:49:ALA:O	18:S:56:HIS:HD2	1.93	0.52
1:A:169:C:O2'	1:A:170:U:H5'	2.09	0.52
1:A:1092:A:H5''	6:G:3:ARG:NH1	2.25	0.52
1:A:45:G:H2'	1:A:46:G:C8	2.45	0.52
1:A:505:G:H4'	1:A:534:U:C4	2.45	0.52
13:N:68:ARG:HH11	13:N:71:GLY:H	1.57	0.51
5:F:70:VAL:HA	5:F:73:GLU:HG3	1.91	0.51
18:S:61:VAL:HA	18:S:65:MET:SD	2.49	0.51
21:U:40:PRO:O	21:U:44:ARG:HB2	2.10	0.51
7:H:17:GLN:OE1	7:H:69:ALA:HB1	2.10	0.51
14:O:80:LEU:O	14:O:84:LEU:HD13	2.10	0.51
4:E:156:ARG:HB2	7:H:43:GLY:HA3	1.91	0.51
1:A:1347:G:H22	1:A:1373:G:H2'	1.72	0.51
1:A:205:A:H2'	1:A:206:C:C6	2.45	0.51
1:A:1461:G:H2'	1:A:1462:C:C6	2.43	0.51
1:A:1524:C:H2'	1:A:1525:G:C8	2.45	0.51
1:A:1150:A:O2'	1:A:1151:A:H5'	2.10	0.51
21:U:39:LYS:O	21:U:43:GLU:HB3	2.10	0.51
17:R:63:TYR:CD2	17:R:63:TYR:N	2.78	0.51
1:A:83:C:HO2'	1:A:84:U:H3'	1.73	0.51
1:A:1349:A:OP1	8:I:121:ARG:HB2	2.11	0.51
1:A:1521:C:H2'	1:A:1522:U:H6	1.75	0.51
1:A:1097:C:H2'	1:A:1098:C:H6	1.76	0.51
1:A:501:C:H1'	1:A:549:C:H1'	1.91	0.51
2:C:13:ILE:N	2:C:13:ILE:HD13	2.24	0.51
13:N:64:ARG:HB2	13:N:77:GLY:O	2.11	0.51
1:A:1459:G:H2'	1:A:1460:C:H6	1.75	0.51
1:A:584:G:O2'	1:A:585:G:H5'	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:224:U:H2'	1:A:225:C:C6	2.45	0.51
1:A:1320:C:C5	18:S:36:ARG:HA	2.46	0.51
8:I:35:GLU:HG3	8:I:44:ARG:HD3	1.91	0.51
1:A:844:G:H2'	1:A:846:G:C8	2.45	0.51
10:K:126:ARG:NE	10:K:126:ARG:HA	2.24	0.51
1:A:81:A:O2'	1:A:82:G:H5'	2.09	0.51
1:A:279:A:C5'	1:A:280:C:H3'	2.40	0.51
1:A:1006:G:H2'	1:A:1007:U:C6	2.45	0.51
1:A:98:A:H2'	1:A:99:C:C6	2.45	0.51
3:D:185:PRO:HB2	3:D:190:LEU:HD12	1.92	0.51
4:E:55:VAL:N	4:E:56:PRO:HD2	2.25	0.51
12:M:36:ALA:HB1	12:M:54:THR:HB	1.92	0.51
1:A:60:A:H4'	1:A:61:G:O5'	2.10	0.51
4:E:113:VAL:HG11	4:E:136:VAL:HG23	1.92	0.51
6:G:131:GLY:O	6:G:134:VAL:HG22	2.11	0.51
19:T:85:LEU:HD23	19:T:86:ALA:N	2.23	0.51
11:L:49:ARG:HH12	11:L:88:ASP:CB	2.24	0.51
5:F:100:SER:HA	17:R:23:LYS:HE2	1.91	0.51
7:H:11:THR:HA	7:H:14:ARG:NH1	2.25	0.51
2:C:34:SER:O	2:C:38:VAL:HG22	2.10	0.51
15:P:20:VAL:HG23	15:P:35:ARG:HA	1.92	0.51
6:G:135:LYS:HE2	6:G:136:LYS:N	2.25	0.51
1:A:1361:G:C2'	1:A:1362:A:H5''	2.36	0.51
20:B:212:TYR:O	20:B:216:VAL:HG22	2.11	0.51
12:M:76:ILE:HG23	12:M:79:LEU:HD12	1.93	0.51
1:A:452:A:H2'	1:A:453:G:O4'	2.09	0.51
20:B:95:TRP:HH2	20:B:100:LEU:HB2	1.75	0.51
1:A:1477:U:H2'	1:A:1478:U:H6	1.75	0.51
1:A:137:U:H2'	1:A:138:G:C8	2.45	0.51
1:A:919:A:O2'	1:A:920:U:H5'	2.11	0.51
11:L:14:LYS:HG2	11:L:15:VAL:N	2.26	0.51
3:D:199:ILE:HD12	3:D:200:VAL:N	2.26	0.51
1:A:448:A:H2'	1:A:449:G:C8	2.46	0.51
7:H:51:GLU:HB3	7:H:57:GLU:HB3	1.91	0.51
1:A:1464:U:H2'	1:A:1465:A:C8	2.45	0.51
1:A:394:G:H2'	1:A:395:C:H6	1.74	0.51
1:A:420:U:H2'	1:A:422:C:C5	2.46	0.51
1:A:398:U:H2'	1:A:399:G:H8	1.76	0.51
9:J:41:PRO:HA	9:J:72:ARG:HD3	1.93	0.51
20:B:205:ALA:HB3	20:B:208:ALA:CB	2.39	0.51
3:D:53:GLN:HB3	3:D:202:LEU:HB2	1.93	0.51
6:G:20:GLU:O	6:G:23:ALA:HB3	2.11	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:130:LYS:O	20:B:134:LEU:HB2	2.10	0.51
6:G:110:ARG:HD3	6:G:118:ARG:HA	1.92	0.51
1:A:462:G:H3'	1:A:463:U:C6	2.45	0.51
1:A:369:G:O2'	1:A:370:C:H5'	2.10	0.51
11:L:113:ARG:HE	11:L:120:ARG:HA	1.75	0.51
1:A:285:C:H2'	1:A:286:C:C6	2.45	0.51
7:H:115:ALA:O	7:H:120:LEU:HD23	2.11	0.51
6:G:99:ALA:O	6:G:103:ILE:HG13	2.10	0.51
11:L:43:LYS:NZ	11:L:44:PRO:HD3	2.25	0.51
1:A:730:G:O2'	1:A:766:A:H5'	2.09	0.51
3:D:31:CYS:SG	3:D:33:ILE:HB	2.51	0.51
21:U:43:GLU:HA	21:U:46:ARG:NE	2.26	0.51
1:A:1118:U:H1'	1:A:1179:A:C4	2.46	0.51
4:E:10:LEU:HA	4:E:39:GLY:O	2.11	0.51
1:A:389:A:N3	1:A:389:A:H2'	2.24	0.51
1:A:738:C:H2'	1:A:739:C:H6	1.75	0.51
1:A:272:C:H2'	1:A:273:U:H6	1.74	0.51
13:N:61:ASN:HB3	13:N:72:PHE:CE2	2.46	0.51
1:A:58:C:O2'	1:A:59:A:H5'	2.11	0.51
3:D:18:LEU:HG	3:D:63:ILE:HG12	1.92	0.51
14:O:52:ARG:HG3	14:O:56:LEU:HD13	1.93	0.51
20:B:16:GLY:HA2	20:B:40:ILE:HG13	1.93	0.51
8:I:55:ASP:HB2	8:I:59:LYS:HG3	1.93	0.51
15:P:39:PHE:CG	15:P:40:ASN:N	2.78	0.51
15:P:46:LYS:C	15:P:48:GLU:H	2.12	0.51
1:A:254:G:O2'	1:A:255:G:H5'	2.11	0.51
16:Q:30:HIS:HB3	16:Q:33:TYR:HB2	1.93	0.51
1:A:176:C:H3'	1:A:177:G:H21	1.76	0.51
1:A:565:U:H3'	1:A:566:G:H2'	1.92	0.51
1:A:791:G:C6	1:A:792:A:N7	2.79	0.51
2:C:171:ARG:HB2	2:C:171:ARG:NH1	2.25	0.51
1:A:1136:C:H3'	1:A:1136:C:OP1	2.10	0.51
1:A:1238:A:H5'	1:A:1336:C:N4	2.26	0.51
8:I:25:GLY:HA3	8:I:57:VAL:HA	1.92	0.51
1:A:734:G:H2'	1:A:735:C:C6	2.45	0.51
1:A:1471:U:O2'	1:A:1472:U:H5'	2.10	0.51
20:B:69:VAL:HB	20:B:162:VAL:CG2	2.40	0.51
1:A:1515:G:O2'	1:A:1516:G:H5'	2.11	0.51
1:A:79:G:H2'	1:A:80:A:H8	1.75	0.51
1:A:612:C:H2'	1:A:613:C:C6	2.46	0.51
5:F:69:GLU:OE1	5:F:70:VAL:HG13	2.11	0.50
13:N:50:LEU:HD23	13:N:51:PRO:HD3	1.92	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:S:20:LYS:O	18:S:23:GLU:HG3	2.11	0.50
14:O:42:PHE:CE1	14:O:55:LEU:HD22	2.46	0.50
8:I:71:ILE:HD12	8:I:71:ILE:N	2.24	0.50
18:S:6:LYS:O	18:S:8:PRO:HD3	2.10	0.50
1:A:493:A:H3'	1:A:494:G:C8	2.46	0.50
1:A:784:A:H2'	1:A:785:G:H8	1.75	0.50
10:K:110:THR:HA	21:U:3:ILE:O	2.12	0.50
10:K:111:ASP:HB2	21:U:19:LYS:HE3	1.91	0.50
1:A:1229:A:H2'	1:A:1230:C:C6	2.46	0.50
2:C:178:ARG:HG2	2:C:206:ILE:HA	1.93	0.50
9:J:44:THR:HG23	9:J:69:THR:O	2.11	0.50
1:A:458:U:H2'	1:A:459:A:H8	1.76	0.50
1:A:1283:U:H2'	1:A:1284:C:C6	2.45	0.50
1:A:1484:C:H2'	1:A:1485:U:O4'	2.11	0.50
1:A:317:U:H2'	1:A:318:G:H8	1.75	0.50
20:B:83:ALA:HA	20:B:88:GLN:NE2	2.26	0.50
4:E:35:LEU:HD22	4:E:133:ILE:HA	1.94	0.50
4:E:87:VAL:HG23	4:E:92:ARG:HA	1.93	0.50
20:B:143:LEU:HB3	20:B:147:LEU:HD12	1.94	0.50
1:A:974:A:OP1	1:A:974:A:H8	1.93	0.50
1:A:1101:A:H4'	1:A:1102:A:O5'	2.11	0.50
1:A:1500:A:H2'	1:A:1501:C:H5'	1.93	0.50
2:C:96:VAL:HB	2:C:97:PRO:HD2	1.93	0.50
1:A:807:A:H2'	1:A:808:C:C6	2.47	0.50
16:Q:39:ARG:HH11	16:Q:39:ARG:HG3	1.75	0.50
1:A:547:A:H4'	1:A:548:G:O5'	2.11	0.50
1:A:586:C:O2'	1:A:878:A:H4'	2.11	0.50
2:C:161:ILE:HD12	2:C:161:ILE:N	2.26	0.50
10:K:33:ILE:HG12	10:K:69:CYS:SG	2.51	0.50
4:E:35:LEU:HD21	4:E:136:VAL:HG11	1.93	0.50
4:E:80:LEU:HA	4:E:146:MET:HE1	1.93	0.50
1:A:720:C:OP1	17:R:40:PRO:HG3	2.11	0.50
1:A:663:A:O3'	17:R:52:ARG:NH2	2.43	0.50
1:A:1258:G:O2'	1:A:1259:C:H5'	2.10	0.50
1:A:34:C:H2'	1:A:35:G:H8	1.76	0.50
7:H:7:ALA:O	7:H:11:THR:HG23	2.11	0.50
1:A:1017:U:H2'	1:A:1018:G:C8	2.45	0.50
1:A:1220:G:H2'	1:A:1221:G:H8	1.76	0.50
1:A:1125:U:HO2'	1:A:1126:U:H2'	1.75	0.50
1:A:1150:A:H4'	9:J:43:PRO:HB3	1.93	0.50
1:A:1151:A:O2'	1:A:1152:A:H8	1.94	0.50
1:A:1124:G:H5''	9:J:37:ARG:O	2.12	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:S:39:ILE:HG21	18:S:61:VAL:HG13	1.93	0.50
6:G:42:VAL:O	6:G:46:LEU:HB2	2.11	0.50
8:I:52:GLU:O	8:I:53:LEU:HD13	2.11	0.50
1:A:1029:U:O3'	1:A:1030:U:H3'	2.11	0.50
1:A:957:U:O2	1:A:959:A:H8	1.94	0.50
1:A:779:C:H5''	10:K:123:PRO:HB3	1.93	0.50
1:A:560:A:H4'	1:A:561:U:H5''	1.92	0.50
17:R:23:LYS:HG3	17:R:24:ASP:N	2.26	0.50
6:G:29:LEU:O	6:G:29:LEU:HD23	2.11	0.50
1:A:538:G:OP2	11:L:111:GLN:HB2	2.11	0.50
11:L:33:CYS:H	11:L:54:VAL:HG13	1.75	0.50
2:C:106:ARG:HH11	2:C:106:ARG:HG2	1.77	0.50
1:A:1219:A:H2'	1:A:1220:G:C8	2.46	0.50
13:N:60:ARG:HE	13:N:62:ARG:HG2	1.76	0.50
18:S:35:ARG:HB3	18:S:50:VAL:HG13	1.91	0.50
8:I:20:ILE:N	8:I:20:ILE:HD12	2.24	0.50
5:F:73:GLU:O	5:F:77:THR:HG23	2.12	0.50
12:M:29:SER:O	12:M:33:LEU:HG	2.11	0.50
17:R:42:ARG:HG3	17:R:43:ILE:N	2.27	0.50
14:O:55:LEU:O	14:O:59:VAL:HG23	2.11	0.50
13:N:26:LEU:HA	13:N:29:ILE:HB	1.94	0.50
3:D:96:ARG:NH1	3:D:133:SER:HA	2.25	0.50
20:B:127:LYS:HD2	20:B:128:LEU:HD13	1.94	0.50
12:M:3:ILE:HD12	12:M:9:PRO:HD2	1.93	0.50
4:E:87:VAL:HG22	4:E:88:HIS:N	2.26	0.50
6:G:12:LEU:HD22	6:G:13:PRO:HD2	1.94	0.50
3:D:55:ARG:HG3	3:D:55:ARG:NH1	2.26	0.50
1:A:1387:G:H2'	1:A:1388:C:C6	2.46	0.50
1:A:312:C:H2'	1:A:313:A:H8	1.77	0.50
1:A:1459:G:H2'	1:A:1460:C:C6	2.45	0.50
1:A:724:G:O2'	1:A:725:G:H5'	2.10	0.50
1:A:86:G:H1'	1:A:87:C:O4'	2.12	0.50
19:T:65:LEU:HG	19:T:66:ILE:HD13	1.93	0.50
19:T:66:ILE:HG23	19:T:70:LYS:HB3	1.92	0.50
18:S:51:HIS:HB2	18:S:56:HIS:CE1	2.47	0.50
1:A:643:C:H2'	1:A:644:U:H6	1.77	0.50
1:A:453:G:H2'	1:A:454:G:C8	2.47	0.50
1:A:1530:G:H2'	1:A:1531:A:H8	1.77	0.50
1:A:9:G:H2'	1:A:10:A:H8	1.77	0.50
6:G:3:ARG:HH11	6:G:3:ARG:HG3	1.76	0.50
1:A:216:U:H2'	1:A:217:C:C6	2.47	0.50
1:A:399:G:H2'	1:A:400:C:C6	2.47	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1254:A:H2'	1:A:1255:G:C8	2.47	0.50
4:E:95:MET:HA	4:E:124:ALA:HB2	1.94	0.50
13:N:11:LYS:HZ3	13:N:11:LYS:N	2.10	0.50
14:O:16:ARG:HA	14:O:16:ARG:HH11	1.76	0.50
1:A:1121:U:O2'	1:A:1122:U:H5'	2.11	0.50
9:J:12:ALA:CB	9:J:96:VAL:HG12	2.41	0.50
20:B:16:GLY:HA2	20:B:40:ILE:CG1	2.42	0.50
1:A:1005:A:H4'	1:A:1037:C:O2	2.12	0.50
8:I:56:MET:O	8:I:57:VAL:HB	2.10	0.50
15:P:25:ARG:CD	15:P:25:ARG:H	2.21	0.50
16:Q:30:HIS:HE1	16:Q:32:ILE:HG22	1.77	0.50
1:A:632:U:H3'	1:A:633:G:H5'	1.94	0.50
1:A:490:C:H2'	1:A:491:G:H8	1.75	0.50
1:A:613:C:H2'	1:A:614:C:C6	2.46	0.50
20:B:128:LEU:HD23	20:B:132:GLU:HB3	1.94	0.50
1:A:893:C:H2'	1:A:894:G:C8	2.47	0.50
1:A:640:A:O2'	1:A:641:U:H5'	2.12	0.50
8:I:30:ASN:O	8:I:31:GLN:HB2	2.11	0.50
20:B:46:VAL:O	20:B:49:PHE:HB2	2.12	0.50
5:F:5:GLU:HA	5:F:63:ASN:HA	1.94	0.50
4:E:28:ARG:CZ	4:E:30:PHE:HB3	2.42	0.50
8:I:56:MET:SD	8:I:57:VAL:HG23	2.52	0.50
1:A:1379:G:O6	6:G:2:ARG:HD3	2.12	0.50
2:C:149:LYS:HE3	2:C:166:TRP:CH2	2.47	0.50
9:J:36:VAL:HA	9:J:76:ILE:HA	1.94	0.50
12:M:89:ARG:HB3	12:M:96:VAL:HG22	1.94	0.50
1:A:658:C:H2'	1:A:659:U:C6	2.44	0.50
2:C:14:VAL:O	2:C:15:LYS:HD2	2.11	0.50
1:A:1437:A:H2'	1:A:1438:G:C8	2.46	0.50
1:A:528:C:H41	11:L:45:ASN:CG	2.15	0.50
7:H:111:THR:H	7:H:114:ALA:HB3	1.76	0.50
8:I:78:ILE:HG22	8:I:82:ILE:HD11	1.92	0.49
12:M:44:ILE:HA	12:M:47:LEU:HD23	1.93	0.49
15:P:28:ARG:HD3	15:P:29:ASN:HD22	1.76	0.49
18:S:10:ILE:HG22	18:S:37:SER:HB3	1.94	0.49
18:S:11:ASP:OD1	18:S:34:SER:HA	2.12	0.49
1:A:239:U:H5'	1:A:239:U:H6	1.76	0.49
9:J:6:ILE:HB	9:J:76:ILE:HD11	1.94	0.49
1:A:772:U:H2'	1:A:773:G:C8	2.46	0.49
11:L:17:LYS:N	11:L:17:LYS:HZ1	2.11	0.49
4:E:53:ARG:HB3	4:E:53:ARG:CZ	2.42	0.49
3:D:120:LYS:O	3:D:145:ARG:HG3	2.12	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:M:43:LYS:N	12:M:43:LYS:HD2	2.26	0.49
18:S:10:ILE:HB	18:S:14:LEU:HD11	1.94	0.49
1:A:1069:C:H5''	4:E:25:LYS:NZ	2.27	0.49
4:E:15:ILE:HB	4:E:35:LEU:O	2.12	0.49
8:I:34:LEU:HD21	8:I:48:ARG:NH2	2.18	0.49
11:L:13:ARG:HG2	11:L:14:LYS:H	1.76	0.49
17:R:56:ARG:O	17:R:60:ARG:HG2	2.12	0.49
1:A:643:C:H2'	1:A:644:U:C6	2.47	0.49
1:A:1317:C:H3'	1:A:1318:A:H8	1.77	0.49
10:K:75:GLU:CD	10:K:75:GLU:N	2.66	0.49
1:A:1134:G:N2	1:A:1135:U:H1'	2.26	0.49
10:K:90:PRO:C	10:K:92:ARG:H	2.16	0.49
16:Q:29:LYS:HG3	16:Q:34:GLY:O	2.12	0.49
7:H:108:GLY:O	7:H:110:MET:HG3	2.12	0.49
15:P:36:VAL:O	15:P:36:VAL:HG13	2.12	0.49
16:Q:74:LEU:HD13	16:Q:75:VAL:N	2.28	0.49
1:A:429:U:OP2	3:D:31:CYS:HB2	2.13	0.49
1:A:1029:U:H5''	1:A:1030:U:C5	2.47	0.49
1:A:1030:U:H4'	1:A:1031:C:OP2	2.12	0.49
7:H:45:ILE:HB	7:H:61:THR:O	2.13	0.49
10:K:106:ILE:HG13	10:K:107:THR:N	2.23	0.49
1:A:1510:C:H2'	1:A:1511:G:C8	2.47	0.49
10:K:30:ILE:HG22	10:K:45:THR:CB	2.42	0.49
1:A:1250:A:H2	1:A:1370:G:H1'	1.77	0.49
1:A:1432:G:O2'	1:A:1468:A:N6	2.45	0.49
1:A:1163:A:H2'	1:A:1164:G:H8	1.77	0.49
2:C:142:ARG:HH21	2:C:143:LEU:HD21	1.77	0.49
7:H:27:PRO:HA	7:H:56:PRO:O	2.12	0.49
9:J:15:HIS:O	9:J:18:ILE:HG22	2.11	0.49
1:A:464:U:H2'	1:A:466:A:OP2	2.11	0.49
1:A:429:U:H3'	3:D:8:LEU:HD23	1.93	0.49
1:A:1118:U:H1'	1:A:1179:A:C5	2.47	0.49
1:A:1413:A:O2'	1:A:1414:U:H5'	2.12	0.49
1:A:634:C:H2'	1:A:635:A:H8	1.77	0.49
1:A:636:U:H2'	1:A:637:C:H6	1.78	0.49
1:A:1127:G:O2'	1:A:1128:C:H5'	2.12	0.49
12:M:50:GLY:O	12:M:54:THR:HG23	2.11	0.49
1:A:320:A:H2'	1:A:321:A:C8	2.47	0.49
1:A:598:U:H4'	7:H:85:TYR:CG	2.46	0.49
7:H:47:ASP:CG	7:H:48:PHE:H	2.16	0.49
1:A:767:A:H2'	1:A:768:A:C8	2.47	0.49
13:N:50:LEU:H	13:N:51:PRO:CD	2.22	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:160:LEU:HA	3:D:163:GLN:CG	2.41	0.49
10:K:86:LYS:HB2	10:K:113:THR:HA	1.94	0.49
1:A:664:G:H5''	17:R:52:ARG:HE	1.77	0.49
2:C:129:PHE:CE2	2:C:156:LEU:HD13	2.47	0.49
1:A:1101:A:H62	20:B:173:LYS:HE3	1.77	0.49
1:A:1500:A:C2'	1:A:1501:C:H5'	2.42	0.49
12:M:22:TYR:CD1	12:M:65:GLU:HA	2.46	0.49
3:D:77:GLU:OE2	3:D:81:LEU:HD21	2.12	0.49
8:I:109:GLN:CD	8:I:110:VAL:H	2.16	0.49
1:A:366:A:O2'	1:A:394:G:N2	2.45	0.49
15:P:6:LEU:N	15:P:6:LEU:HD12	2.27	0.49
1:A:984:C:O2'	1:A:985:C:H5'	2.12	0.49
1:A:50:A:N6	1:A:361:G:H4'	2.28	0.49
1:A:1085:U:H3'	1:A:1086:U:C6	2.48	0.49
12:M:14:ALA:HB2	12:M:42:VAL:HG23	1.95	0.49
18:S:40:PHE:O	18:S:43:MET:HG3	2.11	0.49
1:A:602:A:H2'	1:A:603:U:C6	2.47	0.49
1:A:602:A:O2'	1:A:603:U:H5'	2.12	0.49
1:A:1057:G:O3'	2:C:196:GLY:HA3	2.13	0.49
12:M:90:HIS:HA	12:M:108:ARG:HH22	1.74	0.49
2:C:120:THR:HG22	2:C:188:ALA:HB2	1.94	0.49
16:Q:83:LEU:N	16:Q:83:LEU:HD13	2.27	0.49
2:C:16:PRO:CG	2:C:53:ARG:HH12	2.23	0.49
3:D:22:SER:N	3:D:109:THR:HG22	2.28	0.49
19:T:49:ALA:C	19:T:52:GLU:HB3	2.33	0.49
6:G:14:ASP:OD2	6:G:22:LEU:HB3	2.11	0.49
9:J:8:ILE:HD11	9:J:76:ILE:HG13	1.93	0.49
12:M:86:ARG:HA	12:M:96:VAL:CG1	2.42	0.49
13:N:25:GLU:O	13:N:29:ILE:HG13	2.12	0.49
13:N:29:ILE:HB	13:N:30:ILE:HD12	1.93	0.49
1:A:376:G:H2'	1:A:377:G:C8	2.45	0.49
7:H:4:ASP:OD1	7:H:7:ALA:HB2	2.13	0.49
1:A:1009:U:H2'	1:A:1010:U:C6	2.48	0.49
7:H:113:ARG:NH2	7:H:114:ALA:HA	2.28	0.49
1:A:1527:U:O2'	1:A:1528:U:H5'	2.13	0.49
21:U:13:VAL:HG13	21:U:13:VAL:O	2.12	0.49
1:A:1320:C:N4	18:S:35:ARG:HD3	2.28	0.49
13:N:50:LEU:N	13:N:51:PRO:CD	2.76	0.49
1:A:1339:A:H2'	1:A:1340:A:O4'	2.12	0.49
12:M:21:ILE:HG22	12:M:23:GLY:H	1.77	0.49
18:S:40:PHE:HB2	18:S:43:MET:HE3	1.95	0.49
5:F:51:ILE:HG23	5:F:51:ILE:O	2.12	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:780:A:O2'	1:A:781:A:H5''	2.13	0.49
9:J:76:ILE:O	9:J:76:ILE:HD12	2.11	0.49
1:A:1511:G:O2'	1:A:1512:U:H5'	2.12	0.49
7:H:95:MET:HG2	7:H:98:LEU:HB2	1.93	0.49
5:F:18:VAL:HG21	5:F:58:HIS:CE1	2.48	0.49
1:A:1423:G:H2'	1:A:1424:U:C6	2.48	0.49
1:A:1206:G:H4'	2:C:191:THR:O	2.13	0.49
1:A:398:U:H2'	1:A:399:G:C8	2.47	0.49
20:B:128:LEU:HD23	20:B:132:GLU:CB	2.42	0.49
5:F:53:LYS:HB2	5:F:54:LEU:HD22	1.93	0.49
3:D:16:THR:HG22	3:D:17:ASP:N	2.28	0.49
13:N:79:SER:O	13:N:83:VAL:HG23	2.13	0.49
4:E:88:HIS:CE1	4:E:137:ARG:HD2	2.48	0.49
16:Q:60:ILE:HD13	16:Q:60:ILE:H	1.78	0.49
8:I:22:PRO:HA	8:I:60:LEU:CB	2.43	0.49
2:C:156:LEU:CD1	2:C:165:GLU:HB2	2.43	0.49
1:A:104:G:O2'	1:A:105:G:H5'	2.13	0.49
1:A:69:G:N2	1:A:71:A:N6	2.61	0.49
1:A:1297:G:H1'	1:A:1298:U:C5	2.44	0.49
1:A:502:A:H2'	1:A:503:C:H6	1.76	0.49
1:A:1216:A:H2'	1:A:1217:C:C6	2.47	0.49
1:A:394:G:O2'	1:A:395:C:H5'	2.13	0.49
1:A:137:U:H2'	1:A:138:G:H8	1.78	0.49
5:F:6:ILE:HG13	5:F:6:ILE:O	2.13	0.49
1:A:916:U:O2'	1:A:917:G:H5'	2.12	0.49
20:B:14:HIS:HD2	20:B:202:ASN:H	1.60	0.49
1:A:1238:A:C8	1:A:1303:C:H1'	2.48	0.49
4:E:132:PRO:HG2	4:E:133:ILE:H	1.78	0.49
4:E:136:VAL:HG13	4:E:137:ARG:H	1.78	0.49
3:D:106:PHE:CE1	3:D:158:LEU:HD21	2.48	0.49
11:L:81:ILE:HG23	11:L:94:TYR:HB3	1.95	0.49
15:P:72:ALA:HA	15:P:75:ILE:HD12	1.95	0.49
1:A:1225:A:H5'	1:A:1226:C:OP2	2.13	0.49
1:A:660:C:H2'	1:A:661:G:O4'	2.13	0.49
1:A:847:G:H2'	1:A:848:C:C6	2.48	0.49
20:B:40:ILE:HD13	20:B:201:GLY:HA2	1.93	0.48
12:M:9:PRO:HB2	12:M:17:ALA:HB1	1.95	0.48
20:B:113:LEU:HD23	20:B:114:LYS:N	2.28	0.48
7:H:12:ARG:HG3	7:H:12:ARG:HH11	1.78	0.48
1:A:728:A:H2'	1:A:729:A:H8	1.77	0.48
1:A:591:U:H2'	1:A:592:G:H8	1.78	0.48
1:A:724:G:H2'	1:A:725:G:H8	1.77	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:Q:10:ARG:NH2	16:Q:55:GLY:HA2	2.28	0.48
8:I:50:PRO:HD3	8:I:79:ARG:CG	2.43	0.48
3:D:8:LEU:HD12	3:D:31:CYS:SG	2.53	0.48
1:A:846:G:N3	1:A:846:G:H2'	2.28	0.48
1:A:734:G:O2'	17:R:59:LYS:HD3	2.13	0.48
2:C:155:ARG:H	2:C:162:ALA:HA	1.78	0.48
20:B:75:ALA:C	20:B:79:VAL:HG23	2.33	0.48
20:B:93:HIS:O	20:B:94:ARG:O	2.30	0.48
5:F:68:GLN:HA	5:F:71:ILE:HD11	1.95	0.48
14:O:68:TYR:HA	14:O:71:ARG:HE	1.77	0.48
1:A:820:U:H4'	1:A:821:G:OP2	2.12	0.48
1:A:386:C:C2'	1:A:387:U:H5'	2.44	0.48
1:A:114:U:H2'	1:A:115:G:C8	2.48	0.48
13:N:5:MET:SD	13:N:8:ARG:HD3	2.53	0.48
20:B:209:VAL:HG23	20:B:210:THR:N	2.27	0.48
1:A:1001:C:H2'	1:A:1002:G:H8	1.77	0.48
6:G:67:ASN:HB2	6:G:134:VAL:HG12	1.95	0.48
17:R:42:ARG:HG3	17:R:43:ILE:H	1.78	0.48
2:C:129:PHE:HD2	2:C:156:LEU:HD22	1.78	0.48
2:C:149:LYS:HG3	2:C:168:ARG:HB2	1.96	0.48
1:A:794:A:H2'	1:A:795:C:C6	2.48	0.48
3:D:129:VAL:HG12	3:D:131:ILE:H	1.78	0.48
1:A:908:A:H2'	1:A:909:A:H8	1.79	0.48
11:L:42:LYS:HB3	11:L:44:PRO:HD2	1.94	0.48
4:E:53:ARG:HB3	4:E:53:ARG:NH1	2.28	0.48
6:G:70:PRO:O	6:G:95:ARG:HG3	2.13	0.48
1:A:815:A:H4'	1:A:817:C:C4	2.49	0.48
1:A:1060:U:H5''	9:J:53:ILE:HG12	1.94	0.48
11:L:98:ARG:HD2	11:L:103:CYS:SG	2.53	0.48
1:A:474:G:O2'	1:A:475:C:H5'	2.13	0.48
1:A:475:C:H2'	1:A:476:U:H6	1.78	0.48
11:L:2:THR:HG22	11:L:5:GLN:HE21	1.79	0.48
1:A:586:C:H2'	1:A:587:G:H5'	1.95	0.48
5:F:6:ILE:HG23	5:F:62:MET:HB3	1.95	0.48
1:A:233:C:H2'	1:A:234:C:H6	1.78	0.48
5:F:21:MET:HB3	5:F:25:TYR:CZ	2.48	0.48
1:A:308:C:H2'	1:A:309:A:H8	1.78	0.48
1:A:775:G:H2'	1:A:776:G:H8	1.78	0.48
13:N:97:LYS:HB3	13:N:97:LYS:NZ	2.28	0.48
13:N:68:ARG:HG2	13:N:68:ARG:HH11	1.78	0.48
1:A:923:A:H2'	1:A:924:C:H6	1.77	0.48
19:T:70:LYS:O	19:T:74:HIS:HB2	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:I:32:ARG:HD3	8:I:37:TYR:CD1	2.47	0.48
11:L:66:ILE:N	11:L:66:ILE:HD12	2.28	0.48
2:C:59:PRO:HD2	2:C:62:SER:O	2.13	0.48
1:A:546:A:P	3:D:68:GLU:HB3	2.53	0.48
20:B:10:LYS:O	20:B:13:VAL:HG23	2.13	0.48
2:C:71:ARG:O	2:C:75:VAL:HG23	2.13	0.48
20:B:68:PHE:HE1	20:B:88:GLN:HB3	1.79	0.48
4:E:136:VAL:HG13	4:E:137:ARG:N	2.28	0.48
4:E:37:VAL:HG11	4:E:113:VAL:CG1	2.43	0.48
4:E:17:VAL:HG23	4:E:33:THR:O	2.14	0.48
1:A:113:G:O4'	1:A:354:G:H4'	2.13	0.48
1:A:1009:U:H1'	1:A:1021:A:C2	2.49	0.48
2:C:146:LYS:HB2	2:C:202:PHE:CD2	2.49	0.48
2:C:78:LYS:C	2:C:80:GLY:H	2.16	0.48
3:D:149:LYS:HB2	3:D:177:MET:HG3	1.94	0.48
1:A:1320:C:OP2	18:S:69:LYS:HE3	2.13	0.48
5:F:2:ARG:O	5:F:65:GLU:HA	2.14	0.48
12:M:38:ILE:HD12	12:M:47:LEU:HD11	1.95	0.48
8:I:56:MET:SD	8:I:57:VAL:N	2.87	0.48
8:I:98:ARG:NE	8:I:103:VAL:HG21	2.28	0.48
1:A:411:A:C4	1:A:413:G:H1'	2.49	0.48
5:F:8:PHE:O	5:F:60:VAL:HG23	2.14	0.48
1:A:54:C:H2'	1:A:352:C:H41	1.78	0.48
1:A:614:C:O2'	1:A:615:G:H5'	2.14	0.48
4:E:95:MET:HA	4:E:124:ALA:CB	2.44	0.48
10:K:37:GLN:HB2	10:K:39:ASN:HD22	1.79	0.48
1:A:610:U:O2	1:A:610:U:O4'	2.30	0.48
21:U:20:ARG:HD2	21:U:20:ARG:N	2.29	0.48
18:S:62:THR:O	18:S:66:VAL:HG13	2.14	0.48
8:I:52:GLU:C	8:I:53:LEU:HD22	2.33	0.48
15:P:43:ALA:HA	15:P:46:LYS:HE3	1.96	0.48
20:B:212:TYR:O	20:B:216:VAL:HG13	2.13	0.48
1:A:1522:U:H2'	1:A:1523:G:H8	1.79	0.48
1:A:1234:C:H1'	1:A:1364:U:O2	2.13	0.48
1:A:1451:U:O2	1:A:1451:U:H2'	2.13	0.48
1:A:624:C:H2'	1:A:625:U:C6	2.48	0.48
1:A:1263:C:O2'	1:A:1264:U:H5'	2.14	0.48
15:P:20:VAL:HG21	15:P:32:PHE:CG	2.48	0.48
20:B:63:LYS:HA	20:B:224:ARG:NH1	2.29	0.48
20:B:8:MET:C	20:B:9:LEU:HD12	2.33	0.48
15:P:12:LYS:HD2	15:P:13:LYS:HG3	1.96	0.48
8:I:74:GLN:O	8:I:78:ILE:HG13	2.14	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:N:20:PHE:HB2	13:N:54:SER:OG	2.13	0.48
1:A:1004:A:H2'	1:A:1005:A:O4'	2.14	0.48
1:A:130:A:H1'	1:A:263:A:O2'	2.13	0.48
1:A:599:C:H4'	7:H:121:GLY:HA3	1.96	0.48
20:B:19:THR:HG23	20:B:20:ARG:N	2.23	0.48
1:A:1180:A:OP1	8:I:104:THR:HG22	2.14	0.48
12:M:83:GLY:O	12:M:88:LEU:HD21	2.14	0.48
8:I:129:ARG:HB2	8:I:129:ARG:CZ	2.43	0.48
1:A:1406:U:C2'	1:A:1407:C:H5'	2.43	0.48
20:B:23:ASN:C	20:B:25:LYS:H	2.17	0.48
8:I:12:LYS:HA	8:I:109:GLN:HG2	1.95	0.48
2:C:139:ASN:O	2:C:143:LEU:HD23	2.13	0.48
5:F:52:ASN:HA	5:F:53:LYS:HZ3	1.79	0.48
8:I:83:THR:OG1	8:I:97:LEU:HD22	2.14	0.48
5:F:51:ILE:HD11	5:F:86:ARG:HG3	1.96	0.48
14:O:55:LEU:O	14:O:58:MET:HG2	2.14	0.48
1:A:708:C:O2'	1:A:709:U:H5'	2.14	0.48
1:A:1346:A:N1	1:A:1374:A:H5''	2.29	0.48
10:K:60:PHE:O	10:K:64:VAL:HG12	2.14	0.48
1:A:828:U:H4'	1:A:828:U:OP1	2.14	0.48
20:B:204:ASP:O	20:B:208:ALA:HB3	2.14	0.47
1:A:468:A:H3'	1:A:469:C:C6	2.49	0.47
12:M:14:ALA:O	12:M:17:ALA:HB3	2.14	0.47
4:E:132:PRO:O	4:E:136:VAL:HG12	2.14	0.47
20:B:116:LEU:O	20:B:119:GLN:HB2	2.13	0.47
6:G:129:ASN:HA	6:G:134:VAL:CG1	2.38	0.47
8:I:127:SER:O	8:I:129:ARG:HG3	2.14	0.47
7:H:94:VAL:HG21	7:H:100:ILE:O	2.13	0.47
1:A:454:G:H2'	1:A:455:G:H8	1.79	0.47
6:G:78:ARG:NH1	6:G:80:GLY:H	2.11	0.47
1:A:1299:A:H2'	1:A:1301:U:H1'	1.96	0.47
19:T:3:ILE:HG13	19:T:3:ILE:H	1.47	0.47
7:H:82:LEU:HD13	7:H:82:LEU:O	2.13	0.47
1:A:754:C:H3'	1:A:754:C:O2	2.14	0.47
1:A:1040:U:H2'	1:A:1041:G:C8	2.49	0.47
21:U:20:ARG:HD2	21:U:20:ARG:H	1.79	0.47
3:D:123:MET:CB	3:D:128:VAL:HA	2.44	0.47
6:G:125:ASP:HB3	6:G:131:GLY:H	1.78	0.47
2:C:129:PHE:CD2	2:C:156:LEU:HD22	2.48	0.47
20:B:216:VAL:O	20:B:220:VAL:HG23	2.14	0.47
1:A:1317:C:H3'	1:A:1318:A:C8	2.49	0.47
10:K:74:LYS:HG3	10:K:104:PHE:CZ	2.49	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:N:27:LYS:HG3	13:N:28:ALA:H	1.79	0.47
1:A:898:G:N2	1:A:900:A:H3'	2.29	0.47
16:Q:11:VAL:HG13	16:Q:20:ILE:HG23	1.94	0.47
1:A:1109:C:H2'	1:A:1110:A:O4'	2.14	0.47
7:H:58:LEU:HD22	7:H:60:LEU:HB2	1.96	0.47
1:A:549:C:H2'	1:A:550:G:C8	2.49	0.47
11:L:113:ARG:NE	11:L:120:ARG:HA	2.29	0.47
1:A:36:C:O3'	11:L:119:LYS:HA	2.14	0.47
19:T:49:ALA:O	19:T:52:GLU:HB3	2.14	0.47
1:A:443:C:H2'	1:A:444:G:H8	1.79	0.47
9:J:13:PHE:CD2	9:J:69:THR:HG23	2.49	0.47
20:B:8:MET:HG3	20:B:9:LEU:HD12	1.95	0.47
6:G:75:LYS:HD3	6:G:76:SER:N	2.28	0.47
13:N:79:SER:HG	13:N:82:LYS:HG2	1.79	0.47
1:A:1035:A:H2'	1:A:1036:A:C8	2.49	0.47
1:A:269:C:H2'	1:A:270:A:H8	1.74	0.47
14:O:88:ARG:CA	14:O:88:ARG:HH11	2.20	0.47
1:A:242:G:H2'	1:A:243:A:H5''	1.96	0.47
1:A:1510:C:H2'	1:A:1511:G:H8	1.79	0.47
1:A:411:A:N6	1:A:413:G:H21	2.10	0.47
3:D:44:LYS:HD2	3:D:46:ARG:CG	2.44	0.47
3:D:94:GLU:HG3	3:D:99:ASN:ND2	2.29	0.47
1:A:309:A:O2'	1:A:310:G:H5'	2.14	0.47
1:A:1125:U:O2'	1:A:1126:U:H2'	2.15	0.47
8:I:18:VAL:HA	8:I:64:ILE:HA	1.96	0.47
1:A:1086:U:H3	1:A:1099:G:N2	1.94	0.47
3:D:33:ILE:HD12	3:D:34:GLU:H	1.79	0.47
1:A:1363:A:N3	1:A:1363:A:H2'	2.30	0.47
1:A:1060:U:H2'	1:A:1061:G:H8	1.78	0.47
20:B:130:LYS:HA	20:B:130:LYS:NZ	2.29	0.47
13:N:26:LEU:HD12	13:N:44:VAL:HG13	1.96	0.47
3:D:47:LEU:HD13	3:D:52:VAL:HG22	1.96	0.47
1:A:208:U:O2'	1:A:209:U:H3'	2.13	0.47
14:O:67:ASP:O	14:O:71:ARG:HG3	2.14	0.47
1:A:65:A:C6	1:A:381:C:N3	2.83	0.47
8:I:30:ASN:HD22	8:I:65:THR:HA	1.79	0.47
20:B:46:VAL:HA	20:B:49:PHE:CD2	2.50	0.47
5:F:85:ILE:HG22	5:F:86:ARG:H	1.80	0.47
2:C:119:ILE:CG2	2:C:120:THR:N	2.76	0.47
1:A:1414:U:H2'	1:A:1415:G:C8	2.44	0.47
1:A:502:A:H2'	1:A:503:C:C6	2.49	0.47
1:A:512:U:H2'	1:A:513:C:H6	1.75	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:545:C:O2'	1:A:546:A:H5'	2.15	0.47
1:A:286:C:H2'	1:A:287:U:C6	2.50	0.47
13:N:97:LYS:HB3	13:N:97:LYS:HZ2	1.79	0.47
1:A:904:U:H2'	1:A:905:U:C6	2.50	0.47
1:A:382:A:H2'	1:A:383:A:C8	2.49	0.47
1:A:1120:C:H2'	1:A:1121:U:C6	2.49	0.47
8:I:19:PHE:HB2	8:I:63:TYR:HB3	1.97	0.47
1:A:844:G:H3'	1:A:844:G:OP2	2.14	0.47
17:R:63:TYR:HD2	17:R:63:TYR:N	2.11	0.47
18:S:48:ILE:O	18:S:58:PRO:HA	2.14	0.47
1:A:142:G:N3	1:A:196:A:H2	2.12	0.47
1:A:967:C:H4'	8:I:129:ARG:HG2	1.96	0.47
7:H:10:LEU:CD2	7:H:74:ILE:HD11	2.44	0.47
1:A:659:U:O2'	1:A:660:C:H5'	2.15	0.47
1:A:1406:U:H2'	1:A:1407:C:H5'	1.96	0.47
1:A:44:A:O2'	1:A:45:G:H5'	2.14	0.47
6:G:144:ALA:O	6:G:145:GLU:HB3	2.14	0.47
20:B:80:LYS:HG3	20:B:81:ASP:N	2.29	0.47
1:A:435:A:H2'	1:A:435:A:N3	2.30	0.47
2:C:190:THR:HG22	2:C:191:THR:H	1.78	0.47
1:A:358:U:H2'	1:A:359:G:C8	2.50	0.47
1:A:197:A:H4'	1:A:198:G:O5'	2.13	0.47
13:N:63:CYS:HB3	13:N:68:ARG:H	1.80	0.47
8:I:16:ALA:HA	8:I:66:VAL:HA	1.96	0.47
9:J:41:PRO:O	9:J:42:LEU:HB2	2.15	0.47
5:F:36:ILE:N	5:F:36:ILE:HD12	2.30	0.47
5:F:2:ARG:HB3	5:F:92:THR:OG1	2.14	0.47
3:D:192:ALA:C	3:D:194:ILE:H	2.18	0.47
12:M:77:LYS:O	12:M:80:MET:HG2	2.13	0.47
4:E:92:ARG:HB3	4:E:92:ARG:NH1	2.29	0.47
1:A:429:U:H3'	3:D:8:LEU:CD2	2.45	0.47
1:A:119:A:H4'	1:A:120:A:O4'	2.15	0.47
8:I:123:ARG:CZ	8:I:123:ARG:HB3	2.44	0.47
15:P:3:THR:CG2	15:P:66:THR:HB	2.41	0.47
1:A:762:U:H2'	1:A:763:G:H8	1.79	0.47
1:A:92:U:H2'	1:A:93:U:C6	2.49	0.47
1:A:342:C:O2'	1:A:343:U:H5'	2.15	0.47
1:A:1073:U:H2'	1:A:1074:G:H8	1.78	0.47
1:A:36:C:H4'	11:L:118:VAL:O	2.15	0.47
3:D:188:SER:C	3:D:190:LEU:H	2.18	0.47
2:C:21:TRP:CH2	2:C:31:ASN:HB3	2.50	0.47
1:A:284:C:H2'	1:A:285:C:C6	2.49	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1216:A:H2'	1:A:1217:C:H6	1.80	0.47
1:A:692:U:H2'	1:A:694:A:OP2	2.15	0.47
5:F:54:LEU:HD22	5:F:54:LEU:N	2.28	0.47
10:K:61:ALA:O	10:K:64:VAL:HG13	2.13	0.47
19:T:2:ASN:CG	19:T:3:ILE:N	2.67	0.47
1:A:213:G:H3'	1:A:214:C:H6	1.79	0.47
6:G:30:MET:HA	6:G:38:ALA:CB	2.45	0.47
15:P:21:VAL:HG12	15:P:33:ILE:HD12	1.97	0.47
5:F:11:HIS:CG	5:F:12:PRO:HD2	2.49	0.47
2:C:110:LEU:HD21	2:C:140:ALA:O	2.14	0.47
2:C:110:LEU:HD22	2:C:145:ALA:HB2	1.97	0.47
1:A:1016:A:H4'	1:A:1218:C:H4'	1.96	0.47
1:A:1222:G:C2'	1:A:1223:C:H5'	2.45	0.47
1:A:202:G:H2'	1:A:203:G:H8	1.80	0.47
10:K:88:PRO:HD3	21:U:28:LEU:CD1	2.34	0.47
20:B:116:LEU:HA	20:B:119:GLN:HG3	1.97	0.47
1:A:429:U:H1'	1:A:430:A:H5''	1.96	0.47
20:B:186:VAL:O	20:B:200:PRO:HA	2.14	0.47
13:N:53:ASP:HA	13:N:58:ARG:NE	2.30	0.47
1:A:811:C:O2'	1:A:901:A:N1	2.48	0.47
1:A:224:U:H2'	1:A:225:C:H6	1.80	0.47
11:L:33:CYS:HA	11:L:54:VAL:HA	1.97	0.47
1:A:960:U:H6	1:A:1222:G:O2'	1.98	0.47
1:A:1242:G:H2'	1:A:1243:C:O4'	2.14	0.47
10:K:83:VAL:HG22	10:K:106:ILE:HD11	1.95	0.47
9:J:6:ILE:O	9:J:75:ASP:HA	2.15	0.47
2:C:91:ALA:HB2	2:C:98:ALA:H	1.80	0.47
12:M:90:HIS:CE1	12:M:96:VAL:HG21	2.49	0.47
12:M:92:ARG:NH1	18:S:79:TYR:HD2	2.12	0.47
1:A:364:A:H2'	1:A:365:U:O2	2.14	0.47
8:I:11:ARG:HH21	8:I:12:LYS:HD2	1.80	0.47
19:T:56:ILE:O	19:T:60:GLN:HG2	2.15	0.47
20:B:27:LYS:C	20:B:29:PHE:H	2.18	0.47
15:P:26:ASN:HD22	15:P:26:ASN:HA	1.59	0.47
8:I:78:ILE:HG22	8:I:82:ILE:CD1	2.45	0.47
2:C:72:PRO:O	2:C:76:ILE:HG12	2.13	0.47
3:D:123:MET:HG3	3:D:143:SER:OG	2.15	0.47
1:A:571:U:O2	1:A:918:A:H5'	2.14	0.47
1:A:1081:A:OP1	4:E:21:SER:O	2.33	0.47
12:M:68:LEU:O	12:M:72:ILE:HG22	2.15	0.47
1:A:861:G:H2'	1:A:862:C:H6	1.80	0.47
1:A:193:C:H2'	1:A:194:C:C5	2.49	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:L:106:VAL:CG2	11:L:116:TYR:HB3	2.44	0.47
1:A:908:A:H2'	1:A:909:A:C8	2.50	0.47
8:I:9:GLY:HA3	8:I:81:GLY:N	2.30	0.47
1:A:1239:A:H4'	1:A:1240:U:C5'	2.44	0.47
1:A:716:A:N3	10:K:118:ASN:O	2.48	0.47
1:A:586:C:C2'	1:A:587:G:H5'	2.44	0.47
20:B:131:LYS:HG3	20:B:132:GLU:N	2.30	0.47
21:U:11:PHE:CE1	21:U:13:VAL:HG12	2.50	0.47
1:A:1147:C:H2'	1:A:1148:U:H6	1.80	0.46
1:A:201:G:O2'	1:A:469:C:H4'	2.15	0.46
1:A:1245:C:H2'	1:A:1246:A:H8	1.80	0.46
15:P:43:ALA:CA	15:P:46:LYS:HE3	2.45	0.46
1:A:1266:G:N2	1:A:1268:G:H3'	2.29	0.46
1:A:1360:A:H2'	1:A:1361:G:O4'	2.16	0.46
10:K:112:VAL:HA	17:R:72:ARG:HH21	1.80	0.46
1:A:664:G:P	17:R:52:ARG:HH21	2.38	0.46
1:A:373:A:C1'	1:A:481:G:H1'	2.45	0.46
1:A:1465:A:H2'	1:A:1466:C:C6	2.50	0.46
1:A:1169:A:H2'	1:A:1170:A:C8	2.50	0.46
1:A:787:A:O2'	1:A:788:U:H5'	2.15	0.46
1:A:697:U:H2'	1:A:698:G:H5'	1.98	0.46
11:L:60:PHE:O	11:L:62:VAL:N	2.48	0.46
9:J:18:ILE:HG13	9:J:72:ARG:HG2	1.97	0.46
1:A:1241:G:O2'	1:A:1242:G:H5'	2.15	0.46
1:A:1302:C:H6	1:A:1302:C:H5'	1.80	0.46
19:T:61:ALA:HB1	19:T:67:HIS:HA	1.98	0.46
1:A:817:C:C2	1:A:819:A:O4'	2.68	0.46
1:A:1390:U:O2'	1:A:1391:U:H5'	2.15	0.46
10:K:65:ALA:O	10:K:68:ARG:HB3	2.15	0.46
1:A:1300:G:H1'	1:A:1301:U:C5	2.49	0.46
1:A:805:C:O2'	1:A:806:C:H5'	2.15	0.46
1:A:1175:G:O2'	1:A:1176:A:H5'	2.14	0.46
3:D:187:ARG:CZ	3:D:191:SER:HB3	2.46	0.46
7:H:83:ARG:HB3	7:H:85:TYR:CE1	2.49	0.46
1:A:687:A:C2	1:A:704:A:C5	3.04	0.46
1:A:953:G:H2'	1:A:954:G:O4'	2.16	0.46
8:I:82:ILE:O	8:I:86:LEU:HB2	2.16	0.46
20:B:59:ILE:HG21	20:B:158:ASP:HB3	1.97	0.46
1:A:270:A:H2'	1:A:271:C:O4'	2.16	0.46
1:A:1343:G:H2'	1:A:1344:C:H6	1.80	0.46
20:B:134:LEU:HD12	20:B:134:LEU:HA	1.82	0.46
10:K:108:ASN:HD21	21:U:6:ARG:HD2	1.80	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1291:U:H2'	1:A:1292:G:H8	1.79	0.46
1:A:814:A:H2'	1:A:816:A:O5'	2.14	0.46
20:B:172:ILE:HD12	20:B:172:ILE:N	2.30	0.46
1:A:86:G:O2'	1:A:87:C:O5'	2.27	0.46
1:A:984:C:H2'	1:A:985:C:C6	2.51	0.46
1:A:308:C:H2'	1:A:309:A:C8	2.51	0.46
1:A:1040:U:H2'	1:A:1041:G:O4'	2.16	0.46
1:A:945:G:H21	1:A:1334:G:H4'	1.80	0.46
11:L:78:VAL:O	11:L:102:ASP:HB2	2.16	0.46
1:A:220:G:O2'	1:A:221:C:H5'	2.15	0.46
8:I:16:ALA:HA	8:I:66:VAL:HG23	1.97	0.46
12:M:13:HIS:O	12:M:17:ALA:HB2	2.15	0.46
12:M:44:ILE:O	12:M:47:LEU:HB2	2.15	0.46
1:A:425:G:H2'	1:A:426:U:C6	2.50	0.46
15:P:42:ILE:HG22	15:P:43:ALA:N	2.31	0.46
1:A:1130:A:H2'	1:A:1131:G:C8	2.50	0.46
4:E:45:VAL:HG11	4:E:117:ALA:HB2	1.97	0.46
1:A:1212:U:H4'	1:A:1213:A:C8	2.50	0.46
1:A:1476:A:H2'	1:A:1477:U:O4'	2.14	0.46
14:O:69:LEU:HD11	14:O:76:ARG:CB	2.46	0.46
3:D:40:HIS:O	3:D:43:ARG:HG2	2.15	0.46
11:L:17:LYS:NZ	11:L:17:LYS:N	2.64	0.46
1:A:984:C:H2'	1:A:985:C:H6	1.80	0.46
1:A:1125:U:C6	9:J:40:ILE:HD13	2.51	0.46
1:A:16:A:H2	1:A:1080:A:N3	2.14	0.46
6:G:71:THR:H	6:G:141:HIS:CE1	2.33	0.46
7:H:68:LYS:HG3	7:H:69:ALA:N	2.30	0.46
9:J:8:ILE:H	9:J:8:ILE:HD12	1.80	0.46
3:D:75:TYR:CE1	3:D:200:VAL:HA	2.50	0.46
6:G:74:VAL:HG12	6:G:87:PRO:HB3	1.98	0.46
1:A:1293:C:O2'	1:A:1294:G:H5'	2.14	0.46
1:A:1178:G:H3'	8:I:98:ARG:NH2	2.29	0.46
20:B:93:HIS:HA	20:B:94:ARG:NH2	2.30	0.46
1:A:1095:U:H5''	1:A:1109:C:O2	2.16	0.46
6:G:59:GLU:O	6:G:63:VAL:HG23	2.15	0.46
1:A:707:U:H4'	10:K:21:HIS:CD2	2.50	0.46
1:A:204:G:H2'	1:A:205:A:H8	1.79	0.46
1:A:333:U:H2'	1:A:334:C:C6	2.51	0.46
16:Q:3:LYS:HG3	16:Q:4:ILE:H	1.79	0.46
20:B:129:THR:O	20:B:131:LYS:N	2.48	0.46
4:E:68:ARG:O	4:E:69:ASN:HB2	2.16	0.46
1:A:1181:G:H1'	1:A:1182:G:C5	2.51	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1308:U:H3'	12:M:97:ARG:NH1	2.31	0.46
3:D:90:LEU:HD13	3:D:93:LEU:HD12	1.97	0.46
3:D:24:VAL:O	3:D:27:ILE:HG13	2.14	0.46
1:A:251:G:H1	1:A:271:C:N4	2.13	0.46
16:Q:64:ARG:HG2	16:Q:65:PRO:HD2	1.97	0.46
1:A:1102:A:H2'	1:A:1103:C:C6	2.51	0.46
1:A:373:A:H2'	1:A:374:A:C8	2.47	0.46
1:A:36:C:O2'	1:A:37:U:H5'	2.16	0.46
3:D:2:ARG:HG3	3:D:114:ARG:NH1	2.31	0.46
1:A:586:C:H5''	7:H:81:GLY:HA2	1.98	0.46
1:A:893:C:H2'	1:A:894:G:H8	1.81	0.46
10:K:37:GLN:HB2	10:K:39:ASN:ND2	2.31	0.46
5:F:10:VAL:HG12	5:F:11:HIS:N	2.31	0.46
3:D:162:GLU:C	3:D:164:ARG:H	2.19	0.46
9:J:12:ALA:H	9:J:18:ILE:HD13	1.81	0.46
20:B:160:LEU:HD22	20:B:182:VAL:HA	1.97	0.46
8:I:49:GLN:HA	8:I:52:GLU:HG2	1.98	0.46
3:D:33:ILE:HG13	3:D:34:GLU:N	2.30	0.46
2:C:50:SER:CB	2:C:70:ALA:HB3	2.46	0.46
21:U:33:ARG:HG2	21:U:34:ARG:N	2.28	0.46
9:J:8:ILE:HA	9:J:100:ILE:HG22	1.97	0.46
1:A:1499:A:O2'	1:A:1500:A:H5'	2.16	0.46
10:K:28:ASN:ND2	10:K:29:THR:H	2.14	0.46
1:A:751:U:O2'	14:O:24:THR:HG23	2.16	0.46
1:A:562:U:H4'	1:A:563:A:O5'	2.15	0.46
20:B:102:ASN:HD21	20:B:105:THR:HB	1.81	0.46
6:G:136:LYS:O	6:G:140:VAL:HG23	2.16	0.46
2:C:134:LYS:HA	2:C:167:TYR:HE2	1.81	0.46
8:I:17:ARG:HB2	8:I:65:THR:HB	1.96	0.46
13:N:20:PHE:CD1	13:N:24:ALA:HB2	2.50	0.46
12:M:3:ILE:H	12:M:56:ARG:NH2	2.13	0.46
6:G:13:PRO:O	6:G:14:ASP:C	2.53	0.46
2:C:149:LYS:O	2:C:200:TRP:HE3	1.98	0.46
2:C:122:GLN:O	2:C:127:VAL:HG13	2.16	0.46
11:L:51:VAL:HG12	11:L:52:CYS:N	2.29	0.46
11:L:51:VAL:HG12	11:L:63:THR:HG22	1.97	0.46
1:A:9:G:H5'	4:E:107:GLY:HA3	1.98	0.46
1:A:1252:A:H2'	1:A:1253:G:O4'	2.16	0.46
1:A:395:C:H2'	1:A:396:C:C6	2.50	0.46
1:A:775:G:H2'	1:A:776:G:C8	2.51	0.46
1:A:517:G:H22	1:A:533:A:P	2.39	0.46
9:J:35:GLN:HG2	9:J:78:GLU:OE2	2.14	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:599:C:O2'	1:A:600:A:H5'	2.15	0.46
7:H:77:VAL:HG23	7:H:126:CYS:HA	1.98	0.46
7:H:46:GLU:N	7:H:63:LYS:HB2	2.31	0.46
1:A:241:G:O2'	1:A:242:G:H5'	2.15	0.46
1:A:1318:A:H4'	18:S:9:PHE:CE1	2.50	0.46
19:T:42:ASP:OD1	19:T:44:ALA:HB3	2.16	0.46
20:B:96:LEU:HB2	20:B:99:MET:HE2	1.96	0.46
1:A:1369:C:H2'	1:A:1370:G:C8	2.51	0.46
1:A:62:U:H5''	1:A:385:C:O2'	2.15	0.46
1:A:1276:G:H2'	1:A:1277:C:C6	2.51	0.46
1:A:167:A:O2'	1:A:168:G:H5'	2.16	0.46
1:A:744:C:H2'	1:A:745:G:C8	2.50	0.46
1:A:868:C:H2'	1:A:869:G:O4'	2.16	0.46
5:F:7:VAL:O	5:F:7:VAL:HG13	2.15	0.46
1:A:67:C:H2'	1:A:68:G:C8	2.51	0.46
14:O:30:LEU:HD23	14:O:30:LEU:C	2.36	0.46
5:F:3:HIS:CD2	5:F:65:GLU:HG3	2.49	0.46
12:M:10:ASP:CA	12:M:44:ILE:HD13	2.42	0.46
3:D:25:ARG:HD3	3:D:26:ALA:HB3	1.97	0.46
1:A:865:A:H2'	1:A:866:C:C6	2.51	0.46
19:T:64:GLY:O	19:T:66:ILE:N	2.48	0.46
6:G:129:ASN:HD22	6:G:137:ARG:HH22	1.64	0.46
1:A:642:A:C5	7:H:106:SER:HA	2.51	0.46
13:N:12:ARG:NE	13:N:58:ARG:HH12	2.14	0.46
3:D:61:ARG:HG3	3:D:71:PHE:CD2	2.51	0.46
10:K:70:ALA:C	10:K:72:ALA:N	2.69	0.46
1:A:462:G:H5'	1:A:463:U:P	2.55	0.46
1:A:970:C:H42	8:I:128:LYS:HG2	1.79	0.46
1:A:450:G:N7	1:A:481:G:O6	2.49	0.46
1:A:175:C:H2'	1:A:176:C:H6	1.78	0.46
1:A:1250:A:C2	1:A:1370:G:H1'	2.51	0.46
1:A:1096:C:H2'	1:A:1097:C:H6	1.81	0.46
1:A:627:G:H2'	1:A:628:G:H8	1.81	0.46
1:A:1285:A:HO2'	1:A:1286:U:P	2.39	0.46
12:M:106:ARG:HD3	12:M:111:PRO:HA	1.97	0.46
5:F:32:ALA:O	5:F:33:GLU:HB2	2.16	0.46
1:A:593:U:O2'	1:A:594:U:H5'	2.16	0.46
1:A:1495:U:O2'	1:A:1496:C:H5'	2.16	0.46
20:B:187:ASP:OD1	20:B:203:ASP:HB3	2.16	0.45
21:U:20:ARG:HG3	21:U:24:LYS:HG3	1.99	0.45
21:U:26:GLY:C	21:U:28:LEU:H	2.18	0.45
20:B:151:LYS:HG3	20:B:152:ASP:N	2.31	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:255:G:H5'	16:Q:17:GLU:O	2.16	0.45
20:B:18:GLN:HB2	20:B:188:THR:OG1	2.16	0.45
10:K:122:PRO:HG2	21:U:34:ARG:HA	1.97	0.45
10:K:124:LYS:HA	21:U:34:ARG:CG	2.46	0.45
2:C:63:ILE:O	2:C:65:VAL:HG23	2.16	0.45
13:N:26:LEU:HD23	13:N:27:LYS:N	2.31	0.45
1:A:373:A:H1'	1:A:481:G:H1'	1.98	0.45
20:B:71:THR:HG23	20:B:94:ARG:H	1.78	0.45
1:A:1072:G:H2'	1:A:1073:U:C6	2.51	0.45
1:A:1278:G:H4'	1:A:1279:G:O4'	2.15	0.45
11:L:82:ARG:HG2	11:L:82:ARG:NH1	2.29	0.45
5:F:52:ASN:O	5:F:52:ASN:CG	2.54	0.45
1:A:821:G:O2'	1:A:822:U:H5'	2.16	0.45
12:M:30:LYS:HG3	12:M:40:GLU:OE1	2.16	0.45
1:A:1456:A:H2'	1:A:1457:G:O4'	2.17	0.45
4:E:131:ASN:O	4:E:135:VAL:HG23	2.16	0.45
1:A:292:G:O2'	1:A:609:A:N6	2.49	0.45
1:A:940:C:H2'	1:A:941:G:C8	2.52	0.45
1:A:922:G:H2'	1:A:923:A:C8	2.50	0.45
8:I:56:MET:HA	8:I:59:LYS:HB2	1.97	0.45
8:I:87:MET:HA	8:I:90:ASP:O	2.16	0.45
6:G:137:ARG:HG2	6:G:141:HIS:NE2	2.31	0.45
1:A:81:A:C2'	1:A:82:G:H5'	2.46	0.45
7:H:23:ALA:CB	7:H:61:THR:HA	2.46	0.45
1:A:574:A:H1'	1:A:883:C:O4'	2.16	0.45
11:L:66:ILE:CG2	11:L:71:HIS:HB3	2.44	0.45
1:A:677:U:H3	1:A:713:G:H22	1.62	0.45
7:H:94:VAL:HG12	7:H:99:GLY:HA3	1.98	0.45
16:Q:18:LYS:HG2	16:Q:48:GLU:O	2.16	0.45
6:G:120:ALA:O	6:G:123:LEU:HB2	2.16	0.45
8:I:9:GLY:HA2	8:I:80:HIS:CD2	2.51	0.45
1:A:545:C:H2'	1:A:546:A:C8	2.51	0.45
20:B:172:ILE:CG2	20:B:176:ASN:HD21	2.28	0.45
1:A:1163:A:H2'	1:A:1164:G:C8	2.52	0.45
1:A:1451:U:O3'	1:A:1452:C:H6	2.00	0.45
1:A:79:G:O2'	1:A:80:A:H5'	2.16	0.45
1:A:847:G:H2'	1:A:848:C:H6	1.81	0.45
8:I:20:ILE:HD13	8:I:85:ALA:HB3	1.99	0.45
21:U:25:ALA:O	21:U:27:VAL:N	2.49	0.45
1:A:1024:G:H2'	1:A:1025:U:C6	2.52	0.45
1:A:1305:G:H22	1:A:1331:G:H2'	1.81	0.45
11:L:15:VAL:O	11:L:16:ALA:C	2.54	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:S:4:LEU:HD11	18:S:9:PHE:HB3	1.97	0.45
18:S:42:ASN:ND2	18:S:42:ASN:N	2.62	0.45
5:F:18:VAL:N	5:F:19:PRO:HD2	2.31	0.45
3:D:7:LYS:HB3	3:D:20:LEU:HB3	1.97	0.45
1:A:889:A:N1	1:A:907:A:H5''	2.32	0.45
1:A:1480:A:O2'	1:A:1481:U:H5'	2.17	0.45
18:S:52:ASN:HB2	18:S:76:THR:HG22	1.98	0.45
1:A:1122:U:H2'	1:A:1123:U:C6	2.52	0.45
1:A:1296:C:H4'	1:A:1302:C:H42	1.82	0.45
4:E:21:SER:CB	4:E:28:ARG:HE	2.20	0.45
1:A:255:G:P	16:Q:70:LYS:HZ3	2.40	0.45
1:A:174:A:O2'	1:A:175:C:H5'	2.17	0.45
8:I:10:ARG:CB	8:I:15:ALA:HA	2.46	0.45
1:A:833:G:O2'	1:A:834:U:H5'	2.17	0.45
5:F:18:VAL:O	5:F:22:ILE:HG13	2.15	0.45
1:A:189:A:O2'	1:A:190:A:H5'	2.16	0.45
5:F:45:ARG:NH2	17:R:25:ILE:HD13	2.31	0.45
11:L:31:GLY:HA3	11:L:54:VAL:HG11	1.97	0.45
8:I:29:ILE:HG23	8:I:64:ILE:HB	1.97	0.45
13:N:20:PHE:CD2	13:N:55:SER:HA	2.52	0.45
18:S:40:PHE:HB2	18:S:43:MET:CE	2.47	0.45
4:E:19:ARG:O	4:E:20:VAL:HB	2.16	0.45
1:A:109:A:H4'	1:A:110:C:OP2	2.16	0.45
9:J:6:ILE:O	9:J:8:ILE:HD12	2.16	0.45
1:A:1392:G:H2'	1:A:1393:U:C6	2.51	0.45
1:A:1225:A:H3'	1:A:1226:C:C6	2.52	0.45
12:M:64:VAL:HA	12:M:68:LEU:CD1	2.43	0.45
13:N:30:ILE:CG2	13:N:41:TRP:HB2	2.45	0.45
1:A:1435:G:H2'	1:A:1436:U:C6	2.52	0.45
9:J:80:THR:HB	9:J:83:THR:OG1	2.16	0.45
3:D:97:LEU:HD13	3:D:136:VAL:HG11	1.98	0.45
1:A:112:G:O2'	1:A:113:G:H5'	2.17	0.45
1:A:53:A:C2	1:A:54:C:H1'	2.50	0.45
1:A:1260:G:OP1	1:A:1284:C:H4'	2.17	0.45
1:A:323:U:H2'	1:A:324:G:O4'	2.16	0.45
1:A:1014:A:N3	1:A:1219:A:H1'	2.31	0.45
1:A:1013:G:H2'	1:A:1015:G:OP2	2.16	0.45
5:F:93:LYS:O	5:F:94:HIS:HB2	2.16	0.45
12:M:15:VAL:HG22	12:M:33:LEU:CD1	2.47	0.45
1:A:409:U:OP1	3:D:23:GLY:HA3	2.16	0.45
1:A:16:A:N1	1:A:919:A:H2	2.15	0.45
20:B:117:GLU:HA	20:B:140:LEU:CD2	2.45	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:429:U:H5'	3:D:8:LEU:CG	2.38	0.45
15:P:2:VAL:O	15:P:65:ALA:HA	2.16	0.45
5:F:47:LEU:HD21	5:F:57:ALA:CB	2.47	0.45
6:G:72:VAL:HG12	6:G:89:GLU:CA	2.47	0.45
1:A:25:C:C5'	1:A:524:G:H1'	2.47	0.45
8:I:9:GLY:HA2	8:I:80:HIS:HD2	1.81	0.45
1:A:1527:U:H2'	1:A:1528:U:C6	2.52	0.45
1:A:1159:U:O4'	1:A:1182:G:N2	2.50	0.45
3:D:162:GLU:HA	3:D:166:LYS:NZ	2.32	0.45
3:D:125:ASN:OD1	3:D:140:ASP:HA	2.17	0.45
1:A:936:C:H2'	1:A:937:A:O4'	2.16	0.45
5:F:1:MET:HG2	5:F:67:PRO:HD3	1.99	0.45
20:B:83:ALA:HA	20:B:88:GLN:HE21	1.80	0.45
1:A:864:A:H2'	1:A:865:A:C8	2.52	0.45
1:A:818:G:H3'	1:A:819:A:H5''	1.99	0.45
1:A:250:A:H1'	1:A:252:U:C5	2.52	0.45
12:M:52:ILE:HA	12:M:55:LEU:HG	1.97	0.45
5:F:47:LEU:HD13	5:F:51:ILE:HG22	1.99	0.45
8:I:117:LEU:HD22	8:I:123:ARG:HG2	1.98	0.45
1:A:708:C:H2'	1:A:709:U:C6	2.52	0.45
1:A:949:A:H2'	1:A:950:U:O4'	2.15	0.45
2:C:19:SER:HB2	2:C:39:ARG:NH2	2.32	0.45
11:L:60:PHE:O	11:L:62:VAL:HG13	2.17	0.45
1:A:445:G:H2'	1:A:446:G:O4'	2.17	0.45
1:A:246:A:C2	1:A:282:A:C5	3.05	0.45
15:P:67:ILE:O	15:P:67:ILE:HG23	2.17	0.45
1:A:1152:A:H4'	9:J:15:HIS:CD2	2.52	0.45
1:A:201:G:O2'	1:A:202:G:H5'	2.17	0.45
20:B:221:ARG:HG3	20:B:222:GLU:H	1.81	0.45
3:D:106:PHE:CD1	3:D:158:LEU:HD21	2.52	0.45
1:A:1057:G:H5''	2:C:153:SER:CB	2.47	0.45
10:K:83:VAL:CG2	10:K:106:ILE:HD11	2.47	0.45
20:B:53:LEU:HD13	20:B:216:VAL:HG12	1.98	0.45
1:A:175:C:H2'	1:A:176:C:C6	2.52	0.45
20:B:95:TRP:CH2	20:B:100:LEU:HD13	2.52	0.45
1:A:332:G:H2'	1:A:333:U:H6	1.82	0.45
20:B:23:ASN:O	20:B:25:LYS:N	2.49	0.45
14:O:23:SER:HB3	14:O:26:VAL:CG2	2.47	0.45
3:D:104:MET:SD	3:D:179:GLY:HA3	2.56	0.45
20:B:86:CYS:SG	20:B:87:ASP:N	2.87	0.45
4:E:89:THR:HG22	4:E:90:GLY:N	2.31	0.45
1:A:1243:C:O2'	1:A:1244:G:H5'	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1330:U:H2'	1:A:1331:G:O4'	2.17	0.45
20:B:88:GLN:HG3	20:B:88:GLN:H	1.49	0.45
4:E:19:ARG:HH12	4:E:28:ARG:HH12	1.65	0.45
16:Q:80:LYS:HD2	16:Q:80:LYS:O	2.16	0.45
6:G:11:ILE:HG22	6:G:12:LEU:N	2.32	0.45
7:H:87:ARG:HD3	7:H:90:GLU:OE1	2.17	0.45
15:P:46:LYS:C	15:P:48:GLU:N	2.70	0.45
17:R:63:TYR:C	17:R:64:LEU:HD12	2.37	0.45
1:A:1342:C:O2'	8:I:125:GLN:HB3	2.17	0.45
21:U:48:LYS:HG3	21:U:49:ALA:N	2.31	0.45
1:A:743:A:H2'	1:A:744:C:H6	1.80	0.45
1:A:1020:G:H2'	1:A:1020:G:N3	2.32	0.45
1:A:614:C:C2'	1:A:615:G:H5'	2.47	0.45
1:A:586:C:O2'	1:A:587:G:H5'	2.17	0.45
1:A:356:A:H2'	1:A:357:G:O4'	2.17	0.45
1:A:721:G:H4'	1:A:722:G:O4'	2.17	0.45
8:I:20:ILE:CD1	8:I:85:ALA:HB3	2.47	0.45
3:D:90:LEU:HD11	3:D:194:ILE:HD11	1.99	0.45
20:B:83:ALA:O	20:B:88:GLN:HB2	2.16	0.45
1:A:921:U:H2'	1:A:922:G:H8	1.82	0.45
15:P:52:LEU:CD2	15:P:75:ILE:HA	2.46	0.45
4:E:71:ILE:HD12	4:E:73:VAL:CG2	2.47	0.45
3:D:197:HIS:CE1	3:D:198:LEU:HG	2.52	0.45
10:K:72:ALA:O	10:K:75:GLU:HG2	2.17	0.45
1:A:1411:C:O2'	1:A:1412:C:H5'	2.17	0.45
1:A:313:A:H2'	1:A:314:C:H6	1.81	0.45
1:A:503:C:H2'	1:A:504:C:C6	2.52	0.45
11:L:34:THR:O	11:L:35:ARG:HD2	2.17	0.45
5:F:97:THR:HG22	5:F:98:GLU:N	2.32	0.45
20:B:11:ALA:C	20:B:13:VAL:H	2.20	0.45
1:A:1283:U:H2'	1:A:1284:C:H6	1.82	0.45
1:A:233:C:O2'	1:A:234:C:H5'	2.17	0.45
4:E:64:GLU:O	4:E:68:ARG:HG2	2.17	0.45
1:A:885:G:O2'	1:A:886:G:H5'	2.16	0.45
13:N:16:ALA:O	13:N:20:PHE:HB3	2.17	0.44
1:A:202:G:H2'	1:A:203:G:C8	2.52	0.44
1:A:1002:G:H2'	1:A:1003:G:O4'	2.17	0.44
10:K:88:PRO:HG3	21:U:28:LEU:HD21	1.99	0.44
6:G:14:ASP:HB2	6:G:19:SER:O	2.17	0.44
1:A:797:C:O2'	1:A:798:U:H5'	2.17	0.44
20:B:138:ARG:O	20:B:141:GLU:HB2	2.17	0.44
1:A:1071:C:O2'	1:A:1072:G:H5'	2.16	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:40:GLU:CB	5:F:61:LEU:HB2	2.46	0.44
1:A:669:G:H2'	1:A:670:G:C8	2.52	0.44
1:A:1436:U:H2'	1:A:1437:A:C8	2.52	0.44
1:A:968:A:H3'	1:A:969:A:C5'	2.47	0.44
20:B:129:THR:C	20:B:131:LYS:N	2.69	0.44
1:A:87:C:H2'	1:A:88:U:C6	2.51	0.44
1:A:1454:G:H2'	1:A:1455:G:H8	1.81	0.44
6:G:101:ARG:HG2	6:G:105:GLU:OE2	2.17	0.44
5:F:3:HIS:HA	5:F:64:VAL:O	2.17	0.44
20:B:16:GLY:HA2	20:B:40:ILE:H	1.80	0.44
1:A:1081:A:O2'	1:A:1082:A:H5'	2.17	0.44
2:C:63:ILE:HD12	2:C:90:VAL:HG12	1.99	0.44
11:L:49:ARG:N	11:L:49:ARG:HD2	2.32	0.44
1:A:473:U:H6	1:A:473:U:O5'	2.00	0.44
1:A:454:G:O2'	1:A:455:G:H5'	2.17	0.44
1:A:1313:U:OP2	18:S:5:LYS:HA	2.17	0.44
1:A:366:A:H1'	1:A:395:C:O2	2.16	0.44
1:A:716:A:H1'	10:K:119:GLY:HA2	1.99	0.44
1:A:647:C:H2'	1:A:648:A:C8	2.51	0.44
1:A:526:C:OP2	11:L:87:LYS:HE3	2.18	0.44
1:A:1138:G:H3'	1:A:1138:G:N3	2.33	0.44
1:A:227:G:H2'	1:A:228:A:C8	2.53	0.44
18:S:38:THR:HG22	18:S:68:HIS:O	2.16	0.44
6:G:67:ASN:ND2	6:G:127:ALA:HA	2.32	0.44
2:C:154:GLY:HA2	2:C:163:ARG:H	1.82	0.44
3:D:13:ARG:HG3	3:D:55:ARG:NH1	2.33	0.44
1:A:859:G:O2'	1:A:860:A:H5'	2.16	0.44
13:N:26:LEU:HD23	13:N:27:LYS:H	1.81	0.44
1:A:564:C:C4	16:Q:32:ILE:HD11	2.52	0.44
1:A:1514:G:H2'	1:A:1515:G:H8	1.83	0.44
4:E:33:THR:HG22	4:E:51:LYS:CB	2.46	0.44
6:G:49:LEU:HD21	6:G:60:ALA:CB	2.46	0.44
3:D:20:LEU:C	3:D:21:LYS:HD2	2.38	0.44
1:A:996:A:H2	1:A:1045:C:HO2'	1.63	0.44
1:A:938:A:H1'	1:A:1376:U:O2'	2.17	0.44
1:A:837:U:H2'	1:A:838:G:H8	1.82	0.44
1:A:1498:U:H6	1:A:1498:U:O5'	2.00	0.44
1:A:982:U:H5''	13:N:5:MET:HE1	1.99	0.44
13:N:60:ARG:NH2	13:N:69:PRO:HB3	2.32	0.44
8:I:30:ASN:ND2	8:I:65:THR:HA	2.32	0.44
1:A:1329:A:O2'	1:A:1330:U:H5'	2.17	0.44
12:M:37:GLY:O	12:M:38:ILE:HD13	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1069:C:H5''	4:E:25:LYS:HZ3	1.82	0.44
16:Q:60:ILE:HG22	16:Q:74:LEU:HA	1.99	0.44
10:K:122:PRO:HD2	21:U:35:GLU:HG2	2.00	0.44
10:K:126:ARG:HB2	21:U:33:ARG:HD2	2.00	0.44
13:N:86:ALA:HA	13:N:91:GLU:HG3	1.99	0.44
1:A:175:C:O2	1:A:1447:A:H2	2.01	0.44
1:A:631:C:H3'	1:A:632:U:H5'	1.99	0.44
1:A:634:C:H2'	1:A:635:A:C8	2.52	0.44
5:F:45:ARG:HH22	17:R:25:ILE:HD13	1.81	0.44
2:C:78:LYS:HE3	2:C:79:LYS:NZ	2.32	0.44
1:A:939:G:H2'	1:A:940:C:C6	2.52	0.44
20:B:31:PHE:HB3	20:B:39:ILE:CG2	2.48	0.44
13:N:50:LEU:CG	13:N:51:PRO:HD3	2.48	0.44
18:S:40:PHE:HB3	18:S:41:PRO:HD2	1.98	0.44
1:A:923:A:OP1	4:E:25:LYS:HB3	2.17	0.44
8:I:48:ARG:O	8:I:52:GLU:HG2	2.16	0.44
1:A:254:G:OP1	16:Q:68:LYS:O	2.36	0.44
4:E:148:SER:HB2	4:E:150:GLU:OE1	2.18	0.44
9:J:50:THR:HG22	9:J:62:ARG:HD2	2.00	0.44
11:L:89:LEU:HD22	11:L:89:LEU:N	2.33	0.44
20:B:142:LYS:HA	20:B:145:ASN:CG	2.38	0.44
1:A:1502:A:HO2'	1:A:1503:A:P	2.40	0.44
16:Q:47:ASP:CG	16:Q:50:ASN:HA	2.38	0.44
9:J:32:THR:O	9:J:32:THR:HG23	2.17	0.44
1:A:1299:A:C2'	1:A:1301:U:H1'	2.47	0.44
12:M:57:ASP:O	12:M:61:LYS:HE2	2.16	0.44
1:A:1454:G:H2'	1:A:1455:G:C8	2.53	0.44
1:A:770:C:O2'	1:A:771:G:H5'	2.17	0.44
1:A:49:U:O2	1:A:362:G:H1'	2.18	0.44
7:H:5:PRO:HB2	7:H:32:LYS:NZ	2.32	0.44
5:F:66:ALA:HB1	5:F:70:VAL:HG21	2.00	0.44
1:A:1296:C:H5'	12:M:13:HIS:CE1	2.53	0.44
1:A:570:G:H2'	1:A:571:U:C6	2.53	0.44
6:G:11:ILE:HD12	6:G:11:ILE:N	2.33	0.44
8:I:118:ARG:NH1	8:I:122:ARG:HE	2.16	0.44
12:M:89:ARG:CB	12:M:96:VAL:HG22	2.47	0.44
1:A:861:G:H2'	1:A:862:C:C6	2.52	0.44
12:M:84:CYS:O	12:M:88:LEU:HG	2.16	0.44
1:A:1261:A:H1'	1:A:1275:A:N1	2.32	0.44
1:A:948:C:O2'	1:A:949:A:H5'	2.17	0.44
2:C:35:ASP:O	2:C:39:ARG:HG3	2.17	0.44
1:A:57:G:H2'	1:A:58:C:C6	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:12:PRO:C	5:F:14:GLN:H	2.21	0.44
1:A:594:U:O2'	1:A:595:A:H5'	2.17	0.44
19:T:35:TYR:CG	19:T:36:ALA:N	2.85	0.44
1:A:1105:A:O2'	1:A:1106:G:H5'	2.18	0.44
18:S:33:TRP:C	18:S:35:ARG:H	2.21	0.44
18:S:52:ASN:ND2	18:S:53:GLY:H	2.15	0.44
3:D:25:ARG:O	3:D:27:ILE:N	2.51	0.44
1:A:600:A:OP2	7:H:87:ARG:HG2	2.18	0.44
21:U:39:LYS:N	21:U:40:PRO:CD	2.81	0.44
1:A:338:A:H2'	1:A:339:C:C6	2.53	0.44
3:D:48:SER:O	3:D:49:ASP:C	2.56	0.44
1:A:669:G:H2'	1:A:670:G:H8	1.83	0.44
1:A:686:U:O4	1:A:703:G:H1'	2.18	0.44
9:J:80:THR:O	9:J:84:VAL:HG23	2.18	0.44
9:J:49:PHE:HB2	9:J:65:TYR:HB2	1.99	0.44
11:L:105:GLY:HA3	11:L:117:GLY:O	2.17	0.44
5:F:81:ASN:O	5:F:84:VAL:HG12	2.18	0.44
20:B:16:GLY:HA3	20:B:40:ILE:H	1.83	0.44
1:A:865:A:O2'	1:A:866:C:H5'	2.17	0.44
20:B:112:ARG:O	20:B:116:LEU:HB2	2.17	0.44
6:G:22:LEU:O	6:G:25:PHE:HB3	2.18	0.44
21:U:44:ARG:HG3	21:U:44:ARG:HH11	1.83	0.44
9:J:8:ILE:CD1	9:J:76:ILE:HG13	2.48	0.44
6:G:87:PRO:O	6:G:152:HIS:HB3	2.18	0.44
20:B:99:MET:CA	20:B:106:VAL:HG21	2.44	0.44
6:G:72:VAL:HG12	6:G:89:GLU:CB	2.45	0.44
4:E:11:GLN:HB2	4:E:116:VAL:HB	2.00	0.44
2:C:6:PRO:HB3	2:C:174:LEU:HD21	1.99	0.44
2:C:46:LEU:HB3	2:C:49:ALA:CB	2.48	0.44
20:B:150:ILE:O	20:B:150:ILE:HG12	2.17	0.44
1:A:958:A:N1	18:S:53:GLY:C	2.71	0.44
12:M:2:ARG:N	12:M:2:ARG:HD3	2.31	0.44
12:M:18:LEU:HD13	12:M:33:LEU:HD21	2.00	0.44
18:S:12:LEU:O	18:S:16:LYS:HE2	2.17	0.44
8:I:42:THR:O	8:I:46:VAL:HG22	2.18	0.44
19:T:69:ASN:O	19:T:70:LYS:C	2.57	0.44
21:U:40:PRO:HG2	21:U:41:THR:H	1.83	0.44
1:A:83:C:H4'	1:A:83:C:OP1	2.18	0.44
1:A:5:U:H1'	1:A:6:G:C2	2.53	0.44
1:A:503:C:H2'	1:A:504:C:H6	1.82	0.44
5:F:71:ILE:HG13	5:F:72:ASP:N	2.33	0.44
2:C:178:ARG:HG2	2:C:178:ARG:O	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:L:54:VAL:CG2	11:L:79:ILE:HD11	2.48	0.44
1:A:607:A:H2'	1:A:608:A:C8	2.53	0.44
11:L:65:TYR:HB3	11:L:95:HIS:CD2	2.52	0.44
2:C:126:ARG:NE	2:C:126:ARG:HA	2.33	0.44
18:S:77:ARG:HB3	18:S:77:ARG:HE	1.64	0.44
3:D:123:MET:HA	3:D:128:VAL:HA	2.00	0.43
3:D:160:LEU:H	3:D:160:LEU:CD1	2.16	0.43
1:A:599:C:H4'	7:H:121:GLY:CA	2.47	0.43
21:U:36:PHE:HB3	21:U:40:PRO:CD	2.41	0.43
21:U:39:LYS:H	21:U:39:LYS:HD3	1.82	0.43
5:F:47:LEU:HD13	5:F:51:ILE:CG2	2.47	0.43
1:A:1473:G:O2'	1:A:1474:U:H5'	2.18	0.43
1:A:926:G:H3'	1:A:1505:G:H21	1.82	0.43
1:A:69:G:H21	1:A:71:A:H62	1.65	0.43
10:K:23:HIS:HB3	10:K:30:ILE:HG12	2.00	0.43
1:A:328:C:H4'	1:A:329:A:C5'	2.47	0.43
1:A:993:G:O2'	1:A:994:A:N7	2.51	0.43
1:A:993:G:N2	1:A:996:A:N6	2.66	0.43
1:A:317:U:H2'	1:A:318:G:C8	2.53	0.43
11:L:54:VAL:HG12	11:L:55:ARG:H	1.83	0.43
1:A:1065:U:H1'	1:A:1066:C:OP2	2.18	0.43
12:M:5:GLY:O	12:M:6:ILE:HB	2.18	0.43
1:A:1114:C:O2'	1:A:1115:U:H5'	2.18	0.43
5:F:36:ILE:HD12	5:F:36:ILE:H	1.83	0.43
5:F:67:PRO:O	5:F:70:VAL:HG22	2.17	0.43
21:U:26:GLY:C	21:U:28:LEU:N	2.71	0.43
4:E:87:VAL:HG23	4:E:91:SER:O	2.18	0.43
16:Q:45:VAL:HG11	16:Q:60:ILE:HG21	2.00	0.43
8:I:87:MET:HE2	8:I:88:GLU:HA	2.00	0.43
14:O:42:PHE:CD1	14:O:55:LEU:HD22	2.53	0.43
1:A:789:U:O2'	1:A:791:G:N7	2.44	0.43
1:A:1314:C:H2'	1:A:1315:U:C6	2.53	0.43
7:H:58:LEU:CD2	7:H:60:LEU:HB2	2.47	0.43
1:A:35:G:H2'	1:A:36:C:H6	1.80	0.43
3:D:169:TRP:O	3:D:182:LYS:HB2	2.17	0.43
1:A:1062:U:H2'	1:A:1063:C:C5	2.53	0.43
13:N:48:GLN:HG3	13:N:48:GLN:H	1.68	0.43
8:I:29:ILE:HG23	8:I:64:ILE:C	2.39	0.43
20:B:46:VAL:HA	20:B:49:PHE:HD2	1.84	0.43
13:N:51:PRO:HB2	13:N:54:SER:CB	2.33	0.43
3:D:121:ALA:C	3:D:122:ILE:HD13	2.39	0.43
21:U:26:GLY:O	21:U:30:GLU:HB3	2.17	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1080:A:H4'	4:E:20:VAL:HG13	1.98	0.43
16:Q:60:ILE:HD13	16:Q:60:ILE:N	2.33	0.43
1:A:1057:G:H4'	2:C:196:GLY:N	2.27	0.43
16:Q:30:HIS:CG	16:Q:33:TYR:HB2	2.53	0.43
20:B:94:ARG:N	20:B:94:ARG:HE	2.16	0.43
1:A:1500:A:OP1	1:A:1505:G:OP1	2.36	0.43
1:A:795:C:H1'	1:A:1506:U:C5	2.53	0.43
1:A:1407:C:O2'	1:A:1408:A:H5'	2.17	0.43
1:A:153:C:H2'	1:A:154:U:H6	1.79	0.43
1:A:394:G:H2'	1:A:395:C:C6	2.53	0.43
11:L:43:LYS:CD	11:L:44:PRO:HD3	2.48	0.43
1:A:307:C:H2'	1:A:308:C:H6	1.83	0.43
21:U:15:LEU:C	21:U:17:ARG:H	2.21	0.43
12:M:19:THR:HG22	12:M:29:SER:HB3	2.01	0.43
1:A:409:U:O2'	1:A:410:G:H5'	2.18	0.43
20:B:116:LEU:HA	20:B:119:GLN:CG	2.48	0.43
1:A:845:A:H5''	1:A:846:G:C8	2.53	0.43
8:I:123:ARG:NH1	8:I:123:ARG:HB3	2.32	0.43
9:J:5:ARG:N	9:J:76:ILE:O	2.52	0.43
13:N:23:ARG:C	13:N:25:GLU:H	2.20	0.43
1:A:451:A:H4'	1:A:452:A:O4'	2.18	0.43
4:E:11:GLN:O	4:E:38:VAL:HA	2.18	0.43
1:A:502:A:H2'	1:A:503:C:O4'	2.19	0.43
5:F:43:GLY:HA2	5:F:58:HIS:CD2	2.53	0.43
1:A:880:C:H2'	1:A:881:G:H8	1.84	0.43
1:A:78:A:H2'	1:A:79:G:C8	2.53	0.43
7:H:105:THR:HG21	7:H:110:MET:SD	2.59	0.43
1:A:902:G:H2'	1:A:903:G:H8	1.84	0.43
1:A:496:A:H2'	1:A:497:G:C8	2.52	0.43
20:B:104:LYS:HB2	20:B:104:LYS:NZ	2.33	0.43
1:A:981:U:H2'	1:A:982:U:C5	2.53	0.43
9:J:42:LEU:CD1	9:J:73:LEU:HB2	2.39	0.43
6:G:129:ASN:CA	6:G:134:VAL:HG21	2.47	0.43
1:A:1060:U:H2'	1:A:1061:G:C8	2.52	0.43
1:A:642:A:H2'	1:A:643:C:C6	2.53	0.43
1:A:237:G:H2'	1:A:238:A:C8	2.53	0.43
1:A:6:G:N3	1:A:6:G:C3'	2.81	0.43
1:A:1393:U:O2'	1:A:1394:A:H2'	2.19	0.43
1:A:1026:G:O2'	1:A:1027:C:H5'	2.19	0.43
1:A:222:C:H2'	1:A:223:A:H8	1.82	0.43
1:A:1290:G:H2'	1:A:1291:U:C6	2.54	0.43
13:N:30:ILE:O	13:N:40:ARG:HA	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:521:G:O2'	1:A:522:C:H5'	2.18	0.43
3:D:47:LEU:HD22	3:D:51:GLY:O	2.18	0.43
7:H:9:MET:HG3	7:H:26:MET:SD	2.58	0.43
1:A:215:C:H2'	1:A:216:U:H6	1.82	0.43
10:K:111:ASP:HB3	21:U:3:ILE:N	2.34	0.43
11:L:31:GLY:HA3	11:L:54:VAL:CG1	2.49	0.43
11:L:33:CYS:N	11:L:54:VAL:HG13	2.33	0.43
15:P:21:VAL:O	15:P:33:ILE:HB	2.18	0.43
16:Q:28:VAL:O	16:Q:36:PHE:HA	2.18	0.43
1:A:1222:G:H2'	1:A:1223:C:H5'	2.00	0.43
1:A:1077:G:N1	1:A:1081:A:C6	2.87	0.43
17:R:57:ALA:O	17:R:60:ARG:HG3	2.18	0.43
10:K:91:GLY:O	10:K:95:THR:HG22	2.19	0.43
20:B:165:ALA:HB3	20:B:186:VAL:HG11	2.01	0.43
11:L:37:TYR:O	11:L:38:THR:HG23	2.18	0.43
1:A:375:U:O2'	1:A:376:G:H5'	2.19	0.43
1:A:1096:C:H2'	1:A:1097:C:C6	2.52	0.43
7:H:12:ARG:HG3	7:H:12:ARG:NH1	2.34	0.43
1:A:948:C:H2'	1:A:949:A:H8	1.83	0.43
19:T:4:LYS:HZ1	19:T:6:ALA:CB	2.30	0.43
1:A:186:C:H2'	1:A:187:G:O4'	2.19	0.43
1:A:126:G:H2'	1:A:127:G:O4'	2.18	0.43
1:A:562:U:H5''	1:A:563:A:C4	2.54	0.43
3:D:2:ARG:HG3	3:D:114:ARG:CZ	2.49	0.43
1:A:386:C:O2'	1:A:387:U:H5'	2.18	0.43
20:B:8:MET:SD	20:B:9:LEU:N	2.92	0.43
1:A:828:U:H2'	1:A:829:G:O5'	2.19	0.43
6:G:30:MET:HG3	6:G:35:LYS:HA	2.00	0.43
20:B:35:ASN:HA	20:B:35:ASN:HD22	1.53	0.43
9:J:37:ARG:NH1	9:J:77:VAL:HG11	2.34	0.43
20:B:44:LYS:O	20:B:47:PRO:HD2	2.18	0.43
21:U:20:ARG:C	21:U:22:CYS:H	2.22	0.43
18:S:41:PRO:C	18:S:43:MET:H	2.22	0.43
1:A:251:G:N3	1:A:266:G:O6	2.51	0.43
19:T:64:GLY:H	19:T:67:HIS:CD2	2.37	0.43
3:D:31:CYS:O	3:D:32:LYS:HB2	2.18	0.43
2:C:154:GLY:HA2	2:C:163:ARG:N	2.34	0.43
10:K:106:ILE:O	10:K:107:THR:HG23	2.18	0.43
1:A:1390:U:H2'	1:A:1391:U:C6	2.53	0.43
1:A:957:U:H2'	1:A:959:A:OP2	2.19	0.43
16:Q:30:HIS:CB	16:Q:33:TYR:HB2	2.49	0.43
1:A:25:C:H5'	1:A:524:G:H1'	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:488:C:O2'	1:A:489:C:H5'	2.19	0.43
1:A:389:A:C6	1:A:390:U:H1'	2.53	0.43
7:H:54:THR:HG23	7:H:55:LYS:HG2	2.00	0.43
10:K:59:PRO:HA	10:K:90:PRO:HB2	2.00	0.43
1:A:113:G:O2'	1:A:354:G:H5'	2.19	0.43
10:K:36:ARG:HH11	10:K:36:ARG:HG3	1.83	0.43
1:A:59:A:H3'	1:A:331:G:H22	1.83	0.43
7:H:40:LYS:HD3	7:H:48:PHE:CE1	2.53	0.43
1:A:1366:C:H2'	1:A:1367:C:H6	1.83	0.43
1:A:1469:C:H2'	1:A:1470:U:O4'	2.18	0.43
1:A:1111:A:O2'	1:A:1112:C:H5'	2.19	0.43
10:K:33:ILE:CG1	10:K:73:VAL:HG21	2.46	0.43
20:B:46:VAL:CG1	20:B:47:PRO:HD3	2.33	0.43
6:G:46:LEU:HG	6:G:57:GLU:CB	2.38	0.43
20:B:17:HIS:CG	20:B:18:GLN:H	2.37	0.43
7:H:106:SER:C	7:H:107:LYS:HE2	2.38	0.43
14:O:54:GLY:O	14:O:58:MET:HG2	2.19	0.43
20:B:48:MET:O	20:B:52:ALA:HB3	2.19	0.43
1:A:106:C:HO2'	1:A:107:G:H5'	1.83	0.43
3:D:197:HIS:O	3:D:201:GLU:HG3	2.18	0.43
9:J:57:VAL:HG13	9:J:58:ASN:N	2.33	0.43
11:L:86:VAL:HG12	11:L:89:LEU:H	1.83	0.43
1:A:967:C:H5'	8:I:129:ARG:HA	2.01	0.43
2:C:18:ASN:HB2	13:N:90:GLY:HA3	1.99	0.43
1:A:1313:U:O2'	1:A:1314:C:H5'	2.18	0.43
1:A:1368:A:O2'	1:A:1369:C:H5'	2.19	0.43
20:B:95:TRP:HZ3	20:B:174:GLU:CD	2.22	0.43
5:F:97:THR:O	5:F:98:GLU:CD	2.57	0.43
1:A:993:G:H21	1:A:996:A:N6	2.17	0.43
10:K:19:VAL:HG22	10:K:34:THR:O	2.18	0.43
1:A:300:A:H2'	1:A:301:G:O4'	2.19	0.43
1:A:138:G:C6	1:A:226:G:C6	3.07	0.43
1:A:1484:C:O2'	1:A:1485:U:H5'	2.19	0.43
11:L:79:ILE:C	11:L:101:LEU:HD12	2.39	0.43
5:F:54:LEU:C	5:F:56:LYS:H	2.22	0.43
1:A:282:A:H2'	1:A:282:A:N3	2.33	0.43
1:A:1186:G:H4'	8:I:111:GLU:OE1	2.19	0.43
1:A:542:G:O2'	1:A:543:U:H5'	2.19	0.43
1:A:38:G:O2'	1:A:39:G:H5'	2.19	0.43
1:A:116:A:H8	1:A:116:A:O5'	2.02	0.43
1:A:8:A:H1'	4:E:106:ALA:O	2.18	0.43
20:B:119:GLN:O	20:B:121:GLN:N	2.41	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:K:80:ASN:HB3	10:K:105:ARG:HB3	2.00	0.43
11:L:21:PRO:HG2	11:L:94:TYR:OH	2.19	0.43
3:D:71:PHE:CE1	3:D:89:LEU:HD11	2.54	0.43
1:A:373:A:O2'	1:A:374:A:H5'	2.19	0.43
1:A:618:C:H3'	1:A:620:C:OP2	2.19	0.43
1:A:875:U:O2'	7:H:14:ARG:HD2	2.17	0.43
1:A:537:G:H2'	1:A:538:G:H8	1.84	0.43
8:I:11:ARG:NH2	8:I:12:LYS:HD2	2.34	0.43
1:A:715:A:H2'	1:A:716:A:H8	1.80	0.43
1:A:591:U:OP2	7:H:30:LYS:HE2	2.18	0.43
14:O:49:HIS:O	14:O:52:ARG:HB3	2.19	0.43
20:B:128:LEU:HB3	20:B:132:GLU:HB2	2.01	0.43
5:F:53:LYS:N	5:F:53:LYS:NZ	2.66	0.43
1:A:647:C:H2'	1:A:648:A:H8	1.84	0.43
12:M:100:ARG:HD3	12:M:103:THR:OG1	2.19	0.43
1:A:402:G:O2'	1:A:403:C:H5'	2.19	0.43
20:B:160:LEU:HG	20:B:161:PHE:N	2.33	0.43
8:I:53:LEU:N	8:I:53:LEU:HD22	2.34	0.43
20:B:17:HIS:CG	20:B:18:GLN:N	2.87	0.43
1:A:643:C:H5'	7:H:31:LEU:HD13	2.00	0.43
20:B:165:ALA:H	20:B:186:VAL:HG12	1.83	0.43
20:B:163:ILE:HD12	20:B:185:ILE:HD12	2.00	0.43
1:A:1226:C:H3'	12:M:101:THR:OG1	2.18	0.43
1:A:377:G:H2'	1:A:378:G:H8	1.84	0.43
6:G:78:ARG:HH11	6:G:80:GLY:H	1.67	0.43
4:E:82:HIS:HE1	4:E:147:ASN:H	1.67	0.43
20:B:95:TRP:HH2	20:B:100:LEU:HD22	1.83	0.43
1:A:493:A:H3'	1:A:494:G:H8	1.83	0.43
1:A:218:U:H2'	1:A:219:U:H6	1.80	0.43
5:F:79:ARG:HD3	5:F:79:ARG:HA	1.89	0.43
1:A:1172:C:O2'	1:A:1173:U:H5'	2.19	0.43
1:A:994:A:N3	1:A:994:A:H2'	2.34	0.43
1:A:857:C:H2'	1:A:858:G:O4'	2.19	0.43
11:L:30:ARG:O	11:L:57:THR:HG23	2.19	0.43
2:C:54:ILE:O	2:C:54:ILE:HG23	2.19	0.43
1:A:1014:A:C2	1:A:1219:A:H1'	2.54	0.42
1:A:977:A:O2'	1:A:1223:C:N4	2.52	0.42
1:A:1320:C:H41	18:S:36:ARG:HA	1.84	0.42
1:A:201:G:H2'	1:A:202:G:C8	2.53	0.42
6:G:13:PRO:O	6:G:18:GLY:HA2	2.19	0.42
1:A:1056:U:H2'	1:A:1057:G:H8	1.84	0.42
1:A:695:A:H61	1:A:797:C:C1'	2.28	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:51:A:H61	1:A:314:C:H1'	1.83	0.42
1:A:986:U:H2'	1:A:987:G:C8	2.54	0.42
5:F:9:MET:HB3	5:F:59:TYR:CD2	2.54	0.42
16:Q:39:ARG:NH1	16:Q:39:ARG:HG3	2.33	0.42
11:L:35:ARG:NH2	11:L:36:VAL:HG22	2.34	0.42
1:A:1352:C:H2'	1:A:1353:G:H8	1.81	0.42
2:C:174:LEU:O	2:C:174:LEU:HD23	2.18	0.42
19:T:54:GLN:O	19:T:57:VAL:HG23	2.19	0.42
1:A:623:C:H2'	1:A:624:C:C6	2.54	0.42
4:E:94:PHE:O	4:E:124:ALA:HB1	2.19	0.42
1:A:915:A:H2'	1:A:916:U:H5'	2.01	0.42
1:A:822:U:H2'	1:A:823:C:H6	1.84	0.42
1:A:1187:G:OP1	8:I:114:LYS:HE3	2.19	0.42
1:A:1150:A:O3'	9:J:43:PRO:HA	2.18	0.42
1:A:1035:A:H2'	1:A:1036:A:H8	1.84	0.42
18:S:39:ILE:HG12	18:S:70:LEU:CD1	2.49	0.42
6:G:67:ASN:O	6:G:134:VAL:HA	2.19	0.42
10:K:126:ARG:HE	10:K:126:ARG:HA	1.84	0.42
1:A:979:C:H1'	1:A:1317:C:N4	2.26	0.42
9:J:6:ILE:HD12	9:J:76:ILE:HD11	1.99	0.42
1:A:677:U:H1'	10:K:120:CYS:SG	2.58	0.42
1:A:1446:A:C2'	1:A:1447:A:H5''	2.48	0.42
1:A:826:C:H4'	7:H:12:ARG:NE	2.34	0.42
1:A:42:G:H2'	1:A:43:C:C6	2.53	0.42
3:D:2:ARG:HH22	3:D:132:ALA:CB	2.32	0.42
19:T:52:GLU:HG2	19:T:52:GLU:O	2.19	0.42
16:Q:34:GLY:O	16:Q:35:LYS:C	2.57	0.42
1:A:56:U:H2'	1:A:57:G:H8	1.84	0.42
1:A:1230:C:H2'	1:A:1231:G:H8	1.85	0.42
1:A:878:A:OP1	7:H:80:PRO:HG2	2.19	0.42
1:A:541:G:H2'	1:A:542:G:H8	1.84	0.42
7:H:112:ASP:HB2	7:H:116:ARG:NH2	2.34	0.42
13:N:69:PRO:HG2	13:N:70:HIS:H	1.83	0.42
18:S:2:ARG:NE	18:S:2:ARG:HA	2.35	0.42
9:J:14:ASP:OD1	9:J:17:LEU:HB2	2.18	0.42
9:J:17:LEU:HD22	9:J:96:VAL:HG13	2.01	0.42
10:K:42:GLY:HA3	10:K:73:VAL:HG13	2.00	0.42
18:S:39:ILE:HD13	18:S:65:MET:HB3	2.01	0.42
3:D:24:VAL:HA	3:D:27:ILE:CD1	2.46	0.42
1:A:1078:U:H2'	1:A:1079:G:C8	2.54	0.42
4:E:106:ALA:HB1	4:E:110:MET:CB	2.49	0.42
16:Q:40:THR:HG22	16:Q:41:THR:N	2.34	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:H:125:ILE:HG22	7:H:126:CYS:SG	2.59	0.42
1:A:438:U:H4'	3:D:119:HIS:HD2	1.84	0.42
1:A:974:A:H4'	1:A:975:A:C5'	2.46	0.42
2:C:2:GLN:O	2:C:3:LYS:HB2	2.19	0.42
16:Q:32:ILE:HG23	16:Q:33:TYR:CD2	2.54	0.42
1:A:378:G:H2'	1:A:379:C:C6	2.54	0.42
1:A:1058:G:H2'	1:A:1059:C:C6	2.55	0.42
20:B:55:GLU:O	20:B:58:LYS:HB2	2.19	0.42
10:K:57:SER:O	10:K:90:PRO:HG3	2.19	0.42
14:O:69:LEU:HD11	14:O:76:ARG:HB2	2.02	0.42
1:A:848:C:H2'	1:A:849:G:O4'	2.19	0.42
4:E:52:ALA:H	4:E:58:ALA:HB2	1.84	0.42
5:F:66:ALA:HB1	5:F:67:PRO:HD2	2.01	0.42
18:S:10:ILE:CD1	18:S:14:LEU:HD11	2.49	0.42
1:A:260:G:H2'	1:A:261:U:C6	2.54	0.42
1:A:263:A:H2'	1:A:264:C:C6	2.55	0.42
1:A:602:A:H2'	1:A:603:U:H6	1.85	0.42
15:P:40:ASN:ND2	15:P:43:ALA:HB2	2.34	0.42
1:A:256:U:H3'	1:A:257:G:H8	1.84	0.42
5:F:47:LEU:HB3	17:R:65:SER:OG	2.19	0.42
20:B:96:LEU:HD23	20:B:99:MET:CE	2.49	0.42
8:I:36:GLN:HE21	8:I:36:GLN:N	2.17	0.42
2:C:119:ILE:HD13	2:C:136:ALA:HB2	2.01	0.42
1:A:477:C:H2'	1:A:478:A:C8	2.55	0.42
1:A:706:A:C4'	10:K:30:ILE:HD11	2.48	0.42
14:O:73:ASP:OD1	14:O:75:ALA:HB3	2.19	0.42
1:A:808:C:O2'	1:A:809:G:H5'	2.19	0.42
1:A:1170:A:H3'	1:A:1171:A:H8	1.84	0.42
3:D:78:ALA:HA	3:D:81:LEU:HD12	2.02	0.42
19:T:49:ALA:CA	19:T:52:GLU:HB3	2.49	0.42
1:A:458:U:H2'	1:A:459:A:C8	2.54	0.42
20:B:82:ALA:HB3	20:B:213:LEU:HD22	2.01	0.42
1:A:1046:A:H2'	1:A:1047:G:O4'	2.18	0.42
1:A:1219:A:H2'	1:A:1220:G:H8	1.84	0.42
8:I:62:LEU:N	8:I:62:LEU:HD22	2.34	0.42
1:A:1152:A:H4'	9:J:15:HIS:HD2	1.84	0.42
20:B:16:GLY:HA2	20:B:40:ILE:HD12	2.02	0.42
12:M:13:HIS:HB2	12:M:16:ILE:HG22	2.02	0.42
2:C:166:TRP:HA	2:C:166:TRP:HE3	1.84	0.42
2:C:52:SER:O	2:C:113:LYS:HG2	2.19	0.42
1:A:372:C:H1'	1:A:373:A:OP2	2.20	0.42
1:A:1370:G:O2'	1:A:1371:G:H5'	2.18	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:878:A:C5'	7:H:80:PRO:HG2	2.49	0.42
8:I:66:VAL:HG11	8:I:78:ILE:HD11	2.02	0.42
20:B:59:ILE:O	20:B:62:ARG:HD2	2.20	0.42
13:N:46:LYS:NZ	18:S:10:ILE:HG13	2.34	0.42
1:A:1069:C:O4'	1:A:1191:A:H2	2.01	0.42
6:G:125:ASP:HB3	6:G:131:GLY:N	2.34	0.42
1:A:972:C:P	9:J:59:LYS:HD3	2.59	0.42
9:J:59:LYS:C	9:J:61:ALA:H	2.23	0.42
1:A:82:G:H21	1:A:84:U:H3	1.67	0.42
3:D:115:GLN:HG3	3:D:119:HIS:CE1	2.54	0.42
9:J:55:PRO:O	9:J:56:HIS:HB3	2.19	0.42
2:C:184:ASN:HA	2:C:184:ASN:HD22	1.60	0.42
1:A:9:G:H2'	1:A:10:A:C8	2.55	0.42
1:A:36:C:H5''	11:L:119:LYS:HD2	2.01	0.42
1:A:1374:A:H2'	1:A:1375:A:H8	1.85	0.42
2:C:31:ASN:ND2	2:C:58:ARG:NE	2.66	0.42
20:B:31:PHE:HB3	20:B:39:ILE:HG22	2.01	0.42
20:B:64:GLY:HA2	20:B:158:ASP:OD1	2.20	0.42
15:P:28:ARG:HD3	15:P:29:ASN:ND2	2.35	0.42
1:A:244:U:O4	1:A:906:A:H1'	2.20	0.42
12:M:95:PRO:CA	12:M:108:ARG:HG2	2.50	0.42
1:A:708:C:H2'	1:A:709:U:H6	1.84	0.42
1:A:1426:G:H2'	1:A:1427:C:O4'	2.20	0.42
16:Q:39:ARG:HA	16:Q:39:ARG:CZ	2.50	0.42
1:A:77:A:H2'	1:A:78:A:C8	2.55	0.42
1:A:301:G:H2'	1:A:302:G:C8	2.53	0.42
8:I:95:SER:O	8:I:99:LYS:HB2	2.19	0.42
1:A:1355:G:O2'	1:A:1356:G:H5'	2.19	0.42
1:A:683:G:O2'	1:A:684:U:H5'	2.20	0.42
1:A:1306:A:C2'	1:A:1307:U:H5'	2.49	0.42
20:B:83:ALA:C	20:B:85:SER:H	2.23	0.42
1:A:1033:G:H2'	1:A:1034:G:H5''	2.01	0.42
1:A:279:A:H5'	1:A:281:G:O4'	2.19	0.42
1:A:1007:U:H2'	1:A:1008:U:H6	1.84	0.42
1:A:523:A:H61	11:L:88:ASP:HB2	1.85	0.42
1:A:688:G:O3'	10:K:45:THR:HG21	2.20	0.42
1:A:1476:A:O2'	1:A:1477:U:H5'	2.20	0.42
1:A:553:A:O2'	11:L:25:ALA:HB1	2.20	0.42
10:K:15:VAL:C	10:K:17:ASP:H	2.23	0.42
1:A:87:C:H2'	1:A:88:U:C5	2.55	0.42
19:T:32:LYS:O	19:T:35:TYR:N	2.52	0.42
8:I:19:PHE:HB2	8:I:63:TYR:O	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:E:25:LYS:HG3	4:E:26:GLY:H	1.85	0.42
1:A:430:A:C2'	1:A:431:A:H5'	2.50	0.42
4:E:71:ILE:HG21	4:E:144:GLU:OE2	2.20	0.42
14:O:8:ALA:O	14:O:11:VAL:HB	2.20	0.42
12:M:72:ILE:O	12:M:76:ILE:HG13	2.19	0.42
7:H:24:VAL:CG1	7:H:60:LEU:HB3	2.49	0.42
1:A:152:A:H3'	1:A:153:C:H6	1.85	0.42
19:T:75:LYS:O	19:T:76:ALA:C	2.59	0.42
1:A:586:C:O2'	7:H:3:GLN:NE2	2.53	0.42
20:B:127:LYS:CD	20:B:128:LEU:HD13	2.50	0.42
2:C:76:ILE:O	2:C:82:ASP:N	2.53	0.42
16:Q:52:CYS:SG	16:Q:77:VAL:HG22	2.60	0.42
6:G:130:LYS:N	6:G:134:VAL:HG21	2.35	0.42
8:I:32:ARG:HD3	8:I:37:TYR:HD1	1.85	0.42
3:D:48:SER:O	3:D:52:VAL:HG23	2.19	0.42
1:A:1499:A:H1'	1:A:1520:C:OP1	2.20	0.42
1:A:152:A:H3'	1:A:153:C:C6	2.55	0.42
1:A:1346:A:H61	1:A:1374:A:H3'	1.84	0.42
1:A:499:A:C2	1:A:546:A:N3	2.88	0.42
2:C:38:VAL:HG23	2:C:39:ARG:N	2.35	0.42
1:A:58:C:C2'	1:A:59:A:H5'	2.50	0.42
1:A:1229:A:H2'	1:A:1230:C:H6	1.83	0.42
1:A:822:U:H2'	1:A:823:C:C6	2.54	0.42
1:A:704:A:C2	1:A:705:G:H1'	2.54	0.42
2:C:111:ASP:HB3	2:C:114:LEU:HD12	2.02	0.42
1:A:711:G:O2'	1:A:712:A:H5'	2.20	0.42
1:A:277:C:O2'	1:A:278:G:H5'	2.19	0.42
1:A:853:C:O2'	1:A:854:U:H5'	2.19	0.42
9:J:92:LEU:N	9:J:92:LEU:HD22	2.35	0.42
12:M:43:LYS:C	12:M:45:SER:N	2.74	0.41
1:A:222:C:H2'	1:A:223:A:C8	2.55	0.41
1:A:926:G:N2	1:A:1505:G:H2'	2.35	0.41
1:A:43:C:H2'	1:A:44:A:O4'	2.20	0.41
20:B:25:LYS:HD3	20:B:193:ASP:OD2	2.20	0.41
1:A:635:A:H2'	1:A:636:U:C6	2.54	0.41
1:A:1162:C:H2'	1:A:1163:A:O4'	2.20	0.41
9:J:80:THR:CG2	9:J:82:LYS:HZ2	2.33	0.41
1:A:54:C:N4	1:A:352:C:H2'	2.35	0.41
1:A:67:C:H2'	1:A:68:G:H8	1.84	0.41
1:A:998:C:H2'	1:A:999:C:C6	2.56	0.41
3:D:155:LYS:HG3	3:D:156:ALA:N	2.35	0.41
3:D:159:GLU:C	3:D:161:ALA:H	2.24	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:977:A:H1'	1:A:982:U:O4	2.20	0.41
1:A:1148:U:H2'	1:A:1149:C:O4'	2.20	0.41
9:J:18:ILE:CG1	9:J:72:ARG:HG2	2.50	0.41
2:C:75:VAL:O	2:C:82:ASP:HB2	2.20	0.41
1:A:921:U:O2	4:E:23:THR:HG23	2.20	0.41
4:E:19:ARG:NH1	4:E:28:ARG:HH12	2.18	0.41
8:I:35:GLU:O	8:I:39:GLY:HA3	2.20	0.41
9:J:53:ILE:HG13	13:N:84:ARG:CZ	2.49	0.41
2:C:154:GLY:HA2	2:C:163:ARG:O	2.20	0.41
1:A:1029:U:H2'	1:A:1031:C:C2	2.55	0.41
7:H:124:ILE:O	7:H:125:ILE:HG13	2.20	0.41
20:B:93:HIS:O	20:B:94:ARG:HG2	2.19	0.41
10:K:46:ALA:HA	10:K:65:ALA:HB2	2.01	0.41
20:B:22:TRP:CZ3	20:B:24:PRO:HA	2.55	0.41
1:A:551:U:H2'	1:A:552:U:C6	2.54	0.41
1:A:1015:G:H2'	1:A:1016:A:C8	2.56	0.41
21:U:24:LYS:HZ3	21:U:25:ALA:N	2.00	0.41
12:M:43:LYS:O	12:M:47:LEU:HD23	2.20	0.41
1:A:6:G:C8	4:E:123:LEU:HD21	2.55	0.41
1:A:371:A:O2'	1:A:372:C:H5'	2.20	0.41
1:A:448:A:H2'	1:A:449:G:H8	1.85	0.41
1:A:1503:A:H5'	1:A:1531:A:H1'	2.02	0.41
1:A:824:G:C6	1:A:877:G:C6	3.08	0.41
1:A:991:U:H2'	1:A:1212:U:O2	2.20	0.41
1:A:1127:G:C2'	1:A:1128:C:H5'	2.50	0.41
1:A:301:G:O2'	1:A:302:G:H5'	2.19	0.41
15:P:20:VAL:HG21	15:P:32:PHE:CD2	2.56	0.41
6:G:70:PRO:HD2	6:G:95:ARG:O	2.20	0.41
2:C:17:TRP:HZ2	13:N:95:LEU:O	2.03	0.41
1:A:681:A:H2'	1:A:682:G:C8	2.56	0.41
1:A:298:A:OP1	1:A:298:A:H8	2.02	0.41
1:A:1337:G:H5''	1:A:1338:G:OP1	2.20	0.41
12:M:3:ILE:HA	12:M:56:ARG:HB2	2.01	0.41
18:S:43:MET:C	18:S:46:LEU:HD23	2.40	0.41
16:Q:23:ALA:HA	16:Q:41:THR:O	2.19	0.41
1:A:261:U:H2'	1:A:263:A:OP2	2.19	0.41
1:A:956:U:O2'	1:A:957:U:H5'	2.20	0.41
1:A:1531:A:H2'	1:A:1532:U:H5'	2.02	0.41
1:A:1313:U:OP1	18:S:6:LYS:HD3	2.20	0.41
1:A:493:A:H5'	1:A:494:G:OP2	2.19	0.41
1:A:154:U:H2'	1:A:155:A:H8	1.80	0.41
15:P:12:LYS:C	15:P:14:ARG:H	2.24	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:P:12:LYS:O	15:P:13:LYS:HB2	2.20	0.41
11:L:30:ARG:HA	11:L:80:LEU:HD12	2.02	0.41
1:A:100:G:N7	1:A:101:A:C5	2.88	0.41
1:A:1200:C:H4'	1:A:1201:A:H3'	2.03	0.41
1:A:1202:U:H2'	1:A:1203:C:H5'	2.02	0.41
1:A:1320:C:N4	18:S:36:ARG:HA	2.36	0.41
8:I:18:VAL:HG12	8:I:19:PHE:N	2.36	0.41
20:B:62:ARG:HH11	20:B:62:ARG:HG3	1.86	0.41
1:A:1330:U:H4'	12:M:69:ARG:NH1	2.33	0.41
16:Q:7:LEU:HD21	16:Q:24:ILE:HG21	2.01	0.41
6:G:46:LEU:O	6:G:57:GLU:HG3	2.20	0.41
4:E:143:LEU:C	4:E:145:ASN:H	2.23	0.41
21:U:33:ARG:NE	21:U:34:ARG:HG3	2.36	0.41
5:F:48:ALA:N	17:R:65:SER:OG	2.54	0.41
1:A:975:A:H61	9:J:50:THR:HG21	1.85	0.41
1:A:1140:C:O2'	1:A:1141:C:H5'	2.20	0.41
1:A:1314:C:H2'	1:A:1315:U:H6	1.86	0.41
1:A:1315:U:H5	18:S:5:LYS:HZ1	1.69	0.41
1:A:1261:A:N7	1:A:1274:A:H2	2.17	0.41
11:L:43:LYS:N	11:L:44:PRO:HD2	2.34	0.41
20:B:127:LYS:C	20:B:127:LYS:HD2	2.40	0.41
12:M:26:LYS:O	12:M:30:LYS:HB2	2.20	0.41
1:A:355:C:O2'	1:A:356:A:H5'	2.21	0.41
7:H:29:SER:OG	7:H:32:LYS:HG3	2.20	0.41
7:H:49:LYS:HA	7:H:49:LYS:HD2	1.88	0.41
1:A:1320:C:H2'	1:A:1321:U:O4'	2.20	0.41
1:A:1320:C:N3	18:S:35:ARG:NH1	2.69	0.41
8:I:18:VAL:CG1	8:I:82:ILE:HG12	2.48	0.41
20:B:204:ASP:O	20:B:209:VAL:HG13	2.21	0.41
1:A:203:G:H1'	1:A:465:A:N6	2.35	0.41
20:B:57:ASN:HA	20:B:60:ALA:HB3	2.02	0.41
7:H:88:LYS:CG	7:H:89:ASP:H	2.33	0.41
1:A:1325:C:H2'	1:A:1326:U:H6	1.84	0.41
18:S:51:HIS:HB2	18:S:56:HIS:NE2	2.35	0.41
3:D:89:LEU:HD22	3:D:199:ILE:HD11	2.03	0.41
2:C:112:ALA:O	2:C:113:LYS:C	2.58	0.41
11:L:71:HIS:HD2	11:L:73:LEU:HG	1.86	0.41
1:A:1096:C:O2'	1:A:1097:C:H5'	2.21	0.41
4:E:156:ARG:HB3	7:H:43:GLY:O	2.21	0.41
1:A:832:G:H2'	1:A:833:G:H8	1.86	0.41
6:G:45:ALA:CB	6:G:120:ALA:HB2	2.49	0.41
1:A:1258:G:C4	1:A:1278:G:N2	2.89	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:501:C:OP1	11:L:113:ARG:NH2	2.54	0.41
10:K:47:GLY:C	10:K:49:SER:H	2.24	0.41
1:A:152:A:N6	1:A:170:U:C2	2.88	0.41
6:G:3:ARG:HB3	6:G:4:ARG:H	1.71	0.41
14:O:44:GLU:O	14:O:46:LYS:N	2.51	0.41
1:A:613:C:H2'	1:A:614:C:H6	1.82	0.41
1:A:1483:A:H2'	1:A:1484:C:O4'	2.20	0.41
1:A:1087:G:O2'	1:A:1088:G:H5'	2.20	0.41
2:C:179:ALA:O	2:C:180:ASP:O	2.39	0.41
1:A:577:G:O2'	1:A:578:C:H5'	2.21	0.41
1:A:1120:C:H2'	1:A:1121:U:H6	1.84	0.41
1:A:1125:U:H1'	1:A:1126:U:H6	1.86	0.41
13:N:15:LEU:HB3	13:N:54:SER:CB	2.44	0.41
1:A:1036:A:H2'	1:A:1037:C:O4'	2.20	0.41
1:A:1336:C:O4'	1:A:1337:G:C2	2.74	0.41
1:A:409:U:H2'	1:A:410:G:C8	2.55	0.41
16:Q:80:LYS:H	16:Q:80:LYS:NZ	2.18	0.41
21:U:44:ARG:HG3	21:U:44:ARG:NH1	2.35	0.41
2:C:149:LYS:CB	2:C:168:ARG:HG3	2.51	0.41
20:B:164:ASP:OD1	20:B:186:VAL:HA	2.20	0.41
10:K:70:ALA:O	10:K:72:ALA:N	2.53	0.41
2:C:63:ILE:HD12	2:C:98:ALA:CB	2.48	0.41
14:O:10:ILE:O	14:O:14:PHE:HD1	2.03	0.41
1:A:1226:C:H5''	12:M:94:LEU:HD11	2.03	0.41
20:B:75:ALA:O	20:B:78:ALA:N	2.53	0.41
2:C:188:ALA:HB3	2:C:195:ILE:HB	2.02	0.41
16:Q:18:LYS:H	16:Q:50:ASN:HD21	1.69	0.41
7:H:12:ARG:NH1	7:H:26:MET:HB3	2.35	0.41
3:D:84:ASN:OD1	3:D:87:GLU:HB2	2.20	0.41
1:A:486:U:O2'	1:A:487:A:H5'	2.21	0.41
1:A:187:G:N2	1:A:189:A:H3'	2.36	0.41
1:A:1240:U:H3	6:G:29:LEU:HD23	1.85	0.41
1:A:126:G:H4'	1:A:634:C:O2	2.21	0.41
1:A:637:C:H2'	1:A:638:U:C6	2.56	0.41
1:A:746:A:N1	1:A:747:A:N6	2.68	0.41
6:G:132:THR:HA	6:G:135:LYS:HB3	2.03	0.41
1:A:572:A:N3	1:A:917:G:H1'	2.35	0.41
1:A:516:U:O2'	1:A:517:G:H5'	2.20	0.41
1:A:245:U:H2'	1:A:246:A:H5'	2.03	0.41
2:C:87:ARG:HB2	2:C:100:ILE:CG2	2.51	0.41
16:Q:22:VAL:O	16:Q:42:LYS:HA	2.21	0.41
8:I:112:ARG:HD2	13:N:100:TRP:OXT	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:77:GLU:HG2	20:B:77:GLU:O	2.21	0.41
9:J:17:LEU:HD13	9:J:96:VAL:HG13	2.01	0.41
3:D:116:LEU:O	3:D:121:ALA:HB3	2.20	0.41
12:M:80:MET:C	12:M:82:LEU:H	2.24	0.41
18:S:20:LYS:NZ	18:S:24:SER:HB3	2.36	0.41
16:Q:52:CYS:SG	16:Q:74:LEU:HG	2.61	0.41
1:A:259:G:O2'	1:A:260:G:H5'	2.20	0.41
1:A:599:C:H2'	1:A:600:A:H8	1.85	0.41
1:A:600:A:OP1	7:H:87:ARG:HB3	2.21	0.41
21:U:36:PHE:CD1	21:U:44:ARG:HD3	2.56	0.41
20:B:18:GLN:C	20:B:37:VAL:HG23	2.41	0.41
19:T:38:ILE:HD11	19:T:82:ILE:HA	2.03	0.41
1:A:1178:G:H2'	1:A:1180:A:OP2	2.20	0.41
2:C:123:LEU:HD12	2:C:188:ALA:CB	2.51	0.41
1:A:415:A:N1	1:A:428:G:O6	2.54	0.41
1:A:621:A:H2'	1:A:622:A:H8	1.84	0.41
1:A:1053:G:C6	1:A:1199:U:H2'	2.56	0.41
1:A:987:G:H2'	1:A:988:G:H8	1.85	0.41
1:A:1375:A:P	6:G:24:LYS:HZ3	2.43	0.41
10:K:92:ARG:HH11	10:K:92:ARG:HG2	1.84	0.41
1:A:585:G:H4'	11:L:4:ASN:HD21	1.86	0.41
5:F:6:ILE:HD12	5:F:7:VAL:N	2.35	0.41
2:C:134:LYS:HE3	2:C:138:GLN:HG2	2.02	0.41
1:A:1366:C:H2'	1:A:1367:C:C6	2.55	0.41
1:A:1319:A:H4'	1:A:1320:C:OP1	2.20	0.41
18:S:35:ARG:HB3	18:S:50:VAL:CG1	2.51	0.41
1:A:1125:U:H5'	9:J:40:ILE:HD11	2.03	0.41
5:F:36:ILE:HA	5:F:64:VAL:HG13	2.02	0.41
2:C:85:LYS:O	2:C:89:VAL:HG23	2.21	0.41
1:A:1296:C:C5'	1:A:1302:C:H42	2.34	0.41
12:M:29:SER:HA	12:M:32:ILE:HG22	2.03	0.41
8:I:50:PRO:HD3	8:I:79:ARG:HG3	2.03	0.41
8:I:87:MET:SD	8:I:88:GLU:N	2.93	0.41
8:I:44:ARG:NE	8:I:48:ARG:HH22	2.19	0.41
1:A:264:C:H2'	1:A:265:G:O4'	2.21	0.41
1:A:601:G:O2'	1:A:602:A:H5'	2.21	0.41
3:D:29:THR:CG2	3:D:30:LYS:HD3	2.49	0.41
20:B:26:MET:HG3	20:B:188:THR:O	2.19	0.41
1:A:736:C:H2'	1:A:737:C:H6	1.85	0.41
3:D:148:ALA:O	3:D:154:VAL:HG11	2.21	0.41
20:B:165:ALA:H	20:B:186:VAL:CG1	2.34	0.41
9:J:8:ILE:O	9:J:74:VAL:HB	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:141:G:H2'	1:A:142:G:O4'	2.20	0.41
8:I:28:VAL:HA	8:I:32:ARG:O	2.21	0.41
2:C:112:ALA:CB	2:C:184:ASN:HB2	2.47	0.41
20:B:75:ALA:O	20:B:76:SER:C	2.59	0.41
1:A:451:A:H1'	1:A:452:A:C8	2.56	0.41
6:G:80:GLY:C	6:G:82:SER:H	2.25	0.41
4:E:117:ALA:HB3	4:E:119:VAL:HG23	2.03	0.41
1:A:1073:U:OP1	4:E:61:LYS:HE3	2.21	0.41
1:A:1258:G:C2	1:A:1278:G:N2	2.89	0.41
1:A:170:U:O2'	1:A:171:A:H5'	2.20	0.41
1:A:986:U:H2'	1:A:987:G:O4'	2.21	0.41
1:A:653:U:C6	7:H:55:LYS:HE2	2.56	0.41
1:A:538:G:O3'	11:L:110:LYS:HG3	2.21	0.41
1:A:284:C:O2'	1:A:285:C:H5'	2.21	0.41
3:D:7:LYS:HD2	3:D:21:LYS:NZ	2.35	0.41
1:A:1174:G:O2'	1:A:1175:G:H5'	2.20	0.41
3:D:141:VAL:HA	3:D:179:GLY:O	2.20	0.41
5:F:68:GLN:HA	5:F:71:ILE:HG12	2.02	0.41
1:A:1115:U:H2'	1:A:1116:U:C6	2.56	0.41
4:E:77:ASN:CG	4:E:78:GLY:H	2.19	0.41
1:A:1194:U:H2'	1:A:1195:C:C6	2.56	0.41
20:B:67:LEU:HG	20:B:153:MET:HE2	2.03	0.41
2:C:102:ILE:HD12	2:C:102:ILE:N	2.36	0.41
16:Q:75:VAL:CG2	16:Q:76:ARG:N	2.83	0.41
16:Q:65:PRO:HA	16:Q:71:SER:OG	2.21	0.41
1:A:842:U:O2'	1:A:846:G:N1	2.54	0.41
14:O:31:LEU:O	14:O:35:ILE:HG12	2.21	0.41
1:A:242:G:H2'	1:A:243:A:C5'	2.51	0.41
4:E:105:ILE:HG12	4:E:122:VAL:O	2.21	0.41
1:A:1531:A:C2'	1:A:1532:U:H5'	2.51	0.41
2:C:171:ARG:CB	2:C:171:ARG:HH11	2.27	0.41
1:A:51:A:H4'	1:A:52:C:C5'	2.50	0.41
1:A:1347:G:H8	8:I:108:ARG:HB3	1.85	0.41
21:U:48:LYS:C	21:U:50:SER:N	2.75	0.41
1:A:159:G:N1	1:A:163:C:N4	2.69	0.41
1:A:332:G:O2'	1:A:333:U:H5'	2.21	0.41
1:A:742:G:H2'	1:A:743:A:C8	2.52	0.41
10:K:111:ASP:HB2	21:U:19:LYS:CE	2.51	0.41
1:A:178:C:O2'	1:A:179:A:H5'	2.21	0.41
1:A:1260:G:H4'	1:A:1283:U:O2'	2.20	0.41
1:A:878:A:H5''	7:H:80:PRO:HG2	2.03	0.41
5:F:81:ASN:OD1	5:F:83:ALA:HB3	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:99:GLN:O	2:C:100:ILE:HB	2.21	0.41
16:Q:61:ARG:O	16:Q:61:ARG:HD2	2.21	0.41
1:A:1042:A:H2'	1:A:1043:G:O4'	2.20	0.41
20:B:114:LYS:O	20:B:117:GLU:HB3	2.22	0.40
8:I:44:ARG:O	8:I:48:ARG:HG3	2.21	0.40
8:I:58:GLU:O	8:I:59:LYS:HD2	2.20	0.40
8:I:93:LEU:HD13	8:I:97:LEU:CD1	2.46	0.40
1:A:107:G:O6	19:T:9:ARG:HD3	2.21	0.40
1:A:975:A:N1	9:J:50:THR:HB	2.36	0.40
10:K:14:GLN:HA	10:K:76:TYR:O	2.21	0.40
1:A:1225:A:H5''	1:A:1226:C:C5	2.55	0.40
1:A:450:G:H4'	15:P:41:PRO:HB2	2.03	0.40
1:A:451:A:C1'	1:A:452:A:C8	3.04	0.40
1:A:1071:C:H2'	1:A:1072:G:C8	2.51	0.40
16:Q:13:SER:HB3	16:Q:21:VAL:CB	2.50	0.40
1:A:660:C:H2'	1:A:661:G:C8	2.57	0.40
1:A:33:A:O2'	1:A:34:C:H5'	2.21	0.40
1:A:488:C:H2'	1:A:489:C:H6	1.86	0.40
1:A:1058:G:H2'	1:A:1059:C:H6	1.86	0.40
1:A:633:G:H2'	1:A:634:C:C6	2.56	0.40
3:D:97:LEU:HD13	3:D:136:VAL:CG1	2.51	0.40
11:L:23:LEU:O	11:L:25:ALA:N	2.54	0.40
1:A:78:A:O2'	1:A:79:G:H5'	2.22	0.40
6:G:100:MET:O	6:G:104:VAL:HG23	2.21	0.40
6:G:16:LYS:HB3	6:G:43:TYR:CE1	2.56	0.40
1:A:160:A:H2'	1:A:161:A:C8	2.56	0.40
1:A:584:G:H2'	1:A:585:G:H8	1.85	0.40
2:C:106:ARG:NH1	2:C:106:ARG:HG2	2.35	0.40
1:A:648:A:O2'	1:A:649:A:H5'	2.21	0.40
1:A:999:C:H2'	1:A:1000:A:C8	2.57	0.40
1:A:340:U:O2'	1:A:341:C:H5'	2.21	0.40
1:A:122:G:C2'	1:A:123:U:H5'	2.52	0.40
18:S:52:ASN:CG	18:S:53:GLY:N	2.72	0.40
3:D:117:VAL:HA	3:D:122:ILE:HG12	2.03	0.40
1:A:1296:C:H5''	1:A:1302:C:H42	1.86	0.40
1:A:1080:A:H5''	4:E:20:VAL:HG11	2.03	0.40
4:E:25:LYS:HG3	4:E:26:GLY:N	2.36	0.40
8:I:48:ARG:HA	8:I:51:LEU:HD12	2.03	0.40
21:U:42:THR:O	21:U:45:LYS:N	2.54	0.40
20:B:48:MET:SD	20:B:200:PRO:HD2	2.61	0.40
4:E:104:ILE:HG13	4:E:122:VAL:HG23	2.02	0.40
11:L:73:LEU:HD21	11:L:103:CYS:CB	2.50	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1520:C:H2'	1:A:1521:C:C6	2.57	0.40
1:A:789:U:H2'	1:A:791:G:OP2	2.20	0.40
6:G:3:ARG:HG3	6:G:3:ARG:NH1	2.36	0.40
1:A:1211:U:H5'	1:A:1212:U:H5'	2.03	0.40
12:M:22:TYR:N	12:M:22:TYR:CD2	2.88	0.40
1:A:537:G:H2'	1:A:538:G:C8	2.55	0.40
1:A:1493:A:H1'	23:A:3001:HYG:H362	1.86	0.40
3:D:97:LEU:HA	3:D:100:VAL:CG2	2.51	0.40
14:O:69:LEU:HD12	14:O:77:TYR:HB2	2.01	0.40
1:A:360:G:O2'	1:A:361:G:H5'	2.22	0.40
5:F:55:HIS:CD2	5:F:56:LYS:HE3	2.57	0.40
15:P:22:ALA:HA	15:P:33:ILE:HG13	2.03	0.40
11:L:56:LEU:HD12	11:L:60:PHE:HB2	2.04	0.40
2:C:46:LEU:HB3	2:C:49:ALA:HB3	2.03	0.40
17:R:61:ALA:HB3	17:R:67:LEU:HD12	2.04	0.40
12:M:102:LYS:NZ	12:M:102:LYS:HB2	2.37	0.40
1:A:1220:G:O3'	18:S:35:ARG:HD2	2.20	0.40
1:A:1238:A:C2	1:A:1241:G:N3	2.88	0.40
1:A:1329:A:H5''	12:M:24:VAL:HA	2.03	0.40
12:M:18:LEU:C	12:M:20:SER:N	2.75	0.40
1:A:812:G:O2'	1:A:813:U:C6	2.56	0.40
16:Q:58:VAL:HB	16:Q:74:LEU:CD2	2.51	0.40
16:Q:59:GLU:HG3	16:Q:78:VAL:HG21	2.02	0.40
8:I:44:ARG:HB3	8:I:48:ARG:NH2	2.36	0.40
1:A:1324:A:H4'	1:A:1363:A:OP1	2.22	0.40
4:E:84:VAL:CG1	4:E:146:MET:HB3	2.49	0.40
6:G:92:PRO:HG2	6:G:93:VAL:H	1.86	0.40
10:K:107:THR:HB	10:K:108:ASN:OD1	2.20	0.40
13:N:56:PRO:C	13:N:58:ARG:H	2.25	0.40
9:J:26:VAL:HG12	9:J:30:LYS:HG3	2.04	0.40
9:J:8:ILE:HB	9:J:74:VAL:HB	2.02	0.40
3:D:196:GLU:HG3	3:D:197:HIS:N	2.35	0.40
11:L:73:LEU:HD21	11:L:103:CYS:HB2	2.04	0.40
12:M:85:TYR:HA	12:M:88:LEU:CD1	2.52	0.40
7:H:74:ILE:CG1	7:H:128:VAL:HG22	2.47	0.40
1:A:176:C:H3'	1:A:177:G:N2	2.35	0.40
1:A:1271:A:H5'	1:A:1314:C:C5'	2.49	0.40
4:E:107:GLY:C	4:E:109:ALA:H	2.25	0.40
1:A:549:C:H2'	1:A:550:G:H8	1.86	0.40
1:A:668:G:O2'	1:A:669:G:H5'	2.22	0.40
10:K:51:PHE:HD1	10:K:51:PHE:O	2.04	0.40
1:A:1176:A:H2'	1:A:1177:G:O4'	2.22	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:994:A:C5	1:A:1216:A:H4'	2.56	0.40
1:A:1489:G:H2'	1:A:1490:U:C6	2.55	0.40
1:A:625:U:H4'	15:P:16:PHE:CE1	2.56	0.40
11:L:33:CYS:H	11:L:54:VAL:CG1	2.33	0.40
1:A:930:C:H2'	1:A:931:C:C6	2.56	0.40
1:A:1320:C:H41	18:S:36:ARG:CG	2.30	0.40
1:A:1148:U:O4'	8:I:17:ARG:HD3	2.21	0.40
8:I:54:VAL:HG21	8:I:86:LEU:HD21	2.03	0.40
1:A:120:A:C2'	1:A:121:U:H5''	2.40	0.40
18:S:4:LEU:HD22	18:S:7:GLY:O	2.21	0.40
12:M:88:LEU:O	12:M:92:ARG:HG3	2.22	0.40
1:A:926:G:H5'	1:A:927:G:C5'	2.51	0.40
1:A:1514:G:H2'	1:A:1515:G:C8	2.55	0.40
16:Q:11:VAL:HG13	16:Q:20:ILE:CG2	2.52	0.40
4:E:33:THR:HB	4:E:49:TYR:CE1	2.57	0.40
1:A:1256:A:O4'	1:A:1278:G:N2	2.54	0.40
1:A:618:C:N3	1:A:622:A:N6	2.64	0.40
10:K:18:GLY:HA2	10:K:36:ARG:NH1	2.37	0.40
1:A:95:C:O2	1:A:95:C:C2'	2.69	0.40
11:L:56:LEU:HG	11:L:60:PHE:O	2.21	0.40
2:C:45:GLU:C	2:C:46:LEU:HD22	2.42	0.40
1:A:144:G:H2'	1:A:145:G:O4'	2.22	0.40
5:F:34:GLY:C	5:F:35:LYS:HD2	2.42	0.40
8:I:40:ARG:C	8:I:41:GLU:HG3	2.41	0.40
13:N:78:LEU:HD23	13:N:82:LYS:HB3	2.02	0.40
18:S:2:ARG:NE	18:S:2:ARG:CA	2.85	0.40
1:A:469:C:O2'	1:A:470:C:H5'	2.22	0.40
12:M:43:LYS:C	12:M:45:SER:H	2.24	0.40
20:B:218:ALA:O	20:B:222:GLU:N	2.53	0.40
4:E:110:MET:O	4:E:113:VAL:HG22	2.22	0.40
19:T:20:ASN:O	19:T:24:ARG:HB2	2.22	0.40
1:A:261:U:OP2	19:T:70:LYS:HE2	2.21	0.40
15:P:43:ALA:HB1	15:P:46:LYS:HE3	2.03	0.40
1:A:423:G:H3'	1:A:423:G:N3	2.37	0.40
15:P:71:VAL:HG13	15:P:72:ALA:N	2.37	0.40
20:B:185:ILE:HA	20:B:199:ILE:O	2.20	0.40
1:A:105:G:H2'	1:A:106:C:C6	2.56	0.40
8:I:119:LYS:C	8:I:121:ARG:H	2.25	0.40
1:A:1388:C:O2'	1:A:1389:C:H5'	2.21	0.40
20:B:184:ALA:HB3	20:B:195:VAL:HG21	2.03	0.40
10:K:34:THR:HA	10:K:41:LEU:CG	2.50	0.40
14:O:77:TYR:CZ	14:O:81:ILE:HD11	2.56	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:134:LYS:HA	2:C:167:TYR:CE2	2.56	0.40
9:J:71:LEU:H	9:J:71:LEU:HD23	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	204/232 (88%)	148 (72%)	40 (20%)	16 (8%)	1	22
3	D	203/205 (99%)	134 (66%)	54 (27%)	15 (7%)	2	24
4	E	148/166 (89%)	117 (79%)	25 (17%)	6 (4%)	4	44
5	F	98/135 (73%)	67 (68%)	21 (21%)	10 (10%)	1	14
6	G	150/178 (84%)	124 (83%)	20 (13%)	6 (4%)	5	44
7	H	127/129 (98%)	90 (71%)	28 (22%)	9 (7%)	2	25
8	I	125/129 (97%)	88 (70%)	29 (23%)	8 (6%)	2	29
9	J	96/103 (93%)	68 (71%)	18 (19%)	10 (10%)	1	14
10	K	115/128 (90%)	80 (70%)	27 (24%)	8 (7%)	2	26
11	L	121/123 (98%)	79 (65%)	28 (23%)	14 (12%)	1	12
12	M	111/117 (95%)	69 (62%)	38 (34%)	4 (4%)	5	49
13	N	92/100 (92%)	56 (61%)	26 (28%)	10 (11%)	1	13
14	O	86/89 (97%)	65 (76%)	16 (19%)	5 (6%)	3	32
15	P	78/82 (95%)	53 (68%)	15 (19%)	10 (13%)	0	10
16	Q	79/83 (95%)	56 (71%)	17 (22%)	6 (8%)	2	23
17	R	53/74 (72%)	41 (77%)	10 (19%)	2 (4%)	5	46
18	S	78/91 (86%)	58 (74%)	18 (23%)	2 (3%)	8	57
19	T	83/86 (96%)	59 (71%)	19 (23%)	5 (6%)	2	31
20	B	216/240 (90%)	148 (68%)	46 (21%)	22 (10%)	1	14
21	U	49/71 (69%)	28 (57%)	14 (29%)	7 (14%)	0	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2312/2561 (90%)	1628 (70%)	509 (22%)	175 (8%)	2	23

All (175) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	112	ALA
2	C	180	ASP
2	C	205	GLU
4	E	20	VAL
5	F	41	ASP
5	F	98	GLU
6	G	14	ASP
8	I	127	SER
9	J	36	VAL
9	J	57	VAL
10	K	126	ARG
11	L	13	ARG
11	L	38	THR
11	L	121	PRO
13	N	50	LEU
14	O	73	ASP
15	P	44	SER
16	Q	32	ILE
16	Q	82	VAL
20	B	22	TRP
20	B	58	LYS
20	B	94	ARG
20	B	188	THR
21	U	23	GLU
2	C	14	VAL
2	C	59	PRO
2	C	100	ILE
3	D	26	ALA
3	D	107	GLY
3	D	168	THR
3	D	189	ASP
3	D	191	SER
3	D	192	ALA
5	F	51	ILE
5	F	92	THR
7	H	2	MET
7	H	66	GLN

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Mol	Chain	Res	Type
7	H	70	VAL
7	H	82	LEU
8	I	8	THR
9	J	74	VAL
9	J	75	ASP
10	K	124	LYS
11	L	14	LYS
11	L	42	LYS
11	L	61	GLU
11	L	117	GLY
12	M	3	ILE
12	M	47	LEU
12	M	104	ASN
13	N	2	LYS
13	N	70	HIS
13	N	71	GLY
14	O	17	ASP
15	P	52	LEU
16	Q	81	ALA
17	R	20	ILE
19	T	65	LEU
20	B	14	HIS
20	B	19	THR
20	B	121	GLN
20	B	128	LEU
20	B	131	LYS
20	B	150	ILE
21	U	25	ALA
21	U	26	GLY
21	U	34	ARG
21	U	35	GLU
2	C	81	GLU
2	C	104	GLU
2	C	153	SER
3	D	24	VAL
3	D	31	CYS
3	D	182	LYS
4	E	144	GLU
6	G	3	ARG
6	G	112	ASP
6	G	151	ALA
7	H	114	ALA

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Mol	Chain	Res	Type
8	I	9	GLY
8	I	34	LEU
8	I	106	ASP
9	J	56	HIS
9	J	93	ALA
10	K	71	ASP
10	K	88	PRO
10	K	125	LYS
11	L	47	ALA
13	N	21	ALA
14	O	33	ALA
16	Q	14	ASP
19	T	41	GLY
19	T	42	ASP
19	T	67	HIS
20	B	15	PHE
20	B	18	GLN
20	B	41	ASN
20	B	76	SER
20	B	120	SER
20	B	130	LYS
20	B	205	ALA
21	U	22	CYS
2	C	3	LYS
2	C	166	TRP
3	D	18	LEU
3	D	22	SER
3	D	27	ILE
3	D	59	LYS
3	D	82	LYS
3	D	167	PRO
5	F	48	ALA
5	F	89	VAL
7	H	30	LYS
8	I	25	GLY
9	J	13	PHE
10	K	107	THR
11	L	23	LEU
11	L	24	GLU
11	L	33	CYS
11	L	122	LYS
13	N	34	ASN

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Mol	Chain	Res	Type
13	N	57	SER
13	N	61	ASN
15	P	17	TYR
15	P	54	LEU
16	Q	35	LYS
20	B	38	HIS
20	B	86	CYS
21	U	9	GLU
2	C	83	VAL
2	C	107	LYS
2	C	145	ALA
2	C	167	TYR
4	E	43	GLY
5	F	55	HIS
5	F	85	ILE
5	F	95	ALA
8	I	55	ASP
9	J	62	ARG
10	K	119	GLY
12	M	15	VAL
13	N	48	GLN
13	N	67	GLY
14	O	75	ALA
16	Q	31	PRO
17	R	33	THR
18	S	27	LYS
20	B	24	PRO
20	B	211	LEU
4	E	56	PRO
5	F	94	HIS
7	H	71	VAL
10	K	16	SER
11	L	83	GLY
15	P	24	SER
15	P	28	ARG
18	S	53	GLY
6	G	15	PRO
8	I	71	ILE
9	J	42	LEU
15	P	33	ILE
15	P	42	ILE
4	E	133	ILE

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Mol	Chain	Res	Type
6	G	92	PRO
9	J	41	PRO
15	P	49	GLY
19	T	3	ILE
20	B	28	PRO
4	E	132	PRO
7	H	125	ILE
7	H	128	VAL
14	O	28	VAL
11	L	15	VAL
15	P	20	VAL
2	C	80	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	170/189 (90%)	145 (85%)	25 (15%)	4	26
3	D	172/172 (100%)	149 (87%)	23 (13%)	6	31
4	E	113/125 (90%)	98 (87%)	15 (13%)	6	31
5	F	87/116 (75%)	75 (86%)	12 (14%)	5	29
6	G	125/146 (86%)	108 (86%)	17 (14%)	5	30
7	H	104/104 (100%)	96 (92%)	8 (8%)	18	64
8	I	105/106 (99%)	93 (89%)	12 (11%)	8	40
9	J	86/90 (96%)	80 (93%)	6 (7%)	21	68
10	K	90/98 (92%)	77 (86%)	13 (14%)	5	27
11	L	103/103 (100%)	84 (82%)	19 (18%)	2	14
12	M	91/95 (96%)	82 (90%)	9 (10%)	11	49
13	N	79/83 (95%)	67 (85%)	12 (15%)	4	25
14	O	76/77 (99%)	70 (92%)	6 (8%)	18	62
15	P	65/65 (100%)	57 (88%)	8 (12%)	7	35
16	Q	75/77 (97%)	65 (87%)	10 (13%)	6	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	R	48/64 (75%)	46 (96%)	2 (4%)	40	84
18	S	71/78 (91%)	53 (75%)	18 (25%)	1	5
19	T	65/65 (100%)	53 (82%)	12 (18%)	2	13
20	B	180/198 (91%)	150 (83%)	30 (17%)	3	19
21	U	44/61 (72%)	35 (80%)	9 (20%)	2	10
All	All	1949/2112 (92%)	1683 (86%)	266 (14%)	5	30

All (266) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	2	GLN
2	C	13	ILE
2	C	17	TRP
2	C	18	ASN
2	C	20	THR
2	C	27	GLU
2	C	35	ASP
2	C	41	TYR
2	C	48	LYS
2	C	62	SER
2	C	69	THR
2	C	87	ARG
2	C	88	LYS
2	C	113	LYS
2	C	128	MET
2	C	131	ARG
2	C	138	GLN
2	C	163	ARG
2	C	166	TRP
2	C	168	ARG
2	C	171	ARG
2	C	175	HIS
2	C	180	ASP
2	C	184	ASN
2	C	206	ILE
3	D	4	LEU
3	D	7	LYS
3	D	18	LEU
3	D	25	ARG
3	D	28	ASP

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Mol	Chain	Res	Type
3	D	39	GLN
3	D	47	LEU
3	D	49	ASP
3	D	55	ARG
3	D	82	LYS
3	D	87	GLU
3	D	94	GLU
3	D	114	ARG
3	D	117	VAL
3	D	125	ASN
3	D	135	GLN
3	D	146	GLU
3	D	147	LYS
3	D	160	LEU
3	D	162	GLU
3	D	168	THR
3	D	190	LEU
3	D	195	ASN
4	E	9	GLU
4	E	19	ARG
4	E	23	THR
4	E	44	ARG
4	E	45	VAL
4	E	55	VAL
4	E	71	ILE
4	E	72	ASN
4	E	81	GLN
4	E	92	ARG
4	E	105	ILE
4	E	123	LEU
4	E	127	TYR
4	E	151	MET
4	E	156	ARG
5	F	6	ILE
5	F	39	LEU
5	F	51	ILE
5	F	55	HIS
5	F	60	VAL
5	F	62	MET
5	F	64	VAL
5	F	69	GLU
5	F	82	ASP

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Mol	Chain	Res	Type
5	F	86	ARG
5	F	94	HIS
5	F	98	GLU
6	G	2	ARG
6	G	3	ARG
6	G	8	GLN
6	G	10	LYS
6	G	21	LEU
6	G	49	LEU
6	G	51	GLN
6	G	55	LYS
6	G	62	GLU
6	G	67	ASN
6	G	78	ARG
6	G	89	GLU
6	G	94	ARG
6	G	96	ASN
6	G	105	GLU
6	G	113	LYS
6	G	125	ASP
7	H	2	MET
7	H	30	LYS
7	H	55	LYS
7	H	61	THR
7	H	72	GLU
7	H	82	LEU
7	H	105	THR
7	H	113	ARG
8	I	36	GLN
8	I	45	MET
8	I	59	LYS
8	I	62	LEU
8	I	87	MET
8	I	93	LEU
8	I	94	ARG
8	I	96	GLU
8	I	105	ARG
8	I	109	GLN
8	I	112	ARG
8	I	114	LYS
9	J	15	HIS
9	J	47	GLU

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Mol	Chain	Res	Type
9	J	69	THR
9	J	77	VAL
9	J	78	GLU
9	J	88	MET
10	K	22	ILE
10	K	31	VAL
10	K	34	THR
10	K	51	PHE
10	K	55	ARG
10	K	64	VAL
10	K	76	TYR
10	K	82	GLU
10	K	83	VAL
10	K	107	THR
10	K	115	ILE
10	K	118	ASN
10	K	121	ARG
11	L	13	ARG
11	L	14	LYS
11	L	15	VAL
11	L	17	LYS
11	L	18	SER
11	L	19	ASN
11	L	28	GLN
11	L	33	CYS
11	L	35	ARG
11	L	38	THR
11	L	40	THR
11	L	43	LYS
11	L	61	GLU
11	L	63	THR
11	L	95	HIS
11	L	102	ASP
11	L	107	LYS
11	L	119	LYS
11	L	122	LYS
12	M	2	ARG
12	M	16	ILE
12	M	28	ARG
12	M	41	ASP
12	M	43	LYS
12	M	71	GLU

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Mol	Chain	Res	Type
12	M	80	MET
12	M	88	LEU
12	M	102	LYS
13	N	11	LYS
13	N	19	TYR
13	N	20	PHE
13	N	25	GLU
13	N	27	LYS
13	N	41	TRP
13	N	48	GLN
13	N	49	THR
13	N	50	LEU
13	N	53	ASP
13	N	58	ARG
13	N	65	GLN
14	O	17	ASP
14	O	53	ARG
14	O	65	LEU
14	O	69	LEU
14	O	87	ARG
14	O	88	ARG
15	P	12	LYS
15	P	23	ASP
15	P	26	ASN
15	P	28	ARG
15	P	45	GLU
15	P	51	ARG
15	P	55	ASP
15	P	68	SER
16	Q	3	LYS
16	Q	4	ILE
16	Q	7	LEU
16	Q	8	GLN
16	Q	39	ARG
16	Q	41	THR
16	Q	56	ASP
16	Q	60	ILE
16	Q	80	LYS
16	Q	83	LEU
17	R	23	LYS
17	R	38	ILE
18	S	2	ARG

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Mol	Chain	Res	Type
18	S	4	LEU
18	S	6	LYS
18	S	10	ILE
18	S	13	HIS
18	S	20	LYS
18	S	23	GLU
18	S	26	ASP
18	S	27	LYS
18	S	28	LYS
18	S	32	THR
18	S	35	ARG
18	S	38	THR
18	S	42	ASN
18	S	47	THR
18	S	60	PHE
18	S	64	GLU
18	S	77	ARG
19	T	3	ILE
19	T	4	LYS
19	T	35	TYR
19	T	43	LYS
19	T	51	ASN
19	T	52	GLU
19	T	53	MET
19	T	57	VAL
19	T	67	HIS
19	T	68	LYS
19	T	74	HIS
19	T	84	LYS
20	B	8	MET
20	B	31	PHE
20	B	35	ASN
20	B	46	VAL
20	B	49	PHE
20	B	57	ASN
20	B	62	ARG
20	B	67	LEU
20	B	72	LYS
20	B	87	ASP
20	B	88	GLN
20	B	94	ARG
20	B	95	TRP

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Mol	Chain	Res	Type
20	B	104	LYS
20	B	113	LEU
20	B	115	ASP
20	B	116	LEU
20	B	117	GLU
20	B	121	GLN
20	B	126	ASP
20	B	127	LYS
20	B	130	LYS
20	B	134	LEU
20	B	145	ASN
20	B	160	LEU
20	B	176	ASN
20	B	196	ASP
20	B	199	ILE
20	B	202	ASN
20	B	212	TYR
21	U	11	PHE
21	U	15	LEU
21	U	16	ARG
21	U	22	CYS
21	U	24	LYS
21	U	32	ARG
21	U	34	ARG
21	U	38	GLU
21	U	44	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	2	GLN
2	C	7	ASN
2	C	31	ASN
2	C	68	HIS
2	C	139	ASN
3	D	35	GLN
3	D	39	GLN
3	D	53	GLN
3	D	70	GLN
3	D	135	GLN
3	D	195	ASN
4	E	18	ASN

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Mol	Chain	Res	Type
4	E	72	ASN
4	E	81	GLN
4	E	131	ASN
5	F	46	GLN
6	G	27	ASN
6	G	67	ASN
6	G	121	ASN
6	G	129	ASN
6	G	141	HIS
7	H	3	GLN
7	H	117	GLN
8	I	30	ASN
8	I	31	GLN
8	I	36	GLN
8	I	80	HIS
8	I	109	GLN
9	J	15	HIS
9	J	20	GLN
9	J	35	GLN
9	J	56	HIS
9	J	70	HIS
10	K	14	GLN
10	K	28	ASN
10	K	39	ASN
10	K	118	ASN
11	L	5	GLN
11	L	28	GLN
11	L	45	ASN
11	L	71	HIS
12	M	7	ASN
13	N	34	ASN
13	N	48	GLN
13	N	61	ASN
14	O	27	GLN
14	O	36	ASN
14	O	39	GLN
14	O	61	GLN
15	P	9	HIS
15	P	29	ASN
15	P	40	ASN
16	Q	50	ASN
17	R	53	GLN

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Mol	Chain	Res	Type
17	R	73	HIS
18	S	42	ASN
18	S	56	HIS
18	S	68	HIS
19	T	67	HIS
19	T	74	HIS
20	B	14	HIS
20	B	23	ASN
20	B	35	ASN
20	B	41	ASN
20	B	119	GLN
20	B	121	GLN
20	B	145	ASN
20	B	169	HIS
20	B	202	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1529/1542 (99%)	240 (15%)	27 (1%)

All (240) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	9	G
1	A	14	U
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	52	C
1	A	54	C
1	A	55	A
1	A	68	G
1	A	71	A
1	A	83	C
1	A	84	U
1	A	85	U
1	A	86	G
1	A	87	C

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Mol	Chain	Res	Type
1	A	91	U
1	A	121	U
1	A	130	A
1	A	131	A
1	A	149	A
1	A	164	G
1	A	177	G
1	A	182	A
1	A	183	C
1	A	197	A
1	A	206	C
1	A	209	U
1	A	210	C
1	A	233	C
1	A	239	U
1	A	240	G
1	A	243	A
1	A	244	U
1	A	245	U
1	A	247	G
1	A	250	A
1	A	251	G
1	A	253	A
1	A	256	U
1	A	257	G
1	A	258	G
1	A	266	G
1	A	267	C
1	A	280	C
1	A	289	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	330	C
1	A	332	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	372	C
1	A	373	A
1	A	381	C

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Mol	Chain	Res	Type
1	A	384	G
1	A	392	C
1	A	397	A
1	A	398	U
1	A	406	G
1	A	408	A
1	A	411	A
1	A	412	A
1	A	413	G
1	A	415	A
1	A	421	U
1	A	422	C
1	A	429	U
1	A	430	A
1	A	435	A
1	A	438	U
1	A	460	A
1	A	461	A
1	A	462	G
1	A	463	U
1	A	464	U
1	A	465	A
1	A	466	A
1	A	467	U
1	A	468	A
1	A	479	U
1	A	484	G
1	A	485	U
1	A	486	U
1	A	493	A
1	A	500	G
1	A	511	C
1	A	518	C
1	A	527	G
1	A	532	A
1	A	547	A
1	A	559	A
1	A	562	U
1	A	572	A
1	A	573	A
1	A	576	C
1	A	577	G

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Mol	Chain	Res	Type
1	A	596	A
1	A	633	G
1	A	653	U
1	A	661	G
1	A	665	A
1	A	687	A
1	A	695	A
1	A	700	G
1	A	721	G
1	A	724	G
1	A	731	G
1	A	747	A
1	A	748	G
1	A	755	G
1	A	777	A
1	A	781	A
1	A	782	A
1	A	785	G
1	A	793	U
1	A	794	A
1	A	812	G
1	A	815	A
1	A	817	C
1	A	818	G
1	A	819	A
1	A	828	U
1	A	829	G
1	A	841	C
1	A	843	U
1	A	844	G
1	A	845	A
1	A	846	G
1	A	847	G
1	A	849	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	961	U
1	A	966	G

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Mol	Chain	Res	Type
1	A	968	A
1	A	969	A
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	984	C
1	A	991	U
1	A	992	U
1	A	993	G
1	A	1003	G
1	A	1004	A
1	A	1010	U
1	A	1011	C
1	A	1019	A
1	A	1020	G
1	A	1028	C
1	A	1030	U
1	A	1031	C
1	A	1034	G
1	A	1035	A
1	A	1041	G
1	A	1049	U
1	A	1050	G
1	A	1054	C
1	A	1065	U
1	A	1066	C
1	A	1081	A
1	A	1094	G
1	A	1101	A
1	A	1136	C
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1146	A
1	A	1159	U
1	A	1167	A
1	A	1168	U
1	A	1174	G
1	A	1179	A
1	A	1181	G
1	A	1184	G

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Mol	Chain	Res	Type
1	A	1196	A
1	A	1197	A
1	A	1202	U
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1238	A
1	A	1240	U
1	A	1250	A
1	A	1256	A
1	A	1261	A
1	A	1278	G
1	A	1279	G
1	A	1280	A
1	A	1281	C
1	A	1285	A
1	A	1286	U
1	A	1287	A
1	A	1297	G
1	A	1300	G
1	A	1301	U
1	A	1302	C
1	A	1303	C
1	A	1305	G
1	A	1316	G
1	A	1317	C
1	A	1323	G
1	A	1336	C
1	A	1362	A
1	A	1363	A
1	A	1364	U
1	A	1388	C
1	A	1398	A
1	A	1400	C
1	A	1401	G
1	A	1432	G
1	A	1446	A
1	A	1448	C
1	A	1452	C

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Mol	Chain	Res	Type
1	A	1490	U
1	A	1491	G
1	A	1492	A
1	A	1493	A
1	A	1494	G
1	A	1497	G
1	A	1503	A
1	A	1506	U
1	A	1517	G
1	A	1520	C
1	A	1529	G
1	A	1530	G
1	A	1534	A

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	51	A
1	A	239	U
1	A	243	A
1	A	266	G
1	A	279	A
1	A	328	C
1	A	366	A
1	A	372	C
1	A	412	A
1	A	428	G
1	A	429	U
1	A	484	G
1	A	960	U
1	A	975	A
1	A	1030	U
1	A	1049	U
1	A	1065	U
1	A	1201	A
1	A	1212	U
1	A	1213	A
1	A	1226	C
1	A	1285	A
1	A	1302	C
1	A	1362	A
1	A	1397	C

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Mol	Chain	Res	Type
1	A	1451	U
1	A	1492	A

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 63 ligands modelled in this entry, 62 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	HYG	A	3001	-	39,39,39	1.50	7 (17%)	60,60,60	1.45	6 (10%)

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
23	HYG	A	3001	-	-	1/14/87/87	0/2/4/4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	3001	HYG	C3-C2	5.00	1.56	1.52
23	A	3001	HYG	C27-C33	2.65	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	3001	HYG	O22-C17	-2.31	1.38	1.43
23	A	3001	HYG	O28-C23	2.18	1.44	1.40
23	A	3001	HYG	C16-C15	2.10	1.57	1.53
23	A	3001	HYG	C34-C33	2.08	1.55	1.51
23	A	3001	HYG	C3-C4	2.02	1.56	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	3001	HYG	C23-O28-C27	4.38	115.84	111.82
23	A	3001	HYG	O22-C17-C16	4.35	122.21	111.24
23	A	3001	HYG	C10-N9-C4	3.77	115.93	113.82
23	A	3001	HYG	O8-C1-C2	-3.36	101.78	109.66
23	A	3001	HYG	O35-C34-C33	-2.92	103.94	111.25
23	A	3001	HYG	C26-C25-C24	-2.12	108.26	111.31

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	A	3001	HYG	C26-C27-C33-N36

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1530/1542 (99%)	-0.09	46 (3%) 48 22	8, 57, 142, 180	0
2	C	206/232 (88%)	1.52	60 (29%) 1 1	15, 81, 138, 180	0
3	D	205/205 (100%)	2.18	91 (44%) 1 1	5, 63, 135, 180	0
4	E	150/166 (90%)	2.85	82 (54%) 0 1	5, 62, 135, 175	0
5	F	100/135 (74%)	2.36	53 (53%) 0 1	14, 78, 126, 166	0
6	G	152/178 (85%)	2.48	84 (55%) 0 1	27, 98, 156, 177	0
7	H	129/129 (100%)	2.87	75 (58%) 0 1	5, 53, 117, 153	0
8	I	127/129 (98%)	1.28	31 (24%) 1 2	32, 103, 162, 180	0
9	J	98/103 (95%)	3.43	71 (72%) 0 0	42, 107, 156, 180	0
10	K	117/128 (91%)	2.05	58 (49%) 1 1	5, 57, 112, 179	0
11	L	123/123 (100%)	2.52	67 (54%) 0 1	5, 44, 109, 165	0
12	M	113/117 (96%)	2.33	52 (46%) 1 1	32, 108, 156, 180	0
13	N	96/100 (96%)	2.11	44 (45%) 1 1	38, 99, 137, 171	0
14	O	88/89 (98%)	2.10	44 (50%) 0 1	8, 54, 111, 165	0
15	P	80/82 (97%)	2.72	51 (63%) 0 1	5, 51, 143, 164	0
16	Q	81/83 (97%)	0.83	15 (18%) 2 2	5, 51, 121, 157	0
17	R	55/74 (74%)	1.24	12 (21%) 1 2	13, 69, 132, 149	0
18	S	80/91 (87%)	0.49	11 (13%) 4 3	49, 113, 171, 180	0
19	T	85/86 (98%)	2.26	42 (49%) 1 1	14, 58, 121, 177	0
20	B	218/240 (90%)	1.98	76 (34%) 1 1	26, 106, 160, 180	0
21	U	51/71 (71%)	2.10	23 (45%) 1 1	19, 85, 151, 180	0
All	All	3884/4103 (94%)	1.25	1088 (28%) 1 1	5, 71, 147, 180	0

All (1088) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	E	12	GLU	11.4
4	E	54	GLU	11.4
6	G	152	HIS	11.1
7	H	126	CYS	10.7
2	C	133	MET	10.6
12	M	9	PRO	10.5
9	J	5	ARG	10.2
17	R	19	GLU	10.0
2	C	167	TYR	9.9
13	N	24	ALA	9.8
2	C	165	GLU	9.7
9	J	66	GLU	9.4
10	K	13	LYS	9.3
7	H	127	TYR	9.2
2	C	128	MET	9.1
3	D	146	GLU	8.8
3	D	149	LYS	8.6
4	E	11	GLN	8.6
4	E	13	LYS	8.5
3	D	64	TYR	8.5
20	B	72	LYS	8.5
4	E	111	ARG	8.4
13	N	82	LYS	8.4
20	B	73	ARG	8.3
9	J	68	ARG	8.3
4	E	46	GLY	8.3
15	P	80	LYS	8.3
11	L	95	HIS	8.2
12	M	11	HIS	8.2
7	H	9	MET	8.1
2	C	130	ARG	8.0
20	B	77	GLU	7.8
4	E	110	MET	7.8
4	E	36	THR	7.8
7	H	76	ARG	7.8
7	H	78	SER	7.8
1	A	5	U	7.7
20	B	153	MET	7.6
2	C	166	TRP	7.6
9	J	35	GLN	7.6
3	D	147	LYS	7.6
20	B	164	ASP	7.6
13	N	96	LYS	7.6

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Mol	Chain	Res	Type	RSRZ
9	J	65	TYR	7.6
19	T	48	LYS	7.5
11	L	94	TYR	7.5
11	L	55	ARG	7.5
7	H	90	GLU	7.5
6	G	84	TYR	7.5
3	D	56	GLU	7.5
9	J	102	LEU	7.5
9	J	79	PRO	7.4
20	B	159	ALA	7.4
13	N	97	LYS	7.3
7	H	83	ARG	7.3
11	L	84	GLY	7.3
3	D	63	ILE	7.3
21	U	3	ILE	7.3
7	H	75	GLN	7.2
10	K	59	PRO	7.2
6	G	105	GLU	7.2
10	K	12	ARG	7.2
15	P	67	ILE	7.1
2	C	129	PHE	7.1
11	L	58	ASN	7.0
4	E	14	LEU	7.0
4	E	60	GLN	7.0
4	E	53	ARG	7.0
11	L	59	GLY	7.0
20	B	17	HIS	7.0
13	N	98	ALA	7.0
9	J	50	THR	6.9
12	M	47	LEU	6.9
20	B	158	ASP	6.9
7	H	32	LYS	6.9
6	G	73	GLU	6.8
5	F	32	ALA	6.8
10	K	55	ARG	6.8
1	A	1346	A	6.8
9	J	78	GLU	6.7
19	T	86	ALA	6.7
14	O	88	ARG	6.7
10	K	58	THR	6.7
7	H	89	ASP	6.7
11	L	81	ILE	6.6

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Mol	Chain	Res	Type	RSRZ
4	E	63	MET	6.6
3	D	127	ARG	6.6
19	T	35	TYR	6.6
20	B	66	ILE	6.6
20	B	163	ILE	6.6
12	M	44	ILE	6.6
20	B	150	ILE	6.6
6	G	153	TYR	6.5
3	D	150	LYS	6.5
12	M	43	LYS	6.5
4	E	56	PRO	6.4
19	T	68	LYS	6.4
20	B	67	LEU	6.4
4	E	107	GLY	6.4
3	D	176	LYS	6.4
6	G	86	VAL	6.4
12	M	10	ASP	6.4
2	C	131	ARG	6.4
18	S	15	LEU	6.4
20	B	160	LEU	6.3
4	E	59	ILE	6.3
4	E	144	GLU	6.3
20	B	76	SER	6.3
6	G	106	ALA	6.3
2	C	156	LEU	6.2
6	G	9	ARG	6.2
4	E	15	ILE	6.2
2	C	198	LYS	6.2
2	C	124	GLU	6.2
3	D	62	ARG	6.2
7	H	93	LYS	6.2
6	G	12	LEU	6.2
21	U	15	LEU	6.1
11	L	29	LYS	6.1
4	E	16	ALA	6.1
2	C	126	ARG	6.1
11	L	123	ALA	6.1
2	C	151	GLU	6.0
15	P	66	THR	6.0
4	E	70	MET	6.0
20	B	91	VAL	6.0
4	E	44	ARG	6.0

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Mol	Chain	Res	Type	RSRZ
12	M	46	GLU	6.0
7	H	92	PRO	6.0
5	F	21	MET	6.0
4	E	47	PHE	6.0
6	G	22	LEU	6.0
3	D	145	ARG	6.0
9	J	49	PHE	5.9
7	H	91	LEU	5.9
19	T	43	LYS	5.9
11	L	96	THR	5.9
9	J	12	ALA	5.9
7	H	99	GLY	5.9
13	N	26	LEU	5.9
4	E	35	LEU	5.9
15	P	6	LEU	5.9
9	J	87	LEU	5.9
4	E	28	ARG	5.9
7	H	84	ILE	5.9
7	H	97	GLY	5.8
6	G	74	VAL	5.8
15	P	79	ASN	5.8
3	D	65	GLY	5.8
19	T	71	ALA	5.8
11	L	60	PHE	5.8
1	A	1202	U	5.8
19	T	67	HIS	5.8
1	A	1397	C	5.7
4	E	39	GLY	5.7
6	G	85	GLN	5.7
7	H	77	VAL	5.7
5	F	22	ILE	5.7
15	P	47	GLU	5.7
4	E	38	VAL	5.7
12	M	8	ILE	5.7
5	F	1	MET	5.7
7	H	42	GLU	5.7
11	L	30	ARG	5.6
14	O	62	ARG	5.6
7	H	100	ILE	5.6
11	L	80	LEU	5.6
4	E	115	GLU	5.6
10	K	63	GLN	5.6

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Mol	Chain	Res	Type	RSRZ
17	R	50	TYR	5.6
3	D	61	ARG	5.5
13	N	78	LEU	5.5
6	G	46	LEU	5.5
7	H	129	ALA	5.5
3	D	43	ARG	5.5
4	E	30	PHE	5.5
7	H	35	ILE	5.5
20	B	65	LYS	5.5
4	E	109	ALA	5.5
8	I	121	ARG	5.5
9	J	77	VAL	5.5
8	I	123	ARG	5.5
3	D	7	LYS	5.4
4	E	55	VAL	5.4
12	M	56	ARG	5.4
4	E	117	ALA	5.4
20	B	93	HIS	5.4
11	L	122	LYS	5.4
6	G	89	GLU	5.4
1	A	6	G	5.4
12	M	61	LYS	5.4
11	L	24	GLU	5.4
7	H	43	GLY	5.3
15	P	61	VAL	5.3
17	R	53	GLN	5.3
14	O	35	ILE	5.3
9	J	64	GLN	5.3
3	D	193	ASP	5.3
7	H	112	ASP	5.3
3	D	177	MET	5.3
4	E	57	ALA	5.3
12	M	12	LYS	5.3
4	E	37	VAL	5.3
6	G	10	LYS	5.3
12	M	112	ARG	5.3
19	T	74	HIS	5.3
3	D	126	GLY	5.2
15	P	77	GLU	5.2
20	B	43	GLU	5.2
7	H	72	GLU	5.2
9	J	34	ALA	5.2

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Mol	Chain	Res	Type	RSRZ
4	E	19	ARG	5.2
6	G	108	ARG	5.2
11	L	23	LEU	5.2
4	E	108	GLY	5.2
3	D	120	LYS	5.2
5	F	33	GLU	5.2
13	N	25	GLU	5.2
11	L	93	ARG	5.2
13	N	85	GLU	5.2
9	J	30	LYS	5.2
13	N	80	ARG	5.1
14	O	58	MET	5.1
20	B	71	THR	5.1
16	Q	5	ARG	5.1
4	E	45	VAL	5.1
12	M	52	ILE	5.1
19	T	36	ALA	5.1
2	C	150	VAL	5.1
8	I	109	GLN	5.1
6	G	11	ILE	5.1
19	T	75	LYS	5.1
7	H	79	ARG	5.1
5	F	68	GLN	5.1
11	L	21	PRO	5.1
13	N	71	GLY	5.0
2	C	125	ARG	5.0
20	B	123	GLY	5.0
20	B	124	THR	5.0
21	U	14	ALA	5.0
7	H	68	LYS	5.0
20	B	204	ASP	5.0
4	E	10	LEU	5.0
5	F	35	LYS	5.0
19	T	45	ALA	5.0
14	O	87	ARG	5.0
20	B	92	ASN	4.9
6	G	151	ALA	4.9
15	P	4	ILE	4.9
20	B	154	GLY	4.9
3	D	16	THR	4.9
9	J	36	VAL	4.9
11	L	12	ALA	4.9

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Mol	Chain	Res	Type	RSRZ
4	E	112	ALA	4.9
2	C	164	THR	4.9
19	T	69	ASN	4.9
9	J	67	ILE	4.9
12	M	31	ALA	4.9
10	K	111	ASP	4.9
11	L	82	ARG	4.9
20	B	70	GLY	4.8
3	D	66	VAL	4.8
19	T	52	GLU	4.8
3	D	46	ARG	4.8
8	I	117	LEU	4.8
20	B	157	PRO	4.8
7	H	98	LEU	4.8
4	E	48	GLY	4.8
11	L	31	GLY	4.8
6	G	21	LEU	4.8
20	B	68	PHE	4.8
20	B	162	VAL	4.8
7	H	4	ASP	4.8
4	E	34	ALA	4.8
15	P	68	SER	4.8
3	D	82	LYS	4.8
11	L	43	LYS	4.8
3	D	144	ILE	4.8
9	J	27	GLU	4.7
5	F	30	THR	4.7
9	J	44	THR	4.7
20	B	167	HIS	4.7
7	H	102	VAL	4.7
3	D	14	GLU	4.7
2	C	169	GLU	4.7
4	E	18	ASN	4.7
7	H	101	ALA	4.7
7	H	6	ILE	4.7
19	T	70	LYS	4.7
9	J	90	LEU	4.7
5	F	23	GLU	4.7
2	C	138	GLN	4.7
4	E	31	SER	4.7
15	P	35	ARG	4.7
7	H	96	ALA	4.7

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Mol	Chain	Res	Type	RSRZ
16	Q	82	VAL	4.7
5	F	69	GLU	4.7
20	B	166	ASP	4.7
19	T	37	ALA	4.7
5	F	29	ILE	4.6
9	J	84	VAL	4.6
4	E	17	VAL	4.6
3	D	53	GLN	4.6
5	F	24	ARG	4.6
19	T	46	ALA	4.6
7	H	128	VAL	4.6
7	H	69	ALA	4.6
12	M	18	LEU	4.6
21	U	16	ARG	4.6
11	L	56	LEU	4.6
7	H	17	GLN	4.6
6	G	107	ALA	4.6
12	M	1	ALA	4.6
1	A	1534	A	4.6
3	D	123	MET	4.6
21	U	17	ARG	4.6
1	A	443	C	4.6
9	J	88	MET	4.6
5	F	67	PRO	4.6
2	C	132	ALA	4.6
6	G	143	MET	4.6
19	T	72	ALA	4.5
5	F	64	VAL	4.5
9	J	51	VAL	4.5
21	U	13	VAL	4.5
4	E	140	ILE	4.5
5	F	47	LEU	4.5
10	K	110	THR	4.5
3	D	148	ALA	4.5
9	J	83	THR	4.5
9	J	100	ILE	4.5
7	H	44	PHE	4.5
3	D	194	ILE	4.5
19	T	53	MET	4.5
11	L	14	LYS	4.5
7	H	7	ALA	4.5
20	B	128	LEU	4.5

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Mol	Chain	Res	Type	RSRZ
20	B	169	HIS	4.5
5	F	46	GLN	4.5
8	I	129	ARG	4.5
15	P	62	GLY	4.4
12	M	6	ILE	4.4
9	J	37	ARG	4.4
9	J	69	THR	4.4
7	H	39	LEU	4.4
15	P	43	ALA	4.4
21	U	19	LYS	4.4
15	P	45	GLU	4.4
3	D	121	ALA	4.4
20	B	75	ALA	4.4
7	H	125	ILE	4.4
13	N	76	PHE	4.4
5	F	79	ARG	4.4
3	D	151	GLN	4.3
11	L	74	GLN	4.3
6	G	150	PHE	4.3
6	G	145	GLU	4.3
8	I	11	ARG	4.3
3	D	116	LEU	4.3
11	L	15	VAL	4.3
4	E	52	ALA	4.3
2	C	127	VAL	4.3
11	L	63	THR	4.3
10	K	62	ALA	4.3
8	I	108	ARG	4.3
7	H	10	LEU	4.3
9	J	29	ALA	4.3
4	E	113	VAL	4.3
6	G	52	ARG	4.3
13	N	84	ARG	4.3
6	G	88	VAL	4.3
20	B	74	ALA	4.3
2	C	145	ALA	4.3
7	H	124	ILE	4.3
10	K	51	PHE	4.3
3	D	155	LYS	4.3
5	F	25	TYR	4.3
8	I	101	GLY	4.3
13	N	95	LEU	4.3

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Mol	Chain	Res	Type	RSRZ
4	E	9	GLU	4.3
9	J	46	LYS	4.2
11	L	26	CYS	4.2
13	N	81	ILE	4.2
14	O	59	VAL	4.2
8	I	106	ASP	4.2
6	G	77	ARG	4.2
12	M	55	LEU	4.2
11	L	22	ALA	4.2
5	F	26	THR	4.2
11	L	13	ARG	4.2
15	P	59	HIS	4.2
7	H	14	ARG	4.2
9	J	16	ARG	4.2
11	L	57	THR	4.2
6	G	25	PHE	4.2
10	K	14	GLN	4.2
14	O	39	GLN	4.2
5	F	55	HIS	4.2
5	F	62	MET	4.2
20	B	69	VAL	4.2
1	A	632	U	4.2
1	A	1451	U	4.2
2	C	187	GLU	4.2
9	J	47	GLU	4.2
21	U	18	PHE	4.2
10	K	93	GLU	4.2
9	J	70	HIS	4.1
3	D	10	LEU	4.1
9	J	63	ASP	4.1
6	G	119	LEU	4.1
10	K	23	HIS	4.1
3	D	195	ASN	4.1
4	E	143	LEU	4.1
2	C	159	ALA	4.1
12	M	4	ALA	4.1
21	U	24	LYS	4.1
6	G	87	PRO	4.1
9	J	91	ASP	4.1
12	M	57	ASP	4.1
6	G	29	LEU	4.1
3	D	153	ARG	4.1

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Mol	Chain	Res	Type	RSRZ
7	H	94	VAL	4.1
16	Q	83	LEU	4.1
5	F	4	TYR	4.1
7	H	111	THR	4.1
11	L	64	SER	4.1
13	N	68	ARG	4.1
13	N	29	ILE	4.0
4	E	29	ILE	4.0
19	T	73	ARG	4.0
7	H	74	ILE	4.0
6	G	16	LYS	4.0
14	O	86	LEU	4.0
3	D	49	ASP	4.0
20	B	165	ALA	4.0
20	B	149	GLY	4.0
6	G	49	LEU	4.0
15	P	65	ALA	4.0
10	K	84	MET	4.0
12	M	7	ASN	4.0
4	E	133	ILE	4.0
6	G	120	ALA	4.0
15	P	3	THR	4.0
15	P	69	ASP	4.0
4	E	58	ALA	4.0
10	K	82	GLU	4.0
20	B	224	ARG	4.0
7	H	8	ASP	4.0
6	G	100	MET	4.0
10	K	97	ARG	4.0
19	T	33	LYS	4.0
10	K	96	ILE	4.0
12	M	3	ILE	4.0
20	B	136	ARG	4.0
11	L	79	ILE	3.9
20	B	90	PHE	3.9
2	C	13	ILE	3.9
7	H	31	LEU	3.9
21	U	7	GLU	3.9
7	H	5	PRO	3.9
6	G	142	ARG	3.9
2	C	152	VAL	3.9
12	M	30	LYS	3.9

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Mol	Chain	Res	Type	RSRZ
11	L	61	GLU	3.9
19	T	39	GLU	3.9
4	E	139	THR	3.9
14	O	52	ARG	3.9
4	E	134	ASN	3.9
9	J	21	ALA	3.9
10	K	20	ALA	3.9
11	L	54	VAL	3.9
19	T	4	LYS	3.9
6	G	123	LEU	3.9
20	B	80	LYS	3.9
7	H	36	ALA	3.9
7	H	33	VAL	3.9
6	G	42	VAL	3.9
1	A	490	C	3.9
9	J	6	ILE	3.9
2	C	123	LEU	3.9
14	O	67	ASP	3.9
5	F	28	ALA	3.8
19	T	47	GLN	3.8
9	J	8	ILE	3.8
9	J	39	PRO	3.8
11	L	75	GLU	3.8
20	B	79	VAL	3.8
3	D	60	VAL	3.8
5	F	31	GLY	3.8
3	D	57	LYS	3.8
3	D	205	LYS	3.8
3	D	114	ARG	3.8
13	N	73	LEU	3.8
20	B	156	LEU	3.8
3	D	108	ALA	3.8
8	I	120	ALA	3.8
10	K	74	LYS	3.8
10	K	109	ILE	3.8
9	J	10	LEU	3.7
14	O	77	TYR	3.7
14	O	30	LEU	3.7
3	D	128	VAL	3.7
4	E	118	GLY	3.7
1	A	485	U	3.7
7	H	38	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
20	B	185	ILE	3.7
9	J	17	LEU	3.7
9	J	7	ARG	3.7
9	J	48	ARG	3.7
12	M	28	ARG	3.7
12	M	113	LYS	3.7
14	O	84	LEU	3.7
20	B	31	PHE	3.7
3	D	45	PRO	3.7
2	C	197	VAL	3.7
6	G	60	ALA	3.7
13	N	66	THR	3.7
4	E	40	ASP	3.7
15	P	57	ILE	3.7
19	T	38	ILE	3.7
12	M	81	ASP	3.6
4	E	116	VAL	3.6
1	A	1344	C	3.6
9	J	18	ILE	3.6
10	K	79	LYS	3.6
4	E	142	GLY	3.6
6	G	117	LEU	3.6
8	I	96	GLU	3.6
14	O	32	THR	3.6
13	N	28	ALA	3.6
8	I	99	LYS	3.6
7	H	88	LYS	3.6
3	D	196	GLU	3.6
2	C	134	LYS	3.6
3	D	20	LEU	3.6
1	A	629	A	3.6
3	D	15	GLY	3.6
1	A	1492	A	3.6
13	N	21	ALA	3.6
20	B	87	ASP	3.6
7	H	70	VAL	3.6
3	D	44	LYS	3.5
20	B	161	PHE	3.5
20	B	63	LYS	3.5
3	D	22	SER	3.5
1	A	27	G	3.5
3	D	178	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
9	J	53	ILE	3.5
4	E	49	TYR	3.5
15	P	22	ALA	3.5
4	E	136	VAL	3.5
15	P	41	PRO	3.5
5	F	34	GLY	3.5
4	E	71	ILE	3.5
12	M	59	VAL	3.5
14	O	36	ASN	3.5
7	H	95	MET	3.5
5	F	2	ARG	3.5
10	K	50	GLY	3.5
21	U	36	PHE	3.5
19	T	49	ALA	3.5
14	O	34	GLN	3.5
1	A	1348	U	3.5
5	F	54	LEU	3.5
16	Q	7	LEU	3.5
7	H	34	ALA	3.4
5	F	73	GLU	3.4
6	G	58	LEU	3.4
6	G	45	ALA	3.4
13	N	20	PHE	3.4
20	B	127	LYS	3.4
15	P	5	ARG	3.4
15	P	63	GLN	3.4
8	I	79	ARG	3.4
20	B	172	ILE	3.4
11	L	83	GLY	3.4
20	B	129	THR	3.4
1	A	1257	A	3.4
15	P	52	LEU	3.4
5	F	70	VAL	3.4
7	H	41	GLU	3.3
10	K	15	VAL	3.3
11	L	42	LYS	3.3
16	Q	6	THR	3.3
19	T	44	ALA	3.3
19	T	5	SER	3.3
17	R	47	ARG	3.3
3	D	112	GLU	3.3
11	L	101	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
2	C	185	THR	3.3
5	F	36	ILE	3.3
12	M	42	VAL	3.3
20	B	168	GLU	3.3
10	K	80	ASN	3.3
3	D	143	SER	3.3
13	N	72	PHE	3.3
14	O	55	LEU	3.3
15	P	54	LEU	3.3
6	G	55	LYS	3.3
13	N	45	LEU	3.3
11	L	76	HIS	3.3
6	G	20	GLU	3.3
2	C	137	VAL	3.3
1	A	962	C	3.3
21	U	53	LYS	3.3
9	J	13	PHE	3.3
13	N	65	GLN	3.3
20	B	125	PHE	3.3
1	A	845	A	3.3
8	I	111	GLU	3.3
19	T	42	ASP	3.3
13	N	83	VAL	3.3
13	N	79	SER	3.3
10	K	106	ILE	3.2
9	J	28	THR	3.2
20	B	94	ARG	3.2
12	M	32	ILE	3.2
5	F	53	LYS	3.2
9	J	86	ALA	3.2
14	O	8	ALA	3.2
13	N	27	LYS	3.2
19	T	51	ASN	3.2
11	L	25	ALA	3.2
13	N	44	VAL	3.2
14	O	5	GLU	3.2
3	D	154	VAL	3.2
11	L	62	VAL	3.2
1	A	1347	G	3.2
3	D	4	LEU	3.2
20	B	44	LYS	3.2
10	K	24	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
15	P	42	ILE	3.2
1	A	232	G	3.2
4	E	135	VAL	3.2
3	D	109	THR	3.2
6	G	146	ALA	3.2
12	M	19	THR	3.2
6	G	43	TYR	3.2
6	G	94	ARG	3.1
10	K	100	ASN	3.2
13	N	43	ALA	3.2
14	O	63	ARG	3.1
2	C	119	ILE	3.1
20	B	155	GLY	3.1
3	D	54	LEU	3.1
12	M	51	GLN	3.1
7	H	85	TYR	3.1
10	K	99	LEU	3.1
14	O	83	ARG	3.1
17	R	71	ASP	3.1
3	D	110	ARG	3.1
16	Q	4	ILE	3.1
12	M	34	ALA	3.1
6	G	72	VAL	3.1
11	L	103	CYS	3.1
10	K	54	SER	3.1
6	G	144	ALA	3.1
19	T	7	LYS	3.1
2	C	12	GLY	3.1
11	L	85	ARG	3.1
5	F	65	GLU	3.1
6	G	141	HIS	3.1
7	H	73	SER	3.1
3	D	129	VAL	3.1
9	J	73	LEU	3.1
21	U	46	ARG	3.1
15	P	76	LYS	3.1
21	U	20	ARG	3.1
20	B	184	ALA	3.1
2	C	121	SER	3.1
14	O	60	SER	3.1
3	D	59	LYS	3.1
3	D	3	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
15	P	39	PHE	3.1
2	C	168	ARG	3.1
6	G	24	LYS	3.0
15	P	60	TRP	3.0
2	C	163	ARG	3.0
6	G	51	GLN	3.0
9	J	80	THR	3.0
6	G	7	GLY	3.0
3	D	164	ARG	3.0
10	K	67	GLU	3.0
12	M	58	GLU	3.0
20	B	89	PHE	3.0
13	N	42	ASN	3.0
10	K	92	ARG	3.0
20	B	151	LYS	3.0
2	C	120	THR	3.0
20	B	194	GLY	3.0
3	D	18	LEU	3.0
2	C	74	ILE	3.0
1	A	630	A	3.0
13	N	56	PRO	3.0
21	U	23	GLU	3.0
5	F	37	HIS	3.0
4	E	21	SER	3.0
7	H	86	LYS	3.0
7	H	103	VAL	3.0
10	K	95	THR	3.0
3	D	202	LEU	3.0
4	E	114	LEU	3.0
12	M	2	ARG	3.0
20	B	206	ILE	3.0
11	L	28	GLN	3.0
21	U	49	ALA	3.0
14	O	73	ASP	3.0
6	G	8	GLN	3.0
3	D	106	PHE	3.0
11	L	33	CYS	3.0
1	A	489	C	3.0
11	L	52	CYS	2.9
8	I	102	PHE	2.9
7	H	2	MET	2.9
2	C	186	SER	2.9

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Mol	Chain	Res	Type	RSRZ
14	O	41	HIS	2.9
10	K	83	VAL	2.9
13	N	48	GLN	2.9
8	I	100	ALA	2.9
18	S	19	GLU	2.9
4	E	51	LYS	2.9
5	F	93	LYS	2.9
4	E	67	ARG	2.9
10	K	60	PHE	2.9
20	B	78	ALA	2.9
15	P	71	VAL	2.9
6	G	47	GLU	2.9
7	H	80	PRO	2.9
3	D	48	SER	2.9
4	E	132	PRO	2.9
20	B	203	ASP	2.9
5	F	27	ALA	2.9
8	I	75	ALA	2.9
9	J	76	ILE	2.9
11	L	97	VAL	2.9
15	P	78	VAL	2.9
8	I	97	LEU	2.9
4	E	137	ARG	2.9
15	P	19	VAL	2.9
6	G	101	ARG	2.9
9	J	89	ARG	2.9
7	H	40	LYS	2.9
1	A	1374	A	2.8
8	I	122	ARG	2.8
8	I	38	PHE	2.8
6	G	147	ASN	2.8
5	F	86	ARG	2.8
13	N	75	LYS	2.8
10	K	104	PHE	2.8
6	G	79	VAL	2.8
7	H	63	LYS	2.8
1	A	444	G	2.8
3	D	104	MET	2.8
13	N	47	LEU	2.8
9	J	85	ASP	2.8
3	D	130	ASN	2.8
6	G	59	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
9	J	56	HIS	2.8
11	L	117	GLY	2.8
15	P	34	GLU	2.8
18	S	16	LYS	2.8
1	A	1204	A	2.8
6	G	81	GLY	2.8
6	G	75	LYS	2.8
9	J	96	VAL	2.8
15	P	2	VAL	2.8
9	J	74	VAL	2.8
2	C	178	ARG	2.8
12	M	40	GLU	2.8
3	D	19	PHE	2.8
2	C	48	LYS	2.8
6	G	80	GLY	2.8
1	A	1186	G	2.8
11	L	121	PRO	2.8
12	M	45	SER	2.8
7	H	117	GLN	2.8
4	E	32	PHE	2.8
3	D	55	ARG	2.8
6	G	149	ALA	2.8
7	H	13	ILE	2.7
7	H	113	ARG	2.7
17	R	72	ARG	2.7
6	G	48	THR	2.7
7	H	116	ARG	2.7
12	M	62	PHE	2.7
6	G	103	ILE	2.7
12	M	41	ASP	2.7
1	A	491	G	2.7
6	G	91	ARG	2.7
7	H	71	VAL	2.7
3	D	122	ILE	2.7
1	A	461	A	2.7
1	A	877	G	2.7
10	K	85	VAL	2.7
20	B	186	VAL	2.7
19	T	31	ILE	2.7
14	O	74	VAL	2.7
8	I	12	LYS	2.7
3	D	117	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
9	J	26	VAL	2.7
10	K	91	GLY	2.7
16	Q	62	GLU	2.7
5	F	9	MET	2.7
15	P	56	ARG	2.7
10	K	86	LYS	2.7
20	B	181	PRO	2.7
15	P	44	SER	2.7
14	O	76	ARG	2.6
19	T	40	ALA	2.6
15	P	32	PHE	2.6
2	C	142	ARG	2.6
13	N	23	ARG	2.6
14	O	78	THR	2.6
17	R	73	HIS	2.6
6	G	27	ASN	2.6
10	K	94	SER	2.6
14	O	37	HIS	2.6
18	S	40	PHE	2.6
9	J	11	LYS	2.6
11	L	20	VAL	2.6
1	A	1203	C	2.6
9	J	43	PRO	2.6
18	S	8	PRO	2.6
7	H	67	GLY	2.6
10	K	81	LEU	2.6
21	U	5	VAL	2.6
10	K	16	SER	2.6
2	C	189	HIS	2.6
3	D	161	ALA	2.6
11	L	65	TYR	2.6
14	O	70	LYS	2.6
19	T	50	PHE	2.6
16	Q	60	ILE	2.6
1	A	28	A	2.6
6	G	41	ILE	2.6
14	O	9	LYS	2.6
3	D	102	TYR	2.6
2	C	157	GLY	2.6
11	L	99	GLY	2.6
5	F	3	HIS	2.6
9	J	24	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
14	O	29	ALA	2.6
8	I	76	GLY	2.6
5	F	88	MET	2.6
14	O	16	ARG	2.6
11	L	78	VAL	2.6
19	T	76	ALA	2.6
13	N	94	GLY	2.6
1	A	973	G	2.6
9	J	25	ILE	2.6
10	K	56	LYS	2.6
4	E	20	VAL	2.6
5	F	8	PHE	2.6
12	M	21	ILE	2.6
21	U	6	ARG	2.6
19	T	10	ALA	2.6
4	E	61	LYS	2.5
5	F	66	ALA	2.5
12	M	85	TYR	2.5
3	D	199	ILE	2.5
6	G	104	VAL	2.5
9	J	20	GLN	2.5
15	P	20	VAL	2.5
7	H	82	LEU	2.5
3	D	50	TYR	2.5
20	B	220	VAL	2.5
13	N	49	THR	2.5
14	O	46	LYS	2.5
15	P	17	TYR	2.5
20	B	130	LYS	2.5
14	O	42	PHE	2.5
13	N	100	TRP	2.5
1	A	974	A	2.5
12	M	48	SER	2.5
20	B	107	ARG	2.5
4	E	50	GLY	2.5
14	O	79	ARG	2.5
3	D	40	HIS	2.5
10	K	57	SER	2.5
11	L	16	ALA	2.5
15	P	21	VAL	2.5
17	R	20	ILE	2.5
18	S	39	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
5	F	20	GLY	2.5
11	L	115	LYS	2.5
14	O	66	LEU	2.5
21	U	10	PRO	2.5
14	O	75	ALA	2.5
5	F	74	LEU	2.5
11	L	44	PRO	2.5
3	D	107	GLY	2.5
15	P	37	GLY	2.5
3	D	105	GLY	2.5
2	C	146	LYS	2.5
20	B	205	ALA	2.5
10	K	61	ALA	2.5
12	M	91	ARG	2.5
6	G	35	LYS	2.5
8	I	116	GLY	2.5
8	I	15	ALA	2.5
9	J	97	ASP	2.4
20	B	126	ASP	2.4
20	B	139	GLU	2.4
6	G	130	LYS	2.4
10	K	17	ASP	2.4
2	C	46	LEU	2.4
10	K	108	ASN	2.4
18	S	65	MET	2.4
19	T	41	GLY	2.4
6	G	122	GLU	2.4
7	H	45	ILE	2.4
19	T	58	ASP	2.4
3	D	198	LEU	2.4
4	E	25	LYS	2.4
5	F	90	MET	2.4
3	D	72	ARG	2.4
17	R	43	ILE	2.4
19	T	66	ILE	2.4
11	L	10	PRO	2.4
9	J	60	ASP	2.4
8	I	103	VAL	2.4
2	C	141	MET	2.4
6	G	109	LYS	2.4
6	G	26	VAL	2.4
7	H	123	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
11	L	32	VAL	2.4
15	P	64	GLY	2.4
19	T	54	GLN	2.4
4	E	69	ASN	2.4
16	Q	61	ARG	2.4
1	A	1493	A	2.4
3	D	152	SER	2.4
10	K	105	ARG	2.4
4	E	43	GLY	2.4
3	D	158	LEU	2.4
21	U	12	ASP	2.4
12	M	33	LEU	2.4
13	N	74	ARG	2.4
18	S	73	PHE	2.4
3	D	42	ALA	2.4
8	I	124	PRO	2.4
19	T	34	VAL	2.4
3	D	166	LYS	2.4
15	P	51	ARG	2.3
6	G	83	THR	2.3
2	C	196	GLY	2.3
3	D	67	LEU	2.3
3	D	203	TYR	2.3
14	O	31	LEU	2.3
2	C	135	ARG	2.3
4	E	141	ASP	2.3
5	F	83	ALA	2.3
15	P	58	ALA	2.3
10	K	33	ILE	2.3
12	M	63	VAL	2.3
4	E	138	ALA	2.3
5	F	61	LEU	2.3
6	G	28	ILE	2.3
1	A	436	C	2.3
9	J	62	ARG	2.3
14	O	61	GLN	2.3
16	Q	36	PHE	2.3
10	K	25	SER	2.3
15	P	10	GLY	2.3
6	G	121	ASN	2.3
1	A	185	U	2.3
9	J	22	THR	2.3

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Mol	Chain	Res	Type	RSRZ
19	T	57	VAL	2.3
11	L	91	GLY	2.3
13	N	88	MET	2.3
5	F	6	ILE	2.3
12	M	77	LYS	2.3
15	P	50	THR	2.3
16	Q	33	TYR	2.2
2	C	143	LEU	2.2
4	E	22	LYS	2.2
12	M	82	LEU	2.2
15	P	75	ILE	2.2
12	M	111	PRO	2.2
1	A	363	A	2.2
9	J	32	THR	2.2
10	K	112	VAL	2.2
6	G	39	GLU	2.2
7	H	87	ARG	2.2
9	J	82	LYS	2.2
10	K	76	TYR	2.2
11	L	35	ARG	2.2
11	L	53	ARG	2.2
15	P	33	ILE	2.2
4	E	84	VAL	2.2
5	F	51	ILE	2.2
7	H	81	GLY	2.2
2	C	154	GLY	2.2
8	I	89	TYR	2.2
2	C	14	VAL	2.2
2	C	44	LYS	2.2
5	F	5	GLU	2.2
5	F	56	LYS	2.2
3	D	124	VAL	2.2
11	L	41	PRO	2.2
9	J	72	ARG	2.2
20	B	42	LEU	2.2
1	A	1349	A	2.2
15	P	38	PHE	2.2
11	L	100	ALA	2.2
16	Q	3	LYS	2.2
6	G	92	PRO	2.2
17	R	66	LEU	2.2
20	B	198	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
4	E	86	GLY	2.2
1	A	1533	C	2.2
6	G	17	PHE	2.2
12	M	35	ALA	2.2
12	M	60	ALA	2.2
10	K	70	ALA	2.2
6	G	115	MET	2.2
10	K	64	VAL	2.2
3	D	2	ARG	2.2
1	A	442	G	2.2
18	S	41	PRO	2.2
5	F	85	ILE	2.2
3	D	159	GLU	2.2
4	E	33	THR	2.2
18	S	17	LYS	2.2
12	M	53	ASP	2.2
16	Q	10	ARG	2.2
15	P	11	ALA	2.2
1	A	225	C	2.1
21	U	4	LYS	2.1
5	F	60	VAL	2.1
11	L	102	ASP	2.1
1	A	224	U	2.1
1	A	975	A	2.1
16	Q	25	GLU	2.1
12	M	29	SER	2.1
10	K	102	ALA	2.1
13	N	22	LYS	2.1
4	E	68	ARG	2.1
2	C	41	TYR	2.1
8	I	126	PHE	2.1
2	C	40	GLN	2.1
2	C	153	SER	2.1
4	E	91	SER	2.1
14	O	40	GLY	2.1
4	E	41	GLY	2.1
5	F	94	HIS	2.1
20	B	114	LYS	2.1
20	B	132	GLU	2.1
2	C	122	GLN	2.1
3	D	52	VAL	2.1
13	N	87	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
16	Q	8	GLN	2.1
10	K	77	GLY	2.1
1	A	1201	A	2.1
2	C	22	PHE	2.1
1	A	449	G	2.1
2	C	188	ALA	2.1
8	I	91	GLU	2.1
17	R	64	LEU	2.1
14	O	28	VAL	2.1
18	S	66	VAL	2.1
2	C	179	ALA	2.1
6	G	4	ARG	2.1
19	T	30	PHE	2.1
8	I	112	ARG	2.1
12	M	49	GLU	2.1
14	O	82	GLU	2.1
21	U	50	SER	2.1
11	L	116	TYR	2.0
10	K	36	ARG	2.0
8	I	114	LYS	2.0
14	O	57	ARG	2.0
15	P	7	ALA	2.0
2	C	108	PRO	2.0
21	U	32	ARG	2.0
6	G	82	SER	2.0
17	R	49	LYS	2.0
10	K	88	PRO	2.0
11	L	92	VAL	2.0
14	O	54	GLY	2.0
9	J	14	ASP	2.0
20	B	138	ARG	2.0
3	D	171	GLU	2.0
13	N	86	ALA	2.0
9	J	38	GLY	2.0
10	K	29	THR	2.0
6	G	13	PRO	2.0
6	G	76	SER	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
22	MG	A	2168	1/1	0.41	15.71	50,50,50,50	1
22	MG	A	2346	1/1	0.21	10.87	106,106,106,106	0
22	MG	A	2042	1/1	0.22	3.08	93,93,93,93	0
22	MG	A	2360	1/1	0.29	2.97	80,80,80,80	0
22	MG	A	2182	1/1	0.20	2.29	23,23,23,23	1
22	MG	A	2236	1/1	0.26	1.75	128,128,128,128	0
22	MG	A	2062	1/1	0.69	1.63	132,132,132,132	0
22	MG	A	2196	1/1	0.25	1.43	28,28,28,28	0
22	MG	A	2283	1/1	0.19	1.35	121,121,121,121	0
22	MG	A	2302	1/1	0.29	1.01	8,8,8,8	0
22	MG	A	2049	1/1	0.24	0.87	67,67,67,67	0
22	MG	A	2023	1/1	0.19	0.84	24,24,24,24	0
22	MG	A	2121	1/1	0.15	0.79	125,125,125,125	0
22	MG	A	2324	1/1	0.14	0.68	104,104,104,104	0
22	MG	A	2148	1/1	0.29	0.53	50,50,50,50	0
22	MG	A	2340	1/1	0.14	0.31	99,99,99,99	0
22	MG	A	2245	1/1	0.20	0.26	48,48,48,48	0
22	MG	A	2273	1/1	0.27	0.13	48,48,48,48	0
22	MG	A	2213	1/1	0.22	-0.02	6,6,6,6	0
22	MG	A	2366	1/1	0.27	-0.03	23,23,23,23	0
22	MG	A	2068	1/1	0.19	-0.07	93,93,93,93	0
23	HYG	A	3001	36/36	0.20	-0.10	45,45,45,45	0
22	MG	A	2334	1/1	0.18	-0.14	5,5,5,5	0
22	MG	A	2056	1/1	0.17	-0.24	33,33,33,33	0
22	MG	E	2155	1/1	0.24	-0.28	127,127,127,127	0
22	MG	A	2036	1/1	0.07	-0.72	46,46,46,46	0
22	MG	A	2141	1/1	0.21	-0.77	29,29,29,29	0
22	MG	A	2097	1/1	0.19	-0.77	5,5,5,5	0
22	MG	A	2084	1/1	0.13	-0.81	149,149,149,149	0
22	MG	A	2261	1/1	0.09	-0.84	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
22	MG	A	2091	1/1	0.07	-0.88	53,53,53,53	0
22	MG	A	2107	1/1	0.10	-0.88	73,73,73,73	0
22	MG	A	2114	1/1	0.06	-0.97	73,73,73,73	0
22	MG	A	2295	1/1	0.05	-1.05	74,74,74,74	0
22	MG	A	2202	1/1	0.12	-1.10	33,33,33,33	0
22	MG	A	2225	1/1	0.08	-1.31	101,101,101,101	0
22	MG	A	2256	1/1	0.09	-1.32	58,58,58,58	0
22	MG	A	2231	1/1	0.09	-1.33	94,94,94,94	0
22	MG	A	2330	1/1	0.11	-1.37	11,11,11,11	0
22	MG	A	2208	1/1	0.10	-1.43	56,56,56,56	0
22	MG	A	2250	1/1	0.07	-1.54	46,46,46,46	0
22	MG	A	2077	1/1	0.08	-1.64	47,47,47,47	0
22	MG	A	2007	1/1	0.07	-1.68	5,5,5,5	0
22	MG	A	2353	1/1	0.10	-1.80	94,94,94,94	0
22	MG	A	2319	1/1	0.07	-1.85	30,30,30,30	0
22	MG	A	2011	1/1	0.05	-2.12	35,35,35,35	0
22	MG	A	2101	1/1	0.09	-2.15	6,6,6,6	0
22	MG	A	2306	1/1	0.08	-2.19	39,39,39,39	0
22	MG	A	2073	1/1	0.08	-2.22	73,73,73,73	0
22	MG	A	2267	1/1	0.10	-2.33	59,59,59,59	0
22	MG	A	2016	1/1	0.08	-2.38	8,8,8,8	0
22	MG	A	2218	1/1	0.09	-2.57	89,89,89,89	0
22	MG	A	2189	1/1	0.13	-2.60	7,7,7,7	0
22	MG	A	2175	1/1	0.12	-2.78	75,75,75,75	0
22	MG	A	2288	1/1	0.05	-3.10	58,58,58,58	0
22	MG	A	2278	1/1	0.08	-3.53	57,57,57,57	0
22	MG	A	2001	1/1	0.06	-3.85	5,5,5,5	0
22	MG	A	2029	1/1	0.07	-4.31	95,95,95,95	0
22	MG	A	2128	1/1	0.09	-5.62	63,63,63,63	0
22	MG	A	2239	1/1	0.04	-5.69	16,16,16,16	0
22	MG	A	2312	1/1	0.20	-	73,73,73,73	0
22	MG	A	2161	1/1	0.38	-	26,26,26,26	1
22	MG	A	2134	1/1	0.13	-	137,137,137,137	0

6.5 Other polymers ⓘ

There are no such residues in this entry.