



Full wwPDB X-ray Structure Validation Report

Sep 15, 2014 – 11:17 AM EDT

PDB ID : 1VVL
Title : Crystal Structure of Frameshift Suppressor tRNA SufA6 Bound to Codon CCC-U on the Ribosome
Authors : Maehigashi, T.; Dunkle, J.A.; Dunham, C.M.
Deposited on : 2013-06-07
Resolution : 3.22 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>

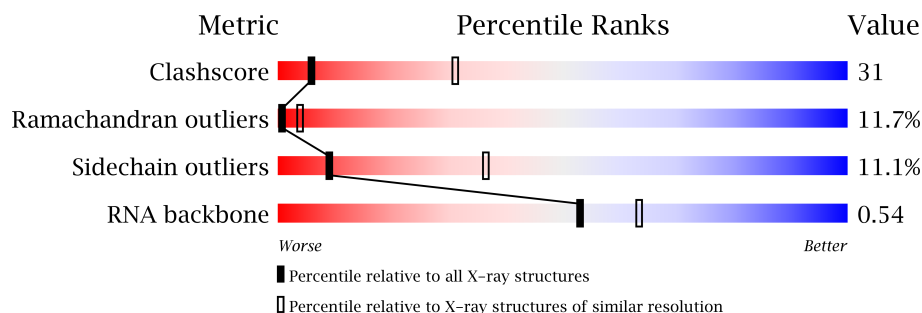
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23489

1 Overall quality at a glance

The reported resolution of this entry is 3.22 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1072 (3.28-3.16)
Ramachandran outliers	78287	1052 (3.28-3.16)
Sidechain outliers	78261	1051 (3.28-3.16)
RNA backbone	1838	1004 (3.74-2.70)





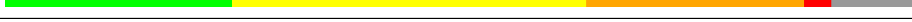

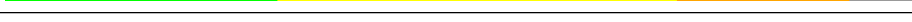

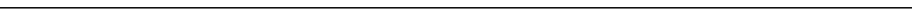

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	1522	
2	B	256	
3	C	239	
4	D	209	
5	E	162	
6	F	101	
7	G	156	
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	132	
13	M	126	
14	N	61	

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Mol	Chain	Length	Quality of chain
15	O	89	
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	U	27	
22	V	77	
23	X	25	
24	Y	18	

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 53707 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 rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1500	Total	C	N	O	P	0	0	0
			32247	14353	5981	10414	1499			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	237	Total	C	N	O	S	0	0	0
			1924	1228	344	347	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	205	Total	C	N	O	S	0	0	0
			1605	1011	313	280	1			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	151	Total	C	N	O	S	0	0	0
			1155	729	218	204	4			

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	99	Total	C	N	O	S	0	0	0
			801	504	157	139	1			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	125	Total	C	N	O	S	0	0	0
			975	614	196	164	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	121	Total	C	N	O	S	0	0	0
			964	597	199	166	2			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	84	Total	C	N	O	S	0	0	0
			705	446	140	118	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	100	Total	C	N	O	S	0	0	0
			834	534	155	143	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	70	Total	C	N	O	0	0	0
			574	367	112	95			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	84	Total	C	N	O	S	0	0	0
			674	430	126	116	2			

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	U	25	Total	C	N	O	0	0	0
			217	134	52	31			

- Molecule 22 is a RNA chain called P-site tRNA fMet.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	V	77	Total	C	N	O	P	0	0	0
			1644	732	297	538	77			

- Molecule 23 is a RNA chain called A-site ASL SufA6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	X	8	Total	C	N	O	P	0	0	0
			167	75	28	56	8			

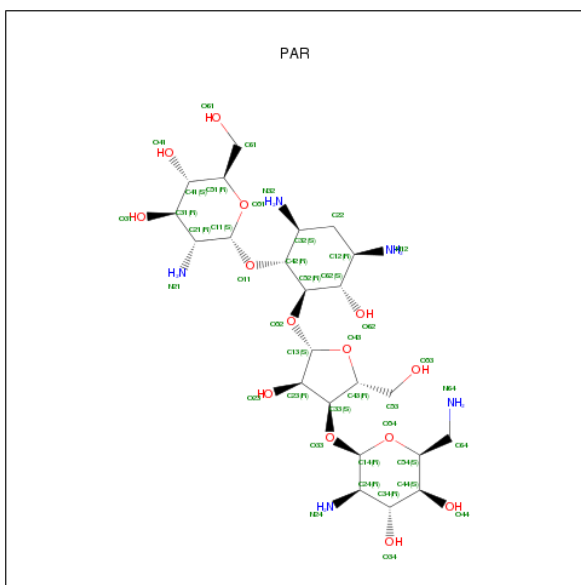
- Molecule 24 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	Y	14	Total	C	N	O	P	0	0	0
			303	135	55	99	14			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	H	1	Total	Mg	0	0
			1	1		
25	A	66	Total	Mg	0	0
			66	66		
25	V	2	Total	Mg	0	0
			2	2		
25	F	1	Total	Mg	0	0
			1	1		
25	M	1	Total	Mg	0	0
			1	1		

- Molecule 26 is PAROMOMYCIN (three-letter code: PAR) (formula: C₂₃H₄₅N₅O₁₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
26	A	1	Total	C	N	O	0	0
			42	23	5	14		

- Molecule 27 is ZINC ION (three-letter code: ZN) (formula: Zn).

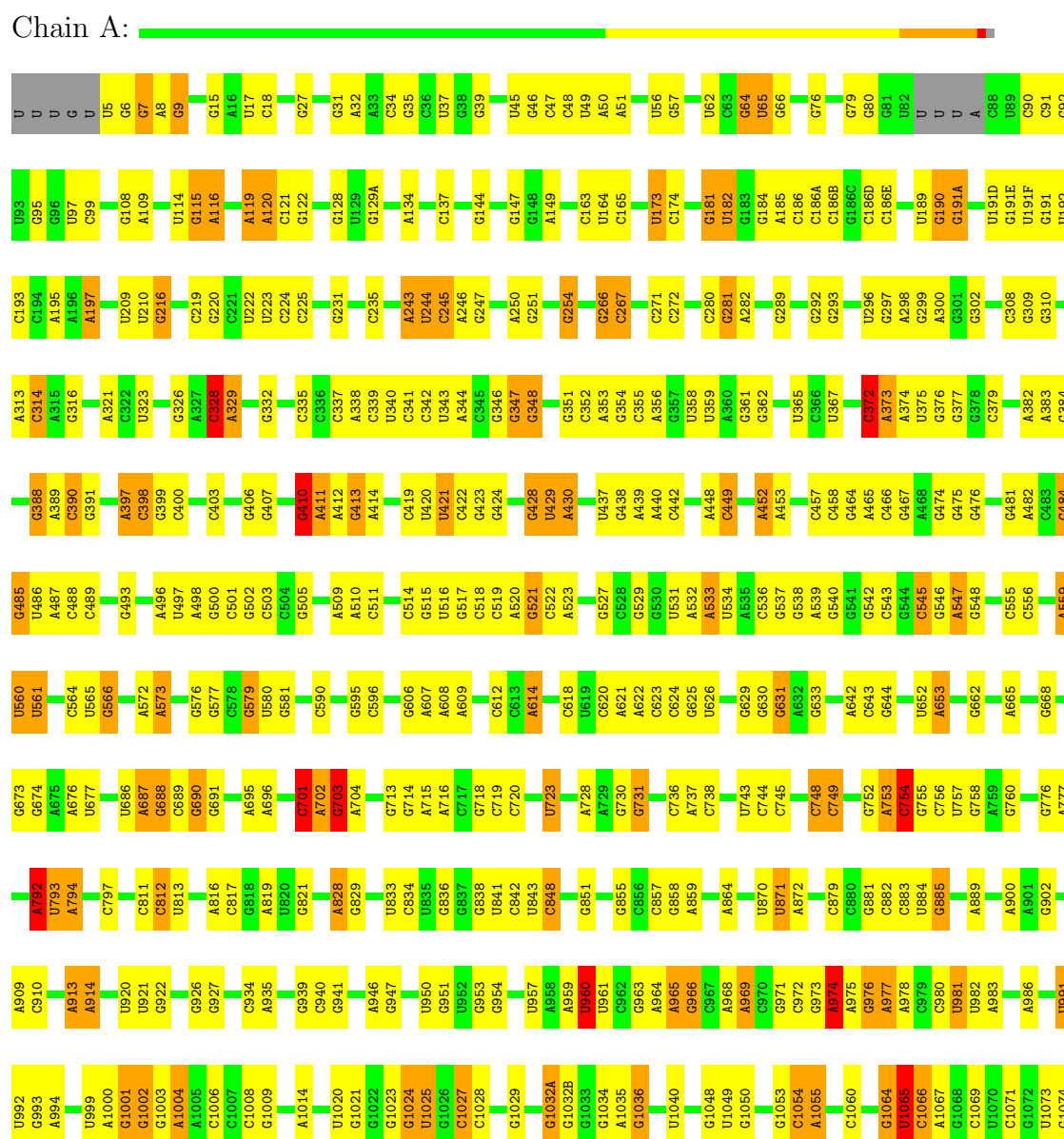
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
27	D	1	Total Zn 1 1	0	0
27	N	1	Total Zn 1 1	0	0

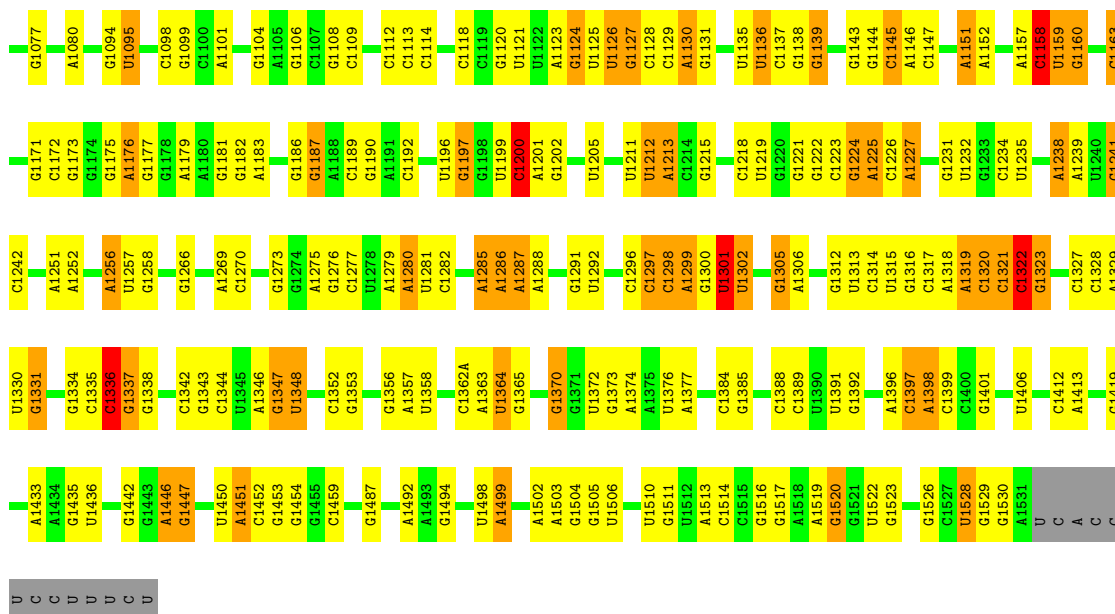
3 Residue-property plots

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.

Note EDS was not executed.

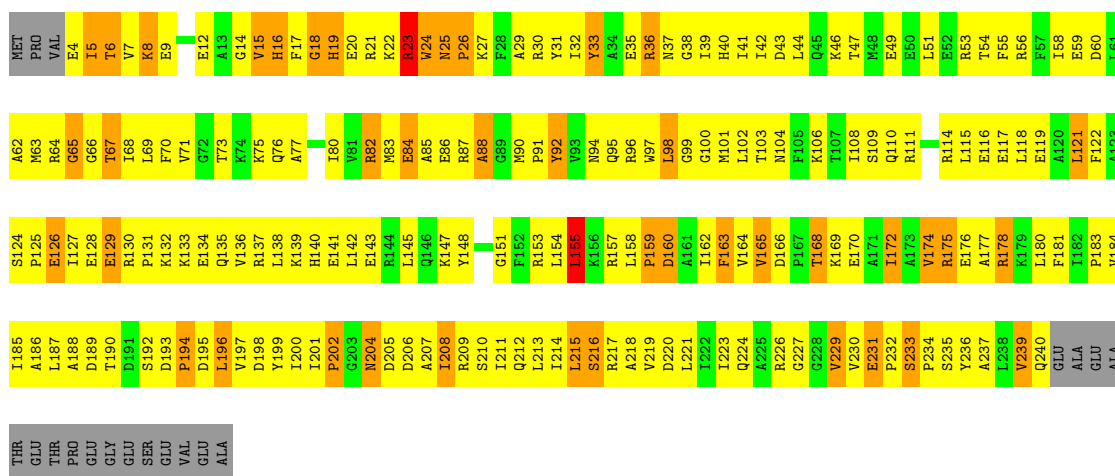
• Molecule 1: 16S rRNA





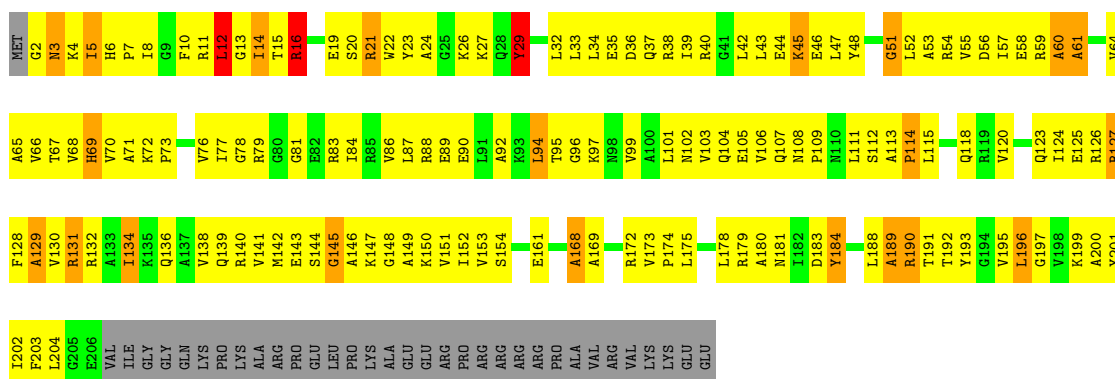
- Molecule 2: 30S ribosomal protein S2

Chain B:



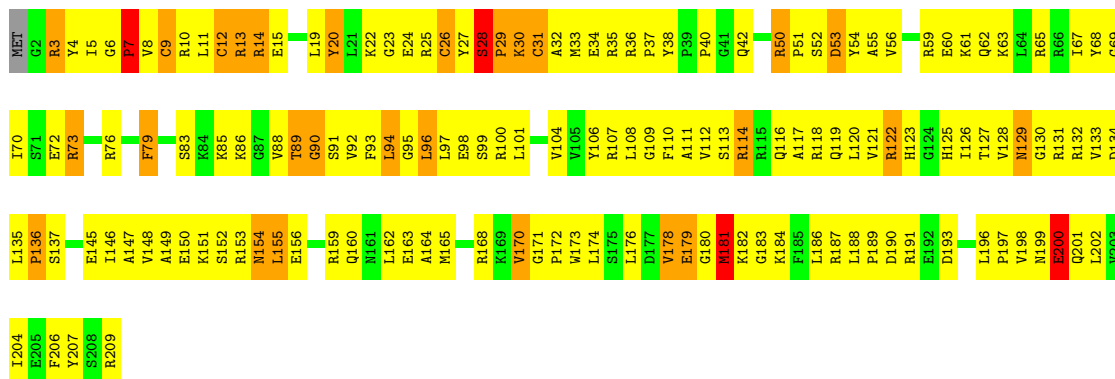
- Molecule 3: 30S ribosomal protein S3

Chain C:



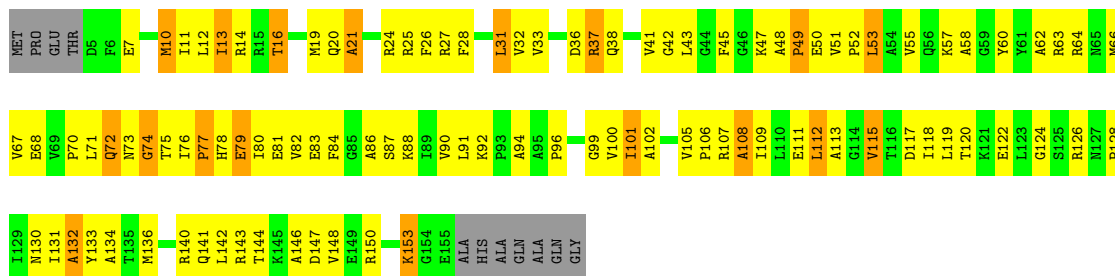
- Molecule 4: 30S ribosomal protein S4

Chain D:



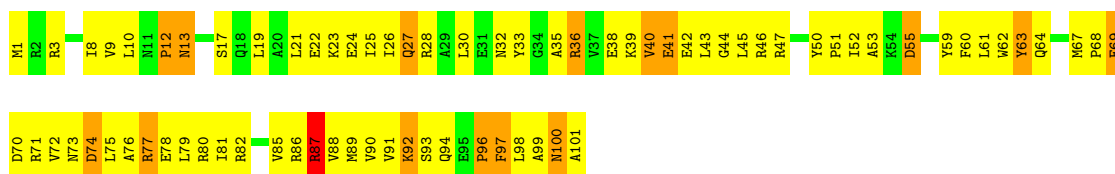
- Molecule 5: 30S ribosomal protein S5

Chain E:



- Molecule 6: 30S ribosomal protein S6

Chain F:



- Molecule 7: 30S ribosomal protein S7

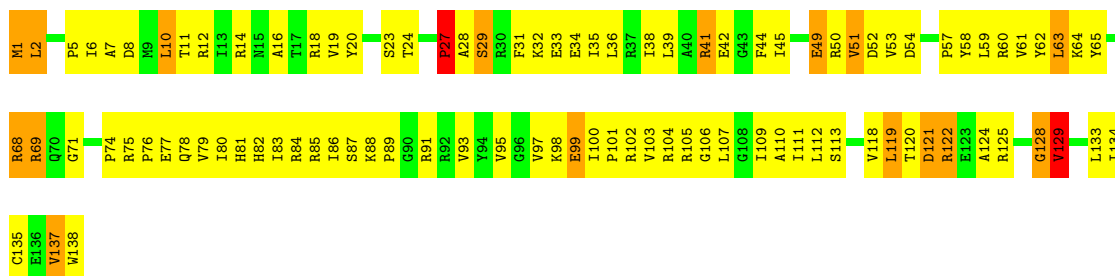
Chain G:



- Molecule 8: 30S ribosomal protein S8

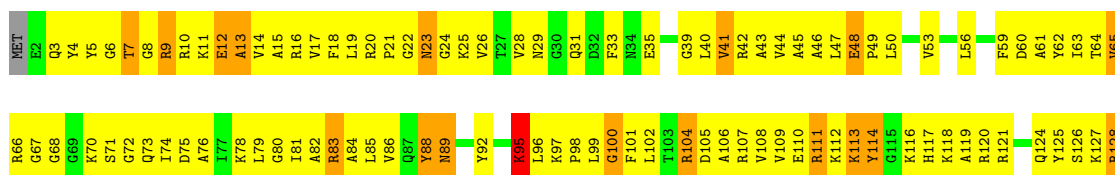
Chain H:





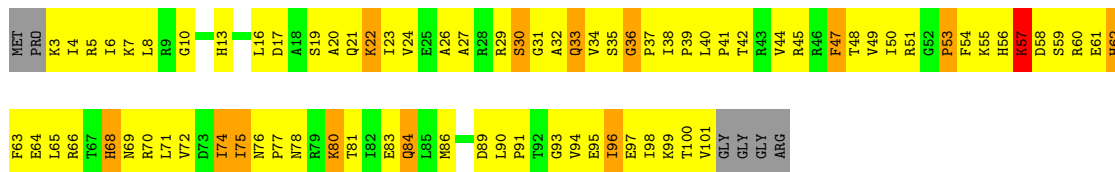
• Molecule 9: 30S ribosomal protein S9

Chain I:



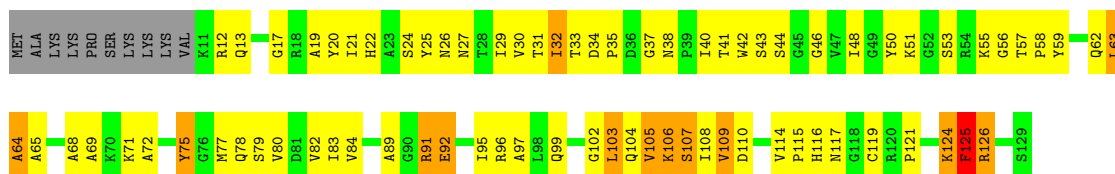
• Molecule 10: 30S ribosomal protein S10

Chain J:



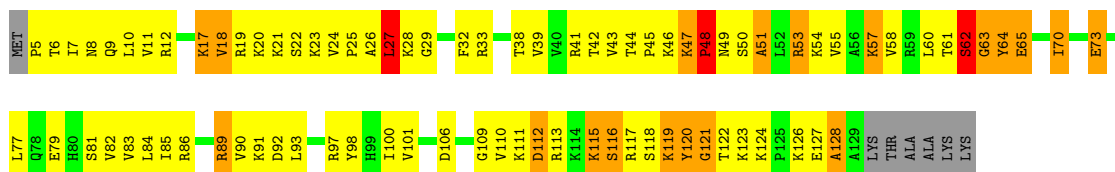
• Molecule 11: 30S ribosomal protein S11

Chain K:



• Molecule 12: 30S ribosomal protein S12

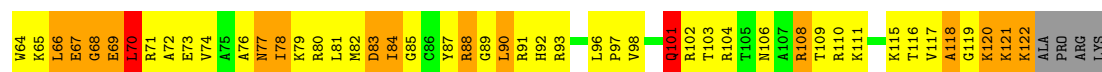
Chain L:



• Molecule 13: 30S ribosomal protein S13

Chain M:





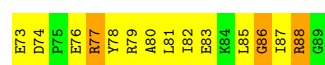
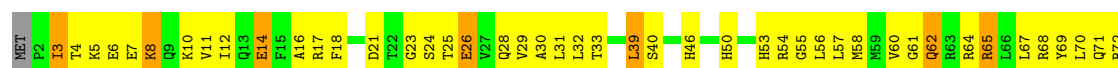
- Molecule 14: 30S ribosomal protein S14

Chain N:



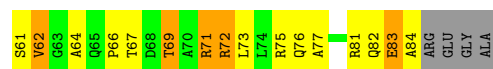
- Molecule 15: 30S ribosomal protein S15

Chain O:



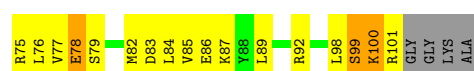
- Molecule 16: 30S ribosomal protein S16

Chain P:



- Molecule 17: 30S ribosomal protein S17

Chain Q:



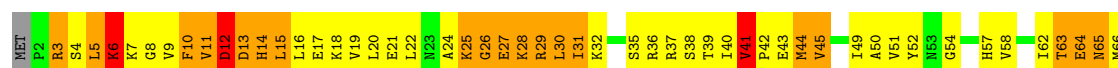
- Molecule 18: 30S ribosomal protein S18

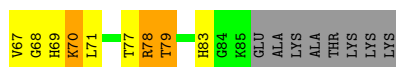
Chain R:



- Molecule 19: 30S ribosomal protein S19

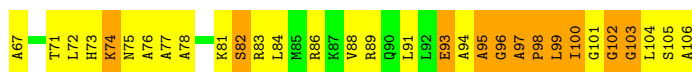
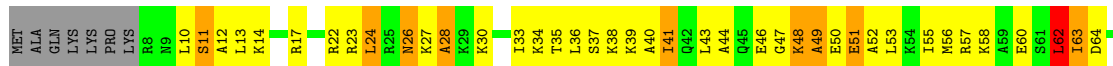
Chain S:





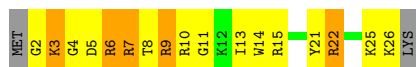
- Molecule 20: 30S ribosomal protein S20

Chain T:



- Molecule 21: 30S ribosomal protein S21

Chain U:



- Molecule 22: P-site tRNA fMet

Chain V:



- Molecule 23: A-site ASL SufA6

Chain X:



- Molecule 24: messenger RNA

Chain Y:



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.20Å 450.23Å 621.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.97 – 3.22	Depositor
% Data completeness (in resolution range)	98.5 (34.97-3.22)	Depositor
R_{merge}	0.25	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PHENIX	Depositor
R, R_{free}	0.229 , 0.260	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	53707	wwPDB-VP
Average B, all atoms (Å ²)	106.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, PAR, 1MG

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	0.31	0/36098	0.86	46/56341 (0.1%)
2	B	0.35	0/1959	0.65	0/2642
3	C	0.36	0/1629	0.60	0/2195
4	D	0.41	0/1733	0.68	1/2318 (0.0%)
5	E	0.38	0/1171	0.66	0/1576
6	F	0.43	0/856	0.68	0/1154
7	G	0.37	0/1276	0.60	0/1709
8	H	0.40	0/1136	0.69	0/1527
9	I	0.36	0/1029	0.67	0/1379
10	J	0.35	0/814	0.61	0/1095
11	K	0.40	0/900	0.67	0/1213
12	L	0.45	0/991	1.00	4/1327 (0.3%)
13	M	0.34	0/974	0.66	0/1303
14	N	0.42	0/501	0.68	0/664
15	O	0.39	0/745	0.67	0/992
16	P	0.36	0/721	0.67	0/970
17	Q	0.37	0/847	0.68	0/1131
18	R	0.39	0/579	0.72	0/768
19	S	0.36	0/689	0.84	2/926 (0.2%)
20	T	0.33	0/765	0.69	0/1007
21	U	0.37	0/221	0.63	0/288
22	V	0.52	0/1836	0.99	5/2859 (0.2%)
23	X	0.39	0/185	0.72	0/285
24	Y	0.52	0/311	0.88	0/483
All	All	0.34	0/57966	0.82	58/86152 (0.1%)

There are no bond length outliers.

All (58) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	47	LYS	C-N-CD	-20.48	75.56	120.60
22	V	17	C	C2-N1-C1'	11.77	131.75	118.80
1	A	1322	C	C2-N1-C1'	9.46	129.20	118.80
12	L	47	LYS	C-N-CA	8.81	159.00	122.00
22	V	17	C	C6-N1-C1'	-8.74	110.32	120.80
1	A	960	U	N3-C2-O2	-8.65	116.15	122.20
1	A	372	C	C2-N1-C1'	8.63	128.29	118.80
1	A	1301	U	C2-N1-C1'	8.12	127.44	117.70
1	A	1158	C	C2-N1-C1'	7.96	127.56	118.80
1	A	960	U	N1-C2-O2	7.82	128.28	122.80
1	A	1322	C	N1-C2-O2	7.43	123.36	118.90
1	A	1301	U	N1-C2-O2	7.43	128.00	122.80
1	A	1322	C	C6-N1-C1'	-7.36	111.97	120.80
22	V	17	C	N1-C2-O2	7.12	123.17	118.90
1	A	1158	C	N1-C2-O2	6.99	123.09	118.90
1	A	372	C	N1-C2-O2	6.86	123.02	118.90
1	A	1301	U	N3-C2-O2	-6.64	117.55	122.20
1	A	372	C	C6-N1-C1'	-6.51	112.98	120.80
12	L	48	PRO	CA-N-CD	-6.41	102.52	111.50
1	A	328	C	N1-C2-O2	6.34	122.71	118.90
4	D	28	SER	C-N-CD	6.27	141.57	128.40
1	A	792	A	P-O3'-C3'	6.23	127.18	119.70
1	A	1158	C	C6-N1-C2	-6.18	117.83	120.30
1	A	328	C	C2-N1-C1'	5.95	125.34	118.80
22	V	17	C	C6-N1-C2	-5.92	117.93	120.30
1	A	372	C	C5-C6-N1	5.88	123.94	121.00
1	A	254	G	O5'-P-OP1	-5.87	100.42	105.70
1	A	690	G	O4'-C1'-N9	5.87	112.89	108.20
1	A	410	G	P-O3'-C3'	5.86	126.73	119.70
12	L	119	LYS	N-CA-C	-5.85	95.21	111.00
1	A	1322	C	C5-C6-N1	5.79	123.89	121.00
1	A	812	C	P-O3'-C3'	5.77	126.62	119.70
1	A	1065	U	P-O3'-C3'	5.74	126.59	119.70
19	S	6	LYS	N-CA-C	-5.67	95.70	111.00
1	A	701	C	P-O3'-C3'	5.61	126.43	119.70
1	A	1301	U	C6-N1-C1'	-5.60	113.36	121.20
1	A	1200	C	P-O3'-C3'	5.59	126.41	119.70
22	V	17	C	C5-C6-N1	5.50	123.75	121.00
1	A	1336	C	C2-N1-C1'	5.49	124.84	118.80
1	A	723	U	C2-N1-C1'	5.48	124.28	117.70
1	A	687	A	P-O3'-C3'	5.48	126.27	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1151	A	O4'-C1'-N9	5.48	112.58	108.20
1	A	1158	C	N3-C2-O2	-5.47	118.07	121.90
1	A	1200	C	OP2-P-O3'	5.47	117.23	105.20
1	A	328	C	N3-C2-O2	-5.40	118.12	121.90
1	A	974	A	O4'-C1'-N9	5.30	112.44	108.20
1	A	449	C	C6-N1-C2	-5.25	118.20	120.30
1	A	1528	U	P-O3'-C3'	5.22	125.96	119.70
1	A	533	A	P-O3'-C3'	5.20	125.93	119.70
1	A	1336	C	C6-N1-C2	-5.19	118.22	120.30
1	A	1065	U	OP2-P-O3'	5.18	116.60	105.20
1	A	1158	C	C6-N1-C1'	-5.18	114.58	120.80
1	A	328	C	P-O3'-C3'	5.17	125.90	119.70
19	S	79	THR	N-CA-C	-5.16	97.06	111.00
1	A	913	A	P-O3'-C3'	5.15	125.88	119.70
1	A	1027	C	OP1-P-O3'	5.06	116.33	105.20
1	A	703	G	P-O3'-C3'	5.02	125.72	119.70
1	A	754	C	C2-N1-C1'	5.01	124.31	118.80

There are no chirality outliers.

There are no planarity outliers.

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	32247	0	16278	483	0
2	B	1924	0	1975	287	0
3	C	1605	0	1668	207	0
4	D	1703	0	1764	240	0
5	E	1155	0	1213	136	0
6	F	843	0	857	94	0
7	G	1257	0	1296	145	0
8	H	1116	0	1175	140	0
9	I	1010	0	1037	141	0
10	J	801	0	849	148	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	K	885	0	904	100	0
12	L	975	0	1062	104	0
13	M	964	0	1034	151	0
14	N	492	0	530	98	0
15	O	734	0	771	75	0
16	P	705	0	725	112	0
17	Q	834	0	904	83	0
18	R	574	0	644	66	0
19	S	674	0	699	103	0
20	T	763	0	860	105	0
21	U	217	0	234	26	0
22	V	1644	0	836	23	0
23	X	167	0	87	12	0
24	Y	303	0	154	11	0
25	A	66	0	0	0	0
25	F	1	0	0	0	0
25	H	1	0	0	0	0
25	M	1	0	0	0	0
25	V	2	0	0	0	0
26	A	42	0	45	1	0
27	D	1	0	0	0	0
27	N	1	0	0	0	0
All	All	53707	0	37601	2831	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 31.

All (2831) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:49:VAL:HG21	14:N:41:ARG:CB	1.49	1.42
10:J:49:VAL:CG2	14:N:41:ARG:CB	2.04	1.36
4:D:22:LYS:HG3	4:D:26:CYS:SG	1.70	1.31
10:J:49:VAL:CG2	14:N:41:ARG:HB2	1.62	1.29
14:N:25:VAL:HG23	14:N:38:GLY:O	1.37	1.25
2:B:101:MET:HA	2:B:108:ILE:HG13	1.25	1.17
10:J:49:VAL:CG2	14:N:41:ARG:HB3	1.71	1.14
19:S:41:VAL:HB	19:S:42:PRO:HA	1.26	1.14
10:J:6:ILE:HG22	10:J:98:ILE:HG13	1.30	1.13
4:D:12:CYS:HA	4:D:19:LEU:HD21	1.24	1.12
4:D:22:LYS:CG	4:D:26:CYS:SG	2.38	1.10
3:C:15:THR:HG23	3:C:181:ASN:HA	1.35	1.08
11:K:79:SER:HB2	11:K:106:LYS:HD2	1.35	1.08

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:49:VAL:HG21	14:N:41:ARG:HB3	1.24	1.07
15:O:87:ILE:HG22	15:O:88:ARG:H	1.18	1.07
10:J:49:VAL:CG1	14:N:41:ARG:HD2	1.85	1.06
11:K:51:LYS:HA	11:K:55:LYS:HD3	1.36	1.05
13:M:88:ARG:HB3	13:M:88:ARG:HH11	1.19	1.05
13:M:49:THR:HG22	13:M:51:ALA:H	1.22	1.05
5:E:11:ILE:HD11	5:E:31:LEU:HD12	1.38	1.05
13:M:3:ARG:HA	13:M:9:ILE:HG21	1.35	1.05
2:B:80:ILE:HD11	2:B:208:ILE:HG23	1.33	1.04
2:B:4:GLU:HG2	2:B:5:ILE:H	1.19	1.04
2:B:18:GLY:H	2:B:42:ILE:HG22	1.21	1.04
10:J:49:VAL:CG1	14:N:41:ARG:HB2	1.88	1.03
4:D:12:CYS:HA	4:D:19:LEU:CD2	1.87	1.03
7:G:78:ARG:HG3	7:G:79:ARG:H	1.24	1.01
19:S:41:VAL:HB	19:S:42:PRO:CA	1.91	1.01
10:J:49:VAL:HG13	14:N:41:ARG:CD	1.90	1.01
8:H:29:SER:HB3	8:H:32:LYS:HG3	1.39	1.00
3:C:95:THR:HG22	3:C:96:GLY:H	1.27	0.99
8:H:84:ARG:HH12	8:H:86:ILE:HD13	1.28	0.99
8:H:23:SER:HA	8:H:63:LEU:HD22	1.45	0.99
10:J:6:ILE:HD11	10:J:72:VAL:HB	1.44	0.99
3:C:181:ASN:HD21	3:C:204:LEU:HD12	1.27	0.98
2:B:196:LEU:HD12	2:B:197:VAL:HG23	1.45	0.98
4:D:94:LEU:H	4:D:94:LEU:HD12	1.28	0.98
3:C:19:GLU:HA	3:C:54:ARG:HH12	1.29	0.97
3:C:16:ARG:HD2	3:C:54:ARG:HH21	1.28	0.97
4:D:29:PRO:HG2	4:D:30:LYS:CD	1.94	0.97
10:J:49:VAL:HG22	14:N:41:ARG:CB	1.92	0.96
4:D:30:LYS:HG3	4:D:35:ARG:NE	1.80	0.96
2:B:7:VAL:HG21	2:B:217:ARG:HH11	1.30	0.96
2:B:8:LYS:H	2:B:8:LYS:HD3	1.30	0.96
4:D:30:LYS:CB	4:D:35:ARG:HG3	1.96	0.96
7:G:62:PHE:HA	7:G:124:LEU:HD21	1.47	0.95
16:P:4:ILE:HD11	16:P:64:ALA:HB1	1.46	0.95
10:J:75:ILE:HG13	10:J:76:ASN:H	1.31	0.95
1:A:1286:A:H5"	21:U:26:LYS:HD2	1.48	0.95
10:J:32:ALA:HB3	10:J:76:ASN:HB2	1.47	0.95
12:L:6:THR:H	12:L:9:GLN:HE21	1.15	0.95
4:D:28:SER:HB2	4:D:29:PRO:HD3	1.49	0.95
6:F:86:ARG:O	6:F:87:ARG:HG2	1.66	0.94
3:C:16:ARG:HB2	3:C:16:ARG:HH11	1.30	0.94
13:M:90:LEU:HA	13:M:93:ARG:HD2	1.50	0.93

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:15:ASP:HB3	7:G:20:ASP:H	1.31	0.93
13:M:57:ARG:HB2	13:M:57:ARG:HH11	1.32	0.93
19:S:40:ILE:HG12	19:S:41:VAL:HG22	1.51	0.93
20:T:49:ALA:HB1	20:T:99:LEU:HB2	1.51	0.93
5:E:53:LEU:H	5:E:53:LEU:HD12	1.34	0.92
12:L:10:LEU:HD13	17:Q:32:TYR:CE2	2.05	0.92
8:H:6:ILE:HB	8:H:85:ARG:NH1	1.85	0.92
4:D:30:LYS:HB3	4:D:35:ARG:HG3	1.52	0.92
2:B:32:ILE:HD11	2:B:40:HIS:HB3	1.52	0.91
4:D:9:CYS:SG	4:D:31:CYS:O	2.28	0.91
10:J:8:LEU:HD11	10:J:23:ILE:HD12	1.49	0.91
17:Q:4:LYS:HE3	17:Q:6:LEU:HD21	1.51	0.91
6:F:24:GLU:HA	6:F:27:GLN:HG3	1.49	0.91
3:C:11:ARG:HB3	3:C:15:THR:HB	1.48	0.91
3:C:20:SER:HB2	3:C:40:ARG:HH22	1.34	0.91
3:C:70:VAL:HG12	3:C:72:LYS:H	1.34	0.91
8:H:6:ILE:H	8:H:6:ILE:HD12	1.35	0.91
15:O:82:ILE:HD11	15:O:88:ARG:HG3	1.51	0.91
2:B:33:TYR:HB2	2:B:43:ASP:HB2	1.53	0.91
5:E:101:ILE:HD11	5:E:119:LEU:HD23	1.52	0.91
4:D:29:PRO:HG2	4:D:30:LYS:CE	2.01	0.91
2:B:77:ALA:HB2	2:B:211:ILE:HD13	1.53	0.91
4:D:170:VAL:HG22	4:D:171:GLY:H	1.34	0.91
4:D:29:PRO:HG2	4:D:30:LYS:HD3	1.49	0.91
1:A:1223:C:H5''	1:A:1224:G:H5''	1.53	0.91
5:E:100:VAL:HG22	5:E:118:ILE:HG22	1.52	0.90
2:B:7:VAL:HG21	2:B:217:ARG:NH1	1.87	0.89
13:M:121:LYS:NZ	24:Y:40:G:OP1	2.04	0.89
19:S:64:GLU:O	19:S:67:VAL:HG23	1.73	0.89
10:J:74:ILE:H	10:J:74:ILE:HD13	1.38	0.89
5:E:41:VAL:HG11	5:E:113:ALA:HB2	1.54	0.89
2:B:126:GLU:HG3	2:B:129:GLU:HG3	1.54	0.88
2:B:18:GLY:N	2:B:42:ILE:HG22	1.86	0.88
8:H:51:VAL:HG21	8:H:60:ARG:HG2	1.55	0.88
13:M:97:PRO:HB2	13:M:101:GLN:NE2	1.89	0.88
11:K:99:GLN:HG2	11:K:105:VAL:HG21	1.53	0.88
20:T:23:ARG:HA	20:T:26:ASN:HD21	1.36	0.87
19:S:41:VAL:HG13	19:S:44:MET:HB2	1.57	0.87
2:B:96:ARG:H	2:B:96:ARG:HD2	1.38	0.87
1:A:1318:A:H4'	19:S:11:VAL:HG11	1.55	0.87
1:A:1049:U:HO2'	14:N:2:ALA:N	1.73	0.87
21:U:6:ARG:HE	21:U:15:ARG:CZ	1.87	0.87

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:O:56:LEU:O	15:O:60:VAL:HG23	1.75	0.87
19:S:8:GLY:O	19:S:9:VAL:HG22	1.75	0.87
1:A:235:C:H5'	17:Q:70:ARG:HG2	1.57	0.86
23:X:6:C:O2'	23:X:7:U:OP1	1.93	0.86
10:J:47:PHE:HE1	10:J:63:PHE:HB2	1.40	0.86
19:S:27:GLU:O	19:S:28:LYS:HG2	1.74	0.86
1:A:1123:A:H4'	10:J:36:GLY:HA3	1.58	0.86
5:E:71:LEU:O	5:E:72:GLN:HG3	1.73	0.86
2:B:67:THR:HG21	2:B:155:LEU:HD21	1.57	0.86
11:K:32:ILE:HD12	11:K:72:ALA:HB2	1.56	0.86
4:D:114:ARG:HG3	4:D:114:ARG:HH11	1.39	0.86
10:J:49:VAL:HG13	14:N:41:ARG:HD2	0.94	0.86
23:X:2:U:O2'	23:X:3:G:H5'	1.74	0.86
13:M:14:ARG:H	13:M:44:ARG:HD3	1.41	0.86
13:M:4:ILE:H	13:M:9:ILE:CG2	1.88	0.86
4:D:22:LYS:CB	4:D:26:CYS:SG	2.64	0.85
1:A:559:A:H4'	1:A:560:U:H3'	1.58	0.85
20:T:36:LEU:HD13	20:T:39:LYS:HD3	1.57	0.85
24:Y:29:U:H2'	24:Y:30:C:C6	2.11	0.84
10:J:49:VAL:HG21	14:N:41:ARG:HB2	1.23	0.84
1:A:954:G:H4'	13:M:121:LYS:HG3	1.60	0.84
10:J:7:LYS:HB2	10:J:97:GLU:HB2	1.57	0.84
10:J:49:VAL:CB	14:N:41:ARG:HB2	2.08	0.84
14:N:23:ARG:O	14:N:24:CYS:O	1.95	0.84
15:O:82:ILE:HD11	15:O:88:ARG:CG	2.07	0.84
7:G:44:TYR:HA	7:G:47:CYS:SG	2.17	0.84
14:N:21:TYR:HE2	14:N:23:ARG:HH21	1.24	0.84
4:D:22:LYS:HB2	4:D:26:CYS:SG	2.18	0.84
5:E:81:GLU:HB3	5:E:90:VAL:HG22	1.60	0.84
17:Q:59:ILE:HG22	17:Q:73:VAL:HA	1.60	0.84
14:N:8:GLU:OE2	14:N:11:LYS:HD2	1.78	0.84
4:D:25:ARG:NH1	4:D:30:LYS:HE3	1.93	0.83
4:D:96:LEU:HD22	4:D:96:LEU:H	1.43	0.83
5:E:51:VAL:HB	5:E:52:PRO:HD3	1.59	0.83
13:M:23:TYR:HB3	13:M:67:GLU:HG2	1.60	0.83
10:J:37:PRO:HA	10:J:72:VAL:HG22	1.59	0.83
19:S:50:ALA:HB1	19:S:57:HIS:HB3	1.60	0.83
15:O:3:ILE:HD13	15:O:3:ILE:H	1.40	0.83
12:L:8:ASN:OD1	17:Q:34:LYS:HE2	1.77	0.83
12:L:38:THR:HG23	12:L:39:VAL:HG23	1.60	0.83
14:N:12:ARG:C	14:N:14:PRO:HD2	1.98	0.83
2:B:193:ASP:OD2	2:B:196:LEU:HG	1.78	0.82

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1189:C:OP1	10:J:51:ARG:NH2	2.12	0.82
2:B:204:ASN:ND2	2:B:206:ASP:H	1.77	0.82
3:C:113:ALA:HB3	3:C:114:PRO:HD3	1.61	0.82
7:G:78:ARG:HG3	7:G:79:ARG:N	1.93	0.82
10:J:49:VAL:HG11	14:N:41:ARG:HB2	1.58	0.82
2:B:185:ILE:HG22	2:B:199:TYR:HB2	1.60	0.82
1:A:677:U:H3	1:A:713:G:H1	1.27	0.82
14:N:41:ARG:NH2	14:N:42:ILE:HD11	1.94	0.82
2:B:196:LEU:CD1	2:B:197:VAL:HG23	2.10	0.81
12:L:86:ARG:HB2	12:L:101:VAL:HG22	1.62	0.81
10:J:63:PHE:HD1	14:N:58:LYS:HA	1.43	0.81
2:B:84:GLU:OE1	2:B:216:SER:HA	1.80	0.81
10:J:4:ILE:HB	10:J:74:ILE:HD11	1.60	0.81
16:P:4:ILE:CD1	16:P:64:ALA:HB1	2.09	0.81
2:B:178:ARG:HH21	8:H:74:PRO:HB3	1.46	0.81
16:P:51:VAL:HG12	16:P:52:ASP:H	1.46	0.81
7:G:111:ARG:HH11	7:G:111:ARG:HB3	1.46	0.81
23:X:4:C:C2'	23:X:5:C:H5'	2.11	0.81
1:A:1139:G:N2	1:A:1143:G:O6	2.14	0.81
4:D:108:LEU:HD11	4:D:174:LEU:HD22	1.60	0.81
3:C:15:THR:CG2	3:C:181:ASN:HA	2.08	0.81
1:A:686:U:H1'	11:K:42:TRP:HE1	1.46	0.81
3:C:47:LEU:HD11	3:C:76:VAL:HG12	1.62	0.81
3:C:52:LEU:H	3:C:52:LEU:HD23	1.46	0.80
5:E:50:GLU:HB3	5:E:53:LEU:HD13	1.61	0.80
2:B:4:GLU:HG2	2:B:5:ILE:N	1.95	0.80
10:J:6:ILE:HD12	10:J:6:ILE:O	1.81	0.80
1:A:375:U:H4'	16:P:17:TYR:HE2	1.46	0.80
1:A:1502:A:H2	1:A:1505:G:H1	1.26	0.80
1:A:1316:G:H22	1:A:1319:A:H5''	1.45	0.80
16:P:51:VAL:HG12	16:P:52:ASP:N	1.97	0.80
3:C:20:SER:HB2	3:C:40:ARG:NH2	1.95	0.80
16:P:4:ILE:HG13	16:P:21:VAL:HG12	1.64	0.80
3:C:138:VAL:HG13	3:C:149:ALA:HB1	1.64	0.80
5:E:126:ARG:HG3	5:E:126:ARG:HH11	1.47	0.80
8:H:84:ARG:HG3	8:H:84:ARG:HH11	1.44	0.80
4:D:12:CYS:CA	4:D:19:LEU:HD21	2.10	0.79
14:N:24:CYS:SG	14:N:39:LEU:HA	2.22	0.79
2:B:35:GLU:O	2:B:36:ARG:HD3	1.82	0.79
9:I:19:LEU:HD23	9:I:61:ALA:HB2	1.63	0.79
2:B:212:GLN:CD	2:B:235:SER:HB2	2.02	0.79
11:K:124:LYS:HD2	11:K:125:PHE:HE1	1.45	0.79

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:48:PRO:HD2	12:L:49:ASN:N	1.97	0.79
19:S:41:VAL:HG12	19:S:44:MET:N	1.98	0.79
20:T:89:ARG:HH21	20:T:104:LEU:HD21	1.47	0.79
1:A:1106:G:H5"	3:C:172:ARG:HG2	1.64	0.79
5:E:10:MET:HB3	5:E:32:VAL:HG22	1.63	0.79
8:H:20:TYR:HA	8:H:65:TYR:CE2	2.18	0.79
12:L:6:THR:N	12:L:9:GLN:HE21	1.80	0.79
18:R:56:THR:HB	18:R:58:LEU:CD1	2.13	0.78
4:D:30:LYS:HD3	4:D:30:LYS:N	1.98	0.78
20:T:50:GLU:HG3	20:T:51:GLU:N	1.97	0.78
4:D:28:SER:HB2	4:D:29:PRO:CD	2.14	0.78
10:J:40:LEU:HB2	10:J:69:ASN:HB3	1.65	0.78
11:K:32:ILE:CD1	11:K:72:ALA:HB2	2.12	0.78
13:M:4:ILE:H	13:M:9:ILE:HG21	1.47	0.78
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.66	0.78
9:I:15:ALA:HB2	9:I:65:VAL:HG23	1.65	0.78
3:C:181:ASN:ND2	3:C:204:LEU:HD12	1.99	0.78
7:G:113:GLU:HB2	7:G:119:ARG:HG2	1.66	0.78
18:R:43:PHE:HE2	18:R:58:LEU:HD11	1.47	0.78
2:B:101:MET:CA	2:B:108:ILE:HG13	2.11	0.78
2:B:122:PHE:HD1	2:B:139:LYS:HZ1	1.30	0.78
2:B:18:GLY:H	2:B:42:ILE:CG2	1.95	0.77
5:E:11:ILE:CD1	5:E:31:LEU:HD12	2.13	0.77
10:J:16:LEU:HD23	10:J:94:VAL:HG13	1.66	0.77
20:T:100:ILE:HG13	20:T:102:GLY:H	1.48	0.77
6:F:24:GLU:HA	6:F:27:GLN:CG	2.14	0.77
2:B:239:VAL:HG12	2:B:240:GLN:NE2	1.99	0.77
2:B:44:LEU:H	2:B:44:LEU:HD12	1.48	0.77
4:D:9:CYS:SG	4:D:22:LYS:HD2	2.25	0.77
2:B:21:ARG:HG3	2:B:38:GLY:C	2.05	0.77
6:F:23:LYS:O	6:F:27:GLN:HG2	1.85	0.77
17:Q:41:LYS:NZ	17:Q:92:ARG:HH22	1.82	0.77
8:H:100:ILE:HB	8:H:125:ARG:HH12	1.47	0.77
17:Q:59:ILE:HD13	17:Q:59:ILE:H	1.50	0.77
4:D:76:ARG:HD2	4:D:207:TYR:CE2	2.20	0.77
5:E:12:LEU:HD23	5:E:13:ILE:N	2.00	0.77
1:A:951:G:OP2	13:M:102:ARG:NH2	2.18	0.77
16:P:6:LEU:HB3	16:P:17:TYR:HD2	1.50	0.77
20:T:26:ASN:O	20:T:30:LYS:HB2	1.86	0.76
2:B:187:LEU:HA	2:B:201:ILE:HB	1.65	0.76
13:M:88:ARG:CB	13:M:88:ARG:HH11	1.96	0.76
7:G:148:ASN:N	7:G:148:ASN:HD22	1.82	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:I:83:ARG:O	9:I:86:VAL:HG12	1.84	0.76
21:U:10:ARG:HG2	21:U:13:ILE:HD12	1.68	0.76
20:T:13:LEU:HD12	20:T:14:LYS:N	2.00	0.76
4:D:153:ARG:NH1	4:D:181:MET:HG3	2.00	0.76
13:M:15:VAL:HG23	13:M:43:THR:O	1.84	0.76
1:A:1151:A:H1'	10:J:39:PRO:HB2	1.66	0.76
5:E:72:GLN:NE2	5:E:144:THR:HG22	2.00	0.76
16:P:22:THR:HA	16:P:33:ILE:HG12	1.66	0.76
5:E:53:LEU:H	5:E:53:LEU:CD1	1.99	0.76
8:H:5:PRO:O	8:H:8:ASP:HB3	1.85	0.76
10:J:38:ILE:HG12	10:J:71:LEU:O	1.86	0.76
6:F:91:VAL:HG13	18:R:72:ARG:HH12	1.51	0.76
3:C:59:ARG:HH22	3:C:97:LYS:HE3	1.51	0.75
5:E:42:GLY:HA3	5:E:66:MET:HG2	1.68	0.75
14:N:22:THR:O	14:N:23:ARG:HB2	1.86	0.75
14:N:43:CYS:O	14:N:44:LEU:C	2.22	0.75
18:R:53:ARG:HH21	18:R:60:ALA:N	1.84	0.75
8:H:91:ARG:HG2	8:H:91:ARG:HH11	1.52	0.75
1:A:448:A:OP2	1:A:485:G:N2	2.18	0.75
1:A:973:G:OP1	10:J:57:LYS:NZ	2.19	0.75
5:E:11:ILE:HD11	5:E:31:LEU:CD1	2.16	0.75
7:G:37:ASN:ND2	9:I:40:LEU:HD23	2.00	0.75
9:I:53:VAL:HB	9:I:95:LYS:HE3	1.67	0.75
20:T:58:LYS:HE3	20:T:62:LEU:HD11	1.69	0.75
2:B:117:GLU:O	2:B:121:LEU:HB2	1.86	0.75
4:D:26:CYS:HA	4:D:31:CYS:HB2	1.67	0.75
5:E:45:PHE:CE2	5:E:47:LYS:HD2	2.22	0.75
12:L:48:PRO:HD2	12:L:49:ASN:H	1.52	0.75
11:K:48:ILE:HD11	11:K:64:ALA:HA	1.67	0.75
19:S:39:THR:HG22	19:S:40:ILE:H	1.50	0.75
1:A:1305:G:H22	1:A:1331:G:H2'	1.52	0.75
10:J:27:ALA:HB1	10:J:34:VAL:HG21	1.69	0.75
19:S:41:VAL:HG12	19:S:44:MET:H	1.50	0.75
13:M:3:ARG:CA	13:M:9:ILE:HG21	2.13	0.75
20:T:35:THR:O	20:T:39:LYS:HG3	1.87	0.75
16:P:43:LYS:HG2	16:P:48:TRP:CE3	2.22	0.74
13:M:37:THR:HG21	13:M:39:ILE:HD11	1.68	0.74
9:I:113:LYS:H	9:I:113:LYS:HD2	1.51	0.74
15:O:87:ILE:HG22	15:O:88:ARG:N	2.00	0.74
15:O:70:LEU:O	15:O:70:LEU:HD12	1.88	0.74
2:B:178:ARG:HD2	8:H:71:GLY:HA2	1.68	0.74
5:E:72:GLN:HE21	5:E:144:THR:HG22	1.53	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:33:GLN:O	10:J:75:ILE:HG12	1.87	0.74
1:A:1054:C:OP2	1:A:1197:G:OP2	2.05	0.74
2:B:168:THR:HB	2:B:192:SER:HB2	1.70	0.74
2:B:47:THR:O	2:B:51:LEU:HG	1.87	0.74
7:G:9:VAL:HG13	7:G:94:ARG:HE	1.53	0.74
6:F:19:LEU:O	6:F:19:LEU:HD23	1.88	0.74
23:X:2:U:C2'	23:X:3:G:H5'	2.17	0.74
7:G:23:VAL:HG12	7:G:27:ILE:HD11	1.69	0.74
2:B:115:LEU:HD13	2:B:145:LEU:HB3	1.68	0.74
3:C:86:VAL:O	3:C:89:GLU:HB3	1.88	0.74
4:D:91:SER:HA	4:D:94:LEU:HD13	1.70	0.74
10:J:3:LYS:HD2	10:J:77:PRO:HD3	1.70	0.73
14:N:40:CYS:SG	14:N:42:ILE:HB	2.27	0.73
3:C:134:ILE:HD11	3:C:153:VAL:HG21	1.70	0.73
12:L:10:LEU:HD13	17:Q:32:TYR:HE2	1.53	0.73
7:G:79:ARG:HH22	7:G:82:GLY:HA2	1.50	0.73
2:B:132:LYS:HA	2:B:135:GLN:HB2	1.71	0.73
16:P:45:THR:HG23	16:P:46:PRO:HD2	1.70	0.73
16:P:43:LYS:O	16:P:45:THR:N	2.21	0.73
19:S:3:ARG:HG3	19:S:4:SER:H	1.52	0.73
20:T:50:GLU:HG3	20:T:51:GLU:H	1.54	0.73
5:E:10:MET:CB	5:E:32:VAL:HG22	2.18	0.73
13:M:121:LYS:HA	13:M:121:LYS:HE2	1.71	0.73
4:D:30:LYS:HB2	4:D:35:ARG:HG3	1.70	0.72
11:K:48:ILE:HD12	11:K:63:LEU:HB3	1.71	0.72
6:F:25:ILE:HD13	6:F:28:ARG:NH1	2.05	0.72
3:C:13:GLY:HA3	14:N:57:ARG:NH2	2.04	0.72
4:D:30:LYS:HG3	4:D:35:ARG:HE	1.52	0.72
12:L:126:LYS:HB2	12:L:126:LYS:NZ	2.04	0.72
15:O:71:GLN:HB2	15:O:78:TYR:CD1	2.25	0.72
4:D:146:ILE:HD12	4:D:146:ILE:N	2.04	0.72
5:E:36:ASP:OD2	5:E:38:GLN:HB2	1.86	0.72
7:G:78:ARG:HH12	7:G:80:VAL:HG23	1.52	0.72
16:P:72:ARG:C	16:P:72:ARG:HD3	2.10	0.72
6:F:72:VAL:CG2	6:F:90:VAL:HG11	2.20	0.72
10:J:49:VAL:HG22	14:N:41:ARG:HB3	1.59	0.72
15:O:79:ARG:O	15:O:82:ILE:HG22	1.90	0.72
20:T:27:LYS:O	20:T:30:LYS:HB3	1.89	0.72
20:T:97:ALA:O	20:T:99:LEU:HD13	1.89	0.72
6:F:77:ARG:HH11	6:F:77:ARG:HB2	1.53	0.72
1:A:1002:G:H2'	1:A:1003:G:H8	1.54	0.72
2:B:21:ARG:O	2:B:23:ARG:HD3	1.90	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:20:TYR:HD1	8:H:65:TYR:CD2	2.07	0.72
10:J:75:ILE:HG13	10:J:76:ASN:N	2.05	0.72
16:P:60:LEU:HA	16:P:64:ALA:HB3	1.71	0.72
10:J:98:ILE:H	10:J:98:ILE:HD12	1.55	0.72
8:H:10:LEU:N	8:H:10:LEU:HD23	2.04	0.71
13:M:49:THR:HG22	13:M:51:ALA:N	2.01	0.71
2:B:187:LEU:HD11	2:B:204:ASN:O	1.91	0.71
20:T:57:ARG:HD3	20:T:102:GLY:O	1.90	0.71
1:A:191:G:C4	20:T:105:SER:HB3	2.25	0.71
4:D:25:ARG:HH12	4:D:30:LYS:HE3	1.56	0.71
19:S:40:ILE:HG13	19:S:44:MET:SD	2.30	0.71
10:J:49:VAL:O	10:J:60:ARG:HB3	1.90	0.71
20:T:83:ARG:HA	20:T:86:ARG:HB3	1.72	0.71
23:X:4:C:H2'	23:X:5:C:H5'	1.72	0.71
1:A:1277:C:HO2'	1:A:1279:A:H8	1.39	0.71
1:A:1348:U:H4'	9:I:120:ARG:HD2	1.73	0.71
11:K:17:GLY:HA3	11:K:77:MET:CE	2.20	0.71
2:B:59:GLU:O	2:B:62:ALA:HB3	1.90	0.71
2:B:75:LYS:HD3	2:B:75:LYS:O	1.89	0.71
8:H:41:ARG:HH11	8:H:41:ARG:CB	2.03	0.71
16:P:20:VAL:HG21	16:P:32:TYR:CG	2.25	0.71
8:H:84:ARG:HH12	8:H:86:ILE:CD1	2.02	0.71
18:R:56:THR:HB	18:R:58:LEU:HD12	1.71	0.71
3:C:16:ARG:NH1	3:C:16:ARG:HB2	2.04	0.71
10:J:5:ARG:HG3	10:J:71:LEU:HD11	1.72	0.71
11:K:124:LYS:HD2	11:K:125:PHE:CE1	2.25	0.71
20:T:23:ARG:CA	20:T:26:ASN:HD21	2.03	0.71
2:B:8:LYS:N	2:B:8:LYS:HD3	2.03	0.71
4:D:190:ASP:HB3	4:D:193:ASP:OD1	1.91	0.71
5:E:78:HIS:HE1	5:E:143:ARG:H	1.38	0.71
13:M:121:LYS:HE2	13:M:121:LYS:CA	2.21	0.70
20:T:63:ILE:HG22	20:T:77:ALA:HB1	1.73	0.70
2:B:126:GLU:CG	2:B:129:GLU:HG3	2.20	0.70
9:I:15:ALA:HA	9:I:64:THR:O	1.91	0.70
1:A:489:C:OP1	4:D:132:ARG:NH2	2.24	0.70
2:B:214:ILE:HA	2:B:217:ARG:HH21	1.55	0.70
5:E:76:ILE:HB	5:E:77:PRO:HD2	1.72	0.70
10:J:6:ILE:HG13	10:J:72:VAL:O	1.91	0.70
1:A:522:C:H41	12:L:53:ARG:HH22	1.39	0.70
15:O:74:ASP:CG	15:O:77:ARG:HG2	2.12	0.70
3:C:152:ILE:HB	3:C:199:LYS:HB2	1.73	0.70
6:F:60:PHE:C	6:F:61:LEU:HD12	2.12	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:87:SER:HB2	8:H:93:VAL:HB	1.74	0.70
16:P:14:ASN:N	16:P:15:PRO:HD3	2.07	0.70
19:S:51:VAL:O	19:S:57:HIS:HA	1.92	0.70
17:Q:52:LYS:HD2	17:Q:55:ASP:OD1	1.91	0.70
3:C:16:ARG:HD2	3:C:54:ARG:NH2	2.03	0.70
15:O:65:ARG:HH11	15:O:65:ARG:HB2	1.56	0.70
5:E:82:VAL:HG12	5:E:83:GLU:N	2.06	0.69
3:C:147:LYS:O	3:C:203:PHE:HB3	1.92	0.69
9:I:113:LYS:N	9:I:113:LYS:HD2	2.07	0.69
9:I:62:TYR:C	9:I:63:ILE:HD12	2.12	0.69
13:M:4:ILE:N	13:M:9:ILE:HG21	2.06	0.69
2:B:95:GLN:HE21	2:B:147:LYS:HE2	1.56	0.69
4:D:120:LEU:HD22	4:D:125:HIS:HB2	1.74	0.69
7:G:78:ARG:HH12	7:G:80:VAL:CG2	2.04	0.69
10:J:38:ILE:HG13	10:J:38:ILE:O	1.92	0.69
2:B:162:ILE:O	2:B:162:ILE:HG13	1.92	0.69
3:C:123:GLN:O	3:C:128:PHE:HB2	1.91	0.69
4:D:30:LYS:H	4:D:30:LYS:HD3	1.57	0.69
12:L:24:VAL:HG12	12:L:24:VAL:O	1.90	0.69
21:U:6:ARG:HE	21:U:15:ARG:NE	1.91	0.69
8:H:31:PHE:CE2	8:H:35:ILE:HD11	2.27	0.69
17:Q:4:LYS:CE	17:Q:6:LEU:HD21	2.21	0.69
1:A:1347:G:N2	1:A:1374:A:OP2	2.24	0.69
2:B:126:GLU:HG2	2:B:126:GLU:O	1.92	0.69
2:B:172:ILE:H	2:B:172:ILE:HD12	1.56	0.69
2:B:212:GLN:NE2	2:B:216:SER:HB2	2.08	0.69
4:D:188:LEU:HD23	4:D:189:PRO:HD2	1.75	0.69
6:F:3:ARG:HB3	6:F:93:SER:HB2	1.74	0.69
8:H:6:ILE:N	8:H:6:ILE:HD12	2.08	0.69
2:B:101:MET:HA	2:B:108:ILE:CG1	2.14	0.69
8:H:49:GLU:HG3	8:H:51:VAL:HG13	1.74	0.69
16:P:1:MET:O	16:P:24:ALA:HB2	1.92	0.69
3:C:105:GLU:HG2	3:C:106:VAL:H	1.58	0.69
8:H:112:LEU:HA	8:H:134:ILE:HG12	1.75	0.69
10:J:54:PHE:CZ	10:J:55:LYS:NZ	2.61	0.69
6:F:100:ASN:ND2	18:R:23:LYS:HE3	2.08	0.69
20:T:47:GLY:O	20:T:49:ALA:N	2.20	0.69
20:T:64:ASP:HA	20:T:67:ALA:HB3	1.74	0.69
3:C:195:VAL:HG12	3:C:196:LEU:N	2.08	0.68
7:G:155:ARG:HD3	7:G:155:ARG:N	2.07	0.68
9:I:46:ALA:HA	9:I:78:LYS:HB2	1.75	0.68
1:A:1305:G:H5'	21:U:4:GLY:HA3	1.76	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1314:C:OP1	19:S:6:LYS:HE3	1.92	0.68
2:B:165:VAL:HG23	2:B:166:ASP:H	1.57	0.68
16:P:3:LYS:C	16:P:4:ILE:HD12	2.14	0.68
20:T:97:ALA:O	20:T:99:LEU:N	2.27	0.68
3:C:150:LYS:HB3	3:C:201:TYR:HB2	1.75	0.68
9:I:28:VAL:HG13	9:I:63:ILE:CG2	2.24	0.68
13:M:90:LEU:CA	13:M:93:ARG:HD2	2.23	0.68
2:B:162:ILE:HD11	2:B:184:VAL:HG13	1.74	0.68
14:N:26:ARG:NH1	14:N:43:CYS:SG	2.67	0.68
4:D:198:VAL:HG12	4:D:199:ASN:N	2.09	0.68
11:K:124:LYS:HB3	11:K:125:PHE:HD1	1.58	0.68
20:T:89:ARG:NH2	20:T:104:LEU:HD21	2.09	0.68
5:E:53:LEU:N	5:E:53:LEU:HD12	2.09	0.68
14:N:6:LEU:HD23	14:N:6:LEU:O	1.93	0.68
3:C:107:GLN:H	3:C:107:GLN:CD	1.97	0.68
9:I:48:GLU:N	9:I:49:PRO:HD2	2.09	0.68
2:B:178:ARG:HD2	8:H:71:GLY:CA	2.24	0.68
10:J:48:THR:HA	10:J:62:HIS:HB3	1.75	0.68
16:P:66:PRO:HG2	16:P:71:ARG:NH1	2.09	0.68
17:Q:59:ILE:HD13	17:Q:59:ILE:N	2.08	0.68
1:A:752:G:H1'	1:A:754:C:H41	1.59	0.68
4:D:96:LEU:HD22	4:D:96:LEU:N	2.07	0.68
2:B:215:LEU:O	2:B:219:VAL:HG23	1.94	0.67
7:G:79:ARG:NH2	7:G:82:GLY:HA2	2.09	0.67
7:G:8:GLU:CD	7:G:8:GLU:H	1.97	0.67
14:N:25:VAL:CG2	14:N:38:GLY:O	2.31	0.67
1:A:439:A:OP2	1:A:493:G:N1	2.28	0.67
4:D:165:MET:HE3	4:D:165:MET:HA	1.77	0.67
6:F:67:MET:HB2	6:F:68:PRO:HD2	1.75	0.67
8:H:14:ARG:O	8:H:18:ARG:HD3	1.94	0.67
10:J:96:ILE:HD13	10:J:96:ILE:N	2.09	0.67
17:Q:74:LEU:HD12	17:Q:75:ARG:HG2	1.76	0.67
2:B:24:TRP:H	2:B:24:TRP:HD1	1.43	0.67
2:B:7:VAL:HG22	2:B:8:LYS:HD3	1.76	0.67
4:D:173:TRP:CD2	4:D:189:PRO:HB3	2.29	0.67
8:H:100:ILE:HB	8:H:125:ARG:NH1	2.10	0.67
10:J:6:ILE:HG22	10:J:98:ILE:CG1	2.16	0.67
1:A:1239:A:O2'	1:A:1298:C:N4	2.27	0.67
1:A:1104:G:H4'	2:B:111:ARG:NH1	2.10	0.67
7:G:120:ILE:O	7:G:124:LEU:HB2	1.95	0.67
7:G:50:ILE:HB	7:G:58:PRO:HB3	1.75	0.67
11:K:95:ILE:HD12	11:K:108:ILE:HD13	1.77	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:23:TYR:CB	13:M:67:GLU:HG2	2.25	0.67
1:A:1297:C:O2'	7:G:114:ARG:NH2	2.27	0.67
1:A:1459:C:OP1	20:T:27:LYS:NZ	2.26	0.67
1:A:346:G:H1'	1:A:347:G:H5'	1.77	0.67
1:A:939:G:H5''	7:G:102:ARG:HH22	1.60	0.67
6:F:96:PRO:HB3	18:R:30:ASP:OD2	1.95	0.67
7:G:28:ASN:O	7:G:31:MET:HB3	1.95	0.67
9:I:33:PHE:CZ	9:I:47:LEU:HD21	2.30	0.67
13:M:78:ILE:HG23	13:M:92:HIS:ND1	2.09	0.67
1:A:1071:C:H5''	5:E:49:PRO:HG2	1.75	0.67
8:H:20:TYR:HE2	8:H:75:ARG:HD2	1.60	0.67
9:I:112:LYS:HA	9:I:119:ALA:HB2	1.77	0.67
13:M:3:ARG:HD2	13:M:9:ILE:HG12	1.77	0.67
18:R:70:ILE:O	18:R:74:ARG:HG3	1.95	0.67
2:B:164:VAL:HB	2:B:186:ALA:CB	2.25	0.67
2:B:71:VAL:CG2	2:B:164:VAL:HG22	2.25	0.67
4:D:52:SER:HB3	4:D:55:ALA:HB2	1.77	0.67
1:A:1199:U:H4'	10:J:54:PHE:CZ	2.30	0.67
13:M:13:LYS:HA	13:M:44:ARG:HD2	1.77	0.67
1:A:377:G:OP1	16:P:5:ARG:NH1	2.25	0.67
19:S:31:ILE:HG23	19:S:49:ILE:HA	1.75	0.67
20:T:83:ARG:HA	20:T:86:ARG:HD3	1.76	0.67
1:A:921:U:O2'	5:E:19:MET:O	2.12	0.66
7:G:141:VAL:HG12	7:G:141:VAL:O	1.95	0.66
8:H:10:LEU:H	8:H:10:LEU:HD23	1.60	0.66
20:T:36:LEU:HD12	20:T:55:ILE:HG23	1.76	0.66
7:G:138:LYS:HE2	7:G:142:GLU:OE2	1.94	0.66
8:H:6:ILE:H	8:H:6:ILE:CD1	2.07	0.66
19:S:65:ASN:HD22	19:S:65:ASN:N	1.93	0.66
13:M:117:VAL:HG22	13:M:118:ALA:H	1.59	0.66
16:P:21:VAL:HG11	16:P:59:TRP:CD1	2.30	0.66
1:A:474:G:H5'	16:P:81:ARG:HG3	1.78	0.66
1:A:1065:U:O5'	1:A:1190:G:N2	2.29	0.66
3:C:101:LEU:HD23	3:C:102:ASN:N	2.11	0.66
3:C:73:PRO:O	3:C:76:VAL:HG22	1.96	0.66
14:N:40:CYS:SG	14:N:43:CYS:N	2.67	0.66
1:A:1392:G:H21	1:A:1502:A:H8	1.42	0.66
2:B:87:ARG:HH11	2:B:223:ILE:CD1	2.09	0.66
2:B:25:ASN:O	2:B:27:LYS:N	2.28	0.66
1:A:27:G:H4'	4:D:209:ARG:HG3	1.77	0.66
5:E:75:THR:HG23	5:E:76:ILE:N	2.11	0.66
7:G:78:ARG:NH1	7:G:80:VAL:HG23	2.11	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:81:LEU:O	13:M:84:ILE:HG22	1.95	0.66
17:Q:56:VAL:HB	17:Q:78:GLU:HB3	1.76	0.66
8:H:23:SER:HA	8:H:63:LEU:CD2	2.24	0.66
10:J:99:LYS:O	10:J:100:THR:HG23	1.96	0.66
15:O:25:THR:HG21	15:O:70:LEU:HB2	1.77	0.66
1:A:1124:G:H3'	1:A:1145:C:N4	2.10	0.66
7:G:69:VAL:O	7:G:69:VAL:HG12	1.95	0.66
12:L:25:PRO:C	12:L:27:LEU:H	1.98	0.66
1:A:1305:G:N2	1:A:1331:G:H2'	2.11	0.65
3:C:140:ARG:HB2	3:C:140:ARG:CZ	2.25	0.65
6:F:41:GLU:O	6:F:43:LEU:HD12	1.96	0.65
12:L:11:VAL:HG13	17:Q:29:HIS:HD2	1.61	0.65
2:B:87:ARG:O	2:B:87:ARG:HD2	1.95	0.65
17:Q:27:PHE:CZ	17:Q:36:ILE:HD11	2.31	0.65
2:B:164:VAL:HB	2:B:186:ALA:HB2	1.78	0.65
2:B:178:ARG:NE	8:H:71:GLY:O	2.29	0.65
4:D:94:LEU:H	4:D:94:LEU:CD1	2.08	0.65
9:I:28:VAL:HA	9:I:63:ILE:HB	1.79	0.65
10:J:38:ILE:HD11	10:J:71:LEU:HB3	1.78	0.65
16:P:45:THR:HG22	16:P:47:ASP:H	1.60	0.65
19:S:3:ARG:CZ	19:S:8:GLY:HA2	2.26	0.65
4:D:122:ARG:HD3	4:D:122:ARG:O	1.97	0.65
4:D:28:SER:CB	4:D:29:PRO:HD3	2.25	0.65
4:D:52:SER:O	4:D:56:VAL:HG23	1.95	0.65
21:U:25:LYS:HE2	21:U:26:LYS:O	1.96	0.65
1:A:1356:G:H2'	1:A:1357:A:C8	2.32	0.65
3:C:70:VAL:HG12	3:C:71:ALA:N	2.10	0.65
7:G:11:GLN:O	7:G:12:LEU:HD13	1.97	0.65
12:L:115:LYS:O	12:L:117:ARG:HG3	1.97	0.65
12:L:21:LYS:HD2	12:L:21:LYS:N	2.11	0.65
4:D:13:ARG:HD3	4:D:38:TYR:O	1.97	0.65
5:E:83:GLU:HG2	5:E:88:LYS:HG3	1.78	0.65
8:H:20:TYR:HA	8:H:65:TYR:HE2	1.60	0.65
10:J:34:VAL:HG22	10:J:74:ILE:HG22	1.77	0.65
13:M:74:VAL:O	13:M:78:ILE:HG13	1.96	0.65
16:P:6:LEU:HD23	16:P:17:TYR:CD2	2.32	0.65
2:B:17:PHE:HD2	2:B:44:LEU:HD21	1.61	0.65
10:J:6:ILE:HD11	10:J:72:VAL:CB	2.24	0.65
10:J:81:THR:C	10:J:83:GLU:H	1.99	0.65
15:O:74:ASP:OD1	15:O:77:ARG:N	2.30	0.65
18:R:43:PHE:CE2	18:R:58:LEU:HD11	2.31	0.65
19:S:21:GLU:O	19:S:25:LYS:HB3	1.97	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:T:44:ALA:HB2	20:T:88:VAL:HG13	1.78	0.65
4:D:52:SER:HB3	4:D:55:ALA:CB	2.27	0.65
5:E:41:VAL:CG1	5:E:113:ALA:HB2	2.25	0.65
8:H:20:TYR:CE2	8:H:75:ARG:HD2	2.32	0.65
10:J:27:ALA:CB	10:J:34:VAL:HG21	2.27	0.65
12:L:39:VAL:HB	12:L:57:LYS:HB2	1.79	0.65
6:F:98:LEU:HB3	18:R:30:ASP:HA	1.79	0.65
6:F:50:TYR:CE1	18:R:77:GLY:HA2	2.32	0.65
19:S:15:LEU:O	19:S:19:VAL:N	2.26	0.65
20:T:83:ARG:CA	20:T:86:ARG:HB3	2.27	0.65
7:G:21:VAL:HG23	7:G:22:LEU:H	1.60	0.65
15:O:8:LYS:O	15:O:12:ILE:HG13	1.97	0.65
16:P:51:VAL:HG21	16:P:77:ALA:HB2	1.78	0.65
2:B:155:LEU:HD12	2:B:157:ARG:O	1.97	0.65
2:B:14:GLY:O	2:B:15:VAL:HG13	1.96	0.65
10:J:39:PRO:HB3	10:J:70:ARG:HH12	1.60	0.65
4:D:79:PHE:HD2	4:D:79:PHE:C	2.00	0.64
19:S:10:PHE:CG	19:S:11:VAL:N	2.65	0.64
12:L:26:ALA:O	12:L:27:LEU:O	2.14	0.64
19:S:35:SER:O	19:S:71:LEU:HD12	1.96	0.64
24:Y:29:U:H2'	24:Y:30:C:H6	1.61	0.64
3:C:138:VAL:HG13	3:C:149:ALA:CB	2.27	0.64
16:P:21:VAL:HG23	16:P:33:ILE:HB	1.77	0.64
2:B:67:THR:HG21	2:B:155:LEU:CD2	2.27	0.64
9:I:53:VAL:HG21	9:I:92:TYR:CE1	2.32	0.64
14:N:7:ILE:HG13	14:N:8:GLU:N	2.12	0.64
22:V:6:G:H1	22:V:67:C:H42	1.45	0.64
2:B:158:LEU:HD12	2:B:158:LEU:O	1.98	0.64
3:C:58:GLU:O	3:C:64:VAL:HA	1.98	0.64
4:D:170:VAL:HG22	4:D:171:GLY:N	2.12	0.64
6:F:12:PRO:HG2	6:F:13:ASN:H	1.62	0.64
10:J:54:PHE:C	10:J:55:LYS:HG3	2.18	0.64
16:P:58:TYR:O	16:P:62:VAL:HG22	1.96	0.64
18:R:73:ALA:HB3	18:R:79:LEU:HD12	1.78	0.64
1:A:192:U:H4'	20:T:102:GLY:O	1.98	0.64
4:D:29:PRO:HG2	4:D:30:LYS:NZ	2.12	0.64
13:M:4:ILE:H	13:M:9:ILE:HG22	1.62	0.64
1:A:191:G:O2'	20:T:101:GLY:O	2.16	0.64
1:A:642:A:N3	8:H:113:SER:OG	2.28	0.64
2:B:60:ASP:HB3	2:B:64:ARG:NH1	2.13	0.64
3:C:34:LEU:HD21	3:C:38:ARG:HD2	1.79	0.64
4:D:61:LYS:HD2	4:D:206:PHE:CE2	2.32	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:41:VAL:HG12	5:E:112:LEU:O	1.97	0.64
6:F:92:LYS:HZ2	6:F:92:LYS:HB2	1.62	0.64
11:K:103:LEU:HD22	11:K:103:LEU:H	1.62	0.64
1:A:1318:A:H4'	19:S:11:VAL:CG1	2.28	0.64
14:N:53:LEU:HB3	14:N:56:VAL:HG21	1.80	0.64
1:A:1175:G:H2'	1:A:1176:A:C8	2.32	0.64
2:B:134:GLU:HA	2:B:137:ARG:HB3	1.80	0.64
10:J:42:THR:HG23	10:J:68:HIS:HA	1.80	0.64
12:L:18:VAL:HG23	12:L:19:ARG:H	1.63	0.64
13:M:51:ALA:O	13:M:55:ARG:HG3	1.97	0.64
1:A:1288:A:N3	1:A:1352:C:O2'	2.30	0.64
1:A:719:C:O2'	18:R:49:LYS:HB3	1.97	0.64
9:I:62:TYR:O	9:I:63:ILE:HD12	1.98	0.64
9:I:97:LYS:HB3	9:I:98:PRO:HD3	1.79	0.64
11:K:17:GLY:HA3	11:K:77:MET:HE3	1.78	0.64
15:O:8:LYS:NZ	15:O:8:LYS:HB2	2.13	0.64
16:P:51:VAL:CG1	16:P:52:ASP:H	2.11	0.64
20:T:26:ASN:HB2	20:T:71:THR:HG23	1.79	0.64
1:A:1002:G:H2'	1:A:1003:G:C8	2.32	0.63
3:C:181:ASN:ND2	3:C:204:LEU:HB2	2.13	0.63
7:G:148:ASN:N	7:G:148:ASN:ND2	2.46	0.63
8:H:97:VAL:HG13	8:H:98:LYS:N	2.13	0.63
9:I:47:LEU:N	9:I:47:LEU:HD22	2.14	0.63
19:S:21:GLU:HG3	19:S:22:LEU:N	2.11	0.63
1:A:523:A:H61	12:L:92:ASP:HB2	1.63	0.63
19:S:39:THR:HG22	19:S:40:ILE:N	2.14	0.63
21:U:15:ARG:HH11	21:U:15:ARG:HG2	1.63	0.63
2:B:20:GLU:HB2	2:B:190:THR:OG1	1.98	0.63
20:T:14:LYS:HA	20:T:17:ARG:NH1	2.14	0.63
8:H:112:LEU:HD12	8:H:112:LEU:O	1.98	0.63
1:A:963:G:H21	10:J:55:LYS:HD3	1.64	0.63
11:K:48:ILE:HD11	11:K:64:ALA:CA	2.28	0.63
14:N:18:VAL:HG23	14:N:19:ARG:H	1.63	0.63
2:B:8:LYS:CD	2:B:8:LYS:H	2.09	0.63
3:C:95:THR:HG22	3:C:96:GLY:N	2.07	0.63
9:I:5:TYR:O	9:I:84:ALA:HA	1.98	0.63
1:A:420:U:H4'	1:A:421:U:H5	1.63	0.63
1:A:581:G:N2	1:A:760:G:N7	2.45	0.63
4:D:30:LYS:CG	4:D:35:ARG:HE	2.11	0.63
8:H:28:ALA:HB3	8:H:57:PRO:HB2	1.79	0.63
19:S:15:LEU:O	19:S:19:VAL:HG23	1.98	0.63
2:B:187:LEU:HD12	2:B:205:ASP:HA	1.79	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:21:ARG:HB2	2:B:39:ILE:HA	1.80	0.63
4:D:30:LYS:HA	4:D:34:GLU:HB2	1.79	0.63
7:G:9:VAL:CG1	7:G:94:ARG:HE	2.12	0.63
8:H:6:ILE:HB	8:H:85:ARG:HH12	1.62	0.63
15:O:61:GLY:C	15:O:65:ARG:HH12	2.02	0.63
3:C:34:LEU:CD2	3:C:38:ARG:HD2	2.29	0.63
12:L:62:SER:O	12:L:64:TYR:HD1	1.81	0.63
12:L:85:ILE:HD11	12:L:98:TYR:HB2	1.81	0.63
3:C:3:ASN:N	3:C:3:ASN:HD22	1.96	0.63
9:I:59:PHE:HZ	9:I:88:TYR:CE1	2.17	0.63
11:K:12:ARG:HG2	11:K:13:GLN:N	2.14	0.63
12:L:86:ARG:HB2	12:L:101:VAL:CG2	2.28	0.63
13:M:40:ASN:HD21	13:M:42:ALA:HB3	1.64	0.63
1:A:375:U:H4'	16:P:17:TYR:CE2	2.33	0.62
3:C:189:ALA:O	3:C:191:THR:HG23	1.99	0.62
3:C:70:VAL:HG12	3:C:72:LYS:N	2.11	0.62
7:G:113:GLU:CG	7:G:119:ARG:HG2	2.28	0.62
9:I:118:LYS:O	9:I:119:ALA:HB3	1.99	0.62
11:K:19:ALA:HA	11:K:32:ILE:HG22	1.80	0.62
11:K:58:PRO:HD3	11:K:89:ALA:HB1	1.81	0.62
2:B:236:TYR:CD2	2:B:239:VAL:HG21	2.34	0.62
2:B:66:GLY:O	2:B:67:THR:HG23	2.00	0.62
7:G:140:ASP:HA	7:G:143:ARG:NH1	2.14	0.62
8:H:42:GLU:HG3	8:H:109:ILE:HD12	1.80	0.62
2:B:214:ILE:HD13	2:B:217:ARG:NH2	2.14	0.62
5:E:51:VAL:O	5:E:55:VAL:HG23	1.99	0.62
6:F:8:ILE:HD11	6:F:79:LEU:HD13	1.81	0.62
18:R:82:THR:HG22	18:R:83:GLU:N	2.15	0.62
5:E:50:GLU:HG3	5:E:52:PRO:HD2	1.79	0.62
7:G:140:ASP:C	7:G:142:GLU:H	2.03	0.62
9:I:17:VAL:HG21	9:I:81:ILE:N	2.14	0.62
17:Q:11:VAL:HG23	17:Q:20:THR:HB	1.79	0.62
12:L:11:VAL:HG13	17:Q:29:HIS:CD2	2.34	0.62
2:B:23:ARG:HD3	2:B:23:ARG:H	1.64	0.62
4:D:106:TYR:HE1	4:D:112:VAL:O	1.82	0.62
5:E:78:HIS:CD2	8:H:104:ARG:HG2	2.35	0.62
8:H:84:ARG:HG3	8:H:84:ARG:NH1	2.10	0.62
9:I:13:ALA:HB2	9:I:67:GLY:O	2.00	0.62
9:I:65:VAL:HG21	9:I:73:GLN:HB3	1.81	0.62
1:A:503:C:OP2	12:L:116:SER:HB3	2.00	0.62
18:R:25:THR:HG22	18:R:25:THR:O	2.00	0.62
1:A:973:G:H3'	1:A:974:A:H5''	1.82	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:127:ARG:HG2	3:C:127:ARG:HH11	1.64	0.62
9:I:116:LYS:O	9:I:118:LYS:N	2.32	0.62
4:D:153:ARG:HD3	4:D:181:MET:SD	2.39	0.62
1:A:939:G:H5''	7:G:102:ARG:NH2	2.15	0.62
11:K:57:THR:HG22	11:K:59:TYR:H	1.64	0.62
14:N:41:ARG:HH21	14:N:42:ILE:HD11	1.62	0.62
1:A:1129:C:H4'	1:A:1130:A:H5'	1.81	0.62
13:M:97:PRO:HB2	13:M:101:GLN:HE22	1.65	0.62
5:E:51:VAL:HB	5:E:52:PRO:CD	2.30	0.62
6:F:77:ARG:NH1	6:F:77:ARG:HB2	2.15	0.62
14:N:23:ARG:NH1	14:N:30:ALA:HB2	2.14	0.62
4:D:196:LEU:C	4:D:198:VAL:H	2.02	0.62
6:F:10:LEU:HD13	6:F:61:LEU:CD1	2.30	0.62
5:E:148:VAL:HG21	8:H:107:LEU:HD13	1.81	0.62
8:H:16:ALA:HB2	8:H:24:THR:HG21	1.82	0.62
8:H:29:SER:HB3	8:H:32:LYS:CG	2.22	0.61
13:M:117:VAL:HG22	13:M:118:ALA:N	2.15	0.61
13:M:66:LEU:HA	13:M:70:LEU:HD23	1.81	0.61
13:M:69:GLU:O	13:M:72:ALA:N	2.32	0.61
14:N:18:VAL:HG23	14:N:19:ARG:N	2.14	0.61
15:O:68:ARG:O	15:O:72:ARG:HB2	2.00	0.61
15:O:26:GLU:CD	15:O:77:ARG:HH12	2.03	0.61
1:A:1322:C:O2'	1:A:1323:G:H5'	2.00	0.61
11:K:121:PRO:HD2	11:K:126:ARG:HD3	1.82	0.61
16:P:66:PRO:HG2	16:P:71:ARG:HH12	1.64	0.61
2:B:108:ILE:O	2:B:111:ARG:HB2	2.01	0.61
3:C:111:LEU:HD21	3:C:144:SER:O	2.01	0.61
14:N:23:ARG:CD	14:N:28:GLY:O	2.49	0.61
10:J:53:PRO:HA	14:N:42:ILE:HD12	1.82	0.61
1:A:1330:U:OP1	13:M:25:ILE:O	2.18	0.61
5:E:91:LEU:HA	5:E:120:THR:HG22	1.81	0.61
7:G:15:ASP:O	7:G:19:GLY:HA2	2.00	0.61
8:H:39:LEU:O	8:H:45:ILE:HG12	2.01	0.61
2:B:178:ARG:NH2	8:H:74:PRO:HB3	2.15	0.61
10:J:98:ILE:N	10:J:98:ILE:HD12	2.15	0.61
12:L:126:LYS:C	12:L:128:ALA:H	2.03	0.61
12:L:48:PRO:CD	12:L:49:ASN:H	2.10	0.61
16:P:4:ILE:HG13	16:P:21:VAL:CG1	2.29	0.61
19:S:11:VAL:O	19:S:12:ASP:HB2	2.00	0.61
1:A:662:G:O2'	1:A:836:G:OP1	2.19	0.61
4:D:162:LEU:CD1	4:D:181:MET:HB3	2.31	0.61
11:K:12:ARG:HG2	11:K:13:GLN:H	1.63	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:X:8:A:O5'	23:X:8:A:H8	1.83	0.61
1:A:1053:G:H5'	1:A:1054:C:H5'	1.81	0.61
4:D:11:LEU:HA	4:D:14:ARG:HB2	1.82	0.61
10:J:34:VAL:CG2	10:J:74:ILE:HG22	2.30	0.61
17:Q:67:LYS:HA	17:Q:70:ARG:NH1	2.15	0.61
1:A:1224:G:C6	1:A:1322:C:H1'	2.35	0.61
1:A:1347:G:C8	9:I:107:ARG:HB3	2.34	0.61
2:B:80:ILE:CD1	2:B:208:ILE:HG23	2.22	0.61
4:D:129:ASN:HA	4:D:145:GLU:HB2	1.82	0.61
7:G:113:GLU:CB	7:G:119:ARG:HG2	2.29	0.61
1:A:963:G:N3	10:J:55:LYS:NZ	2.47	0.61
2:B:115:LEU:CD2	2:B:153:ARG:HD3	2.30	0.61
3:C:70:VAL:O	3:C:106:VAL:HG23	2.01	0.61
4:D:90:GLY:CA	4:D:204:ILE:HD11	2.30	0.61
11:K:99:GLN:HG2	11:K:105:VAL:CG2	2.28	0.61
13:M:36:LYS:HD3	13:M:36:LYS:C	2.20	0.61
6:F:98:LEU:O	6:F:98:LEU:HD12	2.01	0.61
1:A:974:A:H1'	14:N:31:ARG:HE	1.65	0.61
16:P:20:VAL:HG21	16:P:32:TYR:CD2	2.35	0.61
17:Q:65:ILE:N	17:Q:65:ILE:HD12	2.15	0.61
20:T:84:LEU:O	20:T:88:VAL:HG23	2.01	0.61
2:B:194:PRO:HG2	2:B:195:ASP:H	1.64	0.61
4:D:29:PRO:CG	4:D:30:LYS:HD3	2.28	0.61
13:M:9:ILE:HD12	13:M:9:ILE:O	2.01	0.61
20:T:34:LYS:O	20:T:38:LYS:HB2	2.01	0.61
2:B:60:ASP:O	2:B:64:ARG:HG2	2.01	0.60
3:C:47:LEU:O	3:C:52:LEU:HD22	2.01	0.60
4:D:90:GLY:HA2	4:D:204:ILE:HD11	1.83	0.60
2:B:141:GLU:O	2:B:145:LEU:HD23	2.01	0.60
3:C:3:ASN:N	3:C:3:ASN:ND2	2.48	0.60
4:D:146:ILE:HD12	4:D:146:ILE:H	1.66	0.60
4:D:149:ALA:HB3	4:D:152:SER:HB2	1.82	0.60
6:F:69:GLU:O	6:F:72:VAL:HG12	2.01	0.60
8:H:118:VAL:C	8:H:119:LEU:HD23	2.22	0.60
11:K:41:THR:HG21	11:K:71:LYS:HB2	1.83	0.60
15:O:5:LYS:O	15:O:8:LYS:HG2	2.01	0.60
16:P:40:ASP:OD2	16:P:42:ARG:HB2	2.02	0.60
2:B:132:LYS:HA	2:B:135:GLN:CD	2.22	0.60
3:C:88:ARG:NH1	3:C:101:LEU:H	1.99	0.60
3:C:88:ARG:O	3:C:99:VAL:HG21	2.01	0.60
4:D:196:LEU:N	4:D:196:LEU:HD12	2.15	0.60
8:H:49:GLU:O	8:H:51:VAL:HG13	2.02	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:78:GLN:O	11:K:103:LEU:HA	2.01	0.60
14:N:23:ARG:HD2	14:N:28:GLY:O	2.00	0.60
15:O:74:ASP:OD1	15:O:77:ARG:HG2	2.00	0.60
20:T:101:GLY:O	20:T:103:GLY:N	2.35	0.60
2:B:114:ARG:O	2:B:117:GLU:HB2	2.01	0.60
4:D:76:ARG:HD2	4:D:207:TYR:HE2	1.66	0.60
4:D:79:PHE:CD2	4:D:79:PHE:C	2.71	0.60
6:F:1:MET:HA	6:F:67:MET:O	2.02	0.60
9:I:28:VAL:HG13	9:I:63:ILE:HG22	1.83	0.60
10:J:32:ALA:H	10:J:78:ASN:HD21	1.49	0.60
16:P:20:VAL:HG22	16:P:21:VAL:N	2.16	0.60
16:P:8:ARG:HH11	16:P:8:ARG:HG2	1.64	0.60
2:B:221:LEU:O	2:B:221:LEU:HD13	2.02	0.60
2:B:17:PHE:CD2	2:B:44:LEU:HD11	2.36	0.60
5:E:43:LEU:HD21	5:E:132:ALA:HB1	1.83	0.60
19:S:12:ASP:OD1	19:S:37:ARG:HD2	2.00	0.60
1:A:1158:C:H4'	2:B:133:LYS:HZ1	1.65	0.60
2:B:4:GLU:CG	2:B:5:ILE:H	1.99	0.60
8:H:86:ILE:HG22	8:H:93:VAL:HG21	1.84	0.60
9:I:3:GLN:HB3	9:I:20:ARG:HG2	1.82	0.60
1:A:1152:A:H5''	10:J:13:HIS:CD2	2.36	0.60
1:A:1074:G:H4'	2:B:104:ASN:HB2	1.84	0.60
1:A:1321:C:H5''	1:A:1322:C:H5''	1.84	0.60
3:C:141:VAL:O	3:C:146:ALA:HB3	2.01	0.60
6:F:61:LEU:HB3	6:F:63:TYR:HE2	1.67	0.60
9:I:9:ARG:CB	9:I:14:VAL:HG22	2.31	0.60
4:D:11:LEU:O	4:D:14:ARG:N	2.35	0.60
4:D:96:LEU:CD2	4:D:96:LEU:H	2.11	0.60
6:F:97:PHE:C	6:F:97:PHE:HD2	2.05	0.60
8:H:58:TYR:O	8:H:59:LEU:HD23	2.00	0.60
9:I:114:TYR:HD2	9:I:114:TYR:O	1.85	0.60
12:L:54:LYS:CD	12:L:54:LYS:N	2.64	0.60
14:N:15:LYS:HD2	14:N:16:PHE:CZ	2.37	0.60
20:T:104:LEU:HD12	20:T:105:SER:H	1.66	0.60
4:D:114:ARG:NH1	4:D:114:ARG:HG3	2.13	0.60
5:E:74:GLY:O	5:E:115:VAL:HA	2.01	0.60
9:I:85:LEU:HD12	9:I:85:LEU:O	2.02	0.60
10:J:29:ARG:HG2	10:J:29:ARG:O	2.00	0.60
10:J:5:ARG:O	10:J:98:ILE:HA	2.01	0.60
13:M:37:THR:CG2	13:M:39:ILE:HD11	2.31	0.60
15:O:4:THR:HB	15:O:6:GLU:OE2	2.02	0.60
19:S:25:LYS:O	19:S:26:GLY:O	2.20	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1152:A:H5''	10:J:13:HIS:HD2	1.66	0.60
3:C:130:VAL:O	3:C:134:ILE:HG12	2.01	0.60
3:C:189:ALA:HB3	3:C:196:LEU:HB2	1.84	0.60
20:T:96:GLY:O	20:T:97:ALA:HB3	2.02	0.60
5:E:131:ILE:O	5:E:134:ALA:HB3	2.01	0.59
1:A:521:G:H4'	12:L:73:GLU:HG3	1.84	0.59
13:M:96:LEU:HB3	13:M:97:PRO:HD2	1.83	0.59
3:C:13:GLY:HA3	14:N:57:ARG:CZ	2.31	0.59
17:Q:76:LEU:HD12	17:Q:77:VAL:H	1.66	0.59
2:B:124:SER:HB2	2:B:125:PRO:HD2	1.85	0.59
5:E:42:GLY:HA2	5:E:136:MET:HE1	1.82	0.59
7:G:79:ARG:HH11	7:G:79:ARG:HG2	1.66	0.59
1:A:1306:A:N6	1:A:1331:G:H1'	2.18	0.59
1:A:17:U:H2'	1:A:18:C:C6	2.37	0.59
2:B:188:ALA:HB3	2:B:200:ILE:HG23	1.84	0.59
3:C:60:ALA:O	3:C:61:ALA:CB	2.50	0.59
7:G:23:VAL:HG12	7:G:27:ILE:CD1	2.32	0.59
7:G:66:VAL:O	7:G:70:LYS:HG3	2.02	0.59
8:H:41:ARG:HH11	8:H:41:ARG:HB3	1.66	0.59
9:I:111:ARG:HG2	9:I:112:LYS:N	2.16	0.59
11:K:34:ASP:HB3	11:K:40:ILE:HD11	1.84	0.59
11:K:91:ARG:HH22	18:R:88:LYS:HZ3	1.49	0.59
12:L:48:PRO:CD	12:L:49:ASN:N	2.57	0.59
14:N:44:LEU:HD12	14:N:48:ALA:HB2	1.84	0.59
19:S:16:LEU:O	19:S:20:LEU:HG	2.01	0.59
1:A:715:A:H2'	1:A:716:A:C8	2.38	0.59
1:A:991:U:O4	1:A:1212:U:O2'	2.14	0.59
5:E:72:GLN:O	5:E:73:ASN:HB3	2.02	0.59
6:F:44:GLY:HA2	6:F:59:TYR:CZ	2.37	0.59
8:H:86:ILE:HG13	8:H:133:LEU:HD22	1.84	0.59
10:J:31:GLY:HA3	10:J:78:ASN:ND2	2.18	0.59
13:M:45:VAL:O	13:M:45:VAL:HG22	2.02	0.59
20:T:58:LYS:O	20:T:62:LEU:HD12	2.02	0.59
1:A:1226:C:O2'	13:M:111:LYS:NZ	2.34	0.59
3:C:149:ALA:O	3:C:169:ALA:HA	2.02	0.59
5:E:33:VAL:HG11	5:E:109:ILE:HA	1.83	0.59
6:F:26:ILE:O	6:F:30:LEU:HG	2.02	0.59
2:B:19:HIS:NE2	2:B:206:ASP:HB2	2.18	0.59
3:C:127:ARG:CG	3:C:127:ARG:HH11	2.15	0.59
5:E:79:GLU:HB3	5:E:92:LYS:HA	1.84	0.59
10:J:13:HIS:HB3	10:J:68:HIS:CE1	2.37	0.59
11:K:51:LYS:CA	11:K:55:LYS:HD3	2.21	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:46:LYS:HG2	12:L:47:LYS:H	1.67	0.59
1:A:754:C:H5'	15:O:72:ARG:HH22	1.68	0.59
16:P:43:LYS:HA	16:P:48:TRP:HB2	1.84	0.59
20:T:104:LEU:HD12	20:T:105:SER:N	2.18	0.59
2:B:115:LEU:HD23	2:B:153:ARG:HD3	1.84	0.59
4:D:173:TRP:O	4:D:186:LEU:HB2	2.02	0.59
5:E:68:GLU:HG3	5:E:68:GLU:O	2.02	0.59
9:I:96:LEU:HD23	9:I:102:LEU:HD12	1.84	0.59
14:N:19:ARG:O	14:N:20:ALA:C	2.40	0.59
1:A:1114:C:H1'	14:N:60:SER:HB2	1.83	0.59
1:A:7:G:H5'	1:A:298:A:O4'	2.03	0.59
2:B:69:LEU:O	2:B:162:ILE:HA	2.02	0.59
3:C:36:ASP:HB3	3:C:40:ARG:HH12	1.68	0.59
4:D:163:GLU:C	4:D:165:MET:H	2.03	0.59
8:H:41:ARG:HH11	8:H:41:ARG:CG	2.16	0.59
9:I:17:VAL:HG13	9:I:81:ILE:HD13	1.85	0.59
9:I:40:LEU:HD11	9:I:70:LYS:HG2	1.84	0.59
9:I:66:ARG:HH11	9:I:66:ARG:HG2	1.68	0.59
9:I:9:ARG:HB3	9:I:14:VAL:HG13	1.85	0.59
1:A:1226:C:O2'	13:M:103:THR:O	2.15	0.59
1:A:922:G:H4'	5:E:20:GLN:HA	1.83	0.59
6:F:45:LEU:HD12	6:F:59:TYR:HD1	1.66	0.59
12:L:70:ILE:HD13	12:L:77:LEU:HD12	1.83	0.59
14:N:24:CYS:SG	14:N:40:CYS:N	2.76	0.59
1:A:673:G:H2'	1:A:674:G:C8	2.37	0.59
2:B:187:LEU:CD1	2:B:205:ASP:HA	2.33	0.59
2:B:80:ILE:HD11	2:B:208:ILE:CG2	2.22	0.59
8:H:12:ARG:HH12	8:H:27:PRO:HD2	1.67	0.59
12:L:126:LYS:HB2	12:L:126:LYS:HZ3	1.68	0.59
12:L:54:LYS:HD2	12:L:54:LYS:N	2.18	0.59
13:M:84:ILE:HG23	13:M:85:GLY:N	2.17	0.59
1:A:1014:A:H4'	19:S:14:HIS:CD2	2.37	0.59
22:V:53:G:H4'	22:V:54:U:OP1	2.02	0.59
24:Y:39:C:O2'	24:Y:40:G:OP1	2.21	0.59
2:B:47:THR:HG22	2:B:51:LEU:HG	1.85	0.58
5:E:102:ALA:HB2	5:E:120:THR:OG1	2.03	0.58
12:L:5:PRO:HA	12:L:9:GLN:NE2	2.17	0.58
16:P:53:VAL:HG23	16:P:54:GLU:N	2.18	0.58
17:Q:92:ARG:HH11	17:Q:92:ARG:HG3	1.68	0.58
18:R:31:LEU:HD23	18:R:31:LEU:H	1.67	0.58
4:D:13:ARG:HA	4:D:33:MET:HE3	1.85	0.58
6:F:62:TRP:C	6:F:63:TYR:HD2	2.06	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:T:37:SER:HB3	20:T:84:LEU:HD23	1.85	0.58
4:D:196:LEU:O	4:D:198:VAL:N	2.31	0.58
5:E:111:GLU:C	5:E:113:ALA:H	2.07	0.58
5:E:42:GLY:CA	5:E:66:MET:HG2	2.33	0.58
5:E:78:HIS:CE1	5:E:143:ARG:H	2.20	0.58
6:F:97:PHE:O	18:R:31:LEU:HD23	2.04	0.58
7:G:85:TYR:HE1	7:G:154:TYR:CE1	2.21	0.58
9:I:79:LEU:O	9:I:82:ALA:HB3	2.03	0.58
14:N:23:ARG:CZ	14:N:30:ALA:HB2	2.32	0.58
16:P:28:ARG:HH11	16:P:28:ARG:HG2	1.68	0.58
18:R:36:ASN:ND2	18:R:36:ASN:O	2.32	0.58
19:S:40:ILE:HD11	19:S:62:ILE:HG21	1.85	0.58
1:A:1055:A:O2'	3:C:161:GLU:OE2	2.16	0.58
3:C:77:ILE:O	3:C:84:ILE:HG22	2.02	0.58
4:D:156:GLU:O	4:D:160:GLN:HG3	2.03	0.58
1:A:816:A:OP1	1:A:1526:G:O2'	2.20	0.58
7:G:49:ILE:O	7:G:53:LYS:HB3	2.04	0.58
8:H:10:LEU:H	8:H:10:LEU:CD2	2.15	0.58
12:L:33:ARG:O	12:L:85:ILE:HG22	2.03	0.58
14:N:23:ARG:H	14:N:33:VAL:HG11	1.67	0.58
17:Q:32:TYR:O	17:Q:34:LYS:N	2.37	0.58
5:E:153:LYS:NZ	5:E:153:LYS:HB2	2.18	0.58
10:J:3:LYS:O	10:J:100:THR:HG22	2.04	0.58
13:M:19:LEU:H	13:M:19:LEU:HD22	1.68	0.58
1:A:1187:G:H21	14:N:60:SER:HB3	1.67	0.58
2:B:212:GLN:NE2	2:B:235:SER:HB2	2.18	0.58
4:D:22:LYS:O	4:D:113:SER:HB3	2.03	0.58
1:A:1118:C:OP1	9:I:9:ARG:HD3	2.03	0.58
13:M:56:LEU:HD13	13:M:60:VAL:HG23	1.86	0.58
16:P:51:VAL:CG1	16:P:52:ASP:N	2.65	0.58
19:S:9:VAL:HG23	19:S:9:VAL:O	2.04	0.58
1:A:1014:A:H4'	19:S:14:HIS:NE2	2.18	0.58
2:B:21:ARG:HG3	2:B:38:GLY:O	2.01	0.58
3:C:105:GLU:HG2	3:C:106:VAL:N	2.18	0.58
11:K:21:ILE:HG13	11:K:30:VAL:HG12	1.86	0.58
1:A:184:G:H2'	1:A:185:A:H8	1.68	0.58
11:K:30:VAL:HG21	11:K:65:ALA:HA	1.85	0.58
19:S:17:GLU:HA	19:S:20:LEU:HD12	1.86	0.58
7:G:69:VAL:HG11	7:G:104:LEU:CD2	2.34	0.57
13:M:81:LEU:HB3	13:M:89:GLY:CA	2.34	0.57
16:P:21:VAL:HG22	16:P:34:GLU:O	2.04	0.57
2:B:140:HIS:HA	2:B:143:GLU:OE1	2.04	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:80:ILE:HG21	2:B:212:GLN:HA	1.84	0.57
2:B:111:ARG:NE	2:B:111:ARG:HA	2.19	0.57
2:B:37:ASN:C	2:B:39:ILE:H	2.07	0.57
3:C:14:ILE:HG12	3:C:15:THR:N	2.19	0.57
3:C:181:ASN:HD22	3:C:204:LEU:HB2	1.68	0.57
4:D:100:ARG:HH22	4:D:137:SER:HB3	1.70	0.57
15:O:26:GLU:CD	15:O:77:ARG:NH1	2.58	0.57
2:B:12:GLU:O	2:B:16:HIS:ND1	2.36	0.57
2:B:97:TRP:HH2	2:B:176:GLU:HB2	1.69	0.57
1:A:1112:C:H1'	3:C:179:ARG:HH11	1.68	0.57
11:K:32:ILE:O	11:K:40:ILE:HG12	2.04	0.57
11:K:69:ALA:HB1	11:K:103:LEU:HD21	1.85	0.57
13:M:82:MET:O	13:M:84:ILE:N	2.38	0.57
1:A:1159:U:O2'	1:A:1160:G:N7	2.36	0.57
3:C:57:ILE:HG23	3:C:64:VAL:HG13	1.86	0.57
3:C:77:ILE:O	3:C:83:ARG:HB3	2.05	0.57
6:F:99:ALA:O	6:F:100:ASN:HB2	2.04	0.57
7:G:16:LEU:CD1	9:I:45:ALA:HB2	2.34	0.57
10:J:64:GLU:OE2	10:J:66:ARG:HD2	2.05	0.57
13:M:121:LYS:NZ	24:Y:39:C:O2'	2.38	0.57
19:S:65:ASN:N	19:S:65:ASN:ND2	2.52	0.57
1:A:516:U:O2'	1:A:519:C:N3	2.35	0.57
1:A:1073:U:O2'	2:B:104:ASN:OD1	2.21	0.57
3:C:90:GLU:O	3:C:94:LEU:HG	2.05	0.57
1:A:428:G:O3'	4:D:36:ARG:NH2	2.38	0.57
4:D:50:ARG:HD2	4:D:50:ARG:O	2.05	0.57
5:E:140:ARG:HB2	5:E:140:ARG:HH11	1.69	0.57
6:F:39:LYS:HD2	6:F:64:GLN:NE2	2.19	0.57
10:J:22:LYS:C	10:J:22:LYS:HD2	2.25	0.57
16:P:76:GLN:HG2	16:P:76:GLN:O	2.05	0.57
4:D:191:ARG:NH1	4:D:200:GLU:OE1	2.37	0.57
14:N:13:THR:N	14:N:14:PRO:CD	2.68	0.57
14:N:44:LEU:C	14:N:44:LEU:HD12	2.24	0.57
20:T:10:LEU:HG	20:T:12:ALA:H	1.70	0.57
1:A:45:U:H2'	1:A:46:G:C8	2.40	0.57
1:A:15:G:H4'	5:E:24:ARG:NH1	2.20	0.57
7:G:113:GLU:HB2	7:G:119:ARG:CG	2.35	0.57
10:J:74:ILE:HD13	10:J:74:ILE:N	2.16	0.57
18:R:85:LEU:HD23	18:R:88:LYS:HD2	1.86	0.57
1:A:1292:U:OP1	7:G:41:ARG:NH2	2.38	0.57
1:A:1346:A:H5'	9:I:120:ARG:HH12	1.68	0.57
1:A:1391:U:H2'	1:A:1392:G:C8	2.39	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:106:LYS:O	2:B:110:GLN:HG3	2.05	0.57
2:B:30:ARG:HH21	2:B:194:PRO:CG	2.17	0.57
3:C:76:VAL:HG21	3:C:103:VAL:CG1	2.34	0.57
4:D:119:GLN:HG3	4:D:123:HIS:CD2	2.40	0.57
8:H:84:ARG:NH1	8:H:86:ILE:HD13	2.11	0.57
10:J:94:VAL:HG12	10:J:95:GLU:N	2.19	0.57
11:K:29:ILE:HG13	11:K:43:SER:O	2.04	0.57
9:I:17:VAL:CG1	9:I:81:ILE:HD13	2.35	0.57
1:A:1152:A:OP1	10:J:68:HIS:NE2	2.36	0.57
11:K:69:ALA:HB1	11:K:103:LEU:CD2	2.35	0.57
13:M:69:GLU:O	13:M:71:ARG:N	2.38	0.57
16:P:14:ASN:N	16:P:15:PRO:CD	2.67	0.57
1:A:1118:C:H1'	1:A:1179:A:C4	2.40	0.56
3:C:59:ARG:HH12	3:C:97:LYS:HE3	1.70	0.56
3:C:59:ARG:NH2	3:C:97:LYS:HE3	2.20	0.56
11:K:21:ILE:HD12	11:K:21:ILE:N	2.19	0.56
12:L:45:PRO:HD3	12:L:51:ALA:O	2.04	0.56
15:O:53:HIS:CE1	15:O:57:LEU:HD11	2.40	0.56
17:Q:6:LEU:O	17:Q:58:GLU:HA	2.05	0.56
18:R:57:GLY:O	18:R:58:LEU:C	2.44	0.56
2:B:77:ALA:CB	2:B:211:ILE:HG21	2.35	0.56
3:C:7:PRO:O	3:C:11:ARG:HG2	2.05	0.56
7:G:121:ALA:O	7:G:125:MET:N	2.37	0.56
7:G:18:TYR:HD2	7:G:59:LEU:HD22	1.70	0.56
8:H:119:LEU:HD12	8:H:124:ALA:HA	1.87	0.56
16:P:7:ALA:O	16:P:9:PHE:CD2	2.58	0.56
20:T:47:GLY:C	20:T:49:ALA:H	2.07	0.56
20:T:53:LEU:HA	20:T:56:MET:HB3	1.87	0.56
2:B:60:ASP:HB3	2:B:64:ARG:CZ	2.35	0.56
12:L:58:VAL:O	12:L:65:GLU:HA	2.06	0.56
12:L:82:VAL:HG23	12:L:106:ASP:OD2	2.04	0.56
13:M:84:ILE:CG2	13:M:85:GLY:N	2.68	0.56
19:S:40:ILE:HG12	19:S:41:VAL:N	2.20	0.56
21:U:7:ARG:O	21:U:8:THR:HG23	2.05	0.56
1:A:713:G:H2'	1:A:714:G:C8	2.40	0.56
1:A:920:U:H2'	1:A:921:U:C6	2.41	0.56
3:C:188:LEU:O	3:C:189:ALA:HB2	2.05	0.56
9:I:10:ARG:CD	9:I:105:ASP:HB2	2.35	0.56
13:M:73:GLU:O	13:M:77:ASN:N	2.33	0.56
14:N:25:VAL:N	14:N:38:GLY:O	2.38	0.56
20:T:82:SER:O	20:T:86:ARG:HB2	2.06	0.56
3:C:114:PRO:O	3:C:118:GLN:HG3	2.05	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:42:GLN:HG2	4:D:42:GLN:O	2.05	0.56
6:F:97:PHE:C	6:F:97:PHE:CD2	2.76	0.56
16:P:4:ILE:HA	16:P:20:VAL:O	2.05	0.56
1:A:1064:G:O2'	1:A:1065:U:O5'	2.21	0.56
1:A:954:G:H21	1:A:1227:A:H62	1.52	0.56
1:A:411:A:C5	1:A:413:G:H1'	2.40	0.56
3:C:77:ILE:C	3:C:83:ARG:HB3	2.26	0.56
8:H:19:VAL:O	8:H:20:TYR:HB2	2.05	0.56
8:H:77:GLU:HG2	8:H:78:GLN:H	1.71	0.56
9:I:9:ARG:HB2	9:I:14:VAL:HG22	1.88	0.56
10:J:24:VAL:HG21	10:J:37:PRO:HG3	1.86	0.56
12:L:18:VAL:O	12:L:19:ARG:HB2	2.04	0.56
13:M:4:ILE:HG22	13:M:5:ALA:N	2.19	0.56
17:Q:50:LYS:HG3	17:Q:51:TYR:CE1	2.41	0.56
17:Q:84:LEU:C	17:Q:86:GLU:H	2.08	0.56
19:S:15:LEU:HD23	19:S:15:LEU:N	2.19	0.56
3:C:33:LEU:O	3:C:37:GLN:HG2	2.04	0.56
4:D:165:MET:CE	4:D:165:MET:HA	2.36	0.56
5:E:99:GLY:O	5:E:117:ASP:HA	2.06	0.56
5:E:82:VAL:CG1	5:E:83:GLU:N	2.68	0.56
9:I:33:PHE:CE2	9:I:47:LEU:HD21	2.40	0.56
15:O:24:SER:O	15:O:28:GLN:HG3	2.06	0.56
15:O:76:GLU:C	15:O:78:TYR:H	2.08	0.56
1:A:411:A:H62	1:A:413:G:H21	1.53	0.56
2:B:7:VAL:HG22	2:B:8:LYS:N	2.21	0.56
3:C:134:ILE:CD1	3:C:153:VAL:HG21	2.35	0.56
3:C:6:HIS:CD2	3:C:7:PRO:HD2	2.41	0.56
3:C:95:THR:CG2	3:C:96:GLY:H	2.10	0.56
5:E:140:ARG:HH11	5:E:140:ARG:CB	2.18	0.56
6:F:33:TYR:HE2	6:F:74:ASP:HB3	1.71	0.56
13:M:89:GLY:O	13:M:92:HIS:HB2	2.06	0.56
14:N:15:LYS:O	14:N:16:PHE:O	2.24	0.56
20:T:94:ALA:O	20:T:95:ALA:CB	2.54	0.56
3:C:45:LYS:HD2	3:C:46:GLU:HG3	1.87	0.56
4:D:110:PHE:CE2	4:D:148:VAL:HG23	2.41	0.56
8:H:7:ALA:HB2	8:H:85:ARG:HD3	1.87	0.56
13:M:49:THR:HB	13:M:52:GLU:HG3	1.86	0.56
2:B:102:LEU:HB3	2:B:180:LEU:CD1	2.36	0.56
1:A:545:C:OP2	4:D:62:GLN:NE2	2.39	0.56
7:G:42:ILE:O	7:G:117:ALA:HB2	2.05	0.56
7:G:148:ASN:C	7:G:150:ALA:H	2.08	0.56
7:G:73:MET:HG2	7:G:90:GLU:HA	1.87	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:38:ILE:HD12	8:H:118:VAL:HG12	1.87	0.56
8:H:49:GLU:HG3	8:H:51:VAL:CG1	2.35	0.56
9:I:114:TYR:CD2	9:I:114:TYR:O	2.59	0.56
12:L:83:VAL:HG22	12:L:84:LEU:H	1.70	0.56
16:P:48:TRP:O	16:P:49:LEU:HB2	2.06	0.56
17:Q:41:LYS:HZ1	17:Q:92:ARG:HH22	1.53	0.56
1:A:457:C:H42	1:A:475:G:H1	1.54	0.56
7:G:62:PHE:HA	7:G:124:LEU:CD2	2.27	0.56
10:J:35:SER:O	10:J:72:VAL:HG13	2.05	0.56
10:J:89:ASP:C	10:J:90:LEU:HD12	2.26	0.56
11:K:125:PHE:N	11:K:125:PHE:CD1	2.74	0.56
11:K:41:THR:HG21	11:K:71:LYS:CB	2.36	0.56
12:L:111:LYS:O	12:L:112:ASP:HB2	2.05	0.56
17:Q:84:LEU:C	17:Q:86:GLU:N	2.60	0.56
20:T:74:LYS:C	20:T:76:ALA:H	2.10	0.56
3:C:180:ALA:O	3:C:181:ASN:HB3	2.06	0.55
10:J:26:ALA:HA	10:J:29:ARG:NH2	2.21	0.55
13:M:80:ARG:O	13:M:84:ILE:HB	2.06	0.55
14:N:44:LEU:CD1	14:N:48:ALA:HB2	2.36	0.55
1:A:1151:A:H2'	1:A:1152:A:H8	1.71	0.55
2:B:46:LYS:HA	2:B:49:GLU:OE1	2.06	0.55
5:E:126:ARG:HG3	5:E:126:ARG:NH1	2.19	0.55
7:G:46:ALA:HB2	7:G:117:ALA:HB1	1.88	0.55
8:H:128:GLY:O	8:H:129:VAL:HG13	2.06	0.55
13:M:81:LEU:HB3	13:M:89:GLY:HA2	1.88	0.55
16:P:53:VAL:HG23	16:P:54:GLU:H	1.70	0.55
1:A:1014:A:H4'	19:S:14:HIS:HE2	1.71	0.55
19:S:18:LYS:O	19:S:22:LEU:HD13	2.06	0.55
21:U:6:ARG:HH21	21:U:15:ARG:HE	1.53	0.55
1:A:1095:U:H5''	1:A:1109:C:O2	2.06	0.55
1:A:939:G:H5''	7:G:102:ARG:HH12	1.71	0.55
2:B:204:ASN:HD22	2:B:205:ASP:N	2.04	0.55
5:E:7:GLU:HG2	5:E:112:LEU:HD22	1.88	0.55
8:H:82:HIS:HD2	8:H:83:ILE:N	2.03	0.55
15:O:65:ARG:NH1	15:O:65:ARG:HB2	2.20	0.55
16:P:59:TRP:CE3	16:P:59:TRP:HA	2.42	0.55
2:B:217:ARG:HA	2:B:220:ASP:OD2	2.06	0.55
3:C:20:SER:CB	3:C:40:ARG:HH22	2.14	0.55
5:E:144:THR:O	5:E:148:VAL:HG23	2.06	0.55
9:I:82:ALA:O	9:I:86:VAL:HB	2.06	0.55
10:J:6:ILE:CG2	10:J:98:ILE:HG13	2.21	0.55
11:K:125:PHE:HD1	11:K:125:PHE:H	1.54	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:34:ASP:N	11:K:40:ILE:HD11	2.20	0.55
11:K:50:TYR:HH	11:K:59:TYR:HE2	1.54	0.55
16:P:47:ASP:C	16:P:49:LEU:H	2.09	0.55
1:A:757:U:H2'	1:A:758:G:O4'	2.07	0.55
2:B:169:LYS:HD3	2:B:169:LYS:O	2.06	0.55
3:C:112:SER:OG	3:C:115:LEU:HG	2.06	0.55
7:G:20:ASP:HB3	7:G:23:VAL:HG23	1.88	0.55
8:H:49:GLU:O	8:H:51:VAL:N	2.39	0.55
19:S:41:VAL:CB	19:S:42:PRO:CA	2.76	0.55
4:D:126:ILE:HG22	4:D:127:THR:N	2.22	0.55
5:E:92:LYS:O	5:E:118:ILE:HD12	2.07	0.55
8:H:23:SER:HB2	8:H:61:VAL:O	2.07	0.55
17:Q:62:SER:HB3	17:Q:72:ARG:HH21	1.72	0.55
19:S:7:LYS:HG3	19:S:8:GLY:N	2.22	0.55
1:A:1372:U:OP1	9:I:71:SER:HB3	2.06	0.55
3:C:11:ARG:HH21	3:C:180:ALA:HB3	1.70	0.55
3:C:188:LEU:HD22	3:C:188:LEU:N	2.21	0.55
8:H:102:ARG:HH11	8:H:105:ARG:CZ	2.19	0.55
9:I:45:ALA:O	9:I:48:GLU:HG2	2.07	0.55
10:J:16:LEU:HD13	10:J:16:LEU:O	2.07	0.55
10:J:32:ALA:O	10:J:33:GLN:O	2.25	0.55
14:N:25:VAL:HG23	14:N:38:GLY:C	2.21	0.55
1:A:1376:U:H2'	1:A:1377:A:C8	2.42	0.55
7:G:37:ASN:HD21	9:I:40:LEU:HD23	1.69	0.55
9:I:40:LEU:HD11	9:I:70:LYS:CG	2.37	0.55
12:L:79:GLU:O	12:L:79:GLU:HG2	2.06	0.55
15:O:29:VAL:HG11	15:O:67:LEU:HD21	1.89	0.55
15:O:77:ARG:HA	15:O:80:ALA:CB	2.36	0.55
2:B:214:ILE:HA	2:B:217:ARG:NH2	2.21	0.55
7:G:50:ILE:CB	7:G:58:PRO:HB3	2.37	0.55
7:G:50:ILE:O	7:G:50:ILE:HG22	2.07	0.55
9:I:66:ARG:NH1	9:I:66:ARG:HG2	2.22	0.55
14:N:22:THR:HB	14:N:33:VAL:HG11	1.89	0.55
1:A:1205:U:H5'	3:C:190:ARG:NH2	2.22	0.54
2:B:68:ILE:HD12	2:B:68:ILE:N	2.21	0.54
2:B:80:ILE:CG2	2:B:212:GLN:HA	2.35	0.54
3:C:134:ILE:HG21	3:C:168:ALA:HB3	1.89	0.54
12:L:83:VAL:HG22	12:L:84:LEU:N	2.21	0.54
16:P:21:VAL:O	16:P:33:ILE:N	2.39	0.54
17:Q:33:GLY:O	17:Q:34:LYS:O	2.25	0.54
23:X:6:C:HO2'	23:X:7:U:P	2.28	0.54
1:A:347:G:O2'	1:A:348:G:OP2	2.20	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:41:ILE:HD12	2:B:41:ILE:N	2.21	0.54
3:C:43:LEU:O	3:C:47:LEU:HB3	2.08	0.54
9:I:70:LYS:O	9:I:74:ILE:HG13	2.07	0.54
10:J:19:SER:O	10:J:23:ILE:HG13	2.07	0.54
14:N:24:CYS:SG	14:N:39:LEU:CA	2.94	0.54
16:P:43:LYS:HA	16:P:48:TRP:CB	2.37	0.54
6:F:91:VAL:CG1	18:R:72:ARG:HH12	2.18	0.54
21:U:21:TYR:O	21:U:22:ARG:HB2	2.05	0.54
1:A:114:U:H2'	1:A:115:G:C8	2.41	0.54
1:A:1053:G:O6	1:A:1199:U:H2'	2.06	0.54
1:A:1499:A:H1'	1:A:1520:G:H5'	1.89	0.54
1:A:745:C:OP1	1:A:851:G:O2'	2.24	0.54
6:F:52:ILE:O	6:F:53:ALA:HB3	2.07	0.54
11:K:125:PHE:N	11:K:125:PHE:HD1	2.05	0.54
16:P:4:ILE:N	16:P:4:ILE:HD12	2.23	0.54
1:A:1128:C:H42	1:A:1144:G:H1	1.54	0.54
1:A:686:U:O4	1:A:703:G:H1'	2.08	0.54
2:B:83:MET:O	2:B:85:ALA:N	2.41	0.54
3:C:107:GLN:N	3:C:107:GLN:CD	2.61	0.54
3:C:181:ASN:HD21	3:C:204:LEU:CD1	2.12	0.54
4:D:13:ARG:HD2	4:D:40:PRO:HD3	1.89	0.54
8:H:97:VAL:CG1	8:H:98:LYS:N	2.70	0.54
13:M:121:LYS:HE2	13:M:121:LYS:N	2.22	0.54
16:P:28:ARG:HG2	16:P:28:ARG:NH1	2.22	0.54
1:A:1095:U:P	1:A:1108:G:H1	2.30	0.54
4:D:19:LEU:N	4:D:19:LEU:HD23	2.23	0.54
7:G:62:PHE:O	7:G:66:VAL:HG23	2.06	0.54
8:H:51:VAL:HG11	8:H:60:ARG:CG	2.37	0.54
10:J:101:VAL:HG22	10:J:101:VAL:O	2.07	0.54
15:O:21:ASP:OD1	15:O:24:SER:HB2	2.07	0.54
15:O:87:ILE:CG2	15:O:88:ARG:H	2.00	0.54
18:R:39:VAL:HA	18:R:42:ARG:NH1	2.23	0.54
20:T:43:LEU:HA	20:T:46:GLU:HB3	1.88	0.54
2:B:142:LEU:C	2:B:142:LEU:HD23	2.27	0.54
4:D:33:MET:HE1	4:D:37:PRO:HA	1.89	0.54
13:M:34:LEU:CD1	13:M:41:PRO:HG3	2.38	0.54
3:C:109:PRO:O	3:C:115:LEU:HD12	2.08	0.54
8:H:101:PRO:HG2	8:H:133:LEU:HD11	1.89	0.54
16:P:3:LYS:O	16:P:21:VAL:HA	2.08	0.54
1:A:1297:C:H4'	1:A:1298:C:H5'	1.90	0.54
2:B:170:GLU:HA	2:B:172:ILE:HD12	1.90	0.54
4:D:23:GLY:HA3	4:D:112:VAL:CG2	2.38	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:102:ARG:NH1	8:H:105:ARG:NH1	2.55	0.54
12:L:83:VAL:CG2	12:L:100:ILE:HG23	2.38	0.54
12:L:10:LEU:HD13	17:Q:32:TYR:CD2	2.41	0.54
21:U:6:ARG:O	21:U:8:THR:N	2.39	0.54
1:A:1446:A:O2'	1:A:1447:G:O5'	2.24	0.54
2:B:16:HIS:CE1	2:B:209:ARG:HH21	2.25	0.54
2:B:55:PHE:HA	2:B:58:ILE:HB	1.88	0.54
3:C:92:ALA:HB2	3:C:99:VAL:CG1	2.37	0.54
4:D:79:PHE:CE2	4:D:83:SER:HB2	2.43	0.54
6:F:78:GLU:OE2	6:F:81:ILE:HD12	2.08	0.54
6:F:92:LYS:NZ	6:F:92:LYS:HB2	2.22	0.54
7:G:13:GLN:O	7:G:24:THR:HG21	2.08	0.54
11:K:24:SER:HB3	11:K:27:ASN:O	2.08	0.54
12:L:6:THR:OG1	12:L:9:GLN:HG3	2.08	0.54
14:N:13:THR:N	14:N:14:PRO:HD2	2.22	0.54
1:A:1363:A:H4'	1:A:1364:U:H5''	1.89	0.54
3:C:53:ALA:HB2	3:C:115:LEU:HD21	1.90	0.54
9:I:99:LEU:O	9:I:101:PHE:N	2.41	0.54
3:C:195:VAL:CG1	3:C:196:LEU:N	2.71	0.53
7:G:102:ARG:O	7:G:106:GLN:HG3	2.08	0.53
8:H:77:GLU:HG2	8:H:78:GLN:N	2.22	0.53
16:P:75:ARG:C	16:P:77:ALA:H	2.11	0.53
19:S:15:LEU:CD2	19:S:15:LEU:H	2.21	0.53
22:V:68:C:H2'	22:V:69:C:C6	2.42	0.53
2:B:134:GLU:O	2:B:138:LEU:HD12	2.07	0.53
3:C:51:GLY:O	3:C:70:VAL:HG13	2.08	0.53
5:E:12:LEU:O	5:E:13:ILE:HD12	2.08	0.53
6:F:41:GLU:HG2	6:F:43:LEU:HD11	1.89	0.53
7:G:12:LEU:N	7:G:12:LEU:HD22	2.23	0.53
9:I:13:ALA:HA	9:I:66:ARG:O	2.08	0.53
13:M:76:ALA:O	13:M:79:LYS:HB3	2.09	0.53
14:N:23:ARG:O	14:N:24:CYS:C	2.46	0.53
18:R:25:THR:C	18:R:26:LEU:HD23	2.29	0.53
13:M:66:LEU:O	13:M:67:GLU:C	2.46	0.53
15:O:7:GLU:O	15:O:11:VAL:HG23	2.08	0.53
1:A:690:G:H2'	1:A:691:G:O4'	2.09	0.53
1:A:701:C:H1'	1:A:703:G:C6	2.43	0.53
1:A:939:G:H5''	7:G:102:ARG:NH1	2.23	0.53
2:B:134:GLU:HB3	2:B:138:LEU:CD1	2.39	0.53
2:B:187:LEU:HD22	2:B:201:ILE:O	2.07	0.53
2:B:75:LYS:HD3	2:B:75:LYS:C	2.29	0.53
4:D:198:VAL:HG12	4:D:199:ASN:H	1.74	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:I:28:VAL:HG13	9:I:63:ILE:HG21	1.89	0.53
9:I:4:TYR:CE2	9:I:88:TYR:HB2	2.44	0.53
10:J:61:GLU:HG3	14:N:58:LYS:HE2	1.90	0.53
12:L:42:THR:HA	12:L:53:ARG:O	2.08	0.53
17:Q:5:VAL:O	17:Q:6:LEU:HD23	2.09	0.53
18:R:58:LEU:HD12	18:R:58:LEU:H	1.72	0.53
23:X:6:C:O2'	23:X:7:U:P	2.66	0.53
1:A:612:C:O2	1:A:629:G:N2	2.41	0.53
2:B:24:TRP:CE2	2:B:26:PRO:HD3	2.44	0.53
3:C:173:VAL:HG12	3:C:173:VAL:O	2.08	0.53
3:C:3:ASN:ND2	3:C:3:ASN:H	2.05	0.53
4:D:153:ARG:NH1	4:D:181:MET:CG	2.71	0.53
4:D:173:TRP:CD1	4:D:174:LEU:HG	2.44	0.53
5:E:140:ARG:HB2	5:E:140:ARG:NH1	2.23	0.53
1:A:677:U:H1'	11:K:119:CYS:SG	2.48	0.53
1:A:522:C:H41	12:L:53:ARG:NH2	2.06	0.53
1:A:119:A:H4'	1:A:120:A:O5'	2.07	0.53
1:A:411:A:C4	1:A:413:G:H1'	2.44	0.53
1:A:885:G:O2'	1:A:914:A:N1	2.37	0.53
3:C:78:GLY:HA3	3:C:83:ARG:CB	2.38	0.53
7:G:137:LYS:O	7:G:141:VAL:HG23	2.07	0.53
11:K:20:TYR:HB2	11:K:31:THR:O	2.07	0.53
17:Q:11:VAL:HG22	17:Q:20:THR:O	2.09	0.53
1:A:688:G:H2'	1:A:689:C:H6	1.74	0.53
2:B:87:ARG:HH11	2:B:223:ILE:HD12	1.73	0.53
2:B:96:ARG:H	2:B:96:ARG:CD	2.16	0.53
4:D:147:ALA:HA	4:D:182:LYS:HA	1.91	0.53
5:E:36:ASP:OD1	5:E:37:ARG:N	2.42	0.53
10:J:16:LEU:O	10:J:20:ALA:HB2	2.08	0.53
13:M:39:ILE:HD11	13:M:56:LEU:HB2	1.90	0.53
13:M:3:ARG:HA	13:M:9:ILE:CG2	2.22	0.53
16:P:72:ARG:HD3	16:P:73:LEU:HD23	1.91	0.53
18:R:51:LEU:HD22	18:R:55:ARG:HD2	1.89	0.53
21:U:14:TRP:CZ3	21:U:15:ARG:HD3	2.43	0.53
24:Y:39:C:HO2'	24:Y:40:G:P	2.31	0.53
1:A:1120:G:H2'	1:A:1121:U:C6	2.44	0.53
1:A:606:G:H22	1:A:631:G:H5'	1.72	0.53
2:B:233:SER:OG	2:B:234:PRO:HD2	2.09	0.53
2:B:5:ILE:HD13	2:B:5:ILE:N	2.24	0.53
6:F:75:LEU:HD23	6:F:79:LEU:HG	1.91	0.53
1:A:1172:C:H2'	1:A:1173:G:C8	2.44	0.53
1:A:980:C:H5'	1:A:981:U:OP2	2.09	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:200:ILE:HG22	2:B:201:ILE:N	2.24	0.53
4:D:172:PRO:HB2	4:D:193:ASP:OD2	2.08	0.53
4:D:206:PHE:HD2	4:D:207:TYR:CD1	2.27	0.53
5:E:101:ILE:HG12	5:E:101:ILE:O	2.08	0.53
9:I:47:LEU:HB3	9:I:50:LEU:HD12	1.90	0.53
13:M:92:HIS:CD2	13:M:98:VAL:HG21	2.43	0.53
15:O:6:GLU:H	15:O:6:GLU:CD	2.12	0.53
19:S:29:ARG:HD3	19:S:30:LEU:HD13	1.91	0.53
1:A:1397:C:H1'	23:X:8:A:N6	2.24	0.53
1:A:243:A:H4'	1:A:244:U:O5'	2.07	0.53
3:C:134:ILE:CG2	3:C:168:ALA:HB3	2.39	0.53
3:C:29:TYR:OH	14:N:54:PRO:HD2	2.09	0.53
4:D:108:LEU:HD11	4:D:174:LEU:CD2	2.37	0.53
7:G:95:ARG:CZ	7:G:99:LEU:HD11	2.38	0.53
9:I:53:VAL:CB	9:I:95:LYS:HE3	2.36	0.53
1:A:1329:A:P	13:M:28:ALA:HB3	2.49	0.53
17:Q:65:ILE:H	17:Q:65:ILE:HD12	1.74	0.53
18:R:29:PHE:N	18:R:29:PHE:CD2	2.76	0.53
20:T:30:LYS:HE2	20:T:72:LEU:HD12	1.91	0.53
2:B:102:LEU:HB3	2:B:180:LEU:HD12	1.90	0.52
2:B:206:ASP:O	2:B:207:ALA:HB3	2.08	0.52
4:D:120:LEU:HD22	4:D:125:HIS:CB	2.38	0.52
13:M:73:GLU:O	13:M:76:ALA:N	2.42	0.52
16:P:1:MET:SD	16:P:3:LYS:HE3	2.49	0.52
1:A:501:C:OP1	12:L:117:ARG:NH2	2.40	0.52
1:A:1112:C:H1'	3:C:179:ARG:NH1	2.24	0.52
6:F:89:MET:HG2	6:F:89:MET:O	2.09	0.52
7:G:89:MET:CE	7:G:156:TRP:H	2.22	0.52
18:R:44:LEU:HD12	18:R:44:LEU:N	2.24	0.52
22:V:4:G:HO2'	22:V:5:G:H8	1.56	0.52
1:A:964:A:N3	1:A:969:A:O2'	2.40	0.52
3:C:140:ARG:HG3	3:C:140:ARG:HH11	1.75	0.52
4:D:176:LEU:HD12	4:D:182:LYS:O	2.10	0.52
4:D:13:ARG:HB3	4:D:33:MET:HE2	1.91	0.52
13:M:87:TYR:CE1	13:M:91:ARG:HD3	2.44	0.52
15:O:62:GLN:N	15:O:65:ARG:HH12	2.06	0.52
19:S:11:VAL:O	19:S:11:VAL:HG13	2.10	0.52
19:S:65:ASN:H	19:S:65:ASN:ND2	2.08	0.52
22:V:15:G:H22	22:V:48:C:H42	1.58	0.52
1:A:1321:C:H3'	1:A:1322:C:H5''	1.91	0.52
2:B:9:GLU:N	2:B:9:GLU:OE2	2.42	0.52
5:E:87:SER:HB3	5:E:131:ILE:CD1	2.38	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:87:SER:HA	8:H:93:VAL:HG23	1.91	0.52
9:I:113:LYS:HD3	9:I:119:ALA:O	2.09	0.52
15:O:26:GLU:HA	15:O:81:LEU:HD22	1.90	0.52
11:K:91:ARG:NH2	18:R:88:LYS:NZ	2.58	0.52
19:S:50:ALA:CB	19:S:57:HIS:HB3	2.37	0.52
1:A:1343:G:H2'	1:A:1344:C:C6	2.44	0.52
1:A:1513:A:H2'	1:A:1514:C:C6	2.44	0.52
1:A:164:U:H2'	1:A:165:C:C6	2.45	0.52
1:A:718:G:H5'	11:K:117:ASN:OD1	2.10	0.52
2:B:188:ALA:HB3	2:B:200:ILE:CG2	2.40	0.52
8:H:100:ILE:CB	8:H:125:ARG:HH12	2.20	0.52
12:L:127:GLU:O	12:L:128:ALA:HB3	2.10	0.52
1:A:1238:A:H62	1:A:1299:A:N6	2.08	0.52
1:A:65:U:H5''	1:A:65:U:H6	1.75	0.52
4:D:10:ARG:O	4:D:14:ARG:HB2	2.08	0.52
4:D:106:TYR:CE1	4:D:112:VAL:O	2.62	0.52
9:I:13:ALA:HB2	9:I:68:GLY:HA3	1.91	0.52
10:J:4:ILE:HB	10:J:74:ILE:CD1	2.37	0.52
1:A:1314:C:H5	19:S:4:SER:HB2	1.75	0.52
1:A:1348:U:C4	1:A:1374:A:H2	2.28	0.52
1:A:280:C:C2	17:Q:38:ARG:HG3	2.44	0.52
4:D:29:PRO:CG	4:D:30:LYS:NZ	2.73	0.52
4:D:31:CYS:O	4:D:32:ALA:HB3	2.10	0.52
7:G:85:TYR:HE1	7:G:154:TYR:HE1	1.56	0.52
16:P:34:GLU:OE1	16:P:55:ARG:HD3	2.10	0.52
20:T:89:ARG:HH22	20:T:106:ALA:HB2	1.75	0.52
2:B:92:TYR:CE1	2:B:151:GLY:HA3	2.45	0.52
3:C:22:TRP:CZ3	3:C:32:LEU:HD12	2.45	0.52
9:I:13:ALA:HB2	9:I:67:GLY:C	2.29	0.52
10:J:39:PRO:HB3	10:J:70:ARG:NH1	2.23	0.52
12:L:32:PHE:HE1	12:L:86:ARG:HG3	1.73	0.52
13:M:81:LEU:HD13	13:M:88:ARG:HD2	1.91	0.52
1:A:620:C:H2'	1:A:621:A:O4'	2.10	0.52
2:B:232:PRO:O	2:B:233:SER:O	2.27	0.52
3:C:150:LYS:HG3	3:C:169:ALA:HB2	1.92	0.52
6:F:10:LEU:HD13	6:F:61:LEU:HD11	1.92	0.52
6:F:99:ALA:HB1	18:R:23:LYS:NZ	2.25	0.52
7:G:106:GLN:O	7:G:110:GLN:HG3	2.10	0.52
7:G:151:TYR:HA	7:G:153:HIS:CE1	2.45	0.52
13:M:34:LEU:HD12	13:M:41:PRO:HG3	1.92	0.52
14:N:7:ILE:CG1	14:N:8:GLU:N	2.72	0.52
15:O:16:ALA:HB1	15:O:21:ASP:HB3	1.92	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1053:G:N7	1:A:1199:U:H3'	2.24	0.52
1:A:1297:C:HO2'	1:A:1298:C:C5'	2.23	0.52
1:A:1297:C:O2'	1:A:1298:C:O5'	2.26	0.52
1:A:1412:C:H2'	1:A:1413:A:C8	2.45	0.52
5:E:60:TYR:CE1	5:E:64:ARG:NH2	2.77	0.52
19:S:63:THR:O	19:S:66:MET:HG2	2.09	0.52
1:A:1001:G:H2'	1:A:1002:G:O4'	2.10	0.51
1:A:115:G:H4'	1:A:116:A:O5'	2.09	0.51
1:A:1176:A:H2'	1:A:1177:G:H5'	1.92	0.51
3:C:11:ARG:O	3:C:13:GLY:N	2.43	0.51
3:C:35:GLU:OE2	3:C:95:THR:HG23	2.10	0.51
4:D:196:LEU:H	4:D:196:LEU:HD12	1.75	0.51
4:D:65:ARG:NH1	4:D:70:ILE:O	2.43	0.51
13:M:66:LEU:O	13:M:68:GLY:N	2.43	0.51
13:M:98:VAL:O	13:M:98:VAL:HG12	2.10	0.51
18:R:64:ARG:O	18:R:66:LEU:N	2.43	0.51
19:S:40:ILE:HG23	19:S:67:VAL:O	2.11	0.51
1:A:190:G:HO2'	1:A:191(A):G:P	2.33	0.51
1:A:281:G:HO2'	1:A:282:A:H8	1.58	0.51
2:B:53:ARG:O	2:B:56:ARG:HB2	2.10	0.51
3:C:112:SER:HB3	3:C:115:LEU:HD12	1.92	0.51
3:C:195:VAL:HG12	3:C:196:LEU:H	1.75	0.51
3:C:40:ARG:O	3:C:44:GLU:HG3	2.11	0.51
6:F:10:LEU:HD13	6:F:61:LEU:HD13	1.92	0.51
9:I:126:SER:O	9:I:128:ARG:N	2.35	0.51
16:P:21:VAL:O	16:P:33:ILE:HG12	2.11	0.51
17:Q:48:GLU:O	17:Q:49:GLU:C	2.48	0.51
1:A:266:G:O2'	1:A:267:C:OP2	2.24	0.51
1:A:9:G:OP1	5:E:122:GLU:N	2.38	0.51
3:C:22:TRP:CH2	3:C:32:LEU:HB2	2.45	0.51
4:D:127:THR:CG2	4:D:128:VAL:N	2.73	0.51
6:F:69:GLU:C	6:F:71:ARG:H	2.13	0.51
10:J:17:ASP:HA	10:J:20:ALA:HB3	1.93	0.51
1:A:797:C:OP1	11:K:124:LYS:HE2	2.11	0.51
13:M:90:LEU:CB	13:M:93:ARG:HD2	2.41	0.51
1:A:1510:U:H2'	1:A:1511:G:C8	2.45	0.51
3:C:36:ASP:HB3	3:C:40:ARG:NH1	2.25	0.51
4:D:12:CYS:HA	4:D:19:LEU:HD23	1.83	0.51
6:F:30:LEU:O	6:F:35:ALA:HB3	2.10	0.51
6:F:63:TYR:N	6:F:63:TYR:HD2	2.09	0.51
6:F:75:LEU:HD21	6:F:79:LEU:HD11	1.91	0.51
7:G:15:ASP:CB	7:G:20:ASP:H	2.13	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:2:ALA:O	13:M:9:ILE:HB	2.10	0.51
15:O:17:ARG:NH1	15:O:77:ARG:NH1	2.59	0.51
19:S:15:LEU:HD23	19:S:15:LEU:H	1.75	0.51
19:S:3:ARG:HG3	19:S:4:SER:N	2.24	0.51
20:T:83:ARG:O	20:T:86:ARG:HB3	2.10	0.51
4:D:162:LEU:HD11	4:D:181:MET:HB3	1.92	0.51
5:E:107:ARG:O	5:E:108:ALA:C	2.49	0.51
6:F:86:ARG:O	6:F:87:ARG:CG	2.50	0.51
8:H:102:ARG:NH1	8:H:105:ARG:HH12	2.09	0.51
13:M:87:TYR:C	13:M:89:GLY:N	2.64	0.51
1:A:1392:G:N2	1:A:1502:A:H8	2.08	0.51
2:B:134:GLU:HB3	2:B:138:LEU:HD12	1.93	0.51
2:B:24:TRP:CE3	2:B:26:PRO:HA	2.45	0.51
4:D:54:TYR:CE1	4:D:206:PHE:HE1	2.29	0.51
9:I:3:GLN:HB3	9:I:20:ARG:CG	2.40	0.51
13:M:9:ILE:HD12	13:M:9:ILE:C	2.31	0.51
1:A:390:C:H2'	1:A:391:G:C8	2.46	0.51
1:A:864:A:H5'	5:E:86:ALA:HB2	1.91	0.51
1:A:960:U:O2	1:A:960:U:H2'	2.11	0.51
2:B:82:ARG:HA	2:B:92:TYR:CE2	2.45	0.51
5:E:101:ILE:HD13	5:E:101:ILE:N	2.25	0.51
1:A:1346:A:C5'	9:I:120:ARG:HH12	2.24	0.51
10:J:54:PHE:O	10:J:55:LYS:HG3	2.11	0.51
13:M:16:ASP:HB3	13:M:34:LEU:HD11	1.93	0.51
21:U:10:ARG:HH11	21:U:10:ARG:HG3	1.76	0.51
21:U:3:LYS:HB3	21:U:14:TRP:CD1	2.45	0.51
1:A:1301:U:H3'	1:A:1302:U:H5'	1.93	0.51
2:B:187:LEU:HD13	2:B:187:LEU:O	2.11	0.51
3:C:113:ALA:C	3:C:115:LEU:H	2.14	0.51
3:C:175:LEU:HD12	3:C:175:LEU:H	1.75	0.51
3:C:21:ARG:CD	3:C:21:ARG:N	2.74	0.51
4:D:52:SER:O	4:D:53:ASP:C	2.49	0.51
9:I:88:TYR:O	9:I:89:ASN:CB	2.58	0.51
10:J:81:THR:C	10:J:83:GLU:N	2.64	0.51
13:M:57:ARG:HH11	13:M:57:ARG:CB	2.14	0.51
1:A:429:U:H4'	1:A:430:A:OP1	2.10	0.51
3:C:48:TYR:O	3:C:51:GLY:N	2.41	0.51
4:D:112:VAL:HG12	4:D:116:GLN:OE1	2.11	0.51
4:D:22:LYS:HB2	4:D:26:CYS:CB	2.41	0.51
7:G:16:LEU:HD11	9:I:45:ALA:HB2	1.92	0.51
8:H:10:LEU:N	8:H:10:LEU:CD2	2.70	0.51
9:I:79:LEU:HD22	9:I:101:PHE:O	2.11	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:P:45:THR:HG23	16:P:46:PRO:CD	2.39	0.51
1:A:323:U:H5'	20:T:23:ARG:HB2	1.93	0.51
1:A:190:G:O2'	1:A:191(A):G:OP2	2.28	0.51
4:D:155:LEU:O	4:D:159:ARG:HG2	2.10	0.51
4:D:83:SER:HA	4:D:89:THR:HG23	1.92	0.51
6:F:101:ALA:HA	18:R:28:GLU:OE1	2.11	0.51
8:H:104:ARG:HD2	8:H:138:TRP:CD2	2.46	0.51
9:I:29:ASN:OD1	9:I:64:THR:HA	2.11	0.51
11:K:46:GLY:HA2	11:K:50:TYR:O	2.10	0.51
12:L:23:LYS:O	12:L:24:VAL:HG23	2.10	0.51
13:M:120:LYS:O	13:M:121:LYS:HB2	2.11	0.51
16:P:1:MET:O	16:P:3:LYS:HG3	2.11	0.51
19:S:26:GLY:O	19:S:27:GLU:HB2	2.11	0.51
1:A:1320:C:N4	19:S:36:ARG:HG3	2.26	0.50
1:A:543:C:OP1	4:D:14:ARG:NE	2.44	0.50
2:B:23:ARG:HH11	2:B:23:ARG:HG2	1.76	0.50
3:C:132:ARG:O	3:C:136:GLN:HB2	2.11	0.50
3:C:99:VAL:O	3:C:99:VAL:HG23	2.11	0.50
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.92	0.50
4:D:206:PHE:CD2	4:D:207:TYR:CD1	2.99	0.50
5:E:83:GLU:HG2	5:E:88:LYS:CG	2.41	0.50
7:G:23:VAL:O	7:G:27:ILE:CD1	2.60	0.50
9:I:10:ARG:HG3	9:I:105:ASP:HB2	1.92	0.50
13:M:30:ALA:O	13:M:31:LYS:C	2.49	0.50
14:N:8:GLU:C	14:N:10:ALA:H	2.13	0.50
11:K:91:ARG:HH22	18:R:88:LYS:NZ	2.09	0.50
19:S:43:GLU:OE2	19:S:43:GLU:N	2.44	0.50
21:U:14:TRP:CE3	21:U:15:ARG:HD3	2.46	0.50
1:A:1218:C:H2'	1:A:1219:U:C6	2.46	0.50
1:A:1266:G:N2	1:A:1269:A:OP2	2.32	0.50
1:A:411:A:N6	1:A:413:G:H21	2.09	0.50
5:E:45:PHE:CD2	5:E:47:LYS:HD2	2.47	0.50
8:H:12:ARG:NH1	8:H:27:PRO:HD2	2.25	0.50
13:M:66:LEU:O	13:M:70:LEU:HB2	2.11	0.50
16:P:83:GLU:HG3	16:P:84:ALA:H	1.77	0.50
3:C:139:GLN:O	3:C:143:GLU:HB2	2.11	0.50
4:D:107:ARG:C	4:D:109:GLY:H	2.14	0.50
4:D:13:ARG:CB	4:D:33:MET:CE	2.89	0.50
4:D:162:LEU:HD13	4:D:181:MET:HB3	1.92	0.50
6:F:63:TYR:CD2	6:F:63:TYR:N	2.79	0.50
8:H:83:ILE:HB	8:H:137:VAL:HG13	1.93	0.50
22:V:68:C:H2'	22:V:69:C:H6	1.76	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1024:G:H4'	1:A:1024:G:OP1	2.11	0.50
1:A:1064:G:HO2'	1:A:1065:U:P	2.34	0.50
1:A:1124:G:H5''	1:A:1145:C:H41	1.75	0.50
1:A:341:C:H2'	1:A:342:C:C6	2.45	0.50
2:B:200:ILE:O	2:B:201:ILE:HD13	2.12	0.50
2:B:53:ARG:HA	2:B:56:ARG:HG3	1.93	0.50
7:G:50:ILE:HA	7:G:54:THR:HG22	1.94	0.50
8:H:51:VAL:HG11	8:H:60:ARG:HG3	1.92	0.50
8:H:95:VAL:HB	8:H:99:GLU:O	2.12	0.50
9:I:53:VAL:HG21	9:I:92:TYR:CZ	2.45	0.50
10:J:84:GLN:C	10:J:86:MET:H	2.14	0.50
13:M:82:MET:O	13:M:83:ASP:C	2.49	0.50
16:P:20:VAL:HG23	16:P:34:GLU:O	2.11	0.50
16:P:59:TRP:HA	16:P:59:TRP:HE3	1.76	0.50
2:B:170:GLU:HA	2:B:172:ILE:CD1	2.41	0.50
3:C:34:LEU:O	3:C:38:ARG:HG3	2.11	0.50
3:C:52:LEU:H	3:C:52:LEU:CD2	2.20	0.50
3:C:70:VAL:CG1	3:C:71:ALA:N	2.73	0.50
4:D:178:VAL:O	4:D:180:GLY:N	2.44	0.50
10:J:98:ILE:H	10:J:98:ILE:CD1	2.24	0.50
14:N:43:CYS:O	14:N:46:GLU:N	2.43	0.50
14:N:48:ALA:CA	14:N:53:LEU:HD12	2.42	0.50
1:A:1023:G:H3'	1:A:1024:G:H5''	1.93	0.50
1:A:565:U:H5''	1:A:566:G:H2'	1.93	0.50
2:B:15:VAL:H	2:B:16:HIS:HD1	1.59	0.50
7:G:50:ILE:HG21	7:G:58:PRO:HA	1.93	0.50
8:H:20:TYR:HD1	8:H:65:TYR:HD2	1.55	0.50
9:I:5:TYR:HA	9:I:17:VAL:O	2.12	0.50
10:J:56:HIS:O	10:J:58:ASP:O	2.30	0.50
15:O:26:GLU:OE2	15:O:77:ARG:NH1	2.43	0.50
1:A:222:U:H2'	1:A:223:U:H6	1.76	0.50
1:A:836:G:C6	1:A:851:G:C6	3.00	0.50
5:E:12:LEU:HD23	5:E:13:ILE:H	1.76	0.50
7:G:11:GLN:C	7:G:12:LEU:HD22	2.31	0.50
8:H:84:ARG:O	8:H:135:CYS:HB2	2.12	0.50
9:I:48:GLU:N	9:I:49:PRO:CD	2.74	0.50
14:N:22:THR:O	14:N:23:ARG:CB	2.59	0.50
18:R:30:ASP:C	18:R:32:ARG:H	2.16	0.50
3:C:11:ARG:HG3	3:C:15:THR:HG21	1.94	0.50
3:C:184:TYR:HA	3:C:200:ALA:O	2.12	0.50
4:D:128:VAL:O	4:D:130:GLY:N	2.45	0.50
10:J:22:LYS:NZ	10:J:23:ILE:HG12	2.27	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:28:LYS:O	12:L:29:GLY:C	2.50	0.50
16:P:39:TYR:OH	16:P:41:PRO:HB3	2.11	0.50
17:Q:13:ASP:C	17:Q:15:MET:H	2.15	0.50
19:S:41:VAL:CG1	19:S:45:VAL:N	2.74	0.50
20:T:49:ALA:CB	20:T:99:LEU:HD22	2.42	0.50
1:A:210:U:O2'	1:A:216:G:N7	2.45	0.50
2:B:16:HIS:HB3	2:B:210:SER:CB	2.42	0.50
3:C:36:ASP:HA	3:C:39:ILE:HD12	1.94	0.50
4:D:13:ARG:HH22	4:D:36:ARG:CZ	2.24	0.50
4:D:28:SER:CB	4:D:29:PRO:CD	2.85	0.50
12:L:24:VAL:CG1	12:L:24:VAL:O	2.58	0.50
12:L:10:LEU:HB3	17:Q:32:TYR:CE2	2.47	0.50
21:U:2:GLY:O	21:U:4:GLY:N	2.45	0.50
22:V:75:C:H2'	22:V:76:A:O4'	2.12	0.50
1:A:1297:C:HO2'	1:A:1298:C:P	2.35	0.49
9:I:83:ARG:HA	9:I:86:VAL:CG1	2.41	0.49
11:K:32:ILE:HD12	11:K:72:ALA:CB	2.36	0.49
16:P:39:TYR:CE2	16:P:41:PRO:HD3	2.47	0.49
21:U:6:ARG:HE	21:U:15:ARG:NH2	2.09	0.49
1:A:173:U:H5''	1:A:197:A:O4'	2.12	0.49
1:A:618:C:N3	1:A:622:A:N6	2.59	0.49
3:C:35:GLU:O	3:C:39:ILE:HG13	2.12	0.49
5:E:32:VAL:O	5:E:43:LEU:HD12	2.12	0.49
5:E:82:VAL:HG12	5:E:83:GLU:H	1.77	0.49
6:F:72:VAL:HG13	6:F:73:ASN:N	2.27	0.49
8:H:29:SER:CB	8:H:32:LYS:HG3	2.28	0.49
1:A:537:G:H5''	12:L:113:ARG:HH12	1.76	0.49
13:M:108:ARG:O	13:M:109:THR:C	2.50	0.49
15:O:17:ARG:NH1	15:O:77:ARG:CZ	2.74	0.49
1:A:1034:G:H2'	1:A:1035:A:C8	2.47	0.49
1:A:296:U:H2'	1:A:297:G:C8	2.47	0.49
3:C:178:LEU:HD22	3:C:178:LEU:N	2.27	0.49
4:D:206:PHE:HD2	4:D:207:TYR:CE1	2.30	0.49
4:D:13:ARG:CA	4:D:33:MET:HE3	2.43	0.49
16:P:83:GLU:HA	16:P:83:GLU:OE2	2.12	0.49
1:A:1235:U:O2'	1:A:1305:G:O5'	2.30	0.49
1:A:811:C:H4'	1:A:900:A:N6	2.27	0.49
4:D:30:LYS:CG	4:D:35:ARG:NE	2.64	0.49
5:E:78:HIS:HA	8:H:105:ARG:HB2	1.94	0.49
11:K:29:ILE:HG13	11:K:44:SER:HB3	1.93	0.49
11:K:62:GLN:O	11:K:63:LEU:C	2.51	0.49
14:N:8:GLU:O	14:N:10:ALA:N	2.45	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:T:37:SER:O	20:T:41:ILE:HG12	2.12	0.49
21:U:6:ARG:HH21	21:U:15:ARG:NE	2.09	0.49
1:A:448:A:H2'	1:A:449:C:O2	2.12	0.49
2:B:103:THR:N	2:B:180:LEU:HD11	2.27	0.49
4:D:23:GLY:H	4:D:26:CYS:HB2	1.77	0.49
5:E:11:ILE:CG1	5:E:31:LEU:HD12	2.42	0.49
8:H:14:ARG:HG2	8:H:14:ARG:O	2.12	0.49
9:I:105:ASP:C	9:I:107:ARG:H	2.14	0.49
12:L:6:THR:O	12:L:7:ILE:C	2.51	0.49
13:M:120:LYS:O	13:M:121:LYS:CB	2.60	0.49
13:M:14:ARG:HG3	13:M:16:ASP:OD2	2.13	0.49
19:S:62:ILE:C	19:S:63:THR:HG22	2.32	0.49
2:B:181:PHE:O	2:B:183:PRO:HD3	2.12	0.49
4:D:9:CYS:SG	4:D:22:LYS:CE	3.01	0.49
5:E:42:GLY:CA	5:E:136:MET:HE1	2.42	0.49
9:I:43:ALA:C	9:I:45:ALA:H	2.16	0.49
9:I:79:LEU:HD13	9:I:79:LEU:O	2.12	0.49
15:O:77:ARG:HA	15:O:80:ALA:HB3	1.95	0.49
6:F:101:ALA:HA	18:R:28:GLU:HG2	1.95	0.49
20:T:97:ALA:HB3	20:T:99:LEU:CD1	2.43	0.49
3:C:173:VAL:N	3:C:174:PRO:HD3	2.28	0.49
4:D:9:CYS:SG	4:D:22:LYS:CD	2.98	0.49
6:F:100:ASN:HD22	6:F:100:ASN:HA	1.47	0.49
6:F:51:PRO:HA	6:F:55:ASP:O	2.13	0.49
9:I:110:GLU:O	9:I:110:GLU:HG3	2.12	0.49
12:L:62:SER:C	12:L:64:TYR:H	2.14	0.49
13:M:102:ARG:HG3	13:M:102:ARG:O	2.11	0.49
17:Q:74:LEU:HD12	17:Q:75:ARG:NE	2.28	0.49
11:K:110:ASP:HB2	18:R:88:LYS:HD3	1.95	0.49
1:A:1494:G:N7	26:A:1667:PAR:N32	2.61	0.49
1:A:244:U:H4'	1:A:245:C:O5'	2.12	0.49
2:B:16:HIS:HB3	2:B:210:SER:HB2	1.95	0.49
2:B:42:ILE:HD11	2:B:202:PRO:HB2	1.95	0.49
5:E:41:VAL:CG1	5:E:112:LEU:O	2.60	0.49
6:F:97:PHE:CD2	18:R:31:LEU:HD21	2.48	0.49
9:I:43:ALA:HA	9:I:74:ILE:HD13	1.94	0.49
10:J:49:VAL:HG22	14:N:41:ARG:CG	2.42	0.49
10:J:33:GLN:HB2	10:J:75:ILE:CD1	2.43	0.49
15:O:8:LYS:HZ2	15:O:8:LYS:HB2	1.75	0.49
16:P:43:LYS:HE2	16:P:48:TRP:CZ3	2.47	0.49
20:T:53:LEU:HA	20:T:56:MET:CB	2.43	0.49
20:T:60:GLU:HG3	20:T:81:LYS:HE3	1.94	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1336:C:H1'	1:A:1337:G:C2	2.47	0.49
1:A:977:A:O2'	1:A:981:U:N3	2.43	0.49
2:B:207:ALA:O	2:B:209:ARG:N	2.45	0.49
8:H:61:VAL:HG12	8:H:63:LEU:HD13	1.94	0.49
9:I:18:PHE:O	9:I:61:ALA:HA	2.13	0.49
9:I:79:LEU:O	9:I:83:ARG:HG2	2.13	0.49
1:A:1151:A:N3	10:J:39:PRO:HG3	2.27	0.49
10:J:49:VAL:HG23	14:N:34:TYR:OH	2.13	0.49
10:J:49:VAL:CG1	10:J:50:ILE:N	2.76	0.49
10:J:94:VAL:CG1	10:J:95:GLU:N	2.76	0.49
11:K:25:TYR:CD1	11:K:25:TYR:N	2.80	0.49
13:M:4:ILE:HG22	13:M:5:ALA:H	1.76	0.49
1:A:719:C:C2	18:R:50:ILE:HD13	2.48	0.49
1:A:1314:C:C5	19:S:4:SER:HB2	2.48	0.49
1:A:1192:C:O2	5:E:25:ARG:NH2	2.44	0.49
1:A:184:G:H2'	1:A:185:A:C8	2.47	0.49
2:B:170:GLU:C	2:B:172:ILE:HD12	2.33	0.49
2:B:180:LEU:O	2:B:181:PHE:HB2	2.13	0.49
2:B:39:ILE:O	2:B:41:ILE:HD12	2.12	0.49
2:B:68:ILE:O	2:B:91:PRO:HD2	2.13	0.49
4:D:30:LYS:HD2	4:D:35:ARG:HH21	1.78	0.49
8:H:122:ARG:O	8:H:125:ARG:N	2.46	0.49
9:I:112:LYS:HD3	9:I:113:LYS:O	2.13	0.49
11:K:82:VAL:O	11:K:108:ILE:HA	2.13	0.49
17:Q:63:ARG:HG2	17:Q:64:PRO:N	2.28	0.49
20:T:26:ASN:CB	20:T:71:THR:HG23	2.43	0.49
13:M:119:GLY:HA3	22:V:29:G:OP1	2.13	0.49
1:A:1151:A:H1'	10:J:39:PRO:CB	2.39	0.48
1:A:737:A:H2'	1:A:738:C:C6	2.48	0.48
3:C:188:LEU:CD2	3:C:188:LEU:N	2.76	0.48
14:N:23:ARG:HD3	14:N:28:GLY:O	2.13	0.48
1:A:1435:G:H2'	1:A:1436:U:C6	2.48	0.48
2:B:193:ASP:OD2	2:B:196:LEU:CG	2.57	0.48
2:B:7:VAL:CG2	2:B:8:LYS:HD3	2.43	0.48
5:E:78:HIS:CE1	5:E:142:LEU:HD23	2.48	0.48
9:I:113:LYS:H	9:I:119:ALA:HA	1.77	0.48
12:L:38:THR:CG2	12:L:57:LYS:HB3	2.44	0.48
13:M:3:ARG:HA	13:M:9:ILE:HG12	1.94	0.48
1:A:1151:A:H2'	1:A:1152:A:C8	2.48	0.48
1:A:842:C:O2'	1:A:848:C:N4	2.43	0.48
2:B:214:ILE:O	2:B:218:ALA:HB2	2.13	0.48
5:E:100:VAL:O	5:E:107:ARG:NH2	2.47	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:51:VAL:CB	5:E:52:PRO:HD3	2.38	0.48
1:A:1346:A:C5	7:G:10:ARG:NH1	2.81	0.48
9:I:18:PHE:HB2	9:I:62:TYR:HB3	1.96	0.48
11:K:106:LYS:O	11:K:107:SER:HB3	2.12	0.48
11:K:19:ALA:CB	11:K:32:ILE:HG22	2.42	0.48
12:L:119:LYS:C	12:L:120:TYR:HD1	2.16	0.48
17:Q:67:LYS:HA	17:Q:70:ARG:HH12	1.76	0.48
22:V:4:G:O2'	22:V:5:G:H8	1.96	0.48
1:A:97:U:H2'	1:A:99:C:C6	2.49	0.48
2:B:5:ILE:HG21	2:B:224:GLN:HG2	1.95	0.48
4:D:118:ARG:NH2	4:D:136:PRO:HB2	2.28	0.48
4:D:121:VAL:O	4:D:134:ASP:HA	2.14	0.48
7:G:78:ARG:HH11	7:G:78:ARG:HG3	1.78	0.48
15:O:32:LEU:O	15:O:33:THR:C	2.51	0.48
16:P:43:LYS:C	16:P:45:THR:H	2.14	0.48
19:S:27:GLU:O	19:S:28:LYS:CG	2.53	0.48
1:A:1327:C:H2'	1:A:1328:C:C6	2.49	0.48
1:A:738:C:H5''	6:F:69:GLU:HB2	1.95	0.48
4:D:100:ARG:CZ	4:D:137:SER:HA	2.43	0.48
4:D:196:LEU:HB3	4:D:197:PRO:HD2	1.96	0.48
7:G:80:VAL:HG12	7:G:81:GLY:N	2.28	0.48
9:I:118:LYS:CB	9:I:118:LYS:NZ	2.76	0.48
13:M:73:GLU:O	13:M:76:ALA:HB3	2.13	0.48
19:S:36:ARG:NH1	19:S:36:ARG:HB3	2.28	0.48
1:A:792:A:O2'	1:A:794:A:N7	2.45	0.48
1:A:1158:C:H4'	2:B:133:LYS:NZ	2.27	0.48
2:B:154:LEU:O	2:B:155:LEU:HB2	2.13	0.48
2:B:15:VAL:H	2:B:16:HIS:CE1	2.30	0.48
2:B:200:ILE:H	2:B:200:ILE:HD12	1.79	0.48
2:B:16:HIS:HD2	2:B:210:SER:HA	1.77	0.48
4:D:163:GLU:O	4:D:165:MET:N	2.46	0.48
8:H:45:ILE:O	8:H:45:ILE:HG13	2.13	0.48
11:K:34:ASP:HB2	11:K:35:PRO:HD2	1.95	0.48
15:O:50:HIS:O	15:O:53:HIS:N	2.47	0.48
1:A:1004:A:O5'	1:A:1025:U:N3	2.46	0.48
1:A:186:C:H5'	20:T:78:ALA:HB1	1.96	0.48
1:A:579:G:H5'	1:A:728:A:H1'	1.96	0.48
2:B:140:HIS:C	2:B:142:LEU:H	2.16	0.48
4:D:183:GLY:C	4:D:184:LYS:HG3	2.34	0.48
4:D:196:LEU:C	4:D:198:VAL:N	2.66	0.48
8:H:109:ILE:HG12	8:H:110:ALA:N	2.27	0.48
10:J:3:LYS:O	10:J:100:THR:HA	2.14	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:19:ALA:CA	11:K:32:ILE:HG22	2.43	0.48
16:P:57:ARG:HG3	16:P:57:ARG:HH11	1.78	0.48
16:P:71:ARG:HB2	16:P:71:ARG:HH11	1.79	0.48
19:S:24:ALA:O	19:S:25:LYS:HB2	2.13	0.48
1:A:1450:U:O2'	1:A:1451:A:N7	2.43	0.48
4:D:165:MET:CE	4:D:168:ARG:HD2	2.44	0.48
5:E:84:PHE:HD2	5:E:130:ASN:O	1.97	0.48
9:I:128:ARG:HD3	22:V:32:C:OP2	2.13	0.48
11:K:41:THR:HG22	11:K:42:TRP:N	2.28	0.48
15:O:61:GLY:C	15:O:65:ARG:NH1	2.67	0.48
16:P:21:VAL:HG23	16:P:34:GLU:H	1.79	0.48
1:A:1396:A:H4'	1:A:1397:C:C5'	2.44	0.48
1:A:542:G:OP1	4:D:10:ARG:NH2	2.47	0.48
2:B:87:ARG:NH1	2:B:220:ASP:OD1	2.46	0.48
3:C:71:ALA:HA	3:C:106:VAL:HB	1.95	0.48
4:D:13:ARG:HA	4:D:33:MET:CE	2.44	0.48
6:F:89:MET:O	6:F:90:VAL:C	2.51	0.48
7:G:97:GLN:O	7:G:101:LEU:HG	2.14	0.48
8:H:86:ILE:HG12	8:H:135:CYS:HA	1.96	0.48
8:H:6:ILE:O	8:H:10:LEU:HG	2.14	0.48
11:K:48:ILE:HG21	11:K:63:LEU:HD13	1.96	0.48
12:L:27:LEU:C	12:L:29:GLY:N	2.64	0.48
15:O:39:LEU:O	15:O:40:SER:C	2.50	0.48
16:P:60:LEU:CA	16:P:64:ALA:HB3	2.43	0.48
21:U:9:ARG:HG2	21:U:9:ARG:HH11	1.78	0.48
1:A:1399:C:C2	1:A:1502:A:N6	2.82	0.48
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.78	0.48
2:B:24:TRP:CD1	2:B:26:PRO:HD3	2.49	0.48
4:D:163:GLU:C	4:D:165:MET:N	2.66	0.48
4:D:153:ARG:CZ	4:D:181:MET:HG3	2.44	0.48
4:D:6:GLY:O	4:D:8:VAL:HG23	2.14	0.48
5:E:10:MET:HB2	5:E:32:VAL:HG22	1.94	0.48
5:E:87:SER:HB3	5:E:131:ILE:HD13	1.95	0.48
7:G:63:LYS:HD2	7:G:63:LYS:O	2.13	0.48
7:G:79:ARG:O	7:G:80:VAL:HG23	2.14	0.48
9:I:33:PHE:HZ	9:I:47:LEU:HD21	1.76	0.48
9:I:17:VAL:HG11	9:I:81:ILE:HA	1.96	0.48
10:J:39:PRO:CB	10:J:70:ARG:HH12	2.27	0.48
11:K:115:PRO:C	11:K:117:ASN:H	2.17	0.48
12:L:127:GLU:O	12:L:128:ALA:CB	2.62	0.48
13:M:117:VAL:O	13:M:118:ALA:C	2.51	0.48
13:M:12:ASN:O	13:M:13:LYS:HB2	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:Q:3:LYS:HD2	17:Q:60:ILE:HD11	1.95	0.48
18:R:31:LEU:HD23	18:R:31:LEU:N	2.29	0.48
19:S:9:VAL:O	19:S:10:PHE:HB3	2.13	0.48
20:T:37:SER:HB3	20:T:84:LEU:CD2	2.44	0.48
24:Y:40:G:O2'	24:Y:41:A:H5'	2.13	0.48
1:A:608:A:H2'	1:A:609:A:O4'	2.14	0.47
1:A:953:G:H5'	1:A:965:A:H61	1.79	0.47
2:B:24:TRP:CZ3	2:B:26:PRO:HA	2.49	0.47
3:C:153:VAL:HA	3:C:197:GLY:O	2.13	0.47
4:D:3:ARG:O	4:D:5:ILE:HG13	2.14	0.47
7:G:51:GLN:HA	7:G:51:GLN:OE1	2.14	0.47
9:I:7:THR:O	9:I:83:ARG:HD2	2.14	0.47
10:J:4:ILE:CB	10:J:74:ILE:HD11	2.36	0.47
11:K:13:GLN:HG3	11:K:75:TYR:O	2.14	0.47
12:L:85:ILE:HD11	12:L:98:TYR:CB	2.43	0.47
13:M:50:GLU:O	13:M:54:VAL:HG23	2.13	0.47
19:S:11:VAL:O	19:S:12:ASP:CB	2.61	0.47
20:T:50:GLU:HA	20:T:100:ILE:CG2	2.44	0.47
20:T:64:ASP:O	20:T:67:ALA:N	2.47	0.47
2:B:206:ASP:HA	2:B:211:ILE:HD11	1.94	0.47
5:E:75:THR:HG23	5:E:76:ILE:O	2.14	0.47
5:E:82:VAL:CG1	5:E:83:GLU:H	2.27	0.47
7:G:69:VAL:O	7:G:69:VAL:CG1	2.62	0.47
7:G:8:GLU:CD	7:G:8:GLU:N	2.67	0.47
8:H:44:PHE:CD1	8:H:80:ILE:HG12	2.49	0.47
9:I:22:GLY:HA3	9:I:60:ASP:OD2	2.13	0.47
1:A:986:A:N3	19:S:52:TYR:OH	2.47	0.47
20:T:13:LEU:C	20:T:13:LEU:HD12	2.34	0.47
20:T:30:LYS:O	20:T:33:ILE:HG12	2.14	0.47
23:X:4:C:C3'	23:X:5:C:H5'	2.41	0.47
1:A:1147:C:O2	9:I:16:ARG:NH1	2.47	0.47
1:A:339:C:H2'	1:A:340:U:C6	2.49	0.47
1:A:560:U:H5'	1:A:566:G:N2	2.29	0.47
1:A:973:G:O4'	10:J:55:LYS:HG2	2.13	0.47
2:B:116:GLU:HA	2:B:119:GLU:HB3	1.96	0.47
3:C:16:ARG:NH2	3:C:183:ASP:OD2	2.47	0.47
4:D:135:LEU:O	4:D:137:SER:N	2.48	0.47
5:E:96:PRO:HA	5:E:117:ASP:OD2	2.14	0.47
6:F:22:GLU:CD	6:F:82:ARG:HH21	2.18	0.47
7:G:44:TYR:C	7:G:46:ALA:N	2.66	0.47
9:I:42:ARG:NH2	9:I:75:ASP:OD2	2.47	0.47
10:J:24:VAL:HG21	10:J:37:PRO:CG	2.43	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:6:LEU:CD2	14:N:23:ARG:NH2	2.77	0.47
15:O:24:SER:OG	15:O:25:THR:N	2.47	0.47
12:L:10:LEU:CD1	17:Q:32:TYR:CE2	2.90	0.47
22:V:19:G:H4'	22:V:20:U:OP2	2.14	0.47
1:A:309:G:O2'	1:A:607:A:N1	2.45	0.47
1:A:792:A:H1'	1:A:793:U:OP2	2.14	0.47
2:B:164:VAL:HB	2:B:186:ALA:HB1	1.95	0.47
1:A:1256:A:P	3:C:26:LYS:HZ3	2.37	0.47
4:D:198:VAL:CG1	4:D:199:ASN:N	2.75	0.47
4:D:60:GLU:O	4:D:63:LYS:HB3	2.14	0.47
7:G:79:ARG:NH1	7:G:79:ARG:HG2	2.29	0.47
9:I:9:ARG:HA	9:I:76:ALA:HB1	1.97	0.47
13:M:90:LEU:HA	13:M:93:ARG:CD	2.34	0.47
14:N:15:LYS:HD2	14:N:16:PHE:CE2	2.49	0.47
18:R:31:LEU:CD2	18:R:31:LEU:H	2.27	0.47
1:A:1277:C:O2'	1:A:1279:A:H8	1.96	0.47
1:A:266:G:H5''	1:A:267:C:C5	2.49	0.47
1:A:362:G:N2	1:A:365:U:OP2	2.47	0.47
3:C:76:VAL:HG21	3:C:103:VAL:HG11	1.95	0.47
5:E:141:GLN:HA	5:E:143:ARG:HH12	1.79	0.47
7:G:107:ALA:CB	7:G:134:ALA:HB2	2.44	0.47
8:H:39:LEU:HD11	8:H:111:ILE:HD11	1.96	0.47
10:J:84:GLN:H	10:J:84:GLN:HG3	1.50	0.47
11:K:124:LYS:O	11:K:126:ARG:N	2.40	0.47
14:N:8:GLU:C	14:N:10:ALA:N	2.68	0.47
17:Q:98:LEU:O	17:Q:99:SER:C	2.53	0.47
20:T:28:ALA:C	20:T:30:LYS:N	2.67	0.47
1:A:1074:G:C4'	2:B:104:ASN:HB2	2.44	0.47
1:A:1327:C:H2'	1:A:1328:C:H6	1.78	0.47
1:A:686:U:HO2'	11:K:42:TRP:HE1	1.62	0.47
2:B:69:LEU:HB3	2:B:162:ILE:HG22	1.95	0.47
3:C:148:GLY:O	3:C:202:ILE:HA	2.13	0.47
10:J:40:LEU:HB2	10:J:69:ASN:CB	2.40	0.47
12:L:50:SER:O	12:L:51:ALA:HB2	2.14	0.47
13:M:72:ALA:O	13:M:76:ALA:HB2	2.14	0.47
14:N:36:PHE:CD1	14:N:36:PHE:C	2.88	0.47
16:P:34:GLU:HG2	16:P:35:LYS:N	2.29	0.47
1:A:1032(A):G:H2'	1:A:1032(B):G:C8	2.50	0.47
1:A:1305:G:OP1	21:U:2:GLY:HA2	2.14	0.47
1:A:191(D):U:H2'	1:A:191(E):G:C8	2.50	0.47
1:A:64:G:H4'	1:A:65:U:O5'	2.15	0.47
4:D:135:LEU:C	4:D:137:SER:H	2.18	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:173:TRP:C	4:D:186:LEU:HB2	2.35	0.47
4:D:30:LYS:H	4:D:30:LYS:CD	2.23	0.47
6:F:79:LEU:O	6:F:85:VAL:HG11	2.14	0.47
8:H:33:GLU:C	8:H:35:ILE:N	2.65	0.47
8:H:82:HIS:CD2	8:H:83:ILE:N	2.82	0.47
8:H:86:ILE:HG22	8:H:87:SER:N	2.29	0.47
9:I:112:LYS:HD3	9:I:112:LYS:C	2.35	0.47
17:Q:76:LEU:HD11	17:Q:79:SER:H	1.80	0.47
1:A:15:G:H4'	5:E:24:ARG:HH12	1.80	0.47
1:A:313:A:H2'	1:A:314:C:C6	2.50	0.47
1:A:438:G:H4'	4:D:123:HIS:CE1	2.50	0.47
1:A:537:G:H5''	12:L:113:ARG:NH1	2.30	0.47
1:A:748:C:H1'	1:A:749:C:H5	1.79	0.47
2:B:168:THR:CB	2:B:192:SER:HB2	2.41	0.47
2:B:220:ASP:O	2:B:223:ILE:N	2.48	0.47
3:C:11:ARG:HG2	3:C:11:ARG:HH11	1.80	0.47
3:C:203:PHE:O	3:C:204:LEU:HD23	2.15	0.47
4:D:154:ASN:O	4:D:155:LEU:O	2.32	0.47
4:D:165:MET:HE3	4:D:168:ARG:HD2	1.97	0.47
6:F:19:LEU:HD23	6:F:19:LEU:C	2.35	0.47
8:H:80:ILE:HG23	8:H:137:VAL:HG12	1.97	0.47
10:J:74:ILE:HG12	10:J:74:ILE:O	2.13	0.47
11:K:32:ILE:HD11	11:K:68:ALA:O	2.14	0.47
14:N:41:ARG:HH11	14:N:41:ARG:CG	2.28	0.47
16:P:40:ASP:C	16:P:42:ARG:H	2.17	0.47
18:R:32:ARG:HH11	18:R:65:ILE:HD13	1.80	0.47
18:R:82:THR:HG22	18:R:83:GLU:H	1.79	0.47
2:B:95:GLN:NE2	2:B:147:LYS:HE2	2.27	0.47
2:B:223:ILE:HA	2:B:226:ARG:HB3	1.97	0.47
2:B:5:ILE:O	2:B:6:THR:O	2.32	0.47
3:C:23:TYR:CG	3:C:24:ALA:N	2.83	0.47
4:D:110:PHE:H	4:D:110:PHE:HD1	1.63	0.47
6:F:40:VAL:HG22	6:F:41:GLU:N	2.30	0.47
13:M:23:TYR:HB3	13:M:67:GLU:CG	2.39	0.47
16:P:69:THR:O	16:P:73:LEU:HG	2.14	0.47
21:U:15:ARG:NH1	21:U:15:ARG:HG2	2.29	0.47
1:A:1186:G:O3'	9:I:113:LYS:NZ	2.47	0.47
1:A:457:C:H2'	1:A:458:C:H6	1.80	0.47
1:A:560:U:H4'	1:A:561:U:O5'	2.15	0.47
1:A:792:A:H4'	1:A:793:U:O5'	2.15	0.47
2:B:71:VAL:HG23	2:B:164:VAL:HG13	1.97	0.47
3:C:195:VAL:CG1	3:C:196:LEU:H	2.27	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:9:CYS:SG	4:D:22:LYS:HE3	2.55	0.47
7:G:70:LYS:O	7:G:138:LYS:HE3	2.15	0.47
13:M:8:GLU:C	13:M:9:ILE:HG23	2.34	0.47
15:O:76:GLU:O	15:O:78:TYR:N	2.48	0.47
17:Q:59:ILE:N	17:Q:59:ILE:CD1	2.78	0.47
17:Q:63:ARG:HG2	17:Q:64:PRO:CD	2.45	0.47
2:B:86:GLU:C	2:B:88:ALA:H	2.17	0.47
3:C:172:ARG:O	3:C:173:VAL:HG23	2.15	0.47
3:C:58:GLU:O	3:C:59:ARG:HG3	2.15	0.47
4:D:146:ILE:HG22	4:D:146:ILE:O	2.15	0.47
4:D:30:LYS:CD	4:D:30:LYS:N	2.73	0.47
4:D:7:PRO:O	4:D:10:ARG:HG2	2.15	0.47
6:F:41:GLU:HG2	6:F:43:LEU:CD1	2.44	0.47
9:I:106:ALA:O	9:I:108:VAL:HG13	2.15	0.47
10:J:80:LYS:HB2	10:J:80:LYS:NZ	2.30	0.47
11:K:104:GLN:O	11:K:106:LYS:HG3	2.15	0.47
21:U:14:TRP:CE3	21:U:15:ARG:NH1	2.83	0.47
2:B:172:ILE:O	2:B:175:ARG:CB	2.63	0.46
2:B:174:VAL:O	2:B:178:ARG:HB3	2.16	0.46
5:E:101:ILE:CD1	5:E:119:LEU:HD23	2.36	0.46
11:K:96:ARG:O	11:K:97:ALA:C	2.54	0.46
15:O:82:ILE:O	15:O:86:GLY:N	2.49	0.46
18:R:46:GLU:HG3	18:R:47:THR:N	2.29	0.46
19:S:40:ILE:CG1	19:S:41:VAL:N	2.78	0.46
20:T:26:ASN:ND2	20:T:26:ASN:N	2.62	0.46
20:T:53:LEU:HD12	20:T:100:ILE:HG23	1.98	0.46
20:T:49:ALA:HB2	20:T:99:LEU:HD22	1.97	0.46
20:T:99:LEU:O	20:T:100:ILE:HB	2.15	0.46
1:A:128:G:O2'	17:Q:3:LYS:NZ	2.48	0.46
1:A:243:A:H4'	1:A:244:U:H3'	1.97	0.46
3:C:87:LEU:C	3:C:89:GLU:N	2.65	0.46
7:G:92:SER:HB3	7:G:95:ARG:CB	2.45	0.46
8:H:28:ALA:CB	8:H:57:PRO:HB2	2.45	0.46
11:K:102:GLY:O	11:K:103:LEU:C	2.53	0.46
13:M:80:ARG:O	13:M:82:MET:O	2.34	0.46
17:Q:29:HIS:N	17:Q:33:GLY:O	2.48	0.46
19:S:24:ALA:O	19:S:25:LYS:CB	2.63	0.46
1:A:1053:G:N7	1:A:1200:C:H5''	2.31	0.46
1:A:753:A:H4'	1:A:754:C:O5'	2.15	0.46
2:B:17:PHE:CD2	2:B:44:LEU:HD21	2.47	0.46
5:E:96:PRO:HA	5:E:117:ASP:CG	2.35	0.46
5:E:13:ILE:O	5:E:13:ILE:HG22	2.14	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:89:MET:HE1	7:G:156:TRP:H	1.80	0.46
7:G:50:ILE:CG2	7:G:61:VAL:HG21	2.45	0.46
8:H:39:LEU:C	8:H:45:ILE:HG12	2.35	0.46
10:J:47:PHE:CE1	10:J:63:PHE:HB2	2.33	0.46
12:L:115:LYS:O	12:L:117:ARG:N	2.47	0.46
13:M:30:ALA:O	13:M:33:ALA:N	2.47	0.46
13:M:23:TYR:HB2	13:M:67:GLU:OE1	2.15	0.46
1:A:1118:C:OP1	9:I:104:ARG:NH1	2.44	0.46
1:A:1126:U:H1'	1:A:1280:A:N7	2.29	0.46
1:A:97:U:H2'	1:A:99:C:H6	1.80	0.46
2:B:195:ASP:O	8:H:68:ARG:NH2	2.48	0.46
3:C:95:THR:CG2	3:C:97:LYS:HZ3	2.28	0.46
1:A:1231:G:O3'	9:I:126:SER:OG	2.32	0.46
10:J:95:GLU:OE2	10:J:95:GLU:HA	2.16	0.46
12:L:126:LYS:C	12:L:128:ALA:N	2.69	0.46
13:M:65:LYS:NZ	13:M:69:GLU:HG2	2.31	0.46
10:J:49:VAL:HG22	14:N:41:ARG:CD	2.45	0.46
10:J:63:PHE:CD1	14:N:58:LYS:HA	2.35	0.46
16:P:25:ARG:HH11	16:P:25:ARG:HG3	1.79	0.46
1:A:1113:C:H2'	1:A:1114:C:H6	1.81	0.46
1:A:1127:G:H2'	1:A:1128:C:C6	2.51	0.46
1:A:308:C:H2'	1:A:309:G:H8	1.80	0.46
1:A:374:A:C6	1:A:375:U:C4	3.03	0.46
1:A:475:G:H2'	1:A:476:G:C8	2.51	0.46
2:B:224:GLN:HA	2:B:229:VAL:HG23	1.97	0.46
3:C:113:ALA:O	3:C:115:LEU:N	2.48	0.46
5:E:12:LEU:HD21	5:E:14:ARG:HB3	1.98	0.46
5:E:55:VAL:O	5:E:58:ALA:HB3	2.16	0.46
7:G:95:ARG:NE	7:G:99:LEU:HD11	2.30	0.46
10:J:44:VAL:HG12	10:J:45:ARG:N	2.30	0.46
11:K:34:ASP:HB2	11:K:35:PRO:CD	2.45	0.46
1:A:538:G:OP1	12:L:113:ARG:HD2	2.14	0.46
1:A:64:G:H5'	1:A:65:U:H5'	1.98	0.46
1:A:838:G:C5	1:A:842:C:H1'	2.50	0.46
3:C:108:ASN:HB3	3:C:111:LEU:HG	1.98	0.46
5:E:150:ARG:HG2	5:E:150:ARG:O	2.16	0.46
6:F:68:PRO:HG3	6:F:71:ARG:NH2	2.31	0.46
9:I:28:VAL:O	9:I:29:ASN:C	2.53	0.46
9:I:40:LEU:C	9:I:42:ARG:H	2.18	0.46
12:L:43:VAL:HG23	12:L:93:LEU:HD22	1.97	0.46
13:M:87:TYR:C	13:M:89:GLY:H	2.19	0.46
14:N:41:ARG:HH11	14:N:41:ARG:HG2	1.79	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:R:43:PHE:C	18:R:51:LEU:HD12	2.36	0.46
20:T:44:ALA:O	20:T:91:LEU:HB3	2.16	0.46
1:A:1322:C:H2'	1:A:1322:C:O2	2.16	0.46
1:A:397:A:H5'	1:A:398:C:OP1	2.16	0.46
1:A:999:U:H2'	1:A:1000:A:C8	2.50	0.46
2:B:170:GLU:CA	2:B:172:ILE:HD12	2.46	0.46
2:B:162:ILE:CD1	2:B:184:VAL:HG13	2.44	0.46
4:D:187:ARG:HH11	4:D:187:ARG:HG2	1.81	0.46
6:F:101:ALA:HA	18:R:28:GLU:CG	2.46	0.46
6:F:3:ARG:HH11	6:F:3:ARG:HG3	1.81	0.46
7:G:54:THR:HG23	7:G:54:THR:O	2.16	0.46
7:G:57:GLU:O	7:G:59:LEU:N	2.49	0.46
8:H:110:ALA:HB3	8:H:121:ASP:HB3	1.98	0.46
8:H:49:GLU:HG3	8:H:49:GLU:O	2.15	0.46
8:H:86:ILE:HG13	8:H:133:LEU:CD2	2.44	0.46
9:I:59:PHE:CZ	9:I:88:TYR:CE1	3.01	0.46
20:T:56:MET:HG3	20:T:88:VAL:HG21	1.98	0.46
20:T:98:PRO:O	20:T:100:ILE:N	2.42	0.46
1:A:1135:U:H4'	1:A:1136:U:H5	1.81	0.46
1:A:192:U:H2'	1:A:193:C:C6	2.51	0.46
1:A:219:C:H2'	1:A:220:G:O4'	2.15	0.46
1:A:34:C:H2'	1:A:35:G:C8	2.51	0.46
1:A:946:A:H2'	1:A:947:G:C8	2.50	0.46
2:B:163:PHE:CE1	2:B:215:LEU:HD22	2.50	0.46
2:B:92:TYR:C	2:B:92:TYR:CD1	2.88	0.46
3:C:124:ILE:C	3:C:126:ARG:H	2.19	0.46
3:C:15:THR:O	3:C:15:THR:HG22	2.15	0.46
3:C:87:LEU:C	3:C:89:GLU:H	2.20	0.46
4:D:13:ARG:NH2	4:D:36:ARG:NH2	2.64	0.46
6:F:72:VAL:HG23	6:F:90:VAL:HG11	1.98	0.46
11:K:41:THR:CG2	11:K:42:TRP:N	2.79	0.46
15:O:76:GLU:C	15:O:78:TYR:N	2.68	0.46
16:P:30:GLY:O	16:P:31:LYS:C	2.54	0.46
1:A:376:G:H5''	16:P:5:ARG:HD2	1.98	0.46
22:V:49:G:O6	22:V:65:C:N4	2.49	0.46
24:Y:40:G:H2'	24:Y:41:A:C8	2.51	0.46
1:A:186(A):C:H2'	1:A:186(B):C:C6	2.50	0.46
2:B:77:ALA:HB1	2:B:211:ILE:HG21	1.97	0.46
2:B:95:GLN:HA	2:B:95:GLN:OE1	2.16	0.46
3:C:68:VAL:HG12	3:C:70:VAL:HG23	1.98	0.46
3:C:6:HIS:C	3:C:8:ILE:H	2.18	0.46
6:F:44:GLY:HA2	6:F:59:TYR:CE2	2.51	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:I:11:LYS:O	9:I:12:GLU:HB2	2.16	0.46
11:K:80:VAL:O	11:K:106:LYS:HD3	2.15	0.46
12:L:27:LEU:HD13	12:L:28:LYS:N	2.30	0.46
12:L:6:THR:H	12:L:9:GLN:NE2	1.97	0.46
13:M:10:PRO:HG3	13:M:18:ALA:O	2.16	0.46
13:M:3:ARG:O	13:M:4:ILE:HD13	2.16	0.46
17:Q:100:LYS:O	17:Q:101:ARG:HB2	2.15	0.46
19:S:63:THR:HG23	19:S:66:MET:CE	2.46	0.46
20:T:22:ARG:O	20:T:26:ASN:ND2	2.49	0.46
24:Y:39:C:O2'	24:Y:40:G:P	2.74	0.46
1:A:37:U:O2'	1:A:500:G:H4'	2.16	0.46
1:A:643:C:H2'	1:A:644:G:H8	1.81	0.46
3:C:8:ILE:C	3:C:10:PHE:N	2.69	0.46
4:D:126:ILE:HG22	4:D:127:THR:H	1.80	0.46
4:D:180:GLY:O	4:D:181:MET:C	2.54	0.46
4:D:29:PRO:CD	4:D:30:LYS:H	2.29	0.46
4:D:79:PHE:HE2	4:D:83:SER:HB2	1.79	0.46
8:H:68:ARG:HH11	8:H:68:ARG:HG2	1.81	0.46
9:I:5:TYR:OH	9:I:7:THR:HG23	2.15	0.46
10:J:4:ILE:O	10:J:74:ILE:HD13	2.16	0.46
1:A:302:G:O3'	12:L:17:LYS:HE2	2.16	0.46
17:Q:84:LEU:O	17:Q:86:GLU:N	2.49	0.46
20:T:98:PRO:C	20:T:100:ILE:H	2.18	0.46
20:T:93:GLU:O	20:T:93:GLU:HG2	2.15	0.46
1:A:1238:A:H62	1:A:1299:A:H61	1.63	0.45
1:A:254:G:OP1	17:Q:67:LYS:O	2.33	0.45
3:C:127:ARG:CG	3:C:127:ARG:NH1	2.74	0.45
3:C:172:ARG:O	3:C:173:VAL:CG2	2.63	0.45
3:C:43:LEU:HD22	3:C:47:LEU:CD2	2.46	0.45
3:C:53:ALA:O	3:C:54:ARG:HB2	2.16	0.45
4:D:100:ARG:NH2	4:D:137:SER:HA	2.31	0.45
4:D:133:VAL:HG12	4:D:135:LEU:H	1.81	0.45
5:E:12:LEU:HB3	5:E:31:LEU:HB2	1.98	0.45
7:G:107:ALA:O	7:G:110:GLN:HB2	2.15	0.45
8:H:91:ARG:NH1	8:H:91:ARG:HG2	2.25	0.45
10:J:96:ILE:N	10:J:96:ILE:CD1	2.79	0.45
11:K:121:PRO:HD2	11:K:126:ARG:CD	2.46	0.45
12:L:113:ARG:NH2	12:L:120:TYR:CE2	2.85	0.45
14:N:26:ARG:NE	14:N:47:LEU:HD21	2.30	0.45
15:O:30:ALA:HA	15:O:85:LEU:HD11	1.97	0.45
1:A:375:U:C4'	16:P:17:TYR:HE2	2.22	0.45
18:R:43:PHE:C	18:R:44:LEU:HD12	2.36	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:T:71:THR:HG22	20:T:72:LEU:N	2.31	0.45
4:D:173:TRP:NE1	4:D:174:LEU:HG	2.31	0.45
4:D:52:SER:N	4:D:55:ALA:HB3	2.32	0.45
4:D:92:VAL:O	4:D:96:LEU:CD2	2.64	0.45
4:D:93:PHE:CZ	4:D:97:LEU:HD11	2.51	0.45
5:E:64:ARG:HG3	5:E:64:ARG:HH11	1.82	0.45
6:F:69:GLU:O	6:F:71:ARG:N	2.48	0.45
7:G:50:ILE:HG21	7:G:61:VAL:HG21	1.97	0.45
7:G:95:ARG:HG2	7:G:99:LEU:HD12	1.98	0.45
1:A:1291:G:H4'	9:I:39:GLY:HA3	1.98	0.45
13:M:28:ALA:C	13:M:30:ALA:N	2.70	0.45
1:A:191(F):U:O2	20:T:105:SER:HB2	2.16	0.45
1:A:1234:C:H4'	1:A:1364:U:H1'	1.97	0.45
2:B:24:TRP:CZ2	2:B:26:PRO:HB3	2.51	0.45
2:B:96:ARG:HD2	2:B:96:ARG:N	2.20	0.45
4:D:29:PRO:HD2	4:D:30:LYS:H	1.80	0.45
6:F:40:VAL:HG22	6:F:41:GLU:H	1.80	0.45
15:O:5:LYS:O	15:O:8:LYS:CG	2.63	0.45
16:P:40:ASP:O	16:P:42:ARG:N	2.50	0.45
19:S:10:PHE:CD1	19:S:38:SER:HB2	2.52	0.45
1:A:222:U:H2'	1:A:223:U:C6	2.52	0.45
1:A:355:C:H1'	1:A:388:G:H2'	1.98	0.45
2:B:30:ARG:O	2:B:31:TYR:HD2	2.00	0.45
3:C:134:ILE:HG23	3:C:151:VAL:HB	1.98	0.45
3:C:34:LEU:HD23	3:C:34:LEU:C	2.37	0.45
4:D:150:GLU:C	4:D:152:SER:H	2.20	0.45
4:D:52:SER:H	4:D:55:ALA:HB3	1.82	0.45
8:H:33:GLU:O	8:H:35:ILE:N	2.49	0.45
13:M:23:TYR:HB3	13:M:67:GLU:HA	1.98	0.45
13:M:66:LEU:HB2	13:M:67:GLU:H	1.61	0.45
15:O:82:ILE:HD11	15:O:88:ARG:HG2	1.95	0.45
16:P:13:HIS:C	16:P:15:PRO:HD3	2.36	0.45
1:A:1213:A:N6	1:A:1215:G:N3	2.65	0.45
1:A:714:G:H2'	1:A:715:A:C8	2.52	0.45
2:B:22:LYS:O	2:B:24:TRP:N	2.50	0.45
3:C:78:GLY:HA3	3:C:83:ARG:HB3	1.98	0.45
4:D:114:ARG:CG	4:D:114:ARG:NH1	2.77	0.45
4:D:13:ARG:CB	4:D:33:MET:HE2	2.47	0.45
7:G:108:ALA:C	7:G:110:GLN:H	2.19	0.45
8:H:97:VAL:CG1	8:H:98:LYS:H	2.30	0.45
1:A:1370:G:O3'	9:I:12:GLU:HG3	2.17	0.45
9:I:42:ARG:O	9:I:45:ALA:HB3	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:I:80:GLY:C	9:I:82:ALA:N	2.70	0.45
12:L:61:THR:O	12:L:63:GLY:N	2.45	0.45
12:L:64:TYR:O	12:L:65:GLU:HB2	2.16	0.45
16:P:19:ILE:HB	16:P:37:GLY:O	2.16	0.45
16:P:58:TYR:O	16:P:61:SER:OG	2.27	0.45
1:A:193:C:OP1	20:T:57:ARG:HD2	2.16	0.45
1:A:410:G:H2'	1:A:429:U:C4	2.52	0.45
1:A:972:C:H4'	10:J:57:LYS:HG3	1.97	0.45
2:B:240:GLN:O	2:B:240:GLN:HG2	2.16	0.45
2:B:33:TYR:O	2:B:33:TYR:HD1	2.00	0.45
3:C:108:ASN:HB3	3:C:111:LEU:HD12	1.99	0.45
4:D:104:VAL:O	4:D:107:ARG:N	2.49	0.45
4:D:101:LEU:HD21	4:D:121:VAL:HG13	1.98	0.45
6:F:35:ALA:HA	6:F:67:MET:HB3	1.99	0.45
7:G:95:ARG:HH11	7:G:95:ARG:HG3	1.82	0.45
8:H:41:ARG:CG	8:H:41:ARG:NH1	2.76	0.45
10:J:21:GLN:O	10:J:21:GLN:HG2	2.16	0.45
20:T:96:GLY:O	20:T:99:LEU:HD13	2.16	0.45
1:A:1060:C:C5	3:C:2:GLY:HA2	2.50	0.45
1:A:652:U:H1'	1:A:653:A:H2	1.79	0.45
2:B:15:VAL:HG23	2:B:209:ARG:HE	1.80	0.45
2:B:214:ILE:HD13	2:B:217:ARG:HH22	1.81	0.45
2:B:24:TRP:CD2	2:B:26:PRO:HD3	2.52	0.45
3:C:92:ALA:HB2	3:C:99:VAL:HG11	1.99	0.45
5:E:52:PRO:HB2	5:E:53:LEU:HD12	1.97	0.45
5:E:80:ILE:HG13	5:E:82:VAL:HG23	1.99	0.45
6:F:9:VAL:HB	6:F:87:ARG:HB2	1.97	0.45
7:G:148:ASN:C	7:G:150:ALA:N	2.69	0.45
11:K:32:ILE:HD11	11:K:72:ALA:HB2	1.96	0.45
14:N:23:ARG:C	14:N:24:CYS:O	2.54	0.45
1:A:1127:G:H21	1:A:1147:C:H41	1.65	0.45
1:A:1346:A:C4	7:G:10:ARG:NH1	2.85	0.45
3:C:42:LEU:HD12	3:C:45:LYS:HZ3	1.82	0.45
5:E:77:PRO:HG2	5:E:142:LEU:HD22	1.98	0.45
5:E:7:GLU:HB3	5:E:112:LEU:HD13	1.99	0.45
9:I:83:ARG:C	9:I:86:VAL:HG12	2.36	0.45
10:J:51:ARG:HG2	10:J:51:ARG:HH11	1.81	0.45
10:J:38:ILE:CD1	10:J:71:LEU:HB3	2.46	0.45
15:O:82:ILE:CG2	15:O:83:GLU:N	2.79	0.45
16:P:50:LYS:HD3	16:P:50:LYS:O	2.16	0.45
1:A:377:G:P	16:P:5:ARG:HH11	2.40	0.45
17:Q:41:LYS:HZ3	17:Q:92:ARG:HH22	1.60	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:R:63:GLN:OE1	18:R:63:GLN:HA	2.17	0.45
20:T:24:LEU:HD13	20:T:24:LEU:O	2.17	0.45
23:X:5:C:H2'	23:X:6:C:C6	2.51	0.45
1:A:1067:A:N1	1:A:1108:G:O2'	2.40	0.45
1:A:922:G:N3	1:A:1398:A:H2	2.14	0.45
1:A:437:U:H2'	1:A:438:G:O4'	2.16	0.45
1:A:475:G:H2'	1:A:476:G:H8	1.82	0.45
4:D:120:LEU:CD2	4:D:125:HIS:HB2	2.46	0.45
4:D:199:ASN:O	4:D:201:GLN:N	2.49	0.45
4:D:94:LEU:O	4:D:98:GLU:N	2.50	0.45
5:E:36:ASP:C	5:E:37:ARG:HG2	2.38	0.45
8:H:86:ILE:CG1	8:H:133:LEU:HD22	2.46	0.45
10:J:29:ARG:HH11	10:J:29:ARG:HG2	1.81	0.45
10:J:63:PHE:HB3	14:N:57:ARG:O	2.17	0.45
11:K:83:ILE:HG12	11:K:109:VAL:HG23	1.98	0.45
13:M:108:ARG:O	13:M:111:LYS:N	2.48	0.45
13:M:110:ARG:HH11	13:M:110:ARG:HG3	1.82	0.45
13:M:3:ARG:HD2	13:M:9:ILE:CG1	2.45	0.45
13:M:39:ILE:HD12	13:M:56:LEU:HD23	1.99	0.45
13:M:57:ARG:HD2	13:M:61:GLU:OE2	2.17	0.45
20:T:10:LEU:C	20:T:12:ALA:H	2.20	0.45
2:B:95:GLN:NE2	2:B:96:ARG:NH1	2.65	0.45
7:G:111:ARG:HD2	7:G:123:GLU:HB2	1.99	0.45
7:G:26:PHE:HZ	7:G:120:ILE:HG23	1.82	0.45
10:J:62:HIS:N	10:J:62:HIS:CD2	2.85	0.45
1:A:35:G:N2	12:L:118:SER:OG	2.48	0.45
13:M:15:VAL:O	13:M:19:LEU:CD2	2.64	0.45
16:P:39:TYR:CZ	16:P:41:PRO:HB3	2.52	0.45
17:Q:3:LYS:HD3	17:Q:61:GLU:O	2.16	0.45
18:R:82:THR:CG2	18:R:83:GLU:N	2.79	0.45
1:A:1222:G:OP1	19:S:77:THR:HG21	2.17	0.45
1:A:1305:G:C5'	21:U:4:GLY:HA3	2.46	0.45
1:A:539:A:H2'	1:A:540:G:C8	2.52	0.44
1:A:625:G:H2'	1:A:626:U:H6	1.81	0.44
2:B:30:ARG:HH21	2:B:194:PRO:HG2	1.82	0.44
3:C:140:ARG:CG	3:C:140:ARG:HH11	2.30	0.44
3:C:43:LEU:HD11	3:C:66:VAL:HG11	1.98	0.44
8:H:64:LYS:HB3	8:H:79:VAL:HG21	1.98	0.44
8:H:82:HIS:CD2	8:H:82:HIS:C	2.91	0.44
19:S:41:VAL:HG13	19:S:44:MET:CB	2.39	0.44
19:S:69:HIS:O	19:S:70:LYS:O	2.34	0.44
20:T:28:ALA:O	20:T:30:LYS:N	2.50	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:328:C:H4'	1:A:329:A:H5'	1.99	0.44
1:A:501:C:H2'	1:A:502:G:C8	2.51	0.44
1:A:529:G:O6	12:L:49:ASN:HA	2.16	0.44
1:A:757:U:O2'	1:A:879:C:O2	2.34	0.44
2:B:189:ASP:OD2	2:B:205:ASP:OD1	2.35	0.44
1:A:1190:G:OP1	3:C:5:ILE:HD12	2.17	0.44
4:D:122:ARG:HA	4:D:134:ASP:HB2	2.00	0.44
4:D:13:ARG:CB	4:D:33:MET:HE3	2.47	0.44
4:D:178:VAL:O	4:D:181:MET:N	2.50	0.44
4:D:25:ARG:CZ	4:D:30:LYS:HE3	2.46	0.44
4:D:3:ARG:O	4:D:4:TYR:C	2.55	0.44
5:E:12:LEU:HB3	5:E:31:LEU:CB	2.47	0.44
10:J:33:GLN:HB2	10:J:75:ILE:HD11	1.99	0.44
13:M:101:GLN:HE21	13:M:101:GLN:HB2	1.66	0.44
13:M:16:ASP:O	13:M:19:LEU:HD23	2.17	0.44
1:A:1048:G:OP1	14:N:3:ARG:HB3	2.17	0.44
1:A:668:G:O2'	15:O:46:HIS:HB3	2.16	0.44
15:O:54:ARG:O	15:O:55:GLY:C	2.55	0.44
20:T:84:LEU:C	20:T:84:LEU:HD13	2.36	0.44
20:T:89:ARG:HH12	20:T:106:ALA:HB1	1.82	0.44
1:A:939:G:H1	1:A:1344:C:H42	1.65	0.44
1:A:857:C:H2'	1:A:858:G:O4'	2.17	0.44
1:A:976:G:H5''	1:A:1358:U:O2'	2.17	0.44
2:B:98:LEU:O	2:B:101:MET:HG3	2.17	0.44
3:C:22:TRP:HB3	3:C:59:ARG:HB2	1.99	0.44
3:C:73:PRO:O	3:C:77:ILE:HG13	2.16	0.44
4:D:72:GLU:O	4:D:73:ARG:C	2.52	0.44
5:E:31:LEU:HD23	5:E:45:PHE:CD1	2.53	0.44
7:G:40:ALA:O	7:G:41:ARG:C	2.54	0.44
12:L:120:TYR:O	12:L:121:GLY:O	2.36	0.44
13:M:56:LEU:O	13:M:56:LEU:HD13	2.17	0.44
15:O:29:VAL:HB	15:O:81:LEU:HD21	1.99	0.44
17:Q:33:GLY:O	17:Q:34:LYS:C	2.55	0.44
17:Q:48:GLU:O	17:Q:50:LYS:N	2.50	0.44
20:T:48:LYS:HB3	20:T:51:GLU:CG	2.47	0.44
20:T:44:ALA:HB1	20:T:91:LEU:HB2	2.00	0.44
1:A:1241:G:H2'	1:A:1242:C:C6	2.52	0.44
1:A:793:U:O2	1:A:1516:G:H4'	2.17	0.44
1:A:281:G:H8	1:A:281:G:OP2	2.00	0.44
1:A:407:G:O2'	4:D:116:GLN:HG3	2.18	0.44
2:B:51:LEU:O	2:B:55:PHE:HD2	2.00	0.44
6:F:76:ALA:HB1	6:F:80:ARG:HH21	1.82	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:F:3:ARG:HG2	6:F:93:SER:OG	2.17	0.44
9:I:47:LEU:H	9:I:47:LEU:HD22	1.81	0.44
9:I:4:TYR:CZ	9:I:88:TYR:HB2	2.51	0.44
12:L:120:TYR:CD1	12:L:120:TYR:N	2.86	0.44
13:M:66:LEU:C	13:M:70:LEU:HB2	2.38	0.44
16:P:15:PRO:O	16:P:16:HIS:ND1	2.51	0.44
17:Q:13:ASP:O	17:Q:15:MET:N	2.51	0.44
20:T:83:ARG:C	20:T:86:ARG:HB3	2.38	0.44
1:A:1098:C:H2'	1:A:1099:G:O4'	2.18	0.44
1:A:519:C:H2'	1:A:520:A:O4'	2.17	0.44
1:A:580:U:H2'	1:A:581:G:O4'	2.18	0.44
2:B:77:ALA:HB2	2:B:211:ILE:HG21	1.99	0.44
3:C:42:LEU:HD12	3:C:45:LYS:NZ	2.32	0.44
3:C:69:HIS:N	3:C:69:HIS:ND1	2.66	0.44
4:D:60:GLU:HG2	4:D:202:LEU:HD12	2.00	0.44
4:D:206:PHE:CD2	4:D:207:TYR:CE1	3.05	0.44
4:D:76:ARG:O	4:D:79:PHE:HB3	2.17	0.44
5:E:147:ASP:OD2	5:E:147:ASP:N	2.50	0.44
5:E:62:ALA:C	5:E:64:ARG:H	2.21	0.44
7:G:45:ASP:O	7:G:49:ILE:HG12	2.17	0.44
9:I:7:THR:O	9:I:83:ARG:CD	2.66	0.44
11:K:48:ILE:HD11	11:K:64:ALA:N	2.32	0.44
12:L:117:ARG:NH2	12:L:124:LYS:HD3	2.32	0.44
1:A:1269:A:N1	1:A:1312:G:O2'	2.39	0.44
1:A:457:C:N4	1:A:475:G:H1	2.16	0.44
2:B:178:ARG:HD2	8:H:71:GLY:C	2.37	0.44
2:B:192:SER:OG	2:B:193:ASP:N	2.50	0.44
2:B:229:VAL:O	2:B:229:VAL:HG12	2.17	0.44
2:B:29:ALA:O	2:B:32:ILE:HG22	2.17	0.44
1:A:403:C:H4'	4:D:122:ARG:NH2	2.33	0.44
4:D:68:TYR:O	4:D:69:GLY:C	2.55	0.44
5:E:67:VAL:HG22	5:E:68:GLU:N	2.33	0.44
7:G:140:ASP:HA	7:G:143:ARG:HH11	1.79	0.44
7:G:62:PHE:O	7:G:64:GLN:N	2.51	0.44
10:J:70:ARG:HG3	10:J:70:ARG:HH11	1.83	0.44
11:K:77:MET:HE3	11:K:80:VAL:HG12	1.98	0.44
12:L:44:THR:HA	12:L:45:PRO:HD3	1.70	0.44
13:M:90:LEU:HD12	13:M:91:ARG:N	2.33	0.44
16:P:83:GLU:HG3	16:P:84:ALA:N	2.33	0.44
1:A:986:A:H1'	19:S:54:GLY:O	2.17	0.44
1:A:1069:C:O3'	5:E:25:ARG:NH1	2.50	0.44
1:A:1225:A:OP1	13:M:102:ARG:HA	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1251:A:H2'	1:A:1252:A:C8	2.53	0.44
1:A:1374:A:O2'	7:G:28:ASN:HB3	2.17	0.44
1:A:983:A:N1	1:A:1222:G:N2	2.63	0.44
5:E:101:ILE:H	5:E:101:ILE:HD13	1.82	0.44
7:G:15:ASP:HB3	7:G:20:ASP:N	2.15	0.44
8:H:16:ALA:HB2	8:H:24:THR:CG2	2.45	0.44
8:H:88:LYS:HB3	8:H:89:PRO:HD2	2.00	0.44
9:I:13:ALA:HB2	9:I:68:GLY:CA	2.47	0.44
9:I:5:TYR:CD2	9:I:6:GLY:N	2.86	0.44
10:J:54:PHE:CD2	10:J:55:LYS:HD2	2.52	0.44
10:J:61:GLU:CG	14:N:58:LYS:HE2	2.47	0.44
20:T:36:LEU:C	20:T:38:LYS:N	2.71	0.44
1:A:1287:A:H2'	1:A:1288:A:C8	2.53	0.44
2:B:132:LYS:HA	2:B:135:GLN:CB	2.43	0.44
2:B:47:THR:HG22	2:B:51:LEU:CG	2.48	0.44
1:A:939:G:H5''	7:G:102:ARG:CZ	2.47	0.44
7:G:16:LEU:HD13	9:I:45:ALA:HB2	1.99	0.44
8:H:28:ALA:O	8:H:29:SER:HB2	2.18	0.44
11:K:53:SER:C	11:K:55:LYS:H	2.20	0.44
13:M:36:LYS:CD	13:M:36:LYS:C	2.86	0.44
15:O:10:LYS:O	15:O:14:GLU:HB2	2.18	0.44
16:P:72:ARG:CD	16:P:73:LEU:HD23	2.47	0.44
17:Q:92:ARG:HG3	17:Q:92:ARG:NH1	2.30	0.44
1:A:1080:A:H5''	5:E:16:THR:HG21	2.00	0.44
8:H:118:VAL:O	8:H:119:LEU:HD23	2.17	0.44
10:J:10:GLY:O	10:J:68:HIS:N	2.51	0.44
10:J:38:ILE:CG1	10:J:71:LEU:HB3	2.48	0.44
11:K:13:GLN:HG3	11:K:75:TYR:CA	2.48	0.44
13:M:53:VAL:HG12	13:M:57:ARG:HH12	1.82	0.44
18:R:20:ALA:O	18:R:21:LYS:HG3	2.18	0.44
20:T:50:GLU:O	20:T:52:ALA:N	2.51	0.44
22:V:58:A:O2'	22:V:60:U:OP2	2.16	0.44
2:B:136:VAL:O	2:B:140:HIS:N	2.44	0.43
2:B:17:PHE:CG	2:B:44:LEU:HD11	2.53	0.43
2:B:87:ARG:NH1	2:B:223:ILE:HD12	2.33	0.43
2:B:87:ARG:HH11	2:B:223:ILE:HD11	1.83	0.43
4:D:146:ILE:H	4:D:146:ILE:CD1	2.30	0.43
1:A:1376:U:P	7:G:94:ARG:HH12	2.39	0.43
8:H:23:SER:HB3	8:H:62:TYR:HA	2.00	0.43
1:A:966:G:O2'	9:I:127:LYS:O	2.34	0.43
10:J:100:THR:O	10:J:101:VAL:HB	2.17	0.43
10:J:6:ILE:O	10:J:71:LEU:HD12	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:106:LYS:O	11:K:107:SER:CB	2.65	0.43
11:K:34:ASP:OD1	11:K:38:ASN:HB2	2.18	0.43
1:A:1226:C:N4	13:M:104:ARG:HD2	2.32	0.43
13:M:69:GLU:O	13:M:70:LEU:C	2.56	0.43
19:S:51:VAL:HG12	19:S:52:TYR:N	2.33	0.43
19:S:45:VAL:O	19:S:62:ILE:O	2.35	0.43
1:A:116:A:H61	1:A:313:A:H1'	1.83	0.43
1:A:1205:U:H1'	3:C:195:VAL:HG23	1.99	0.43
1:A:1297:C:O2'	1:A:1298:C:P	2.76	0.43
1:A:1301:U:H2'	1:A:1301:U:O2	2.17	0.43
1:A:458:C:H2'	1:A:464:G:H8	1.83	0.43
1:A:701:C:H4'	1:A:702:A:H5''	2.00	0.43
2:B:115:LEU:HD21	2:B:153:ARG:HD3	1.99	0.43
4:D:25:ARG:C	4:D:27:TYR:H	2.21	0.43
1:A:546:G:P	4:D:72:GLU:HB3	2.58	0.43
7:G:15:ASP:OD1	7:G:23:VAL:HG11	2.18	0.43
9:I:10:ARG:NE	9:I:105:ASP:CB	2.81	0.43
9:I:43:ALA:O	9:I:45:ALA:N	2.51	0.43
12:L:27:LEU:HD13	12:L:28:LYS:H	1.83	0.43
15:O:25:THR:HG22	15:O:70:LEU:HD22	1.99	0.43
16:P:23:ASP:O	16:P:26:ARG:HB2	2.18	0.43
20:T:101:GLY:C	20:T:103:GLY:H	2.21	0.43
1:A:1314:C:H2'	1:A:1315:U:C6	2.52	0.43
1:A:1388:C:H2'	1:A:1389:C:H6	1.83	0.43
1:A:181:G:O2'	1:A:182:U:O5'	2.35	0.43
1:A:555:C:H2'	1:A:556:C:C6	2.53	0.43
1:A:909:A:H2'	1:A:910:C:O4'	2.18	0.43
2:B:100:GLY:N	2:B:176:GLU:OE2	2.51	0.43
4:D:90:GLY:HA3	4:D:204:ILE:HD11	2.01	0.43
7:G:38:LEU:O	7:G:42:ILE:HG13	2.17	0.43
10:J:54:PHE:CE2	10:J:55:LYS:HD2	2.52	0.43
11:K:75:TYR:N	11:K:75:TYR:CD1	2.86	0.43
12:L:119:LYS:HB2	12:L:120:TYR:HD1	1.83	0.43
13:M:19:LEU:HD22	13:M:19:LEU:N	2.33	0.43
1:A:1223:C:P	19:S:78:ARG:HH12	2.41	0.43
1:A:192:U:H4'	20:T:103:GLY:HA2	2.00	0.43
24:Y:39:C:H4'	24:Y:40:G:OP1	2.18	0.43
1:A:1296:C:H3'	1:A:1297:C:C6	2.53	0.43
1:A:501:C:H2'	1:A:502:G:H8	1.83	0.43
2:B:231:GLU:HA	2:B:232:PRO:HD3	1.83	0.43
3:C:106:VAL:HG11	3:C:109:PRO:HA	2.00	0.43
3:C:14:ILE:C	3:C:16:ARG:H	2.21	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:95:GLY:O	4:D:99:SER:N	2.51	0.43
6:F:61:LEU:HD23	6:F:63:TYR:OH	2.17	0.43
6:F:88:VAL:HG12	6:F:89:MET:N	2.34	0.43
6:F:91:VAL:CG1	18:R:72:ARG:NH1	2.82	0.43
7:G:78:ARG:HH11	7:G:78:ARG:CG	2.31	0.43
9:I:100:GLY:C	9:I:102:LEU:N	2.72	0.43
10:J:90:LEU:N	10:J:91:PRO:CD	2.81	0.43
11:K:105:VAL:O	11:K:105:VAL:HG23	2.19	0.43
12:L:91:LYS:HE2	12:L:91:LYS:HB2	1.76	0.43
16:P:21:VAL:HG23	16:P:34:GLU:N	2.34	0.43
19:S:36:ARG:NH1	19:S:52:TYR:O	2.51	0.43
1:A:1211:U:H5'	1:A:1212:U:OP1	2.17	0.43
1:A:246:A:N6	1:A:281:G:H1'	2.33	0.43
1:A:520:A:N1	1:A:536:C:H1'	2.33	0.43
1:A:676:A:H1'	11:K:115:PRO:HB3	1.99	0.43
1:A:833:U:H2'	1:A:834:C:C6	2.53	0.43
1:A:855:G:OP2	1:A:871:U:N3	2.36	0.43
2:B:109:SER:C	2:B:111:ARG:H	2.21	0.43
2:B:142:LEU:HD23	2:B:142:LEU:O	2.19	0.43
2:B:47:THR:O	2:B:51:LEU:N	2.32	0.43
2:B:90:MET:HA	2:B:91:PRO:HD3	1.82	0.43
3:C:27:LYS:HB3	3:C:27:LYS:NZ	2.34	0.43
3:C:67:THR:O	3:C:69:HIS:CE1	2.72	0.43
3:C:69:HIS:HA	3:C:104:GLN:HB2	2.00	0.43
4:D:132:ARG:HH11	4:D:132:ARG:HG2	1.83	0.43
4:D:163:GLU:HA	4:D:163:GLU:OE2	2.19	0.43
7:G:23:VAL:O	7:G:27:ILE:HD12	2.19	0.43
7:G:60:LYS:O	7:G:61:VAL:C	2.57	0.43
9:I:41:VAL:HG12	9:I:41:VAL:O	2.18	0.43
10:J:51:ARG:NH1	10:J:51:ARG:HG2	2.33	0.43
11:K:20:TYR:C	11:K:21:ILE:HD12	2.38	0.43
12:L:22:SER:C	12:L:24:VAL:H	2.22	0.43
15:O:77:ARG:HA	15:O:80:ALA:HB2	1.99	0.43
15:O:83:GLU:C	15:O:85:LEU:N	2.71	0.43
22:V:15:G:N2	22:V:48:C:H42	2.17	0.43
22:V:4:G:C6	22:V:70:G:N1	2.87	0.43
1:A:1175:G:H2'	1:A:1176:A:H8	1.83	0.43
1:A:756:C:H2'	1:A:757:U:O4'	2.18	0.43
2:B:32:ILE:HD13	2:B:190:THR:CG2	2.48	0.43
7:G:111:ARG:HH11	7:G:111:ARG:CB	2.23	0.43
7:G:122:HIS:HA	7:G:125:MET:HB2	2.00	0.43
7:G:88:PRO:HB3	7:G:145:ALA:HA	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:155:ARG:H	7:G:155:ARG:HD3	1.83	0.43
11:K:62:GLN:O	11:K:64:ALA:N	2.52	0.43
14:N:12:ARG:C	14:N:14:PRO:CD	2.81	0.43
16:P:72:ARG:O	16:P:72:ARG:HD3	2.18	0.43
19:S:21:GLU:HG3	19:S:22:LEU:CD1	2.49	0.43
22:V:54:U:C4	22:V:55:U:C4	3.06	0.43
2:B:77:ALA:HB1	2:B:165:VAL:HG11	2.00	0.43
2:B:200:ILE:HD12	2:B:200:ILE:N	2.34	0.43
2:B:33:TYR:CD1	2:B:33:TYR:C	2.92	0.43
2:B:95:GLN:HE21	2:B:147:LYS:CE	2.28	0.43
3:C:59:ARG:HH12	3:C:97:LYS:CD	2.31	0.43
4:D:90:GLY:O	4:D:93:PHE:HB3	2.19	0.43
5:E:126:ARG:CG	5:E:126:ARG:NH1	2.79	0.43
6:F:73:ASN:O	6:F:76:ALA:HB3	2.19	0.43
8:H:64:LYS:CB	8:H:79:VAL:HG21	2.48	0.43
9:I:95:LYS:C	9:I:95:LYS:HD3	2.39	0.43
10:J:16:LEU:HD13	10:J:16:LEU:C	2.38	0.43
12:L:120:TYR:O	12:L:121:GLY:C	2.57	0.43
15:O:64:ARG:CD	15:O:68:ARG:NH2	2.82	0.43
18:R:29:PHE:HD2	18:R:29:PHE:N	2.17	0.43
18:R:43:PHE:HA	18:R:51:LEU:HD12	2.01	0.43
1:A:56:U:H2'	1:A:57:G:C8	2.54	0.43
1:A:953:G:H2'	1:A:954:G:O4'	2.19	0.43
2:B:54:THR:HG21	2:B:201:ILE:HD11	2.00	0.43
4:D:25:ARG:NH1	4:D:30:LYS:CE	2.75	0.43
5:E:62:ALA:O	5:E:64:ARG:N	2.51	0.43
6:F:22:GLU:OE1	6:F:82:ARG:NH2	2.46	0.43
6:F:85:VAL:O	6:F:85:VAL:HG12	2.18	0.43
7:G:148:ASN:O	7:G:150:ALA:N	2.51	0.43
8:H:20:TYR:CD1	8:H:65:TYR:HD2	2.35	0.43
11:K:44:SER:O	11:K:48:ILE:HG12	2.18	0.43
11:K:75:TYR:HD1	11:K:75:TYR:N	2.17	0.43
14:N:17:LYS:HG3	14:N:18:VAL:N	2.33	0.43
18:R:53:ARG:C	18:R:55:ARG:H	2.22	0.43
20:T:44:ALA:C	20:T:91:LEU:HB3	2.39	0.43
1:A:1285:A:H4'	1:A:1286:A:O5'	2.19	0.43
1:A:452:A:O2'	1:A:453:A:O4'	2.35	0.43
2:B:127:ILE:HG23	2:B:128:GLU:N	2.34	0.43
2:B:188:ALA:CB	2:B:200:ILE:HG23	2.47	0.43
2:B:68:ILE:HB	2:B:70:PHE:HE1	1.82	0.43
2:B:92:TYR:C	2:B:92:TYR:HD1	2.21	0.43
3:C:12:LEU:C	3:C:14:ILE:H	2.22	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:188:LEU:HD12	3:C:195:VAL:CG1	2.48	0.43
4:D:52:SER:O	4:D:55:ALA:N	2.52	0.43
5:E:48:ALA:HB2	5:E:57:LYS:HD3	2.00	0.43
5:E:94:ALA:HB2	5:E:119:LEU:HG	2.00	0.43
8:H:91:ARG:CG	8:H:91:ARG:HH11	2.23	0.43
9:I:26:VAL:CG1	9:I:63:ILE:HD13	2.49	0.43
12:L:27:LEU:C	12:L:29:GLY:H	2.20	0.43
15:O:83:GLU:HA	15:O:83:GLU:OE1	2.19	0.43
1:A:310:G:H4'	16:P:31:LYS:HD3	2.01	0.43
1:A:1055:A:N7	1:A:1200:C:N4	2.67	0.43
1:A:109:A:C6	1:A:326:G:C6	3.07	0.43
2:B:162:ILE:O	2:B:185:ILE:HG13	2.19	0.43
3:C:101:LEU:C	3:C:101:LEU:HD23	2.38	0.43
5:E:105:VAL:HB	5:E:106:PRO:CD	2.49	0.43
6:F:27:GLN:H	6:F:27:GLN:HG2	1.65	0.43
11:K:108:ILE:HG21	18:R:88:LYS:OXT	2.19	0.43
1:A:376:G:OP1	16:P:5:ARG:HB2	2.19	0.43
16:P:75:ARG:C	16:P:77:ALA:N	2.72	0.43
18:R:73:ALA:HB3	18:R:79:LEU:CD1	2.47	0.43
22:V:43:A:H2'	22:V:44:A:C8	2.54	0.43
1:A:514:C:H2'	1:A:515:G:C8	2.53	0.42
2:B:95:GLN:HB3	2:B:148:TYR:HD1	1.84	0.42
2:B:16:HIS:CD2	2:B:213:LEU:HD13	2.54	0.42
2:B:211:ILE:O	2:B:215:LEU:HB2	2.19	0.42
3:C:22:TRP:CB	3:C:59:ARG:HB2	2.48	0.42
3:C:76:VAL:CG2	3:C:103:VAL:HG11	2.49	0.42
10:J:75:ILE:CG1	10:J:76:ASN:H	2.17	0.42
16:P:20:VAL:CG2	16:P:21:VAL:N	2.81	0.42
16:P:55:ARG:O	16:P:56:ALA:C	2.57	0.42
17:Q:22:LEU:HD13	17:Q:41:LYS:HG2	2.02	0.42
17:Q:77:VAL:O	17:Q:78:GLU:HB2	2.18	0.42
19:S:29:ARG:HG2	19:S:29:ARG:HH11	1.84	0.42
19:S:62:ILE:HG22	19:S:63:THR:N	2.34	0.42
19:S:66:MET:O	19:S:66:MET:HG3	2.19	0.42
1:A:1069:C:O2'	5:E:25:ARG:NH1	2.50	0.42
1:A:191(D):U:H2'	1:A:191(E):G:H8	1.83	0.42
1:A:292:G:C5	1:A:293:G:H1'	2.53	0.42
1:A:308:C:H2'	1:A:309:G:C8	2.54	0.42
1:A:399:G:H2'	1:A:400:C:C6	2.54	0.42
1:A:452:A:C6	1:A:453:A:C6	3.07	0.42
2:B:33:TYR:C	2:B:33:TYR:HD1	2.23	0.42
4:D:19:LEU:O	4:D:20:TYR:C	2.57	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:22:LYS:CD	4:D:26:CYS:SG	3.05	0.42
5:E:20:GLN:O	5:E:21:ALA:C	2.57	0.42
6:F:23:LYS:HG2	6:F:27:GLN:OE1	2.18	0.42
9:I:29:ASN:OD1	9:I:65:VAL:N	2.48	0.42
10:J:30:SER:OG	10:J:81:THR:HG22	2.19	0.42
1:A:950:U:H3'	13:M:102:ARG:NH2	2.34	0.42
15:O:25:THR:O	15:O:29:VAL:HG23	2.18	0.42
15:O:8:LYS:NZ	15:O:31:LEU:HD11	2.34	0.42
16:P:40:ASP:C	16:P:42:ARG:N	2.73	0.42
22:V:53:G:HO2'	22:V:54:U:H6	1.66	0.42
1:A:1065:U:O2'	1:A:1066:C:OP2	2.25	0.42
1:A:1163:C:H42	1:A:1173:G:H1	1.67	0.42
1:A:191:G:N9	20:T:105:SER:HB3	2.33	0.42
2:B:99:GLY:O	2:B:108:ILE:HD11	2.19	0.42
3:C:149:ALA:O	3:C:169:ALA:CA	2.67	0.42
3:C:83:ARG:O	3:C:86:VAL:HG22	2.20	0.42
4:D:127:THR:HG23	4:D:130:GLY:O	2.20	0.42
7:G:126:ASP:N	7:G:126:ASP:OD2	2.53	0.42
7:G:75:VAL:HG13	7:G:145:ALA:HA	2.00	0.42
7:G:79:ARG:HH12	7:G:82:GLY:HA2	1.84	0.42
8:H:109:ILE:HD11	8:H:120:THR:HG22	2.00	0.42
13:M:87:TYR:HA	13:M:90:LEU:HG	2.01	0.42
15:O:17:ARG:HD3	15:O:26:GLU:HG3	2.01	0.42
16:P:12:LYS:HE2	16:P:12:LYS:HB3	1.73	0.42
1:A:760:G:O2'	17:Q:98:LEU:HD23	2.19	0.42
19:S:29:ARG:HD3	19:S:30:LEU:H	1.83	0.42
19:S:41:VAL:CG1	19:S:45:VAL:H	2.32	0.42
19:S:8:GLY:O	19:S:9:VAL:CG2	2.57	0.42
22:V:1:C:O2'	22:V:2:G:H5'	2.19	0.42
1:A:372:C:HO2'	1:A:373:A:P	2.41	0.42
1:A:430:A:P	4:D:9:CYS:H	2.42	0.42
1:A:743:U:H2'	1:A:744:C:C6	2.54	0.42
2:B:60:ASP:C	2:B:62:ALA:N	2.72	0.42
3:C:113:ALA:C	3:C:115:LEU:N	2.73	0.42
4:D:24:GLU:O	4:D:28:SER:OG	2.21	0.42
7:G:79:ARG:NH1	7:G:82:GLY:HA2	2.35	0.42
10:J:49:VAL:HG13	10:J:50:ILE:N	2.35	0.42
13:M:54:VAL:O	13:M:58:GLU:OE2	2.37	0.42
14:N:47:LEU:O	14:N:48:ALA:C	2.57	0.42
18:R:63:GLN:O	18:R:66:LEU:HB3	2.18	0.42
18:R:64:ARG:O	18:R:65:ILE:C	2.58	0.42
18:R:74:ARG:NH2	18:R:81:PHE:HA	2.35	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:U:6:ARG:C	21:U:8:THR:H	2.20	0.42
1:A:190:G:O2'	1:A:191(A):G:P	2.76	0.42
3:C:35:GLU:O	3:C:38:ARG:N	2.53	0.42
4:D:150:GLU:O	4:D:152:SER:N	2.53	0.42
5:E:71:LEU:HD11	5:E:113:ALA:O	2.20	0.42
11:K:124:LYS:HB3	11:K:125:PHE:H	1.67	0.42
12:L:10:LEU:CD1	17:Q:32:TYR:CD2	3.02	0.42
1:A:1221:G:OP1	19:S:36:ARG:HD3	2.19	0.42
1:A:1384:C:H2'	1:A:1385:G:H8	1.84	0.42
1:A:347:G:O2'	1:A:348:G:P	2.78	0.42
1:A:736:C:H2'	1:A:737:A:C8	2.54	0.42
2:B:158:LEU:C	2:B:158:LEU:HD12	2.39	0.42
3:C:143:GLU:C	3:C:145:GLY:H	2.23	0.42
3:C:142:MET:HG2	3:C:149:ALA:HB2	2.01	0.42
6:F:45:LEU:O	6:F:46:ARG:HB2	2.19	0.42
8:H:33:GLU:O	8:H:36:LEU:N	2.53	0.42
9:I:25:LYS:O	9:I:60:ASP:OD1	2.37	0.42
9:I:71:SER:O	9:I:74:ILE:N	2.52	0.42
12:L:38:THR:HG22	12:L:57:LYS:HB3	2.01	0.42
13:M:4:ILE:CG2	13:M:5:ALA:H	2.29	0.42
17:Q:77:VAL:O	17:Q:77:VAL:HG12	2.20	0.42
19:S:30:LEU:O	19:S:31:ILE:HB	2.19	0.42
20:T:96:GLY:O	20:T:99:LEU:CD1	2.67	0.42
24:Y:36:G:C2	24:Y:37:IMG:C4	3.07	0.42
1:A:376:G:O3'	16:P:5:ARG:HD2	2.20	0.42
2:B:204:ASN:C	2:B:204:ASN:HD22	2.22	0.42
2:B:69:LEU:HD12	2:B:91:PRO:O	2.19	0.42
3:C:58:GLU:HB2	3:C:65:ALA:HB3	2.01	0.42
3:C:88:ARG:NH2	3:C:101:LEU:O	2.53	0.42
4:D:29:PRO:CG	4:D:30:LYS:CE	2.86	0.42
4:D:59:ARG:NE	4:D:59:ARG:HA	2.34	0.42
4:D:93:PHE:CE1	4:D:97:LEU:HD11	2.55	0.42
7:G:18:TYR:CD2	7:G:59:LEU:HD13	2.55	0.42
8:H:86:ILE:CB	8:H:133:LEU:HD22	2.49	0.42
8:H:95:VAL:HG23	8:H:95:VAL:O	2.20	0.42
11:K:21:ILE:HD13	11:K:84:VAL:HG12	2.02	0.42
1:A:881:G:P	12:L:12:ARG:HH22	2.43	0.42
13:M:13:LYS:HA	13:M:44:ARG:CD	2.48	0.42
1:A:1049:U:O2'	14:N:2:ALA:N	2.45	0.42
17:Q:82:MET:C	17:Q:84:LEU:N	2.72	0.42
18:R:76:LEU:HD22	18:R:76:LEU:N	2.35	0.42
19:S:15:LEU:CD2	19:S:15:LEU:N	2.79	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:S:7:LYS:CG	19:S:8:GLY:N	2.83	0.42
20:T:13:LEU:CD1	20:T:17:ARG:NH1	2.82	0.42
22:V:17:C:H2'	22:V:17:C:O2	2.20	0.42
1:A:45:U:H2'	1:A:46:G:H8	1.79	0.42
1:A:573:A:N3	1:A:883:C:O2'	2.51	0.42
1:A:828:A:H2'	1:A:829:G:O4'	2.19	0.42
2:B:109:SER:C	2:B:111:ARG:N	2.73	0.42
2:B:130:ARG:NH2	2:B:138:LEU:HD21	2.34	0.42
2:B:162:ILE:O	2:B:185:ILE:CG1	2.67	0.42
2:B:197:VAL:CG1	2:B:198:ASP:N	2.82	0.42
2:B:200:ILE:CG2	2:B:201:ILE:N	2.83	0.42
2:B:67:THR:C	2:B:68:ILE:HD12	2.40	0.42
3:C:47:LEU:HD11	3:C:76:VAL:CG1	2.42	0.42
5:E:31:LEU:HD23	5:E:45:PHE:HD1	1.84	0.42
6:F:46:ARG:HG3	6:F:47:ARG:N	2.34	0.42
17:Q:27:PHE:HA	17:Q:28:PRO:HD3	1.92	0.42
17:Q:76:LEU:HD21	17:Q:79:SER:HB2	2.01	0.42
19:S:18:LYS:O	19:S:18:LYS:HD2	2.19	0.42
19:S:41:VAL:HG11	19:S:45:VAL:HG13	2.02	0.42
20:T:10:LEU:O	20:T:12:ALA:N	2.53	0.42
20:T:99:LEU:O	20:T:100:ILE:CB	2.68	0.42
1:A:1316:G:N2	1:A:1319:A:H5''	2.25	0.42
1:A:1347:G:N2	1:A:1373:G:H2'	2.34	0.42
1:A:720:C:H5''	18:R:52:PRO:HA	2.02	0.42
6:F:36:ARG:CZ	6:F:38:GLU:HG2	2.49	0.42
8:H:102:ARG:NH1	8:H:105:ARG:CZ	2.80	0.42
9:I:35:GLU:HG2	9:I:35:GLU:O	2.19	0.42
9:I:6:GLY:HA3	9:I:84:ALA:HB2	2.01	0.42
11:K:72:ALA:HB1	11:K:77:MET:HG2	2.02	0.42
16:P:21:VAL:HG21	16:P:59:TRP:NE1	2.35	0.42
20:T:36:LEU:HD13	20:T:36:LEU:HA	1.82	0.42
21:U:5:ASP:O	21:U:11:GLY:HA3	2.20	0.42
1:A:1129:C:H5'	1:A:1130:A:OP1	2.19	0.42
1:A:1275:A:H2'	1:A:1276:G:O4'	2.20	0.42
1:A:1313:U:OP1	19:S:5:LEU:HB2	2.19	0.42
1:A:62:U:O2'	1:A:379:C:O2	2.34	0.42
2:B:142:LEU:O	2:B:145:LEU:HB2	2.19	0.42
3:C:120:VAL:O	3:C:123:GLN:HB2	2.20	0.42
4:D:178:VAL:HG12	4:D:179:GLU:N	2.35	0.42
5:E:26:PHE:CD1	5:E:26:PHE:N	2.87	0.42
6:F:45:LEU:CD1	6:F:59:TYR:HD1	2.31	0.42
7:G:11:GLN:HG3	7:G:12:LEU:H	1.85	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:140:ASP:O	7:G:142:GLU:N	2.52	0.42
7:G:80:VAL:CG1	7:G:81:GLY:N	2.83	0.42
7:G:95:ARG:O	7:G:96:GLN:C	2.58	0.42
1:A:590:C:OP1	8:H:29:SER:HA	2.20	0.42
8:H:74:PRO:O	8:H:75:ARG:C	2.58	0.42
9:I:22:GLY:O	9:I:23:ASN:C	2.57	0.42
10:J:29:ARG:O	10:J:30:SER:HB3	2.20	0.42
13:M:16:ASP:HB3	13:M:34:LEU:CD1	2.49	0.42
13:M:88:ARG:HD2	13:M:88:ARG:O	2.19	0.42
1:A:1316:G:H5''	14:N:17:LYS:CE	2.50	0.42
14:N:9:LYS:HG2	14:N:9:LYS:O	2.19	0.42
15:O:3:ILE:N	15:O:3:ILE:HD13	2.22	0.42
15:O:71:GLN:HB2	15:O:78:TYR:CE1	2.54	0.42
16:P:45:THR:CG2	16:P:46:PRO:HD2	2.47	0.42
17:Q:11:VAL:HG23	17:Q:12:SER:N	2.35	0.42
19:S:58:VAL:HG23	19:S:58:VAL:O	2.20	0.42
20:T:96:GLY:O	20:T:97:ALA:CB	2.64	0.42
23:X:4:C:H2'	23:X:4:C:O2	2.20	0.42
2:B:125:PRO:O	2:B:126:GLU:HB2	2.20	0.41
2:B:159:PRO:HB2	2:B:160:ASP:H	1.74	0.41
4:D:111:ALA:HB3	4:D:117:ALA:HB2	2.02	0.41
4:D:101:LEU:CD2	4:D:121:VAL:HG11	2.50	0.41
4:D:150:GLU:C	4:D:152:SER:N	2.73	0.41
4:D:31:CYS:SG	4:D:31:CYS:O	2.78	0.41
7:G:44:TYR:O	7:G:47:CYS:N	2.53	0.41
8:H:122:ARG:HG3	8:H:122:ARG:HH11	1.85	0.41
8:H:53:VAL:HG12	8:H:54:ASP:OD2	2.20	0.41
11:K:33:THR:HB	11:K:37:GLY:C	2.40	0.41
1:A:1227:A:OP2	13:M:111:LYS:HE3	2.19	0.41
22:V:23:C:H2'	22:V:24:U:C6	2.55	0.41
1:A:149:A:H4'	1:A:1450:U:C4	2.55	0.41
1:A:382:A:H2'	1:A:383:A:C8	2.56	0.41
1:A:881:G:H2'	1:A:882:C:O4'	2.19	0.41
2:B:155:LEU:C	2:B:157:ARG:H	2.23	0.41
2:B:163:PHE:CD2	2:B:185:ILE:HD12	2.54	0.41
2:B:231:GLU:HG3	2:B:233:SER:H	1.86	0.41
2:B:5:ILE:HB	2:B:221:LEU:HD23	2.01	0.41
4:D:198:VAL:CG1	4:D:199:ASN:H	2.32	0.41
4:D:13:ARG:NH2	4:D:36:ARG:CZ	2.83	0.41
7:G:17:VAL:HG12	7:G:18:TYR:CD1	2.55	0.41
8:H:6:ILE:HB	8:H:85:ARG:HH11	1.74	0.41
9:I:118:LYS:HZ2	9:I:118:LYS:HB2	1.85	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:119:GLY:O	13:M:120:LYS:O	2.38	0.41
14:N:22:THR:HB	14:N:33:VAL:CG1	2.50	0.41
14:N:3:ARG:CG	14:N:4:LYS:N	2.83	0.41
15:O:54:ARG:NH1	15:O:58:MET:SD	2.93	0.41
17:Q:11:VAL:CG2	17:Q:20:THR:HB	2.50	0.41
20:T:95:ALA:O	20:T:97:ALA:N	2.54	0.41
1:A:1226:C:H2'	13:M:103:THR:HB	2.02	0.41
1:A:1344:C:HO2'	1:A:1348:U:HO2'	1.66	0.41
1:A:1388:C:H2'	1:A:1389:C:C6	2.55	0.41
1:A:224:C:H2'	1:A:225:C:C6	2.55	0.41
1:A:358:U:H2'	1:A:359:U:H6	1.85	0.41
2:B:97:TRP:HZ3	2:B:172:ILE:HG22	1.85	0.41
1:A:410:G:OP2	4:D:25:ARG:HG3	2.20	0.41
8:H:85:ARG:HA	8:H:135:CYS:HB3	2.02	0.41
9:I:43:ALA:C	9:I:45:ALA:N	2.73	0.41
9:I:8:GLY:CA	9:I:79:LEU:HD12	2.49	0.41
13:M:47:ASP:O	13:M:48:LEU:HB3	2.20	0.41
14:N:41:ARG:HG3	14:N:42:ILE:N	2.35	0.41
14:N:48:ALA:HA	14:N:53:LEU:HD12	2.01	0.41
16:P:22:THR:HB	16:P:32:TYR:HB3	2.03	0.41
1:A:134:A:H61	16:P:25:ARG:NH1	2.17	0.41
17:Q:74:LEU:O	17:Q:74:LEU:HD13	2.20	0.41
18:R:84:LYS:H	18:R:84:LYS:HG2	1.56	0.41
20:T:101:GLY:C	20:T:103:GLY:N	2.73	0.41
20:T:50:GLU:HA	20:T:100:ILE:HG22	2.02	0.41
1:A:337:C:H2'	1:A:338:A:C8	2.56	0.41
4:D:94:LEU:HA	4:D:97:LEU:HD12	2.01	0.41
5:E:31:LEU:HD22	5:E:31:LEU:HA	1.86	0.41
7:G:79:ARG:CZ	7:G:82:GLY:HA2	2.51	0.41
8:H:11:THR:HA	8:H:14:ARG:NH1	2.35	0.41
10:J:45:ARG:HH11	10:J:45:ARG:HG3	1.86	0.41
10:J:45:ARG:HB2	10:J:65:LEU:HB3	2.03	0.41
11:K:56:GLY:O	11:K:89:ALA:HB3	2.21	0.41
12:L:117:ARG:HB3	12:L:122:THR:HB	2.02	0.41
19:S:41:VAL:HG12	19:S:45:VAL:H	1.84	0.41
1:A:547:A:H4'	1:A:548:G:O5'	2.20	0.41
1:A:625:G:H2'	1:A:626:U:C6	2.54	0.41
1:A:643:C:H2'	1:A:644:G:C8	2.56	0.41
1:A:730:G:C5	1:A:731:G:H1'	2.56	0.41
4:D:36:ARG:HA	4:D:37:PRO:HD2	1.82	0.41
7:G:118:VAL:HG23	7:G:119:ARG:N	2.35	0.41
2:B:178:ARG:CD	8:H:71:GLY:C	2.89	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:I:118:LYS:HB3	9:I:118:LYS:NZ	2.34	0.41
9:I:83:ARG:HA	9:I:86:VAL:HG12	2.02	0.41
11:K:92:GLU:O	11:K:95:ILE:N	2.54	0.41
12:L:90:VAL:HG12	12:L:92:ASP:H	1.85	0.41
16:P:8:ARG:NH1	16:P:8:ARG:HG2	2.32	0.41
18:R:20:ALA:C	18:R:21:LYS:HG3	2.41	0.41
1:A:1223:C:P	1:A:1224:G:H2'	2.60	0.41
1:A:487:A:H2'	1:A:488:C:O4'	2.20	0.41
2:B:168:THR:CG2	2:B:192:SER:HB2	2.51	0.41
2:B:166:ASP:O	2:B:170:GLU:OE1	2.38	0.41
3:C:78:GLY:HA3	3:C:83:ARG:HB2	2.03	0.41
4:D:30:LYS:HG3	4:D:35:ARG:CZ	2.47	0.41
5:E:153:LYS:C	5:E:153:LYS:HD3	2.40	0.41
6:F:36:ARG:NH2	6:F:38:GLU:HG2	2.35	0.41
6:F:3:ARG:HB3	6:F:93:SER:CB	2.47	0.41
6:F:92:LYS:NZ	6:F:92:LYS:CB	2.84	0.41
7:G:24:THR:HA	7:G:27:ILE:HD13	2.02	0.41
7:G:78:ARG:CG	7:G:78:ARG:NH1	2.84	0.41
7:G:92:SER:HB3	7:G:95:ARG:HB2	2.03	0.41
9:I:71:SER:O	9:I:72:GLY:C	2.58	0.41
10:J:40:LEU:HB3	10:J:41:PRO:HD2	2.02	0.41
10:J:71:LEU:HD12	10:J:72:VAL:H	1.85	0.41
11:K:22:HIS:HB3	11:K:29:ILE:HG22	2.03	0.41
11:K:20:TYR:N	11:K:31:THR:O	2.54	0.41
12:L:21:LYS:N	12:L:21:LYS:CD	2.83	0.41
17:Q:89:LEU:HA	17:Q:89:LEU:HD23	1.93	0.41
18:R:53:ARG:O	18:R:55:ARG:N	2.53	0.41
19:S:4:SER:O	19:S:5:LEU:HD13	2.20	0.41
21:U:2:GLY:C	21:U:4:GLY:H	2.23	0.41
1:A:271:C:H2'	1:A:272:C:C6	2.56	0.41
1:A:49:U:C2	1:A:361:G:N2	2.88	0.41
2:B:115:LEU:O	2:B:119:GLU:N	2.54	0.41
3:C:108:ASN:CG	3:C:111:LEU:HG	2.41	0.41
3:C:55:VAL:HG12	3:C:55:VAL:O	2.20	0.41
4:D:30:LYS:HB3	4:D:35:ARG:CG	2.36	0.41
5:E:132:ALA:O	5:E:133:TYR:C	2.59	0.41
7:G:121:ALA:O	7:G:125:MET:HG3	2.21	0.41
7:G:22:LEU:O	7:G:25:ALA:HB3	2.21	0.41
12:L:53:ARG:HH12	12:L:92:ASP:CB	2.33	0.41
13:M:82:MET:HG2	13:M:93:ARG:HG3	2.03	0.41
14:N:18:VAL:CG2	14:N:19:ARG:H	2.32	0.41
15:O:74:ASP:C	15:O:76:GLU:H	2.24	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:80:ARG:NH1	19:S:65:ASN:O	2.51	0.41
22:V:16:C:O2'	22:V:17:C:OP1	2.39	0.41
22:V:21:A:N6	22:V:46:G:H2'	2.36	0.41
1:A:1065:U:C5	1:A:1190:G:H1'	2.55	0.41
1:A:1077:G:N2	1:A:1080:A:OP2	2.52	0.41
1:A:1065:U:P	1:A:1190:G:H22	2.44	0.41
1:A:1305:G:HO2'	1:A:1306:A:P	2.44	0.41
1:A:299:G:H2'	1:A:300:A:C8	2.56	0.41
1:A:390:C:O3'	16:P:28:ARG:NH2	2.53	0.41
1:A:484:G:H4'	1:A:485:G:O5'	2.20	0.41
2:B:71:VAL:HG23	2:B:164:VAL:HG22	2.02	0.41
2:B:32:ILE:HD13	2:B:190:THR:HG21	2.03	0.41
3:C:108:ASN:HB3	3:C:111:LEU:CG	2.51	0.41
1:A:614:A:OP1	4:D:85:LYS:NZ	2.54	0.41
5:E:10:MET:CE	5:E:13:ILE:HD13	2.51	0.41
5:E:68:GLU:CG	5:E:68:GLU:O	2.68	0.41
7:G:103:TRP:O	7:G:104:LEU:C	2.59	0.41
7:G:101:LEU:O	7:G:104:LEU:HB2	2.20	0.41
7:G:141:VAL:CG1	7:G:141:VAL:O	2.65	0.41
12:L:109:GLY:HA3	12:L:121:GLY:O	2.20	0.41
13:M:110:ARG:O	13:M:110:ARG:HG3	2.20	0.41
15:O:25:THR:CG2	15:O:70:LEU:HB2	2.48	0.41
16:P:6:LEU:N	16:P:6:LEU:CD1	2.84	0.41
12:L:10:LEU:HB3	17:Q:32:TYR:CZ	2.56	0.41
19:S:39:THR:HG23	19:S:68:GLY:O	2.21	0.41
1:A:1221:G:O3'	19:S:77:THR:HG21	2.21	0.41
1:A:335:C:O2'	1:A:1433:A:N3	2.49	0.41
1:A:244:U:H4'	1:A:245:C:C5'	2.51	0.41
3:C:47:LEU:CD1	3:C:76:VAL:HG12	2.42	0.41
3:C:92:ALA:HB2	3:C:99:VAL:HG13	2.03	0.41
5:E:32:VAL:CG2	5:E:58:ALA:HB1	2.51	0.41
10:J:8:LEU:HD11	10:J:23:ILE:CD1	2.37	0.41
1:A:686:U:O2'	11:K:42:TRP:NE1	2.54	0.41
12:L:43:VAL:HG13	12:L:55:VAL:HG21	2.03	0.41
13:M:117:VAL:O	13:M:119:GLY:N	2.53	0.41
13:M:15:VAL:O	13:M:19:LEU:HD22	2.21	0.41
13:M:8:GLU:C	13:M:9:ILE:CG2	2.90	0.41
15:O:69:TYR:CZ	15:O:73:GLU:HG3	2.56	0.41
16:P:50:LYS:HD3	16:P:50:LYS:C	2.42	0.41
1:A:1305:G:O2'	1:A:1306:A:H8	2.04	0.41
1:A:950:U:H2'	1:A:951:G:C8	2.56	0.41
2:B:223:ILE:O	2:B:226:ARG:HB3	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:37:ASN:C	2:B:39:ILE:N	2.73	0.41
3:C:23:TYR:CD2	3:C:24:ALA:N	2.88	0.41
4:D:15:GLU:OE1	4:D:15:GLU:N	2.54	0.41
8:H:18:ARG:HA	8:H:18:ARG:HD2	1.92	0.41
9:I:13:ALA:H	9:I:68:GLY:HA3	1.86	0.41
9:I:49:PRO:O	9:I:85:LEU:HD21	2.20	0.41
9:I:88:TYR:O	9:I:89:ASN:HB2	2.20	0.41
12:L:53:ARG:HH12	12:L:92:ASP:HB3	1.85	0.41
12:L:89:ARG:HB3	12:L:97:ARG:HA	2.02	0.41
13:M:28:ALA:C	13:M:30:ALA:H	2.25	0.41
16:P:20:VAL:HG22	16:P:21:VAL:H	1.83	0.41
17:Q:60:ILE:O	17:Q:60:ILE:HG23	2.21	0.41
17:Q:67:LYS:O	17:Q:68:ARG:HB3	2.21	0.41
17:Q:86:GLU:O	17:Q:87:LYS:C	2.60	0.41
1:A:1232:U:OP1	9:I:124:GLN:NE2	2.45	0.41
1:A:1301:U:O3'	13:M:21:TYR:OH	2.34	0.41
1:A:922:G:O2'	1:A:1398:A:N1	2.47	0.41
1:A:186(D):C:H2'	1:A:186(E):C:C6	2.55	0.41
1:A:189:U:H3	17:Q:63:ARG:HB3	1.86	0.41
1:A:957:U:H2'	1:A:959:A:OP2	2.20	0.41
2:B:62:ALA:O	2:B:65:GLY:N	2.53	0.41
2:B:95:GLN:O	2:B:96:ARG:C	2.59	0.41
3:C:46:GLU:C	3:C:48:TYR:H	2.23	0.41
5:E:41:VAL:O	5:E:66:MET:HA	2.21	0.41
5:E:90:VAL:C	5:E:91:LEU:HD12	2.42	0.41
6:F:75:LEU:HD23	6:F:75:LEU:C	2.41	0.41
8:H:38:ILE:CD1	8:H:118:VAL:HG12	2.49	0.41
8:H:1:MET:O	8:H:2:LEU:HB2	2.21	0.41
12:L:8:ASN:O	12:L:11:VAL:HG23	2.20	0.41
12:L:62:SER:HB2	12:L:64:TYR:CD1	2.56	0.41
1:A:1330:U:H4'	13:M:23:TYR:CZ	2.56	0.41
15:O:3:ILE:CD1	15:O:3:ILE:H	2.20	0.41
1:A:624:C:O3'	16:P:10:GLY:HA2	2.21	0.41
17:Q:11:VAL:HG23	17:Q:12:SER:H	1.85	0.41
17:Q:85:VAL:HG12	17:Q:85:VAL:O	2.20	0.41
18:R:52:PRO:HG2	18:R:55:ARG:HG2	2.04	0.41
19:S:29:ARG:HG2	19:S:29:ARG:NH1	2.36	0.41
20:T:47:GLY:C	20:T:49:ALA:N	2.72	0.41
1:A:1004:A:H1'	1:A:1036:G:C2	2.56	0.40
1:A:1224:G:O2'	19:S:78:ARG:NH2	2.50	0.40
1:A:1451:A:N3	1:A:1451:A:H2'	2.35	0.40
1:A:189:U:C2	17:Q:72:ARG:NH1	2.89	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:300:A:O2'	1:A:564:C:N3	2.46	0.40
3:C:140:ARG:HB2	3:C:140:ARG:NH1	2.36	0.40
3:C:178:LEU:CD2	3:C:178:LEU:N	2.85	0.40
3:C:59:ARG:NH1	3:C:97:LYS:HE3	2.34	0.40
4:D:110:PHE:HE2	4:D:148:VAL:HG23	1.86	0.40
4:D:14:ARG:HD3	4:D:14:ARG:HA	1.89	0.40
4:D:199:ASN:OD1	4:D:201:GLN:HB3	2.21	0.40
4:D:29:PRO:HD2	4:D:30:LYS:HE2	2.03	0.40
5:E:27:ARG:CG	5:E:28:PHE:N	2.84	0.40
11:K:83:ILE:HG12	11:K:109:VAL:CG2	2.51	0.40
13:M:36:LYS:HE3	13:M:59:TYR:CD1	2.57	0.40
15:O:50:HIS:O	15:O:53:HIS:HB3	2.20	0.40
17:Q:51:TYR:HA	17:Q:52:LYS:HZ2	1.85	0.40
17:Q:63:ARG:HA	17:Q:64:PRO:HD3	1.94	0.40
18:R:37:VAL:O	18:R:40:LEU:N	2.54	0.40
18:R:74:ARG:HG2	18:R:79:LEU:HB2	2.02	0.40
20:T:44:ALA:HB3	20:T:91:LEU:HD12	2.03	0.40
1:A:1522:U:H2'	1:A:1523:G:H8	1.86	0.40
1:A:695:A:H2'	1:A:696:A:C8	2.57	0.40
2:B:143:GLU:O	2:B:147:LYS:HB2	2.21	0.40
2:B:212:GLN:O	2:B:212:GLN:NE2	2.54	0.40
2:B:17:PHE:HB2	2:B:42:ILE:CG2	2.50	0.40
3:C:128:PHE:O	3:C:130:VAL:N	2.54	0.40
4:D:52:SER:HB3	4:D:55:ALA:HB3	2.01	0.40
5:E:48:ALA:C	5:E:50:GLU:H	2.24	0.40
5:E:64:ARG:HB2	5:E:64:ARG:CZ	2.51	0.40
7:G:140:ASP:C	7:G:142:GLU:N	2.68	0.40
7:G:87:VAL:HG11	7:G:155:ARG:HA	2.03	0.40
10:J:101:VAL:HG13	10:J:101:VAL:O	2.22	0.40
12:L:11:VAL:HG21	17:Q:34:LYS:HD3	2.03	0.40
13:M:39:ILE:CD1	13:M:56:LEU:HB2	2.51	0.40
14:N:34:TYR:N	14:N:34:TYR:CD1	2.89	0.40
10:J:65:LEU:HA	14:N:55:GLY:O	2.21	0.40
15:O:11:VAL:O	15:O:12:ILE:C	2.60	0.40
19:S:31:ILE:O	19:S:31:ILE:HG23	2.21	0.40
19:S:32:LYS:HA	19:S:50:ALA:HB3	2.03	0.40
1:A:1347:G:H22	1:A:1374:A:P	2.41	0.40
1:A:940:C:H2'	1:A:941:G:C8	2.57	0.40
2:B:130:ARG:HH22	2:B:138:LEU:HD21	1.85	0.40
3:C:113:ALA:HB3	3:C:114:PRO:CD	2.43	0.40
4:D:96:LEU:C	4:D:98:GLU:N	2.72	0.40
5:E:72:GLN:C	5:E:74:GLY:H	2.23	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:100:ILE:HA	8:H:101:PRO:HD3	1.85	0.40
11:K:25:TYR:H	11:K:25:TYR:HD1	1.69	0.40
16:P:26:ARG:HH21	16:P:31:LYS:HG2	1.86	0.40
1:A:186:C:O3'	20:T:82:SER:HB3	2.21	0.40
1:A:452:A:O2'	1:A:453:A:O5'	2.39	0.40
2:B:132:LYS:HA	2:B:135:GLN:CG	2.52	0.40
2:B:5:ILE:CG2	2:B:224:GLN:HG2	2.51	0.40
3:C:129:ALA:C	3:C:131:ARG:N	2.72	0.40
3:C:138:VAL:HG22	3:C:151:VAL:HG23	2.03	0.40
3:C:13:GLY:O	3:C:14:ILE:HB	2.21	0.40
4:D:11:LEU:O	4:D:12:CYS:C	2.60	0.40
5:E:101:ILE:HD13	5:E:118:ILE:O	2.21	0.40
7:G:69:VAL:HG12	7:G:100:ALA:HA	2.03	0.40
8:H:109:ILE:HG13	8:H:120:THR:HB	2.03	0.40
1:A:1342:C:H4'	9:I:125:TYR:HB3	2.03	0.40
10:J:22:LYS:C	10:J:22:LYS:CD	2.89	0.40
13:M:122:LYS:O	13:M:122:LYS:HE2	2.21	0.40
1:A:1329:A:H5''	13:M:29:ARG:HG3	2.02	0.40
14:N:48:ALA:O	14:N:51:GLY:N	2.53	0.40
16:P:22:THR:CA	16:P:33:ILE:HG12	2.42	0.40
19:S:39:THR:O	19:S:40:ILE:HB	2.20	0.40
20:T:82:SER:O	20:T:86:ARG:CB	2.70	0.40
1:A:1113:C:H2'	1:A:1114:C:C6	2.56	0.40
1:A:267:C:OP2	17:Q:67:LYS:HD2	2.21	0.40
2:B:114:ARG:O	2:B:118:LEU:HG	2.21	0.40
2:B:76:GLN:OE1	2:B:206:ASP:HB3	2.21	0.40
3:C:59:ARG:HH12	3:C:97:LYS:CE	2.33	0.40
3:C:70:VAL:CG1	3:C:71:ALA:H	2.35	0.40
4:D:129:ASN:CA	4:D:145:GLU:HB2	2.51	0.40
4:D:3:ARG:HB3	4:D:69:GLY:O	2.22	0.40
4:D:63:LYS:O	4:D:67:ILE:HG13	2.21	0.40
5:E:31:LEU:HD13	5:E:43:LEU:HD11	2.04	0.40
6:F:61:LEU:HB3	6:F:63:TYR:CE2	2.53	0.40
6:F:98:LEU:C	6:F:98:LEU:HD12	2.41	0.40
8:H:105:ARG:O	8:H:107:LEU:N	2.47	0.40
8:H:97:VAL:O	8:H:100:ILE:HG13	2.21	0.40
9:I:105:ASP:C	9:I:107:ARG:N	2.74	0.40
13:M:4:ILE:O	13:M:5:ALA:C	2.60	0.40
13:M:54:VAL:HG12	13:M:54:VAL:O	2.21	0.40
13:M:84:ILE:HA	13:M:84:ILE:HD12	1.90	0.40
15:O:77:ARG:CA	15:O:80:ALA:HB3	2.52	0.40
16:P:39:TYR:CD2	16:P:41:PRO:HD3	2.56	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:Q:8:GLY:HA3	17:Q:21:VAL:HG12	2.03	0.40
17:Q:83:ASP:O	17:Q:87:LYS:HG2	2.21	0.40
19:S:10:PHE:CD2	19:S:11:VAL:N	2.90	0.40
20:T:48:LYS:O	20:T:49:ALA:C	2.59	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	B	235/256 (92%)	153 (65%)	52 (22%)	30 (13%)	0	3
3	C	203/239 (85%)	128 (63%)	56 (28%)	19 (9%)	1	8
4	D	206/209 (99%)	136 (66%)	50 (24%)	20 (10%)	1	7
5	E	149/162 (92%)	103 (69%)	31 (21%)	15 (10%)	1	7
6	F	99/101 (98%)	66 (67%)	24 (24%)	9 (9%)	1	8
7	G	153/156 (98%)	102 (67%)	36 (24%)	15 (10%)	1	7
8	H	136/138 (99%)	92 (68%)	29 (21%)	15 (11%)	1	5
9	I	125/128 (98%)	77 (62%)	32 (26%)	16 (13%)	0	3
10	J	97/105 (92%)	68 (70%)	20 (21%)	9 (9%)	1	8
11	K	117/129 (91%)	87 (74%)	21 (18%)	9 (8%)	1	11
12	L	123/132 (93%)	85 (69%)	24 (20%)	14 (11%)	1	4
13	M	119/126 (94%)	71 (60%)	28 (24%)	20 (17%)	0	1
14	N	58/61 (95%)	31 (53%)	15 (26%)	12 (21%)	0	0
15	O	86/89 (97%)	61 (71%)	19 (22%)	6 (7%)	2	14
16	P	82/88 (93%)	48 (58%)	23 (28%)	11 (13%)	0	2
17	Q	98/105 (93%)	75 (76%)	15 (15%)	8 (8%)	1	10
18	R	68/88 (77%)	46 (68%)	14 (21%)	8 (12%)	1	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	S	82/93 (88%)	47 (57%)	17 (21%)	18 (22%)	0	0
20	T	97/106 (92%)	63 (65%)	16 (16%)	18 (19%)	0	1
21	U	23/27 (85%)	15 (65%)	4 (17%)	4 (17%)	0	1
All	All	2356/2538 (93%)	1554 (66%)	526 (22%)	276 (12%)	1	4

All (276) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	6	THR
2	B	15	VAL
2	B	26	PRO
2	B	84	GLU
2	B	88	ALA
2	B	126	GLU
2	B	230	VAL
2	B	233	SER
3	C	4	LYS
3	C	12	LEU
3	C	14	ILE
3	C	29	TYR
3	C	61	ALA
3	C	189	ALA
3	C	190	ARG
4	D	28	SER
4	D	29	PRO
4	D	51	PRO
4	D	89	THR
4	D	129	ASN
4	D	154	ASN
4	D	155	LEU
4	D	178	VAL
5	E	146	ALA
7	G	5	ARG
7	G	7	ALA
8	H	50	ARG
8	H	129	VAL
9	I	23	ASN
9	I	56	LEU
9	I	95	LYS
9	I	111	ARG
9	I	117	HIS

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Mol	Chain	Res	Type
10	J	30	SER
10	J	33	GLN
11	K	91	ARG
12	L	18	VAL
12	L	27	LEU
12	L	48	PRO
12	L	62	SER
12	L	121	GLY
13	M	67	GLU
13	M	70	LEU
13	M	83	ASP
13	M	106	ASN
13	M	108	ARG
13	M	118	ALA
14	N	3	ARG
14	N	16	PHE
14	N	23	ARG
14	N	24	CYS
14	N	44	LEU
15	O	88	ARG
16	P	44	THR
16	P	67	THR
17	Q	34	LYS
17	Q	49	GLU
18	R	22	VAL
19	S	3	ARG
19	S	12	ASP
19	S	14	HIS
19	S	25	LYS
19	S	26	GLY
19	S	31	ILE
19	S	41	VAL
19	S	70	LYS
19	S	78	ARG
19	S	79	THR
20	T	48	LYS
20	T	49	ALA
20	T	74	LYS
20	T	95	ALA
20	T	96	GLY
20	T	100	ILE
21	U	7	ARG

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Mol	Chain	Res	Type
21	U	9	ARG
21	U	22	ARG
2	B	18	GLY
2	B	65	GLY
2	B	208	ILE
2	B	216	SER
2	B	237	ALA
3	C	60	ALA
3	C	79	ARG
3	C	129	ALA
3	C	145	GLY
4	D	7	PRO
4	D	20	TYR
4	D	164	ALA
4	D	170	VAL
4	D	179	GLU
4	D	181	MET
4	D	200	GLU
5	E	21	ALA
5	E	63	ARG
5	E	108	ALA
6	F	70	ASP
7	G	4	ARG
7	G	63	LYS
7	G	141	VAL
8	H	68	ARG
8	H	69	ARG
8	H	76	PRO
8	H	122	ARG
8	H	128	GLY
9	I	31	GLN
9	I	41	VAL
9	I	100	GLY
9	I	109	VAL
10	J	36	GLY
10	J	68	HIS
11	K	103	LEU
11	K	107	SER
11	K	124	LYS
11	K	125	PHE
11	K	126	ARG
12	L	65	GLU

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Mol	Chain	Res	Type
12	L	110	VAL
12	L	115	LYS
12	L	116	SER
12	L	128	ALA
13	M	49	THR
13	M	68	GLY
13	M	120	LYS
14	N	14	PRO
14	N	15	LYS
14	N	27	CYS
15	O	77	ARG
16	P	49	LEU
17	Q	14	LYS
17	Q	33	GLY
17	Q	78	GLU
17	Q	100	LYS
18	R	27	GLY
18	R	54	ARG
18	R	64	ARG
18	R	65	ILE
19	S	13	ASP
19	S	45	VAL
20	T	11	SER
20	T	28	ALA
20	T	62	LEU
20	T	99	LEU
20	T	102	GLY
20	T	103	GLY
21	U	3	LYS
2	B	155	LEU
2	B	159	PRO
2	B	175	ARG
3	C	16	ARG
3	C	45	LYS
3	C	81	GLY
4	D	26	CYS
4	D	136	PRO
5	E	37	ARG
6	F	41	GLU
6	F	87	ARG
7	G	35	LYS
7	G	62	PHE

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Mol	Chain	Res	Type
7	G	149	ARG
8	H	2	LEU
9	I	12	GLU
9	I	13	ALA
10	J	57	LYS
12	L	51	ALA
12	L	123	LYS
13	M	12	ASN
13	M	101	GLN
13	M	121	LYS
14	N	9	LYS
15	O	14	GLU
15	O	23	GLY
16	P	8	ARG
16	P	83	GLU
17	Q	30	PRO
17	Q	99	SER
18	R	55	ARG
19	S	6	LYS
19	S	27	GLU
19	S	64	GLU
20	T	82	SER
20	T	98	PRO
2	B	19	HIS
2	B	131	PRO
2	B	160	ASP
2	B	177	ALA
3	C	168	ALA
4	D	151	LYS
5	E	70	PRO
5	E	72	GLN
5	E	124	GLY
6	F	13	ASN
6	F	40	VAL
6	F	42	GLU
7	G	41	ARG
7	G	109	ASN
7	G	116	ALA
7	G	117	ALA
8	H	27	PRO
8	H	49	GLU
10	J	93	GLY

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Mol	Chain	Res	Type
12	L	64	TYR
13	M	4	ILE
13	M	14	ARG
13	M	69	GLU
13	M	77	ASN
14	N	26	ARG
14	N	48	ALA
15	O	86	GLY
16	P	26	ARG
16	P	28	ARG
16	P	48	TRP
19	S	28	LYS
19	S	44	MET
20	T	40	ALA
20	T	51	GLU
2	B	23	ARG
2	B	25	ASN
2	B	98	LEU
2	B	129	GLU
2	B	194	PRO
2	B	229	VAL
2	B	231	GLU
3	C	125	GLU
5	E	74	GLY
5	E	77	PRO
5	E	112	LEU
5	E	128	PRO
5	E	132	ALA
6	F	12	PRO
6	F	32	ASN
6	F	96	PRO
8	H	29	SER
8	H	34	GLU
8	H	103	VAL
9	I	44	VAL
9	I	88	TYR
9	I	89	ASN
10	J	53	PRO
10	J	59	SER
10	J	75	ILE
11	K	64	ALA
11	K	105	VAL

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Mol	Chain	Res	Type
12	L	63	GLY
18	R	58	LEU
19	S	11	VAL
3	C	51	GLY
5	E	115	VAL
11	K	106	LYS
13	M	48	LEU
14	N	20	ALA
16	P	57	ARG
2	B	202	PRO
2	B	239	VAL
4	D	88	VAL
5	E	49	PRO
7	G	55	GLY
7	G	58	PRO
8	H	106	GLY
18	R	37	VAL
20	T	63	ILE
2	B	227	GLY
3	C	114	PRO
4	D	90	GLY
9	I	24	GLY
13	M	60	VAL
15	O	18	PHE
16	P	53	VAL
3	C	134	ILE
13	M	84	ILE
9	I	21	PRO
13	M	78	ILE
7	G	14	PRO
8	H	51	VAL
16	P	41	PRO
20	T	97	ALA

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	B	205/220 (93%)	181 (88%)	24 (12%)	8	34
3	C	159/188 (85%)	143 (90%)	16 (10%)	11	41
4	D	180/181 (99%)	160 (89%)	20 (11%)	9	36
5	E	116/123 (94%)	108 (93%)	8 (7%)	22	65
6	F	90/90 (100%)	76 (84%)	14 (16%)	4	17
7	G	126/127 (99%)	114 (90%)	12 (10%)	12	44
8	H	119/119 (100%)	106 (89%)	13 (11%)	9	37
9	I	98/99 (99%)	87 (89%)	11 (11%)	9	36
10	J	89/92 (97%)	81 (91%)	8 (9%)	14	48
11	K	90/99 (91%)	81 (90%)	9 (10%)	11	41
12	L	104/109 (95%)	90 (86%)	14 (14%)	6	26
13	M	97/101 (96%)	81 (84%)	16 (16%)	3	14
14	N	49/50 (98%)	40 (82%)	9 (18%)	2	11
15	O	79/80 (99%)	73 (92%)	6 (8%)	19	60
16	P	72/74 (97%)	63 (88%)	9 (12%)	7	30
17	Q	95/97 (98%)	89 (94%)	6 (6%)	25	69
18	R	61/77 (79%)	54 (88%)	7 (12%)	8	35
19	S	73/80 (91%)	62 (85%)	11 (15%)	4	19
20	T	76/82 (93%)	68 (90%)	8 (10%)	10	39
21	U	20/22 (91%)	19 (95%)	1 (5%)	34	78
All	All	1998/2110 (95%)	1776 (89%)	222 (11%)	9	36

All (222) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	5	ILE
2	B	8	LYS
2	B	16	HIS
2	B	23	ARG
2	B	24	TRP
2	B	33	TYR
2	B	36	ARG
2	B	63	MET
2	B	67	THR
2	B	73	THR
2	B	82	ARG

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Mol	Chain	Res	Type
2	B	92	TYR
2	B	94	ASN
2	B	121	LEU
2	B	155	LEU
2	B	163	PHE
2	B	165	VAL
2	B	168	THR
2	B	172	ILE
2	B	174	VAL
2	B	178	ARG
2	B	196	LEU
2	B	204	ASN
2	B	215	LEU
3	C	3	ASN
3	C	5	ILE
3	C	12	LEU
3	C	16	ARG
3	C	21	ARG
3	C	29	TYR
3	C	56	ASP
3	C	69	HIS
3	C	94	LEU
3	C	127	ARG
3	C	131	ARG
3	C	154	SER
3	C	184	TYR
3	C	192	THR
3	C	193	TYR
3	C	196	LEU
4	D	3	ARG
4	D	7	PRO
4	D	9	CYS
4	D	12	CYS
4	D	13	ARG
4	D	14	ARG
4	D	30	LYS
4	D	31	CYS
4	D	50	ARG
4	D	53	ASP
4	D	73	ARG
4	D	79	PHE
4	D	86	LYS

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Mol	Chain	Res	Type
4	D	94	LEU
4	D	96	LEU
4	D	114	ARG
4	D	122	ARG
4	D	131	ARG
4	D	181	MET
4	D	200	GLU
5	E	10	MET
5	E	13	ILE
5	E	16	THR
5	E	31	LEU
5	E	53	LEU
5	E	79	GLU
5	E	101	ILE
5	E	153	LYS
6	F	17	SER
6	F	21	LEU
6	F	27	GLN
6	F	36	ARG
6	F	55	ASP
6	F	63	TYR
6	F	69	GLU
6	F	74	ASP
6	F	77	ARG
6	F	87	ARG
6	F	92	LYS
6	F	94	GLN
6	F	97	PHE
6	F	100	ASN
7	G	8	GLU
7	G	12	LEU
7	G	38	LEU
7	G	78	ARG
7	G	84	ASN
7	G	98	SER
7	G	111	ARG
7	G	114	ARG
7	G	124	LEU
7	G	137	LYS
7	G	148	ASN
7	G	155	ARG
8	H	1	MET

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Mol	Chain	Res	Type
8	H	10	LEU
8	H	27	PRO
8	H	41	ARG
8	H	52	ASP
8	H	63	LEU
8	H	69	ARG
8	H	81	HIS
8	H	99	GLU
8	H	119	LEU
8	H	121	ASP
8	H	129	VAL
8	H	137	VAL
9	I	7	THR
9	I	9	ARG
9	I	48	GLU
9	I	65	VAL
9	I	83	ARG
9	I	95	LYS
9	I	104	ARG
9	I	113	LYS
9	I	114	TYR
9	I	121	ARG
9	I	128	ARG
10	J	22	LYS
10	J	47	PHE
10	J	57	LYS
10	J	62	HIS
10	J	74	ILE
10	J	80	LYS
10	J	84	GLN
10	J	96	ILE
11	K	26	ASN
11	K	32	ILE
11	K	63	LEU
11	K	75	TYR
11	K	92	GLU
11	K	109	VAL
11	K	114	VAL
11	K	116	HIS
11	K	125	PHE
12	L	17	LYS
12	L	20	LYS

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Mol	Chain	Res	Type
12	L	27	LEU
12	L	41	ARG
12	L	53	ARG
12	L	57	LYS
12	L	60	LEU
12	L	62	SER
12	L	70	ILE
12	L	73	GLU
12	L	81	SER
12	L	89	ARG
12	L	112	ASP
12	L	120	TYR
13	M	3	ARG
13	M	8	GLU
13	M	13	LYS
13	M	35	GLU
13	M	47	ASP
13	M	56	LEU
13	M	57	ARG
13	M	64	TRP
13	M	66	LEU
13	M	70	LEU
13	M	88	ARG
13	M	90	LEU
13	M	101	GLN
13	M	115	LYS
13	M	116	THR
13	M	122	LYS
14	N	3	ARG
14	N	12	ARG
14	N	14	PRO
14	N	16	PHE
14	N	26	ARG
14	N	29	ARG
14	N	41	ARG
14	N	43	CYS
14	N	44	LEU
15	O	3	ILE
15	O	8	LYS
15	O	26	GLU
15	O	39	LEU
15	O	62	GLN

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Mol	Chain	Res	Type
15	O	65	ARG
16	P	1	MET
16	P	26	ARG
16	P	28	ARG
16	P	59	TRP
16	P	62	VAL
16	P	69	THR
16	P	71	ARG
16	P	72	ARG
16	P	82	GLN
17	Q	12	SER
17	Q	48	GLU
17	Q	52	LYS
17	Q	59	ILE
17	Q	68	ARG
17	Q	74	LEU
18	R	26	LEU
18	R	29	PHE
18	R	32	ARG
18	R	36	ASN
18	R	46	GLU
18	R	54	ARG
18	R	55	ARG
19	S	5	LEU
19	S	10	PHE
19	S	12	ASP
19	S	13	ASP
19	S	15	LEU
19	S	29	ARG
19	S	30	LEU
19	S	41	VAL
19	S	63	THR
19	S	65	ASN
19	S	83	HIS
20	T	11	SER
20	T	24	LEU
20	T	26	ASN
20	T	41	ILE
20	T	62	LEU
20	T	73	HIS
20	T	75	ASN
20	T	93	GLU

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Mol	Chain	Res	Type
21	U	6	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	95	GLN
2	B	135	GLN
2	B	204	ASN
2	B	212	GLN
3	C	181	ASN
5	E	72	GLN
5	E	78	HIS
6	F	64	GLN
6	F	100	ASN
7	G	28	ASN
7	G	37	ASN
7	G	86	GLN
7	G	148	ASN
9	I	89	ASN
10	J	78	ASN
11	K	117	ASN
12	L	9	GLN
13	M	40	ASN
13	M	101	GLN
15	O	53	HIS
19	S	65	ASN
20	T	26	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1499/1522 (98%)	296 (19%)	46 (3%)
22	V	76/77 (98%)	30 (39%)	1 (1%)
23	X	7/25 (28%)	5 (71%)	1 (14%)
24	Y	13/18 (72%)	5 (38%)	1 (7%)
All	All	1595/1642 (97%)	336 (21%)	49 (3%)

All (336) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	G
1	A	8	A
1	A	9	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	50	A
1	A	51	A
1	A	64	G
1	A	65	U
1	A	66	G
1	A	76	G
1	A	79	G
1	A	80	G
1	A	90	C
1	A	91	C
1	A	92	G
1	A	95	G
1	A	108	G
1	A	116	A
1	A	120	A
1	A	121	C
1	A	122	G
1	A	129(A)	G
1	A	137	C
1	A	144	G
1	A	147	G
1	A	163	C
1	A	173	U
1	A	174	C
1	A	182	U
1	A	190	G
1	A	191(A)	G
1	A	195	A
1	A	197	A
1	A	209	U
1	A	216	G
1	A	231	G
1	A	244	U
1	A	245	C
1	A	247	G

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Mol	Chain	Res	Type
1	A	251	G
1	A	267	C
1	A	281	G
1	A	289	G
1	A	314	C
1	A	316	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	332	G
1	A	343	U
1	A	344	A
1	A	347	G
1	A	348	G
1	A	351	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	356	A
1	A	367	U
1	A	373	A
1	A	384	G
1	A	388	G
1	A	389	A
1	A	390	C
1	A	397	A
1	A	398	C
1	A	406	G
1	A	411	A
1	A	412	A
1	A	413	G
1	A	414	A
1	A	419	C
1	A	421	U
1	A	422	C
1	A	423	G
1	A	424	G
1	A	429	U
1	A	430	A
1	A	440	A
1	A	442	C
1	A	452	A

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Mol	Chain	Res	Type
1	A	465	A
1	A	466	C
1	A	467	G
1	A	482	A
1	A	485	G
1	A	486	U
1	A	496	A
1	A	497	U
1	A	498	A
1	A	505	G
1	A	509	A
1	A	510	A
1	A	511	C
1	A	517	G
1	A	518	C
1	A	521	G
1	A	527	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	545	C
1	A	547	A
1	A	559	A
1	A	561	U
1	A	566	G
1	A	572	A
1	A	573	A
1	A	576	G
1	A	577	G
1	A	579	G
1	A	596	C
1	A	614	A
1	A	623	C
1	A	630	G
1	A	631	G
1	A	633	G
1	A	653	A
1	A	665	A
1	A	688	G
1	A	701	C
1	A	702	A

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Mol	Chain	Res	Type
1	A	703	G
1	A	704	A
1	A	723	U
1	A	731	G
1	A	748	C
1	A	749	C
1	A	753	A
1	A	754	C
1	A	755	G
1	A	776	G
1	A	777	A
1	A	792	A
1	A	793	U
1	A	794	A
1	A	813	U
1	A	817	C
1	A	819	A
1	A	821	G
1	A	828	A
1	A	841	U
1	A	843	U
1	A	848	C
1	A	859	A
1	A	870	U
1	A	871	U
1	A	872	A
1	A	884	U
1	A	885	G
1	A	889	A
1	A	902	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
1	A	968	A
1	A	969	A
1	A	971	G
1	A	974	A

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Mol	Chain	Res	Type
1	A	975	A
1	A	976	G
1	A	977	A
1	A	978	A
1	A	981	U
1	A	982	U
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1001	G
1	A	1002	G
1	A	1004	A
1	A	1006	C
1	A	1008	C
1	A	1009	G
1	A	1020	U
1	A	1021	G
1	A	1024	G
1	A	1025	U
1	A	1028	C
1	A	1029	G
1	A	1032(A)	G
1	A	1036	G
1	A	1040	U
1	A	1050	G
1	A	1054	C
1	A	1055	A
1	A	1064	G
1	A	1065	U
1	A	1066	C
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1130	A
1	A	1131	G
1	A	1136	U
1	A	1137	C

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Mol	Chain	Res	Type
1	A	1138	G
1	A	1139	G
1	A	1145	C
1	A	1146	A
1	A	1157	A
1	A	1158	C
1	A	1159	U
1	A	1160	G
1	A	1163	C
1	A	1171	G
1	A	1176	A
1	A	1181	G
1	A	1182	G
1	A	1183	A
1	A	1187	G
1	A	1196	U
1	A	1197	G
1	A	1200	C
1	A	1201	A
1	A	1202	G
1	A	1212	U
1	A	1213	A
1	A	1224	G
1	A	1225	A
1	A	1227	A
1	A	1238	A
1	A	1241	G
1	A	1256	A
1	A	1257	U
1	A	1258	G
1	A	1270	C
1	A	1273	G
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1286	A
1	A	1287	A
1	A	1297	C
1	A	1298	C
1	A	1299	A
1	A	1300	G
1	A	1301	U

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Mol	Chain	Res	Type
1	A	1302	U
1	A	1305	G
1	A	1317	C
1	A	1319	A
1	A	1320	C
1	A	1321	C
1	A	1322	C
1	A	1323	G
1	A	1331	G
1	A	1334	G
1	A	1335	C
1	A	1336	C
1	A	1337	G
1	A	1338	G
1	A	1347	G
1	A	1348	U
1	A	1353	G
1	A	1362(A)	C
1	A	1364	U
1	A	1365	G
1	A	1370	G
1	A	1397	C
1	A	1398	A
1	A	1401	G
1	A	1406	U
1	A	1419	G
1	A	1442	G
1	A	1446	A
1	A	1447	G
1	A	1451	A
1	A	1452	C
1	A	1453	G
1	A	1454	G
1	A	1487	G
1	A	1492	A
1	A	1499	A
1	A	1504	G
1	A	1506	U
1	A	1517	G
1	A	1519	A
1	A	1520	G
1	A	1529	G

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Mol	Chain	Res	Type
1	A	1530	G
22	V	3	C
22	V	4	G
22	V	5	G
22	V	7	G
22	V	8	U
22	V	14	A
22	V	16	C
22	V	17	C
22	V	17(A)	U
22	V	18	G
22	V	19	G
22	V	21	A
22	V	22	G
22	V	25	C
22	V	31	G
22	V	37	A
22	V	42	G
22	V	47	U
22	V	48	C
22	V	49	G
22	V	50	U
22	V	51	C
22	V	52	G
22	V	54	U
22	V	59	A
22	V	63	G
22	V	67	C
22	V	72	A
22	V	75	C
22	V	76	A
23	X	3	G
23	X	4	C
23	X	5	C
23	X	7	U
23	X	8	A
24	Y	31	G
24	Y	33	U
24	Y	36	G
24	Y	39	C
24	Y	40	G

All (49) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	5	U
1	A	31	G
1	A	64	G
1	A	115	G
1	A	119	A
1	A	181	G
1	A	190	G
1	A	243	A
1	A	244	U
1	A	250	A
1	A	266	G
1	A	328	C
1	A	372	C
1	A	410	G
1	A	412	A
1	A	428	G
1	A	481	G
1	A	484	G
1	A	485	G
1	A	509	A
1	A	533	A
1	A	560	U
1	A	595	G
1	A	687	A
1	A	701	C
1	A	703	G
1	A	753	A
1	A	792	A
1	A	812	C
1	A	913	A
1	A	934	C
1	A	960	U
1	A	965	A
1	A	992	U
1	A	1027	C
1	A	1064	G
1	A	1065	U
1	A	1200	C
1	A	1285	A
1	A	1297	C
1	A	1336	C
1	A	1347	G
1	A	1446	A

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Mol	Chain	Res	Type
1	A	1498	U
1	A	1503	A
1	A	1528	U
22	V	53	G
23	X	6	C
24	Y	39	C

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	1MG	Y	37	24	24,26,27	3.02	6 (25%)	34,39,42	3.99	12 (35%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	1MG	Y	37	24	-	0/8/25/26	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	Y	37	1MG	C4-N3	8.23	1.49	1.35
24	Y	37	1MG	C2-N1	7.46	1.47	1.37
24	Y	37	1MG	C2-N2	6.66	1.48	1.33
24	Y	37	1MG	P-OP1	4.81	1.52	1.46
24	Y	37	1MG	C5-N7	-3.70	1.33	1.38
24	Y	37	1MG	C8-N9	-2.07	1.33	1.36

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	Y	37	1MG	C6-C5-N7	-17.40	133.31	134.24
24	Y	37	1MG	C6-N1-C2	11.86	123.96	120.71
24	Y	37	1MG	N2-C2-N1	3.91	123.76	118.45
24	Y	37	1MG	N3-C4-N9	3.77	132.43	126.91
24	Y	37	1MG	C8-N9-C4	3.31	109.65	106.96
24	Y	37	1MG	C5-C4-N3	-3.24	122.34	126.07
24	Y	37	1MG	N3-C2-N1	-2.63	119.09	123.84
24	Y	37	1MG	C4-C5-N7	-2.60	106.90	109.41
24	Y	37	1MG	C1'-N9-C4	-2.39	122.50	126.64
24	Y	37	1MG	C8-N7-C5	2.32	110.79	103.58
24	Y	37	1MG	C2-N3-C4	2.18	117.92	115.30
24	Y	37	1MG	N7-C8-N9	-2.10	107.43	112.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 74 ligands modelled in this entry, 73 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	$\# Z > 2$
26	PAR	A	1667	-	45,45,45	1.31	7 (15%)	67,67,67	1.40	8 (11%)

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
26	PAR	A	1667	-	-	0/18/94/94	0/4/4/4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	A	1667	PAR	C52-C42	3.21	1.58	1.52
26	A	1667	PAR	C64-C54	2.90	1.59	1.51
26	A	1667	PAR	O54-C14	2.87	1.49	1.41
26	A	1667	PAR	O51-C11	2.31	1.47	1.41
26	A	1667	PAR	C11-C21	2.18	1.56	1.52
26	A	1667	PAR	C31-C21	2.06	1.56	1.53
26	A	1667	PAR	C14-C24	2.03	1.56	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	1667	PAR	O52-C13-C23	4.73	115.94	107.50
26	A	1667	PAR	C14-O54-C54	3.86	121.19	113.73
26	A	1667	PAR	O33-C14-C24	3.34	114.68	108.08
26	A	1667	PAR	O11-C42-C52	3.14	115.41	107.42
26	A	1667	PAR	O11-C42-C32	-3.03	101.73	108.97
26	A	1667	PAR	O54-C54-C64	2.93	111.55	105.97
26	A	1667	PAR	C22-C32-C42	2.16	114.72	109.37
26	A	1667	PAR	O54-C54-C44	-2.12	105.80	109.73

There are no chirality outliers.

There are no torsion outliers.

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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.